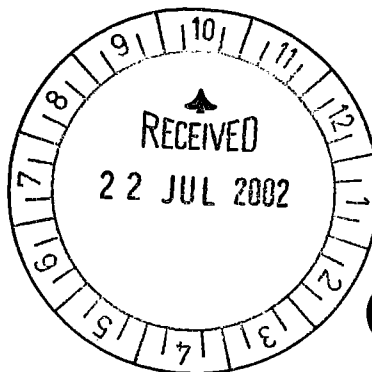


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Dow AgroSciences

**Supplementary References for Dow AgroSciences Application A 446 -
corn line 1507
July 2002**

- 1 ✓ EPA (2001) 'Pesticide Fact Sheet for *Bacillus thuringiensis* subspecies Cry 1F Protein and the Genetic Material Necessary for its production (plasmid insert PHI 8999) in Corn.'
- Evans SL (1998) 'Equivalency of microbial and maize expressed Cry1F protein; characterization of test substances for biochemical and toxicological studies.' (Mycogen c/o Dow AgroSciences LCC, San Diego). Submitted June 2001.
- 2 ✗ Gallagher.S.P., Grimes J, Beavers JB (1999) 'Transgenic corn expressing *Bacillus thuringiensis* var. *aizawai* (Bt) CRY1F delta-endotoxin: A dietary toxicity study with the Northern Bobwhite.' (Mycogen c/o Dow AgroSciences LCC, San Diego)
- 3 ✓ Gao Y (2002) 'Equivalency between transgenic corn-produced and microbially-derived Cry1F protein.'
- 4 Gao Y, Collins RA (2002) 'Gel electrophoresis, Western Blot and ELISA of truncated cry1F delta-endotoxin following heat treatment.' (Dow AgroSciences LLC, Indianapolis, IN)
Herman RA (2000) 'Thermolability of Cry1F(truncated) Delta-Endotoxin.' (Dow AgroSciences LLC, Indianapolis, IN). Submitted June 2002.
- 5 Japanese MAFF (2002) 'Letter of approval from MAFF and MHLW Japan.'
- 6 Kuhn JO (1998) 'Acute oral toxicity study in mice.' (Dow AgroSciences LLC/Mycogen Corporation, San Diego). Raw data and protocols only - overview submitted June 2001.
- 7 Schafer BW, Korjagin VA (2002) 'In vitro simulated Gastric Fluid digestibility study of Truncated cry1F delta-endotoxin derived from *Pseudomonas fluorescens*.' (Dow AgroSciences LLC, Indianapolis, IN)
- 8 Schafer BW, Schwedler DA (2001) 'Characterisation of the recombinant Cry1F protein derived from *Pseudomonas fluorescens* and transgenic maize.' (Dow AgroSciences LLC, Indianapolis, IN)
- 9 Stelman SJ (2002) 'Comparison of the amino acid sequence of the *Bacillus thuringiensis* var. *aizawai* cry1F insect control protein as expressed in *Zea mays* event 1507 to assess homology to known protein toxins.' (Dow AgroSciences LLC, San Diego, CA)

United States
Environmental Protection
Agency

Office of Prevention,
Pesticides
and Toxic Substances
(7501C)



PESTICIDE FACT SHEET

Name of Chemical(s): *Bacillus thuringiensis* subspecies Cry1F Protein and the
Genetic Material Necessary for Its Production
(Plasmid Insert PHI 8999) in Corn

Reason for Issuance: New Registration

Date Issued: May 2001

EPA Publication Number:

I. DESCRIPTION OF THE PLANT PESTICIDE

Bacillus thuringiensis subspecies Cry1F Protein and the Genetic Material Necessary for
Its Production (Plasmid Insert PHI 8999) in Corn

OPP Chemical Code: 006481

Trade Name: Herculex J I Insect Protection, Pioneer Brand Seed Corn with Herculex J I

Year of Initial Registration: 2001

Pesticide Type: Plant-Pesticide

U.S. and Foreign Producers: Mycogen Seeds
c/o Dow Agrosiences LLC
9330 Zionsville Road
Indianapolis, IN 46268-1054

Pioneer Hi-Bred International, Inc.
7250 NW 62nd Avenue
P.O. Box 552
Johnston, Iowa 50131-0552

II. USE SITES AND LIMITATIONS

Bacillus thuringiensis subspecies Cry1F protein and the genetic material necessary for its production (plasmid insert PHI 8999) in corn is registered for full commercial use in field corn originating from maize line 1507 until September 30, 2001.

III. BT CROP REASSESSMENT PROCESS

EPA is currently engaged in a comprehensive reassessment of the time-limited registrations for all existing B.t. corn and cotton plant-pesticides. This reassessment has been designed to assure that the decisions on the renewal of these registrations are based on the most current health and ecological data. Current registrations are set to expire September 30, 2001. As part of EPA's reassessment, the Agency will decide whether to extend the registrations and whether to include any additional terms and conditions of such registrations for issues including insect resistance management, the protection of non-target organisms, and other measures necessary to ensure full public and environmental safety.

During this reassessment, EPA will conduct an open and transparent public process that incorporates sound and current science, public involvement, and balanced decision making. The major components of the process and time frames for action are as follows:

Comprehensive risk assessments. This review incorporated all available scientific information on B.t. products, including results of recent scientific studies and recommendations from various individuals and organizations. (Summer/Fall 2000) *Completed.*

Scientific Peer Review and public comment. After completing our scientific risk assessment, the Agency provided the registrants of the products an opportunity to review the risk assessment and suggest technical corrections to the Agency. After technical corrections were made, EPA released the risk assessments and invited public comment and scientific peer review. That release included EPA's regulatory assessment and the underlying data, along with registrants' technical error correction comments and the corrective actions taken by the Agency. All of these materials were placed in the Bt crop reassessment docket. (Fall 2000) *Completed.*

Recommendations from the Scientific Advisory Panel, National Academy of Sciences, public comments, and the Administration-wide review. Since there are many organizations providing regulatory and scientific recommendations to EPA, this period will be used to consider and incorporate as appropriate recommendations into our revised risk assessment. This will include recommendations from the Scientific Advisory Panel on insect resistance management, ecological and public health aspects of our regulatory program, along with consideration of issues identified in the report released by the National Academy of Sciences titled: "Genetically Modified Pest-Protected Plants, Science and Regulation" and the Administration-wide review. Any available recommendation from the Administration-wide review will also be addressed at this time. (Fall 2000, Winter 2000/1) *Ongoing. SAP Meeting Held October 18,19,*

and 20, 2000. *SAP Report Released March 12, 2001.*

Revised risk assessments and propose registration requirements. After incorporating the appropriate recommendations, the Agency will revise its risk assessments, and develop registration decision documents for future growing seasons. This will include any necessary terms and conditions for issues including insect resistance management, the protection of non-target organisms, and other measures necessary to ensure full public and environmental safety. The Agency will ask for public comment on the revised risk assessment and any proposed regulatory actions. *Spring 2001*

Final decisions on B.t. registrations. This will complete the scientific and public process with EPA providing decisions on the B.t. registrations for the 2002 growing season. At this time, EPA will announce final regulatory conclusions regarding these registrations. *Summer 2001*

IV. SCIENCE ASSESSMENT

A. Product Analysis

1. Product Analysis - Cry1F

A modified (synthetic, truncated) form of the *cry1Fa2* gene and the phosphinothricin acetyl transferase (*pat*) gene were inserted into maize plants by microprojectile bombardment. Digestion of the genomic DNA of maize line 1507 with *NheI* or *HindIII* and Southern hybridization with probes specific for *cry1F*, *kan^r* and *pat* genes yielded indications of the complexity of the gene integration pattern and copy number. Hybridization patterns suggested that the copy number of introduced / integrated *cry1F* and *pat* genes is one. It is most likely that the TC 1507 line contains one functional *cry1F* gene and partial copies (1 or 2) of the gene which are non-functional.

B. Human Health Assessment

1. Mammalian Toxicity and Allergenicity Assessment

Data have been submitted demonstrating the lack of mammalian toxicity at high levels of exposure to the pure Cry1F protein. These data demonstrate the safety of the products at levels well above maximum possible exposure levels that are reasonably anticipated in the crops. This is similar to the Agency position regarding toxicity and the requirement of residue data for the microbial *Bacillus thuringiensis* products from which this plant-pesticide was derived. [See 40 CFR Sec. 158.740(b)(2)(i).] For microbial products, further toxicity testing and residue data are triggered by significant acute effects in studies such as the mouse oral toxicity study, to verify the observed effects and clarify the source of these effects (Tiers II & III).

The acute oral toxicity data submitted support the prediction that the Cry1F protein would be

non-toxic to humans. Male and female mice (5 of each) were dosed with 15 % (w/v) of the test substance, which consisted of *Bacillus thuringiensis* var. *aizawai* Cry1F protein at a net concentration of 11.4 %. Two doses were administered approximately an hour apart to achieve the dose totaling 33.7 mL / kg body weight. Outward clinical signs and body weights were observed and recorded throughout the 14 day study. Gross necropsies performed at the end of the study indicated no findings of toxicity. No mortality or clinical signs were noted during the study. An LD₅₀ was estimated at >5050 mg / kg body weight of this microbially produced test material. The actual dose administered contained 576 mg Cry1F protein / kg body weight. At this dose, no LD₅₀ was demonstrated as no toxicity was observed. Cry1F maize seeds contain 0.0017 to 0.0034 mg of Cry1F / gram of corn kernel tissue.

When proteins are toxic, they are known to act via acute mechanisms and at very low dose levels [Sjoblad, Roy D., *et al.* "Toxicological Considerations for Protein Components of Biological Pesticide Products," Regulatory Toxicology and Pharmacology 15, 3-9 (1992)]. Therefore, since no effects were shown to be caused by the plant-pesticides, even at relatively high dose levels, the Cry1F protein is not considered toxic. Further, amino acid sequence comparisons showed no similarity between Cry1F protein to known toxic proteins available in public protein databases.

Since Cry1F is a protein, allergenic sensitivities were considered. Current scientific knowledge suggests that common food allergens tend to be resistant to degradation by heat, acid, and proteases, may be glycosylated and present at high concentrations in the food.

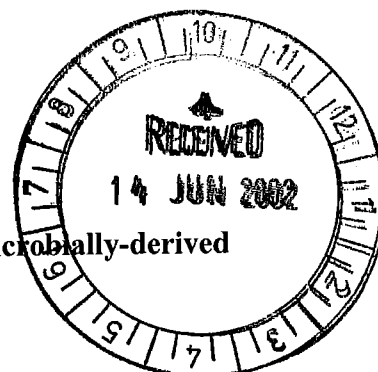
Data has been submitted which demonstrates that the Cry1F protein is rapidly degraded by gastric fluid *in vitro* and is non-glycosylated. In a solution of Cry1F:pepsin at a molar ratio of 1:100, complete degradation of Cry1F to amino acids and small peptides occurred in 5 minutes. A heat lability study demonstrated the loss of bioactivity of Cry1F protein to neonate tobacco budworm larvae after 30 minutes at 75 EC. Studies submitted to EPA done in laboratory animals have not indicated any potential for allergic reactions to *B. thuringiensis* or its components, including the δ -endotoxin of the crystal protein. Additionally, a comparison of amino acid sequences of known allergens uncovered no evidence of any homology with Cry1F, even at the level of 8 contiguous amino acids residues.

The potential for the Cry1F protein to be a food allergen is minimal. Regarding toxicity to the immune system, the acute oral toxicity data submitted support the prediction that the Cry1F protein would be non-toxic to humans. When proteins are toxic, they are known to act via acute mechanisms and at very low dose levels [Sjoblad, Roy D., *et al.* "Toxicological Considerations for Protein Components of Biological Pesticide Products," Regulatory Toxicology and Pharmacology 15, 3-9 (1992)]. Therefore, since no effects were shown to be caused by the plant-pesticides, even at relatively high dose levels, the Cry1F protein is not considered toxic.]

2. Aggregate Exposures

Pursuant to FFDCA section 408(b)(2)(D)(vi), EPA considers available information concerning

Equivalency between transgenic corn-produced and microbially-derived Cry1F protein



The rationale for using microbial material for toxicology studies has been in place for many years and has been accepted by regulatory agencies around the world. The reason is that it is not possible to isolate active functional protein from plants in sufficient quantities (multi-grams) to perform the required toxicology and other regulatory studies. Therefore, a recombinant protein is produced in large quantity with a high expression system such as bacteria, and a small quantity of the protein is isolated from plants. Characterization studies are conducted to demonstrate the physico-chemical and biological equivalency or comparability of the protein from the two sources.

The bacterial Cry1F was produced with recombinant *Pseudomonas fluorescens* strain MR872. The full-length *cryIF* gene was transformed and inserted into the bacterium, and the translated protein was a full-length Cry1F with a molecular weight of 130 kDa. This full length Cry1F was then isolated and enzymatically cleaved *in vitro* with trypsin into an active truncated Cry1F. This truncated Cry1F was compared to the Cry1F protein isolated from the transgenic corn in these aspects: primary structure, molecular weight, immunoreactivity to Cry1F specific antibodies, N-terminal sequencing, peptide mass fingerprinting by MALDI-TOF MS, the lack of glycosylation, and insecticidal activity. The following is a summary of the findings. The details of the studies are fully documented in reports MYCO98-001 and GH-C 5294 (attach reports).

The studies concluded that the truncated microbial Cry1F and the transgenic corn derived Cry1F were equivalent in biochemical characteristics and biological activities.

Primary structure/sequence:

The plant and microbial Cry1F protein primary structure (sequences) are defined in Table 1 and compared in Figure 1 (identical to Figure 3 of the monograph). **MR872** is the Cry1F protein produced by recombinant *Pseudomonas fluorescens* strain MR872. **Cry1Fa2syn** is the protein sequence that is expressed in *B.t.* Cry1F maize line 1507. **Cry1Fa2** is the naturally occurring protein sequence from *Bacillus thuringiensis* var. *aizawai* strain PS811 (it is provided here as reference and was not used in any of the laboratory studies).

Bt toxins in nature are protoxins, meaning that they are larger than necessary for the activity. Pieces of peptides on the carboxyl domain, and in some cases also at amino terminus, are removed, usually by insect gut proteases, leaving in place a core sequence of amino acids comprising the active toxin. Precise cleavage has not been shown to be required for activity of typical Bt toxins. Figure 1 (Figure 3 in the monograph) shows the entire protoxin sequence of Cry1Fa2. Computer simulations of digestion, coupled with size estimates, indicate that the protein in nature most likely is cleaved at amino acid 612 on the C-terminus. Actual data from laboratory digestions and computer simulations indicate that the N terminus is processed down to residue 28. Thus, an activated toxin

produced from Cry1F protoxin in nature would be expected to contain amino acids 28 to 612.

The protein produced in plants (**Cry1Fa2syn**) contains amino acids from 1 to 605, thus after proteolytic cleavage at the N-terminus the active toxin would be expected to consist of amino acids 28 to 605. The microbial protein (**MR872**) was produced using nearly the full Cry1Fa2 sequence (there is deletion and/or substitution of amino acids 781-812). As part of the preparation process, the MR872 protoxin (full-length) was subjected to controlled cleavage by trypsin, followed by additional purification to yield the expected Cry1F toxin containing amino acids 28 to 612 (truncated).

Overall from the primary structure point of view, the sequence differences between the plant and microbial-derived toxins are: 1) a phenylalanine to leucine substitution at position 604 (based on the occurrence of leucine in the homologous position of other Cry1F proteins), and 2) approximately 7 additional amino acids are present on the C-terminus of the microbial toxin. These differences represent only 1% of the amino acid sequence of the plant and microbial toxins, and the differences are restricted to the non-functional outermost C-terminus.

Molecular weight and immunoreactivity:

Both plant and microbial Cry1F are immunoreactive to antibodies specific for Cry1F. An immunoaffinity column was generated using the antibodies, and the plant Cry1F was purified with the column from transgenic corn plant leaf extract. The plant purified Cry1F was used in further characterization studies. In transgenic plant, the Cry1F was initially expressed as a protein of about 68 kDa (amino acids 1-605). However, this protein was subject to the cleavage of plant proteases, resulting the formation of a N-terminal truncated form at approximately 65 kDa (amino acids 28-605). Depending on the growth stages of plant tissues and sample extraction procedure, either the doublet bands (68 and 65 kDa) or a major 65 kDa band can be detected by SDS-PAGE and Western blot (MYCO98-001, GH-C 5294). This 65 kDa band is the active core toxin, and this molecular weight is very similar to that of the truncated microbial Cry1F.

N-terminal sequencing:

✓ N-terminal sequencing data showed that both the plant derived 65 kDa Cry1F band and the truncated microbial Cry1F had N-terminal amino acid corresponding to amino acid 28 (MYCO98-001).

Tryptic peptide mass fingerprints:

MALDI-TOF MS tryptic peptide fingerprints of the plant produced and microbially-derived truncated Cry1F is shown in Table 2 (identical to Table 1 of report GH-C 5294). In the trypsin digest of *P. fluorescens*-derived truncated Cry1F protein, 19 peptides were identified matching the theoretical deduced peptide masses of Cry1F. The peptide fragments detected were between residues 32 and 546 of Cry1F. In the trypsin digest of

the transgenic corn derived Cry1F protein, 20 peptides were identified matching the theoretical deduced peptide masses.

Lack of glycosylation

Both the plant derived and truncated microbial Cry1F had no detectable carbohydrates (GH-C 5294).

Biological activity (insecticidal potency)

Biological potency data showed essentially indistinguishable LC₅₀s between plant and microbial protein on 4 insect species, clearly indicating that the materials are functionally interchangeable (MYC098-001).

Table 1. Definition of Cry1F sequence nomenclature used in Figure 3 of the Japanese monograph.




Cry1F Sequence	Description	Amino Acid Sequence, Before Cleavage (Protoxin)	Amino Acid Sequence, After Cleavage (Toxin)
MR872	Cry1F sequence expressed in <i>Pseudomonas fluorescens</i> strain MR872	1-1175, except 781-812	28-612
Cry1Fa2syn	Cry1F sequence expressed in <i>B.t.</i> Cry1F maize line 1507	1-605, F604L 	28-605, F604L 
Cry1Fa2	Cry1F sequence naturally occurring in <i>Bacillus thuringiensis</i> var. <i>aizawai</i> strain PS811	1-1175	28-612

Figure 1. Alignment of the amino acid sequences of the delta-endotoxin proteins comparing a microbially derived Cry1F protein (MR872), the modified plant Cry1F protein (Cry1F syn), and B.t.a Cry1F full length protein (Cry1F).

The consensus sequence represents identical residues among all three genetic versions encoding the Cry1F protein. The positions of putative protease cleavage sites at the start (about residue 28 or 31) and end (about residue 612 or 615) of the active core protein are marked with a ↓. Note the single F₆₀₄L substitution in the transgenic polypeptide. This difference is due to codon changes resulting from the introduction of a restriction enzyme site that enables gene cloning of the alternative C-terminal half of the full length protein.



	1				50
MR872	MENNIQNQCV	PYNCLNNPEV	EILNEERSTG	RLPLDISLSL	TRFLLSEFVP
Cry1Fa2syn	MENNIQNQCV	PYNCLNNPEV	EILNEERSTG	RLPLDISLSL	TRFLLSEFVP
Cry1Fa2	MENNIQNQCV	PYNCLNNPEV	EILNEERSTG	RLPLDISLSL	TRFLLSEFVP
Consensus	MENNIQNQCV	PYNCLNNPEV	EILNEERSTG	RLPLDISLSL	TRFLLSEFVP
	51				100
MR872	GVGVAFGLFD	LIWGFITPSD	WSLFLLQIEQ	LIEQRIETLE	RNRAITTLRG
Cry1Fa2syn	GVGVAFGLFD	LIWGFITPSD	WSLFLLQIEQ	LIEQRIETLE	RNRAITTLRG
Cry1Fa2	GVGVAFGLFD	LIWGFITPSD	WSLFLLQIEQ	LIEQRIETLE	RNRAITTLRG
Consensus	GVGVAFGLFD	LIWGFITPSD	WSLFLLQIEQ	LIEQRIETLE	RNRAITTLRG
	101				150
MR872	LADSYEIIYIE	ALREWEANPN	NAQLREDVRI	RFANTDDALI	TAINNFTLTS
Cry1Fa2syn	LADSYEIIYIE	ALREWEANPN	NAQLREDVRI	RFANTDDALI	TAINNFTLTS
Cry1Fa2	LADSYEIIYIE	ALREWEANPN	NAQLREDVRI	RFANTDDALI	TAINNFTLTS
Consensus	LADSYEIIYIE	ALREWEANPN	NAQLREDVRI	RFANTDDALI	TAINNFTLTS
	151				200
MR872	FEIPLLSVYV	QAANLHLSLL	RDAVSFGQGW	GLDIATVNNH	YNRLINLIHR
Cry1Fa2syn	FEIPLLSVYV	QAANLHLSLL	RDAVSFGQGW	GLDIATVNNH	YNRLINLIHR
Cry1Fa2	FEIPLLSVYV	QAANLHLSLL	RDAVSFGQGW	GLDIATVNNH	YNRLINLIHR
Consensus	FEIPLLSVYV	QAANLHLSLL	RDAVSFGQGW	GLDIATVNNH	YNRLINLIHR
	201				250
MR872	YTKHCLDTYN	QGLENLRGTN	TRQWARFNQF	RRDLTLTVLD	IVALFPNYDV
Cry1Fa2syn	YTKHCLDTYN	QGLENLRGTN	TRQWARFNQF	RRDLTLTVLD	IVALFPNYDV
Cry1Fa2	YTKHCLDTYN	QGLENLRGTN	TRQWARFNQF	RRDLTLTVLD	IVALFPNYDV
Consensus	YTKHCLDTYN	QGLENLRGTN	TRQWARFNQF	RRDLTLTVLD	IVALFPNYDV
	251				300
MR872	RTYPIQTSSQ	LTREIYTSSV	IEDSPVSANI	PNGFNRAEFG	VRPPLMDFM
Cry1Fa2syn	RTYPIQTSSQ	LTREIYTSSV	IEDSPVSANI	PNGFNRAEFG	VRPPLMDFM
Cry1Fa2	RTYPIQTSSQ	LTREIYTSSV	IEDSPVSANI	PNGFNRAEFG	VRPPLMDFM
Consensus	RTYPIQTSSQ	LTREIYTSSV	IEDSPVSANI	PNGFNRAEFG	VRPPLMDFM
	301				350
MR872	NSLFVTAETV	RSQTVWGGHL	VSSRNTAGNR	INFPSYGVFN	PGGAIWIAD
Cry1Fa2syn	NSLFVTAETV	RSQTVWGGHL	VSSRNTAGNR	INFPSYGVFN	PGGAIWIAD
Cry1Fa2	NSLFVTAETV	RSQTVWGGHL	VSSRNTAGNR	INFPSYGVFN	PGGAIWIAD
Consensus	NSLFVTAETV	RSQTVWGGHL	VSSRNTAGNR	INFPSYGVFN	PGGAIWIAD
	351				400
MR872	DPRPFYRTLS	DPVFVRGGFG	NPHYVLGLRG	VAFQQTGTNH	TRTFRNSGTI
Cry1Fa2syn	DPRPFYRTLS	DPVFVRGGFG	NPHYVLGLRG	VAFQQTGTNH	TRTFRNSGTI
Cry1Fa2	DPRPFYRTLS	DPVFVRGGFG	NPHYVLGLRG	VAFQQTGTNH	TRTFRNSGTI
Consensus	DPRPFYRTLS	DPVFVRGGFG	NPHYVLGLRG	VAFQQTGTNH	TRTFRNSGTI
	401				450
MR872	DSLDEIPPQD	NSGAPWNDYS	HVLNHVTFVR	WPGEISGSDS	WRAPMFSWTH
Cry1Fa2syn	DSLDEIPPQD	NSGAPWNDYS	HVLNHVTFVR	WPGEISGSDS	WRAPMFSWTH
Cry1Fa2	DSLDEIPPQD	NSGAPWNDYS	HVLNHVTFVR	WPGEISGSDS	WRAPMFSWTH
Consensus	DSLDEIPPQD	NSGAPWNDYS	HVLNHVTFVR	WPGEISGSDS	WRAPMFSWTH

	451				500
MR872	RSATPTNTID	PERITQIPLV	KAHTLQSGTT	VVRGPGFTGG	DILRRTSGGP
Cry1Fa2syn	RSATPTNTID	PERITQIPLV	KAHTLQSGTT	VVRGPGFTGG	DILRRTSGGP
Cry1Fa2	RSATPTNTID	PERITQIPLV	KAHTLQSGTT	VVRGPGFTGG	DILRRTSGGP
Consensus	RSATPTNTID	PERITQIPLV	KAHTLQSGTT	VVRGPGFTGG	DILRRTSGGP
	501				550
MR872	FAYTIVNING	QLPQRYRARI	RYASTTNLRI	YVTVAGERIF	AGQFNKTMDT
Cry1Fa2syn	FAYTIVNING	QLPQRYRARI	RYASTTNLRI	YVTVAGERIF	AGQFNKTMDT
Cry1Fa2	FAYTIVNING	QLPQRYRARI	RYASTTNLRI	YVTVAGERIF	AGQFNKTMDT
Consensus	FAYTIVNING	QLPQRYRARI	RYASTTNLRI	YVTVAGERIF	AGQFNKTMDT
	551				600
MR872	GDPLTFQSFS	YATINTAFTF	PMSQSSFTVG	ADTFSSGNEV	YIDRFELIPV
Cry1Fa2syn	GDPLTFQSFS	YATINTAFTF	PMSQSSFTVG	ADTFSSGNEV	YIDRFELIPV
Cry1Fa2	GDPLTFQSFS	YATINTAFTF	PMSQSSFTVG	ADTFSSGNEV	YIDRFELIPV
Consensus	GDPLTFQSFS	YATINTAFTF	PMSQSSFTVG	ADTFSSGNEV	YIDRFELIPV
	601				650
MR872	TATFEAEYDL	ERAQKAVNAL	FTSINQIGIK	TDVTDYHIDR	VSNLVECLSD
Cry1Fa2syn	TATLE*.....
Cry1Fa2	TATFEAEYDL	ERAQKAVNAL	FTSINQIGIK	TDVTDYHIDQ	VSNLVDCLSD
Consensus	TAT-E-----	-----	-----	-----	-----
	651				700
MR872	BFCLDEKKEL	SEKVKHAKRL	SDERNLLQDP	NFRGINRQLD	RGWRGSTDIT
Cry1Fa2syn
Cry1Fa2	BFCLDEKKEL	SEKVKHAKRL	SDERNLLQDP	NFKGINRQLD	RGWRGSTDIT
Consensus	-----	-----	-----	-----	-----
	701				750
MR872	IQGGDDVFKE	NYVTLLGTFD	ECYLTLYLYQK	IDESKLKAYT	RYQLRGYIED
Cry1Fa2syn
Cry1Fa2	IQRGDDVFKE	NYVTLPGTFD	ECYPTLYLYQK	IDESKLKPYT	RYQLRGYIED
Consensus	-----	-----	-----	-----	-----
	751				800
MR872	SQDLEIYLIR	YNAKHETVNV	PGTGSWLWRLS	APSPI.....
Cry1Fa2syn
Cry1Fa2	SQDLEIYLIR	YNAKHETVNV	LGTGSWLWPLS	VQSPIRKCGE	PNRCAPHLEW
Consensus	-----	-----	-----	-----	-----
	801				850
MR872GKCAHSHSH	FSLDIDVGCT	DLNEDLGWVW	IFKIKTQDGH
Cry1Fa2syn
Cry1Fa2	NPDLDCSCRD	GEKCAHSHSH	FSLDIDVGCT	DLNEDLDWVW	IFKIKTQDGH
Consensus	-----	-----	-----	-----	-----
	851				900
MR872	ARLGNLEFLE	EKPLVGEALA	RVKRAEKKWR	DKREKLEWET	NIVYKEAKES
Cry1Fa2syn
Cry1Fa2	ARLGNLEFLE	EKPLVGEALA	RVKRAEKKWR	DKREKLELET	NIVYKEAKES
Consensus	-----	-----	-----	-----	-----
	901				950
MR872	VDALFVNSQY	DRLQADTNIA	MIHAADKRVH	SIREAYLPBL	SVIPGVNAAI
Cry1Fa2syn
Cry1Fa2	VDALFVNSQY	DQLQADTNIA	MIHAADKRVH	RIREAYLPBL	SVIPGVNVDI
Consensus	-----	-----	-----	-----	-----
	951				1000
MR872	FEBLEGRIFT	AFSLYDARNV	IKNGDFNNGL	SCWNVKGHVD	VEEQNNHRSV
Cry1Fa2syn
Cry1Fa2	FBELKGRIFT	AFFLYDARNV	IKNGDFNNGL	SCWNVKGHVD	VEEQNNHRSV
Consensus	-----	-----	-----	-----	-----
	1001				1050
MR872	LVPPEWEAEV	SQEVRCVCPGR	GYILRVTAAYK	EGYGEQCVTI	HEIENNTDEL
Cry1Fa2syn
Cry1Fa2	LVPPEWEAEV	SQEVRCVCPGR	GYILRVTAAYK	EGYGEQCVTI	HEIENNTDEL

Consensus	-----				
	1051				1100
MR872	KFSNCVEEEV	YPNNTVTCND	YTATQEEYEG	TYTSRNRGYD	GAYESNSSVP
Cry1Fa2syn
Cry1Fa2	KFSNCVEEEV	YPNNTVTCND	YTANQEEYGG	AYTSRNRGYD	ETYGSNSSVP
Consensus	-----	-----	-----	-----	-----
	1101				1150
MR872	ADYASAYEEK	AYTDGRRDNP	CESNRGYGDY	TPLPAGYVTK	ELEYFPETDK
Cry1Fa2syn
Cry1Fa2	ADYASVYEEK	SYTDGRRDNP	CESNRGYGDY	TPLPAGYVTK	ELEYFPETDK
Consensus	-----	-----	-----	-----	-----
	1151		1175		
MR872	VWIEIGETEG	TFIVDSVELL	LMEE*		
Cry1Fa2syn		
Cry1Fa2	VWIEIGETEG	TFIVDSVELL	LMEE*		
Consensus	-----	-----	-----		

Table 2. Tryptic Peptide Mass Data (m/z $[M+H]^+$) of Cry 1F Proteins Obtained by MALDI-TOF MS

Full Length Cry1Fsynpro residue #	Theoretical mass (m/z)	<i>P. fluorescens</i> trypsinized Cry1F [$M+H$]	TC1507 Maize Cry1F [$M+H$]
32-42	1227.72	1227.70	1227.68
100-113	1612.81	1612.81	1612.79
114-125	1441.67	1441.66	1441.65
172-193	2434.15	2434.21	2434.16
194-200	878.55	878.51	878.50
204-217	1675.79	1675.75	1675.75
252-263	1394.72	1394.69	1394.68
264-286	2509.21	2509.24	2509.19
312-324	1413.71	1413.70	1413.68
358-366	1033.56	1033.52	1033.52
367-379	1386.71	1386.70	1386.69
380-392	1416.68	1416.67	1416.67
431-442	1376.62	1376.62	1376.59
452-463	1301.63	1301.60	1301.58
464-471	911.58	911.53	911.52
472-483	1269.68	1269.66	1269.65
484-494	1089.56	1089.53	1089.52
522-529	925.46	ND ^b	925.43
530-538	1007.54	1007.51	1007.50
539-546	924.48	924.44	924.43

Note:

^a Two digit decimals were used for mass data in this table although raw data obtained from the MALDI-TOF-MS spectrometer were shown in 4 digit decimals. A peptide was considered a match if its m/z is within m/z 0.1 error range of its theoretical m/z .

^b ND: not detected.

aggregate exposures from the pesticide residue in food and all other non-occupational exposures, including drinking water from ground water or surface water and exposure through pesticide use in gardens, lawns, or buildings (residential and other indoor uses).

The Agency has considered available information on the aggregate exposure levels of consumers (and major identifiable subgroups of consumers) to the pesticide chemical residue and to other related substances. These considerations include dietary exposure under the tolerance exemption and all other tolerances or exemptions in effect for the plant-pesticide chemical residue, and exposure from non-occupational sources. Exposure via the skin or inhalation is not likely since the plant-pesticide is contained within plant cells, which essentially eliminates these exposure routes or reduces these exposure routes to negligible. Oral exposure, at very low levels, may occur from ingestion of processed corn products and, potentially, drinking water. However a lack of mammalian toxicity and the digestibility of the plant-pesticides have been demonstrated. The use sites for the Cry1F protein are all agricultural for control of insects. Therefore, exposure via residential or lawn use to infants and children is not expected. Even if negligible exposure should occur, the Agency concludes that such exposure would present no risk due to the lack of toxicity demonstrated for the Cry1F protein.

3. Cumulative Effects

Pursuant to FFDCA Section 408(b)(2)(D)(v), EPA has considered available information on the cumulative effects of such residues and other substances that have a common mechanism of toxicity. These considerations included the cumulative effects on infants and children of such residues and other substances with a common mechanism of toxicity. Because there is no indication of mammalian toxicity to these plant-pesticides, we conclude that there are no cumulative effects for the Cry1F protein.

4. Determination of Safety for U.S. Population, Infants and Children

a) Toxicity and Allergenicity Conclusions

The data submitted and cited regarding potential health effects for the Cry1F protein include the characterization of the expressed Cry1F protein in corn, as well as the acute oral toxicity, heat stability, and *in vitro* digestibility of the proteins. The results of these studies were determined applicable to evaluate human risk and the validity, completeness, and reliability of the available data from the studies were considered.

Adequate information was submitted to show that the Cry1F test material derived from microbial cultures was biochemically and, functionally similar to the protein produced by the plant-pesticide ingredients in corn. Production of microbially produced protein was chosen in order to obtain sufficient material for testing.

The acute oral toxicity data submitted supports the prediction that the Cry1F protein would be non-toxic to humans. When proteins are toxic, they are known to act via acute mechanisms and

at very low dose levels [Sjoblad, Roy D., et al. "Toxicological Considerations for Protein Components of Biological Pesticide Products," Regulatory Toxicology and Pharmacology 15, 3-9 (1992)]. Since no effects were shown to be caused by Cry1F protein, even at relatively high dose levels (>5,050 mg test substance / kg body weight; 576 mg Cry1F / kg body weight), the Cry1F protein is not considered toxic. This is similar to the Agency position regarding toxicity and the requirement of residue data for the microbial *Bacillus thuringiensis* products from which this plant-pesticide was derived. [See 40 CFR Sec. 158.740(b)(2)(i).] For microbial products, further toxicity testing and residue data are triggered by significant acute effects in studies such as the mouse oral toxicity study to verify the observed effects and clarify the source of these effects (Tiers II & III).

Although Cry1F expression level data was required for an environmental fate and effects assessment, residue chemistry data were not required for a human health effects assessment of the subject plant-pesticide ingredients because of the lack of mammalian toxicity.

Both (1) available information concerning the dietary consumption patterns of consumers (and major identifiable subgroups of consumers including infants and children); and (2) safety factors which, in the opinion of experts qualified by scientific training and experience to evaluate the safety of food additives, are generally recognized as appropriate for the use of animal experimentation data were not evaluated. The lack of mammalian toxicity at high levels of exposure to the Cry1F protein demonstrates the safety of the product at levels well above possible maximum exposure levels anticipated in the crop.

The genetic material necessary for the production of the plant-pesticides active ingredients are the nucleic acids (DNA, RNA) which comprise (1) genetic material encoding these proteins and (2) their regulatory regions. "Regulatory regions" are the genetic material, such as promoters, terminators, and enhancers, that control the expression of the genetic material encoding the proteins. DNA and RNA are common to all forms of plant and animal life and the Agency knows of no instance where these nucleic acids have been associated with toxic effects related to their consumption as a component of food. These ubiquitous nucleic acids, as they appear in the subject active ingredient, have been adequately characterized by the applicant. Therefore, no mammalian toxicity is anticipated from dietary exposure to the genetic material necessary for the production of the subject active plant pesticidal ingredients.

b) Infants and Children Risk Conclusions

FFDCA section 408(b)(2)(C) provides that EPA shall assess the available information about consumption patterns among infants and children, special susceptibility of infants and children to pesticide chemical residues and the cumulative effects on infants and children of the residues and other substances with a common mechanism of toxicity. In addition, FFDCA section 408(B)(2)(C) also provides that EPA shall apply an additional tenfold margin of safety for infants and children in the case of threshold effects to account for pre- and post-natal toxicity and the completeness of the database unless EPA determines that a different margin of safety will be safe for infants and children.

In this instance, based on all the available information, the Agency concludes that there is a finding of no toxicity for the Cry1F protein and the genetic material necessary for its production. Thus, there are no threshold effects of concern and, as a result, the provision requiring an additional margin of safety does not apply. Further, the provisions of consumption patterns, special susceptibility, and cumulative effects do not apply.

c) Overall Safety Conclusion

There is a reasonable certainty that no harm will result from aggregate exposure to the U.S. population, including infants and children, to the Cry1F protein and the genetic material necessary for its production. This includes all anticipated dietary exposures and all other exposures for which there is reliable information.

The Agency has arrived at this conclusion because, as discussed above, no toxicity to mammals has been observed for the plant-pesticides.

5. Other Considerations

a) Endocrine Disruptors

The pesticidal active ingredients are proteins, derived from sources that are not known to exert an influence on the endocrine system. Therefore, the Agency is not requiring information on the endocrine effects of these plant-pesticides at this time.

b) Analytical Method(s)

A validated method for extraction and direct ELISA analysis of Cry1F in corn grain has been submitted and found acceptable by the Agency.

c) Codex Maximum Residue Level

No Codex maximum residue levels exists for the plant-pesticides *Bacillus thuringiensis* Cry1F protein and the genetic material necessary for its production in corn.

6. Tolerance Exemption

Therefore, 40 CFR chapter I is to be amended as follows:

Bacillus thuringiensis Cry1F Protein and the Genetic Material Necessary for its Production in Corn.

Bacillus thuringiensis Cry1F protein and the genetic material necessary for its production in corn are exempt from the requirement of a tolerance when used as plant-pesticides in the food and feed commodities of field corn, sweet corn and popcorn. "Genetic material necessary for its production" means the genetic material which comprise (1) genetic material encoding the Cry1F protein and (2) its regulatory regions. "Regulatory regions" are the genetic material, such as promoters, terminators, and enhancers, that control the expression of the genetic material encoding the Cry1F protein.

C. Environmental Assessment

1. Ecological Effects Hazard Assessment

This environment hazard assessment includes outcrossing and potential for weeds to develop if pollen from Cry1F corn was to fertilize other plants, horizontal gene transfer, expression of Cry1F protein in plant tissues, ecological effects including effects on monarch butterflies, fate of Bt proteins in the environment and effects on endangered species, particularly Lepidoptera. Studies have been submitted which demonstrate no effects under test conditions to representative species of birds (Bobwhite quail), non-target soil organisms (*Collembola* and Earthworm), honey bees, ladybird beetle, green lacewing, parasitic wasp, the monarch butterfly, aquatic invertebrates (*Daphnia magna*) and non-target insects in corn fields. In addition, it has been shown that conventional processes used in the commercial preparation of fish food inactivate any Cry1F protein present in corn grain. Cry1F protein in soil has been shown to degrade rapidly to very low levels.

2. Outcrossing and Weediness

The movement of transgenes from the host plant into weeds and other crops has been a significant concern due to the possibility of novel exposures to the pesticidal substance. The Agency has determined that there is no significant risk of gene capture and expression of Cry1F protein by wild or weedy relatives of corn in the U.S., its possessions or territories. Domesticated corn does not have a reasonable possibility of passing its traits to wild maize species. Feral species related to corn, as found within the United States, cannot be pollinated due to differences in chromosome number, phenology (periodicity or timing of events within an organism's life cycle as related to climate, e.g., flowering time) and habitat.

However, concern over species related to maize (*Zea mays* ssp. *mays*), such as *Tripsacum* species and the teosintes, as potential recipients of gene flow from genetically modified *Zea mays* calls for a closer look at this topic. Some *Zea* spp., such as the teosintes, are known to be interfertile with maize and are discussed as potential recipients of pollen directed gene flow from maize. This issue is of particular concern based upon the increased planting of genetically modified maize.

a) *Zea mays* ssp. *mays* - Maize

The origin of corn is thought to be in Mexico or Central America, based largely on archaeological evidence of early cob-like maize in indigenous cultures approximately 7200 years ago. *Zea mays* is a wind-pollinated, monoecious, annual species with imperfect flowers. This means that spatially separate tassels (male flowers) and silks (female flowers) are found on the same plant, a feature which limits inbreeding. A large variety of types are known to exist (e.g., dent, flint, flour, pop, sweet) and have been selected for specific seed characteristics through standard breeding techniques. Maize cultivars and landraces are known to be diploid ($2n = 20$) and interfertile to a large degree. However, some evidence for genetic incompatibility exists within the species (e.g., popcorn x dent crosses; Mexican maize landraces x Chalco teosinte). *Zea mays* has been domesticated for its current use by selection of key agronomic characters, such as a non-shattering rachis, grain yield and resistance to pests.

A recent study has indicated that cross-pollination of commercial maize cultivars at 100 ft downwind from the source of genetically modified maize was 1 %, and this proportion declined exponentially to 0.1 % at 130 ft and further declined to 0.03 % at 160 ft. At 1000 ft, the farthest distance measured, no cross-pollination was detected. For production of Foundation Seed, a distance of 660 ft has been generally required to ensure separation of pollen types. The relatively large size of corn pollen and its short viability period under most conditions preclude long distance transfer for purposes of outcrossing. Under conditions of high temperature or low humidity, corn pollen may only survive for a matter of minutes. Under more favorable conditions in the field or with controlled handling in the laboratory, pollen life may be extended to several hours.

b) *Tripsacum* species - Gama Grass

A close relative of corn or maize is the genus *Tripsacum*. Sixteen species of *Tripsacum* are known worldwide and generally recognized by taxonomists and agrostologists; most of the 16 different *Tripsacum* species recognized are native to Mexico, Central and South America, but three occur within the U.S.. In the Manual of Grasses of the United States, A. S. Hitchcock (revisions by Agnes Chase; 1971) reports the presence of three species of *Tripsacum* in the continental United States: *T. dactyloides*, *T. floridanum* and *T. lanceolatum*. Of these, *T. dactyloides*, Eastern Gama Grass, is the only species of widespread occurrence and of any agricultural importance. It is commonly grown as a forage grass and has been the subject of some agronomic improvement (i.e., selection and classical breeding). *T. floridanum* is known from southern Florida and *T. lanceolatum* is present in the Mule Mountains of Arizona and possibly southern New Mexico.

For the species occurring in the United States, *T. floridanum* has a diploid chromosome number of $2n = 36$ and is native to Southern Florida; *T. dactyloides* includes $2n = 36$ forms which are native to the central and western U.S., and $2n = 72$ forms which extend along the Eastern seaboard and along the Gulf Coast from Florida to Texas, but which have also been found in IL.

and KS; these latter forms may represent tetraploids ($x = 9$ or 18); and *T. lanceolatum* ($2n = 72$) which occurs in the Southwestern U.S. *Tripsacum* differs from corn in many respects, including chromosome number (*T. dactyloides* $n = 18$; *Zea mays* $n = 10$). Many species of *Tripsacum* can cross with *Zea*, or at least some accessions of each species can cross, but only with difficulty and the resulting hybrids are primarily male and female sterile. *Tripsacum* / maize hybrids have not been observed in the field, but have been accomplished in the laboratory using special techniques under highly controlled conditions.

Eastern Gama Grass is considered by some to be an ancestor of *Zea mays* or cultivated maize, while others dispute this, based largely on the disparity in chromosome number between the two species (maize $n = 10$; Gama Grass $x = 9$ or 18 , with diploid, triploid and tetraploid races existing; $2n = 36$ or 72), as well as radically different phenotypic appearance. Albeit with some difficulty, hybrids between the two species have been made. In most cases these progeny have been sterile or viable only by culturing with *in vitro* >embryo rescue= techniques.

Even though some *Tripsacum* species occur in areas where maize is cultivated, gene introgression from maize under natural conditions is highly unlikely, if not impossible. Hybrids of *Tripsacum* species with *Zea mays* are difficult to obtain outside of the controlled conditions of laboratory and greenhouse. Seed obtained from such crosses are often sterile or progeny have greatly reduced fertility. Approximately 10 - 20% of maize-*Tripsacum* hybrids will set seed when backcrossed to maize, and none are able to withstand even the mildest winters. The only known case of a naturally occurring *Zea* - *Tripsacum* hybrid is a species native to Guatemala known as *Tripsacum andersonii*. It is 100% male and nearly 99% female sterile and is thought to have arisen from an outcrossing to teosinte, but the lineage is uncertain. *Zea mays* is not known to harbor properties that indicate it has weedy potential and, other than occasional volunteer plants in the previous season=s corn field, maize is not considered as a weed in the U.S.

Relatively few accessions of *T. dactyloides* will cross with maize and the majority of progeny aren=t fertile or viable even in those that do. In controlled crosses, if the female parent is maize, there is a greater likelihood of obtaining viable seed. When these hybrids have been backcrossed to maize in attempts to introgress *Tripsacum* genes for quality enhancement or disease resistance, the *Tripsacum* chromosomes are typically lost in successive generations. In many instances where hybridization has been directed between these two species, the resultant genome is lacking in most or all of the chromosomal complements of one of the parent species in subsequent generations.

Conclusion: The possibility of maize contributing genetic material to Eastern Gama Grass through random pollen flow in agricultural or natural situations is extremely remote based upon experience trying to create hybrids under the optimal laboratory conditions. No other known grass species present in the continental U.S. would interbreed with commercial maize populations (*i.e.*, be recipients of pollen-directed gene flow). None of the sexually compatible relatives of corn in the U.S. are considered to be serious, principal, or common weeds in the U.S.

c) *Zea* species - Teosintes

Teosintes, specifically *Z. mays* ssp. *mexicana* (Schrader) Iltis, *Z. mays* ssp. *parviglumis* Iltis and Doebley, *Z. mays* ssp. *huehuetenangensis* (Iltis and Doebley) Doebley, *Z. luxurians* (Durieu and Ascherson) Bird, *Z. perennis* (Hitchc.) Reeves and Mangelsdorf and *Z. diploperennis* Iltis, Doebley and Guzman, have co-existed and co-evolved in close proximity to maize in the Americas over thousands of years, however, maize and teosinte maintain distinct genetic constitutions despite sporadic introgression.

The teosintes retain a reduced cob-like fruit/inflorescence that shatters more than cultivated maize, but still restricts the movement of seeds as compared to more widely dispersed weedy species. Hence, the dispersal of large numbers of seeds, as is typical of weeds, is not characteristic of teosintes or maize. In their native habitat, some teosintes have been observed to be spread by animals feeding on the plants. Teosintes and teosinte-maize hybrids do not survive even mild winters and could not propagate in the U.S. corn belt. Additionally, some types have strict day length requirements that preclude flowering within a normal season (*i.e.*, they would be induced to flower in November or December) and, hence, seed production under our temperate climate.

Since both teosinte and *Tripsacum* are included in botanical gardens in the U.S., the possibility exists (although unlikely) that exchange of genes could occur between corn and its wild relatives.

EPA is not aware, however, of any such case being reported in the United States. Gene exchange between cultivated corn and transformed corn would be similar to what naturally occurs at the present time within cultivated corn hybrids and landraces. Plant architecture and reproductive capacity of the intercrossed plants will be similar to normal corn, and the chance that a weedy type of corn will result from outcrossing with cultivated corn is extremely remote.

Like corn, *Zea mays* ssp. *mexicana* (annual teosinte) and *Zea diploperennis* (diploid perennial teosinte) have 10 pairs of chromosomes, are wind pollinated, and tend to outcross, but are highly variable species which are often genetically compatible and interfertile with corn, especially when maize acts as the female parent. *Zea perennis* (perennial teosinte) has 20 pairs of chromosomes and forms less stable hybrids with maize. Corn and compatible species of teosinte are capable of hybridization when in proximity to each other. In Mexico and Guatemala, teosintes exist as weeds around the margins of corn fields. The F1 hybrids have been found to vary in their fertility and vigor. Those that are fertile are capable of backcrossing to corn. A few isolated populations of annual and perennial teosinte were said to exist in Florida and Texas, respectively. The Florida populations were presumably an escape from previous use of *Z. mays* ssp. *mexicana* as a forage grass, but local botanists have not documented any natural populations of this species for approximately twenty-five years. No teosinte populations are reported to exist in the State of Texas. Further, given the day length characteristics of *Z. diploperennis*, it is highly unlikely a sustaining population would result from introduction of this species. *Z. mays* ssp. *mexicana*, *Z. mays* ssp. *parviglumis*, *Z. luxurians* and *Z. diploperennis* may cross with maize to produce fertile hybrids in many instances. None of these teosinte species have, however, been shown to be aggressive weeds in their native or introduced habitats. Except for special

plantings as noted above, teosinte is not present in the U.S. or its territories. Its natural distribution is limited to Mexico, Honduras, Nicaragua, El Salvador and Guatemala.

Given the cultural and biological relationships of various teosinte species and cultivated maize over the previous two millennia, it would appear that significant gene exchange has occurred (based upon morphological characters) between these two groups of plants and that no weedy types have successfully evolved as a result. More recent cytogenetic, biochemical and molecular analyses have indicated that the degree of gene exchange is far less than previously thought. Partial and complete gametophytic incompatibility has been documented among cultivated maize, landraces and teosinte. The former is demonstrated by differential pollen growth and a skewed recovery of alleles linked to incompatibility genes. Complete incompatibility mechanisms serve to isolate a species or subspecies and are evidenced as pollen exclusion or non-functioning of pollen types on certain genotypes. Attempts to cross six collections of *Zea mays* ssp. *mexicana* with U.S. maize cultivars (W22, W23) yielded no or few seeds in five of the six groups.

Conclusion: Based on the ability of maize to hybridize with some teosintes, the suggestion of previous genetic exchange amongst these species over centuries, and their general growth habits, any introgression of genes into wild teosinte from *Zea mays* is not considered to be a significant agricultural or environmental risk. The growth habits of teosintes are such that the potential for serious weedy propagation and development is not biologically plausible in the United States.

Summary:

The potential for pollen-directed gene flow from maize to Eastern Gama Grass is extremely remote. This is evidenced by the difficulty with which *Tripsacum dactyloides* x *Zea mays* hybrids are produced in structured breeding programs. Additionally, the genus does not represent any species considered as serious or pernicious weeds in the United States or its territories. Any introgression of genes into this species as a result of cross fertilization with genetically-modified maize is not expected to result in a species that is weedy or difficult to control. In many instances where hybridization has been directed between these two species, the resultant genome is lacking in most or all of the maize chromosomal complement in subsequent generations.

Many of the *Zea* species loosely referred to as Ateosintes[®] will produce viable offspring when crossed with *Zea mays* ssp. *mays*. None of these plants are known to harbor weedy characteristics and none of the native teosinte species, subspecies or races are considered to be aggressive weeds in their native or introduced habitats. In fact, many are on the brink of extinction where they are indigenous and will be lost without human intervention (*i.e.*, conservation measures). Further, none of the landraces or cultivated lines of *Zea mays* are considered to have weedy potential and are generally considered to be incapable of survival in the wild as a result of breeding practices (*i.e.*, selection) during domestication of the crop.

3. Ecological Exposure and Risk Characterization

a. Ecological Exposure

1) Maximum Expression of Cry1F Protein in Various Corn Tissues

Cry1F protein from inbred and hybrid maize 1507 pollen, grain, grain-derived feeds and a microbial source was evaluated biochemically using ELISA, SDS-PAGE and Western Blotting, and for bioactivity using insect bioassays. Transgene expression was found throughout the different plant tissues across the growing season. The level of the Cry1F proteins was higher in tissues and in whole plants during vegetative growth through pollen shed and declined with plant senescence. PAT expression was found to be typically below the detection limit.

a) Cry1F and PAT protein expression in hybrid maize samples:

Test line grain samples contained an average Cry1F expression of 89.8 (71.2 to 114.8) pg / μ g total protein. Leaf sample expression from Cry1F maize lines was 110.9 (56.6 to 148.9) pg / μ g total protein. Pollen and silk samples yielded 135.5 (113.4 to 168.2) pg/ μ g total protein for pollen (31 to 33 ng/mg pollen) and 50.3 (26.8 to 79.8) pg / μ g total protein for silk. The Cry1F expression for stalk samples was 550.0 (355.9 to 737.4) pg / μ g total protein. For whole plant samples, the expression level averaged 1063.8 (803.2 to 1572.7) pg / μ g total protein. In senescent whole plant samples the expression of Cry1F was 714.3 (622.2 to 845.3) pg / μ g total protein. Of the leaf samples tested for PAT expression, the test line samples ranged from below the LOD to 40.8 pg / μ g total protein. All of the following tissues were below the LOD for PAT: pollen, silk, stalk and grain from both test and control lines. Both whole plant samples and senescent whole plant samples were negative or below the LOD for PAT.

b) Cry1F and PAT protein expression in inbred maize samples:

Test line grain samples contained an average Cry1F expression of 112.2 (66.5 to 141.5) pg / μ g total protein. Leaf sample expression from Cry1F maize lines was 169.5 (79.3 to 209.4) pg / μ g total protein. Pollen and silk samples yielded 207.5 (186.3 to 231.1) pg/ μ g total protein for pollen and 58.9 (36.2 to 89.8) pg / μ g total protein for silk. The Cry1F expression for stalk samples was 637.8 (480.5 to 849.0) pg / μ g total protein. For whole plant samples, the expression level averaged 1357.8 (1283.5 to 1428.0) pg / μ g total protein. In senescent whole plant samples the expression of Cry1F was 677.5 (470.5 to 968.3) pg / μ g total protein. Of the leaf samples tested for PAT expression, the test line samples ranged from below the LOD to 58.2 pg / μ g total protein. All of the following tissues were below the LOD for PAT: pollen, silk, stalk and grain from both test and control lines. Both whole plant samples and senescent whole plant samples were negative or below the LOD for PAT.

2) Half-Life and Estimated Environmental Concentration

Based on a bioassay with the tobacco budworm (*Heliothis virescens*), a target species, purified Cry1F proteins incorporated into test soils biodegraded with a half-life of approximately 3.13 days (Table 2). This half-life is very comparable with the 4-7 days in published reports for other Cry proteins. The study does not, however, adequately address the duration and the amount of residual Cry 1F protein in the soil.

Much of the Cry1F that will be exposed to the soil or soil organisms in the field consists of the protein in various corn tissues, e.g. incorporation of crop debris at the end of the growing season, pollen, or root tissue. Several published studies indicate that Cry proteins expressed in transgenic corn degrade more rapidly in the soil than purified Cry protein. Testing of purified protein degradation in the soil, therefore, may result in higher soil half-life than the degradation of plant incorporated Cry1F. Therefore addition of purified Cry protein is likely a more rigorous test of degradation rates than addition of Cry1F corn tissue. The reported 3.13 day half life of purified protein does, however, indicate that the Cry1F protein will be degraded rapidly in the soil to levels below those that could pose a hazard to non-target organisms.

RECOMMENDATIONS: There is no evidence to indicate that prolonged exposure to trace amounts of Cry protein in the soil affects non-target organisms. The submitted data do not, however, sufficiently address the issue of residual Cry protein accumulation in the soil. The soil degradation study should be carried out for a longer period of time to determine the duration and the amount of residual Cry 1F protein in agricultural soil. Also, the soil used in the study should be actual field soil containing the microbial flora normally found in the field. This will give a more accurate rate of degradation of the Cry protein in the agricultural environment because microbial populations in the rhizosphere are commonly 100 fold higher than in bulk soil. Bulk soil generally does not support populations of microorganisms as high as those in the rhizosphere or those in soils with high organic content (plant residues). In addition, field soil high in organic content should result in lower (if any) soil binding of Cry proteins.

Estimated Environmental Concentration (EEC): The amounts of Cry1F protein in an acre of corn (if 25,000 corn plants/acre at harvest were left in the field) is approximately 20.5 g/acre. As a result the expected maximum environmental concentration (EEC) of Cry1F protein will be 23 micrograms/kg dry soil (15 cm deep). This does not include any additional Cry protein in the soil as a result of root exudation (if root exudation is shown to occur).

RECOMMENDATIONS: Data for Cry1F protein expression in plant roots and data on Cry protein exudation by roots should be submitted for review.

3) Effects on soil microbial flora

Limited published data do not indicate that Cry proteins have any measurable effect on microbial populations in the soil, even at levels much higher than expected from Cry1F Bt corn cultivation. Due to frequent fluctuations of organic and other inputs into agricultural soil, at any particular time, soil samples are likely to display radically different abundances and diversity of

microorganisms. There is no evidence to suggest that the numerous processes mediated by soil microorganisms do not persist across the spectrum from undisturbed soil under native vegetation to intensively cultivated soil under continuous cropping and chemical treatments. Without better information regarding the range of what constitutes natural microbial communities or microbial communities in current agroecosystems, and the consequences of such changes, it is not possible to assign a significance to apparently minor changes in microbial populations when they do occur. Constant fluctuations of soil microbial communities are typical of most soil ecosystems.

Summary: The low concentration of Cry protein in the soil has not been shown to have any adverse effects on non-lepidopteran organisms. Sufficient evidence exists to suggest that adverse impacts of Cry proteins in the soil are not likely, although the levels of expression in the root should be determined to assure that unexpectedly high levels of root expression do not exist. The EEC of Cry1F from corn (23 µg/kg dry soil) is well below levels used in toxicity tests which were performed at multiples of the expected environmental concentration in the soil.

4) Horizontal Transfer of Transgenes to Plants and Soil Organisms

Microbial transformation with large concentrations of plant transgenes has only been accomplished at low frequencies and under artificial optimized conditions in the laboratory, and only where homology to existing DNA in the recipient bacteria occurs. Under conditions where homology does not occur, horizontal transfer has not been observed. Therefore, DNA transfer occurs rarely if at all from plants to bacteria. In addition, because homologous sequences already exist in soil bacteria (such as native soil *Bacillus thuringiensis*) horizontal transfer of the same sequences from plants, if it were to occur, would not constitute a new phenomenon. Bt species are generally common in soil, if not always abundant, and therefore various *cry* genes have been available for long periods of time for horizontal transfer from Bt to plants or other soil species. Similarly, antibiotic resistance genes and promoter genes used in making Bt plants have long been present in the soil microorganisms and decaying plant material. Therefore the likelihood of an adverse impact or new horizontal gene transfer that is not already capable of taking place in the soil is extremely unlikely.

b. Risk Characterization for Terrestrial Animals

1) Avian

The dietary LC₅₀ value for corn grain (meal) expressing *Bacillus thuringiensis* var. *aizawai* Cry1F protein in corn grain when fed to juvenile northern bobwhite for 5 days was determined to be greater than 100,000 ppm (10% corn meal). The no-observed-effect concentration was also 100,000 ppm. The study is scientifically sound and no treatment mortality or behavior change was observed between the dosed and control replicates. These data show that there will be no adverse effects on avian wildlife from incidental field exposure to Cry1F corn. These data are, however, not sufficient to make a hazard assessment from repeated exposure(s) to higher doses of Bt corn. The study is rated as supplemental because the concentration tested (10% corn in the

diet) is too low to assess hazards to non-target birds from continuous exposure to higher levels of Cry1F protein.

RECOMMENDATIONS: A six week study with 60 to 70% corn in the diet is necessary to assess hazards from chronic exposure of wild and domesticated fowl.

2) Mammalian Wildlife

Since the anticipated exposure of mammalian wildlife is considered high, risk to wild mammals from Bt Cry1F is a potential concern. Direct wild mammal testing, however, is required only when human toxicology data are inadequate for assessment of hazard to wild mammals. The human health effects data submitted to EPA indicate that there is no significant toxicity to rodents from acute oral testing at the maximum hazard dose. In light of this toxicology information, no risk to mammalian wildlife is expected.

3) Plants

Since the active ingredient in this product is an insect toxin (*Bt* endotoxin) that has never shown any toxicity to plants, the plant toxicity studies have been waived.

4) Nontarget Beneficial Organism Studies

a) Honey Bees

The reviewed capped honey bee brood cell study where larvae were fed Cry 1F corn pollen and pure Cry1F protein showed normal larval development and emergence of healthy adult honey bees. This study shows that at levels higher than the expected environmental exposure, the proposed use of Cry1F protein in corn is not likely to have any measurable deleterious effects on the honey bee (*Apis mellifera*). The data showed no significant difference between treatment mortality or behavior change between the dosed and control replicates. As a result, no discernible detrimental effects to honey bees are expected from the proposed uses of the Cry1F producing corn. The data adequately address potential toxicity concerns for foraging honey bees exposed to Cry1F protein expressed in corn pollen in the field. In addition, since corn is wind pollinated, few honey bees are expected to be exposed.

b) Lady beetle predator:

Adult lady beetles (*Hippodamia convergens*) fed a concentration of Bt Cry1F protein at 15x the expected rate found in corn pollen resulted in no mortality or signs of toxicity over a 29 day period. Therefore, the NOEC was determined to be >15x the concentration of Cry1F found in pollen and the LC₅₀ was determined to be > 480 ppm a.i (the test concentration). The submitted study shows that corn containing the Cry1F protein should not cause significant adverse effects to lady bird beetle predators. The test insects were exposed to a dose of active ingredient

approximating the amount that would be ingested by the beetles feeding on aphids under field conditions. As a result, no discernible beneficial beetle population effects are expected from the proposed uses of the Cry1F producing corn. This conclusion is confirmed by adult and larval lady beetle abundance found in the field census study. These studies adequately address potential concerns for Cry1F protein expressed in corn to beneficial beetles.

c) Green lacewing

Green lacewing larvae fed a concentration of Bt Cry1F protein at 15x the expected rate found in corn pollen resulted in no mortality or signs of toxicity due to feeding on Cry1F over a 13 day period. Therefore, the NOEC was determined to be >15x the concentration of Cry1F found in pollen and the LC₅₀ was determined to be > 480 ppm a.i (the test concentration). These laboratory findings do not show significant detrimental effects and provide data that show a lack of risk to beneficial insects at Cry1F levels that will be encountered in the field use situation. These findings confirm published field studies on the effects of *B.t.* crops on insect predators showing no significant differences in the density of beneficial insects, including green lacewings. The conclusions are also confirmed by the adult and larval green lacewing abundance found in a field census study submitted with this application.

d) Parasitic wasp

Parasitic Hymenoptera (*Brachymeria intermedia*) fed a concentration of Bt Cry1F protein at 10x the expected rate found in corn pollen showed no mortality or signs of toxicity over a 12 day period. Therefore, the NOEC was determined to be >10x the concentration of Cry1F found in pollen. The LC₅₀ was determined to be > 320 ppm a.i (the test concentration). As a result, no adverse effect to parasitic wasps are expected from field exposure to Cry1F protein producing corn. The conclusions are also confirmed by the parasitic wasp abundance found in a field census study submitted with this application

e) Monarch butterfly

An additional scientifically sound study submitted by Dow AgroSciences showed that Cry1F is non-toxic to neonate monarch butterfly larvae when fed a #10,000 ng/mL diet dose. First instar larval weight and mortality were recorded after seven days of feeding. There was no mortality to monarchs fed 10,000 ng/mL diet, the highest rate tested. There was some growth inhibition at 10,000 ng/mL diet. Since pollen doses equivalent to 10,000 ng/mL diet are not likely to occur on milkweed leaves in nature, it can be concluded that Cry1F protein will not pose a risk to monarchs.

RECOMMENDATIONS: The conclusions should be confirmed by providing data showing that the amounts of Cry protein found in pollen on milkweed leaves in the field are at concentrations less than the 10,000 ng/mL diet used in this study. The NOEC of pollen on milkweed leaves also has to be determined.

f) Non-target Insects in the Field

A field study was conducted to determine whether Cry1F Bt corn had any significant negative impact on natural non-target insect populations. Results from a field evaluation study indicate that the transgenic corn lines 1507 and 1360 do not adversely affect the number of beneficial arthropods in the field. In general line 1507 showed larger numbers of beneficial insects. Beneficial insects counted in this study were: lady beetles (*Cycloneda munda* & *Coleomegilla maculata*), predacious Carabids, brown lacewings (Hemerobiidae), green lacewings (*Chrysoperla plorabunda*), minute pirate bugs (*Orius insidiosus*), assassin bugs (Reduviidae), damsel bugs (Nabidae), Ichneumonid and Braconids (parasitic wasps), damselflies and dragonflies, and spiders. Data included counts of adult and larval lady beetles and lacewings. This field census study adequately addresses potential concerns for Cry1F protein expressed in corn to non-target insect populations.

RECOMMENDATIONS: It is recommended that the beneficial insect monitoring should continue into the first few years of commercial use of Cry1F corn crops to confirm the single season effects and findings and to gather data on long range non-target insect effects and abundance.

g) Earthworm:

The submitted data show that Cry1F protein has no measurable deleterious effects on earthworms, a representative beneficial soil invertebrate species. This suggests that the proposed uses of the Cry1F protein in corn are not likely to have any measurable population effects on beneficial soil invertebrates. The one limit test concentration of 2.26 mg Cry1F/kg dry soil represented more than 100X the estimated concentration present in the top six inches of an acre of soil following the incorporation of 25,000 senescent corn plants. This concentration is higher than any amount of Cry protein that may be present in the soil during any stage of the growing season (such as from root exudation). Based on the results of this study, Cry1F transgenic corn plantings will have no adverse effects on earthworms.

h) Collembola:

Since Collembola feed on decaying plant material in the soil, they may be exposed to Cry1F protein in corn found in the field. A study was conducted to determine if there may be adverse effects of Cry1F on Collembola. The study is scientifically sound and no treatment mortality or behavior change was observed between the dosed and control replicates after 28 days. The results of this study indicate that at levels that would reasonably be expected to be found in the field, collembola were not affected by chronic exposure to Cry1F protein. The exposure rates in this study are 1560-, 388-, and 79-fold-higher than the expected field concentration. The reviewed data show that *Bacillus thuringiensis* Cry1F corn protein has no measurable deleterious effects on collembola (*Folsomia candida*), a representative beneficial soil insect species. This indicates

that the proposed uses of the Cry1F protein in corn are not likely to have any measurable population effects on beneficial soil insects.

c. Risk Characterization for Aquatic Animals

Aquatic species: There is no evidence for sensitivity of aquatic (including endangered) species to Cry proteins. Toxicity studies with *Daphnia magna*, a very sensitive aquatic test organism, show no hazard for fish or invertebrates exposed to either corn pollen or to bacterially expressed Cry1F protein. In addition, aquatic exposure from Bt crops is extremely small. A simple standard pond scenario (1-ha pond, 2-m deep draining a 10-ha watershed planted with corn) was used to develop a worst case EEC for Cry1F protein on the basis of corn pollen loadings from airborne pollen deposition and agricultural runoff. Airborne pollen deposition results in water concentrations of approximately 1.25 ng Cry1F/mL and the contribution of Cry1F to the pond through agricultural runoff is <0.15 ng/mL. Thus, total water concentration of 1.4 ng Cry1F protein/L is projected under worst case conditions

1) Aquatic Invertebrates

The major source of Bt Cry1F protein in fresh water would be corn pollen. Toxicity studies with corn pollen containing Cry1F proteins conducted using the sensitive aquatic indicator species *Daphnia magna* show the no-mortality concentration and NOEC to be >100 mg a.i./L. There were no overt signs of toxicity to daphnids exposed to 100 mg Bt Cry1F pollen/L. The amount of pollen tested was considered to well exceed field exposure. These data indicate that the expected environmental concentration of corn pollen from the proposed use of Cry1F protein in corn is not likely to have any measurable population effects on aquatic invertebrates.

2) Fish

The registrant has requested a waiver of freshwater fish testing for transgenic maize containing *Bacillus thuringiensis* var. *aizawai* (Bt) Cry 1F protein. The basis of the waiver is the lack of significant exposure to fish and the low content of Cry1F protein in corn kernels in commercially manufactured fish diets (in aquafarms). Submitted data show that following processing there were undetectable levels of Cry1F protein in fish food containing Cry 1F maize. The submitted data are sufficient to conclude that the low aquatic EEC and the lack of measurable concentrations of Cry1F protein in commercial fish diets are unlikely to present hazardous exposures to fish. Accordingly the registrant's request to waive fish toxicity studies is acceptable.

3) Estuarine and Marine Animals

The Estuarine fish study was not required for this product because of very low or no potential for exposure.

d. Impacts on Endangered Species

The primary route of exposure to Cry1F protein in corn is through ingestion of corn tissue. There are no reports of threatened or endangered species feeding on corn plants, therefore such species would not be exposed to corn tissue containing the Cry1F protein. Since Cry1F corn pollen have shown no toxicity at the expected environmental concentration rates (EEC) to mammals, birds, plants, aquatic species, insect and other invertebrate species tested a "may effect" situation for endangered land and aquatic species is not anticipated given the current use pattern for this product. In its evaluation of endangered and threatened species, EPA considered all of the species listed in the Greenpeace and Environment Defense Fund petitions. In addition, EPA does not expect that any threatened or endangered plant species will be affected by outcrossing to wild relatives or by competition with such entities. Hybrid corn does not exist in the wild, nor are there wild plants that can interbreed with corn in the United States.

Because of the selectivity of Cry1F protein for lepidopteran species, endangered species concerns are mainly restricted to the order Lepidoptera. The majority of endangered lepidopteran species have very restricted habitat range that does not encroach on corn production areas. For example, Mitchell's satyr butterfly occur in wetlands fed by seeps and springs known as fens, and their larvae, which are present throughout the summer, feed primarily on sedges. No Mitchell satyr populations have been seen in close proximity to corn fields.

Examination of an overlay map showing the county level distribution of endangered lepidopteran species (as listed by the U.S. Fish and Wildlife Service) relative to corn production counties in the US, shows that they do not occur in agricultural areas where corn is grown, nor is corn considered a host plant for these species. The overlay map when combined with restricted habitat range clearly indicates that any potential concern for endangered or threatened butterfly species, including those listed in the Greenpeace petition is restricted to the Karner blue butterfly.

The Karner blue is found along the northern extent of the range of wild lupine, where there are prolonged periods of winter snowpack, primarily in parts of Wisconsin, Michigan, Minnesota, Indiana, New Hampshire and New York. The Karner blue requires wild lupine (*Lupinus perennis*) as an oviposition substrate and larval food source, while the adults feed on wild flowers. Wild lupine does not occur in corn fields, although there are anecdotal reports of wild lupine growing 'within a couple of hundred meters of corn fields. Wild lupine grows on dry, sandy soils in pine barrens, oak savannah, forest trails and previously disturbed habitats such as utility rights-of-way, military installations, airports, highway corridors, sand roads and abandoned sand pits. There are recent reports that wild lupine may, in rare instances, grow in the vicinity of corn fields, especially in cases where the field may have been fallow in the previous season. However, there are no reports of Karner blue larvae or wild lupine within one meter of corn fields.

Karner blue oviposition overlap with corn pollen shed is also minimal. Although first generation

Karner blues emerge in mid-April, prior to pollen anthesis, second generation larvae emerge in June-July when there may be some overlap with pollen-shed. However, there should be no risk of Karner blue exposure to maize pollen because larvae typically occur on wild lupines in full sunlight in open areas of savannas or barrens and not within corn fields.

Because Cry1F protein is active against Lepidoptera, some activity against the Karner blue at high dose levels would not be surprising. However, data on the levels of Cry1F pollen exceeding the NOEL inside the 1 meter corn field perimeter are not available. Testing of Karner blue larvae directly is difficult due to its endangered status. Although close relatives of the Karner blue butterfly are available, data from related lepidopteran species do not predict susceptibility to low levels of Bt proteins, even within the same genus. Since susceptibility of the Karner blue is not necessarily equivalent to other species from the genus *Lycaeides* and tests cannot be conducted with the Karner blue, determining a NOEL is difficult to impossible. However, the Karner blue is probably no more sensitive to Cry1F than monarch butterflies and will not consume toxic levels of Bt in the field.

Conclusion: Exposure of Karner blue butterflies to harmful levels of Cry1F corn pollen is not expected. Likewise, a review of the preferred habitats of other lepidopteran species listed as endangered by the U.S. Fish and Wildlife Service, including the endangered Mitchell satyr butterfly, indicates that no exposure to harmful levels of Cry1F protein containing pollen will take place. Therefore, EPA believes that this action will have no effect on listed species. However, because of the lack of direct testing of Cry1F effects on the endangered Karner blue butterfly (*Lycaeides melissa samuelis*) and recent information on the possibility of exposure of the Karner blue to corn pollen under certain rare circumstances (such as replanting of fallow fields), at this time geographic restrictions are needed for this product to eliminate potential exposure of Karner blue butterflies to Cry1F corn pollen. Without geographic restrictions, at this time it is not possible to make a definitive *Ano effect@* finding without a consultation with the US Fish and Wildlife Service. The Agency plans to conduct further work to understand the extent to which the practice of replanting fallow fields might expose Karner blue butterflies to Bt corn pollen.

4. Endangered Species Statement

Of particular concern is the endangered Karner blue butterfly (*Lycaeides melissa samuelis*) with populations in Illinois, Indiana, Michigan, Minnesota, New Hampshire, New York, and Wisconsin. Because of the potential for *B. t.* Cry protein containing pollen to affect Lepidoptera adversely, Cry1F maize must not be near habitats of the Karner blue butterfly in the following counties where the Karner blue butterfly is known to exist in scattered populations: Illinois - Lake; Indiana - Porter and Lake; Michigan - Allegan, Lake, Monroe, Montcalm, Muskegon, Newaygo and Oceana; Minnesota - Anoka and Winona; New Hampshire - Merrimack; New York - Albany, Saratoga, Schenectady and Warren; Wisconsin - Adams, Barron, Burnett, Chippewa, Clark, Dunn, Eau Claire, Green Lake, Jackson, Juneau, Kenosha, Marquette, Menominee, Monroe, Oconto, Outagamie, Polk, Portage, Sauk, Shawano, St. Croix, Waupaca,

Waushara, Wood; (this list is from the Wisconsin Statewide Karner Blue Butterfly Habitat Conservation Plan and Environmental Impact Statement). Although it is unlikely that sufficient Cry1F expressing pollen would accumulate on the wild lupine (*Lupinus perennis*) that constitutes the sole food source for the butterfly larvae, this precaution is needed in the lack of adequate data from the field indicating the precise proximity of wild lupine to corn fields in the above named counties.

D. Resistance Management

The following requirements for Cry1F event 1507 are based on the Agency's requirements for Cry1Ab expressing corn. This is due to the possibility of cross-resistance between Cry1Ab and Cry1F. Modifications of these requirements may result following the Agency's comprehensive reassessment of B.t. plant-pesticides.

1) Several aspects of the Insect Resistance Management Plan will operate in synergy to promote grower compliance, however, the cornerstones of the compliance program must be the:

a) Grower Guides

Grower Guides and/or Product Use Guides must be submitted to the Agency at the time of distribution to growers. These Guides must be distributed to each seed customer and updated on an annual basis, as needed. The Guides provide complete information for growers regarding routine IRM practices that must be employed, and will be a primary educational and reference tool. Agreed-upon requirements and additional information that cannot be included in the Grower Guides for 2001 (e.g., because the requirements were enacted after printing and distribution of the Grower Guides) must be conveyed via supplemental communications to Cry1F field corn seed customers.

b) Stewardship Agreement (grower agreement).

Each grower who purchases Cry1F field corn seed must be required to sign a Stewardship Agreement, which will obligate the grower to follow the required IRM and non-target insect protection practices as specified in the Grower Guide/Product Use Guide and/or in supplements thereof.

c) A Strong and Multi-Pronged Grower Education Program.

A variety of methods must be employed to promote grower education and to continue to reinforce the need for adherence to all aspects of the IRM program.

d) Additional mechanisms must also be used to promote grower compliance, including:

Training of sales personnel, seed dealers and technical support staff. Coordination and reinforcement of IRM requirements through other organizations (e.g., NC-205, the Cooperative

Extension Service, USDA, National Corn Growers Assn. (NCGA), American Crop Protection Assn., Biotechnology Industry Organization, crop consultants and other crop professionals).

2) (Stewardship Agreements/Grower Agreements) will specify that growers must adhere to the refuge requirements as described in the Grower Guide/Product Use Guide and/or in supplements to the Grower Guide/Product Use Guide. Specifically, growers must plant a minimum structured refuge of at least 20% non-Bt corn. Insecticide treatments for control of European corn borer, corn earworm and/or Southwestern corn borer may be applied only if economic thresholds are reached for one or more of these target pests. Economic thresholds will be determined using methods recommended by local or regional professionals (e.g., Extension Service agents, crop consultants). Instructions to growers will specify that microbial Bt insecticides must not be applied to non-Bt corn refuges.

3) For the 2001 growing season, grower agreements (Stewardship Agreements) for Cry1F field corn grown in cotton-growing areas will specify that growers must adhere to the refuge requirements as described in the Grower Guide/Product Use Guide and/or in supplements to the Grower/ Product Use Guide. Specifically, growers in these areas must plant a minimum structured refuge of 50% non-Bt corn. Cotton growing areas include the following States: Alabama, Arkansas, Georgia, Florida, Louisiana, North Carolina, Mississippi, South Carolina, Oklahoma (only the counties of Bryan, Caddo, Canadian, Garvin, and Grady), Tennessee (only the counties of Carroll, Chester, Crockett, Fayette, Franklin, Gibson, Hardeman, Hardin, Haywood, Henderson, Lake, Lauderdale, Lawrence, Lincoln, McNairy, Madison, Obion, Rutherford, Shelby, and Tipton), Texas (except the counties of Carson, Dallam, Hansford, Hartley, Hutchinson, Lipscomb, Moore, Ochiltree, Roberts, and Sherman), Virginia (only the counties of Greensville, Isle of Wight, Northampton, Southampton, Sussex, Suffolk) and Missouri (only the counties of Butler, Dunkin, Mississippi, New Madrid, Pemiscot, Scott, Stoddard).

4) Requirements for refuge deployment will be described in the Grower Guides/Product Use Guides as described in Section D of the Industry IRM Plan submitted on April 19, 1999. Growers must continue to be required to plant only non-Bt corn in the refuge and to plant the refuge within 2 mile of their Cry1F corn acreage. In regions of the corn belt where conventional insecticides have historically been used to control ECB and SWCB, growers wanting the option to treat these pests must plant the refuge within 3 mile of their Cry1F corn. Refuge planting options include: separate fields, blocks within fields (e.g., along the edges or headlands), and strips across the field. When planting the refuge in strips across the field, growers must be instructed to plant multiple non-Bt rows whenever possible.

5) The registrants will monitor for the development of resistance using baseline susceptibility data and/or a discriminating concentration assay when such an assay is available. The registrants will proceed with efforts to develop a discriminating concentration assay. The registrants will ensure that monitoring studies are conducted annually to determine the susceptibility of ECB and corn earworm (CEW) populations to the Cry1Ab protein. This resistance monitoring

program will be developed to measure increased tolerance to Bt corn above the various regional baseline ranges.

Populations of ECB and CEW will be collected from representative distribution areas that contain Cry1F corn plant-pesticide and monitored/screened for resistance, with particular focus on those areas of highest distribution. The results of monitoring studies will be communicated to the Agency on an annual basis, by January 31 of the year following the population collections for a given growing season.

In addition, the registrants will instruct its customers (growers and seed distributors) to contact the registrants (e.g., via a toll-free customer service number) if incidents of unexpected levels of ECB and/or CEW damage occur.

Upon exclusion of the causes specified in section 7a of this document, the registrants will investigate and identify the cause for this damage by local field sampling of plant tissue from corn hybrids that contain Cry1F corn plant-pesticide and sampling of ECB & CEW populations, followed by appropriate in vitro and in planta assays. Upon the registrant's confirmation by immunoassay that the plants contain Cry1F protein, bioassays will be conducted to determine whether the collected ECB population exhibits a resistant phenotype.

Until such time that a discriminating concentration assay is established and validated by the registrant, the registrant will utilize the following to define a confirmed instance of ECB and/or CEW resistance:

Progeny from the sampled ECB or CEW population will exhibit both of the following characteristics in bioassays initiated with neonates

1. An LC50 in a standard Cry1F diet bioassay that exceeds the upper limit of the 95% confidence interval of the mean historical LC50 for susceptible ECB or CEW populations, as established by the ongoing baseline monitoring program. The source of Cry1F crystal protein standard for this bioassay will be *Bacillus thuringiensis* subspecies *aizawai*.
2. > 30% survival and > 25% leaf area damaged in a 5-day bioassay using Cry1F-positive leaf tissue under controlled laboratory conditions.

Based upon continued experience and research, this working definition of confirmed resistance may warrant further refinement. In the event that the registrant finds it appropriate to alter the criteria specified in the working definition, the registrant must obtain Agency approval in establishing a more suitable definition.

The insect monitoring programs must include Southwestern corn borer (SWCB) and corn earworm (CEW), in addition to European corn borer (ECB). The program must focus monitoring in areas that typically have a high density of Bt corn or have historically been prone to high

levels of corn borer pressure and where the refuge areas may more likely be treated with insecticides.

6) The current definition of confirmed insect resistance must be used as described in Section E of the Industry IRM Plan. Agency approval will be sought prior to implementation of any modified definition of confirmed insect resistance.

7) a) When field resistance has been demonstrated to have occurred, you must stop sale and distribution of Cry1F corn in the counties where the field resistance has been shown until an effective local mitigation plan approved by EPA has been implemented. The registrant assumes responsibility for the implementation of resistance mitigation actions undertaken in response to the occurrence of resistance during the 2001 growing season. EPA interprets "suspected resistance" to mean, in the case of reported product failure, that the corn in question has been confirmed to be Cry1F corn, that the seed used had the proper percentage of corn expressing Cry1F protein, that the relevant plant tissues are expressing the expected level of Cry1F protein, that it has been ruled out that species not susceptible to the protein could be responsible for the damage, that no climatic or cultural reasons could be responsible for the damage, and that other reasonable causes for the observed product failure have been ruled out. The Agency does not interpret "suspected resistance" to mean grower reports of possible control failures, nor should extensive field studies and testing to fully scientifically confirm insect resistance be completed before responsive measures are undertaken.

7) b) The registrant will maintain a (confidential) database to track sales (units and location) of its Cry1F corn on a county-by-county basis. The registrant will provide annually, on a CBI basis, sales data for each state indicating the number of units of corn hybrids that contain the registrant's Cry1F corn plant-pesticide that were sold. As part of the overall sales report, the registrant will provide a listing of an estimate of the acreage planted within such states and counties with sales limitations. This information will be provided by January 31 of the year following each growing season.

8) The registrants will provide grower education. The registrants will agree to include an active partnership with such parties as: university extension entomologists and agronomists, consultants, and corn grower groups. The registrants will implement a grower education program (in part, as requested by the registrants, through the Grower Agreement setting forth any resistance management requirements) directed at increasing grower awareness of resistance management, in order to promote responsible product use. Insect Resistance Management educational materials for the 2001 growing season must be provided to the Agency as they become available for distribution. IRM educational materials must be developed and distributed at the same time that growers receive seed. Survey results and other available information must be used to identify geographic areas of non-compliance with insect resistance management plans. As described in the Industry IRM Plan submitted to EPA on April 19, 1999, an intensified grower education program will be conducted in these geographic areas prior to the following growing season. If individual non-compliant growers are identified, they must be prohibited from

future purchases of Cry1F corn seed.

E. Benefits

Registration of *Bacillus thuringiensis* subspecies Cry1F protein and the genetic material necessary for its production (plasmid insert PHI 8999) in corn is in the public interest because the new pesticide is comparatively less risky to health or the environment than currently registered pesticides and the benefits (including economic benefits) from the use of the new active ingredient exceed those of alternative registered pesticides and other available non-chemical techniques.

V. DATA GAPS

The following data was determined necessary to complete the pending products= database for registration until September 30, 2001.

1) A longer soil degradation study in actual field soil.

There is no evidence to indicate that prolonged exposure to trace amounts of Cry protein in the soil affects non-target organisms. The submitted data do not, however, sufficiently address the issue of residual Cry protein accumulation in the soil. The soil degradation study should be carried out for a longer period of time to determine the duration and the amount of residual Cry 1F protein in agricultural soil. Also, the soil used in the study should be actual field soil containing the microbial flora normally found in the field. This will give a more accurate rate of degradation of the Cry protein in the agricultural environment because microbial populations in the rhizosphere are commonly 100 fold higher than in bulk soil. Bulk soil generally does not support populations of microorganisms as high as those in the rhizosphere or those in soils with high organic content (plant residues). In addition, field soil high in organic content should result in lower (if any) soil binding of Cry proteins.

2) Confirmatory Monarch butterfly data.

An additional scientifically sound study submitted by Dow AgroSciences showed that Cry1F is non-toxic to neonate monarch butterfly larvae when fed a #10,000 ng/mL diet dose. First instar larval weight and mortality were recorded after seven days of feeding. There was no mortality to monarchs fed 10,000 ng/mL diet, the highest rate tested. There was some growth inhibition at 10,000 ng/mL diet. Since pollen doses equivalent to 10,000 ng/mL diet are not likely to occur on milkweed leaves in nature, it can be concluded that Cry1F protein will not pose a risk to monarchs.

The conclusions should be confirmed by providing data showing that the amounts of Cry protein found in pollen on milkweed leaves in the field are at concentrations less than the 10,000 ng/mL.

diet used in this study. The NOEC of pollen on milkweed leaves also has to be determined.

3) Continuation of beneficial insect field monitoring.

The beneficial insect monitoring should continue into the first few years of commercial use of Cry1F corn crops to confirm the single season Anso effects findings and to gather data on long range non-target insect effects and abundance.

4) Insect resistance management data.

The registrants will confer with the EPA as the registrants develop various aspects of its resistance management research program. The registrants agree, as a condition of these registrations, to generate data and to submit annually progress reports on or before January 31st each year on the following areas as a basis for developing a long-term resistance management strategy which include:

a) The registrants must submit available research data on CEW relative to resistance development and the registrants= plans for producing resistance predictive models to cover regional management zones in the cotton belt based on Helicoverpa zea biology and cotton, corn, soybeans, and other host plants. These models must be field tested and must be modified based on the field testing performed during the period of the conditional registration. EPA might modify the terms of the conditional registration based upon the field testing validation of the model and might require refuge in the future. EPA notes that there is some scientific work and even some models for H. zea on other crops in at least NC and TX that could be used for reference. EPA wants to be in close communication with the registrants as the model development and testing is ongoing. The requirement for development of resistance predictive models may be modified if the registrants provide the results of research that demonstrates resistance to CEW would have no significant impact on the efficacy of foliar Bt products and other Bt crops. Actual usage data of Bta on crops to control specific pests as well as successes and failures and field validated research would be necessary to support such a waiver request.

b) ECB pest biology and behavior including adult movement and mating patterns, larval movement, survival on silks, kernels, and stalks, and overwintering survival and fecundity on non-corn hosts. A combination of a comprehensive literature review and research can fulfill this condition.

c) The feasibility of "structured" refuge options for ECB including both "block" refuge, "50-50 early/late season patchwork;" research needs to be done in both northern and southern areas on ECB as well as CEW.

d) Development of a discriminating concentration (diagnostic concentration) assay for field resistance (field screening) for ECB, CEW and SWCB. Sampling will be done in accordance with the Industry Plan to determine if increases in Cry1F toxin tolerance are occurring before

crop failures develop. Increased tolerance levels need to be identified before field failure occurs. In monitoring for tunneling damage, the number of trivial tunnels may be less indicative of resistance development than the total extent of tunneling damage (e.g. length of tunnels). The extent of tunneling damage must be monitored as well as the number of tunnels.

e) Effects of corn producing the Cry1F delta endotoxin on pests other than ECB, including but not limited to CEW, fall armyworm, and the stalk borer complex.

f) The biology of ECB resistance including receptor-mediated resistance and its potential effect on population fitness, as well as the effects on insect susceptibility to other Cry proteins.

g) You must assess the feasibility of using the F2 screen, sentinel plots, and in-field screening kits to increase the sensitivity of resistance monitoring in 2001. By January 31, 2002, you must provide the Agency with the results from these investigations.

h) You must implement a survey approach similar to the Iowa State University Bt Corn Survey (e.g., Pilcher and Rice, 1999) A statistically valid sample, as determined by Independent market research, of Bt corn growers in key states will be surveyed by a third-party. Bt corn growers will be included based upon a proportionately stratified random sample designed to balance the survey evenly across seed companies and geographies. In addition to demographic information, the survey will include questions related to insect resistance management such as:

- 1) What is your primary source of information on Bt corn?
- 2) What percentage of your acres were planted to Bt corn this year?
- 3) Are you following a recommended insect resistance management strategy?
- 4) If you plant most of your acreage to Bt corn, are you likely to scout your non-Bt corn for economically damaging populations of corn borers?
- 5) Did you treat your Bt corn acres with an insecticide?
- 6) What planting pattern did you use for your refuge?
 - ° Planted Bt corn as one block in one field.
 - ° Planted Bt corn in one block in every field.
 - ° Split seed boxes in the planter and alternated every row or several rows with Bt and non-Bt corn in every field.
 - ° Planted Bt corn in large strips alternated with large strips of a non-Bt corn hybrid.
 - ° Planted Bt corn in an entire field and planted the border around the field with non-Bt corn.
 - ° Planted pivot corners to non-Bt corn with the irrigated area of the

field planted to Bt corn.

5) Analytical methods and method validation for the Cry1F protein in corn have been received and are acceptable, but additional confirmatory methods and standard post-registration EPA laboratory method validation are required.

Although, Cry1F protein plant root expression and exudation data and a 6 week avian feeding study with 60 -70% Cry1F corn in the diet were identified as deficiencies for a non-expiring full commercial use registration, they are not considered data gaps for a registration expiring on September 30, 2001. At this time in the reassessment process, these data have not been required of other Bt corn plant-pesticide registrants.

VI.. CONTACT PERSON AT EPA

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Arlington, VA 22202
[REDACTED]
[REDACTED]

DISCLAIMER: The information in this Pesticide Fact Sheet is a summary only and is not to be used to satisfy data requirements for pesticide registration. Contact the Regulatory Action Leader listed above for further information.

A446

This study does not use
Corn line 1507 but another
line expressing cryIF.1. Not
used in safety assessment.

TRANSGENIC CORN EXPRESSING *Bacillus thuringiensis* var. *aizawai* (Bt) CRYIF DELTA-
ENDOTOXIN:

A DIETARY TOXICITY STUDY WITH THE NORTHERN BOBWHITE

WILDLIFE INTERNATIONAL LTD. PROJECT NO.: 354-116

FIFRA SUBDIVISION E, SECTION 71-2

AUTHORS:



STUDY INITIATION: July 22, 1999

STUDY COMPLETION: December 14, 1999

SUBMITTED TO

Mycogen c/o Dow AgroSciences LLC Corporation
5501 Oberlin Drive
San Diego, California 92121

Wildlife International, Ltd.

8598 Commerce Drive
Easton, Maryland 21601

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STATEMENT OF NO DATA CONFIDENTIALITY CLAIMS

No claim of confidentiality is made for any information contained in this study on the basis of its falling within the scope of FIFRA section 10(d) (1)(A), (B), or (C).

Company: Mycogen Seeds c/o Dow AgroSciences LLC (Typed Name)

Company Agent: [REDACTED] (Typed Name)

Title: Registration Manager

Signature: [REDACTED]

Date: 12/15/99

- 3 -

GOOD LABORATORY PRACTICE COMPLIANCE STATEMENT

SPONSOR: Mycogen Corporation c/o Dow AgroSciences LLC

TITLE: Transgenic Corn Expressing *Bacillus thuringiensis* var. *aizawai* (Bt) Cry1F delta-endotoxin:
A Dietary Toxicity Study with the Northern Bobwhite

WILDLIFE INTERNATIONAL LTD. PROJECT NO.: 354-116

STUDY COMPLETION: December 14, 1999

This study was conducted in compliance with Good Laboratory Practice Standards as published by the U.S. Environmental Protection Agency, 40 CFR Part 160, 17 August 1989; OECD Principles of Good Laboratory Practice, (ENV/MC/CHEM (98) 17); and Japan MAFF, 59 NohSan, Notification No. 3850, Agricultural Production Bureau, 10 August 1984, with the following exceptions:

Homogeneity of the test substance in the diet was not determined. The stability of the test substance under the conditions of storage at the test site was not conducted in compliance with Good Laboratory Practice Standards.

STUDY DIRECTOR:

DATE

12/14/99

Senior Biologist

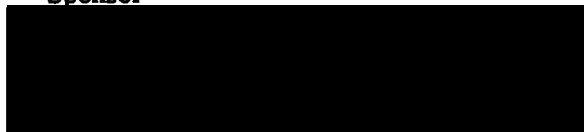
SPONSOR'S APPROVAL:

Mycogen Seeds c/o Dow AgroSciences LLC

DATE

12/15/99

Sponsor



DATE

12/15/99

This study was examined for compliance with Good Laboratory Practice Standards as published by the U.S. Environmental Protection Agency, 40 CFR part 160, 17 August 1989; OECD Principles of Good Laboratory Practice, (ENV/MC/CHEM (98) 17); and Japan MAFF, 59 NohSan, Notification No. 3850, Agricultural Production Bureau, 10 August 1984. The dates of all audits and inspections and the dates any findings were reported to the Study Director and Laboratory Management were as follows. Reviews conducted by Monsanto AG Regulatory Quality Assurance Unit are included in the Quality Assurance Statement for the analytical subreport in Appendix III.

ACTIVITY	DATE CONDUCTED	DATE REPORTED TO:	
		STUDY DIRECTOR	MANAGEMENT
Diet preparation and Test Substance Preparation	July 22, 1999	July 22, 1999	July 22, 1999
Feed Consumption and Analytical Sampling	July 27, 1999	July 27, 1999	August 9, 1999
Biological Data and Draft Report	November 1-3, 1999	November 3, 1999	November 5, 1999
Final Report	December 9, 1999	December 9, 1999	December 9, 1999

DATE 12/14/99
Manager, Regulatory and Technical Support

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REPORT SIGNATURE PAGE

This report accurately represents the data developed during the study.

PREPARED
BY:

[REDACTED]

Senior Biologist

12/14/99
Study Completion Date

APPROVED
BY:

[REDACTED]

Director, Avian Toxicology

12/14/99
Study Completion Date

[REDACTED]

Manager, Regulatory and Technical Support

12/14/99
Date

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SUMMARY

SPONSOR: Mycogen Corporation c/o Dow AgroSciences LLC

TEST SUBSTANCES: A genetically modified corn line expressing *Bacillus thuringiensis* var. *aizawai* (Bt) Cry1F delta-endotoxin

CONTROL SUBSTANCES: A non-genetically modified corn line with a similar genetic background

WILDLIFE INTERNATIONAL, LTD. PROJECT NO.: 354-116

STUDY: Transgenic Corn Expressing *Bacillus thuringiensis* var. *aizawai* (Bt) Cry1F delta-endotoxin: A Dietary Toxicity Study with the Northern Bobwhite

RESULTS: The dietary LC50 value for northern bobwhite exposed to transgenic corn expressing *Bacillus thuringiensis* var. *aizawai* (Bt) Cry1F delta-endotoxin from a genetically modified corn line was estimated to be greater than 100,000 ppm (10% of diet), the highest concentration tested. The no mortality concentration and the no-observed-effect concentration were 100,000 ppm.

TEST DATES: Hatch - July 12, 1999
Acclimation - July 12, 1999 to July 22, 1999
Experimental Start - July 22, 1999
Biological Termination - July 30, 1999
Analytical Termination - November 18, 1999

NOMINAL TEST

CONCENTRATIONS: 100,000 ppm (10% of diet)

TEST ANIMALS: Northern Bobwhite (*Colinus virginianus*)

AGE TEST ANIMALS: 10 days of age at test initiation

SOURCE TEST ANIMALS: Wildlife International, Ltd. Production Flock
8598 Commerce Drive
Easton, Maryland 21601

STUDY COMPLETION: December 14, 1999

INTRODUCTION

This study was conducted by Wildlife International, Ltd. for Dow AgroSciences LLC/Mycogen Corporation at the Wildlife International, Ltd. toxicology facility in Easton, Maryland. The in-life portion of the test was conducted from July 22, 1999 to July 30, 1999. Raw data generated at Wildlife International, Ltd. and a certified copy of the final report are filed under Project Number 354-116 in archives located on the Wildlife International, Ltd. site.

OBJECTIVE

The objective of this study was to evaluate the effects of corn grain (meal) expressing *Bacillus thuringiensis* var. *aizawai* (Bt) Cry1F delta-endotoxin, when administered to juvenile northern bobwhite in the diet for five days.

MATERIALS AND METHODS

The methods used in conducting this study are based upon procedures specified in Section 71-2 of the U.S. Environmental Protection Agency's Registration Guidelines, *Pesticide Assessment Guidelines, FIFRA Subdivision E, Hazard Evaluation: Wildlife and Aquatic Organisms* (1) and upon ASTM Standard E857-87, "Standard Practice for Conducting Subacute Dietary Toxicity Tests with Avian Species" (2).

Test and Control Substances

The test substance was ground corn seed from a corn line genetically modified to express *Bacillus thuringiensis* var. *aizawai* (Bt) Cry1F delta-endotoxin to provide protection against certain insect pests. The test substance was received from Dow AgroSciences LLC on July 1, 1999 and was assigned Wildlife International, Ltd. Identification Number 4999. It was identified as: Transgenic Corn Seed (Cry1F TR) TSN 101791; Lot No. 2722} RL0016. A summary of the GLP characterization of the test substance is presented in Appendix I.

The control substance was ground corn grain from a corn line that is genetically similar to the test substance. The control substance was received from Dow AgroSciences LLC on July 1, 1999 and was assigned Wildlife International, Ltd. Identification number 5000. The control substance was

identified as: Control Substance Corn Seed TSN 101792; Lot No. 2722. The test and control substances were stored frozen at approximately -20°C.

Treatment Groups

The test consisted of a genetically modified corn line (test substance) and a non-genetically modified parental line (control substance). Bobwhite chicks were assigned to each corn line by indiscriminate draw. Each line tested included six replicates of five birds each. Bobwhite chicks were fed diet containing 10% of the appropriate test or control substance and 90% basal ration for 5 days. Following the five day exposure period all groups were given untreated basal diet for three days.

Duration of the Test

The primary phases of this test and their durations were:

1. Acclimation - 10 days.
2. Exposure - 5 days.
3. Post-exposure observation - 3 days.

Test Birds

All northern bobwhite (*Colinus virginianus*) were 10 days of age and appeared to be in good health at initiation of the test. The birds were obtained from Wildlife International, Ltd. Production Flock, Easton, MD and were hatched on July 12, 1999. Birds ranged in weight from 18 to 23 grams at test initiation. All birds were from the same hatch, pen-reared and phenotypically indistinguishable from wild birds. All birds were acclimated to the caging and facilities from the day of hatch until initiation of the test.

Birds were assigned to two experimental groups. Each group contained thirty chicks. Birds were housed in brooding pens containing five birds each. The birds used in this study were immature and could not be differentiated by sex.

Animal Diet

All test birds were fed a game bird ration formulated to Wildlife International, Ltd.'s specifications (Appendix II) throughout acclimation and testing. The chicks were given a vitamin

supplement in their water from the day they were hatched until the initiation of the test. Water, from the town of Easton public water supply, and feed were provided ad libitum during acclimation and during the test. The birds received no form of antibiotic medication during acclimation or the test.

Diet Preparation

Test diets were prepared by incorporating the appropriate test and control substances directly into basal ration using a Hobart (Model Number AS200T) mixer (Appendix III). An amount of diet sufficient to last the five-day exposure period was prepared on the day of the test initiation and stored frozen. The birds were presented a portion of the diet daily during the exposure period.

Diet Sampling

Samples of diets for the test and control substances were collected at Day 0 and Day 5. One verification sample was collected from each diet at preparation on Day 0. At the end of the exposure period (Day 5), one sample was collected from each treatment group diet. The day 5 samples were collected from feed composited by treatment group remaining in the feeders. Samples were stored frozen until transferred to Mycogen Corporation c/o Dow AgroSciences LLC.

Analysis of Diet

The diet samples were shipped to the Sponsor and analyzed for the presence of Cry1F delta-endotoxin protein to confirm the identity of the test substance (Appendix I).

Housing and Environmental Conditions

During acclimation and testing, all birds were housed indoors in batteries of thermostatically controlled brooding pens manufactured by Beacon Steel Products Co. (Model No. B735Q). Each pen had floor space that measured approximately 72 X 90 cm. Ceiling height was approximately 23 cm. External walls, ceilings and floors were constructed of galvanized steel wire and sheeting.

Birds were assigned to pens by indiscriminate draw. Each group of birds was identified by pen number and test concentration. Individual birds were identified by colored leg bands. Six pens that contained five chicks each were assigned to each corn line.

During the test the average temperature in the brooding compartment of the pens was $38.0^{\circ}\text{C} \pm 2.0^{\circ}\text{C}$ (SD). Average ambient room temperature for this study was $28.5^{\circ}\text{C} \pm 0.8^{\circ}\text{C}$ (SD) with an average relative humidity of $62\% \pm 8\%$ (SD). The photoperiod (maintained by a time clock) was sixteen hours of light per day during acclimation and throughout the test. The light source was fluorescent lights which closely approximate noon-day sunlight. The birds were exposed to an average of approximately 254 lux of illumination.

Housing and husbandry practices were based on guidelines established by the National Research Council (3).

Observations

All birds were observed daily during acclimation. Birds exhibiting abnormal behavior or physical injury were not used. All birds were observed at least twice daily following test initiation through Day 8 of the test. A record was maintained of all mortality, signs of toxicity and abnormal behavior.

Animal Body Weights/Feed Consumption

Individual body weights were measured at the initiation of the test, on Day 5, and at termination of the test on Day 8. Average feed consumption values were determined by pen for each day of the exposure period (Days 1, 2, 3, 4, 5) and for the post-exposure observation period (Days 6-8). Feed consumption was determined by measuring the change in the weight of the feed presented to the birds over a given period of time. The accuracy of feed consumption values may have been affected by the unavoidable wastage of feed by the birds.

Statistical Analyses

Because no mortalities occurred in the treatment groups, an LC50 value could not be calculated. However, based upon the biological response obtained in the treatment groups, the toxicity values were estimated to be greater than the highest concentration tested. The no-observed-effect concentrations were determined by evaluation of the mortality, clinical signs, body weight and feed consumption data.

RESULTS

Analysis of Diet

Biochemical analysis by ELISA of diet samples confirmed that the Cry1F protein was present in the Cry1F expressed test substance. The Cry1F protein was not detected in diets containing the control substance corn seed.

Mortalities and Clinical Observations

There were no mortalities in the non-genetically modified parental corn line control group. Two birds in the control group suffered foot lesions as a result of penmate aggression during the course of the test. One bird noted with foot lesions was also noted with wing droop and as lame. Five other control birds were noted as nostril-picked, another form of penmate aggression, on Day 5 of the test. Otherwise, all birds in the control group were normal in appearance and behavior throughout the test.

There were no mortalities or overt signs of toxicity in the genetically modified corn line tested. One bird was noted limping and with foot lesions on Day 8 of the test. All other birds in this group were normal in appearance and behavior for the duration of the test.

Body Weight and Feed Consumption

When compared to the non-genetically modified parental corn line control group, there were no apparent treatment related effects on body weight or feed consumption in the genetically modified corn line tested (Tables 2 and 3 and Appendices V and VI).

CONCLUSION

The dietary LC50 value for northern bobwhite exposed to transgenic corn expressing *Bacillus thuringiensis* var. *aizawai* (Bt) Cry1F delta-endotoxin from a genetically modified corn line, was estimated to be greater than 100,000 ppm (10% of diet), the highest concentration tested. The no mortality concentration and the no-observed-effect concentration were 100,000 ppm.

REFERENCES

- 1 U.S. Environmental Protection Agency. 1982. *Pesticide Assessment Guidelines, FIFRA Subdivision E, Hazard Evaluation: Wildlife and Aquatic Organisms*, subsection 71-2, Environmental Protection Agency, Office of Pesticide Programs. Washington, D.C.
- 2 American Society for Testing and Materials. 1987. Standard Practice for Conducting Subacute Dietary Toxicity Tests with Avian Species. ASTM Standard E857-87. Annual Book of ASTM Standards, Vol. 11.04. Philadelphia, PA.
- 3 National Research Council. 1996. *Guide for the Care and Use of Laboratory Animals*. Washington, D.C. National Academy Press. 125 pp.

TABLE 1
Cumulative Mortality from a Northern Bobwhite Acute Dietary
Toxicity Study with Transgenic Corn Expressing *Bacillus thuringiensis* var. *aizawai* (Bt) Cry1F delta-endotoxin

Experimental Group	No. Dead Per No. Exposed Exposure Period						No. Dead Per No. Exposed Post-Exposure Period		
	Day 0	Day 1	Day 2	Day 3	Day 4	Day 5	Day 6	Day 7	Day 8
Corn Seed TSN 101792 (Control)	0/30	0/30	0/30	0/30	0/30	0/30	0/30	0/30	0/30
Corn Expressing Bt Cry1F delta-endotoxin TSN 101791	0/30	0/30	0/30	0/30	0/30	0/30	0/30	0/30	0/30

The toxicity value was estimated to be greater than 100,000 ppm, the highest concentration tested.

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TABLE 2
Mean Body Weight (g) from a Northern Bobwhite Acute Dietary Toxicity Study
with Transgenic Corn Expressing *Bacillus thuringiensis* var. *aizawai* (Bt) Cry1F delta-endotoxin

Experimental Group		Exposure Period			Post-Exposure Period		Total Change ¹
		Day 0	Change ¹	Day 5	Change ¹	Day 8	
Corn Seed TSN 101792 (Control)	Mean	21	9	29	8	37	17
	SD	1	4	4	3	7	6
Corn Expressing Bt Cry1F delta-endotoxin TSN 101791	Mean	20	9	29	7	37	17
	SD	1	2	3	3	6	5

¹Mean change is calculated separately from the mean body weights using individual body weights (See Appendix V).

TABLE 3

Mean Feed Consumption (g/bird/day) from a Northern Bobwhite Acute Dietary Toxicity Study with Transgenic Corn Expressing *Bacillus thuringiensis* var. *aizawai* (Bt) Cry1F delta-endotoxin

Experimental Group		Exposure Period					Post-Exposure Period
		Days 0-1	1-2	2-3	3-4	4-5	6-8
Corn Seed TSN 101792 (Control)	Mean	7	7	8	8	7	9
	SD	1	1	1	1	1	1
Corn Expressing Bt Cry1F delta-endotoxin TSN 101791	Mean	6	6	9	8	8	9
	SD	1	1	2	1	1	3

APPENDIX I
TEST SUBSTANCE CHARACTERIZATION

Dow AgroSciences LLC
Study ID: 990027
Page 1 of 2

SUMMARY

(In accordance with 40 CFR part 152, this summary is available
for public release after registration)

STUDY TITLE

Characterization of Expressed Cry1F Protein in Maize Tissues (Pollen, Grain, Grain-Containing
Feed, and Purified Maize-Expressed Cry1F Protein) and Microbial Expressed Cry1F Delta
Endotoxin by Biological and Biochemical Procedures

DATA REQUIREMENTS

Not Applicable

AUTHORS

██████████

STUDY COMPLETED ON

November 18, 1999

PERFORMING LABORATORIES

Global Environmental Chemistry Laboratory—Indianapolis Lab
Dow AgroSciences LLC
9330 Zionsville Road
Indianapolis, Indiana 46268-1054

Pioneer Hi-Bred International
7300 NW 62nd Ave.
Johnston, Iowa 50131

LABORATORY STUDY ID

990027

Delta AgriSciences LLC
Study ID: 000027
Page 2 of 2

Characterization of Expressed Cry1F Protein in Maize Tissues (Pollen, Grain, Grain-Containing Feed, and Purified Maize-Expressed Cry1F Protein) and Microbial Expressed Cry1F Delta Endotoxin by Biological and Biochemical Procedures

SUMMARY

This report contains characterization information of maize lines that have been modified to express the Cry1F protein to support regulatory submissions including equivalency and toxicological studies. Maize tissues expressing Cry1F protein (pollen, grain, grain-containing feed and purified maize-expressed Cry1F protein) and microbial expressed Cry1F protein were evaluated and characterized by biological and biochemical analysis. The biological analysis results confirmed the biological activity of the pollen, grain, purified maize-expressed Cry1F protein and bacterially derived Cry1F protein when tested with susceptible insect species, either European corn borer or tobacco budworm. The biochemical analysis was performed to quantify and characterize the extractable Cry1F protein of the pollen, grain, purified maize-expressed Cry1F protein and bacterially derived Cry1F protein. The biochemical analysis of the tissues included ELISA and SDS-PAGE followed by Western Blotting. Biochemical analysis data demonstrated the test materials contained immunoreactive Cry1F protein at the expected molecular weight.

Dow AgroSciences LLC
Study ID: 990027
Page 1 of 71

STUDY TITLE

Characterization of Expressed Cry1F Protein in Maize Tissues (Pollen, Grain, Grain-Containing Feed, and Purified Maize-Expressed Cry1F Protein) and Microbial Expressed Cry1F Delta Endotoxin by Biological and Biochemical Procedures

DATA REQUIREMENTS

Not Applicable

AUTHORS

[REDACTED]
[REDACTED]
[REDACTED]

STUDY COMPLETED ON

November 18, 1999

PERFORMING LABORATORY

Global Environmental Chemistry Laboratory—Indianapolis Lab
Dow AgroSciences LLC
9330 Zionsville Road
Indianapolis, Indiana 46268-1054

Pioneer Hi-Bred International
7300 NW 62nd Ave.
Johnston, Iowa 50131

LABORATORY STUDY ID

990027

Dow AgroSciences LLC
Study ID: 990027
Page 2

STATEMENT OF NO DATA CONFIDENTIALITY CLAIMS

Compound: Cry1F Delta Endotoxin Protein

Title: Characterization of Expressed Cry1F Protein in Maize Tissues (Pollen, Grain, Grain-Containing Feed, and Purified Maize-Expressed Cry1F Protein) and Microbial Expressed Cry1F Delta Endotoxin by Biological and Biochemical Procedures

No claim of confidentiality is made for any information contained in this study on the basis of its falling within the scope of FIFRA Section 10 (d)(1)(A)(B), or (C).*

Company: Dow AgroSciences LLC

Company Agent: [REDACTED]

Title: Regulatory Manager

Signature: [REDACTED]

Date: 11/17/99

*In the United States, the above statement supersedes all other statements of confidentiality that may occur elsewhere in this report.

THIS DATA MAY BE CONSIDERED CONFIDENTIAL IN COUNTRIES OUTSIDE THE UNITED STATES.

Dow AgroSciences LLC
Study ID: 990027
Page 3

STATEMENT OF COMPLIANCE WITH GOOD LABORATORY PRACTICE STANDARDS

Title: Characterization of Expressed Cry1F Protein in Maize Tissues (Pollen, Grain, Grain-Containing Feed, and Purified Maize-Expressed Cry1F Protein) and Microbial Expressed *Cry1F* Delta Endotoxin by Biological and Biochemical Procedures

Study Initiation Date: August 4, 1998 **Study Completion Date:** November 18, 1999
Experimental Start Date: August 4, 1998 **Experiment Termination Date:** September 24, 1999

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

Organisation for Economic Co-Operation and Development
ISBN 92-64-12367-9, Paris 1982

At Pioneer Hi-Bred, during the first three biological experiments (8/98, 9/98, and 2/99) the laboratory was working towards being GLP compliant; therefore, several GLP-required elements were not yet in place. GLP training and personnel record information was instituted for scientists performing bioassay tests during the course of this study. Protocols and SOPs had been approved, and Quality Assurance conducted in-phase inspections but in some instances SOPs were not present or available during the conduct of the study. On several occasions data were not recorded or corrected exactly as required by GLPs. Maintenance logs were not in place for some equipment used in the study, some reagents were not properly labeled and calibrations were not always performed. The GLP required documentation of the two reference substances used in the biochemical study was not performed (the bacterially derived Cry1F protein and the BioRad BSA protein).

At Dow AgroSciences, management-approved SOPs specific to the insect bioassay were not in place. The GLP required documentation for reference standards were not met.

[Redacted Signature]
Dow AgroSciences LLC

11/17/99
Date

[Redacted Signature]
Dow AgroSciences LLC

11/17/99
Date

[Redacted Signature]
Dow AgroSciences LLC

11/18/99
Date

Dow AgroSciences LLC
Study ID: 990027
Page 4

**Dow AgroSciences Quality Assurance Unit
Good Laboratory Practice Statement Page**

Compound: Cry IF Protein

Study ID: 990027

Title: Characterization of Expressed CryIF Protein in Maize Tissues (Pollen, Grain, Grain Containing Feed, and Purified Maize-Expressed CryIF Protein) and Microbial Expressed CryIF Delta Endotoxin by Biological and Biochemical Procedures

Study Initiation Date: 8/4/98

Study Completion Date: 11/18/99

GLP Quality Assurance Inspections		
Date of GLP Inspection(s)	Date Reported to the Study Director and to Management	Phases of the Study which received a GLP Inspection by the Quality Assurance Unit
8/4/98	8/12/98	Elisa, extraction, Bradford assay, Bioassay of pollen (PHI)
2/23/99	3/1/99	Bioassay of microbial tox lot
6/17/99	6/18/99	Bioassays of pollen, microbial protein (PHI)
8/11/99	8/12/99	Bioassay for Amendment 8 - Test/Control substance preparation, dilution, application, test system placement
8/19/99	8/25/99	Sample prep for Elisa assay of corn grain, quail and fish feed
9/22/99	9/23/99	Raw data and draft report (PHI)
9/22-24/99	9/24/99	Raw data and draft report (PHI)
11/1-4/99	11/16/99	Raw data and draft report

QUALITY ASSURANCE STATEMENT:

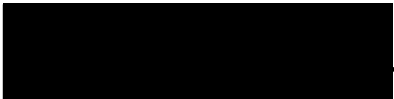
The Quality Assurance Unit has reviewed the final study report and has determined that the report reflects the raw data generated during the conduct of this study.


Dow AgroSciences, Quality Assurance


11/18/99
Date

Dow AgroSciences LLC
Study ID: 990027
Page 5

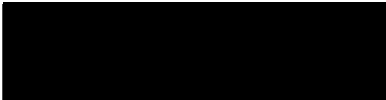
SIGNATURE PAGE

 _____ 11/18/99
Date


Author
Dow AgroSciences LLC

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Date

Co-Author
Dow AgroSciences LLC

 _____ 10/21/99
Date

Reviewer
Dow AgroSciences LLC

 _____ 10/21/99
Date

Reviewer
Dow AgroSciences LLC

 _____ 10/21/99
Date

Reviewer

 _____ 10/21/99
Date

Reviewer
Dow AgroSciences LLC

 _____ 10/21/99
Date

Global ECL Group Leader
Dow AgroSciences LLC

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Study ID: 990027
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Characterization of Expressed Cry1F Protein in Maize Tissues (Pollen, Grain, Grain-Containing Feed, and Purified Maize-Expressed Cry1F Protein) and Microbial Expressed Cry1F Delta Endotoxin by Biological and Biochemical Procedures

ABSTRACT

This report contains characterization information used in support of regulatory submissions for maize lines that have been modified to express the Cry1F protein. The activity of maize tissues expressing Cry1F protein (pollen, grain, grain-containing feed and purified maize-expressed Cry1F protein) and microbial derived Cry1F protein were evaluated and characterized by biological and biochemical analysis.

Biological analysis of the purified maize-expressed Cry1F protein, the bacterially derived Cry1F protein, and maize pollen test substances demonstrates that the Cry1F protein present in all test substances was active against European corn borer (ECB) at all time points tested. Activity of each test substance analyzed is summarized in the following table:

ECB Potency

Test Substance	Activity
1507 - Maize pollen	100% mortality at high dose of 0.2 mg Cry1F/ μ L buffer diet overlay
5XH751 - Control pollen	No activity
1568-022A - Purified Maize-expressed Protein Control	0-36% Mortality
1568-022B - Purified Maize-expressed Cry1F Protein	LC ₅₀ = <0.03 μ g Cry1F/mL diet
101788 - Microbial Cry1F Powder	LC ₅₀ = <0.02 μ g - 0.06 μ g Cry1F/mL diet

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The potency of the test substance against tobacco budworm (TBW) was measured by determining the GI_{50} (concentration that inhibits growth by 50%). LC_{50} s (concentration that kills 50% of the insects) were not useful for indexing the potency of the test substances due to insufficient mortality at the highest concentrations tested. Biological analysis of the maize grain and feeds containing maize grain with TBW are summarized in the following tables:

TBW Potency Estimates with Cry1F Maize Grain, Quail Feed, and Fish Feed

Test Substance	GI_{50} (95% confidence limits) in % Cry1F Maize Grain ^a
maize grain expressing Cry1F	0.15 (0.07-0.32)
0-day quail feed containing Cry1F expressing maize	0.15 (0.06-0.41)
5-day quail feed containing Cry1F expressing maize	0.20 (0.05-0.77)
fish feed containing Cry1F expressing maize	>7.7

^aExpressed as a percent of maize grain expressing Cry1F applied in the treatment suspensions.

TBW Weights with Fish Feed at 7.7% Maize

Test Substance	Insect Weight (mg)
Cry1F fish feed	875.7 ^a
control fish feed	1032.3 ^a
agar control	1214.9 ^a
2:1 acetone:water	1253.7 ^a

^aThe means were not significantly different ($\alpha = 0.05$) based on analysis of variance (1).

TBW results demonstrate comparable activity between the maize grain and the maize grain component of the quail feed. No statistically significant difference in activity was observed between fish feed containing Cry1F and the three controls.

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Biochemical analysis by ELISA of the purified maize-expressed Cry1F protein, microbial derived Cry1F protein, maize grain, feeds containing maize grain and maize pollen test substances demonstrate that the Cry1F protein was present in all Cry1F expressed test substances. The range of quantitation of extractable Cry1F protein is summarized in the following table:

Test and Control Substances (sample number and identification)	Cry1F Concentration (ng Cry1F/mg) ^a
1507 - Maize pollen	30.7 - 32.8
5XH751 - Control pollen	ND ^b
1568-022A - Purified Maize-expressed Protein Control	ND
1568-022B - Purified Maize-expressed Cry1F Protein	1511.33 ± 268.9
101788 - Microbial Cry1F Powder	114,000
TSN101791 - maize grain containing Cry1F	2.2 - 3.5
TSN101792 - Control maize	ND
TSN101834 - fish feed containing control maize	ND
TSN101835 - fish feed containing Cry1F expressing maize	ND
TSN101862 - quail feed, Day 0 containing Cry1F expressing maize	0.2 - 1.1
TSN101863 - quail feed, Day 0 containing control maize	ND
TSN101864 - quail feed, Day 5 containing Cry1F expressing maize	0.2 - 0.6

^a ng Cry1F/mg of tissue or powder weighed.

^b ND = not detectable, below the limit of detection of the ELISA (0.04 ng/mg), 5 mg sample extracted.

Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and Western immunoblotting results indicated an expected immunoreactive molecular weight band of ~64kDa as previously reported (2) in both the microbial expressed Cry1F protein and the maize grain expressed Cry1F protein.

APPENDIX II

DIET FORMULATION
WILDLIFE INTERNATIONAL, LTD. GAME BIRD RATION¹

INGREDIENTS	PERCENT (%)
Fine Corn Meal	44.83
Soy Bean Meal, 48% Protein	30.65
Wheat Midds	6.50
Protein Base	6.00
Agway Special, 60% Protein	4.00
Alfalfa Meal, 20% Protein	3.00
Dried Whey	2.50
Ground Limestone	0.90
Eastman CalPhos	0.60
Methionine Premix + Liquid	0.35
Vitamin and Mineral Premix (see below)	0.32
GL Ferm (Fermatco) ²	0.25
Salt Iodized	0.10
Total	100.00

VITAMIN AND MINERAL PREMIX

AMOUNT ADDED PER TON

Vitamin D ₃	2,000,000 I.C.U.
Vitamin A	7,000,000 I.U.
Riboflavin	6 grams
Niacin	40 grams
Pantothenic Acid	10 grams
Vitamin B ₁₂	8 mgs
Folic Acid	600 mgs
Biotin	64 mgs
Pyridoxine	1.2 grams
Thiamine	1.2 grams
Vitamin E	20,000 I.U.
Vitamin K (Menadione Dimethylpyrimidinol Bisulfite)	5.8 grams
Manganese	102 grams
Zinc	47 grams
Copper	6.8 grams
Iodine	1.5 grams
Iron	51 grams
Selenium	182 mgs

¹ The guaranteed analysis is a minimum of 27% protein, a minimum of 2.5% crude fat and a maximum of 5% crude fiber.

² Fermentation By-Products (Source of Unidentified Growth Factors).

APPENDIX III
DIET PREPARATION

Weight of constituents used to prepare diet:

Experimental Group	Control or Test Substance (g)	Basal Ration (g)
Corn Seed TSN 101792 (Control)	900.0	8100.0
Corn Expressing Bt Cry1F delta-endotoxin TSN 101791	900.0	8100.0

Diets were prepared as follows:

- 5000.0 g of basal ration was weighed into a tared Hobart mixing bowl.
- The bowl was retared and 900.0 grams of the appropriate test or control substance was added to the mixing bowl.
- An additional 3100.0 grams of basal ration was weighed and added to the bowl.
- All constituents were mixed in the Hobart mixer for approximately 10 minutes.
- The experimental diets were placed in labeled bags.

APPENDIX IV
Cumulative Mortality by Pen from a Northern Bobwhite Acute Dietary Toxicity Study
with Transgenic Corn Expressing *Bacillus thuringiensis* var. *aizawai* (Bt) Cry1F delta-endotoxin

Experimental Group	No. Dead Per No. Exposed Exposure Period							No. Dead Per No. Exposed Post-Exposure Period		
	Pen	Day 0	Day 1	Day 2	Day 3	Day 4	Day 5	Day 6	Day 7	Day 8
Corn Seed TSN 101792 (Control)	1	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5
	2	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5
	3	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5
	4	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5
	5	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5
	6	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5
Corn Expressing Bt Cry1F delta-endotoxin TSN 101791	1	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5
	2	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5
	3	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5
	4	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5
	5	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5
	6	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5	0/5

The LC50 value was estimated to be greater than 100,000 ppm, the highest nominal concentration tested.

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APPENDIX V

Individual Body Weights (g) from a Northern Bobwhite
 Acute Dietary Toxicity Study with Transgenic Corn Expressing *Bacillus thuringiensis* var. *aizawai*
 (Bt) Cry1F delta-endotoxin
 Page 1

Experimental Group	Bird	Day 0	Change	Day 5	Change	Day 8	Total Change
Corn Seed TSN 101792 (CONTROL)	1	19	1	20	5	25	6
	2	20	5	25	6	31	11
	3	19	3	22	5	27	8
	4	20	7	27	8	35	15
	5	21	9	30	10	40	19
	Mean	20	5	25	7	32	12
	SD	1	3	4	2	6	5
	1	23	6	29	7	36	13
	2	21	9	30	10	40	19
	3	22	12	34	9	43	21
	4	18	10	28	10	38	20
	5	21	10	31	7	38	17
	Mean	21	9	30	9	39	18
	SD	2	2	2	2	3	3
	1	22	10	32	9	41	19
	2	22	13	35	8	43	21
	3	20	10	30	5	35	15
	4	20	6	26	5	31	11
	5	18	10	28	8	36	18
	Mean	20	10	30	7	37	17
	SD	2	2	3	2	5	4
	1	20	9	29	9	38	18
	2	19	-3	16	-2	14	-5
	3	21	11	32	11	43	22
	4	22	11	33	10	43	21
	5	22	10	32	8	40	18
	Mean	21	8	28	7	36	15
	SD	1	6	7	5	12	11

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APPENDIX V

Individual Body Weights (g) from a Northern Bobwhite
 Acute Dietary Toxicity Study with Transgenic Corn Expressing *Bacillus thuringiensis* var. *aizawai*
 (Bt) Cry1F delta-endotoxin
 Page 2

Experimental Group	Bird	Day 0	Change	Day 5	Change	Day 8	Total Change
Corn Seed TSN 101792 (CONTROL)	1	20	11	31	10	41	21
	2	20	8	28	7	35	15
	3	20	9	29	10	39	19
	4	23	12	35	12	47	24
	5	18	8	26	8	34	16
	Mean	20	10	30	9	39	19
	SD	2	2	3	2	5	4
	1	20	10	30	7	37	17
	2	20	10	30	9	39	19
	3	23	14	37	8	45	22
	4	22	8	30	9	39	17
	5	21	12	33	8	41	20
	Mean	21	11	32	8	40	19
	SD	1	2	3	1	3	2

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APPENDIX V

Individual Body Weights (g) from a Northern Bobwhite
 Acute Dietary Toxicity Study with Transgenic Corn Expressing *Bacillus thuringiensis* var. *aizawai*
 (Bt) Cry1F delta-endotoxin
 Page 3

Experimental Group	Bird	Day 0	Change	Day 5	Change	Day 8	Total Change
Corn Expressing Bt Cry1F delta-endotoxin TSN 101791	1	19	11	30	10	40	21
	2	19	7	26	5	31	12
	3	20	12	32	9	41	21
	4	19	9	28	8	36	17
	5	22	10	32	9	41	19
	Mean	20	10	30	8	38	18
	SD	1	2	3	2	4	4
	1	19	3	22	4	26	7
	2	21	10	31	9	40	19
	3	21	8	29	-1	28	7
	4	18	8	26	0	26	8
	5	20	8	28	0	28	8
	Mean	20	7	27	2	30	10
	SD	1	3	3	4	6	5
	1	23	11	34	8	42	19
	2	19	5	24	4	28	9
	3	23	13	36	11	47	24
	4	19	10	29	10	39	20
	5	21	10	31	8	39	18
	Mean	21	10	31	8	39	18
	SD	2	3	5	3	7	6
	1	20	10	30	7	37	17
	2	20	11	31	11	42	22
	3	20	9	29	8	37	17
	4	23	11	34	8	42	19
	5	19	11	30	8	38	19
	Mean	20	10	31	8	39	19
	SD	2	1	2	2	3	2

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APPENDIX V

Individual Body Weights (g) from a Northern Bobwhite
 Acute Dietary Toxicity Study with Transgenic Corn Expressing *Bacillus thuringiensis* var. *aizawai*
 (Bt) Cry1F delta-endotoxin
 Page 4

Experimental Group	Bird	Day 0	Change	Day 5	Change	Day 8	Total Change
Corn Expressing Bt Cry1F delta-endotoxin TSN 101791	1	20	8	28	8	36	16
	2	18	7	25	7	32	14
	3	20	11	31	9	40	20
	4	19	7	26	9	35	16
	5	21	10	31	8	39	18
	Mean	20	9	28	8	36	17
	SD	1	2	3	1	3	2
	1	20	12	32	8	40	20
	2	19	3	22	5	27	8
	3	22	10	32	10	42	20
	4	20	12	32	10	42	22
	5	19	11	30	11	41	22
	Mean	20	10	30	9	38	18
	SD	1	4	4	2	6	6

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APPENDIX VI

Feed Consumption (g/bird/day) by Pen from a Northern Bobwhite Acute
Dietary Toxicity Study with Transgenic Corn Expressing *Bacillus thuringiensis* var. *aizawai*
(Bt) Cry1F delta-endotoxin
Page 1

Experimental Group	Pen	Exposure Period					Post- Exposure Period
		Days 0-1	1-2	2-3	3-4	4-5	6-8
Corn Seed TSN 101792 (Control)	1	6	5	6	7	7	8
	2	7	7	8	8	7	8
	3	8	7	8	9	7	9
	4	7	9	8	7	6	8
	5	6	6	7	7	7	9
	6	7	7	9	8	8	9
Corn Expressing Bt Cry1F delta-endotoxin TSN 101791	1	7	7	9	9	8	10
	2	5	5	7	6	5	5
	3	5	6	8	8	8	8
	4	7	6	8	8	8	9
	5	7	7	12	10	8	13
	6	6	6	8	7	8	7

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APPENDIX VII
PERSONNEL INVOLVED IN THE STUDY

The following key Wildlife International, Ltd. Personnel were involved in the conduct or management of this study:

- (1) [REDACTED], Wildlife Toxicologist
- (2) [REDACTED], Director of Avian Toxicology
- (3) [REDACTED], Manager, Avian Toxicology
- (4) [REDACTED], Senior Biologist
- (5) [REDACTED] Senior Biologist

Equivalency between transgenic corn-produced and microbially-derived Cry1F protein

Yong Gao (2002)
Dow AgroSciences
Indianapolis

The rationale for using microbial material for toxicology studies has been in place for many years and has been accepted by regulatory agencies around the world. The reason is that it is not possible to isolate active protein from plants in sufficient quantities (multi-grams) to perform the required toxicology and other regulatory studies. Therefore, a recombinant protein is produced in large quantity with a high expression system such as bacteria, and a small quantity of the protein is isolated from plants. Characterization studies are conducted to demonstrate the physico-chemical and biological equivalency or comparability of the protein from the two sources.

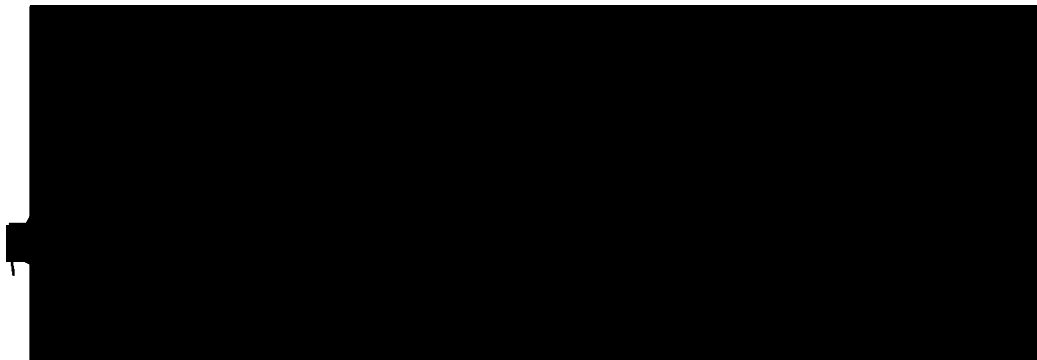
The microbial Cry1F was produced with recombinant *Pseudomonas fluorescens* strain MR872. The full-length *cry1F* gene was transformed and inserted into the bacterium, and the translated protein was a full-length Cry1F with a molecular weight of 130 kDa. This full length Cry1F was then isolated and enzymatically cleaved *in vitro* with trypsin into an active truncated Cry1F. This truncated Cry1F was compared to the Cry1F protein isolated from the transgenic corn in these aspects: primary structure, molecular weight, immunoreactivity to Cry1F specific antibodies, N-terminal sequencing, peptide mass fingerprinting by MALDI-TOF MS, the lack of glycosylation, and insecticidal activity. The following is a summary of the findings. The details of the studies are fully documented in reports by Evans (submitted as ref 15) and (Schafer and Schwedler 2001).

The studies concluded that the truncated microbial Cry1F and the transgenic corn derived Cry1F were equivalent in biochemical characteristics and biological activities.

Primary structure/sequence:

The plant and microbial Cry1F protein primary structure (sequences) are defined in Table 1 and compared in Figure 1. **MR872** is the Cry1F protein produced by recombinant *Pseudomonas fluorescens* strain MR872. **Cry1Fa2syn** is the protein sequence that is expressed in *B.t.* Cry1F maize line 1507. **Cry1Fa2** is the naturally occurring protein sequence from *Bacillus thuringiensis* var. *aizawai* strain PS811 (it is provided here as reference and was not used in any of the laboratory studies).

Bt toxins in nature are protoxins, meaning that they are larger than necessary for activity. Pieces of peptides on the carboxyl domain, and in some cases also at amino terminus, are removed, usually by insect gut proteases, leaving in place a core sequence of amino acids comprising the active toxin. Precise cleavage has not been shown to be required for activity of typical Bt toxins. Figure 1 shows the entire protoxin sequence of Cry1Fa2. Computer simulations of digestion, coupled with size estimates, indicate that the protein in nature most likely is cleaved at amino acid 612 on the C-terminus. Actual data from laboratory digestions and computer simulations indicate that the N terminus is processed



down to residue 28. Thus, an activated toxin produced from Cry1F protoxin in nature would be expected to contain amino acids 28 to 612.

The protein produced in plants (**Cry1Fa2syn**) contains amino acids from 1 to 605, thus after proteolytic cleavage at the N-terminus the active toxin would be expected to consist of amino acids 28 to 605. The microbial protein (**MR872**) was produced using nearly the full Cry1Fa2 sequence (there is deletion and/or substitution of amino acids 781-812). As part of the preparation process, the MR872 protoxin (full-length) was subjected to controlled cleavage by trypsin, followed by additional purification to yield the expected truncated Cry1F toxin containing amino acids 28 to 612.

✓ Overall from the primary structure point of view, the sequence differences between the plant and microbial-derived toxins are: 1) a phenylalanine to leucine substitution at position 604 (based on the occurrence of leucine in the homologous position of other Cry1F proteins), and 2) approximately 7 additional amino acids are present on the C-terminus of the microbial toxin. These differences represent only 1% of the amino acid sequence of the plant and microbial toxins, and the differences are restricted to the non-functional outermost C-terminus.

Molecular weight and immunoreactivity:

Both plant and microbial Cry1F are immunoreactive to antibodies specific for Cry1F. An immunoaffinity column was generated using the antibodies and it was used to purify the plant Cry1F from transgenic corn plant leaf extract. The plant purified Cry1F was used in further characterization studies. In transgenic plants, the Cry1F was initially expressed as a protein of about 68 kDa (amino acids 1-605). However, this protein was subject to cleavage by plant proteases, resulting in the formation of an N-terminal truncated form at approximately 65 kDa (amino acids 28-605). Depending on the growth stages of plant tissues and sample extraction procedure, either a combination of both bands (68 and 65 kDa) or a single major 65 kDa band can be detected by SDS-PAGE and Western blot (Evans 1998; Schafer and Schwedler 2001). This 65 kDa band is the active core toxin, and this molecular weight is very similar to that of the truncated microbial Cry1F. //

N-terminal sequencing:

N-terminal sequencing data showed that both the plant derived 65 kDa Cry1F band and the truncated microbial Cry1F had N-terminal amino acid corresponding to amino acid residue 28 (Evans 1998).

Tryptic peptide mass fingerprints:

MALDI-TOF MS tryptic peptide fingerprints of the plant produced and microbially-derived truncated Cry1F is shown in Table 2 (Table 1 of (Schafer and Schwedler 2001)). In the trypsin digest of *P. fluorescens*-derived truncated Cry1F protein, 19 peptides were identified matching the theoretical deduced peptide masses of Cry1F. The peptide fragments detected were between residues 32 and 546 of Cry1F. In the trypsin digest of

the transgenic corn derived Cry1F protein, 20 peptides were identified matching the theoretical deduced peptide masses.

Lack of glycosylation

Both the plant derived and truncated microbial Cry1F had no detectable carbohydrates (Schafer and Schwedler 2001).

Biological activity (insecticidal potency)

Biological potency data showed essentially indistinguishable LC_{50} 's between plant and microbial Cry1F protein on 4 insect species, clearly indicating that the materials are functionally interchangeable (Evans 1998).

Table 1. Definition of Cry1F sequence nomenclature used in Figure 1

Cry1F Sequence	Description	Amino Acid Sequence, Before Cleavage (Protoxin)	Amino Acid Sequence, After Cleavage (Toxin)
MR872	Cry1F sequence expressed in <i>Pseudomonas fluorescens</i> strain MR872	1-1174, except 781-812	28-612
Cry1Fa2syn	Cry1F sequence expressed in <i>B.t.</i> Cry1F maize line 1507	1-605, F604L	28-605, F604L
Cry1Fa2	Cry1F sequence naturally occurring in <i>Bacillus thuringiensis</i> var. <i>aizawai</i> strain PS811	1-1174	28-612

Figure 1. Alignment of the amino acid sequences of the delta-endotoxin proteins comparing a microbially derived Cry1F protein (MR872), the modified plant Cry1F protein (Cry1Fa2syn), and B.t.a Cry1F full length protein (Cry1Fa2).

The consensus sequence represents identical residues among all three genetic versions encoding the Cry1F protein. The positions of putative protease cleavage sites at the start (about residue 28 or 31) and end (about residue 612 or 615) of the active core protein are marked with a ↓. Note the single F₆₀₄L substitution in the transgenic polypeptide. This difference is due to codon changes resulting from the introduction of a restriction enzyme site that enables gene cloning of the alternative C-terminal half of the full length protein.

				↓	↓	
	1					50
MR872	MENNIQNQC	PYNCLNNPEV	EILNEERSTG	RLPLDISLSL	TRFLLSEFVP	
Cry1Fa2syn	MENNIQNQC	PYNCLNNPEV	EILNEERSTG	RLPLDISLSL	TRFLLSEFVP	
Cry1Fa2	MENNIQNQC	PYNCLNNPEV	EILNEERSTG	RLPLDISLSL	TRFLLSEFVP	
Consensus	MENNIQNQC	PYNCLNNPEV	EILNEERSTG	RLPLDISLSL	TRFLLSEFVP	
	51					100
MR872	GVGVAFGLFD	LIWGFITPSD	WSLFLLQIEQ	LIEQRIETLE	RNRAITTLRG	
Cry1Fa2syn	GVGVAFGLFD	LIWGFITPSD	WSLFLLQIEQ	LIEQRIETLE	RNRAITTLRG	
Cry1Fa2	GVGVAFGLFD	LIWGFITPSD	WSLFLLQIEQ	LIEQRIETLE	RNRAITTLRG	
Consensus	GVGVAFGLFD	LIWGFITPSD	WSLFLLQIEQ	LIEQRIETLE	RNRAITTLRG	
	101					150
MR872	LADSYEIIYE	ALREWEANPN	NAQLREDVRI	RFANTDDALI	TAINNFTLTS	
Cry1Fa2syn	LADSYEIIYE	ALREWEANPN	NAQLREDVRI	RFANTDDALI	TAINNFTLTS	
Cry1Fa2	LADSYEIIYE	ALREWEANPN	NAQLREDVRI	RFANTDDALI	TAINNFTLTS	
Consensus	LADSYEIIYE	ALREWEANPN	NAQLREDVRI	RFANTDDALI	TAINNFTLTS	
	151					200
MR872	FEIPLLSVYV	QAANLHLSLL	RDAVSFGQGW	GLDIATVNNH	YNRLINLIHR	
Cry1Fa2syn	FEIPLLSVYV	QAANLHLSLL	RDAVSFGQGW	GLDIATVNNH	YNRLINLIHR	
Cry1Fa2	FEIPLLSVYV	QAANLHLSLL	RDAVSFGQGW	GLDIATVNNH	YNRLINLIHR	
Consensus	FEIPLLSVYV	QAANLHLSLL	RDAVSFGQGW	GLDIATVNNH	YNRLINLIHR	
	201					250
MR872	YTKHCLDTYN	QGLENLRGTN	TRQWARFNQF	RRDLTLTVLD	IVALEFPNYDV	
Cry1Fa2syn	YTKHCLDTYN	QGLENLRGTN	TRQWARFNQF	RRDLTLTVLD	IVALEFPNYDV	
Cry1Fa2	YTKHCLDTYN	QGLENLRGTN	TRQWARFNQF	RRDLTLTVLD	IVALEFPNYDV	
Consensus	YTKHCLDTYN	QGLENLRGTN	TRQWARFNQF	RRDLTLTVLD	IVALEFPNYDV	
	251					300
MR872	RTYPIQTSSQ	LTREIYTSSV	IEDSPVSANI	PNGFNRAEFG	VRPPHLMDFM	
Cry1Fa2syn	RTYPIQTSSQ	LTREIYTSSV	IEDSPVSANI	PNGFNRAEFG	VRPPHLMDFM	
Cry1Fa2	RTYPIQTSSQ	LTREIYTSSV	IEDSPVSANI	PNGFNRAEFG	VRPPHLMDFM	
Consensus	RTYPIQTSSQ	LTREIYTSSV	IEDSPVSANI	PNGFNRAEFG	VRPPHLMDFM	
	301					350
MR872	NSLFVTAETV	RSQTVWGGHL	VSSRNTAGNR	INFPSYGVFN	PGGAIWIADE	
Cry1Fa2syn	NSLFVTAETV	RSQTVWGGHL	VSSRNTAGNR	INFPSYGVFN	PGGAIWIADE	
Cry1Fa2	NSLFVTAETV	RSQTVWGGHL	VSSRNTAGNR	INFPSYGVFN	PGGAIWIADE	
Consensus	NSLFVTAETV	RSQTVWGGHL	VSSRNTAGNR	INFPSYGVFN	PGGAIWIADE	
	351					400
MR872	DPRPFYRTLS	DPVFVRGGFG	NPHYVLGLRG	VAFQQTGTNH	TRTFRNSGTI	
Cry1Fa2syn	DPRPFYRTLS	DPVFVRGGFG	NPHYVLGLRG	VAFQQTGTNH	TRTFRNSGTI	
Cry1Fa2	DPRPFYRTLS	DPVFVRGGFG	NPHYVLGLRG	VAFQQTGTNH	TRTFRNSGTI	
Consensus	DPRPFYRTLS	DPVFVRGGFG	NPHYVLGLRG	VAFQQTGTNH	TRTFRNSGTI	
	401					450
MR872	DSLDEIPPQD	NSGAPWNDYS	HVLNHVTFVR	WPGEISGSDS	WRAPMFSWTH	
Cry1Fa2syn	DSLDEIPPQD	NSGAPWNDYS	HVLNHVTFVR	WPGEISGSDS	WRAPMFSWTH	
Cry1Fa2	DSLDEIPPQD	NSGAPWNDYS	HVLNHVTFVR	WPGEISGSDS	WRAPMFSWTH	
Consensus	DSLDEIPPQD	NSGAPWNDYS	HVLNHVTFVR	WPGEISGSDS	WRAPMFSWTH	

	451		500
MR872	RSATPTNTID PERITQIPLV KAHTLQSGTT VVRGPGFTGG DILRRTSGGP		
Cry1Fa2syn	RSATPTNTID PERITQIPLV KAHTLQSGTT VVRGPGFTGG DILRRTSGGP		
Cry1Fa2	RSATPTNTID PERITQIPLV KAHTLQSGTT VVRGPGFTGG DILRRTSGGP		
Consensus	RSATPTNTID PERITQIPLV KAHTLQSGTT VVRGPGFTGG DILRRTSGGP		
	501		550
MR872	FAYTIVNING QLPQRYRARI RYASTTNLRI YVTVAGERIF AGQFNKTMDT		
Cry1Fa2syn	FAYTIVNING QLPQRYRARI RYASTTNLRI YVTVAGERIF AGQFNKTMDT		
Cry1Fa2	FAYTIVNING QLPQRYRARI RYASTTNLRI YVTVAGERIF AGQFNKTMDT		
Consensus	FAYTIVNING QLPQRYRARI RYASTTNLRI YVTVAGERIF AGQFNKTMDT		
	551		600
MR872	GDPLTFQSFS YATINTAFTF PMSQSSFTVG ADTFSSGNEV YIDRFELIPV		
Cry1Fa2syn	GDPLTFQSFS YATINTAFTF PMSQSSFTVG ADTFSSGNEV YIDRFELIPV		
Cry1Fa2	GDPLTFQSFS YATINTAFTF PMSQSSFTVG ADTFSSGNEV YIDRFELIPV		
Consensus	GDPLTFQSFS YATINTAFTF PMSQSSFTVG ADTFSSGNEV YIDRFELIPV		
	↓ ↓		
	601		650
MR872	TATFEAEYDL ERAQKAVNAL FTSINQIGIK TDVTDYHIDR VSNLVECLSD		
Cry1Fa2syn	TATLE*.....		
Cry1Fa2	TATFEAEYDL ERAQKAVNAL FTSINQIGIK TDVTDYHIDQ VSNLVDCLSD		
Consensus	TAT-E-----		
	651		700
MR872	EFCLDEKKEL SEKVKHAKRL SDERNLLQDP NFRGINRQLD RGWRGSTDIT		
Cry1Fa2syn		
Cry1Fa2	EFCLDEKREL SEKVKHAKRL SDERNLLQDP NFKGINRQLD RGWRGSTDIT		
Consensus	-----		
	701		750
MR872	IQGGDDVFKE NYVTLLGTFD ECYLTYLYQK IDESKLKAYT RYQLRGYIED		
Cry1Fa2syn		
Cry1Fa2	IQRGDDVFKE NYVTLPGTFD ECPYTYLYQK IDESKLKPYT RYQLRGYIED		
Consensus	-----		
	751		800
MR872	SQDLEIYLIR YNAKHETVNV PGTGSLWRLS APSPI.....		
Cry1Fa2syn		
Cry1Fa2	SQDLEIYLIR YNAKHETVNV LGTGSLWPLS VQSPIRKCGE PNRCAHLEW		
Consensus	-----		
	801		850
MR872 GKCAHSHH FSLDIDVGCT DLNEDLGWVW IFKIKTQDGH		
Cry1Fa2syn		
Cry1Fa2	NPDLDCSCRD GEKCAHSHH FSLDIDVGCT DLNEDLDVWV IFKIKTQDGH		
Consensus	-----		
	851		900
MR872	ARLGNLEFLE EKPLVGEALA RVKRAEKKWR DKREKLEWET NIVYKEAKES		
Cry1Fa2syn		
Cry1Fa2	ARLGNLEFLE EKPLVGEALA RVKRAEKKWR DKREKLELET NIVYKEAKES		
Consensus	-----		
	901		950
MR872	VDALFVNSQY DRLQADTNIA MIHAADKRVH SIREAYLPEL SVIPGVNAAI		
Cry1Fa2syn		
Cry1Fa2	VDALFVNSQY DQLQADTNIA MIHAADKRVH RIREAYLPEL SVIPGVNVDI		
Consensus	-----		
	951		1000
MR872	FEELEGRIFT AFSLYDARNV IKNGDFNNGL SCWNVKGHVD VEEQNNHRSV		
Cry1Fa2syn		
Cry1Fa2	FEELEGRIFT AFFLYDARNV IKNGDFNNGL SCWNVKGHVD VEEQNNHRSV		
Consensus	-----		
	1001		1050
MR872	LVPWEWAEV SQEVRVCPGR GYILRV TAYK EGYGEGCVTI HEIENNTDEL		
Cry1Fa2syn		
Cry1Fa2	LVPWEWAEV SQEVRVCPGR GYILRV TAYK EGYGEGCVTI HEIENNTDEL		

Consensus	-----	-----	-----	-----	-----
	1051				1100
MR872	KFSNCVEEEV	YPNNTVTCND	YTATQEEYEG	TYTSRNRGYD	GAYESNSSVP
Cry1Fa2syn
Cry1Fa2	KFSNCVEEEV	YPNNTVTCND	YTANQEEYGG	AYTSRNRGYD	ETYGSNSSVP
Consensus	-----	-----	-----	-----	-----
	1101				1150
MR872	ADYASAYEEK	AYTDGRRDNP	CESNRGYGDY	TPLPAGYVTK	ELEYFPETDK
Cry1Fa2syn
Cry1Fa2	ADYASVYEEK	SYTDGRRDNP	CESNRGYGDY	TPLPAGYVTK	ELEYFPETDK
Consensus	-----	-----	-----	-----	-----
	1151		1175		
MR872	VWIEIGETEG	TFIVDSVELL	LMEE*		
Cry1Fa2syn		
Cry1Fa2	VWIEIGETEG	TFIVDSVELL	LMEE*		
Consensus	-----	-----	-----		

Table 2. Tryptic Peptide Mass Data (m/z $[M+H]^+$) of Cry 1F Proteins Obtained by MALDI-TOF MS

Full Length Cry1Fsynpro residue #	Theoretical mass (m/z)	<i>P. fluorescens</i> trypsinized Cry1F [$M+H$]	TC1507 Maize Cry1F [$M+H$]
32-42	1227.72	1227.70	1227.68
100-113	1612.81	1612.81	1612.79
114-125	1441.67	1441.66	1441.65
172-193	2434.15	2434.21	2434.16
194-200	878.55	878.51	878.50
204-217	1675.79	1675.75	1675.75
252-263	1394.72	1394.69	1394.68
264-286	2509.21	2509.24	2509.19
312-324	1413.71	1413.70	1413.68
358-366	1033.56	1033.52	1033.52
367-379	1386.71	1386.70	1386.69
380-392	1416.68	1416.67	1416.67
431-442	1376.62	1376.62	1376.59
452-463	1301.63	1301.60	1301.58
464-471	911.58	911.53	911.52
472-483	1269.68	1269.66	1269.65
484-494	1089.56	1089.53	1089.52
522-529	925.46	ND ^b	925.43
530-538	1007.54	1007.51	1007.50
539-546	924.48	924.44	924.43

Note:

^a Two digit decimals were used for mass data in this table although raw data obtained from the MALDI-TOF-MS spectrometer were shown in 4 digit decimals. A peptide was considered a match if its m/z is within m/z 0.1 error range of its theoretical m/z .

^b ND: not detected.

SUMMARY

(In accordance with 40 CFR part 152, this summary is available
for public release after registration)

STUDY TITLE

Gel Electrophoresis, Western Blot, and ELISA of Truncated Cry1F Delta-endotoxin Following
Heat Treatment

DATA REQUIREMENTS

none

AUTHOR(S)

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STUDY COMPLETED ON

January 14, 2002

PERFORMING LABORATORY

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LABORATORY STUDY ID

GH-C 5366

Gel Electrophoresis, Western Blot, and ELISA of Truncated Cry1F Delta-endotoxin Following Heat Treatment

SUMMARY

Corn plants have been genetically modified through the introduction of a synthetic gene which encodes for a truncated version of an insecticidal crystal protein, Cry1F, isolated from *Bacillus thuringiensis* var. *aizawai* strain PS811. When expressed in corn cultivars, the Cry1F protein provides crop resistance against lepidopteran pests, including the European corn borer (*Ostrinia nubilalis*). The Cry1F corn plants also contain a herbicide-resistant selectable marker gene that expresses the protein phosphinothricin acetyltransferase (PAT). The PAT protein imparts tolerance to glufosinate-ammonium, the active ingredient in Liberty herbicide.

The study demonstrated that there was a significant difference between the detectability of Cry1F protein by an ELISA test kit before and after heat treatment of the protein. If heated for 30 minutes at 75 °C or higher, the Cry1F protein was inactivated and lost its biological activity, as well as detectability (or binding affinity) by the ELISA test kit. Gel electrophoresis and Western blot analysis indicated that the molecular mass of the Cry1F protein (approximately 65 kDa) was unchanged after heat treatment, as would be expected for most proteins including previously registered insecticidal crystal proteins originated from *Bacillus thuringiensis*. The loss of biological activity of Cry1F upon heat treatment indicates the unfolding and destruction of the three-dimensional structure of Cry1F protein. The results of gel electrophoresis and Western blot of non-heated and heat-treated Cry1F protein are extensively discussed in this report.

STUDY TITLE

Gel Electrophoresis, Western Blot, and ELISA of Truncated Cry1F Delta-endotoxin Following Heat Treatment

DATA REQUIREMENTS

none

AUTHOR(S)

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STUDY COMPLETED ON

January 14, 2002

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GH-C 5366

STATEMENT OF NO DATA CONFIDENTIALITY CLAIMS

Compound: Cry1F delta-endotoxin

Title: Gel Electrophoresis, Western Blot, and ELISA of Truncated Cry1F Delta-endotoxin Following Heat Treatment

No claim of confidentiality is made for any information contained in this study on the basis of its falling within the scope of FIFRA Section 10 (d)(1)(A)(B), or (C).*

Company: Dow AgroSciences LLC

Company Agent: [REDACTED]

Title: Regulatory Manager

Signature: _____

Date: _____

*In the United States, the above statement supersedes all other statements of confidentiality that may occur elsewhere in this report.

THIS DATA MAY BE CONSIDERED CONFIDENTIAL IN COUNTRIES OUTSIDE THE UNITED STATES.

STATEMENT OF COMPLIANCE WITH GOOD LABORATORY PRACTICE STANDARDS

Title: Gel Electrophoresis, Western Blot, and ELISA of Truncated Cry1F Delta-endotoxin
Following Heat Treatment

Study Initiation Date: November 27, 2001 Study Completion Date:
Experimental Start Date: November 27, 2001 Experiment Termination Date: January 9, 2002

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

Organisation for Economic Co-Operation and Development
ISBN 92-64-12367-9, Paris 1982

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.

_____ Sponsor Dow AgroSciences LLC	_____ Date
_____ Submitter Dow AgroSciences LLC	_____ Date
_____ Study Director/Author Dow AgroSciences LLC	_____ Date

QUALITY ASSURANCE STATEMENT

Compound: Cry1F delta-endotoxin

Title: Gel Electrophoresis, Western Blot, and ELISA of Truncated Cry1F Delta-endotoxin Following Heat Treatment

Study Initiation Date: November 27, 2001 Study Completion Date: January 14, 2002

NON-GLP STUDY

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Gel Electrophoresis, Western Blot, and ELISA of Truncated Cry1F Delta-endotoxin Following Heat Treatment

ABSTRACT

Corn plants have been genetically modified through the introduction of a synthetic gene which encodes for a truncated version of an insecticidal crystal protein, Cry1F, isolated from *Bacillus thuringiensis* var. *aizawai* strain PS811. When expressed in corn cultivars, the Cry1F protein provides crop resistance against lepidopteran pests, including the European corn borer (*Ostrinia nubilalis*). The Cry1F corn plants also contain a herbicide-resistant selectable marker gene that expresses the protein phosphinothricin acetyltransferase (PAT). The PAT protein imparts tolerance to glufosinate-ammonium, the active ingredient in Liberty herbicide.

The study demonstrated that there was a significant difference between the detectability of Cry1F protein by an ELISA test kit before and after heat treatment of the protein. If heated for 30 minutes at 75 °C or higher, the Cry1F protein was inactivated and lost its biological activity, as well as detectability (or binding affinity) by the ELISA test kit. Gel electrophoresis and Western blot analysis indicated that the molecular mass of the Cry1F protein (approximately 65 kDa) was unchanged after heat treatment, as would be expected for most proteins including previously registered insecticidal crystal proteins originated from *Bacillus thuringiensis*. The loss of biological activity of Cry1F upon heat treatment indicates the unfolding and destruction of the three-dimensional structure of Cry1F protein. The results of gel electrophoresis and Western blot of non-heated and heat-treated Cry1F protein are extensively discussed in this report.

ABBREVIATIONS

β -ME	β -mercaptoethanol
BCIP	5-bromo-4-chloro-3-indolyl phosphate
CAPS	3-(cyclohexylamino)-1-propanesulfonic acid
CBB	Coomassie Brilliant Blue
DAS	Dow AgroSciences LLC
ELISA	enzyme-linked immunosorbent assay
GLP	Good Laboratory Practice
HRP	horseradish peroxidase
IgG	immunoglobulin G
kDa	kilodalton
MAb	monoclonal antibody
min	minute
MW	molecular weight
NBT	p-nitroblue tetrazolium
PAb	polyclonal antibodies
PAT	phosphinothricin acetyltransferase
PBST	phosphate buffered saline with Tween 20
SDS	sodium dodecyl sulfate
SDS-PAGE	sodium dodecyl sulfate-polyacrylamide gel electrophoresis
TSN	test substance number

INTRODUCTION

Corn plants have been genetically modified through the introduction of a synthetic gene which encodes for a truncated version of an insecticidal crystal protein, Cry1F, isolated from *Bacillus thuringiensis* var. *aizawai* strain PS811. When expressed in corn cultivars, the Cry1F protein provides crop resistance against lepidopteran pests, including the European corn borer (*Ostrinia nubilalis*). The Cry1F corn plants also contain a herbicide-resistant selectable marker gene that expresses the protein phosphinothricin acetyltransferase (PAT). The PAT protein imparts tolerance to glufosinate-ammonium, the active ingredient in Liberty herbicide.

Previously, a heat lability study was conducted with the truncated Cry1F protein (Herman 2000). The results indicated that the Cry1F protein lost insecticidal or biological activity following exposure for 30 minutes at temperatures of 75 °C or higher. The current study was carried out with two objectives. The first was to examine the binding affinity (or detectability) differences between non-heated, native (active) Cry1F protein and heat-treated, denatured (inactive) Cry1F protein with an ELISA kit manufactured by Strategic Diagnostics Inc. The second objective was to examine whether there is any significant breakdown of the truncated Cry1F protein following heat treatment by using gel electrophoresis and Western blot analysis with polyclonal antibodies.

MATERIALS AND METHODS

Test Substance

The truncated Cry1F protein was obtained from the Test Substance Coordinator, Dow AgroSciences LLC, 9330 Zionsville Road, Building 304, Indianapolis, IN 46268. The test substance was a recombinant protein produced by a genetically modified strain of *Pseudomonas fluorescens*. The Dow AgroSciences (DAS) test substance number for this lot of the truncated Cry1F protein is TSN 101788. The Cry1F protein was 13.7% of the total solid weight of the lyophilized powder (Collins 2001). It should be pointed out that in this lyophilized preparation,

the purity of the Cry1F protein was >80% in terms of the percentage of Cry1F protein to total proteins (Evans 1998, Collins 2001, Schafer and Schwedler 2001). The dried preparation also contains non-proteinaceous substances such as buffering chemicals and salts, which were present in the liquid formulation before freeze-drying. The non-proteinaceous substances account for the major portion of the weight in the lyophilized powder. This microbially-derived Cry1F protein has been demonstrated to be equivalent to the transgenic corn-produced Cry1F in other studies (Evans 1998, Schafer and Schwedler 2001).

Reference Substance

The pre-stained protein molecular weight (MW) markers from Bio-Rad (catalog #161-0318) were used as MW references in gel electrophoresis and Western blot analysis.

ELISA of Heated and Non-heated Cry1F

A liquid solution of the Cry1F protein was prepared from the lyophilized powder (TSN 101788), and diluted to 1000 ng/mL with PBST (phosphate buffered saline with Tween 20, Sigma catalog # P3563). The solution was divided into 0.5-mL aliquots and heated in different water baths at 1) 75 °C for 30 min, 2) 90 °C for 30 min, or 3) 100 °C for 15 min. The non-heated sample was kept at 4 °C in a refrigerator. After treatment, all samples were kept on ice until analysis by a microtiter plate ELISA test kit available from Strategic Diagnostics Inc (Product Part No. 7020000). The samples were diluted with PBST to certain concentrations when loading into the wells of the ELISA plates. The assay uses a double antibody sandwich ELISA format. Polyclonal antibodies specific to the Cry1F protein are coated onto the microtiter plates. Cry1F samples were incubated in the wells of the plate together with the horseradish peroxidase (HRP)-conjugate of a second antibody which is a monoclonal specific to Cry1F, forming an enzyme-labeled sandwich of the Cry1F protein (Figure 1). After incubation, the plate was washed to remove unbound reagents and proteins. A second incubation was then performed with a substrate solution. After this incubation, the enzyme reaction was stopped, and the color

intensity of the samples and standard was measured at 450 nm using a microplate optical-density reader. The concentration of Cry1F protein in each sample was calculated based on a standard curve generated using non-heated Cry1F protein.

Gel Electrophoresis and Western Blot Analysis of Heated and Non-heated Cry1F

The Cry1F protein (TSN 101788) was suspended in 20 mM CAPS buffer (pH 10.5) at 1 mg lyophilized powder per mL buffer. The solution was mixed with Laemmli sample buffer (Bio-Rad catalog #161-0737) containing 5% freshly added β -mercaptoethanol (β -ME). Separate aliquots of the Cry1F solution were treated 1) heated by boiling at 100 °C for 5 min, 2) heated by boiling at 100 °C for 15 min, and 3) non-heated. The samples were loaded onto 4-15% gradient gels (Bio-Rad catalog #161-1104), and a Mini-PROTEAN III module was used. Electrophoresis was conducted at a constant voltage of 200 V for approximately 30 min. The electrophoresis buffer was Tris/Glycine/SDS buffer from Bio-Rad (catalog #161-0755). After electrophoresis, identical gels were either stained with Coomassie Brilliant Blue (CBB) or electro-blotted to a nitrocellulose membrane with a Mini Trans-Blot electrophoretic transfer cell (Bio-Rad) for 60 min under a constant voltage of 100 V. For immunodetection of the Western blotted membrane, a specific rabbit polyclonal antibody (PAb) against truncated Cry1F was used as the primary antibody (lot #200.310-4, Strategic Diagnostics Inc., Newark, Delaware). A conjugate of goat anti-rabbit IgG (H+L)-alkaline phosphatase (catalog # 31340, Pierce, Rockford, Illinois) was used as the secondary antibody. A substrate solution containing 100 mM Tris, 100 mM NaCl, 5 mM $MgCl_2$, 0.025% 5-bromo-4-chloro-3-indolyl phosphate (BCIP), and 0.05% p-nitroblue tetrazolium chloride (NBT) was used for colorimetric development of the immunoreactive protein bands. This experiment was repeated on two separate test dates.

RESULTS AND DISCUSSION

ELISA Assay of Heated and Non-heated Cry1F Protein

Table 1 shows the ELISA results of the heated and non-heated Cry1F protein. The concentration of Cry1F protein measured in the non-heated sample matched the amount added to the aliquot. When the Cry1F protein was heated to 75 or 90 °C for 30 min, or 100 °C for 15 min, the ELISA kit could no longer detect it at any of the concentrations tested. A small amount of the Cry1F protein was measured in some treatments after heating. The measured level in these heat-treated samples was less than 2% of the amount added.

The current study showed that the Cry1F ELISA could not detect the protein after treatment with heat. The ELISA appeared only to recognize native Cry1F protein which was not denatured or inactivated by the heat treatment. The small amount of protein detected in some treatments is likely due to incomplete denaturing of the sample or experimental error around background optical densities. A study conducted by Herman (2000) demonstrated that truncated Cry1F protein was inactivated and lost its insecticidal or biological activity following exposure to 75 °C or higher for 30 min (Appendix A), suggesting that the three dimensional structure of the Cry1F protein had been destroyed following these heat treatments.

The results indicate that the epitope (i.e., binding site) for the monoclonal antibody (MAb) used in the sandwich ELISA format was destroyed once the Cry1F protein was heated and the three dimensional structure unfolded. An epitope is the region of an antigen that binds to an antibody. Epitopes on protein antigens, such as Cry1F protein, are local surface structures that can be formed by contiguous or non-contiguous amino acid sequences (Berzofsky and Berkower 1984). A preparation of polyclonal antibodies (PAb) contains many different antibodies that recognize a protein antigen through multiple epitopes, including those on the secondary or tertiary structure, and those in the contiguous sequence of a polypeptide chain. After heat treatment, the denatured protein would lose many but not all epitopes that are recognized by the PAb. Also the binding affinity of PAb to a denatured protein would be significantly reduced if the PAb was originally

generated using the native protein as antigen. Thus, even though a PAb preparation often detects a protein in both native and denatured states, the sensitivity to the denatured protein could be dramatically reduced. A monoclonal antibody (MAb), on the other hand, would only recognize and bind to a specific epitope of a protein. If this epitope is a part of the secondary or tertiary structure composed by non-contiguous amino acid sequences, the binding affinity would be lost once the protein is heated to certain temperature and the three-dimensional structure is destroyed. The MAb used in the Cry1F ELISA sandwich seems to be one such example. The advantage of using such an ELISA kit is that one would be able to measure the active Cry1F protein in samples.

The ELISA data (Table 1) and the insect-activity data (Appendix A) appeared to correlate well, and confirm this conclusion. In the 4 °C treatment, the Cry1F protein remained active resulting in 96% growth inhibition and 31% mortality to tobacco budworm at the dosage used (Appendix A), and the complete detection by ELISA (Table 1). After treatments at 75 or 90 °C for 30 min, the Cry1F protein lost biological activity against tobacco budworm (Appendix A), and the ELISA results showed no detection of Cry1F (Table 1).

Gel Electrophoresis and Western Blot Analysis of Heated and Non-heated Cry1F

Heat-treated (100 °C for 5 or 15 minutes) and non-heated (kept at approximately 4 °C in a refrigerator, mixed with Laemmli sample buffer and loaded onto gels directly) Cry1F protein were examined with gel electrophoresis and Western blot analysis. The experiment was conducted once in November 2001 (Figure 2) and again in January 2002 (Figure 3). The experiments on the two test dates used two different aliquots of the same PAb that were stored under different conditions. An aliquot of PAb stored in a refrigerator was used in November 2001, and a newly thawed aliquot stored at -80 °C freezer was employed in January 2002.

Figure 2 and Figure 3 show the photographs of Coomassie Brilliant Blue (CBB) stained gels and PAb detected blotted membranes. In each figure, the same samples were first separated on 4-15% gradient gel. After electrophoresis, one gel was stained with CBB which detects all the

proteins in each lane. A second identical gel was Western-blotted onto a nitrocellulose membrane, which was immuno-detected by using the rabbit PAb specific to Cry1F as the primary antibody, and a goat anti-rabbit IgG (H+L)-alkaline phosphatase conjugate (Pierce) as the secondary antibody. It can be seen from the CBB stained gels (left photograph, labeled as A) that the Cry1F band (approximately 65 kDa) remained essentially unchanged before and after heat treatment. It can also be seen from PAb detected blotted membrane (right photograph, labeled as B) that both heated and non-heated Cry1F were reactive to the PAb.

On the Western blotted membranes, a reactive smear was observed in the non-heated sample lanes (lane 2 of Figures 2B and 3B), while no smear was observed in the heated-sample lanes on the same membrane. In addition, no obvious smear was seen on CBB stained gels regardless whether the protein was subject to heat treatment or not. This observation is expected and is due to several reasons.

First, the reason that a smear in the non-heated sample lanes was seen on Western blot and not on the CBB stained gels was due to the difference of detection limit between PAb and CBB. PAb sensitivity to Cry1F is at the pg level, while CBB sensitivity to proteins on gels is at the level of multi-tens ng or higher. So the same amount of Cry1F protein could be detected on the Western blot, but not enough is present to be visible on CBB stained gels.

Secondly, on the Western blot membrane the phenomenon of a smear in non-heated-sample lanes, but not in the heated-sample lanes is likely the result of multiple factors. The most important factor was the difference in mobility during gel electrophoresis between heated and non-heated Cry1F protein molecules. Normally, during electrophoresis on a polyacrylamide gel, the migration velocity of proteins mainly depends on the charge, mass, and shape of the proteins. When proteins are heated in the presence of SDS and a reducing agent (β -ME), they are denatured and unfolded. In addition, the negatively charged SDS molecules coat the unfolded polypeptide chains with a strong negative charge, which covers up the intrinsic charge of proteins. Thus, in heated protein samples, individual charge differences of the proteins are masked, and all proteins have approximately the same charge/mass ratio. For this reason, the

heated, denatured proteins move in the SDS-PAGE gel only based on molecular weight (Gorg and Westermeier 1999, Speicher 1999). As expected, the heat-treated Cry1F protein moved uniformly on the gels, and appears as a clear band (approximately 65 kDa) on the blotted membrane (lane 3 of Figure 2B, lanes 3 and 4 of Figure 3B). In the non-heated protein sample, the majority of Cry1F molecules also unfolded and was coated by SDS molecules, because SDS can unfold protein molecules without heat treatment but at a much slower rate. The fully coated Cry1F protein molecules in non-heated samples migrated to the expected position similar to the heated Cry1F. However, some Cry1F molecules, especially those in aggregated forms, remained in native state, and were only partially coated by SDS due to the limited accessibility of the native structure. Therefore, these molecules would not move through the gel based exclusively on their molecular weight. Instead, their movements are dependent upon the collective result of their charges, molecular mass, and the ionic or hydrophobic interactions between molecules (which may cause aggregation). The heterogeneity in charge and aggregation among the partially SDS-coated Cry1F molecules caused them to migrate to varying positions on the lane. This spread of Cry1F molecules was detected by the extremely sensitive Western blot analysis with PAb, resulting in a smear in the non-heated-sample lanes on the membrane. It should be noted that smearing phenomenon is very often seen in running native-PAGE gels, where no SDS is added and no heating is applied to protein samples.

Another factor that might also contribute to the smearing phenomenon in non-heated sample lanes was the significant difference between the immunoreactivity (binding affinity) of the PAb to the non-heated Cry1F and to the heated Cry1F. As discussed earlier in this report, even though a PAb preparation can detect Cry1F in both native (non-heated) and denatured (heated) states, the reactivity was significantly higher for non-heated Cry1F than heated Cry1F because many epitopes were lost on heated Cry1F protein molecules. The high reactivity of PAb to non-heated Cry1F enhanced the detection sensitivity for the non-heated sample lanes on the Western blot.

Dow AgroSciences scientists have used the Cry1F specific PAb for Western blot analysis or for making immunoaffinity columns in several studies (Korjagin 2001, Gao *et al.* 2001, Herman and

Gao 2001, Schafer and Schwedler 2001). In all of those studies the Cry1F samples were heated (boiled) before being loaded on gels for Western blot analysis. Therefore, no smear was observed in those studies. In the current study a Cry1F sample was intentionally not heated before loading onto the gels in order to examine the difference between heated and non-heated Cry1F protein on gels and blots.

Finally, it should also be noted that a trace amount of a protein at approximately 50-51 kDa was observed in the non-heated protein sample (lane 2 of Figures 2 and 3, more visible on the Western blot). In the heated lanes (lanes 3 and 4), this band disappeared, while two peptide fragments at apparent molecular weights of approximately 23-25 kDa were detected. This suggests that the 50-51 kDa band might be a dimer of the two peptides linked together by disulfide bond(s) before heat application in the presence of the reducing agent β -ME. This minor dimeric protein was likely generated during the preparation of the microbial Cry1F protein lot.

CONCLUSIONS

The study demonstrated that there was a significant difference between the detectability of Cry1F protein by an ELISA test kit before and after heat treatment of the protein. If heated for 30 minutes at 75 °C or higher, the Cry1F protein was inactivated and lost its biological activity, as well as detectability (or binding affinity) by the ELISA test kit. Gel electrophoresis and Western blot analysis indicated that the molecular mass of the Cry1F protein (approximately 65 kDa) was unchanged after heat treatment, as would be expected for most proteins including previously registered insecticidal crystal proteins originated from *Bacillus thuringiensis*. The loss of biological activity of Cry1F upon heat treatment indicates the unfolding and destruction of the three-dimensional structure of Cry1F protein. The results of gel electrophoresis and Western blot of non-heated and heat-treated Cry1F protein are extensively discussed in this report.

REFERENCES

1. Berzofsky, J. A. and Berkower, I. J. 1984. Antigen-antibody interaction. In *Fundamental Immunology* (Ed by W. E. Paul), p595-644. Raven Press, New York.
2. Collins, R. A. 2001. Certificate of analysis of test/reference/control substances (TSN 101788). Dow AgroSciences Study ID BIOT 013056.
3. Evans, S. L. 1998. Equivalency of microbial and maize expressed Cry1F protein: characterization of test substances for biochemical and toxicological studies. Mycogen Corporation Study ID MYCO98-001.
4. Gao, Y.; Gilbert, J. R.; Schwedler, D. A.; Xu, X. 2001. "Characterization of Cry1F Protein Derived from *Pseudomonas fluorescens* and Transgenic Cotton", unpublished report of Dow AgroSciences LLC, Study ID 010018.
5. Gorg, A. and Westermeier, R. 1999. High resolution gel-electrophoretic techniques: qualitative, quantitative and micropreparative applications. In *Microcharacterization of Proteins* (Ed by R. Kellner, F. Lottspeich, and H. E. Meyer, 2nd edition), p13-24.
6. Herman, R. A. 2000. "Thermolability of Cry1F (truncated) Delta-endotoxin", unpublished report of Dow AgroSciences LLC, Study ID GH-C 5144.
7. Herman, R. A. and Gao, Y. 2001. "Thermolability of Cry1F(synpro) Delta-endotoxin", unpublished report of Dow AgroSciences LLC, Study ID 010069.
8. Korjagin, V. A. 2001. "In vitro Simulated Gastric Fluid Digestibility Study of Microbially Derived Cry1F(synpro).", unpublished report of Dow AgroSciences LLC, Study ID 010081.
9. Schafer, B. W. and Schwedler, D. A. 2001. "Characterization of the Recombinant Cry1F Protein Derived from *Pseudomonas fluorescens* and Transgenic Maize", unpublished report of Dow AgroSciences LLC, Study ID GH-C 5294.
10. Speicher, D. W. 1999. Introduction for Chapter 10 Electrophoresis. In *Current Protocols in Protein Science*. p10.0.1-10.0.3. John Wiley & Sons, New York.

Table 1. ELISA Data of Cry1F Standard Treated at Different Temperatures

Cry1F Concentration ^a (ng/ml)	4 °C (ng/ml) ^b	75 °C 30 min (ng/ml) ^b	90 °C 30 min (ng/ml) ^b	100 °C 15 min (ng/ml) ^b
10.00	10.01	0.00	0.00	0.00
8.00	7.97	0.00	0.00	0.00
6.00	5.87	0.13	0.00	0.00
3.75	3.87	0.00	0.00	0.01
2.00	1.94	0.01	0.00	0.01
0.75	0.65	0.01	0.00	0.01
0.25	0.24	0.02	0.02	0.04

Notes:

^a Expected concentration based on Cry1F added before heat treatment.

^b Detected concentration after treatment.

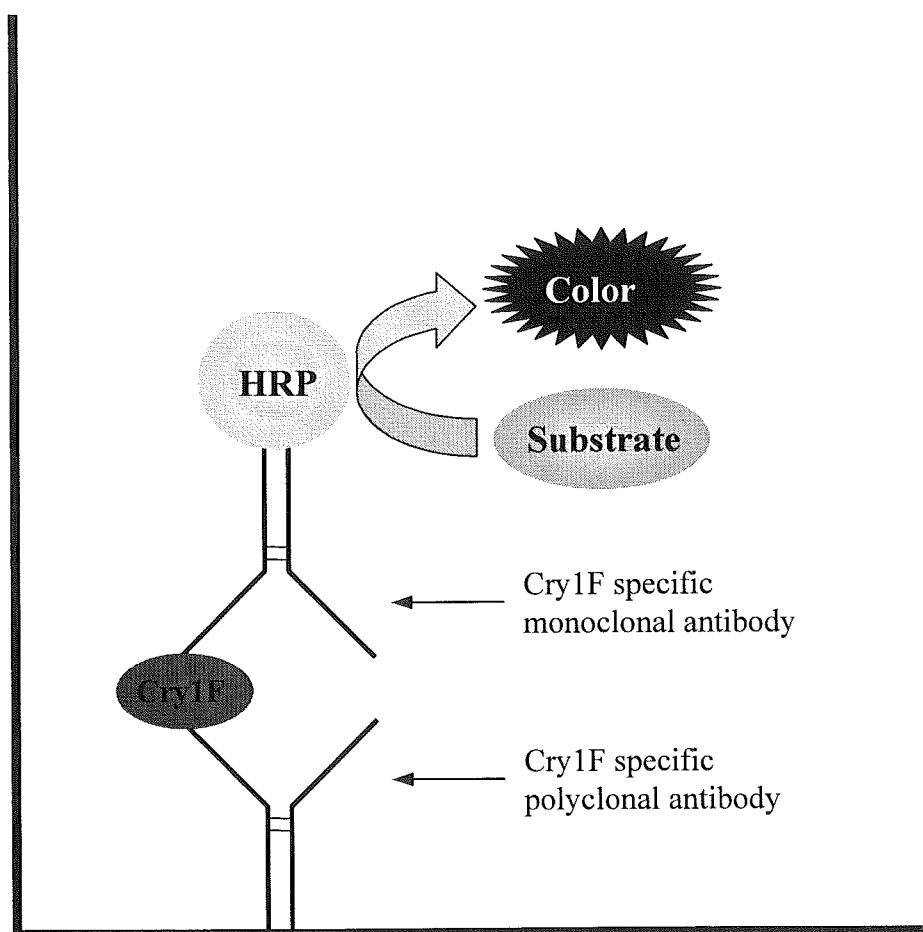


Figure 1. Illustration of the Double Antibody Sandwich ELISA.
HRP: horseradish peroxidase.

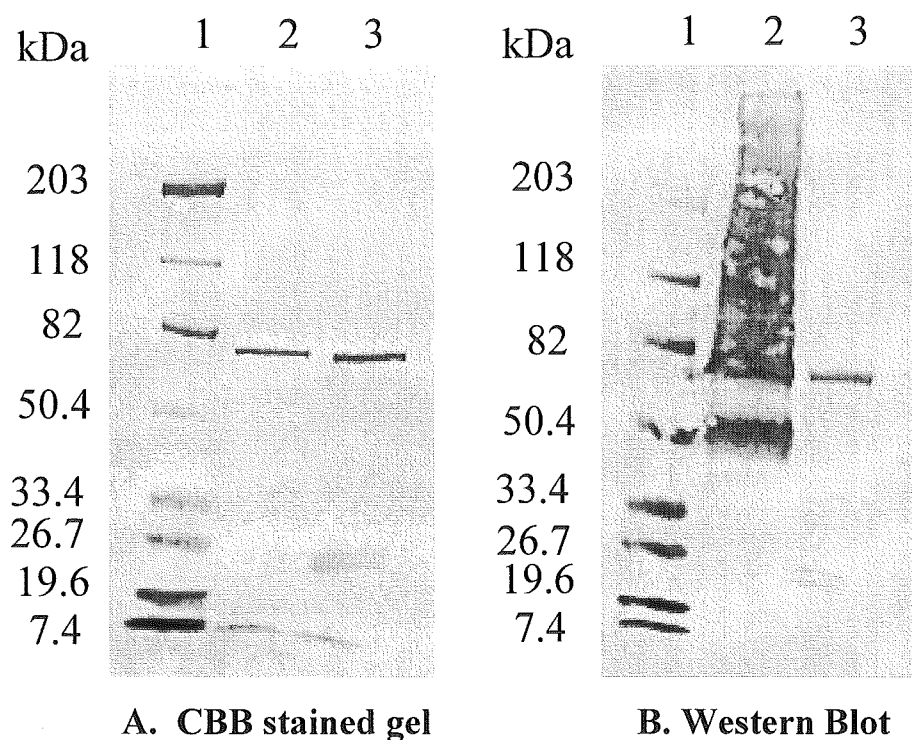


Figure 2. Coomassie Brilliant Blue (CBB) Stained Gel and Western Blotted Membrane of Cry1F Protein Before and After Heat Treatment (Conducted on November 27, 2001).

A: Coomassie Brilliant Blue stained gel

B: Western blotted membrane detected by polyclonal antibodies

Lane 1: pre-stained molecular weight markers (Bio-Rad)

Lane 2: Cry1F, non-heated, loaded 0.7 μ g

Lane 3: Cry1F, heated at 100 $^{\circ}$ C for 15 min, loaded 0.7 μ g

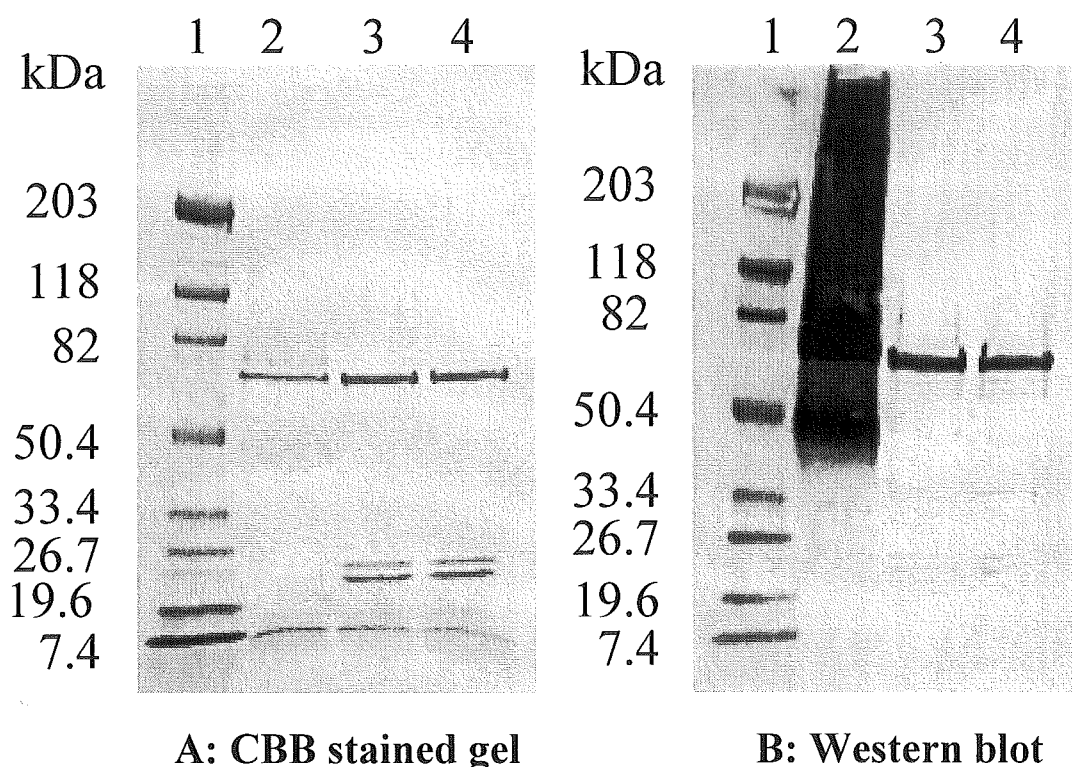


Figure 3. Coomassie Brilliant Blue (CBB) Stained Gel and Western Blotted Membrane of Cry1F Protein Before and After Heat Treatment (Conducted on January 9, 2002).
A: Coomassie Brilliant Blue stained gel
B: Western blotted membrane detected by polyclonal antibodies
Lane 1: pre-stained molecular weight markers (Bio-Rad)
Lane 2: Cry1F, non-heated, loaded 0.7 μ g
Lane 3: Cry1F, heated at 100 $^{\circ}$ C for 5 min, loaded 0.7 μ g
Lane 4: Cry1F, heated at 100 $^{\circ}$ C for 15 min, loaded 0.7 μ g

Appendix A—Biological Activity of Cry1F on Tobacco Budworm Following Heat Treatment

Table A-1. Biological Activity of Cry1F on Tobacco Budworm Following Heat Treatment
(Cited from Dow AgroSciences Study Report GH-C 5144 by R. A. Herman).

Treatment	% of Mortality ^a	% of Growth Inhibition ^b
4 °C	31%	96%
60 °C 30 min	25%	93%
75 °C 30 min	0%	8%
90 °C 30 min	0%	3%

Notes to superscripts:

^a % of mortality was calculated based on the number of dead insects to the total number of insects.

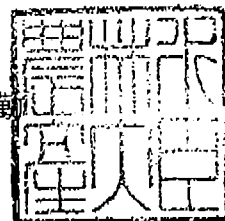
^b % of growth inhibition was calculated based on the reduction in the total weight of live insects in the Cry1F treatments to that of the negative buffer control treatment.



14生畜第994号
平成14年5月23日

ダウ・ケミカル日本株式会社
代表取締役 スティーブン・タトル 殿

農林水産大臣 武部 勤



組換え体利用飼料の安全性評価指針に適合していることの確認について

組換え体利用飼料の安全性評価指針（平成8年4月19日付け8畜B第585号農林水産事務次官依命通知）6の（2）に基づき、平成13年7月10日付けで申請のあった下記の生産物については同指針に適合していることを確認する。

記

生産物の名称：B.tCry1F 害虫抵抗性、グルホシネート耐性トウモロコシ
1507系統

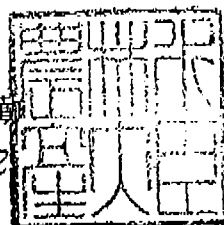


→ May 26, 2002
14 生畜第 994 号
平成 14 年 5 月 23 日

Dow Chemical Japan Limited
ダウ・ケミカル日本株式会社

代表取締役 スティーブン・タトル 殿
(Vice President Steven Tuttle)

農林水産大臣 武部 勤
The Minister of Agriculture
Forestry and Fisheries



Butomu Takebe

組換え体利用飼料の安全性評価指針に適合していることの確認について

Confirmation under "Guideline for Feed Safety"

組換え体利用飼料の安全性評価指針（平成 8 年 4 月 19 日付け 8 畜 B 第 585 号農林水産事務次官依命通知）6 の（2）に基づき、平成 13 年 7 月 10 日付けで申請のあった下記の生産物については同指針に適合していることを確認する。

記

Application Date
July 10, 2001

生産物の名称：Bt.Cry1F 害虫抵抗性、グルホシネート耐性トウモロコシ
1507 系統

Name of apply feed:

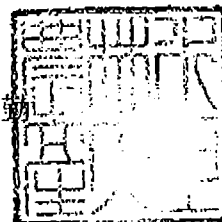
Bt. Cry1F Insect-resistant, Glufosinate
- tolerant Maize line 1507



平成14年6月25日

代表取締役 スティーブン・タトル 殿

農林水産大臣 武部



「農林水産分野等における組換え体の利用のための指針」（平成元年４月
２０日付け元農会第７４７号農林水産事務次官依命通知）第４章の１の規定に
基づき、平成１４年４月１９日付けで申請のあった下記の組換え体利用計画に
ついては、その内容が同指針に適合していることを確認する。

記

B. t. Cry1F害虫抵抗性及びグルホシネート耐性トウモロコシ1507系統の開放系における環境に対する安全性評価



14 農会第377号

平成14年6月25日

Heisei 14 years, June 25

Dow Chemical Japan Limited
 ダウ・ケミカル日本株式会社

June 25, 2002

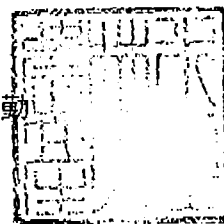
代表取締役 スティーブン・タトル 殿

Vice President Steven Tuttle

農林水産大臣 武部 勤

The Minister of Agriculture,
 Forestry and Fisheries

Tutomu Takebe



「農林水産分野等における組換え体の利用のための指針」に基づく

確認について

Confirmation under "Guidelines for Application of Recombinant DNA Organisms"

「農林水産分野等における組換え体の利用のための指針」（平成元年4月
 20日付け元農会第747号農林水産事務次官依命通知）第4章の1の規定に
 基づき、平成14年4月19日付けで申請のあった下記の組換え体利用計画に
 ついては、その内容が同指針に適合していることを確認する。

application Data: April 19, 2002

記

B. t. Cry1F害虫抵抗性及びグルホシネート耐性トウモロコシ1507系統の開放

系における環境に対する安全性評価

Safety evaluation for open field environment

on B. t. Cry1F Insect-resistant, Glufosinate-tolerant
 maize line 1507.

とうもろこし	福岡県直営技術センター MON863系統	日本モンサント株式会社
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○九州地方整備局告示第百六十八号
次のように道路の区域を変更したので、道路法（昭和二十七年法律第八十号）第十八条第一項の規定に基づき、告示する。

この関係図面は、平成十四年七月八日から二週間一般の縦覧に供する。
平成十四年七月八日
道路の種類 一般国道
路線名 五十号
道路の区域

○九州地方整備局告示第百六十九号
次のように道路の供用を開始するので、道路法（昭和二十七年法律第八十号）第十八条第二項の規定に基づき、告示する。

その関係図面は、平成十四年七月八日から二週間一般の縦覧に供する。
平成十四年七月八日
道路の種類 一般国道
路線名 五十号
道路の区域

○九州地方整備局告示第百七十号
次のように道路の供用を開始するので、道路法（昭和二十七年法律第八十号）第十八条第二項の規定に基づき、告示する。

その関係図面は、平成十四年七月八日から二週間一般の縦覧に供する。
平成十四年七月八日
道路の種類 一般国道
路線名 五十号
道路の区域

九州地方整備局長 江頭 和彦

道路の種類 一般国道
路線名 三三
道路の区域
変更前 敷地の幅員 延長
後別 敷地の幅員 延長
○九州地方整備局告示第百七十一号
次のように道路の区域を変更したので、道路法（昭和二十七年法律第八十号）第十八条第一項の規定に基づき、告示する。

その関係図面は、平成十四年七月八日から二週間一般の縦覧に供する。
平成十四年七月八日
道路の種類 一般国道
路線名 三三
道路の区域

○九州地方整備局告示第百七十二号
次のように道路の供用を開始するので、道路法（昭和二十七年法律第八十号）第十八条第二項の規定に基づき、告示する。

その関係図面は、平成十四年七月八日から二週間一般の縦覧に供する。
平成十四年七月八日
道路の種類 一般国道
路線名 三三
道路の区域

○九州地方整備局告示第百七十三号
次のように道路の供用を開始するので、道路法（昭和二十七年法律第八十号）第十八条第二項の規定に基づき、告示する。

その関係図面は、平成十四年七月八日から二週間一般の縦覧に供する。
平成十四年七月八日
道路の種類 一般国道
路線名 三三
道路の区域

九州地方整備局長 江頭 和彦

○文部科学省告示第五百十号
文化財保護法（昭和二十五年法律第二百四十四号）第八十三条の七第四項において準用する第五十六一条の三第四項の規定により、次の表の上欄に掲げる選定保存技術について、同表の下欄に掲げる若者を当該選定保存技術の保持者として追加認定する。

	氏名	所在地
一	山本 清太郎	東京都港区
二	山本 清太郎	東京都港区
三	山本 清太郎	東京都港区
四	山本 清太郎	東京都港区
五	山本 清太郎	東京都港区
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八十九	山本 清太郎	東京都港区
九十	山本 清太郎	東京都港区
九十一	山本 清太郎	東京都港区
九十二	山本 清太郎	東京都港区
九十三	山本 清太郎	東京都港区
九十四	山本 清太郎	東京都港区
九十五	山本 清太郎	東京都港区
九十六	山本 清太郎	東京都港区
九十七	山本 清太郎	東京都港区
九十八	山本 清太郎	東京都港区
九十九	山本 清太郎	東京都港区
一百	山本 清太郎	東京都港区

平成十四年七月八日
文部科学大臣 遠山 敦子

○文部科学省告示第百五十一号
文化財保護法（昭和二十五年法律第二百四号）第八十三条の七第一項及び第二項の規定により、次の表の上欄に掲げる文化財保存技術を選定保存技術に選定し、同表の下欄に掲げる団体を当該選定保存技術の保存団体として認定する。

保存技術	保存団体
平式十四年七月八日	文部科学大臣 遠山 敦子

文部科学大臣 遠山 敦子

○文部科学省告示第百五十二号
文化財保護法（昭和二十五年法律第二百十四号）第八十三条の七第四項において準用する第五十六条の三第四項の規定により、次の表の上欄に掲げる、選定保存技術について、同表の下欄に掲げる団体を当該選定保存技術の保存団体として追加認定する。

○文化庁告示第八号
文化財保護法（昭和二十五年法律第二百一十四号）第五十六条の十二で準用する同法第三十二條の二第一項の規定により、次の表に掲げる重要有形民俗文化財の管理団体として平取町を指定する。
平成十四年七月八日
文化庁長官 河合 肇雄

○厚生労働省告示第百三十四号
組換えDNA技術応用食品及び添加物の安全性審査の手続(平成十二年厚生省告示第百三十三号)
第三条第二項の規定に基づき、組換えDNA技術応用食品及び添加物の安全性審査の手続を経た生物
又は物(平成十三年厚生労働省告示第百十八号)の一部を改正し、公布の日から適用する。
平成十四年七月八日
厚生労働大臣 坂口 力
衷中

○文部科学省告示第百五十号
文化財保護法（昭和二十五年法律第二百四号）第八十三条の七第四項において準用する第五十六条の三第四項の規定により、次表の上欄に掲げる選定保存技術について、同表の下欄に掲げる者を当該選定保存技術の保持者として追加認定する。

平成十四年七月八日

文部科学大臣 遠山 敦子

○文部科学省告示第百五十一号
文化財保護法（昭和二十五年法律第二百十四号）第八十三条の七第一項及び第二項の規定により、次の表の上欄に掲げる文化財保存技術を選定保存技術に選定し、同表の下欄に掲げる団体を当該選定保存技術の保存団体として認定する。

保存技術	保存団体
平式十四年七月八日	文部科学大臣 遠山 敦子

文部科学大臣 遠山 敦子

平成十四年七月八日

存	団	体	事務所の所在地	波盛町	沖繩県国頭郡本部町字大浜八七四一 本部町教育委員会社会教育課内
表者	<p>第五十六条の十二で準用する同法第三十二条の 文化財の管理団体として平取町を指定する。</p> <p>文化庁長官 河合 雄雄</p>				<p>指定告示</p> <p>平成十四年二月十二日 文部科学省告示第十二号</p> <p>望野 茂 (北海道釧路郡平取町二風谷)</p>

○厚生労働省告示第百二十四号
組換えDNA技術応用食品及び添加物の安全性審査の手続(平成十一年厚生省告示第百三十三号)を組換えDNA技術応用食品及び添加物の安全性審査の手続を経た生物第三家第二項の規定に基づき、組換えDNA技術応用食品及び添加物の安全性審査の手続を經た生物又は物(平成十三年厚生労働省告示第百十八号)の一部を改正し、公布の日から適用する。
平成十四年七月八日
厚生労働大臣 坂口 力
表中



FAX TRANSMISSION

Date : 07/11/2002

To : [REDACTED] DAS Australia

(Fax [REDACTED])

From : [REDACTED], Dow AgroSciences – Tokyo

Number of pages including cover sheet (10 pages)

Dow Chemical Japan Ltd.

(Fax : 81-3-5460-6253)

Dow AgroSciences

(Tel : 81-3-5460-2311)

Tennoz Central Tower

2-24, Higashi Shinagawa 2-chome, Shinagawa-ku, Tokyo 140-8617

This is in reply to your request via e-mail of July 11. Hope it could be of some help to you. Please let me know if there is anything else I can do for you.

Thank you,

[REDACTED]
[REDACTED] Tokyo

an

Attach.

出 人: [REDACTED]
送信日時: [REDACTED] 2002 14:24
宛先: [REDACTED]
件名: Japanese Herculex I approvals

Fumoto san

The Australian authorities have requested that I provide an update on Herculex approvals. Would you please fax to me any appropriate letter from MAFF or MHLW which signifies that Herculex has been approved in your country.

thanks and regards
[REDACTED]

Regulatory Specialist	ph +61	[REDACTED]
Dow AgroSciences	fx +61	(0)2 9776 3199
Locked Bag 502	email	[REDACTED]
Frenchs Forest 1640	mobile	[REDACTED]
NSW AUSTRALIA		[REDACTED]

STILLMEADOW

INCORPORATED

PROTOCOL FOR STUDY 4281-98

Study Title: ACUTE ORAL TOXICITY STUDY IN MICE
(EPA FIFRA Guideline 81-1)

Test Substance: Cry1F *Bacillus thuringiensis* subsp. *aizawai* Delta-endotoxin

Test Facility: STILLMEADOW, Inc.
12852 Park One Drive
Sugar Land, Texas 77478

Approved:

[Redacted Signature]

Study Director
STILLMEADOW, Inc.

26 Aug 98

Date

Approved:

[Redacted Signature]

Vice President
STILLMEADOW, Inc.

8 Jun 98

Date

Reviewed:

[Redacted Signature]

Director, Quality Assurance Unit
STILLMEADOW, Inc. ✓

8 June 98

Date

Sponsor:

Mycogen

[Redacted Signature]

Approved:

[Redacted Signature]

Registration Manager

25 June 98 DS

28 June 98

Date

FF81-1 (Rev: 010198)

12852 Park One Drive ■ Sugar Land, Texas 77478 ■ 281 240-8828 ■ Fax 281 240-8448

PROTOCOL FOR STUDY 4281-98

A. GENERAL

1. Study Title:

ACUTE ORAL TOXICITY STUDY IN MICE

2. Purpose:

To assess the acute oral toxicity potential of the test substance when administered by the oral route (gavage) to mice.

3. Regulatory Compliance:

This study will be conducted in accordance with Pesticide Assessment Guidelines, Subdivision F, Hazard Evaluation: Human and Domestic Animals, Series 81-1.

This study will be conducted in compliance with Good Laboratory Practice Standards:

1. EPA FIFRA: 40 CFR 160
2. OECD: C(81)30 (Final)
3. Japanese MAFF

All procedures in this protocol are in compliance with Animal Welfare Act Regulations. All methods can be found in STILLMEADOW, Inc. Standard Operating Procedures (SOPs).

4. Quality Assurance:

The Protocol is reviewed by the Quality Assurance Unit (QAU). The study information will be entered into the Master Schedule. The study will be inspected at least once during its progress. Further inspections may be scheduled as needed to ensure the integrity of the study. Any deviations from SOPs, the Protocol, or Good Laboratory Practice Standards will be immediately reported to the Study Director and Management. The report will be audited and a statement prepared and signed which shall specify the dates inspections were made and findings reported to Management and to the Study Director.

5. Test Substance:

Cry1F *Bacillus thuringiensis* subsp. *aizawai* Delta-endotoxin. Test substance identification should include the name, batch number, and purity. Information regarding safety, stability, storage conditions, and disposal should also be provided by the Sponsor. The Sponsor assumes responsibility for purity and stability determinations. Analysis and archiving of reserve samples will be the responsibility of the Sponsor.

6. Proposed Schedule:

Testing will begin within approximately three weeks of receipt of the test substance and authorization to conduct the study.

Proposed Start Date: June 17, 1998

Proposed End Date: July 1, 1998

The study will be extended if several dose levels are required.

A. GENERAL (cont.)

7. Study Director:

[REDACTED]

8. Experimental Summary:

The test substance will be administered to mice orally by gavage. The animals will be observed three times on the day of dosing for mortality and signs of pharmacologic and/or toxicologic effects and once daily thereafter for at least 14 days. If a sufficient number of dose levels are tested, an LD₅₀ with slope function and 95% confidence limits will be calculated.

9. Protocol Amendments:

Any alteration in the Protocol will be justified, approved by the Study Director and Sponsor, and recorded in writing.

10. Sponsor Audits:

The Sponsor may send an authorized representative to inspect the test system and/or data on the STILLMEADOW, Inc. premises during normal working hours.

B. EXPERIMENTAL DESIGN

1. Animals



- a. Species: Albino mice
- b. Strain/Source: ICR (Harlan Sprague Dawley, Inc., Houston, TX)
- c. Justification of Species: Rodents are conventionally used to provide an index of toxicity on which human hazard can be judged. Mice were chosen because they require less test substance for dosing.
- d. Quantity and Sex: Five males and five females (nulliparous and non-pregnant) for the initial dose level and 5/sex for any additional dose levels, if required (see B.3.g.).
- e. Age/Weight: Young adult (8 - 12 weeks) Minimum body weight of 21-29 g. Weight variation shall not exceed $\pm 20\%$ of the mean for each sex.
- f. Identification: Ear punch
- g. Acclimation and Health Status: Animals will be acclimated for at least five days prior to testing. Normal weight gain, appearance, and behavior will be factors used to select healthy animals for testing. Only naive animals will be selected.

2. Animal Husbandry

- a. Cages: Polycarbonate boxes with wire tops; hardwood bedding.
- b. Number per Cage: Animals will be housed individually during the study.
- c. Food: PMI Feeds, Inc.™ Formulab #5008, available *ad libitum* prior to fasting and after dosing. Analyzed by manufacturer.
- d. Water: Tap water; available *ad libitum* (water bottles). Municipal water supply analyzed by Texas Natural Resource Conservation Commission (TNRCC) Water Utilities Division.
- e. Contaminants: There are no known contaminants in the feed or water available to laboratory animals that would be expected to interfere with this study.
- f. Environment: Environmental controls for the animal room will be set to maintain a temperature of approximately $22^{\circ}\text{C} \pm 3^{\circ}\text{C}$, a relative humidity range of approximately 30 - 80%, a 12-hour light/dark cycle (regulated automatically), and room ventilation of approximately 10 - 12 air changes per hour.

B. EXPERIMENTAL DESIGN (cont.)

3. Test Substance Administration

- a. Preparation of Animals: Animals will be fasted for at least 16 hours prior to dosing. Food will be made available immediately after dosing.
- b. Reason for Route of Administration: Historically, the oral route has been a route of choice for evaluation of the toxicity potential of a test substance and is a potential route of human exposure.
- c. Assignment of Animals to Groups: Animals will be randomly assigned to groups so that individual body weights will not exceed $\pm 20\%$ of the mean weight for each sex.
- d. Preparation of Test Substance: The test substance will be administered diluted in an appropriate vehicle to the most concentrated workable dilution. All animals in a dose group will receive the same concentration of the test substance. Maximum dose volume will not exceed 2 mL/100 g. The dosing solutions will be prepared and dosed immediately after mixing.
- e. Dosing: The animals will be dosed by gavage with an appropriately-sized stainless steel ball-tipped dosing needle and syringe. Individual doses will be calculated based upon the animal's body weight on the day of test substance administration.
- f. Control Groups:  If the test substance is administered as received, a control group is not necessary. If the test substance is administered in a vehicle for which the toxicity is not known, then a vehicle control group (five males and five females) will be required.
- g. Dose Level:  A single dose level of approximately 5050 mg/kg will be administered to five animals per sex. If no mortality occurs at this level, no further testing is required.

If mortality meets or exceeds 40% in either or both sexes at the level tested, then at least two additional dose levels will be tested for those sexes upon approval by Sponsor. There will be at least five animals (five males and/or five females) per dose level. The number and spacing of dose levels will be chosen in collaboration with the Sponsor so that an LD₅₀ can be determined. If both sexes are tested at a given dose level, then the group will consist of an equal number of males and females.

B. EXPERIMENTAL DESIGN (cont.)

4. Observations

a. Clinical Signs:

Observations for signs of pharmacologic and/or toxicologic effects will be made three times on the day of dosing, and daily thereafter for 14 days. Mortality checks will be performed twice daily, separated by at least 4 hours, throughout the duration of the study. The duration of the study should be determined by the toxic reactions and may be extended beyond 14 days when considered necessary. The nature, onset, severity, and duration of all gross or visible pharmacologic or toxicologic signs will be recorded.

Observations will include: skin, fur, eyes and mucous membranes, somatomotor activity, and behavior pattern. Particular attention will be given to tremors, convulsions, salivation, diarrhea, lethargy, sleep, and coma.

b. Body Weights:

Body weights will be recorded on the day prior to dosing (Day -1), the day of dosing (Day 0), and weekly thereafter (Days 7 and 14), or at the time of discovery after death.

c. Sacrifice of Animals:

All surviving animals will be sacrificed with an overexposure to CO₂.

d. Necropsy:

A gross necropsy will be conducted on each animal at termination of the study or at the time of discovery after death, and the results recorded. The gross necropsy shall include the following:

1. Gross observations of external surfaces; all orifices; and thoracic, abdominal, and pelvic cavities.
2. Upon request of the Sponsor, sections of abnormal tissues may be saved in 10% neutral buffered formalin for possible histopathologic examination. Tissues will be discarded if histopathology is not performed.

5. Evaluation of Results:

Unless only a single dose level is tested, an LD₅₀ with slope function and 95% confidence limits will be calculated for males, females, and males and females combined (if necessitated by mortality in one or both sexes) by the method of Litchfield and Wilcoxon (Litchfield, J.T., Jr., and Wilcoxon, F.: A Simplified Method of Evaluating Dose-Effect Experiments, J. Pharm. & Exp. Ther. 96, 99-115, 1949) or other appropriate method.

6. Test Substance Accountability:

A comprehensive inventory of test substance received and used will be kept. The test substance container(s) will be weighed when received at this facility, and a record of all test substance use will be maintained. Test substance and test substance dosing solutions will be stored in the original containers, or in the equivalent thereof, or in glass containers with Teflon-lined caps.

B. EXPERIMENTAL DESIGN (cont.)

7. Disposal of Unused Test Substance:

Unused test substance will be returned or disposed of at the Sponsor's expense after the termination of the study. The Sponsor should specify return or disposal at the time of study authorization. If returned, the recipient of the test substance will be notified in advance of shipping. The sample will be accompanied by a chain of custody letter describing the sample(s) contained in the shipment.

8. Safety Precautions:

General safety precautions required by laboratory SOPs will be followed. The Sponsor will supply basic toxicity data on the test substance to be used. However, since the toxicity of test substances is often not well characterized, this laboratory will be conservative in setting safety procedures. The Sponsor or Sponsor's Representative shall be notified of any exposures requiring a physician's examination or care.

C. DATA MANAGEMENT

1. Records:

The following records will be maintained during the study and transferred to the STILLMEADOW, Inc. archives upon study termination.

- a. Protocol and Protocol Amendments (if any).
- b. Final report and amendments (if any).
- c. Study correspondence.
- d. Animal receipt/acclimation data.
- e. Test substance receipt, identification as supplied by Sponsor, preparation, administration, and disposition.
- f. Test animal information: number, sex, source, strain.
- g. Body weight data.
- h. Daily observation data for signs of pharmacologic and/or toxicologic effects.
- i. Mortality data, gross necropsy findings, and histopathology findings, if requested.
- ✓ j. Calculations (if any) of the LD₅₀ and slope determinations with 95% confidence limits.
- k. SOP/Protocol deviations
- l. Other pertinent data.

2. Data Storage:

All raw data will be retained at STILLMEADOW, Inc.

C. DATA MANAGEMENT (cont.)

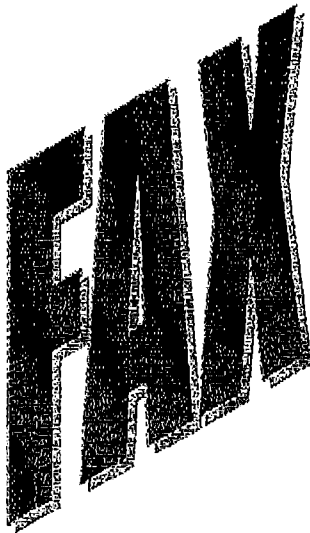
3. Data Reporting:

The final report will include all data as described in the Good Laboratory Practice Standards, including:

- a. Statement from the Quality Assurance Unit.
- b. Signature of the Study Director.
- c. A GLP Compliance Statement signed by the Study Director.
- d. Names of scientific personnel involved in the study.
- e. Dates of study initiation and termination.
- f. Identification, description, preparation, and storage of the test substance.
- g. All pertinent animal data, animal husbandry, dosing information, and observation methods.
- h. Description of the test procedures.
- i. If calculated, the LD₅₀ and slope function data with 95 % confidence limits for males, females, and males and females combined (if necessitated by mortality in one or both sexes).
- j. Individual body weights.
- k. Observations on the nature, onset, severity, and duration of all gross or visible pharmacologic and/or toxicologic signs. Nonroutine findings will be addressed in a discussion section in which the relationship to treatment and historical data will be evaluated.
- l. Individual mortality data, gross necropsy findings, and histopathology findings, if requested.
- m. A reference to this Protocol.

4. Report Submission:

A report will be submitted after termination of the in-life portion of the study (subject to completion of histopathology, if requested).



9330 Zionsville Road
Indianapolis, Indiana
46268

Date: July 11, 2002

To: [REDACTED]

Fax #: [REDACTED]

From: [REDACTED]

Phone: [REDACTED]

Fax: [REDACTED]

Number of pages (including cover sheet): 5

The information transmitted is intended only for the person or entity to which it is addressed and may contain confidential and/or privileged material. If you are not the intended recipient of this message you are hereby notified that any use, review, retransmission, dissemination, distribution, reproduction or any action taken in reliance upon this message is prohibited. If you received this in error, please contact the sender.

Message:

Acute tox study raw data.

MOUSE ACUTE ORAL TOXICITY

Date Rec'd: 14 Aug 98
Strain: HSD ICR(CD-1)
Date(s) Rec'd: 24 Aug 98
Date(s) of Birth: 17 Jul 98

Sample: Cry 1F Bacillus
thuringiensis subsp.
Density: NA g/mL
aizawa: Delta-endotoxin
Vehicle: 2% CMS
Conc: 15.96
Dose Temp: RT
Dose: 33.7 mU/kg
5050 mg/kg

Room No: 133
Study No.: 4281-98
Guideline No.: NA
Client Code: M-5
Fast Tech: HLW
Fast Time: 16.00
Fast Date: 02 Sept 98
Dose Tech: HLW
Dose Start: 10:45/11:46
Dose Stop: 11:01/12:00
Dose Date: 03 Sept 98

Animal Number *	Check When Dosed	Dose Amount (mL)	Body Weights (g)				Scale Hour/Day of Death	Tech Time Date	Necropsy Findings				
			Day -1	Day 0	Day 7	Final							
			02 Sep	03 Sep	10 Sep	17 Sep							
51 -M	✓ ✓	0.451 0.451	27.5	26.8	29.6	30.5	SLOF1 T-SAC	HF 15:15 17 Sep 98	NOA				
52 -M	✓ ✓	0.495 0.495	30.0	29.4	31.8	33.3	T-SAC	HF 15:15 17 Sep 98	NOA				
53 -M	✓ ✓	0.461 0.461	28.2	27.4	30.5	32.8	T-SAC	HF 15:15 17 Sep 98	NOA				
54 -M	✓ ✓	0.476 0.476	29.1	28.3	30.2	31.8	T-SAC	HF 15:15 17 Sep 98	NOA				
55 -M	✓ ✓	0.454 0.454	28.2	27.0	29.1	31.1	T-SAC	HF 15:15 17 Sep 98	NOA				
Calculation Check			Scale > <u>SLOF1</u> <u>017</u> <u>017</u> <u>SLOF1</u>				Males				Day 0 Allowed Body Weight Variation (20%)		
<u>HF</u> <u>10:28</u> <u>03 Sep 98</u>			Tech > <u>CU</u> <u>HLW</u> <u>CU</u> <u>HLW</u> <u>HF</u>				Upper		Lower		Mean		Tech <u>CU</u>
			Time > <u>10:10</u> <u>11:40</u> <u>8:20</u> <u>14:38</u> <u>15:10</u>										Time <u>8:27</u>
			Date > <u>03 Sep</u> <u>03 Sep 98</u> <u>03 Sep</u> <u>10 Sep</u> <u>17 Sep 98</u>				<u>33.3</u>		<u>22.2</u>		<u>27.8</u>		Date <u>03 Sep 98</u>

INSPECTOR: HLW PHASE: obs DATE: 9 Sep 98
* Mice were not housed individually but by sex due to a variability of housing units at time of study HLW 10 Sept 98
STILLMEADOW, INC.

MOUSE ACUTE ORAL TOXICITY

Strain: HSD (SD)

Study No.: 4281-98

Animal Number	Check When Dosed	Dose Amount (mL)	Body Weights (g)				Scale Hour/Day of Death	Tech Time Date	Necropsy Findings
			Day -1	Day 1	Day 7	Final			
56	✓ ✓	0.444 0.444	27.0	26.4	28.1	31.3	TSAL	HF 15:15 17 Sep 98	NOA
57	✓ ✓	0.419 0.419	26.8	24.9	26.9	28.8	TSAL	HF 15:15 17 Sep 98	NOA
58	✓ ✓	0.424 0.424	27.3	25.2	26.3	28.8	TSAL	HF 15:15 17 Sep 98	NOA
59	✓ ✓	0.419 0.419	25.4	24.9	27.1	27.1	TSAL	HF 15:15 17 Sep 98	NOA
60	✓ ✓	0.453 0.453	27.8	26.9	28.0	33.3	TSAL	HF 15:15 17 Sep 98	NOA
Calculation Check			Scale >	54.07	0.7	0.7	56.81	Females	
			Tech >	CU	HLM	CU	HLM	Day 0 Allowed Body Weight Variation (20%)	
			Time	10:12	11:42	5:25	14:40	Upper	Lower
			Date >	03 Sep	07 Sep	03 Sep	12 Sep	Mean	
								30.8	20.5
								25.7	
			Tech	CU					
			Time	8:28					
			Date	03 Sep 98					

12 cu
03 Sep 98

STILLMEADOW, INC.

11-07-02 22:40 TO: Dow AgroSciences Regulatory FROM: 317 337 4549

P03

Group	<u>Males</u>	
Dose Level:	5050	mg/kg

Animal No. 51, 52, 53, 54, 55
Sample: Cry 1F Bacillus thuringiensis
subsp. aizawai Delta-endotoxin

Study No. 4281-98
Time Dosed: 10:45 / 11:46
Date Dosed: 03 Sep 98

[illegible]

v - very slight; s - slight; m - moderate; e - extreme; NOA - No Observation Abnormalities

STILLMEADOW, INC.

SUMMARY

(In accordance with 40 CFR part 152, this summary is available
for public release after registration)

STUDY TITLE

In Vitro Simulated Gastric Fluid Digestibility Study of Truncated Cry1F Delta-endotoxin Derived from *Pseudomonas fluorescens*

DATA REQUIREMENTS

NA

AUTHOR(S)

STUDY COMPLETED ON

January 14, 2002

PERFORMING LABORATORY

**Regulatory Laboratories—Indianapolis Lab
Dow AgroSciences LLC
9330 Zionsville Road
Indianapolis, Indiana 46268-1054**

LABORATORY STUDY ID

GH-C 5367

In Vitro Simulated Gastric Fluid Digestibility Study of Truncated Cry1F Delta-endotoxin
Derived from *Pseudomonas fluorescens*

SUMMARY

Corn plants have been genetically modified through the introduction of a synthetic gene which encodes for a truncated version of an insecticidal protein (Cry1Fa2, commonly referred to as Cry1F) isolated from *Bacillus thuringiensis* var. *aizawai* strain PS811. This protein when expressed in corn cultivars provides crop resistance against lepidopteran pests, including the European corn borer (*Ostrinia nubilalis*). The purpose of this study was to evaluate the digestibility of the truncated Cry1F protein in a simulated gastric fluid (SGF) model. The test and control substances were incubated with SGF for specific time intervals and then analyzed by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and Western blot analysis. Truncated Cry1F was rapidly digested in less than 15 seconds in the simulated gastric model as demonstrated by SDS-PAGE and Western blot analysis.

STUDY TITLE

In Vitro Simulated Gastric Fluid Digestibility Study of Truncated Cry1F Delta-endotoxin
Derived from *Pseudomonas fluorescens*

DATA REQUIREMENTS

NA

AUTHOR(S)

[REDACTED]

STUDY COMPLETED ON

January 14, 2002

PERFORMING LABORATORY

Regulatory Laboratories—Indianapolis Lab
Dow AgroSciences LLC
9330 Zionsville Road
Indianapolis, Indiana 46268-1054

LABORATORY STUDY ID

GH-C 5367

STATEMENT OF NO DATA CONFIDENTIALITY CLAIMS

Compound: Cry1F δ -endotoxin

Title: *In Vitro* Simulated Gastric Fluid Digestibility Study of Truncated Cry1F Delta-endotoxin Derived from *Pseudomonas fluorescens*

No claim of confidentiality is made for any information contained in this study on the basis of its falling within the scope of FIFRA Section 10 (d)(1)(A)(B), or (C).*

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Company Agent: [REDACTED]

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STATEMENT OF COMPLIANCE WITH GOOD LABORATORY PRACTICE STANDARDS

Title: *In Vitro* Simulated Gastric Fluid Digestibility Study of Truncated Cry1F Delta-endotoxin Derived from *Pseudomonas fluorescens*

Study Initiation Date: January 3, 2002 Study Completion Date:
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At the time this study was conducted, it was not subject to Good Laboratory Practice Standards, but was, nevertheless, conducted in accordance with existing and proposed standards.

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QUALITY ASSURANCE STATEMENT

Compound: Cry1F δ -endotoxin

Title: *In Vitro* Simulated Gastric Fluid Digestibility Study of Truncated Cry1F Delta-endotoxin Derived from *Pseudomonas fluorescens*

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NON-GLP STUDY

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ABBREVIATIONS

AI	active ingredient
BCIP	5-bromo-4-chloro-3-indolyl phosphate
BME	2-mercaptoethanol
BSA	bovine serum albumin
CAPS	3-cyclohexylamino-1-propane sulfonic acid
CBB	coomassie brilliant blue
kDa	kiloDalton
MW	molecular weight
PAb	polyclonal antibody
PBST	phosphate buffered saline (10mM phosphate buffer, 138 mM NaCl, 2.7 mM KCl) with 0.05% Tween 20, pH 7.4
SDS-PAGE	sodium dodecyl sulfate – polyacrylamide gel electrophoresis
SGF	simulated gastric fluid
TSN	Dow AgroSciences Test Substance Number

In Vitro Simulated Gastric Fluid Digestibility Study of Truncated Cry1F Delta-endotoxin
Derived from *Pseudomonas fluorescens*

ABSTRACT

Corn plants have been genetically modified through the introduction of a synthetic gene which encodes for a truncated version of an insecticidal protein (Cry1Fa2, commonly referred to as Cry1F) isolated from *Bacillus thuringiensis* var. *aizawai* strain PS811. This protein when expressed in corn cultivars provides crop resistance against lepidopteran pests, including the European corn borer (*Ostrinia nubilalis*). The purpose of this study was to evaluate the digestibility of the truncated Cry1F protein in a simulated gastric fluid (SGF) model. The test and control substances were incubated with SGF for specific time intervals and then analyzed by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and Western blot analysis.

INTRODUCTION

The purpose of this study was to evaluate the digestibility of truncated Cry1F protein in simulated gastric fluid. The protein used as a test substance in this study was produced with a bacterium *Pseudomonas fluorescens* (Pf). The microbially derived Cry1F was shown to be biochemically and insecticidally equivalent to the Cry1F protein produced in transgenic TC1507 corn plants (2, 3). Bovine serum albumin (BSA) and β -lactoglobulin were included in the experimental design of this study for comparative purposes. BSA was used as a positive control for the experiment since it is known to degrade readily in SGF, and β -lactoglobulin was used as a poorly digestible control since it is known to persist in SGF. The test and control proteins were incubated with SGF for specific time intervals and were analyzed by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and Western blot analysis. The biochemical and immunological methods employed in this study are standard techniques for protein analysis. SDS-PAGE separates proteins based on the apparent molecular weight (mass). Western blotting of proteins to a nitrocellulose membrane following SDS-PAGE and immunodetection with a protein specific antibody is widely used to identify the authenticity of a molecule in a crude preparation.

EXPERIMENTAL

Test Substances

The test substance used in this study is listed in the following table:

Test Substance	ID Number	% AI (w/w)	Reference
Cry1F	TSN101788	13.7%	BIOT 013056 (1)

AI: active ingredient

The recombinant truncated Cry1F protein was produced in *P. fluorescens* strain MR872, which was prepared at the Dow AgroSciences facility in San Diego, California. The Cry1F protein was expressed in the bacterial cells as inclusion bodies and after fermentation the inclusion bodies were extracted and washed. The truncated Cry1F was prepared by trypsinolysis of the full length Cry1F protein. The Dow AgroSciences (DAS) test substance number for this lot of the truncated Cry1F protein is TSN 101788. The Cry1F protein was 13.7% of the total solid weight of the lyophilized powder (1). It should be noted that in this lyophilized preparation, the purity of the Cry1F protein was quite high (>80%) in terms of the percentage of Cry1F protein to total protein as determined by SDS-PAGE analysis (1, 2). In the lyophilized powder, besides proteins (Cry1F, its low molecular weight fragments and other proteins), there were also non-proteinaceous substances such as buffering chemicals and salts that were present in the liquid formulation before freeze-drying. The non-proteinaceous substances account for major portion of the weight in the lyophilized powder. This microbially derived Cry1F protein has been demonstrated to be equivalent to the transgenic corn-produced Cry1F in other studies (2, 3).

Control Substances

The positive and negative control substances used in this study are listed in the following table:

Control Substance	Purity	Reference	ID Number
Bovine serum albumin (BSA)	≥ 96%	Sigma Catalog #A9418	Lot 118H0595
β-lactoglobulin	≥ 90%	Sigma Catalog #L7880	Lot 70K7049

Reference Substances

The reference substances used in this study are listed in the following table:

Reference Substance	Product Name	Lot Number	Assay	Reference
Molecular Weight Markers	Bio-Rad Kaleidoscope Prestained Standards	90032	Biochemical/ Western Blotting	Bio-Rad Cat# 161-0324 MW Markers of 213, 128, 85, 42.6, 31.2, 18, and 8.5 kDa
Molecular Weight Markers	BenchMark Protein Ladder	1097741	Biochemical/ SDS-PAGE	GibcoBRL Cat# 10747-012, MW Markers of 220, 160, 120, 100, 90, 80, 70, 60, 50, 40, 30, 25, 20, 15, and 10 kDa

Reference substances were chosen by the procedure used.

Test Methods

Equimolar (~0.074 mM) solutions of the test and control substances were prepared as follows. TSN101788 (Cry1F) was reconstituted by weighing 35.6 mg of lyophilized powder in a 4-mL test tube and adding 1 mL of 10 mM CAPS, pH 11.0. BSA was reconstituted by weighing 24.8 mg of powder in a 15-mL centrifuge tube and adding 5 mL of 3.0 mM NaCl, pH 1.2. β -lactoglobulin was reconstituted by weighing 13.6 mg of powder and adding 5 mL of 3.0 mM NaCl, pH 1.2. Simulated gastric fluid (SGF) (pH ~1.2) containing approximately 0.3% (w/v) pepsin (Sigma Aldrich, St. Louis, MO) was prepared as described in the United States Pharmacopeia (4).

The digestions were performed for time intervals of 0, 15 and 30 seconds, and for 1, 2, 5, 10 and 15 minutes in a water bath set to 37 °C. The three proteins, Cry1F, BSA, and β -lactoglobulin were digested as follows. Three 1.5-mL microcentrifuge tubes, each containing a 285- μ L aliquot of SGF, were placed in the 37 °C water bath. After 5 minutes, 73.2 μ g (15 μ L) of Cry1F, 74.4 μ g (15 μ L) of BSA, and 40.8 μ g (15 μ L) of β -lactoglobulin, respectively, were added to the tubes and a timer was set. After each specified incubation interval, 20 μ L of the reaction mixture was removed and added to tubes containing stop solution (8 μ L sodium carbonate). The stopped reactions were then placed on ice until all of the time points were sampled for the three proteins. An SGF reagent blank was prepared by substituting water for the sample protein and incubating for 0 and 15 minutes at 37 °C. For each of the proteins above, a zero time point (undigested control) was prepared as follows. First, an aliquot of SGF was stopped with sodium carbonate and the respective protein was added to the solution. The digested proteins and their undigested 'controls' were stored in a freezer overnight.

The samples (each protein at each time point) were mixed with Laemmli sample buffer (Bio-Rad Laboratories, Hercules, CA), containing freshly added β -mercaptoethanol (Bio-Rad Laboratories, Hercules, CA). Single 10-20% polyacrylamide gels (Zaxis Inc., Hudson, OH) of BSA and β -lactoglobulin and duplicate gels of Cry1F were set up and loaded as described in the following table.

Protein	Volume of sample loaded per lane for SDS-PAGE analysis	Amount of protein (before digestion) loaded per lane for SDS-PAGE analysis	Volume of sample loaded per lane for Western blot analysis	Amount of protein (before digestion) loaded per lane for Western blot analysis
BSA	25 μ L	~1.77 μ g	N/A	N/A
β -lactoglobulin	25 μ L	~0.97 μ g	N/A	N/A
Cry1F	10 μ L	~0.58 μ g	10 μ L	~ 0.12 μ g

The samples were then electrophoresed at a constant amperage of 30 mA per gel for 60 minutes. The electrophoresis buffer was Tris/Glycine/SDS buffer from Bio-Rad. After separation, three of the gels were stained with Pierce Gel Code Blue Stain. Proteins on the remaining Cry1F gel

were electro-blotted to a nitrocellulose membrane using a Bio-Rad Criterion Blotter under a constant voltage of 100 v. Following protein transfer, the membrane was blocked with PBST and 5% powdered milk. Polyclonal antibody specific to Cry1F (Strategic Diagnostics Incorporated, Newark, NJ, lot #200.310-4) was then added to the blot to allow for protein detection. A conjugate of goat anti-rabbit IgG (H+L)- alkaline phosphatase (Pierce, Rockford, IL) was used as the secondary antibody. A substrate solution containing 100 mM Tris, 100 mM NaCl, 5 mM MgCl₂, 0.025% 5-bromo-4-chloro-3-indolyl phosphate (BCIP), and 0.05% p-nitroblue tetrazolium chloride (NBT) was used for colorimetric development of the immunoreactive protein bands.

RESULTS

The positive and negative controls, BSA and β -lactoglobulin, respectively, responded as expected (Table 1). BSA was not detected at the 15 second time point when subjected to the simulated gastric environment (Figure 2, lane 3). β -lactoglobulin remained readily detectable for 15 minutes (the duration of the experiment) (Figure 1, lane 10). The test protein (Cry1F and its minor degradation fragments) were not detectable at 15 seconds as demonstrated by both SDS-PAGE (Figure 3, Panel B, lane 4) and Western blot analysis (Figure 3, Panel A, lane 4).

CONCLUSION

Truncated microbial Cry1F protein is readily digested by pepsin (<15 seconds) under simulated gastric conditions (pH 1.2) as demonstrated by both SDS-PAGE and Western blot analysis.

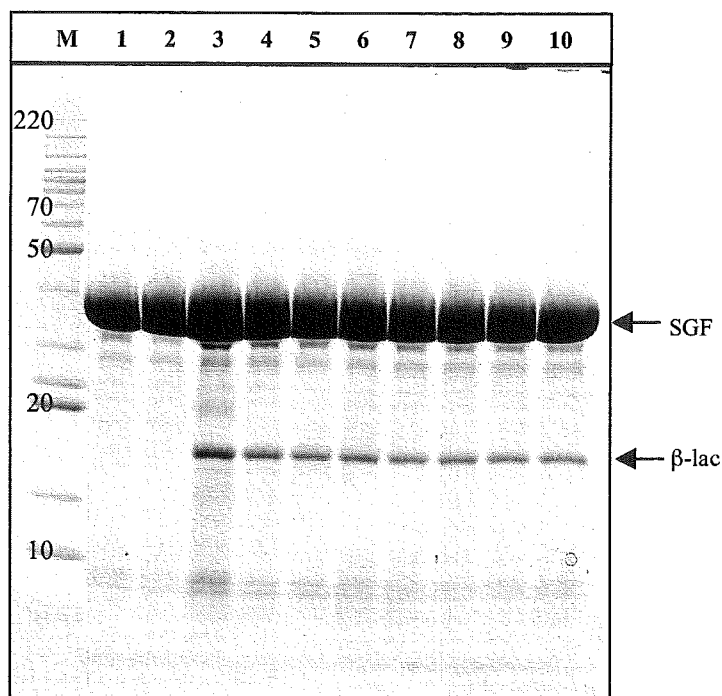
REFERENCES

1. Collins, R. A. (2001). Certificate of analysis of test/reference/control substances (TSN 101788). Dow AgroSciences BIOT 013056.
2. Schafer, B. W. and Schwedler, D. A. (2001). Characterization of the Recombinant Cry1F Protein Derived from *Pseudomonas fluorescens* and Transgenic Maize, GH-C 5294, 21 pp, unpublished report of Dow AgroSciences LLC.
3. Evans, S. L. (1998). Equivalency of Microbial and Maize Expressed Cry1F Protein; Characterization of Test Substances for Biochemical and Toxicological Studies. Mycogen Corporation MYCO98-001.
4. Board of Trustees (ed.) (1995). Simulated Gastric Fluid, TS, pp. 2053 in *The United States Pharmacopeia 23, The National Formulary 18*. United States Pharmacopeial Convention, Inc., Rockville, MD.

Table 1. Results of the *In Vitro* Digestibility Study of Truncated, Microbial Cry1F Protein in Simulated Gastric Fluid

Protein	Digestion time demonstrated by SDS-PAGE analysis	Digestion time demonstrated by Western blot analysis
BSA	<15 seconds	N/A
Cry1F	<15 seconds	<15 seconds
β -lactoglobulin	>15 minutes	N/A





Lane Assignments for β -lactoglobulin SDS-PAGE Gel

M - Benchmark Protein Ladder

1 - SGF Reagent Blank, 0 minute incubation

2 - SGF Reagent Blank, 15 minute incubation

3 - β -lactoglobulin (0.97 μ g), 0 minute digestion

4 - 15 second digestion

5 - 30 second digestion

6 - 1 minute digestion

7 - 2 minute digestion

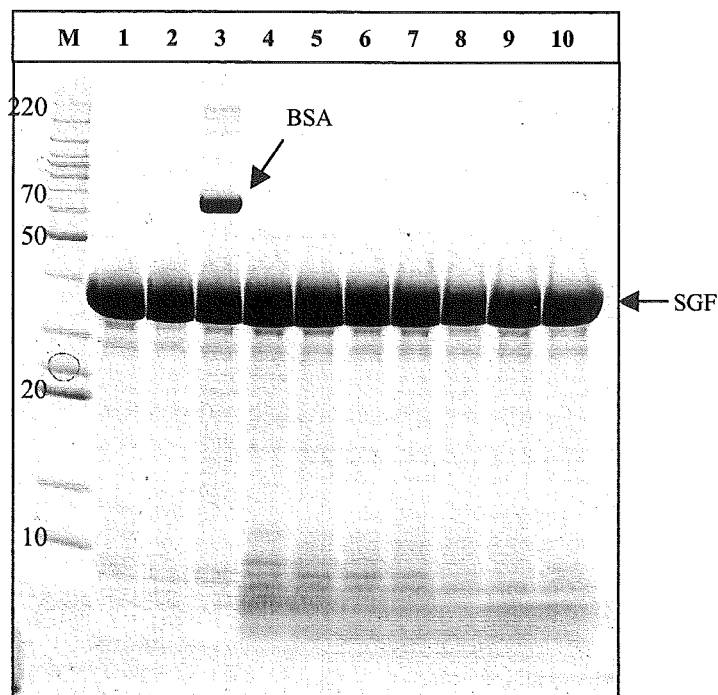
8 - 5 minute digestion

9 - 10 minute digestion

10 - 15 minute digestion

* Note MW markers are labeled in kDa.

Figure 1. SDS-PAGE Analysis of β -lactoglobulin Protein Subjected to Digestion in Simulated Gastric Fluid



Lane Assignments for Bovine Serum Albumin SDS-PAGE Gel

M - Benchmark Protein Ladder

1 - SGF Reagent Blank, 0 minute incubation

2 - SGF Reagent Blank, 15 minute incubation

3 - Bovine Serum Albumin (1.77 μ g), 0 minute digestion

4 - 15 second digestion

5 - 30 second digestion

6 - 1 minute digestion

7 - 2 minute digestion

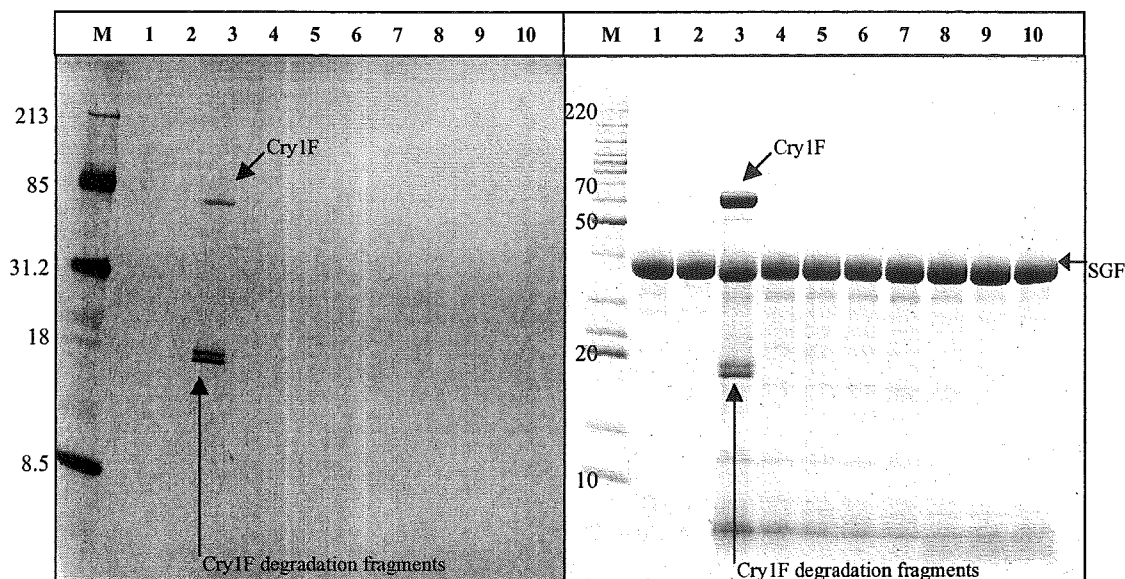
8 - 5 minute digestion

9 - 10 minute digestion

10 - 15 minute digestion

* Note MW markers are labeled in kDa.

Figure 2. SDS-PAGE Analysis of Bovine Serum Albumin Protein Subjected to Digestion in Simulated Gastric Fluid



Panel A: Cry1F Western Blot

Lane Assignments

M - Bio-Rad Prestained Standards

1 - SGF Reagent Blank, 0 minute incubation

2 - SGF Reagent Blank, 15 minute incubation

3 - Cry1F (0.12 µg), 0 minute digestion

4 - 15 second digestion

5 - 30 second digestion

6 - 1 minute digestion

7 - 2 minute digestion

8 - 5 minute digestion

9 - 10 minute digestion

10 - 15 minute digestion

Panel B: Cry1F SDS-PAGE Gel

Lane Assignments

M - Benchmark Protein Ladder

1 - SGF Reagent Blank, 0 minute incubation

2 - SGF Reagent Blank, 15 minute incubation

3 - Cry1F (0.58 µg), 0 minute digestion

4 - 15 second digestion

5 - 30 second digestion

6 - 1 minute digestion

7 - 2 minute digestion

8 - 5 minute digestion

9 - 10 minute digestion

10 - 15 minute digestion

* Note MW markers are labeled in kDa.

Figure 3. Western Blot and SDS-PAGE Analysis of Truncated, Microbial Cry1F Protein Subjected to Digestion in Simulated Gastric Fluid

SUMMARY

(In accordance with 40 CFR part 152, this summary is available
for public release after registration)

STUDY TITLE

Characterization of the Recombinant Cry1F protein Derived from *Pseudomonas fluorescens* and
Transgenic Maize

DATA REQUIREMENTS

None

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STUDY COMPLETED ON

September 18, 2001

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LABORATORY STUDY ID

GH-C 5294

Characterization of the Recombinant Cry1F protein Derived from *Pseudomonas fluorescens* and Transgenic Maize

SUMMARY

Corn plants have been genetically modified by the introduction of a synthetic gene which encodes for a truncated version of an insecticidal protein (Cry1Fa2, commonly referred to as Cry1F) isolated from *Bacillus thuringiensis aizawai* strain PS811. This protein when expressed in corn cultivars confers the crop resistance to lepidopteran pests, including the European corn borer (*Ostrinia nubilalis*). Because it would be difficult to isolate sufficient amounts of biologically active Cry1F protein from corn tissue to perform toxicological studies, the proteins were produced with a bacterium *Pseudomonas fluorescens* (*Pf*) through recombinant DNA technology. The microbial derived Cry1F protein was used in various toxicology and ecotoxicology studies. It was therefore important to characterize the biochemical properties of both the plant and microbial derived proteins.

Sodium dodecyl sulfate polyacrylamide gel electrophoresis (stained with coomassie blue and glycoprotein detection methods), Western blot, and matrix assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) were used to characterize the biochemical properties of the proteins. The Cry1F protein from *Pf* and transgenic maize (event TC1507) were shown to be equivalent with respect to immunoreactivity, peptide mass fingerprints and the lack of post-translational glycosylation. There was a slight difference in the apparent molecular weight of the two proteins but this could be accounted for by additional truncation of the maize derived protein during purification. This data supports the use of the microbial protein for registration of transgenic corn expressing Cry1F.

STUDY TITLE

Characterization of the Recombinant Cry1F protein Derived from *Pseudomonas fluorescens* and Transgenic Maize

DATA REQUIREMENTS

None

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STUDY COMPLETED ON

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STATEMENT OF NO DATA CONFIDENTIALITY CLAIMS

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Title: Characterization of the Recombinant Cry1F protein Derived from *Pseudomonas fluorescens* and Transgenic Maize

No claim of confidentiality is made for any information contained in this study on the basis of its falling within the scope of FIFRA Section 10 (d)(1)(A)(B), or (C).*

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non-GLP

STATEMENT OF COMPLIANCE WITH GOOD LABORATORY PRACTICE STANDARDS

Title: Characterization of the Recombinant Cry1F protein Derived from *Pseudomonas fluorescens* and Transgenic Maize

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United States Environmental Protection Agency
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FEDERAL REGISTER, August 17, 1989

Organisation for Economic Co-Operation and Development
ISBN 92-64-12367-9, Paris 1982

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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_____ Submitter Dow AgroSciences LLC	_____ Date
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_____ Study Director/Author Dow AgroSciences LLC	_____ Date
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QUALITY ASSURANCE STATEMENT

Compound: Cry1F δ -endotoxin

Title: Characterization of the Recombinant Cry1F protein Derived from
Pseudomonas fluorescens and Transgenic Maize

Study Initiation Date: August 2, 2001

Study Completion Date: September 18, 2001

NON-GLP STUDY

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ABBREVIATIONS

BCIP	5-bromo-4-chloro-3-indolyl phosphate
BME	2-mercaptoethanol
CBB	coomassie brilliant blue
CV	column volumes
DTT	dithiothreitol
EDTA	ethylenediamine tetraacetate
IAC	immunoaffinity chromatography
MALDI-TOF MS	matrix-assisted laser desorption/ionization time-of-flight mass spectrometry
MW	molecular weight
NBT	<i>p</i> -nitroblue tetrazolium
PAb	polyclonal antibody
PBST	phosphate buffered saline (10mM phosphate buffer, 138 mM NaCl, 2.7 mM KCl) with 0.05% Tween 20, pH = 7.4
PMSF	phenylmethylsulfonyl fluoride
SDS-PAGE	sodium dodecyl sulfate – polyacrylamide gel electrophoresis
TFA	trifluoroacetic acid
TSN	Dow AgroSciences Test Substance Number

Characterization of the Recombinant Cry1F protein Derived from *Pseudomonas fluorescens* and Transgenic Maize

ABSTRACT

Corn plants have been genetically modified by the introduction of a synthetic gene which encodes for a truncated version of an insecticidal protein (Cry1Fa2, commonly referred to as Cry1F) isolated from *Bacillus thuringiensis aizawai* strain PS811. This protein when expressed in corn cultivars confers the crop resistance to lepidopteran pests, including the European corn borer (*Ostrinia nubilalis*). Because it would be difficult to isolate sufficient amounts of biologically active Cry1F protein from corn tissue to perform toxicological studies, the proteins were produced with a bacterium *Pseudomonas fluorescens* (*Pf*) through recombinant DNA technology. The microbial derived Cry1F protein was used in various toxicology and ecotoxicology studies. It was therefore important to characterize the biochemical properties of both the plant and microbial derived proteins.


Sodium dodecyl sulfate polyacrylamide gel electrophoresis (stained with coomassie blue and glycoprotein detection methods), Western blot, and matrix assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) were used to characterize the biochemical properties of the proteins. The Cry1F protein from *Pf* and transgenic maize (event TC1507) were shown to be equivalent with respect to immunoreactivity, peptide mass fingerprints and the lack of post-translational glycosylation. There was a slight difference in the apparent molecular weight of the two proteins but this could be accounted for by additional truncation of the maize derived protein during purification. This data supports the use of the microbial protein for registration of transgenic corn expressing Cry1F.

INTRODUCTION

Corn plants have been genetically modified by the introduction of a synthetic gene which encodes for a truncated version of an insecticidal protein (Cry1Fa2, commonly referred to as Cry1F) isolated from *Bacillus thuringiensis* var. *aizawai* strain PS811. This protein (approximately 66 kDa) when expressed in corn cultivars confers resistance to lepidopteran pests, including the European corn borer (*Ostrinia nubilalis*). Because it would be difficult to isolate sufficient amounts of biologically active Cry1F protein from corn tissue to perform toxicological studies, the proteins were produced with a bacterium *Pseudomonas fluorescens* (Pf) through recombinant DNA technology. The microbial derived Cry1F protein was used in various toxicology and eco-toxicology studies. It was, therefore, important to characterize the biochemical properties of both the plant and microbial derived proteins.

The biochemical and immunological methods employed in study are among those that have been well established for protein analysis. SDS-PAGE separates proteins based on the apparent molecular weight (mass). Western blotting of proteins to a nitrocellulose membrane following SDS-PAGE, and immunodetection with a protein specific antibody is widely used to identify the authenticity of a molecule in a crude preparation. In addition, staining for carbohydrate moieties linked to polypeptides (following electrophoresis) is a standard test to detect post-translational glycosylation of proteins. When treated with periodic acid, glycols present in glycoproteins are oxidized to aldehydes. The aldehydes are next exposed to a proprietary stain (Pierce Chemical Co.) and the glycols of the glycoprotein are visualized. Peptide mass fingerprinting by MALDI-

TOF MS following trypsinolysis is among the most powerful tools in examining the sequence equivalency between two proteins (Henzel and Stults, 1996).



MATERIALS AND METHODS

Generation and Purification of Test Substances

The recombinant microbial derived Cry1F protein was expressed by *P. fluorescens* strain MR872 and purified as described in Appendix C of Project ID: MYCO98-001 (Evans 1998). The solubilized, truncated Cry1F, TSN101788 (Collins 2001) was aliquoted and stored at -80 °C until use. Transgenic maize TC1507 leaf tissue was harvested fresh at the Mycogen field research station in Windfall, IN. The leaves from the entire corn plant were removed, placed in plastic bags, stored on ice and transported to the Dow AgroSciences Indianapolis laboratory. Upon receipt in the lab, the leaves were stored frozen at -20 °C until use. Corn leaf powder was prepared by grinding the tissue (mid-vein removed) in liquid nitrogen using a mortar and pestle. The proteins were extracted with PBST (Sigma Chemical, Catalog#: P-3563), 1 mM EDTA, 2 mM DTT, 1 mM PMSF, pH 7.4. Large pieces of the leaf tissue were removed by filtering through several layers of cheese cloth followed by centrifugation at 17000xg for 30 minutes. The proteins were fractionated by using 75% ammonium sulfate precipitation and centrifugation. The protein precipitate was resuspended in PBST and filtered through a 0.45 micron membrane. The clarified extract was applied by gravity flow to a 4.2-mL immunoaffinity column specific for Cry1F (Gao *et al.*, 2001) and non-specific proteins were removed by washing with 5 CV of PBST. The bound Cry1F protein was eluted with approximately 25 mL of 50 mM pyridine/acetic acid buffer, pH 3.2 and dried under vacuum centrifugation (sixteen 1.5 mL fractions). The protein was resuspended with 20 mM Tris pH 8.0 buffer and used for the subsequent studies.

SDS-PAGE and Western Blot

SDS-PAGE was performed with Zaxis gels (Zaxis Catalog#: 110-0420T212) and an Integrated Separation Systems gel module. Protein samples were mixed with Laemmli sample buffer (Bio-Rad Catalog#:161-0737) containing 5% freshly added BME and boiled for 5 minutes at 100 °C.

The electrophoresis was conducted at a constant amperage of 40 mA per gel for 60 minutes using Tris/glycine/SDS buffer (Bio-Rad Catalog#: 161-0732). After separation, the gel was cut in half with a fresh razor blade and half was stained with coomassie brilliant blue and half was stained with GelCode Glycoprotein stain (Pierce Catalog#: 24562). In addition, a second gel was prepared and the proteins were electro-blotted to a nitrocellulose membrane (Bio-Rad Catalog#:162-0145) with a Mini Trans-Blot electrophoretic transfer cell for 60 minutes under a constant voltage of 100 volts. For immunodetection, a Cry1F specific polyclonal rabbit antibody (Strategic Diagnostics Inc., Lot#: 200.310-4) was used as the primary antibody. A conjugate of goat anti-rabbit IgG (H+L) and calf intestinal alkaline phosphatase (Pierce Chemical, Catalog#: 31340) was used as the secondary antibody. A substrate solution containing SIGMA *Fast* NBT/BCIP (Sigma Chemical, Catalog#: B5655) was used for colorimetric development and visualization of the immuno-reactive protein bands (DAS notebook #: E1213).

Detection of Post-translational Glycosylation

The *Pseudomonas* derived Cry1F and immunoaffinity purified maize Cry1F protein preparations were separated by SDS-PAGE. After electrophoresis, the gel was cut in half and stained with either CBB to visualize all protein bands, or with GelCode Glycoprotein Staining Kit (Pierce, catalog #24562) to visualize glycoproteins. The procedure for glycoprotein staining was briefly described as the following. After electrophoresis, the gel was fixed in 50% MeOH for 30 min and rinsed with 3% acetic acid. This was followed by an incubation period with the oxidation solution from the test kit for 15 min. The gel was once again rinsed with 3% acetic acid and incubated with GelCode glycoprotein staining reagent for 15 min. Finally, it was immersed in the reduction solution for 10 min, and then rinsed with 3% acetic acid. The glycoproteins were visualized as magenta bands on a light pink background.

MALDI-TOF MS Peptide Mass Fingerprinting of Plant and Microbial Derived Cry1F

MALDI-TOF MS was conducted at the Proteomics Lab of Dow AgroSciences LLC. *P. fluorescens* produced truncated Cry1F and immunoaffinity purified, immunoreactive proteins were further separated from other contaminants by SDS-PAGE. The respective bands were excised from the gel and placed into siliconized Eppendorf microcentrifuge tubes, and destained with 50% acetonitrile in 12.5 mM NH_4HCO_3 . The gel pieces were dried using vacuum centrifugation, and digested with sequencing grade trypsin (Roche Diagnostics, Indianapolis, Indiana) overnight (approximately 16 hours) at 37 °C. The peptides were extracted with 50% acetonitrile in 0.5% TFA. After brief centrifugation to pellet the gel pieces, the supernatant containing the peptides were decanted and dried in a Savant Speed-Vac. The peptides were then suspended in 0.1% TFA and cleaned with ZipTip resin. The post-cleaning peptides were eluted into siliconized microcentrifuge tubes with 75% acetonitrile/0.1% TFA, dried using vacuum centrifugation, and stored at -20 °C freezer until MALDI-TOF MS analysis. The samples were re-dissolved in 6 μL of 0.1% TFA for MALDI analysis. The instrument used was a PerSeptive Biosystems (Framingham, MA) Voyager DE-STR MALDI-TOF mass spectrometer. The instrument utilizes a 337 nm nitrogen laser for the desorption/ionization event and a 3.0 meter reflector time-of-flight tube. On a stainless steel MALDI sample plate, 0.5 μL of the solubilized peptides was mixed with 0.5 μL of MALDI matrix solution (saturated solution of α -cyano-4-hydroxycinnamic acid in 50% acetonitrile, 0.1% TFA) and allowed to air dry. External calibration was performed by using a solution of angiotensin I, ACTH (clip 1-17), ACTH (clip 18-39), and ACTH (clip 7-38). Internal calibration was performed using the autolytic trypsin peak at m/z 2163.05. All mass spectra were collected in the positive ion reflector mode with delayed extraction.

RESULTS AND DISCUSSION

Purification of Cry1F Protein from Transgenic TC1507 Corn Extract

Immunoaffinity chromatography (IAC) was conducted on the TC1507 transgenic corn leaf extract. Fractions (1.5 mL each) were collected from the elution effluent and concentrated to dryness using vacuum centrifugation and resuspended in 40 μ L of Tris buffer ($>30\times$ concentration). Fractions (#3-15) were examined by SDS-PAGE and the results showed that in fractions #7-15, there was a major protein band of an approximate MW of 65 kDa (Data not shown, DAS Notebook E1213). Western blot analysis of fractions 10 and 11 demonstrated the major protein band to be immunoreactive to the specific anti-Cry1F polyclonal antibody (Figure 1, Panel A). It was also observed that below the 65 kDa band, there were several bands which were immunoreactive to the anti-Cry1F antibodies. Although the amounts of these proteins were too low to be seen on SDS-PAGE (Figure 1, Panel B) they were highly antigenic. These minor bands are most likely truncated products of Cry1F which were captured and subsequently purified by IAC in addition to the intact full length protein.

SDS-PAGE and Western Blot Analysis

In the tox lot preparation of *P. fluorescens* MR872 (TSN 101788) the major Cry1F band, as visualized on coomassie stained SDS-PAGE gels, was approximately 66 kDa. As expected (Figure 2), the corresponding maize derived Cry1F was slightly lower at approximately 65 kDa. (Figure 1, Panel B). This is consistent with the previous findings as discussed in the report prepared by Evans (Evans, 1998) where the two proteins were nearly indistinguishable. Predictably, the plant purified fractions contained a number of proteolytic products that were reactive with the anti-Cry1F PAb (Figure 1, Panel A) in addition to the intact protein. This could be accounted for by the need to highly concentrate the purification fractions for visualization on SDS-PAGE which may have contributed to additional protein degradation. As described above, the immunoaffinity column was prepared with anti-Cry1F polyclonal antibodies, and therefore

all available epitopes were most likely captured and purified with the intact Cry1F core protein. These truncation products, though highly immunoreactive, were minor components of the final purified preparation. This was confirmed by the CBB stained gel (Figure 1, Panel B).

Detection of Glycosylation

Detection of carbohydrates possibly covalently linked to Cry1F (microbial and maize derived) was assessed by the GelCode Glycoprotein Staining Kit from Pierce. *P. fluorescens* derived and the immunoaffinity-purified transgenic corn derived Cry1F proteins were electrophoresed simultaneously. A glycoprotein, horseradish peroxidase, was loaded as a positive indicator for glycosylation and a non-glycoprotein, soybean trypsin inhibitor, was employed as a negative control. The results showed that both the corn- and *P. fluorescens*-derived Cry1F proteins had no detectable carbohydrates (Figure 1, Panel C).

Tryptic Peptide Mass Fingerprints

The Cry1F proteins derived from both *P. fluorescens* and transgenic corn TC1507 were separated by SDS-PAGE (Figure 1, Panel B), and the respective bands were excised and subjected to in-gel digestion by trypsin. The resulting peptide mixture was analyzed by MALDI-TOF MS to determine the peptide mass fingerprint coverage. The masses of the detected peptides were compared to those deduced based on potential trypsin cleavage sites on the sequence of Cry1F. Figure 2 illustrates the theoretical cleavage which was generated in silico using PAWS (Protein Analysis Worksheet) freeware from Proteometrics LLC. The predicted amino acid digest (and MW) of the trypsin resistant toxin core of *P. fluorescens* and transgenic corn derived Cry1F proteins are also described in Figure 2. This core, when denatured, is readily digested by trypsin and will generate numerous peptide peaks.

In the trypsin digest of *P. fluorescens*-derived truncated Cry1F protein, 19 peptides were identified matching the theoretical deduced peptide masses of Cry1F (Table 1). The peptide fragments detected were between residues 32 and 546 of Cry1F. In the trypsin digest of the

transgenic corn derived Cry1F protein, 20 peptides were identified matching the theoretical deduced peptide masses (Table 1). The peptide fragments detected were also between residues 32 and 546 of Cry1F. Only the plant Cry1F had an additional match with residues 522-529. The peptide coverage of the protease resistant toxin core for both the microbial and maize derived Cry1F was excellent. There were several unidentified peptides detected in the MALDI-TOF-MS spectrum (Figures 3 and 4). Many factors could contribute to the formation of these non-match peptides, such as over digestion (which resulted in non-specific cleavage), self-digestion products of trypsin, and random breakage of peptides during ionization.

CONCLUSIONS

The current study revealed that the biochemical identity of *P. fluorescens* produced Cry1F protein was equivalent or comparable to that produced in transgenic TC1507 corn plants. As expected, the Cry1F produced in transgenic plants was subject to protease cleavage, resulting in truncated forms and breakdown products. The core toxin of an apparent MW of 65 kDa was predominant in the transgenic corn leaf extract and the core toxin was similar to the truncated Cry1F generated by treating the *P. fluorescens* produced full length Cry1F with trypsin (66 kDa). The Cry1F protein from both expression sources lacked detectable post-translational glycosylation. Tryptic peptide mass fingerprints by in-gel digestion and MALDI-TOF MS, provided direct supporting evidence that the Cry1F produced by *P. fluorescens* and the transgenic corn are equivalent molecules.

REFERENCES

- [1] **Collins, R. A.** (2001). Certificate of analysis of test/reference/control substances (TSN 101788). Dow AgroSciences BIOT 013056.
- [2] **Evans, S. L.** (1998). Equivalency of Microbial and Maize Expressed Cry1F Protein; Characterization of Test Substances for Biochemical and Toxicological Studies. Mycogen Corporation MYCO98-001.
- [3] **Gao, Y., Gilbert, J. R., Schwedler, D. A., and Xu, X.** (2001) Characterization of Cry1F Protein Derived from *Pseudomonas fluorescens* and Transgenic Cotton. Dow AgroSciences Report GH-C 5265, 36 pp.
- [4] **Henzel, W. J. and Stults T. J.** (1996). Matrix-assisted laser desorption/ionization time-of-flight mass analysis of peptides. Current Protocols in Protein Sciences, unit 16.2, John Wiley & Sons Inc., New York, USA.
- [5] **Pierce Chemical Company** (2001). Instructions for GelCode Glycoprotein Staining Kit, Document Number: 0855.

Table 1. Tryptic Peptide Mass Data (m/z $[M+H]^+$) of Cry 1F Proteins Obtained by MALDI-TOF MS

Full Length Cry1Fsynpro residue #	Theoretical mass (m/z)	<i>P. fluorescens</i> trypsinized Cry1F [M+H]	TC1507 Maize Cry1F [M+H]
32-42	1227.72	1227.70	1227.68
100-113	1612.81	1612.81	1612.79
114-125	1441.67	1441.66	1441.65
172-193	2434.15	2434.21	2434.16
194-200	878.55	878.51	878.50
204-217	1675.79	1675.75	1675.75
252-263	1394.72	1394.69	1394.68
264-286	2509.21	2509.24	2509.19
312-324	1413.71	1413.70	1413.68
358-366	1033.56	1033.52	1033.52
367-379	1386.71	1386.70	1386.69
380-392	1416.68	1416.67	1416.67
431-442	1376.62	1376.62	1376.59
452-463	1301.63	1301.60	1301.58
464-471	911.58	911.53	911.52
472-483	1269.68	1269.66	1269.65
484-494	1089.56	1089.53	1089.52
522-529	925.46	ND ^b	925.43
530-538	1007.54	1007.51	1007.50
539-546	924.48	924.44	924.43

Note:

^a Two digit decimals were used for mass data in this table although raw data obtained from the MALDI-TOF-MS spectrometer were shown in 4 digit decimals. A peptide was considered a match if its m/z is within m/z 0.1 error range of its theoretical m/z .

^b ND: not detected.

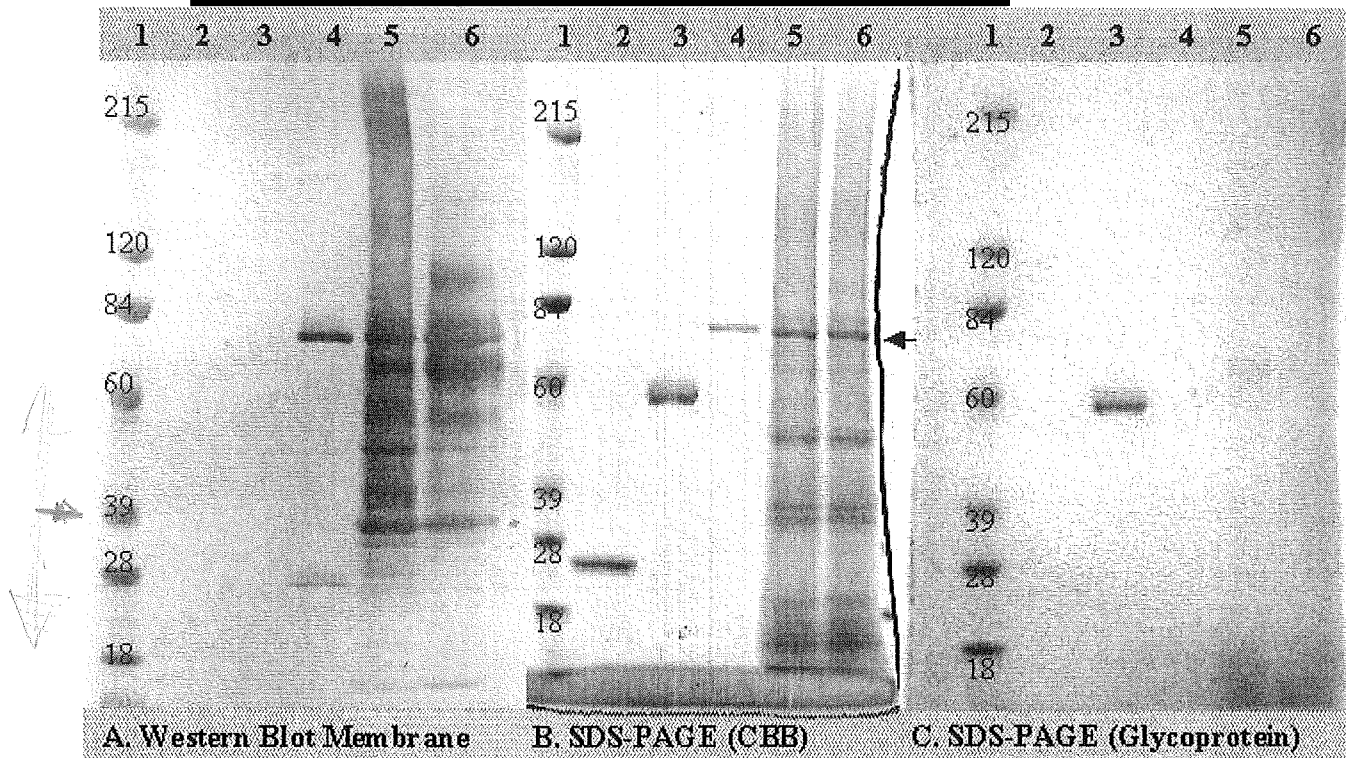


Figure 1. SDS-PAGE and Western Blot Analysis of Microbial and Maize Derived Cry1F Proteins

Panel A: Western Blot detected with rabbit anti-Cry1F polyclonal antibody.

Panel B: SDS-PAGE, 4-20% gradient gel, Coomassie brilliant blue stained.

Panel C: SDS-PAGE, 4-20% gradient gel, GelCode glycoprotein stained

Lane 1: Pre-stained molecular weight markers (Pierce Chemical, BlueRanger)

Lane 2: Soybean Trypsin Inhibitor (MW: 20.1 kDa), 1.25 µg/lane

Lane 3: Horseradish Peroxidase (MW: 44 kDa), 1.25 µg/lane

Lane 4: *P. fluorescens* MR872 derived Cry1F, 0.14 µg/lane

Lane 5: Maize derived, IAC purified Cry1F (Fraction 10)

Lane 6: Maize derived, IAC purified Cry1F (Fraction 11)

*Arrow Denotes Cry1F protein

```

1  M E N N I Q N Q C V P Y N C L N N P E V E I L N E E R s t g 30
31  r L \ P L D I S L S L T R f l l s e f v p g v g v a f g l f d 60
61  l i w g f i t p s d w s l f l l q i e q l i e q r I E T L E 90
91  R n r A I T T L R g l a d s y e i y i e a l r E W E A N P N 120
121 N A Q L R e d v r I R f a n t d d a l i t a i n n f t l t s 150
151 f e i p l l s v y v q a a n l h l s l l r D A V S F G Q G W 180
181 G L D I A T V N N H Y N R l i n l i h r Y T K h c l d t y n 210
211 q g l e n l r G T N T R q w a r F N Q F R r D L T L T V L D 240
241 I V A L F P N Y D V R t y p i q t s s q l t r E I Y T S S V 270
271 I E D S P V S A N I P N G F N R a e f g v r p p h l m d f m 300
301 n s l f v t a e t v r S Q T V W G G H L V S S R n t a g n r 330
331 I N F P S Y G V F N P G G A I W I A D E D P R P F Y R t l s 360
361 d p v f v r G G F G N P H Y V L G L R g v a f q q t g t n h 390
391 t r T F R n s g t i d s l d e i p p q d n s g a p w n d y s 420
421 h v l n h v t f v r W P G E I S G S D S W R a p m f s w t h 450
451 r S A T P T N T I D P E R i t q i p l v k A H T L Q S G T T 480
481 V V R g p g f t g g d i l r R t s g g p f a y t i v n i n g 510
511 q l p q r Y R a r I R y a s t t n l r I Y V T V A G E R i f 540
541 a g q f n k T M D T G D P L T F Q S F S Y A T I N T A F T F 570
571 P M S Q S S F T V G A D T F S S G N E V Y I D R f e l i p v 600
601 t a t l e a e s d l e r A Q K a v n a l f t s s n q i g l k 630
631 T D V T D Y H I D R v s n l v e c l s d e f c l d e k K e l 660
661 s e k V K h a k R l s d e r N L L Q D P N F R g i n r Q L D 690
691 R g w r G S T D I T I Q G G D D V F K e n y v t l l g t f d 720
721 e c y p t y i y q k l D E S K l k A Y T R y q l r G Y I E D 750
751 S Q D L E I Y L I R y n a k H E T A V N V P G T G S L W P L S 780
781 A P S P I G K c a h h s h h f s l d i d v g c t d l n e d l 810
811 g v w v i f k I K t q d g h a r L G N L E F L E E K P L V G 840
841 E A L A R v k R a e k K w r D K r E K l e w e t n i v y k E 870
871 A K e s v d a l f v n s q y d r L Q A D T N I A M I H A A D 900
901 K r V H S I R e a y l p e l s v i p g v n a a i f e e l e g 930
931 r I F T A F S L Y D A R n v i k N G D F N N G L S C W N V K 960
961 g h v d v e e q n n h r S V L V V P E W E A E V S Q E V R v 990
991 c p g r G Y I L R v t a y k E G Y G E G C V T I H E I E N N 1020
1021 T D E L K f s n c v e e e v y p n n t v t c n d y t a t q e 1050
1051 e y e g t y t s r N R g y d g a y e s n s s v p a d y a s a 1080
1081 y e e k A Y T D G R r D N P C E S N R g y g d y t p l p a g 1110
1111 y v t k E L E Y F P E T D K v w i e i g e t e g t f i v d s 1140
1141 v e l l l m e e 1148

```

Note: The molecular weight of the protease resistant Cry1F core is predicted to be 65.8 kDa for the microbial protein (amino acids 28-612) as compared to 65.0 kDa for the maize protein (amino acids 28-605, residue 604 changed to F from L). One amino acid difference exists between the gene expression products and the synthetic maize gene (1 shown in blue). In the synthetic maize gene (amino acids 1-605) a conservative amino acid substitution of leucine (L) to phenylalanine (F) was introduced for cloning purposes (added restriction site). Alternating blocks of upper and lower case letters within the amino acid sequence are used to differentiate the potential peptides after trypsin digestion. The numbers on the left and right sides indicate the amino acid residue numbers.

Figure 2. Amino Acid Sequence of Full Length Microbial MR872 Cry1F

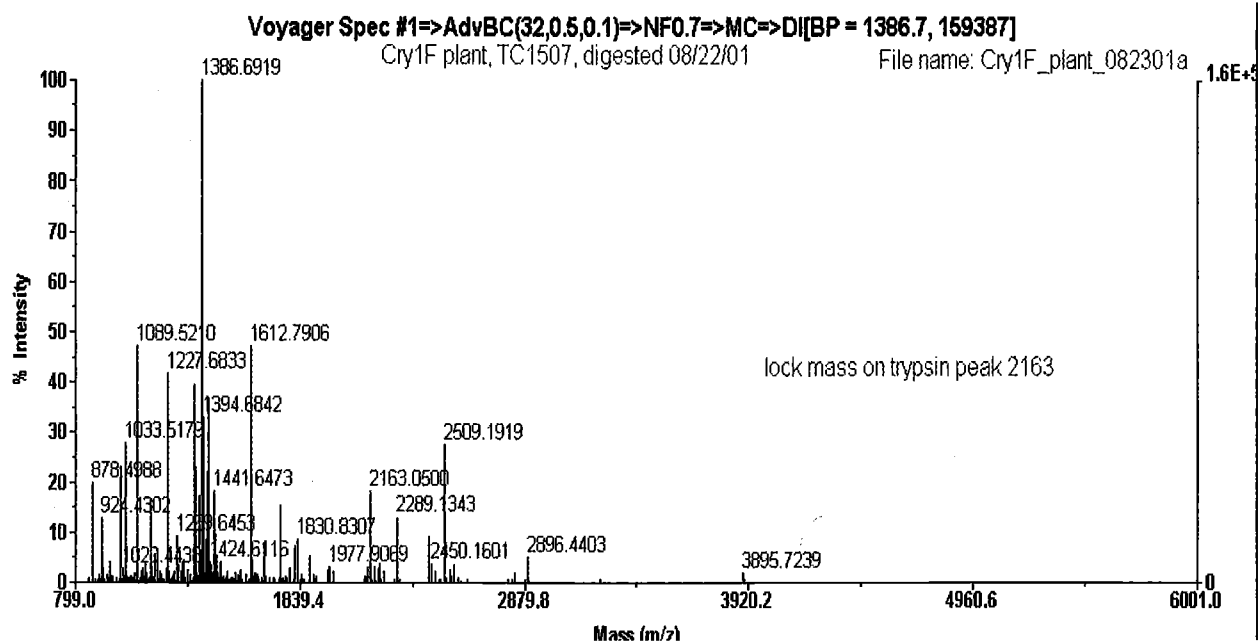


Figure 4. MALDI-TOF Mass Spectrum (deisotoped) of the Trypsin Digest of the Truncated Cry1F Derived from Transgenic Corn Event TC1507. Note: not every peak was labeled.

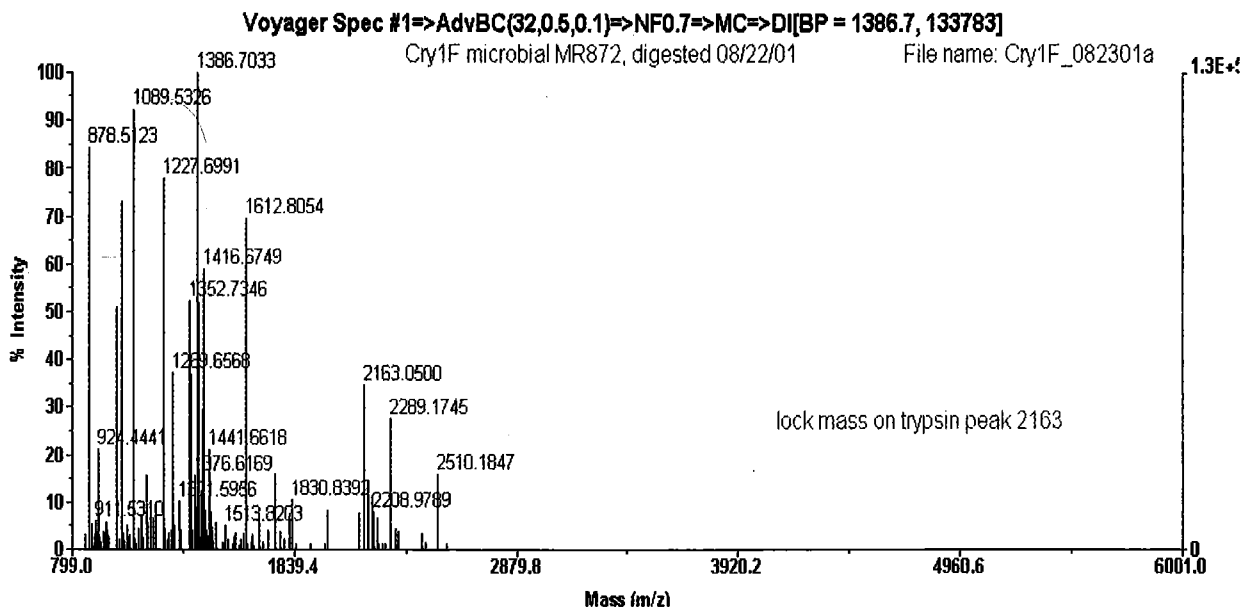


Figure 3. MALDI-TOF Mass Spectrum (deisotoped) of the Trypsin Digest of the Truncated Cry1F Derived from *P. fluorescens* MR872. Note: not every peak was labeled.

SUMMARY

(In accordance with 40 CFR part 152, this summary is available
for public release after registration)

STUDY TITLE

Comparison of the Amino Acid Sequence of the *Bacillus thuringiensis* var. *aizawai* Cry1F Insect
Control Protein as Expressed in *Zea mays* Event 1507 to Assess Homology to Known Protein
Toxins

DATA REQUIREMENTS

None

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LABORATORY STUDY ID

GH-C 5463

Comparison of the Amino Acid Sequence of the *Bacillus thuringiensis* var. *aizawai* Cry1F Insect Control Protein as Expressed in *Zea mays* Event 1507 to Assess Homology to Known Protein Toxins

SUMMARY

In assessing the safety of food proteins to human health, the potential risk of a toxic response to the protein in the diet should be evaluated. Proteins can be introduced into plants to confer a variety of desirable traits. A comparison of the amino-acid sequence of the introduced protein for similarity to known protein toxins is one step in a multilevel analytical process to assess potential toxicity (Codex 2001). In this study, the amino sequence of the Cry1F Insect Control Protein in event 1507 has been evaluated for similarity to known protein toxins. Significant sequence similarity requires a match with an expectation value of at most 1.0 to a protein toxin. In this study, no significant sequence similarity was detected for Cry1F to protein toxins other than insecticidal delta-endotoxins.

STUDY TITLE

Comparison of the Amino Acid Sequence of the *Bacillus thuringiensis* var. *aizawai* Cry1F Insect Control Protein as Expressed in *Zea mays* Event 1507 to Assess Homology to Known Protein Toxins

DATA REQUIREMENTS

None

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STATEMENT OF NO DATA CONFIDENTIALITY CLAIMS

Compound: Cry1F

Title: Comparison of the Amino Acid Sequence of the *Bacillus thuringiensis* var. *aizawai* Cry1F Insect Control Protein as Expressed in *Zea mays* Event 1507 to Assess Homology to Known Protein Toxins

No claim of confidentiality is made for any information contained in this study on the basis of its falling within the scope of FIFRA Section 10 (d)(1)(A)(B), or (C).*

Company: Dow AgroSciences LLC

Company Agent: ██████████

Title: Regulatory Manager

Signature: _____

Date: _____

*In the United States, the above statement supersedes all other statements of confidentiality that may occur elsewhere in this report.

THIS DATA MAY BE CONSIDERED CONFIDENTIAL IN COUNTRIES OUTSIDE THE UNITED STATES.

STATEMENT OF COMPLIANCE WITH GOOD LABORATORY PRACTICE STANDARDS

Title: Comparison of the Amino Acid Sequence of the *Bacillus thuringiensis* var. *aizawai* Cry1F Insect Control Protein as Expressed in *Zea mays* Event 1507 to Assess Homology to Known Protein Toxins

Study Initiation Date: 4/8/02

Study Completion Date:

Experimental Start Date: 4/9/02

Experiment Termination Date: 6/11/02

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

Organisation for Economic Co-Operation and Development
ISBN 92-64-12367-9, Paris 1982

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.

Sponsor
Dow AgroSciences LLC

Date

Submitter
Dow AgroSciences LLC

Date

Study Director/Author
Dow AgroSciences LLC

Date

QUALITY ASSURANCE STATEMENT

Compound: Cry1F

Title: Comparison of the Amino Acid Sequence of the *Bacillus thuringiensis* var. *aizawai* Cry1F Insect Control Protein as Expressed in *Zea mays* Event 1507 to Assess Homology to Known Protein Toxins

Study Initiation Date: 4/8/02

Study Completion Date:

NON-GLP STUDY

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LITERATURE CITED	

Comparison of the Amino Acid Sequence of the *Bacillus thuringiensis* var. *aizawai* Cry1F Insect Control Protein as Expressed in *Zea mays* Event 1507 to Assess Homology to Known Protein Toxins

ABSTRACT

In assessing the safety of food proteins to human health, the potential risk of a toxic response to the protein in the diet should be evaluated. Proteins can be introduced into plants to confer a variety of desirable traits. A comparison of the amino-acid sequence of the introduced protein for similarity to known protein toxins is one step in a multilevel analytical process to assess potential toxicity (Codex 2001). In this study, the amino sequence of the Cry1F Insect Control Protein in event 1507 has been evaluated for similarity to known protein toxins. Significant sequence similarity requires a match with an expectation value of at most 1.0 to a protein toxin. In this study, no significant sequence similarity was detected for Cry1F to protein toxins other than insecticidal delta-endotoxins.

INTRODUCTION

The safety assessment of proteins expressed in transgenic plants may include an evaluation of whether 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 transferred protein includes the comparison of the protein sequence to known protein toxin sequences (Codex 2001). As there is not a standard recognized definition of a protein as a toxin based on its sequence, a comparison should be made to a database of all available protein sequences. 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 which ensures avoidance of false positives (labeling a sequence as related when it is not) employs an expectation value threshold between 0.001 and 0.01 (Pearson, 1999). Although little can be done to avoid false negatives (missing a likely homolog), visual inspection of the quality of less conservative alignments (with $E() < 1$) may help to reduce this occurrence. A protein identified as having significant sequence similarity to a known toxin can then be further assessed using physiochemical tests based on a decision-tree or weight-of-evidence schemes similar to those applied for assessing the allergenic potential of foods (Metcalf *et al*, 1996, Astwood and Fuchs, 1996).

Finally, it should be noted that this evaluation should take into account the biological function of the protein (Codex 2001). For example, *Bacillus thuringiensis* insecticidal delta-endotoxins, the focus of this study, are named toxins based on their effect on insects, but have been approved for human consumption in a number of transgenic food crops due to a lack of mammalian toxicity.

The objective of this study was to compare the sequence of *Bacillus thuringiensis* var. *aizawai* Cry1F Insect Control Protein (Cry1F) (Figure 1) expressed in event 1507 corn plants (*Zea mays*) developed for resistance to corn Lepidopteran pests. Sequence comparison was performed utilizing BLASTP, a local alignment algorithm that performs a search for similarity between a query sequence and a group of sequences using the method of Altschul *et al.* (1990, J. Mol. Biol. 215:403-410).

METHODS

The Cry1F protein in this study comprises residues 1-605 (with a F→L substitution at 604) of the 1174 Cry1Fa sequence, representing the active portion of the cry1Fa protoxin.

Sequence analysis in this study was performed using the BLASTP tools available at the NCBI web site (<http://www.ncbi.nlm.nih.gov/Blast/>) to compare the Cry1F protein against the Protein nr database (contains all non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF). The versions used were April 9, 2002 containing 919,193 sequences, and April 30, 2002, containing 925,521 sequences.

All proteins from the Protein nr database that showed similarity to the Cry1F protein with a statistical expectation value lower than 1.0 were evaluated for potential to be protein toxins.

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71

RESULTS AND CONCLUSION

A statistically significant sequence similarity generally requires a match with an expectation value less than 0.01, although the significance scores of alignments decrease in value as the size of the database grows (Pearson, 1999). Since the database used here is substantially large (greater than 900,000 sequences), less conservative alignments, with $E() < 1$, were also evaluated. Any statistically significant matches need to then be evaluated for their biological relevance as protein toxins.

The BLASTP analysis revealed a total of 181 proteins with $E() < 1.0$. Of those, all but 4 (Table 1) are other known Cry proteins (Crickmore et al, 2002).

1. *Homology to Other Known Cry Proteins*

It is important to note that although Cry proteins are known as delta-endotoxins, their biological function as toxins, and value in transgenic crops, is as biopesticides. Cry1F is closely related to

Cry1Ab (52.4% identity over 614 residue alignment overlap), a protein approved for human consumption in transgenic corn. An exception to this is Cry31Aa1, which shares very low homologies to other Cry proteins (27.3% over 304 residue alignment overlap with Cry1F). Cry31Aa1 has been reported in one study to function as a toxin to leukemic, but not normal, human T-cells, when activated by processing under specific conditions and by specific proteases (Mizuki et al, 2000).

2. Homology to non-Cry proteins

The remainder of this study will focus on the four non-Cry proteins identified in the BLAST analysis (Table 1). These four proteins were each evaluated for their significance as protein toxins and for homology to Cry1F.

Table 1. Non-Cry protein blast hits

NCBI accession	Organism	Description	E()
AAM06002.1	Methanosarcina acetivorans	Hypothetical protein	2.00E-07
CAA98839.1	Saccharomyces cerevisiae	Chromosome IV reading frame ORF YDR017C	0.073
NP_010300.1	Saccharomyces cerevisiae	Chromosome IV reading frame ORF YDR017C	0.073
NP_437949.1	Sinorhizobium meliloti	putative regulatory protein	0.62

2.1 Protein from Methanosarcina acetivorans

The protein from Methanosarcina acetivorans is listed as a hypothetical protein, predicted by translation of genomic DNA sequence. The expectation value of the alignment of Cry1F with this protein, $E() = 2.00e-07$, is statistically significant and suggests a real homology. Blasting this protein back against the NCBI protein nr database, however, reveals statistically significant hits only against Cry proteins (Figure 3.) Cry protein conserved blocks 1 and 2 can also be observed in the sequence (Schnepf et al, 1998), however this protein is too short to represent an active insect toxin (Hofte and Whiteley, 1989). This protein appears to be newly identified as a Cry protein homolog, with no non-Cry homologs in the public protein databank. Other than

delta-endotoxins, discussed above, there is no evidence that this protein is a known toxin, or is homologous to a known toxin.

2.2 *Proteins from Saccharomyces cerevisiae*

It should be noted that the two hits from *Saccharomyces cerevisiae* are the same protein, listed twice because one database submission is C-terminally truncated. Since the region of similarity with Cry1F occurs at the common N-terminus, these hits will be evaluated together as one.

These proteins are thought to be related to the basic leucine zipper family of transcription factors. The region of alignment with Cry1F is from amino acids 134 to 292, and corresponds to the domain I alpha-helical bundles 3 through 7 (Grochulski et al, 1995). The expectation value of 0.073 for the alignment of Cry1F with the *Saccharomyces* proteins falls in the range where significance is not certain. These proteins were blasted back against the NCBI protein nr database (Figures 4 and 5) to determine if homology exists between them and known protein toxins. The expectation value of the alignment of these proteins with Cry1F (Cry1F in database instead of as query sequence), it's nearest potential Cry protein homolog, is $E() = 0.74$ for the truncated protein, and $E() = 1.3$ for the full length protein. These values are statistically near the limit where the alignments would be expected to occur by random chance ($E() = 1$). Statistically significant homology exists between the *Saccharomyces* proteins and several transcription factors, mammalian inositol hexakisphosphate kinases, and ARGIII arginine metabolism regulatory protein. None of these are known protein toxins.

2.3 *Protein from Sinorhizobium meliloti*

The region of alignment with Cry1F is from amino acids 294 to 442, corresponding to domain II. The expectation value of 0.62 for the alignment of Cry1F with these proteins is nearing the statistical limit where there is an equal chance of obtaining such an alignment randomly ($E() = 1$). This protein was blasted back against the NCBI protein nr database (Figure 6) to determine if

any potential homology exists with a protein toxin. It is annotated as a putative regulatory protein, possibly two-component response regulator. It shares statistically significant homology with adenylate cyclase and several transcriptional regulation proteins, including O-linked N-acetyl glucosamine transferase, tetratricopeptide repeat family proteins, and many known and putative two-component response regulator transcription regulator proteins. None of these are known protein toxins.

CONCLUSION

The summary of these local alignment results is that Cry1F shows homology to other Cry family proteins, with a potential distant homology to various transcriptional regulatory proteins.

In conclusion, the results of this study do not show that Cry1F shares significant similarity with known protein toxins aside from other insecticidal delta-endotoxins.

FIGURE 1: Cry1F protein sequence.

```
1  MENNIQNQCV PYNCLNNPEV EILNEERSTG RLPLDISLSL TRFLLSEFVP
51  GVGVAFGFLD LIWGFITPSD WSLFLLQIEQ LIEQRIETLE RNRAITTLRG
101 LADSYEIIYE ALREWEANPN NAQLREDVRI RFANTDDALI TAINNFTLTS
151 FEIPLLSVYV QAANLHLSLL RDAVSFGQGW GLDIATVNNH YNRLINLIHR
201 YTKHCLDTYN QGLENLRGTN TRQWARFNQF RRDLTTLTVLD IVALFPNYDV
251 RTYPIQTSSQ LTREIYTSSV IEDSPVSANI PNGFNRAEFG VRPPHLMDFM
301 NSLFVTAETV RSQTVWGGHL VSSRNTAGNR INFPSYGVFN PGGAIWIAD
351 DPRPFYRTLS DPVFVRGGFG NPHYVLGLRG VAFQQTGTNH TRTFRNSGTI
401 DSLDEIPPDQ NSGAPWWDYS HVLNHVTFVR WPGEISGSDS WRAPMFSWTH
451 RSATPTNTID PERITQIPLV KAHTLQSGTT VVRGPGFTGG DILRRTSGGP
501 FAYTIVNING QLPQRYRARI RYASTTNLRI YVTVAGERIF AGQFNKTM
551 GDPLTFQSFS YATINTAFTF PMSQSSFTVG ADTFSSGNEV YIDRFELIPV
601  TATLE
```

FIGURE 2: Blastp results of Cry1F protein sequence against the NCBI Protein nr database.

BLASTP 2.2.2 [Dec-14-2001]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, 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.

RID: 1018387228-662-10391

Query=

(605 letters)

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF

919,193 sequences; 288,098,425 total letters

If you have any problems or questions with the results of this search
please refer to the BLAST FAQs

Taxonomy reports

Sequences producing significant alignments:	Score (bits)	E Value
sp Q03746 C1FA_BACTA Pesticidial crystal protein cry1Fa (In...	1231	0.0
pir S32649 parasporal crystal protein - Bacillus thuringie...	1060	0.0
dbj BAA25298.1 (AB012288) CryINA67-1 [Bacillus thuringiensis]	1060	0.0
sp O66377 C1FB_BACTM PESTICIDIAL CRYSTAL PROTEIN CRY1FB (IN...	1058	0.0
sp Q03748 C1AE_BACTL PESTICIDIAL CRYSTAL PROTEIN CRY1AE (IN...	583	e-165
sp P21257 CRYT_BACTK 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXI...	579	e-164
gb AAK14336.1 (AF327924) insecticidal crystal protein BTRX...	578	e-164
pir A29125 parasporal crystal protein - Bacillus thuringie...	578	e-164
gb AAG16877.1 (U94191) delta endotoxin [Bacillus thuringie...	578	e-164
gb AAK72985.1 (M60856) cryIA(a) [synthetic construct]	578	e-164
sp P06578 C1AB_BACTK PESTICIDIAL CRYSTAL PROTEIN CRY1AB (IN...	578	e-164
pir A26461 parasporal crystal protein Bt2 - Bacillus thuri...	578	e-164
sp P09667 CRYV_BACTA 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXI...	577	e-163
gb AAK55546.1 AF375608_1 (AF375608) crystal protein Cry1Ab1...	577	e-163
sp P09666 CRYT_BACTA 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXI...	577	e-163
sp Q03744 C1AD_BACTA Pesticidial crystal protein cry1Ad (In...	573	e-162
prf 1409195A_135kd insecticidal protein [Bacillus thuringi...	565	e-160
sp P16478 CRYU_BACTA 135 KD CRYSTAL PROTEIN (DELTA ENDOTOXI...	565	e-160
sp P09665 CRYS_BACTS 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXI...	563	e-159
dbj BAA77213.1 (AB026261) BtT84A1 crystal protein [Bacillu...	563	e-159
pir JC2219 lepidopteran-specific protoxin - Bacillus thuri...	563	e-159
emb CAA70856.1 (Y09663) delta-endotoxin [Bacillus thuringi...	563	e-159
gb AAA86265.1 (U43605) CryIA(a) [Bacillus thuringiensis]	563	e-159
prf 2013214A lepidopteran-specific protoxin [Bacillus thur...	563	e-159
prf 1304168B endotoxin delta 1 [Bacillus thuringiensis]	562	e-159
sp Q45718 C1HB_BACTM Pesticidial crystal protein cry1Hb (In...	562	e-159
sp P09664 CRYS_BACTE 133 KD CRYSTAL PROTEIN (DELTA ENDOTOXI...	560	e-158
pir A22617 parasporal crystal protein - Bacillus thuringie...	560	e-158
gb AAD55382.1 AF154676_1 (AF154676) 135 kDa insecticidal pr...	560	e-158
sp Q45748 C1HA_BACTU PESTICIDIAL CRYSTAL PROTEIN CRY1HA (IN...	554	e-156
sp P19415 C1DA_BACTA PESTICIDIAL CRYSTAL PROTEIN CRY1DA (IN...	553	e-156
gb AAK14337.1 (AF327925) insecticidal crystal protein BTRX...	545	e-154
sp Q45747 C1DB_BACTU PESTICIDIAL CRYSTAL PROTEIN CRY1DB (IN...	535	e-151
gb AAK48937.1 AF358862_2 (AF358862) insecticidal crystal pr...	535	e-151
sp Q45738 C1JA_BACTU PESTICIDIAL CRYSTAL PROTEIN CRY1JA (IN...	535	e-151
sp Q45746 C1GA_BACTU PESTICIDIAL CRYSTAL PROTEIN CRY1GA (IN...	533	e-150
gb AAD46139.1 AF081790_1 (AF081790) insecticidal crystal pr...	533	e-150

pdb 1CIY	Insecticidal Toxin: Structure And Channel Formation	529	e-149
sp P96315 C1AF_BACTU	Pesticidial crystal protein cryIAf (In...	526	e-148
sp Q9ZAZ6 C1GB_BACTZ	Pesticidial crystal protein cryIGb (In...	526	e-148
emb CAA70925.1	(Y09787) delta-endotoxin [Bacillus thuringi...	519	e-146
sp Q9S515 C1AG_BACTU	PESTICIDIAL CRYSTAL PROTEIN CRYIAG (IN...	515	e-145
pir A49785	parasporal crystal protein cryIA(c) - Bacillus ...	514	e-145
gb AAC98807.1	(U63372) truncated CryIAc [synthetic construct]	514	e-145
sp P05068 C1AC_BACTK	Pesticidial crystal protein cryIAc (In...	514	e-145
emb CAA10270.1	(AJ130970) crystal toxin protein [Bacillus ...	513	e-144
gb AAA73077.1	(M73249) [Bacillus thuringiensis gene, compl...	512	e-144
gb AAA22339.1	(M73248) cryIA(c)3 [Bacillus thuringiensis]	512	e-144
gb AAD38701.1	AF148644_1 (AF148644) insecticidal protein Cr...	512	e-144
pir S11445	parasporal crystal protein cryIA.c - Bacillus t...	512	e-144
pir JC7140	protoxin - Bacillus thuringiensis	510	e-143
emb CAA65457.1	(X96682) delta-endotoxin [Bacillus thuringi...	510	e-143
sp P05518 C1CA_BACTE	Pesticidial crystal protein cryICa (In...	510	e-143
emb CAA67557.1	(X99103) delta-endotoxin [synthetic construct]	510	e-143
gb AAC63055.1	(AF023672) CryIA(c) [synthetic construct]	510	e-143
pir A37829	parasporal crystal protein - Bacillus thuringie...	509	e-143
gb AAA22345.1	(M73252) cryIE(a) [Bacillus thuringiensis] >...	509	e-143
sp Q57458 C1EA_BACTX	Pesticidial crystal protein cryIEa (In...	509	e-143
gb AAF37224.1	AF215647_1 (AF215647) toxin CryICa6 [Bacillus...	509	e-143
pir S00944	parasporal crystal protein - Bacillus thuringie...	508	e-143
gb AAA22343.1	(M73251) cryIC(b) [Bacillus thuringiensis]	508	e-143
pir S04181	parasporal crystal protein - Bacillus thuringie...	507	e-142
gb AAB30710.1	insecticidal protein Cry I A (c) product (to...	507	e-142
gb AAD04732.1	(U94323) CryIEa4 [Bacillus thuringiensis]	506	e-142
sp P09663 CRYU_BACTK	131 KD CRYSTAL PROTEIN (DELTA ENDOTOXI...	504	e-141
gb AAA86266.1	(U43606) CryIA(c) [Bacillus thuringiensis]	503	e-141
sp Q45716 C1JB_BACTU	Pesticidial crystal protein cryIJB (In...	502	e-141
emb CAA70506.1	(Y09326) delta-endotoxin [Bacillus thuringi...	501	e-141
sp Q45715 C1KA_BACTM	Pesticidial crystal protein cryIKa (In...	497	e-139
sp P56953 C1CB_BACTG	PESTICIDIAL CRYSTAL PROTEIN CRYICB (IN...	495	e-139
sp Q03745 C1EB_BACTA	Pesticidial crystal protein cryIEb (In...	488	e-137
gb AAD55947.1	(AF177675) Cry IAc insecticidal toxin [synth...	482	e-135
gb AAK14338.1	(AF327926) insecticidal crystal protein BTRX...	475	e-133
sp Q45709 C1IB_BACTE	Pesticidial crystal protein cryIIB (In...	418	e-115
gb AAK66742.1	AF373207_1 (AF373207) CryIIa [Bacillus thurin...	416	e-115
sp Q45739 C1BB_BACTU	PESTICIDIAL CRYSTAL PROTEIN CRYIIBB (IN...	415	e-115
emb CAA70124.1	(Y08920) Bt toxin [Bacillus thuringiensis]	415	e-115
sp Q45774 C1BC_BACTM	PESTICIDIAL CRYSTAL PROTEIN CRYIIB (IN...	415	e-115
sp Q45752 C1IA_BACTK	Pesticidial crystal protein cryIIa (In...	414	e-114
pir S25383	parasporal crystal protein cryV - Bacillus thur...	414	e-114
pir I39814	insecticidal protein cryVI - Bacillus thuringie...	414	e-114
gb AAB00958.1	(L49391) CGCryV gene product [Bacillus thuri...	414	e-114
gb AAC26910.1	(AF076953) insecticidal protein [Bacillus th...	412	e-114
sp Q9XDL1 C1ID_BACTU	Pesticidial crystal protein cryIID (In...	410	e-113
gb AAG43526.1	AF211190_1 (AF211190) CryII [Bacillus thuring...	410	e-113
sp O87404 C1IC_BACTU	Pesticidial crystal protein cryIIC (In...	395	e-109
emb CAA65003.1	(X95704) cryIBa2 [Bacillus thuringiensis] >...	387	e-106
sp P05517 C1BA_BACTK	PESTICIDIAL CRYSTAL PROTEIN CRYIIBa (IN...	386	e-106
gb AAK63251.1	AF368257_1 (AF368257) CryIba [Bacillus thurin...	383	e-105
gb AAK14339.1	(AF327927) insecticidal crystal protein BTRX...	375	e-102
sp Q45733 C9CA_BACTO	Pesticidial crystal protein cry9Ca (In...	372	e-102
sp Q9ZAZ5 C1BD_BACTZ	Pesticidial crystal protein cryIBd (In...	364	2e-99
sp Q45704 C8AA_BACUK	Pesticidial crystal protein cry8Aa (In...	353	3e-96
sp O85805 C1BE_BACTU	Pesticidial crystal protein cryIBe (In...	344	1e-93
sp Q45705 C8BA_BACUK	Pesticidial crystal protein cry8Ba (In...	344	2e-93
gb AAC63366.1	(AF093107) delta-endotoxin [Bacillus thuring...	339	6e-92
pdb 1JI6 A	Chain A, Crystal Structure Of The Insecticidal B...	337	2e-91
sp Q06117 C3BB_BACTU	Pesticidial crystal protein cry3Bb (In...	337	2e-91
sp P17969 C3BA_BACTO	PESTICIDIAL CRYSTAL PROTEIN CRY3BA (IN...	335	6e-91
gb AAA74198.1	(U31633) Cry3Bb2 [Bacillus thuringiensis]	335	8e-91
pir S39536	parasporal crystal protein-related protein - Ba...	333	4e-90
emb CAA52927.1	(X75019) delta-endotoxin [Bacillus thuringi...	333	4e-90
sp O06014 C9DA_BACTP	PESTICIDIAL CRYSTAL PROTEIN CRY9DA (IN...	325	7e-88
sp Q45708 C7AB_BACUK	Pesticidial crystal protein cry7Ab (In...	323	3e-87
sp Q9ZNL9 C9EA_BACTA	Pesticidial crystal protein cry9Ea (In...	322	7e-87
sp Q45707 C7AB_BACUA	Pesticidial crystal protein cry7Ab (In...	319	5e-86

sp P07130 C3AA_BACTT	Pesticidal crystal protein cry3Aa pre...	319	6e-86
pir A27323	parasporal crystal protein CryIIIA - Bacillus t...	319	6e-86
gb AA73184.1	(M84650) crystal toxin [synthetic construct]...	318	8e-86
emb CAA51996.1	(X73600) CryIIIA insecticidal crystal prote...	318	8e-86
pdb 1DLC	Delta-Endotoxin Cryiia (Bt13)	318	8e-86
gb AAA22542.1	(M30503) insect control protein [Bacillus th...	317	3e-85
sp Q03749 C7AA_BACTU	PESTICIDIAL CRYSTAL PROTEIN CRY7AA (IN...	315	7e-85
gb AAB97923.1	(AF042733) delta-endotoxin [Bacillus thuring...	314	2e-84
sp Q9X597 CQAA_BACTF	Pesticidal crystal protein cry26Aa (I...	303	5e-81
sp Q45744 C3CA_BACTK	PESTICIDIAL CRYSTAL PROTEIN CRY3CA (IN...	289	5e-77
sp Q45706 C8CA_BACTP	PESTICIDIAL CRYSTAL PROTEIN CRY8CA (IN...	246	4e-64
sp Q99031 C9AA_BACTG	PESTICIDIAL CRYSTAL PROTEIN CRY9AA PRE...	236	4e-61
emb CAA41425.1	(X58534) crystal protein [Bacillus thuringi...	236	4e-61
pir B42459	hypothetical protein 2 (cryIF 3' region) - Baci...	232	1e-59
gb AAA22349.1	(M63897) ORF [Bacillus thuringiensis]	232	1e-59
dbj BAB78603.1	(AB075462) crystal protein CryE6S [Bacillus...	222	1e-56
dbj BAB72016.2	(AB074413) insecticidal crystal protein bun...	221	2e-56
gb AAG36711.1	(AY008143) crystal protein [Bacillus thuring...	219	7e-56
sp O87905 COAA_BACTJ	Pesticidal crystal protein cry24Aa (I...	214	3e-54
sp O32307 CJAA_BACTJ	Pesticidal crystal protein cry19Aa (I...	206	8e-52
sp O86170 CJBA_BACUH	Pesticidal crystal protein cry19Ba (I...	191	1e-47
dbj BAB78602.1	(AB075461) crystal protein CryE6Q [Bacillus...	189	7e-47
sp P16479 CRYU_BACTI	130 KD CRYSTAL PROTEIN (DELTA ENDOTOXI...	179	8e-44
gb AAG00235.1	AF285775_1 (AF285775) parasporal inclusion pr...	179	8e-44
pir A26858	130K delta-endotoxin - Bacillus thuringiensis s...	179	1e-43
sp P16480 C4AA_BACTI	PESTICIDIAL CRYSTAL PROTEIN CRY4AA (IN...	178	1e-43
sp Q9X682 CSAA_BACTF	Pesticidal crystal protein cry28Aa (I...	178	2e-43
emb CAA34382.1	(X16315) delta-endotoxin (AA 429-726) [Baci...	175	1e-42
pir S04994	Parasporal crystal protein - Bacillus thuringie...	175	1e-42
sp O32321 CKAA_BACUF	Pesticidal crystal protein cry20Aa (I...	173	5e-42
gb AAF01213.1	(AF182196) endotoxin [Bacillus thuringiensis]	171	3e-41
sp O87906 CPAA_BACTJ	Pesticidal crystal protein cry25Aa (I...	164	2e-39
sp P09662 CAAA_BACTI	PESTICIDIAL CRYSTAL PROTEIN CRY10AA (I...	160	4e-38
pir B29838	parasporal crystal protein - Bacillus thuringie...	160	4e-38
emb CAC80986.1	(AJ251978) Cry30Aa protein [Bacillus thurin...	155	1e-36
dbj BAB72018.1	(AB074414) insecticidal crystal protein bun...	155	2e-36
sp Q9S597 CRAA_BACUH	Pesticidal crystal protein cry27Aa (I...	154	3e-36
emb CAC80985.1	(AJ251977) Cry29Aa protein [Bacillus thurin...	142	1e-32
sp Q45882 CGAA_CLOBI	Pesticidal crystal-like protein cry16...	142	1e-32
sp P05519 C4BA_BACTI	PESTICIDIAL CRYSTAL PROTEIN CRY4BA (IN...	128	2e-28
emb CAA30114.1	(X07082) delta-endotoxin (AA 1 - 1136) [Bac...	128	2e-28
gb AAC60477.1	(S72313) delta-endotoxin CryIAb7 [Bacillus t...	122	1e-26
dbj BAB78601.1	(AB075460) crystal protein CryE6L [Bacillus...	115	2e-24
sp P11782 CRYT_BACTI	130 KD CRYSTAL PROTEIN (DELTA ENDOTOXI...	114	2e-24
sp O05102 CHAA_CLOBI	Pesticidal crystal-like protein cry17...	103	5e-21
sp Q9RMG3 C2AD_BACTU	Pesticidal crystal protein cry2Ad (In...	81	4e-14
sp Q45754 CCAA_BACTU	Pesticidal crystal protein cry12Aa (I...	79	1e-13
emb CAA10670.2	(AJ132463) Cry2A protein [Bacillus thuringi...	76	9e-13
emb CAA10671.1	(AJ132464) Cry2Aa protein [Bacillus thuring...	76	9e-13
pdb 1I5P A	Chain A, Insecticidal Crystal Protein Cry2aa	76	1e-12
gb AAC04867.1	(AF047038) insecticidal crystal protein [Bac...	76	1e-12
sp P21253 C2AA_BACTK	Pesticidal crystal protein cry2Aa (In...	76	1e-12
pir A29913	parasporal crystal protein P2 - Bacillus thurin...	76	1e-12
emb CAA10672.1	(AJ132465) Cry2Aa protein [Bacillus thuring...	75	2e-12
sp P21254 C2AB_BACTK	Pesticidal crystal protein cry2Ab (In...	73	8e-12
pir A25140	parasporal crystal protein - Bacillus thuringie...	68	3e-10
sp P57091 CIBA_PAEPP	Parasporal crystal protein cry18Ba (Pa...	67	4e-10
sp Q45358 CIAA_PAEPP	Parasporal crystal protein cry18Aa (Pa...	67	6e-10
sp P57092 CICA_PAEPP	Parasporal crystal protein cry18Ca (Pa...	62	2e-08
gb AAM06002.1	(AE010957) hypothetical protein [Methanosarc...	59	2e-07
sp Q45743 C2AC_BACTU	Pesticidal crystal protein cry2Ac (In...	57	6e-07
sp Q45753 C5AB_BACUD	Pesticidal crystal protein cry5Ab (In...	55	2e-06
sp Q45710 CEAA_BACTS	Pesticidal crystal protein cry14Aa (I...	53	8e-06
sp Q45712 C5BA_BACTU	Pesticidal crystal protein cry5Ba (In...	53	8e-06
sp Q45760 C5AA_BACUD	Pesticidal crystal protein cry5Aa (In...	52	2e-05
dbj BAB11757.1	(AB031065) 81-kDa leukemia toxin [Bacillus ...	52	2e-05
sp P56955 C5AC_BACTU	Pesticidal crystal protein cry5Ac (In...	50	9e-05
sp Q45730 CBBA_BACTJ	Pesticidal crystal protein cry11Ba (I...	48	3e-04
sp P21256 CBAA_BACTI	Pesticidal crystal protein cry11Aa (I...	47	6e-04

sp P56956 CLAA_BACTU	Pesticidal crystal protein cry21Aa (I...	46	0.001
sp Q45755 CDAA_BACTU	Pesticidal crystal protein cry13Aa (I...	44	0.004
sp Q9ZIU5 CBBB_BACTV	Pesticidal crystal protein cry11Bb (I...	44	0.005
emb CAA98839.1	(Z74314) ORF YDR017c [Saccharomyces cerevis...	40	0.073
ref NP_010300.1	(NC_001136) Shows homology to basic leucin...	40	0.073
ref NP_437949.1	(NC_003078) putative regulatory protein, p...	37	0.62

Alignments

>sp|Q03746|C1FA_BACTA Pesticidal crystal protein cry1Fa (Insecticidal delta-endotoxin CryIF(a)) (Crystalline entomocidal protoxin) (134 kDa crystal protein)
 pir||A42459 insecticidal crystal protein CryIF - Bacillus thuringiensis (strain aizawai)
 gb|AAA22347.1| (M73254) cryIF [Bacillus thuringiensis]
 gb|AAA22348.1| (M63897) insecticidal crystal protein [Bacillus thuringiensis]
 Length = 1174

Score = 1231 bits (3185), Expect = 0.0
 Identities = 604/605 (99%), Positives = 604/605 (99%)

Query: 1	MENNIQNQCVPYNCLNNPEVEILNEERSTGRPLDISLSLTRLFLSEFVPGVGVAFGFLD	60
	MENNIQNQCVPYNCLNNPEVEILNEERSTGRPLDISLSLTRLFLSEFVPGVGVAFGFLD	
Sbjct: 1	MENNIQNQCVPYNCLNNPEVEILNEERSTGRPLDISLSLTRLFLSEFVPGVGVAFGFLD	60
Query: 61	LIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSIEIYIEALREWEANPN	120
	LIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSIEIYIEALREWEANPN	
Sbjct: 61	LIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSIEIYIEALREWEANPN	120
Query: 121	NAQLREDVRIREFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW	180
	NAQLREDVRIREFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW	
Sbjct: 121	NAQLREDVRIREFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW	180
Query: 181	GLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRDLTLTVLD	240
	GLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRDLTLTVLD	
Sbjct: 181	GLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRDLTLTVLD	240
Query: 241	IVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM	300
	IVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM	
Sbjct: 241	IVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM	300
Query: 301	NSLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPGGAIWIADEDPRPFYRTLS	360
	NSLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPGGAIWIADEDPRPFYRTLS	
Sbjct: 301	NSLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPGGAIWIADEDPRPFYRTLS	360
Query: 361	DPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDMSGAPWNDYS	420
	DPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDMSGAPWNDYS	
Sbjct: 361	DPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDMSGAPWNDYS	420
Query: 421	HVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT	480
	HVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT	
Sbjct: 421	HVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT	480
Query: 481	VVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYASTTNLRIYVTVAGERIF	540
	VVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYASTTNLRIYVTVAGERIF	
Sbjct: 481	VVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYASTTNLRIYVTVAGERIF	540
Query: 541	AGQFNKMTDGTGDLTFQSFYSATINTAFTFPMSQSSFTVGADTFSSGNEVYIDRFELIPV	600
	AGQFNKMTDGTGDLTFQSFYSATINTAFTFPMSQSSFTVGADTFSSGNEVYIDRFELIPV	
Sbjct: 541	AGQFNKMTDGTGDLTFQSFYSATINTAFTFPMSQSSFTVGADTFSSGNEVYIDRFELIPV	600
Query: 601	TATLE 605	
	TAT E	
Sbjct: 601	TATFE 605	
>pir S32649 parasporal crystal protein - Bacillus thuringiensis		
emb CAA80235.1 (Z22512) crystal protein [Bacillus thuringiensis]		
Length = 1174		

Score = 1060 bits (2740), Expect = 0.0
Identities = 519/605 (85%), Positives = 549/605 (89%), Gaps = 1/605 (0%)

Query: 1 MENNIONQCVYPYNCLNNPEVEILNEERSTGRPLPLDISLSLRFLLSEFVPGVGVAFGLED 60
M+NNIONQCVYPYNCL+NPEVEIL+EERSTGRPLPLDISLSLRFLLSEFVPGVGVAFGLED
Sbjct: 1 MKNNIONQCVYPYNCLSNPEVEILSEERSTGRPLPLDISLSLRFLLSEFVPGVGVAFGLED 60

Query: 61 LIWGFIPTSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEYIEALREWEANPN 120
LIWGFIPTPS+WSLFLQIEQLIEQRIETLERNRAITTLRGLADSYE+Y+EALREWE NPN
Sbjct: 61 LIWGFIPTSEWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEVYLEALREWEENPN 120

Query: 121 NAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW 180
NAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW
Sbjct: 121 NAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW 180

Query: 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNQLENLRGTNTRQWARFNQFRDLTLTVLD 240
GLDIATVNNHYNRLINLIHRYT+HCLDTYNQLENLRGTNTRQW+RFNQFR+LTLTVLD
Sbjct: 181 GLDIATVNNHYNRLINLIHRYTEHCLDTYNQLENLRGTNTRQWSRFNQFRRELTLTVLD 240

Query: 241 IVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM 300
IVALFPNYD R YPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM
Sbjct: 241 IVALFPNYDARAYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM 300

Query: 301 NSLFVTAETVRSQTVWGGHLVSSRNNTAGNRINFPSYGVFNPGGAIWIADDPFPFYRTL 360
NSLFVTAETVRSQTVWGGHLVSSRNNTAGN INFP YG+FNPGGAIWIADDPFPFYRTL
Sbjct: 301 NSLFVTAETVRSQTVWGGHLVSSRNNTAGNPINFPIYGFNPGGAIWIADDPFPFYRTL 360

Query: 361 DPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNGAPWWDYS 420
DPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNGAPWWDYS
Sbjct: 361 DPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNGAPWWDYS 420

Query: 421 HVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
HVLNHVTFVRWPGEI+GSDSWRAPMFSWTHRSA TN I+P ITQIP VKAH L SG+T
Sbjct: 421 HVLNHVTFVRWPGEIAGSDSWRAPMFSWTHRSADRTNIINPNIIITQIPAVKAHNHLSGST 480

Query: 481 VVRGPGFTGGDILRRTSGGPFAITVNINGQLPQYRARIYASTTNLRIYVTVAGERIF 540
VVRGPGFTGGD+LRRT+ G FA VNI G L QRYR RIRYASTT+L+ + + G +
Sbjct: 481 VVRGPGFTGGDLRRTNTGTTFADIRVNITGPLSQRYRVIRYASTTDLQFFTRINGTSVN 540

Query: 541 AGQFNKMTDGTGDLTFQSFSYATINTAFTFPMSSQSFVADTFSSGNEVYIDRFELIPV 600
G F +TM+ G L +F A +T F+F +QS+ET+G FS+ EVYIDR E +P
Sbjct: 541 QGNFQRTMNRGGNLESGNFRTAGFSTPFSFSAQSTFTLTGTQAFSN-QEVYIDRIEFVPA 599

Query: 601 TATLE 605
T E
Sbjct: 600 EVTTE 604

>dbj|BAA25298.1| (AB012288) CryINA67-1 [Bacillus thuringiensis]
Length = 1168

Score = 1060 bits (2740), Expect = 0.0
Identities = 519/605 (85%), Positives = 549/605 (89%), Gaps = 1/605 (0%)

Query: 1 MENNIONQCVYPYNCLNNPEVEILNEERSTGRPLPLDISLSLRFLLSEFVPGVGVAFGLED 60
M+NNIONQCVYPYNCL+NPEVEIL+EERSTGRPLPLDISLSLRFLLSEFVPGVGVAFGLED
Sbjct: 1 MKNNIONQCVYPYNCLSNPEVEILSEERSTGRPLPLDISLSLRFLLSEFVPGVGVAFGLED 60

Query: 61 LIWGFIPTSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEYIEALREWEANPN 120
LIWGFIPTPS+WSLFLQIEQLIEQRIETLERNRAITTLRGLADSYE+Y+EALREWE NPN
Sbjct: 61 LIWGFIPTSEWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEVYLEALREWEENPN 120

Query: 121 NAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW 180
NAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW
Sbjct: 121 NAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW 180

Query: 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNQLENLRGTNTRQWARFNQFRDLTLTVLD 240
GLDIATVNNHYNRLINLIHRYT+HCLDTYNQLENLRGTNTRQW+RFNQFR+LTLTVLD
Sbjct: 181 GLDIATVNNHYNRLINLIHRYTEHCLDTYNQLENLRGTNTRQWSRFNQFRRELTLTVLD 240

Query: 241 IVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM 300
IVALFPNYD R YPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM
Sbjct: 241 IVALFPNYDARAYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM 300

Query: 301 NSLFVTAETVRSQTVWGGHLVSSRNNTAGNRINFPSYGVFNPGGAIWIADEDPRPFYRTLS 360
NSLFVTAETVRSQTVWGGHLVSSRNNTAGN INFP YG+FNPGGAIWIADEDPRPFYRTLS
Sbjct: 301 NSLFVTAETVRSQTVWGGHLVSSRNNTAGNPINFPIYGFNPGGAIWIADEDPRPFYRTLS 360

Query: 361 DPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNSGAPWNDYS 420
DPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNSGAPWNDYS
Sbjct: 361 DPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNSGAPWNDYS 420

Query: 421 HVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
HVLNHVTFVRWPGEI+GSDSWRAPMFSWTHRSA TN I+P ITQIP VKAH L SG+T
Sbjct: 421 HVLNHVTFVRWPGEIAGSDSWRAPMFSWTHRSADRTNIINPNIITQIPAVKAHNHSGST 480

Query: 481 VVRGPGFTGGDILRRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIF 540
VVRGPGFTGGD+LRRRT+ G FA VNI G L QRYR RIRYASTT+L+ + + G +
Sbjct: 481 VVRGPGFTGGDLLRRNTGTTFADIRVNITGPLSQRYRVIRYASTTDLQFFTRINGTSVN 540

Query: 541 AGQFNKTMMDTGDPFLTQSFSYATINTAFTFPMSSQSFVGTADTFSSGNEVYIDRFELIPV 600
G F +TM+ G L +F A +T F+F +QS+FT+G FS+ EVYIDR E +P
Sbjct: 541 QGNFQRTMNRGNLESGNFRTAGFSTFFSNAQSTFTLGTQAFSN-QEVYIDRIEFVPA 599

Query: 601 TATLE 605
T E
Sbjct: 600 EVTFE 604

>sp|O66377|C1FB BACTM PESTICIDIAL CRYSTAL PROTEIN CRY1FB (INSECTICIDAL DELTA-ENDOTOXIN
CRYIF(B)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (132 KDA
CRYSTAL PROTEIN)
gb|AAF21767.1|AF062350_1 (AF062350) crystal protein Cry1Fb [Bacillus thuringiensis serovar
morrisoni]
Length = 1169

Score = 1058 bits (2737), Expect = 0.0
Identities = 519/605 (85%), Positives = 548/605 (89%), Gaps = 1/605 (0%)

Query: 1 MENNIQNQCVPYNCLNPEVEILNEERSTGRPLDISLSLTRFLLSEFVPGVGVAAGLFD 60
M+NNIQNQCVPYNCL+NPEVEIL+EERSTGRPLDISLSLTRFLLSEFVPGVGVAAGLFD
Sbjct: 1 MKNNIQNQCVPYNCLNPEVEILSEERSTGRPLDISLSLTRFLLSEFVPGVGVAAGLFD 60

Query: 61 LIWGFIPTSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEYIEALREWEANPN 120
LIWGFIPT+WSLFLQIEQLIEQRIETLERNRAITTLRGLADSYE+Y+EALREWE NPN
Sbjct: 61 LIWGFIPTSEWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEVYLEALREWEENPN 120

Query: 121 NAQLREDVRIREFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW 180
NAQLREDVRIREFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW
Sbjct: 121 NAQLREDVRIREFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW 180

Query: 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNQLENLRGTNTRQWARFNQFRRDLTLTVLD 240
GLDIATVNNHYNRLINLIHRYT+HCLDTYNQLENLRGTNTRQW+RFNQFRR+LTLTVLD
Sbjct: 181 GLDIATVNNHYNRLINLIHRYTEHCLDTYNQLENLRGTNTRQWSRFNQFRRDLTLTVLD 240

Query: 241 IVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM 300
IVALFPNYD R YPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM
Sbjct: 241 IVALFPNYDARAYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM 300

Query: 301 NSLFVTAETVRSQTVWGGHLVSSRNNTAGNRINFPSYGVFNPGGAIWIADEDPRPFYRTLS 360
NSLFVTAETVRSQTVWGGHLVSSRNNTAGN INFP YGVFNPGGAIWIADEDPRPFYRTLS
Sbjct: 301 NSLFVTAETVRSQTVWGGHLVSSRNNTAGNPINFPIYGVFNPGGAIWIADEDPRPFYRTLS 360

Query: 361 DPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNSGAPWNDYS 420
DPVFVRGGFGNPHYVLGLRGV FQQTGTNHTRTFRNSGTIDSLDEIPPQDNSGAPWNDYS
Sbjct: 361 DPVFVRGGFGNPHYVLGLRGVGFQQTGTNHTRTFRNSGTIDSLDEIPPQDNSGAPWNDYS 420

Query: 421 HVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
HVLNHVTFVRWPGEI+GSDSWRAPMFSWTHRSA TN I+P ITQIP VKAH L SG+T
Sbjct: 421 HVLNHVTFVRWPGEIAGSDSWRAPMFSWTHRSADRTNIINPNIITQIPAVKAHNHSGST 480

Query: 481 VVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIF 540
VVRGPGFTGGD+LRRT+ G FA VNI G L QRYR RIRYASTT+L+ + + G +
Sbjct: 481 VVRGPGFTGGDLLRRTNTGTTFADIRVNITGPLSQRYRVIRYASTTDLQFFTRINGTSVN 540

Query: 541 AGQFNKMTMDTGDPLTFQSFYSYATINTAFTFPMSSQSSFTVGADTFSSGNEVYIDRFELIPV 600
G F +TM+ G L +F A +T F+F +QS+FT+G FS+ EVYIDR E +P
Sbjct: 541 QGNFQRTMNRGGNLESGNFRTAGFTSTPFSFSAQSTFTLGTQAFSN-QEVYIDRIEFVPA 599

Query: 601 TATLE 605
T E
Sbjct: 600 EVTFE 604

>sp|Q03748|C1AE_BACTL PESTICIDIAL CRYSTAL PROTEIN CRYIAE (INSECTICIDAL DELTA-ENDOTOXIN
CRYIA(E)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (134 KDA
CRYSTAL PROTEIN)
pir||A41052 parasporal crystal protein - Bacillus thuringiensis (strain alesti)
gb|AAA22410.1| (M65252) delta-endotoxin [Bacillus thuringiensis]
Length = 1181

Score = 583 bits (1504), Expect = e-165
Identities = 317/614 (51%), Positives = 393/614 (63%), Gaps = 11/614 (1%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFLG 58
M+NN + N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNNPKINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
DLIWGF+ PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY EA REWEA+
Sbjct: 61 IDLIWGFVGPSQWDAFLVQIEQLISQRIEEFARNQAISRLEGLSNLYQIYAEAFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI FT+ ++++PLLSVYVQA NLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLFTVQNYQVPLLSVYVQAVNLHLSVLRDVSVFGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRLTLTV 238
WGLD+AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGLDVATINSRYNDLTRLIGTYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIV+LFPNYD RTYPI+T SQLTREIYT+ V+E+ + R E +R PHLM
Sbjct: 241 LDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQRIEQSIRSPHLM 298

Query: 299 FMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADDPDPF 355
+NS+ + + W GH + S +G FP YG N I + +
Sbjct: 299 ILNSTIITYTDAHGGYYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLQGV 358

Query: 356 YRTLSDPV----FVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS F+ G VL A+ + + +R SGT+DSLDEIPPQDN
Sbjct: 359 YRTLSSTFYRNPFIIGINNQRLSVLDGTEFAYGSSSNLPSAVYRKSGTVDSLDEIPPQDN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R S RAPMFSW HRSA N I +ITQIPL K
Sbjct: 419 NVPPRQGFHRLSHVSMFRSGFSNSSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLTK 478

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIY 531
+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+ +
Sbjct: 479 STNLGSGTSVVGKPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVIRYASTTNLQFH 538

Query: 532 VTVAGERIFAGQFNKMTMDTGDPLTFQSFYSYATINTAFTFPMSSQSSFTVGADTFSSGNEVY 591
++ G I G F+ TM +G L SF T F F S FT+ A F+SGNEVY
Sbjct: 539 TSIDGRPINQGNFSATMSSGGNLQSGSFRTVGFTTFFNFNSGSSVFTLSAHVFNSSGNEVY 598

Query: 592 IDRFELIPVTATLE 605
IDR E +P T E
Sbjct: 599 IDRIEFVPAEVTFE 612

>sp|P21257|CRYT_BACTK 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALINE ENTOMOCIDAL
PROTOXIN) (5.3 CLASS)

pir|I39838 delta-endotoxin (5.3 class) - Bacillus thuringiensis
gb|AAA22420.1| (M37263) 5.3 class delta endotoxin [Bacillus thuringiensis]
Length = 1155

Score = 579 bits (1493), Expect = e-164
Identities = 314/614 (51%), Positives = 392/614 (63%), Gaps = 11/614 (1%)

Query: 1 MNNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + ++++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNTRQWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT H + YN GLE + G ++R W R+NQFRRL+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRLTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIV+LFPNYD RTYPI+T SQLTREIYT+ V+E+ + E +R PHLM
Sbjct: 241 LDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSRGSAQGIEGSIRSPHLM 298

Query: 299 FMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADDP 355
+NS+ + + R + W GH + S +G FP YG N I + +
Sbjct: 299 ILNSITIYTDARHGEYYWSGHQIMASPVGFGPEFTFPLYGTMGAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS ++ R G N VL A+ + + +R SGT+DSLDEIPPQ+N
Sbjct: 359 YRTLSSTLYRRFPNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R S RAPMFSW HRSA N I +ITQIPL K
Sbjct: 419 NVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAFNFIIPSSQITQIPLTK 478

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIY 531
+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+ +
Sbjct: 479 STNLGSGTSVVGKPGFTGGDILRRTSPGQISTLRVNIAPLSQRYRVRIYASTTNLQFH 538

Query: 532 VTVAGERIFAGQFNKMTDGTPLTFQSFYSATINTAFTFPMSSQSSFTVGADTFSSGNEVY 591
++ G I G F+ TM +G L SF + T F F S FT+ A F+SGNEVY
Sbjct: 539 TSIHGRPINQGNFSAFMSSGSNLQSGSFRHLGFTTPFNFSNGSSVFTLSAHVFNSSGNEVY 598

Query: 592 IDRFELIPVTATLE 605
IDR E +P T E
Sbjct: 599 IDRIEFVPAEVTFE 612

>gb|AAK14336.1| (AF327924) insecticidal crystal protein BTRX24 [Bacillus
thuringiensis serovar kunthalarX24]
Length = 1118

Score = 578 bits (1491), Expect = e-164
Identities = 313/614 (50%), Positives = 392/614 (62%), Gaps = 11/614 (1%)

Query: 1 MNNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFL 58
M+NN+ N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + ++++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNQWARFNQFRRDLTLTV 238
WG D AT+N+ YN L LI YT H + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRDLTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIV+LFPNYD RTYPI+T SQLTREIYT+ V+E+ + E +R PHLM
Sbjct: 241 LDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQGIEGSIRSPLHMD 298

Query: 299 FMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADEDPRPF 355
+NS+ + + R + W GH + S +G FP YG N I + +
Sbjct: 299 ILNSITIYTDHAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVVRG---GFGNPHY-VLGLRGVAFQQTGTNHTTRFRNSGTIDSLDEIPPQDN 411
+ R SGT++ R G N VL A+ + + +R SGT+DSLDEIPPQ+N
Sbjct: 359 YRTLSSTLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R S RAPMFSW HRSA N I +ITQIPL K
Sbjct: 419 NVPPRQGFHRLSHVSMFSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLTK 478

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRIRYASTTNLRIY 531
+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+ +
Sbjct: 479 STNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRIRYASTTNLQFH 538

Query: 532 VTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTFPMSSQSFVTGADTFSSGNEVY 591
++ G I G F+ TM +G L +F T F F S FT+ A F+SGNEVY
Sbjct: 539 TSIDGRPINQGNFSAFMSSGNSLQSGAFMTVGFTTFFNFSSNGSSVFTLSAHVFNSSGNEVY 598

Query: 592 IDREFELIPVTATLE 605
IDR E +P T E
Sbjct: 599 IDRIEFVPAEVTFE 612

>pir||A29125 parasporal crystal protein - Bacillus thuringiensis subsp. kurstaki
(strain HD-1)
prf||1310234A insect control protein [Bacillus thuringiensis]
Length = 1156

Score = 578 bits (1489), Expect = e-164
Identities = 314/614 (51%), Positives = 391/614 (63%), Gaps = 11/614 (1%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFLG 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEFARNQAISRLGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + ++++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNQWARFNQFRRDLTLTV 238
WG D AT+N+ YN L LI YT H + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRDLTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIV+LFPNYD RTYPI+T SQLTREIYT+ V+E+ + E +R PHLM
Sbjct: 241 LDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQGIEGSIRSPLHMD 298

Query: 299 FMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADEDPRPF 355
+NS+ + + R + W GH + S +G FP YG N I + +
Sbjct: 299 ILNSITIYTDHAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVVRG---GFGNPHY-VLGLRGVAFQQTGTNHTTRFRNSGTIDSLDEIPPQDN 411
YRTLS ++ R G N VL A+ + + +R SGT+DSLDEIPPQ+N
Sbjct: 359 YRTLSSTLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R S RAPMFSW HRSA N I +ITQIPL K
Sbjct: 419 NVPPRQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLTK 478

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIY 531
+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+ +
Sbjct: 479 STNLGSGTSSVVGKPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIYASTTNLQFH 538

Query: 532 VTVAGERIFAGQFNKTMGTGDLTFQSFYSATINTAFTFPMSSQSSFTVGADTFSSGNEVY 591
++ G I G F+ TM +G L SF T F F S FT+ A F+SGNEVY
Sbjct: 539 TSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTPFNFSNGSSVFTLSAHVFNSGNEVY 598

Query: 592 IDRFELIPVTATLE 605
IDR E +P T E
Sbjct: 599 IDRIEFVPAEVTFE 612

>gb|AAG16877.1| (U94191) delta endotoxin [Bacillus thuringiensis]
Length = 1155

Score = 578 bits (1489), Expect = e-164
Identities = 314/614 (51%), Positives = 391/614 (63%), Gaps = 11/614 (1%)

Query: 1 MENNIQ-NQCVPYNCNLNPEVEILNEER-STGRLPLDISLSLTRFLLSEFVPGVGVAFL 58
M+NN N+C+PYNCNL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNPNINECIPYNCNLNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGFIFGSPQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + +++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLEAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRRDLTLTV 238
WG D AT+NN+ YN L LI YT H + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGFDAAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRDLTLTV 240

Query: 239 LDIVALEFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIV+LEFPNYD RTYPI+T SQLTREIYT+ V+E+ + E +R PHLM
Sbjct: 241 LDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLEN--FDGSFRGSAQGI EGSI RSPHLM 298

Query: 299 FMNSLFVTAETVRSQTVMWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADDPREF 355
+NS+ + + R + W GH + S +G FP YG N I + +
Sbjct: 299 ILNSITIYTDHARGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS ++ R G N VL A+ + + +R SGT+DSLDEIPPQ+N
Sbjct: 359 YRTLSSTLYRRFPNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R S RAPMFSW HRSA N I +ITQIPL K
Sbjct: 419 NVPPRQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLTK 478

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIY 531
+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+ +
Sbjct: 479 STNLGSGTSSVVGKPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIYASTTNLQFH 538

Query: 532 VTVAGERIFAGQFNKTMGTGDLTFQSFYSATINTAFTFPMSSQSSFTVGADTFSSGNEVY 591
++ G I G F+ TM +G L SF T F F S FT+ A F+SGNEVY
Sbjct: 539 TSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTPFNFSNGSSVFTLSAHVFNSGNEVY 598

Query: 592 IDRFELIPVTATLE 605
IDR E +P T E
Sbjct: 599 IDRIEFVPAEVTFE 612

>gb|AAA72985.1| (M60856) cryIA(a) [synthetic construct]
Length = 615

Score = 578 bits (1489), Expect = e-164
Identities = 314/614 (51%), Positives = 391/614 (63%), Gaps = 11/614 (1%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRLFLSEFVPGVGVAFL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + +++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT H + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIV+LFPNYD RTYPI+T SQLTREIYT+ V+E+ + E +R PHLM
Sbjct: 241 LDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLEN--FDGSFRGSAQGIEGSI RPHLM 298

Query: 299 FMNSLFVTAETVRSQTVWGGH--LVSSRNNTAGNRINFPSYGVF-NPGGAIWIADPRPF 355
+NS+ + + R + W GH + S +G FP YG N I + +
Sbjct: 299 ILNSITIIYDHAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVVRG---GFGNPHY-VLGLRGVAFQQTGNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS ++ R G N VL A+ + + +R SGT+DSLDEIPPQ+N
Sbjct: 359 YRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R S RAPMFSW HRSA N I +ITQIPL K
Sbjct: 419 NVPPRQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLTK 478

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRIRYASTTNLRIY 531
+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+ +
Sbjct: 479 STNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIRYASTTNLQFH 538

Query: 532 VTVAGERIFAGQFNKMTDGTPLTFQSFSYATINTAFTFPMSSQSFVADTFSSGNEVY 591
++ G I G F+ TM +G L SF T F F S FT+ A F+SGNEVY
Sbjct: 539 TSIDGRPIQGNFSA TMSSGSNLQSGSFRTVGFTTFFNFSGSSVFTLSAHVFNSSGNEVY 598

Query: 592 IDR FELIPVTATLE 605
IDR E +P T E
Sbjct: 599 IDRIEFVPAEVTTE 612

>sp|P06578|CIAB_BACTK PESTICIDIAL CRYSTAL PROTEIN CRYIAB (INSECTICIDAL DELTA-ENDOTOXIN
CRYIA(B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (130 KDA
CRYSTAL PROTEIN)

pir||JD0002 parasporal crystal protein Bt2 - Bacillus thuringiensis
emb|CAA38701.1| (X54939) unnamed protein product [Bacillus thuringiensis]
gb|AAA22330.1| (M13898) entomocidal protoxin [Bacillus thuringiensis]
gb|AAA22561.1| (M15271) crystal protein precursor [Bacillus thuringiensis]
dbj|BAA00071.1| (D00117) delta-endotoxin [Bacillus thuringiensis]
gb|AAC64003.1| (AF059670) crystal protein [Bacillus thuringiensis serovar
kurstaki]
prf||1304168A endotoxin delta 2 [Bacillus thuringiensis]
Length = 1155

Score = 578 bits (1489), Expect = e-164
Identities = 314/614 (51%), Positives = 391/614 (63%), Gaps = 11/614 (1%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRLFLSEFVPGVGVAFL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + ++++PLLSVYVQAANLHLS+LRD FGQ

Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNTRQWARFNQFRRDLTLTV 238
WG D AT+N+ YN L LI YT H + YN GLE + G ++R W R+NQFRR+LTLTV

Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIV+LFPNYD RTYPI+T SQLTREIYT+ V+E+ + E +R PHLMD

Sbjct: 241 LDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQGIEGSIRSPHLM 298

Query: 299 FMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADPRPF 355
+NS+ + + R + W GH + S +G FP YG N I + +

Sbjct: 299 ILNSITIYTDHARGEYYWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVVRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS ++ R G N VL A+ + + +R SGT+DSLDEIPPQ+N

Sbjct: 359 YRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R S RAPMFSW HRSA N I +ITQIPL K

Sbjct: 419 NVPPRQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLTK 478

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIY 531
+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+ +

Sbjct: 479 STNLGSGTSVVGKPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIRYASTTNLQFH 538

Query: 532 VTVAGERIFAGQFNKMTDGTPLTFQSFYSYATINTAFTFPMSSQSFVTGADTFSSGNEVY 591
++ G I G F+ TM +G L SF T F F S FT+ A F+SGNEVY

Sbjct: 539 TSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTFFNFSNGSSVFTLSAHVFNNGNEVY 598

Query: 592 IDRFELIPVTATLE 605
IDR E +P T E

Sbjct: 599 IDRIEFVPAEVTFE 612

>pir||A26461 parasporal crystal protein Bt2 - Bacillus thuringiensis (strain
berliner 1715)
emb|CAA28405.1| (X04698) delta endotoxin (AA 1-1155) [Bacillus thuringiensis]
Length = 1155

Score = 578 bits (1489), Expect = e-164
Identities = 314/614 (51%), Positives = 391/614 (63%), Gaps = 11/614 (1%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFG 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL

Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+

Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + ++++PLLSVYVQAANLHLS+LRD FGQ

Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNTRQWARFNQFRRDLTLTV 238
WG D AT+N+ YN L LI YT H + YN GLE + G ++R W R+NQFRR+LTLTV

Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIV+LFPNYD RTYPI+T SQLTREIYT+ V+E+ + E +R PHLMD

Sbjct: 241 LDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQGIEGSIRSPHLM 298

Query: 299 FMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADPRPF 355
+NS+ + + R + W GH + S +G FP YG N I + +

Sbjct: 299 ILNSITIYTDHARGEYYWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS ++ R G N VL A+ + + +R SGT+DSLDEIPPQ+N
Sbjct: 359 YRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R S RAPMFSW HRSA N I +ITQIPL K
Sbjct: 419 NVPPRQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLTK 478

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYASTTNLRIY 531
+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+ +
Sbjct: 479 STNLGSGTSVVKGPFTGGDILRRTSPGQISTLRVNITAPLSQRYRVIRYASTTNLQFH 538

Query: 532 VTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTFPMSSQSSFTVGADTFSSGNEVY 591
++ G I G F+ TM +G L SF T F F S FT+ A F+SGNEVY
Sbjct: 539 TSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFTTFFNFSSNGSSVFTLSAHVFNSSGNEVY 598

Query: 592 IDR FELIPVTATLE 605
IDR E +P T E
Sbjct: 599 IDRIEFVPAEVTFE 612

>sp|P09667|CRYV_BACTA 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE ENTOMOCIDAL
PROTOXIN)
pir||A26513 parasporal crystal protein - Bacillus thuringiensis (strain
aizawai)
gb|AAA22551.1| (M16463) insecticidal protein [Bacillus thuringiensis]
Length = 1155

Score = 577 bits (1486), Expect = e-163
Identities = 316/615 (51%), Positives = 393/615 (63%), Gaps = 13/615 (2%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGAVFGL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLELLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAAHLHLRLDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + ++++PLLSVYVQAAHLHL+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAHLHLVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTHKCLDTYNQGLENLRGNTNQWARFNQFRRLTLTV 238
WG D AT+N+ YN L LI YT H + YN GLE + G ++R W R+NQFRRLTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSAN-IPNGFNRAEFVGRPHLM 297
LDIV+LFPNYD RTYPI+T SQLTREIYT+ V+E+ S + G E +R PHLM
Sbjct: 241 LDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSFRALAQGI---EGSIRSPHLM 297

Query: 298 DFMNSLEFVTAETVRSQTVMGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADPRP 354
D +NS+ + + R + W GH + S +G FP YG N I + +
Sbjct: 298 DILNSITIYTDHRGEYYWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQGLGG 357

Query: 355 FYRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQD 410
YRTLS ++ R G N VL A+ + + +R SGT+DSLDEIPPQ+
Sbjct: 358 YVRLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQN 417

Query: 411 NSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLV 470
N+ P +SH L+HV+ R S RAPMFSW HRSA N I +ITQIPL
Sbjct: 418 NNVPPRQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLT 477

Query: 471 KAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYASTTNLRI 530
K+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+
Sbjct: 478 KSTNLGSGTSVVKGPFTGGDILRRTSPGQISTLRVNITAPLSQRYRVIRYASTTNLQF 537

Query: 531 YVTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTFPMSSQSSFTVGADTFSSGNEV 590
+ ++ G I G F+ TM +G L SF T F F S FT+ A F+SGNEV

Sbjct: 538 HTSIDGRPINQGNFSATMSSGSLNLSQSGSFRTVGFTTPFNFSNGSSVFTLSAHVFNSGNEV 597

Query: 591 YIDRFELIPVTATLE 605

YIDR E +P T E

Sbjct: 598 YIDRIEFVPAEVTFE 612

>gb|AAK55546.1|AF375608_1 (AF375608) crystal protein Cry1Ab16 [Bacillus thuringiensis serovar israelensis]
Length = 1155

Score = 577 bits (1486), Expect = e-163

Identities = 313/614 (50%), Positives = 390/614 (62%), Gaps = 11/614 (1%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFL 58

M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL

Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118

D+IWG PS W FL+QIEQLI ORIE RN+AI+ L GL++ Y+IY E+ REWEA+

Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178

P N LRE++RI+F + + AL TAI F + ++ +PLLSVYVQA NLHLS+LRD + FGQ

Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYRVPLLSVYVQAVNLHLSVLRDVLVFGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGTNTRQWARFNQFRDLTLTV 238

WG D AT+N+ YN L LI YT H + YN GLE + G ++R W R+NQFRR+LTLTV

Sbjct: 181 RWGFDAAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298

LDIV+LFPNYD RTYPI+T SQLTREIYT+ V+E+ + E +R PHLMD

Sbjct: 241 LDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSGFRSAQGIEGSIRSPHLM 298

Query: 299 FMNSLFVTAETVRSQTVMGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADDP 355

+NS+ + + R + W GH + S +G FP YG N I + +

Sbjct: 299 ILNSITIYTDHAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411

YRTLS ++ R G N VL A+ + + +R SGT+DSLDEIPPQ+N

Sbjct: 359 YRTLSSTLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSCTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471

+ P +SH L+HV+ R S RAPMFSW HRSA N I +ITQIPL K

Sbjct: 419 NVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLTK 478

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRIRYASTTNLRIY 531

+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+ +

Sbjct: 479 STNLGSGTSVVGKPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRIRYASTTNLQFH 538

Query: 532 VTVAGERIFAGQFNKMTDGDPLTFQSFYSATINTAFTFPMSSQSSFTVGADTFSSGNEVY 591

++ G I G F+ TM +G L SF T F F S FT+ A F+SGNEVY

Sbjct: 539 TSIDGRPINQGNFSATMSSGSLNLSQSGSFRTVGFTTPFNFSNGSSVFTLSAHVFNSGNEVY 598

Query: 592 IDRFELIPVTATLE 605

IDR E +P T E

Sbjct: 599 IDRIEFVPAEVTFE 612

>sp|P09666|CRYT BACTA 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE ENTOMOCIDAL PROTOXIN)

pir||S02134 parasporal crystal protein - Bacillus thuringiensis (strain aizawai IC1)

emb|CAA31620.1| (X13233) delta-endotoxin [Bacillus thuringiensis]
Length = 1155

Score = 577 bits (1486), Expect = e-163

Identities = 313/614 (50%), Positives = 391/614 (62%), Gaps = 11/614 (1%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFL 58

M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL

Sbjct: 1 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+

Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + ++++PLLSVYVQAANLHLS+LRD FGQ

Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNTRQWARFNQFRRDLTLTV 238
WG D AT+N+ YN L LI YT H + YN GLE + G ++R W R+NQFRR+LTLTV

Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRDLTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPLHMD 298
LDIV+LFPNYD RTYPI+T SQLTREIYT+ V+E+ + E +R PHLMD

Sbjct: 241 LDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQGIEGSIIRPHLMD 298

Query: 299 FMNSLFVTAETVRSQTVWGGH--LVSSRNATAGNRINFPSYGVF-NPGGAIWIADEPRPF 355
+NS+ + + R + W GH + S +G FP YG N I + +

Sbjct: 299 ILNSITIYDHAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS ++ R G N VL A+ + + +R SGT+DSLDEIPPQ+N

Sbjct: 359 YRTLSTLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R S R PMFSW HRSA N I +ITQIPL K

Sbjct: 419 NVPPRQGFHSHRLSHVSMFRSGFSNSSVSIIRPPMFSWIHRSAEFNNIIPSSQITQIPLTK 478

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRIRIRYASTTNLRIY 531
+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+++

Sbjct: 479 STNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIRYASTTNLQLH 538

Query: 532 VTVAGERIFAGQFNKMTMDTGDPLTFQSFSYATINTAFTFPMSSQSSFTVGADTFSSGNEVY 591
++ G I G F+ TM +G L SF T F F S ET+ A F+SGNEVY

Sbjct: 539 TSIDGRIINQGNFSATMSSGSNLQSGSFRIVGFTTFFNFSNGSSVFTLSAHVFNSGNEVY 598

Query: 592 IDRFELIPVTATLE 605
IDR E +P T E

Sbjct: 599 IDRIEFVPAEVTTE 612

>sp|Q03744|C1AD_BACTA Pesticidal crystal protein cryIAd (Insecticidal delta-endotoxin
CryIA(d)) (Crystalline entomocidal protoxin) (133 kDa
crystal protein)
gb|AAA22340.1| (M73250) cryIA(d) [Bacillus thuringiensis]
Length = 1179

Score = 573 bits (1476), Expect = e-162
Identities = 312/612 (50%), Positives = 390/612 (62%), Gaps = 15/612 (2%)

Query: 4 NIQNCQVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFGLFDLI 62
N QNCQVPYNCLN+P +EIL ER TG P+DISLSLT+FLLEFVPG G GL DLI

Sbjct: 5 NNQNCQVPYNCLNDPTIEILEGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLDLI 64

Query: 63 WGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNA 122
WGF+ PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY EA REWEA+P N

Sbjct: 65 WGFVGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAEAFREWEADPTNP 124

Query: 123 QLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGL 182
L E++RI+F + + AL TAI FT+ ++++PLLSVYVQAANLHLS+LRD FGQ WG

Sbjct: 125 ALTEEMRIQFNDMNSALTTAIPLFTVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGF 184

Query: 183 DIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNTRQWARFNQFRRDLTLTVLDIV 242
D+AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTVLDIV

Sbjct: 185 DVATINSRYNDLTRLIGTYDYAVRWYNTGLERVWGPDSRDWVRYNQFRRDLTLTVLDIV 244

Query: 243 ALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPLHMDFMNS 302
+LFPNYD RTYPI+T SQLTREIYT+ V+E+ + R E +R PHLMD +NS

Sbjct: 245 SLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSFRGMAQRIEQNIRQPHLMDLLNS 302

Query: 303 LFVTAETVRSQTVWGGHLVSSR--NTAGNRINFPSYGVFNPGGAIWIADEDPRPFYRTLS 360
+ + + R W GH +++ AG FP YG + +RTLS

Sbjct: 303 ITIYTDVHRGFNYWSGHQITASPVGFAGPEFTFPRYGTMGNAAPPVLISTTGLGIFRTLS 362

Query: 361 DPVFVR---GGFGNPHYVLGLRGVAF---QQTGTNHTRTFRNSGTIDSLDEIPPQDNLSGA 414
P++ R G N + L G F T + +R GT+DSL D IPPQDNS

Sbjct: 363 SPLYRRIILGSGPNNQNLFLVDGTEFSFASLTADLPSTIYRQRTVDSL DVI PPQDNSVP 422

Query: 415 PWNDYSHVLNHVTFVRWPGEISGS-DSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAH 473
+SH L+HVT + + +G+ + RAP FSW HRSA +N I +ITQIPL K+

Sbjct: 423 ARAGFSHRLSHVTML---SQAAGAVYTLRAPTFSWHRSAEFNSNLI PSSQITQIPLTKSI 479

Query: 474 TLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVT 533
L SGT+VV+GPGFTGGDILR TS G + V I L QRYR RIRYASTTNL+ + +

Sbjct: 480 NLGSGTSVVKGPFTGGDILRITSPGQISTLRVTITAPLSQRYRVIRYASTTNLQFHTS 539

Query: 534 VAGERIFAGQFNKMTMDTGDPLTFQSFSYATINTAFTFPMSQSSFTVGADTFSSGNEVYID 593
+ G I G F+ TM +G L SF A T F F S FT+ A F+SGNEVYI+

Sbjct: 540 IDGRPINQGNFSATMSSGGNLQSGSFRTAGTTPFNFSNGSSIFTLSAHVFNSGNEVYIE 599

Query: 594 RFELIPVTATLE 605
R E +P T E

Sbjct: 600 RIEFVPAEVTFE 611

>prf||1409195A 135kD insecticidal protein [Bacillus thuringiensis]
Length = 1176

Score = 565 bits (1456), Expect = e-160
Identities = 310/616 (50%), Positives = 390/616 (62%), Gaps = 16/616 (2%)

Query: 1 MENNIQ-NQCVPINCLNPEVEILNEER-STGRLPLDISLSLTRFLLSEFVPGVGVAEGL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL

Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+

Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + +++PLLSVYVQAANLHLS+LRD FGQ

Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G +R W R+NQFRRLTLTV

Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239 LDIVALEFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHMD 298
LDIVALE NYD R YPI+T SQLTREIYT+ V+E+ + R E +R PHLMD

Sbjct: 241 LDIVALEFSNYDSRRYPIRTVSQLTREIYTNPVLEN--FDGSFRGMAQRIEQNIRQPHLMD 298

Query: 299 FMNSLFVTAETVRSQTVWGGHLVSSR--NTAGNRINFPSYGVFNPGGAIWIADEDPRPFY 356
+NS+ + + R W GH +++ +G FP +G + +

Sbjct: 299 ILNSITITYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIF 358

Query: 357 RTLSDPVFVR-----GGFGNPHYVLGLRGVAFQQTGTNHTRT-FRNSGTIDSLDEIPPQD 410
RTLS P++ R G +VL +F TN T +R GT+DSL D IPPQD

Sbjct: 359 RTLSSPLYRRIILGSGPNNQELFVLVDGTEFSFASLTTLNLPSTIYRQRTVDSL DVI PPQD 418

Query: 411 NSGAPWNDYSHVLNHVTFVRWPGEISGS-DSWRAPMFSWTHRSATPTNTIDPERITQIPL 469
NS P +SH L+HVT + + +G+ + RAP FSW HRSA N I +ITQIPL

Sbjct: 419 NSVPPRAGFSHRLSHVTML---SQAAGAVYTLRAPTFSWQHRSAEFNNIIPSSQITQIPL 475

Query: 470 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLR 529
K+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+

Sbjct: 476 TKSTNLGSGTSVVKGPFTGGDILRRTSPGQISTLRVNITAPLSQRYRVIRYASTTNLQ 535

Query: 530 IYVTVAGERIFAGQFNKMTMDTGDPLTFQSFSYATINTAFTFPMSQSSFTVGADTFSSGNE 589

+ ++ G I G F+ TM +G L SF T F F S FT+ A F+SGNE
Sbjct: 536 FHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTFFNFSSNGSSVFTLSAHVFNSGNE 595

Query: 590 VYIDRFELIPVTATLE 605
VYIDR E +P T E

Sbjct: 596 VYIDRIEFVPAEVTFE 611

>sp|P16478|CRYU_BACTA 135 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALINE ENTOMOCIDAL
PROTOXIN)

pir||JT0241 parasporal crystal protein - Bacillus thuringiensis (strain aizawai
IPL7)

dbj|BAA00257.1| (D00348) 135 kDa insecticidal protein [Bacillus thuringiensis]
Length = 1176

Score = 565 bits (1456), Expect = e-160

Identities = 310/616 (50%), Positives = 390/616 (62%), Gaps = 16/616 (2%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFG 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + +++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNROWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGFAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWGPDSRDWRVYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIVALF NYD R YPI+T SQLTREIYT+ V+E+ + R E +R PHLM
Sbjct: 241 LDIVALFSNYSRRYPIRT SQLTREIYTNPVLEN--FDGSFRGMAQRIEQNIRQPHLM 298

Query: 299 FMNSLFVTAETVRSQTVWGGHLVSSR--NTAGNRINFPSYGVFNPGGAIWIADDPREFY 356
+NS+ + + R W GH +++ +G FP +G +
Sbjct: 299 ILNSITIYTDVHRGFNYWGHQITASPVGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIF 358

Query: 357 RTLSDPVFVR-----GGFGNPHYVLGLRGVAFQQTGTNHTRT-FRNSGTIDSLDEIPPQD 410
RTLS P++ R G +VL +F TN T +R GT+DSLIPPQD
Sbjct: 359 RTLSSPLYRRIILGSGPNNQELFVLGDGTEFSFASLTNLPSTIYRQRTVDSLDVIPPQD 418

Query: 411 NSGAPWNDYSHVLNHVTFVRWPGEISGS-DSWRAPMFSWTHRSATPTNTIDPERITQIPL 469
NS P +SH L+HVT + + +G+ + RAP FSW HRSA N I +ITQIPL
Sbjct: 419 NSVPPRAGFSHRLSHVTML---SQAAGAVYTLRAPTFWQHRSAEFNNIIPSSQITQIPL 475

Query: 470 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRIRYASTTNLR 529
K+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+
Sbjct: 476 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVIRYASTTNLQ 535

Query: 530 IYVTVAGERIFAGQFNKMTMDGDLTFQSFYATINTAFTFMSQSSFTVGADTFSSGNE 589
+ ++ G I G F+ TM +G L SF T F F S FT+ A F+SGNE
Sbjct: 536 FHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTFFNFSSNGSSVFTLSAHVFNSGNE 595

Query: 590 VYIDRFELIPVTATLE 605
VYIDR E +P T E

Sbjct: 596 VYIDRIEFVPAEVTFE 611

>sp|P09665|CRYS_BACTS 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALINE ENTOMOCIDAL
PROTOXIN)

pir||A22798 parasporal crystal protein - Bacillus thuringiensis

gb|AAA22552.1| (M10917) insecticidal crystal protein [Bacillus thuringiensis]

prf||1106181A protein,insecticidal crystal [Bacillus thuringiensis serovar sotto]
Length = 934

Score = 563 bits (1451), Expect = e-159

Identities = 309/616 (50%), Positives = 389/616 (62%), Gaps = 16/616 (2%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRLFLSEFVPGVGVAFL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + ++++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLRGTNTRQWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239 LDIIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHMD 298
LDIVAF NYD R YPI+T SQLTREIYT+ V+E+ + R E +R PHMD
Sbjct: 241 LDIIVALFSNYDSRRYPIRTYSQLTREIYTNPVLEN--FDGSFRGMAQRIEQNIRQPHMD 298

Query: 299 FMNSLFVTAETVRSQTVWGHLVSSR--NTAGNRINFPSYGVFNPGGAIWIADDEPRFFY 356
+N + + + R W GH +++ +G FP +G + +
Sbjct: 299 ILNRITIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIF 358

Query: 357 RTLSDPVFVR-----GGFGNPHYVLGLRGVAFQQTGTNHTRT-FRNSGTIDSLDEIPPQD 410
RTLS P++ R G +VL +F TN T +R GT+DSL D IPPQD
Sbjct: 359 RTLSPLYRRIILGSGPNNQELFVLDGTEFSFASLTNLPSTIYRQGTVDSLDVIPPQD 418

Query: 411 NSGAPWNDYSHVLNHVTFVRWPGEISGS-DSWRAPMFSWTHRSATPTNTIDPERITQIPL 469
NS P +SH L+HVT + + +G+ + RAP FSW HRSA N I +ITQIPL
Sbjct: 419 NSVPPRAGFSHRLSHVTML---SQAAGAVYTLRAPTFSWQHRSAEFNNIIPSSQITQIPL 475

Query: 470 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTNL 529
K+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTNL+
Sbjct: 476 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVIRYASTNLQ 535

Query: 530 IYVTVAGERIFAGQFNKMTMDTGDPLTFQSFYATINTAFTFMSQSSFTVGADTFSSGNE 589
+ ++ G I G F+ TM +G L SF T F F S FT+ A F+SGNE
Sbjct: 536 FHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTFNFNSGSSVFTLSAHVFNSGNE 595

Query: 590 VYIDRFELIPVTATLE 605
VYIDR E +P T E
Sbjct: 596 VYIDRIEFVPAEVTFE 611

>dbj|BAA77213.1| (AB026261) BtT84A1 crystal protein [Bacillus thuringiensis]
Length = 1180

Score = 563 bits (1451), Expect = e-159

Identities = 309/616 (50%), Positives = 389/616 (62%), Gaps = 16/616 (2%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRLFLSEFVPGVGVAFL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + ++++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLRGTNTRQWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239 LDIIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHMD 298

Sbjct: 241 LDI VALF NYD R YPI+T SQLTREIYT+ V+E+ + R E +R PHLMD
LDI VALFSNYDSRRYPIRTVSQ LTR E IYTNPVLEN--FDGSFRGMAQRIEQNIRQPHLMD 298

Query: 299 FMNSLFVTAETVRSQTVWGGHLVSSR--NTAGNRINFPSYGVFNPGGAIWIAD EDP RPFY 356
+N + + + R W GH +++ +G FP +G + +

Sbjct: 299 ILNRITIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIF 358

Query: 357 RTLSDPVFVR-----GGFGNPHYVLGLRGVAFQQTGTNHTRT-FRNSGTIDSLDEIPPD 410
RTLS P++ R G +VL +F TN T +R GT+DSL D IPPQD

Sbjct: 359 RTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTLNLPSTIYRQRGTVDSLDVIPPQD 418

Query: 411 NSGAPWNDYSHVLNHVT FVRWPGEISGS-DSWRAPMFSWTHRSATPTNTIDPERITQIPL 469
NS P +SH L+HVT + + +G+ + RAP FSW HRSA N I +ITQIPL

Sbjct: 419 NSVPPRAGFSHRLSHVTML---SQAAGAVYTLRAPTFWQHRSAEFNNIIPSSQITQIPL 475

Query: 470 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRIRYASTTNLR 529
K+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+

Sbjct: 476 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVIRYASTTNLQ 535

Query: 530 IYVTVAGERIFAGQFNKMTDGTDLTFQSFSYATINTAFTFMSQSSFTVGADTFSSGNE 589
+ ++ G I G F+ TM +G L SF T F F S FT+ A F+SGNE

Sbjct: 536 FHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTPFNFSNGSSVFTLSAHVFNSSGNE 595

Query: 590 VYIDRFELIPVTATLE 605
VYIDR E +P T E

Sbjct: 596 VYIDRIEFVPAEVTFE 611

>pir||JC2219 lepidopteran-specific protoxin - Bacillus thuringiensis
dbj|BAA04468.1| (D17518) insecticidal crystal protein [Bacillus thuringiensis]
Length = 1176

Score = 563 bits (1450), Expect = e-159
Identities = 309/616 (50%), Positives = 389/616 (62%), Gaps = 16/616 (2%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLSEFVPGVGVA FGL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL

Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+

Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + ++++PLLSVYVQAANLHLS+LRD FGQ

Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLAVQNYQVPLLSVYVQAANLHLSVL RDSVSVFGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLRGTNTRQWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFR+LTLTV

Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239 LDI VALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMD 298
LDI VALF NYD R YPI+T SQLTREIYT+ V+E+ + R E +R PHLMD

Sbjct: 241 LDI VALFSNYDSRRYPIRTVSQ LTR E IYTNPVLEN--FDGSFRGMAQRIEQNIRQPHLMD 298

Query: 299 FMNSLFVTAETVRSQTVWGGHLVSSR--NTAGNRINFPSYGVFNPGGAIWIAD EDP RPFY 356
+NS+ + + R W GH +++ +G FP +G + +

Sbjct: 299 ILNSITIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIF 358

Query: 357 RTLSDPVFVR-----GGFGNPHYVLGLRGVAFQQTGTNHTRT-FRNSGTIDSLDEIPPD 410
RTLS P++ R G +VL +F TN T +R GT+DSL D IPPQD

Sbjct: 359 RTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTLNLPSTIYRQRGTVDSLDVIPPQD 418

Query: 411 NSGAPWNDYSHVLNHVT FVRWPGEISGS-DSWRAPMFSWTHRSATPTNTIDPERITQIPL 469
NS P +SH L+HVT + + +G+ + RAP FSW HRSA N I +ITQIPL

Sbjct: 419 NSVPPRAGFSHRLSHVTML---SQAAGAVYTLRAPTFWQHRSAEFNNIIPSSQITQIPL 475

Query: 470 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRIRYASTTNLR 529
K+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+

Sbjct: 476 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVIRYASTTNLQ 535

Query: 530 IYVTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTFPMSQSSFTVGADTFSSGNE 589
+ ++ G I G F+ TM +G L SF T F F S FT+ A F+SGNE
Sbjct: 536 FHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTPFNFSNGSSVFTLSAHVFNNGNE 595

Query: 590 VYIDRFELIPVTATLE 605
VYIDR E +P T E
Sbjct: 596 VYIDRIEFVPAEVTTE 611

>emb|CAA70856.1| (Y09663) delta-endotoxin [Bacillus thuringiensis]
Length = 1176

Score = 563 bits (1450), Expect = e-159
Identities = 309/616 (50%), Positives = 389/616 (62%), Gaps = 16/616 (2%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFGL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGFIFGSPQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + ++++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLLVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIVALF NYD R YPI+T SQLTREIYT+ V+E+ + R E +R PHLM
Sbjct: 241 LDIVALFSNYDSRRYPIRTVSQTLTREIYTNPVLEN--FDGSGRMAQRIEQNIRQPHLM 298

Query: 299 FMNSLFVTAETVRSQTVWGGHLVSSR--NTAGNRINFPSYGVFNPGGAIWIADDPFPFY 356
+NS+ + + R W GH +++ +G FP +G + +
Sbjct: 299 ILNSTIYTDVHRGFNYWSGHQITASVPGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIF 358

Query: 357 RTLSDPVFVR-----GGFGNPHYVLGLRGVAFQQTGTNHTRT-FRNSGTIDSLDEIPPQD 410
RTLS P++ R G +VL +F TN T +R GT+DSL D IPPQD
Sbjct: 359 RTLSSPLYRRIILGSGPNNQELFVLDTGTEFSFASLTNLPSITYRQRGTVDSLDVIPPQD 418

Query: 411 NSGAPWNDYSHVLNHVTFVRWPGGEISGS-DSWRAPMFSWTHRSATPTNTIDPERITQIPL 469
NS P +SH L+HVT + + +G+ + RAP FSW HRSA N I +ITQIPL
Sbjct: 419 NSVPPRAGFSHRLSHVTML---SQAAGAVYTLRAPTFWQHRSAEFNIIIPSSQITQIPL 475

Query: 470 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRIRYASTTNLR 529
K+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+
Sbjct: 476 TKSTNLGSGTSVVGKPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVIRYASTTNLQ 535

Query: 530 IYVTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTFPMSQSSFTVGADTFSSGNE 589
+ ++ G I G F+ TM +G L SF T F F S FT+ A F+SGNE
Sbjct: 536 FHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTPFNFSNGSSVFTLSAHVFNNGNE 595

Query: 590 VYIDRFELIPVTATLE 605
VYIDR E +P T E
Sbjct: 596 VYIDRIEFVPAEVTTE 611

>gb|AAA86265.1| (U43605) CryIA(a) [Bacillus thuringiensis]
Length = 620

Score = 563 bits (1450), Expect = e-159
Identities = 309/616 (50%), Positives = 389/616 (62%), Gaps = 16/616 (2%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFGL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + +++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIVALF NYD R YPI+T SQLTREIYT+ V+E+ + R E +R PHLM
Sbjct: 241 LDIVALFSNYDSRRYPRTVSQTLTREIYTNPVLEN--FDGSFRGMAQRIEQNIRQPHLM 298

Query: 299 FMNSLFVTAETVRSQTVWGGHLVSSR--NTAGNRINFPSYGVFNPGGAIWIADPRPFY 356
+NS+ + + R W GH +++ +G FP +G + +
Sbjct: 299 ILNSITIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIF 358

Query: 357 RTLSDPVFVR-----GGFGNPHYVLGLRGVAFQQTGTNHTRT-FRNSGTIDSLDEIPPQD 410
RTLS P++ R G +VL +F TN T +R GT+DSL D IPPQD
Sbjct: 359 RTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTNLPSTIYRQGTVDSLDVIPPQD 418

Query: 411 NSGAPWNDYSHVLNHVTFVRWPGEISGS-DSWRAPMFWSWTHRSATPTNTIDPERITQIPL 469
NS P +SH L+HVT + + +G+ + RAP FSW HRSA N I +ITQIPL
Sbjct: 419 NSVPPRAGFSHRLSHVTML---SQAAGAVYTLRAPTFWQHRSAEFNNIIPSSQITQIPL 475

Query: 470 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLR 529
K+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+
Sbjct: 476 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIYASTTNLQ 535

Query: 530 IYVTVAGERIFAGQFNKMTMDTGDPLTFQSFSYATINTAFTFMSQSSFTVGADTFSSGNE 589
+ ++ G I G F+ TM +G L SF T F F S FT+ A F+SGNE
Sbjct: 536 FHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTPFNFSNGSSVFTLSAHVFNSGNE 595

Query: 590 VYIDRFELIPVTATLE 605
VYIDR E +P T E
Sbjct: 596 VYIDRIEFVPAEVTFE 611

>prf||2013214A lepidopteran-specific protoxin [Bacillus thuringiensis]
Length = 1176

Score = 563 bits (1450), Expect = e-159
Identities = 309/616 (50%), Positives = 389/616 (62%), Gaps = 16/616 (2%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLPLDISLSLTRLFLSEFVPGVGVAFL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + +++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIVALF NYD R YPI+T SQLTREIYT+ V+E+ + R E +R PHLM
Sbjct: 241 LDIVALFSNYDSRRYPRTVSQTLTREIYTNPVLEN--FDGSFRGMAQRIEQNIRQPHLM 298

Query: 299 FMNSLFVTAETVRSQTVWGGHLVSSR--NTAGNRINFPSYGVFNPGGAIWIADPRPFY 356
+NS+ + + R W GH +++ +G FP +G + +
Sbjct: 299 ILNSITIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIF 358

Query: 357 RTLSDPVFVR-----GGFGNPHYVLGLRGVAFQQTGTNHTRT-FRNSGTIDSLDEIPPQD 410
RTLS P++ R G +VL +F TN T +R GT+DSL D IPPQD
Sbjct: 359 RTLS SPLYRRIILGSGPNNQELFVLDGTEFSFASLTTLNLPSTIYRQRTVDSL DVI PPQD 418

Query: 411 NSGAPWNDYSHVLNHVTFVRWPGEISGS-DSWRAPMFSWTHRSATPTNTIDPERITQIPL 469
NS P +SH L+HVT + + +G+ + RAP FSW HRSA N I +ITQIPL
Sbjct: 419 NSVPPRAGFSHRLSHVTML---SQAAGAVYTLRAPTFWSQHRSAEFNNIIPSSQITQIPL 475

Query: 470 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLR 529
K+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+
Sbjct: 476 TKSTNLGSGTSVVKGPFTGGDILRRTSPGQISTLRVNITAPLSQRYRVIRYASTTNLQ 535

Query: 530 IYVTVAGERIFAGQFNKMTDGTPLTFQSFSYATINTAFTFMSQSSFTVGADTFSSGNE 589
+ ++ G I G F+ TM +G L SF T F F S FT+ A F+SGNE
Sbjct: 536 FHTSIDGRPINQGNFSATMSSGNLQSGSFRTVGFTTFFNFNSNGSSVFTLSAHVFNSSGNE 595

Query: 590 VYIDRFELIPVTATLE 605
VYIDR E +P T E
Sbjct: 596 VYIDRIEFVPAEVTFE 611

>prf||1304168B endotoxin delta 1 [Bacillus thuringiensis]
Length = 1176

Score = 562 bits (1449), Expect = e-159
Identities = 309/616 (50%), Positives = 388/616 (62%), Gaps = 16/616 (2%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTFLLSEFVPGVGVAFLG 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W F +QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFPVQIEQLINQRIEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + ++++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTHKCLDTYNQGLENLRGNTNROWARFNQFRRLTLTV 238
WG D AT+N+ YN L LI YT H + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIVALF NYD R YPI+T SQLTREIYT+ V+E+ + R E +R PHLMD
Sbjct: 241 LDIVALFSNYDSRRYPIRTVSQLTREIYTNPVLEN--FDGSFRGMAQRIEQNIQPHLMD 298

Query: 299 FMNSLFVTAETVRSQTVWGGHLVSSR--NTAGNRINFPSYGVFNPGGAIWIADDPREFY 356
+NS+ + + R W GH +++ +G FP +G + +
Sbjct: 299 ILNSITIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIF 358

Query: 357 RTLSDPVFVR-----GGFGNPHYVLGLRGVAFQQTGTNHTRT-FRNSGTIDSLDEIPPQD 410
RTLS P++ R G +VL +F TN T +R GT+DSL D IPPQD
Sbjct: 359 RTLS SPLYRRIILGSGPNNQELFVLDGTEFSFASLTTLNLPSTIYRQRTVDSL DVI PPQD 418

Query: 411 NSGAPWNDYSHVLNHVTFVRWPGEISGS-DSWRAPMFSWTHRSATPTNTIDPERITQIPL 469
NS P +SH L+HVT + + +G+ + RAP FSW HRSA N I +ITQIPL
Sbjct: 419 NSVPPRAGFSHRLSHVTML---SQAAGAVYTLRAPTFWSQHRSAEFNNIIPSSQITQIPL 475

Query: 470 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLR 529
K+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+
Sbjct: 476 TKSTNLGSGTSVVKGPFTGGDILRRTSPGQISTLRVNITAPLSQRYRVIRYASTTNLQ 535

Query: 530 IYVTVAGERIFAGQFNKMTDGTPLTFQSFSYATINTAFTFMSQSSFTVGADTFSSGNE 589
+ ++ G I G F+ TM +G L SF T F F S FT+ A F+SGNE
Sbjct: 536 FHTSIDGRPINQGNFSATMSSGNLQSGSFRTVGFTTFFNFNSNGSSVFTLSAHVFNSSGNE 595

Query: 590 VYIDRFELIPVTATLE 605
VYIDR E +P T E

Sbjct: 596 VYIDRIEFVPAEVTFE 611

>sp|Q45718|C1HB_BACTM Pesticidal crystal protein cry1Hb (Insecticidal delta-endotoxin CryI(b)) (Crystalline entomocidal protoxin) (131 kDa crystal protein)
gb|AAA79694.1| (U35780) crystal toxin [Bacillus thuringiensis]
Length = 1155

Score = 562 bits (1448), Expect = e-159
Identities = 317/615 (51%), Positives = 388/615 (62%), Gaps = 25/615 (4%)

Query: 1 MENNIQNQCVPYNCLNNPEVEILNEERSTGRLP---LDISLSLTRFLLSEFVPGVGVAFG 57
ME N QN+CVYPYNCL NP++E+L+ E + R +ISL LTRFLL +PG FG
Sbjct: 1 MEVNHQNECVYPYNCLKNPKIEMLDIEGISSRSREQVAEISLGLTRFLLSLLPGASFGFG 60

Query: 58 LFDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEA 117
LFD+IWG I P WSLFL QIEQLI+QRIE RN+AI+ L GL DSYE+YIE+LREWEA
Sbjct: 61 LFDIIWGVIGPDQWSLFLTQIEQLIDQRIEAHVRNQAISRLGLGDSYEVYIESLREWEA 120

Query: 118 NPNNAQLREDVRIREFANTDDALITAINNFTLTSEIPLLSVYVQAANLHLSLLRDAVSFG 177
+PNN L++DVR RF+NTD+ALITAI FEIPLL+VYVQAANLHLSLLRDAV FG
Sbjct: 121 SPNNESLQDDVRNRFSTNDNALITAIPILREQGFEIPLLTVYVQAANLHLSLLRDAVYFG 180

Query: 178 QGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRDLTLT 237
Q WGLD ATVNNHYNRLINLI+ Y+ HC +N+GL+N G T AR+ F+R++T++
Sbjct: 181 QRWGLDTATVNNHYNRLINLINTYSDHCAQWFNRGLDNF-GVVT---ARYLDFQREVTTIS 236

Query: 238 VLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 297
VLDIVALFPNYD+RTYPIQT SQLTREIYTS V E S N+ +R PHLM
Sbjct: 237 VLDIVALFPNYDIRTYPIQTLSQLTREIYTSPVAEPG-ASLNVD-----LRNILREPHLM 290

Query: 298 DFMNSLFVTAETVRSQTVWGGHLVSSRNNTA--GNRINFPSYGV-FNPGGAIWIADDP RP 354
DF+ L + W GH +SSR T + I FP YG N +A
Sbjct: 291 DFLTRLVIYTGVGQGGIYHWAGHEISSRTTGNLSSNIQFPLYGTSANADRPFNLAHYSET 350

Query: 355 FYRTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRT----FRNSGTIDSLDEIPPQD 410
YRTL S P++ G +P+ + GV F N+ + +R G++DS E+PP+D
Sbjct: 351 IYRTLAPIYSVSGGISPNRTRAVEGVRFLTARDNNLNSLFLYRKEGSLDSFTELPPEP 410

Query: 411 NSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLV 470
+ P+ YSH L H F R + S+ R P+FSWTHRSA PTN + RITQIP V
Sbjct: 411 ENEPPYIGYSHRLCHARFARSSVLEPSNFARIPVFSWTHRSAGPTNEVSSSRITQIPWV 470

Query: 471 KAHTLQSGTTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRI 530
KAHTL SG V++GPGFTGGDIL R + G V + GQLPQ Y RIRYAS N
Sbjct: 471 KAHTLDSGAFVIKGPFTGGDILTRPNLGTGLALRVTLTGQLPQTYNIRIRYASIANRGG 530

Query: 531 YVTVAGERIFAGQFNKMTMDTGDPLTFQSFSYATINTAFTFPMSSQSSFTVGADTFSSGNEV 590
+ + + F KTMD +PLT +SF+ T+ T TF +Q+ + T G V
Sbjct: 531 TLIFSQPPSYGLTFPKTMDIDEPLTSRSFARTTLFTPTITFQAQAELENL---TIQQG--V 585

Query: 591 YIDRFELIPVTATLE 605
YIDR E IPV AT E
Sbjct: 586 YIDRIEFIPVNATFE 600

>sp|P09664|CRYS_BACTE 133 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE ENTOMOCIDAL PROTOXIN)
sp|P02965|C1AA_BACTK PESTICIDIAL CRYSTAL PROTEIN CRY1AA (INSECTICIDAL DELTA-ENDOTOXIN CRYIA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (133 KDA CRYSTAL PROTEIN)
pir||S02215 parasporal crystal protein (clone pMP36) - Bacillus thuringiensis (strain entomocidus)
emb|CAA31886.1| (X13535) parasporal crystal toxin (AA 1-1176) [Bacillus thuringiensis]
Length = 1176

Score = 560 bits (1443), Expect = e-158
Identities = 308/616 (50%), Positives = 388/616 (62%), Gaps = 16/616 (2%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFG 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W F +QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFPVQIEQLINQRIEEFARNQAISRLGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + ++++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNROWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G +R W R+NQFR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHMD 298
LDIVALF NYD R YPI+T SQLTREIYT+ V+E+ + R E +R PHLMD
Sbjct: 241 LDIVALFSNYDSRRYPITVSQLTREIYTNPVLEN--FDGSFRGMAQRIEQNIRQPHLMD 298

Query: 299 FMNSLFVTAETVRSQTVWGGHLVSSR--NTAGNRINFPSYGVFNPGGAIWIADDEPRPFY 356
+NS+ + + R W GH +++ +G FP +G + +
Sbjct: 299 ILNSITIYTDVHRGFNYWSGHQITASPVGFGPEFAFPLFGNAGNAAPPVLVSLTGLGIF 358

Query: 357 RTLSDPVFVR-----GGFGNPHYVLGLRGVAFQQTGNHTRT-FRNSGTIDSLDEIPPQD 410
RTLS P++ R G +VL +F TN T +R GT+DSL D IPPQD
Sbjct: 359 RTLSSPLYRRIILGSGPNQELFVLDTGTEFSFASLTTLNLPSTIYRQRTVDSLDVIPPQD 418

Query: 411 NSGAPWNDYSHVLNHVTFVRWPGEISGS-DSWRAPMFSWTHRSATPTNTIDPERITQIPL 469
NS P +SH L+HVT + + +G+ + RAP FSW HRSA N I +ITQIPL
Sbjct: 419 NSVPPRAGFSHRLSHVTML---SQAAGAVYTLRAPTFWQHRSAEFNNIIPSSQITQIPL 475

Query: 470 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTNL 529
K+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTNL+
Sbjct: 476 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIRYASTNLQ 535

Query: 530 IYVTVAGERIFAGQFNKMTMDTGDPLTFQSFSYATINTAFTFMSQSSFTVGADTFSSGNE 589
+ ++ G I G F+ TM +G L SF T F F S FT+ A F+SGNE
Sbjct: 536 FHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTFFNFSNGSSVFTLSAHVFNSGNE 595

Query: 590 VYIDREFELIPVTATLE 605
VYIDR E +P T E
Sbjct: 596 VYIDRIEFVPAEVTFE 611

>pir||A22617 parasporal crystal protein - Bacillus thuringiensis
gb|AAA22353.1| (M11250) crystal protein [Bacillus thuringiensis]
Length = 1176

Score = 560 bits (1443), Expect = e-158
Identities = 308/616 (50%), Positives = 388/616 (62%), Gaps = 16/616 (2%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFG 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W F +QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFPVQIEQLINQRIEEFARNQAISRLGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + ++++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNROWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G +R W R+NQFR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHMD 298
LDIVALF NYD R YPI+T SQLTREIYT+ V+E+ + R E +R PHLMD

Sbjct: 241 LDI VALFSNYDSRRYP IRTVSQ LTR E IYTNPVLEN--FDGSFRGMAQR IEQNI RQPHLMD 298

Query: 299 FMNSLFVTAETVRSQTVWGHLVSSR--NTAGNRINFPSYGVFNPGGAIWIAD EDP RPFY 356
+NS+ + + R W GH +++ +G FP +G + +

Sbjct: 299 ILNSIT IYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIF 358

Query: 357 RTLSDPVFVR-----GGFGNPHYVLGLRGVAFQQTGTNHTRT-FRNSGTIDSLDEIPPQD 410
RTLS P++ R G +VL +F TN T +R GT+DSL D IPPQD

Sbjct: 359 RTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTLNLPSTIYRQRGTVDSLDVIPPQD 418

Query: 411 NSGAPWNDYSHVLNHVT FVRWPGEISGS-DSWRAPMFSWTHRSATPTNTIDPERITQIPL 469
NS P +SH L+HVT + + +G+ + RAP FSW HRSA N I +ITQIPL

Sbjct: 419 NSVPPRAGFSHRLSHVTML---SQAAGAVYTLRAPTF SWQHRS AEFNNIIPSSQITQIPL 475

Query: 470 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLR 529
K+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+

Sbjct: 476 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIYASTTNLQ 535

Query: 530 IYVTVAGERIFAGQFNKTM D TGDPLTFQSFSYATINTAFTFMSQSSTFVGADTFSSGNE 589
+ ++ G I G F+ TM +G L SF T F F S FT+ A F+SGNE

Sbjct: 536 FHTSIDGRPINQGNFSATMSSGSLQSGSFRTVGFTT PFNFSNGSSVFTLSAHVFNSGNE 595

Query: 590 VYIDRFELIPVTATLE 605
VYIDR E +P T E

Sbjct: 596 VYIDRIEFVPAEVTFE 611

>gb|AAD55382.1|AF154676_1 (AF154676) 135 kDa insecticidal protein [Bacillus thuringiensis
serovar kurstaki]
Length = 1176

Score = 560 bits (1442), Expect = e-158
Identities = 308/616 (50%), Positives = 387/616 (62%), Gaps = 16/616 (2%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGR LPLDISLSLT RFL LSEFVPGVGVA FGL 58
M+NN N+C+PYNCL+NPEVE+L R TG P+DISLSLT+FL LSEFVPG G GL

Sbjct: 1 MDNPN NINECIPYNCLSNPEVEVLGGRIETGYTPIDISLSLTQFL LSEFVPGAGV LGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+

Sbjct: 61 VDIWGFIFGDSQWDTFLVQIEQLINQRIEEFARNQAISRLEGLSNY+IYI AESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + ++++PLLSVYVQAANLHLS+LRD FGQ

Sbjct: 121 PTNPALREEMRIQNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLRGTNTROWARFNQFRRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTV

Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239 LDI VALFNPYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRP PHLMD 298
LDI VALF NYD R YPI+T SQLTREIYT+ V+E+ + R E +R PHLMD

Sbjct: 241 LDI VALFSNYDSRRYP IRTVSQ LTR E IYTNPVLEN--FDGSFRGMAQR IEQNI RQPHLMD 298

Query: 299 FMNSLFVTAETVRSQTVWGHLVSSR--NTAGNRINFPSYGVFNPGGAIWIAD EDP RPFY 356
+NS+ + + R W GH +++ +G FP +G + +

Sbjct: 299 ILNSIT IYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIF 358

Query: 357 RTLSDPVFVR-----GGFGNPHYVLGLRGVAFQQTGTNHTRT-FRNSGTIDSLDEIPPQD 410
RTLS P++ R G +VL +F TN T +R GT+DSL D IPPQD

Sbjct: 359 RTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTLNLPSTIYRQRGTVDSLDVIPPQD 418

Query: 411 NSGAPWNDYSHVLNHVT FVRWPGEISGS-DSWRAPMFSWTHRSATPTNTIDPERITQIPL 469
NS P +SH L HVT + + +G+ + RAP FSW HRSA N I +ITQIPL

Sbjct: 419 NSVPPRAGFSHRLGHVTML---SQAAGAVYTLRAPTF SWQHRS AEFNNIIPSSQITQIPL 475

Query: 470 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLR 529
K+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+

Sbjct: 476 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIYASTTNLQ 535

Query: 530 IYVTVAGERIFAGQFNKMTMDGDLTFQSFYSYATINTAFTFPMSQSSFTVGADTFSSGNE 589
+ ++ G I G F+ TM +G L SF T F F S FT+ A F+SGNE
Sbjct: 536 FHTSIDGRPINQGNFSATMSSGSLNLSQGSFRTVGFTTPFNFSNGSSVFTLSAHVFNNGNE 595

Query: 590 VYIDRFELIPVTATLE 605
VYIDR E +P T E
Sbjct: 596 VYIDRIEFVPAEVTFE 611

>sp|Q45748|C1HA_BACTU PESTICIDIAL CRYSTAL PROTEIN CRY1HA (INSECTICIDAL DELTA-ENDOTOXIN
CRYIH(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (133 KDA
CRYSTAL PROTEIN)

pir||S32689 parasporal crystal protein - Bacillus thuringiensis
emb|CAA80236.1| (Z22513) crystal protein [Bacillus thuringiensis]
Length = 1172

Score = 554 bits (1427), Expect = e-156
Identities = 312/615 (50%), Positives = 388/615 (62%), Gaps = 29/615 (4%)

Query: 4 NIQNQCVPYNCLNNPEVEILNEERSTGRLP---LDISLSLTFRLLSEFVPGVGVAFLFD 60
N QNQ VPYNCL+NPE EIL+ E + R +ISL LTRFLL +PG F LFD
Sbjct: 5 NNQNQYVPYNCLSNPENEILDIESLSRSREQVAEISLGLTRFLLSLLPGASFQFALFD 64

Query: 61 LIWGFIPTSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPN 120
+IWG I P W+LFL QIEQLI+QRIE RN+AI+ L GL DSYE+YIE+LREWEA+PN
Sbjct: 65 IIWGVIGPDQWNFLAQIEQLIDQRIEAHVRNQAISRLGLGDSYEVYIESLREWEASPN 124

Query: 121 NAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW 180
N L++DVR RF+NTD+ALITAI FEIPLLSVYVQAANLHLSLLRDAV FGQ W
Sbjct: 125 NEALQQDVRNRFSTNDNALITAIPILREQGFIEIPLLSVYVQAANLHLSLLRDAVYFGQRW 184

Query: 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNRQWARFNQFRRDLTLTVLD 240
GLD TVNNHYNRLINLI+ Y+ HC +N+GL+N G + AR+ F+R++T++VLD
Sbjct: 185 GLDVTVNNHYNRLINLINTYSDHCAQWFNRLDNFGGVs-----ARYLDFQREVTISVLD 240

Query: 241 IVALFPNYDVRTYPIQTSSQLTREIYTSSVIE-DSPVSANIPNGFNRAEFGVRPPHLMDF 299
IVALFPNYD+RTYPI T SQTREIYTS V E + ++AN+ N +R PHLMDF
Sbjct: 241 IVALFPNYDIRTYPISTQSQLTREIYTSPVAEPGASLNANLQN-----ILREPHLMDF 293

Query: 300 MNSLFVTAETVRSQTVWGGHLVSSRNATA--GNRINFPSYG-VFNPGGAIWIADDP RPFFY 356
+ L + W GH +SSR T + I FP YG + A + Y
Sbjct: 294 LTRLVIYTGVSQSGIYHWAGHEISSRTTGNLSSNIQFPLYGTAASADRAFNMNIHSETIY 353

Query: 357 RTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRT----FRNSGTIDSLDEIPPQDNS 412
RTLS P++ G +P+ + GV F N+ + +R GT+DS E+PP+D S
Sbjct: 354 RTLSAPIYSVSGGISPNRTRVVEGVRELIARDNNLDSLPLFLYRKEGTLDSTELPPEDES 413

Query: 413 GAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKA 472
P+ YSH L H F R P + S+ R P+FSWTHRSA+PTN + P RITQIP VKA
Sbjct: 414 TPPYIGYSHRLCHARFARSPVILEPSNFARLPVFSWTHRSASPTNEVSPSRITQIPWVKA 473

Query: 473 HTLQSGTTVVRGPGFTGGDILRRT--SGGPFAYTIVNINGQLPQRYRARIRYASTTNLRI 530
HTL SG +V++GPGETGGDI+ R + G V + G+LPQ Y R+RYAS N
Sbjct: 474 HTLASGASVIKPGFTGGDIMTRNNINLGDGLTLRVTVTGRLPQSYIIRLYASVANSSG 533

Query: 531 YVTVAGERIFAGQFNKMTMDGDLTFQSFYSYATINTAFTFPMSQSSFTVGADTFSSGNEV 590
+ + F +TM T +PLT +SF+ T+ T T +Q F + T G V
Sbjct: 534 VFRHLPQPSYGISFPRTMGTDPLTSRSFALTTLFTPITLTRAQEEFNL---TIPRG--V 588

Query: 591 YIDRFELIPVTATLE 605
YIDR E +PV AT E
Sbjct: 589 YIDRIEFVVDATFE 603

>sp|P19415|C1DA_BACTA PESTICIDIAL CRYSTAL PROTEIN CRY1DA (INSECTICIDAL DELTA-ENDOTOXIN
CRYID(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (132 KDA
CRYSTAL PROTEIN)

pir||S11446 parasporal crystal protein cryID - Bacillus thuringiensis
emb|CAA38099.1| (X54160) cryID protein [Bacillus thuringiensis]
Length = 1165

Score = 553 bits (1425), Expect = e-156
Identities = 311/612 (50%), Positives = 385/612 (62%), Gaps = 23/612 (3%)

Query: 1 MENNIQNQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRLFLLSEFVPGVGVAFLG 59
ME N QNQCVPYNCL+NP+ IL EER TG DISL L FL S FVPG G GL
Sbjct: 1 MEINNQNQCVPYNCLSNPKEIILGEERLETGNTVADISLGLINFLYSNFVPGGGFIVGLL 60

Query: 60 DLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANP 119
+LIWGF PS W +FL QIEQLI QRIE RN+AI+ L GL++ Y++Y+ A +WE +P
Sbjct: 61 ELIWGFIGPSQWDIFLAQIEQLISQRIEEFARNQAISRLEGLSNLYKVVYVRAFSWEKDP 120

Query: 120 NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQG 179
N LRE++RI+F + + ALITAI F + ++E+ LLSVYVQAANLHLS+LRD FG+
Sbjct: 121 TNPALREEMRIQFNDMSALITAIPLFRVQNYEVALLSVYVQAANLHLSILRDVSVFGER 180

Query: 180 WGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRDLTLTVL 239
WG D AT+NN Y+ L +LIH YT HC+DTYNQGL L G W +N+FRR LT++VL
Sbjct: 181 WGYDTATINNRYSDLTSLIHVYTNHCVDTYNQGLRRLLEGREFLSDWIVYNNRFRRLTISVL 240

Query: 240 DIVALFPNYDVRTYPIQTSSQLTREIYTS--SVIEDSPVSANIPNGFNRAEFG-VRPPHL 296
DIVA FPNYD+RTYPIQT++QLTRE+Y + E+ +A+ P F+ AE +R PHL
Sbjct: 241 DIVAFFPNYDIRTYPIQTATQLTREYVLDLPFINENLSPAASYPT-FSAAESAIRSPHL 299

Query: 297 MDFMNSLFVTAETVRSQTVWGGHLVSS--RNTAGNRINFPSYG-VFNPGGAIWIADDP 353
+DF+NS + +++ WGGHLV+S T N I P YG N + I
Sbjct: 300 VDFLNSFTIYTDLSLARYAYWGGHLVNSFRGTGTTNLRSPLYGREGNTERPVTITASPSV 359

Query: 354 PFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDMSG 413
P +RTLS G N + V G+ GV FQ T + +R SG IDS E+PPQD S
Sbjct: 360 PIFRTLS----YITGLDNSNPVAGIEGVEFQNTISR--SIYRKS GPIDSFSELPPQDASV 413

Query: 414 APWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAH 473
+P YSH L H TF+ ISG +FSWTHRSA+PTN + P RITQIP VKAH
Sbjct: 414 SPAIGYSHRLCHATFLE---RISG-PRIAGTVFSWTHRSASPTNEVSPSRITQIPVKAH 469

Query: 474 TLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYASTTNLRIYVT 533
TL SG +V++GPGFTGGDIL R S G V G+LPQ Y R RYAS N
Sbjct: 470 TLASGASVIKGPFTGGDILTRNSMGELGLRVTFTRGLPQSYIIRFYASVANRSGTFR 529

Query: 534 VAGERIFAGQFNKMTDGDPLTFQSFYSATINTAFTFPMSSQSFVVGADTFSSGNEVYID 593
+ + F KTMD G+PLT +SF++ T+ T TF +Q F + SG VYID
Sbjct: 530 YSQPPSYGISFPKMTMDAGEPLTSRSFAHTTLFTPTITSRAQEEDL---YIQSG--VYID 584

Query: 594 RFELIPVTATLE 605
R E IPVTAT E
Sbjct: 585 RIEFIPVTATFE 596

>gb|AAK14337.1| (AF327925) insecticidal crystal protein BTRX28 [Bacillus thuringiensis serovar kunthalaRX28]
Length = 1118

Score = 545 bits (1403), Expect = e-154
Identities = 305/619 (49%), Positives = 382/619 (61%), Gaps = 21/619 (3%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRLFLLSEFVPGVGVAFLG 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + ++++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSVFQG 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR++TLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREITLTV 240

Query: 239 LDIIVALEFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSNIPNGFNRAEFGVRPPHLM 298
LDIVALEFPNYD RTYPI+T SQLTREIYT+ V+E+ + E +R PHLMD
Sbjct: 241 LDIIVALEFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQGTTERSIRSPHLM 298

Query: 299 FMNSLFVTAETVRSQTVWGGHLVSSR---NTAGNRINFPSYG---VFNP---GAIW 346
+NS +T + + + G + R G F G +P +
Sbjct: 299 ILNS--ITIYRMHIEDIIIGQIKRLLLEGGQNSLFLYLGRGEMQLHPNRLLLNKVR 356

Query: 347 IADEDPFPFYRTLSDPVFRVGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEI 406
E RP Y + +F G VL A+ + + +R SGT+DSLDEI
Sbjct: 357 ACIEHYRPLY---IEDLFKEGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEI 413

Query: 407 PPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ 466
PPQ+N+ P +SH L+HV+ R S RAPMFSW HRSA N I +ITQ
Sbjct: 414 PPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQ 473

Query: 467 IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTT 526
IPL K+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTT
Sbjct: 474 IPLTKSTNLGSGTSVVGKPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIYASTT 533

Query: 527 NLRIYVTVAGERIFAGQFNKMTMDTGDPLTFQSFYATINTAFTFPMSQSSFTVGADTFSS 586
NL+ + ++ G I G F+ TM +G L SF T F F S FT+ A F+S
Sbjct: 534 NLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRTVGFTTPFNFSNGSSVFTLSAHVFNS 593

Query: 587 GNEVYIDRFELIPVTATLE 605
GNEVYIDR E +P T E
Sbjct: 594 GNEVYIDRIEFVPAEVTFE 612

>sp|Q45747|C1DB_BACTU_PESTICIDIAL_CRYSTAL_PROTEIN_CRY1DB (INSECTICIDAL DELTA-ENDOTOXIN
CRYID(B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (131 KDA
CRYSTAL PROTEIN)
pir||S32647 parasporal crystal protein - Bacillus thuringiensis
emb|CAA80234.1| (Z22511) crystal protein [Bacillus thuringiensis]
Length = 1160

Score = 535 bits (1379), Expect = e-151
Identities = 302/612 (49%), Positives = 379/612 (61%), Gaps = 23/612 (3%)

Query: 1 MENNIQNQCVPYNCLNNPEVEILNEER-STGRPLDISLSLRFLLSEFVPGVGVAFGLF 59
M+ N QNQC+PYNCL+NP+ +L+ ER TG DISL L FL S FVPG G GL
Sbjct: 1 MDINHQNQCIPYNCLSNPDAILLDAERLETGNTVADISLGLINFLYSNFVPGGGFIVGLL 60

Query: 60 DLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANP 119
+LIWGF+ PS W +FL QIEQLI QRIE RN+AI+ L GL+++YEIY E R WE +P
Sbjct: 61 ELIWGFVGPQWEIIFLAQIEQLISQRIEEFARNQAISRLGLESNNYEITYTETFAWEKDP 120

Query: 120 NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQG 179
+N LRE++R +F + ALI AI + ++E+ LLSVYVQAANLHLS+LRD +GQ
Sbjct: 121 SNPALREEMRTQFNVMNSALIAAIPLLRVNRNVEVALLSVYVQAANLHLSVLRDVSFVYQQR 180

Query: 180 WGLDIATVNNHYNRLNLIHRYTKHCLDITYNQGLNLRGTNTRQWARFNQFRDLTLTVL 239
WG D ATVN+ Y+ L LIH YT HC+DTYN GL+NL G+ W +N+FRR LT++VL
Sbjct: 181 WGFDPATVNSRYSDLTRLIHVYTDHCVDTYNDGLKNLEGSRLSDWVYVNRFRRLTISVL 240

Query: 240 DIVALEFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVS--ANIPNGFNRAEFG-VRPPHL 296
DI+A FPNYD+ YPIQT+SQLTRE+Y + +S A+ P F+ AE +R PHL
Sbjct: 241 DIIAFFPNYDIEAYPIQTASQLTREYVLDLPFVNETLSPASYPYPT-FSAAESAIIRSPHL 299

Query: 297 MDFMNSLFVTAETVRSQTVWGGHLVSS--RNTAGNRINFPSYG-VFNPGGAIWIADEDP 353
+DF+NS + +++ S WGGHLV+S T N I P YG N + I+
Sbjct: 300 VDFLNSFTIYTDLSAYAYWGGHLVNSFRTGTTNLRSPLYGREGNTERPVTISASPSV 359

Query: 354 PFYRTLSDPVFRVGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNSG 413
P +RTLS G N + V G+ GV FQ T + +R SG IDS E+PPQD S
Sbjct: 360 PIFRTLS-----YFTGLNNNNPVAGIEGVEFQNTISR--SIYRKSGPIDSFSELPQDVSV 413

Query: 414 APWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAH 473
+P YSH L H TF+ ISG +FSWTHRSA+P N + P RITQIP VKAH

Sbjct: 414 SPAIGYSHRLCHATFLE---RISG-PRIAGTVFSWTHRSASPINEVSPSRITQIPWVKAH 469

Query: 474 TLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVT 533
TL SG +V++GPGFTGGDIL R S G V G+LPQ Y R RYAS N

Sbjct: 470 TLASGASVIKGPFTGGDILTRNSMGDLGALRVFTTGRLPQSYIRFRYASVANRSGTFR 529

Query: 534 VAGERIFAGQFNKMTDGTGDLTFQSFYSATINTAFTFPMSSSFTVGADTFSSGNEVYID 593
+ + F KTMD G+ LT +SF++ T+ T TF +Q F + SG VYID

Sbjct: 530 YSQPPSYGISFPKTM DAGEALTSRFAHTTLFTPTFSRAQEEFDL---YIQSG--VYID 584

Query: 594 RFELIPVTATLE 605

R E IPV AT E

Sbjct: 585 RIEFIPVDATFE 596

>gb|AAK48937.1|AF358862_2 (AF358862) insecticidal crystal protein [Bacillus thuringiensis]
Length = 1160

Score = 535 bits (1379), Expect = e-151

Identities = 302/612 (49%), Positives = 379/612 (61%), Gaps = 23/612 (3%)

Query: 1 MENNIQNCQVPYNCLNNPEVEILNEER-STGRPLDISLSITRFLLEFVPGVGVAFGLF 59
M+ N QNQC+PYNCL+NP+ +L+ ER TG DISL L FL S FVPG G GL

Sbjct: 1 MDINHQNQCIPYNCLSNPDAILLDAERLETGNTVADISLGLINFLYSNFPVGGGFIVGLL 60

Query: 60 DLIWGFITPSDWSLELLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANP 119
+LIWGF+ PS W +FL QIEQLI QRIE RN+AI+ L GL+++YEIY E R WE +P

Sbjct: 61 ELIWGFVGPSQWEIFLAQIEQLISQRIEEFARNQAISRLGLSNNYEIYTETFWAWEKDP 120

Query: 120 NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQG 179
+N LRE++R +F + ALI AI + ++E+ LLSVYVQAANLHLS+LRD +GQ

Sbjct: 121 SNPALREEMRTQFNMNSALIAAIPLLRVRYEVALLSVYVQAANLHLSVLRDVSFVGQR 180

Query: 180 WGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLTVL 239
WG D ATVN+ Y+ L LIH YT HC+DTYN GL+NL G+ W +N+ERR LT++VL

Sbjct: 181 WGFDPATVNSRYSDLTRLIHVYTDHCVDTYNDGLKNLEGSRLSDWVVYNRFRRLTISVL 240

Query: 240 DIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVS--ANIPNGFNRAEFG-VRPPHL 296
DI+A FPNYD+ YPIQT+SQLTRE+Y + +S A+ P F+ AE +R PHL

Sbjct: 241 DIIAFFPNYDIEAYPIQTASQLTREYVLDLPFVNTELSPASYPT-FSAAESAIRSPHL 299

Query: 297 MDFMNSLFVTAETVRSQTVWGGHLVSS--RNTAGNRINFPSYG-VFNPGGAIWIADDP 353
+DF+NS + +++ S WGGHLV+S T N I P YG N + I+

Sbjct: 300 VDFLNSFTIYTDLSLASYAYWGGHLVNSFRGTGTTNLIIRSPLYGREGNTERPVTISASPSV 359

Query: 354 PFYRTLSDPVPFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDMSG 413
P +RTLS G N + V G+ GV FQ T + +R SG IDS E+PPQD S

Sbjct: 360 PIFRTLST----YFTGLNNNNPVAGIEGVEFQNTISR--SIYRKSGPIDSFSELPPQDVSV 413

Query: 414 APWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAH 473
+P YSH L H TF+ ISG +FSWTHRSA+P N + P RITQIP VKAH

Sbjct: 414 SPAIGYSHRLCHATFLE---RISG-PRIAGTVFSWTHRSASPINEVSPSRITQIPWVKAH 469

Query: 474 TLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVT 533
TL SG +V++GPGFTGGDIL R S G V G+LPQ Y R RYAS N

Sbjct: 470 TLASGASVIKGPFTGGDILTRNSMGDLGALRVFTTGRLPQSYIRFRYASVANRSGTFR 529

Query: 534 VAGERIFAGQFNKMTDGTGDLTFQSFYSATINTAFTFPMSSSFTVGADTFSSGNEVYID 593
+ + F KTMD G+ LT +SF++ T+ T TF +Q F + SG VYID

Sbjct: 530 YSQPPSYGISFPKTM DAGEALTSRFAHTTLFTPTFSRAQEEFDL---YIQSG--VYID 584

Query: 594 RFELIPVTATLE 605

R E IPV AT E

Sbjct: 585 RIEFIPVDATFE 596

>sp|Q45738|C1JA BACTU PESTICIDIAL CRYSTAL PROTEIN CRY1JA (INSECTICIDAL DELTA-ENDOTOXIN
CRYIJ(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (133 KDA
CRYSTAL PROTEIN)

gb|AAA22341.1| (L32019) crystal protein [Bacillus thuringiensis]
Length = 1167

Score = 535 bits (1377), Expect = e-151
Identities = 306/613 (49%), Positives = 375/613 (60%), Gaps = 22/613 (3%)

Query: 1 MENNIONQCVPNCLNNPEVEILNEERSTGRPLDISLSLSTRFLLSEFVPGVGVAFGLF 59
ME N Q QC+PYNCL+NPE +L+ ER + PL++SLSL +FLL+ FVPG G GL
Sbjct: 1 MEINNQKQCIPYNCLSNPEEVLDDGERILPDIDPLEVSLSLQFLLNNFVPGGGFISGLV 60

Query: 60 DLIWGFIPTSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANP 119
D IWG + PS+W LFL QIE+LI+QRIE R +AIT L GL +Y+IY EA +EWE++P
Sbjct: 61 DKIWGALRPSEWDLFLAQIERLIDQRIEATVRAKAITELEGLGRNYQIYAEAFKEWESDP 120

Query: 120 NNAQLREDVRIRFANTDDALITAINNFTLTSTFEIPLLSVYVQAANLHLSLLRDAVSFGQG 179
+N + V RF D + I +F + FE+PLLSVYVQAANLHL+LLRD+V FG+
Sbjct: 121 DNEAAKSVIDRFRILDGLIEANIPSFRIIGFEVPLLSVYVQAANLHLALLRDSVIFGER 180

Query: 180 WGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLTVL 239
WGL VN+ YNR I IH Y+ HC+DTYN LE L + QW +NQFRR+LTLTVL
Sbjct: 181 WGLTTKNVNDIYNRQIREIHEYSNHCVDTYNTELERLGFRSIAQWRIYNQFRRELTLTVL 240

Query: 240 DIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSANIPNGFNR-AEFGVRPPHMD 298
DIVALFPNYD R YPIQT SQLTREI TS V E N N E +R PHLMD
Sbjct: 241 DIVALFPNYDSRLYPIQTFSQLTREIVTSPVSEFYGVINSNGNIIGTLTEQQIRPHMD 300

Query: 299 FMNSLFVTAETVRSQTVWGGLVSSRNT--AGNRINFPSYGVFNPGGAIWIADDPFPFY 356
F NS+ + R + W G +++ T AG +++FP G Y
Sbjct: 301 FFSNMIMYTSNDRREHYWSGLEMTAYFTGFAGAQVSFPLVGTGRGESAPPLTVRSVNDGIY 360

Query: 357 RTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTN----HTRTRFNRSGTIDSLDEIPPQDNS 412
R LS P + G VLG RG F N + +R+ GT+DSL IPPQDNS
Sbjct: 361 RILSAPFYSAPFLGT--IVLGSRGKEFDALNNISPPPSTIYRHPGTVDLSLVIIPPQDNS 418

Query: 413 GAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKA 472
P SH L+HVT +P+F WTHRSAT TNTI+P I QIPLVKA
Sbjct: 419 VPPHRGSSSHRLSHVTM-----RASSPIFWHRSATTTNTINPNAIQIPLVKA 467

Query: 473 HTLQSGTTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYV 532
L SG TVVRGPGFTGGDILRRT+ G FA VNI G L QRYR RIRYASTT+L+ +
Sbjct: 468 FNLHSGATVVRGPGFTGGDILRRTNTGTADFMRVNITGPLSQRYRVIRYASTTDLQFFT 527

Query: 533 TVAGERIFAGQFNKMTDGTGDPDTFQSFYATINTAETFPMSQSSFTVGADTFSSGNEVYI 592
+ G + G F +TM+ GD L +F A +T F+F +QS+FT+G FS+ EVYI
Sbjct: 528 RINGTSVNQGNFQRTMNRGDNLESNGNERTAGFSTPFSFNAQSTFTLGTQAFSN-QEVYI 586

Query: 593 DRFELIPVTATLE 605
DR E +P T E
Sbjct: 587 DRIEFVPAEVTFE 599

>sp|Q45746|C1GA_BACTU PESTICIDIAL CRYSTAL PROTEIN CRY1GA (INSECTICIDAL DELTA-ENDOTOXIN
CRY1G(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (132 KDA
CRYSTAL PROTEIN)
pir||S32645 parasporal crystal protein - Bacillus thuringiensis
emb|CAA80233.1| (Z22510) crystal protein [Bacillus thuringiensis]
Length = 1166

Score = 533 bits (1372), Expect = e-150
Identities = 311/615 (50%), Positives = 375/615 (60%), Gaps = 28/615 (4%)

Query: 1 MENNIONQCVPNCLNNPEVEILNEERSTGRPLDISLSLSTRFLLSEFVPGVGVAFGGLFD 60
ME + QNQ +PYNCLNNPE EI N S L +S LTRFLL VP G A GLFD
Sbjct: 1 MEISDQNYQIPYNCLNNPESEIFNARNNSFGLVSQVSSGLTRFLLLEAAVPEAGFALGLFD 60

Query: 61 LIWGFIPTSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPN 120
+IWG + WSLFL QIEQLI Q I LERNRA L GL+ SY +Y+EALREWE +PN
Sbjct: 61 LIWGALGVDQWSLFLRLQIEQLIRQEITELERNRATAITLGLSSSYNLYVEALREWENDPN 120

Query: 121 NAQLREDVRIRFANTDDALITAINNFTLTSTFEIPLLSVYVQAANLHLSLLRDAVSFGQGW 180
N +E VR RF TDDA++T + + + E+ LSVY QAANLHLSLLRDAV FG+ W
Sbjct: 121 NPASQERVTRERLRTDDAIVTGLPTLAIRNLEVNNLSVYTQAANLHLSLLRDAVYFGERW 180

Query: 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRDLTLTVLD 240
GL A + + Y RL + I Y+ HC YNQL + G + R+ F+RDLT++VLD
Sbjct: 181 GLTQANIEDLYTRLTSNIQEYSDHCARWYNQGLNEIGGIS----RRYLDQFQDLTISVLD 236

Query: 241 IVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPLMDFM 300
IVALFPNYD+RTYPI T SQLTREIYTS V V+ NI G + A +R PHLMD+
Sbjct: 237 IVALFPNYDIRTYPIPTQSQLTREIYTSPV-----VAGNINFGLSIANV-LRAPHLMDFI 290

Query: 301 NSLFVTAETVRSQTVWGGHLVSSRNTA---GNRINFPSYGV-FNPGGAIWIA----DEDP 352
+ + + +VRS W GH V SR T GN I FP YGV N + I ++
Sbjct: 291 DRIVYITNSVRSTPYWAGHEVISRRTGQGGQNEIRFPLYGVAANAEPVVTIRPTGTDEQ 350

Query: 353 RPFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRN--SGTIDSLDEIPPQD 410
R +YR S V R G ++ G T + +RN D++DEIP +
Sbjct: 351 RQWYRARSRVVSFRSS-GQDFSLVDAVGFL---TIFSAVSIYRNGFGFNTDTIDEIPIEG 406

Query: 411 NSGAPWNDYSHVLNHVTFVRWPGEISGDSWRAPMFSWTHRSATPTNTIDPERITQIPLV 470
P+ YSH L HV F+ I S RAP+FSWTHRSAT TNTI P+ ITQIPLV
Sbjct: 407 TD--PFTGYSHRLCHVGFLASSPFI--SQYARAPIFSWTHRSATLTNTIAPDVITQIPLV 462

Query: 471 KAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRI 530
KA L SG T+V+GPGFTGGDILRRT+ G F VNI L QRYR RIRYASTT+L+
Sbjct: 463 KAFNLHSGATIVKGPFTGGDILRRTNVGSFGDMRVNITAPLSQRYRVIRYASTTDLQF 522

Query: 531 YVTVAGERIFAGQFNKMTMDTGDPLTFQSFSYATINTAFTEPMSQSSFTVGADTFSSGNEV 590
Y + G I G F+ TMD+GD L + F A T FTF + S+FT+GA FS NEV
Sbjct: 523 YTNINGTTINIGNFSSTMDSGDDLQYGRFRVAGFTTPTFTSDANSTFTIGAFGFSNNEV 582

Query: 591 YIDREFELIPVTATLE 605
YIDR E +P T E
Sbjct: 583 YIDRIEFVPAEVTFE 597

>gb|AAD46139.1|AF081790_1 (AF081790) insecticidal crystal protein [Bacillus thuringiensis]
Length = 1176

Score = 533 bits (1372), Expect = e-150
Identities = 301/616 (48%), Positives = 379/616 (60%), Gaps = 16/616 (2%)

Query: 1 MENNIQ-NQCVPYNCLNPEVEILNEER-STGRLPLDISLSLTRLFLSEFVPGVGVAFL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLFLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLFLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSIEIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRLDAVSFGQ 178
P N LRE++RI+F + + AL TAI + ++++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGFAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPLMD 298
LDIVALF NYD R YPI+T SQLTREIYT+ V+E+ + R E R PHLMD
Sbjct: 241 LDIVALFSNYDSRRYPVRTVSQTLTREIYTNPVLEN--FDGSFRGMAQRIEPEYRQPHLMD 298

Query: 299 FMNSLFVTAETVRSQTVWGGHLVSSR--NTAGNRINFPSYGVFNPGGAIWIADDPFPFY 356
+NS+ + + R W GH +++ +G FP +G + +
Sbjct: 299 ILNSITIYTDVHRGFNYWSGHQITTSFVGFSGPEFAFPPLFGNAGNAAPPVLVSLTGLGIF 358

Query: 357 RTLSDPVFVR-----GGFGNPHYVLGLRGVAFQQTGTNHTRT-FRNSGTIDSLDEIPPQD 410
RTLS P++ R G +VL +F TN T +R GT+DSLID IPPQD
Sbjct: 359 RTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTLNLPSTIYRQRTVDSLVDVIPPQD 418

Query: 411 NSGAPWNDYSHVLNHVTFVRWPGEISGS-DSWRAPMFSWTHRSATPTNTIDPERITQIPL 469
NS P +SH L+HV + + +G+ + RA +F SA N I QIPL

Sbjct: 419 NSVPPRAGFSHRLSHVPM---SQAAGAVYTLRASLFLRLDPSAEFNNIIPSFNTYQIPL 475
Query: 470 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLR 529
K+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+
Sbjct: 476 TKSTNLGSGTSVVKPGFTGGDILRRTSPGLISTLRVNITAPLSQRYRVIRYASTTNLQ 535
Query: 530 IYVTVAGERIFAGQFNKMTMDTGDLPTFQSFYATINTAFTFPMSSQSFVTGADTFSSGNE 589
+ ++ G I G F TM +G L SF T F F S FT+ A F+SGNE
Sbjct: 536 FHTSIDGRPINQNFYATMSSGSNLQSGSFRTVGFTTTFNFSSNGSSVFTLSAHVFNSGNE 595
Query: 590 VYIDRFELIPVTATLE 605
VYIDR E +P T E
Sbjct: 596 VYIDRIEFVPAEVTFE 611

>pdb|1CIY| Insecticidal Toxin: Structure And Channel Formation
Length = 590

Score = 529 bits (1362), Expect = e-149
Identities = 291/586 (49%), Positives = 366/586 (61%), Gaps = 14/586 (2%)

Query: 29 TGRPLDISLSLTLRLLSEFVPGVGVAFLGLFDLIWGFIPTSDWSLFLQLIEQLIEQRIET 88
TG P+DISLSLT+LFLSEFVPG G GL D+IWG PS W FL+QIEQLI QRIE
Sbjct: 3 TGYPIDISLSLTQLLSEFVPGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEE 62
Query: 89 LERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTL 148
RN+AI+ L GL++ Y+IY E+ REWEA+P N LRE++RI+F + + AL TAI +
Sbjct: 63 FARNAQISRLGLESLNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLLAV 122
Query: 149 TSFEIPLLSVYVQAANLHLSLLRDVSVFGQWGLDIATVNNHYNRLINLIHRYTKHCLDT 208
++++PLLSVYVQAANLHLS+LRD FGQ WG D AT+N+ YN L LI YT + +
Sbjct: 123 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQWGFDAATINSRYNDLTRLIGNYTDYAVRW 182
Query: 209 YNQGLENLRGTNTROWARFNQFRRDLTLTVLDIVALEFPNYDVRTYPIQTSSQLTREIYTS 268
YN GLE + G ++R W R+NQFRR+LTLTVLDIVALE NYD R YPI+T SQLTREIYT+
Sbjct: 183 YNTGLERVWGPDSRDWVRYNQFRRDLTLTVLDIVALEFSNYDSRRYPRTVSQTLTREIYTN 242
Query: 269 SVIEDSPVSANIPNGFNRAEFGVRPPLHMDFMNSLFVTAETVRSQTVWGHLVSSR--NT 326
V+E+ + R E +R PHLMD +NS+ + + R W GH +++
Sbjct: 243 PVLEN--FDGSFRGMAQRIEQNIRQPHLMDILNSITIYTDVHRGFNYWSGHQITASPVGF 300
Query: 327 AGNRINFPSYGVFNPGGAIWIADPRPFYRTLSDPVFVR----GGFGNPHYVLGLRGV 381
+G FP +G + +RTLS P++ R G +VL
Sbjct: 301 SGPEFAFPPLFGNAGNAAPPVLVSLTGLGIFRTLSSPLYRRIILGSGPNNQELFVLDGTEF 360
Query: 382 AFQQTGTNHTRT-FRNSGTIDSLDEIPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGS-D 439
+F TN T +R GT+DSL D IPPQDNS P +SH L+HVT + + +G+
Sbjct: 361 SFASLTTLNLPSTIYRQGTVDSLDVIIPPQDNSVPPRAGFSHRLSHVTML---SQAAGAVY 417
Query: 440 SWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGG 499
+ RAP FSW HRSA N I +ITQIPL K+ L SGT+VV+GPGFTGGDILRRTS G
Sbjct: 418 TLRAPTFWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKPGFTGGDILRRTSPG 477
Query: 500 PFAYTIVNINGQLPQRYRARIYASTTNLRIVYVTVAGERIFAGQFNKMTMDTGDLPTFQSF 559
+ VNI L QRYR RIRYASTTNL+ + ++ G I G F+ TM +G L SF
Sbjct: 478 QISTLRVNITAPLSQRYRVIRYASTTNLQFHTSIDGRPINQNFSAATMSSGSNLQSGSF 537
Query: 560 SYATINTAFTFPMSSQSFVTGADTFSSGNEVYIDRFELIPVTATLE 605
T F F S FT+ A F+SGNEVYIDR E +P T E
Sbjct: 538 RTVGFTTTFNFSSNGSSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFE 583

>sp|P96315|C1AF_BACTU Pesticidal crystal protein cryIAf (Insecticidal delta-endotoxin
CryIA(f)) (Crystalline entomocidal protoxin)
gb|AAB82749.1| (U82003) insecticidal crystal protein [Bacillus thuringiensis]
Length = 911

Score = 526 bits (1355), Expect = e-148
Identities = 297/614 (48%), Positives = 377/614 (61%), Gaps = 14/614 (2%)

Query: 1 MENNIQ-NQCVYPNCLNNPEVEILNEER-STGRPLDISLSLTLRLLSEFVPGVGVAFLGL 58

Sbjct: 1 M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IW + FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+

Sbjct: 61 VDIIWEIFSVLSSDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + ++++PLLSVYV + S ++V GQ

Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVTCNYIIS--ESVMCGQ 177

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRDLTLTV 238
G D AT+N+ YN L LI YT H + YN GLE + G ++R W R+NQFRR+LTLTV

Sbjct: 178 RSGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTV 237

Query: 239 LDIIVLFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHMD 298
LDIV+LFPNYD RTYPI+T SQLTREIYT+ V+E+ + E +R PHLMD

Sbjct: 238 LDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLEN--FDGSFRGSAQGIEGSI RSPHMD 295

Query: 299 FMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADPRPF 355
+NS+ + + R + W GH + S +G FP YG N I + +

Sbjct: 296 ILSITIYTDHAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNSAPQQRIVAQLGQGV 355

Query: 356 YRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS ++ R G N VL A+ + + +R SGT+DSLDEIPPQ+N

Sbjct: 356 YRTLSSTLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNN 415

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R S RAPMFSW HRSA N I +ITQIPL K

Sbjct: 416 NVPPRQGFHSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLTK 475

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIY 531
+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR RI YASTTNL+ +

Sbjct: 476 STNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIYASTTNLQFH 535

Query: 532 VTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTFPMSSQSSFTVGADTFSSGNEVY 591
++ G I G F+ TM +G L S T F F S FT+ A F+SGNEVY

Sbjct: 536 TSIDGRPINQGNFSATMSSGRNLQSGSLRTVGFTTPFNFSNGSSVFTLSAHVFNSSGNEVY 595

Query: 592 IDRFELIPVTATLE 605
IDR E +P T E

Sbjct: 596 IDRIEFVPAEVTTE 609

>sp|Q9ZAZ6|C1GB_BACTZ Pesticidal crystal protein cry1Gb (Insecticidal delta-endotoxin
CryIG(b)) (Crystalline entomocidal protoxin) (133 kDa
crystal protein)
gb|AAD10291.1| (U70725) insecticidal crystal protein CryH2 [Bacillus thuringiensis
serovar wuhanensis]
Length = 1169

Score = 526 bits (1354), Expect = e-148
Identities = 301/611 (49%), Positives = 364/611 (59%), Gaps = 21/611 (3%)

Query: 1 MENNIQNCQVPYNCLNNPEVEILNEERSTGRPLDISLSLTRFLLSEFVPGVGVAFLGFD 60
ME N QNCQVPYNCLNNPE EILN + +I L +TR +L F+PG AFGLED

Sbjct: 1 MEINNIQNCQVPYNCLNNPESEILNVAIFSSEQVAEHLKITRLILENFLPGGSFAFGLED 60

Query: 61 LIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPN 120
LIWG WS FL Q+E+LI QRI R +AI L G SY+ YI AL+EWE +P+

Sbjct: 61 LIWGFINEDQWSAFLRQVEELINQRITEFARGQAIQRLVGFGRSYDEYILALKEWENDPD 120

Query: 121 NAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW 180
N +E VR RF TDDAL+T + + FE+ LSVY Q+ANLHL+LLRDAV FG+ W

Sbjct: 121 NPASKERVTRFRRTTDDALLTGVPMAIPGFELATLSVYAQSANLHLALLRDAVFFGERW 180

Query: 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRDLTLTVLD 240
GL +N+ Y+RL N I YT HC+ YN GL NL + +F+R+LT++VLD

Sbjct: 181 GLTQTNINDLYSRLKNSIRDYTNHCVRFYNI GLNLNVIR----PEYYRFQRELTTISVLD 236

Query: 241 IVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM 300
+VALFPNYD+RTYPI T SQLTREIYT +I S G+ + +R PHLMDF+
Sbjct: 237 LVALFPNYDIRTYPIPTKSQTLTREIYTDPII-----SPGAQAGYTLQDV-LREPHLMDFL 290

Query: 301 NSLFVTAETVRSQTVWGGHLV-SSRNTAGNRINFPSYGVFNPGGAIWIADPRP----F 355
N L + R W GH V SSR I FP YG P F
Sbjct: 291 NRLIIYTGEGYRGIRHWAGHEVESSRTGMMTNIRFPLYGTAATAEPTRFITPSTFPGLNLF 350

Query: 356 YRTLSDPVFVRGGFGN---PHYVLGRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNS 412
YRTLS P+F N + + GV F Q N + +R GT+DSLD++P + S
Sbjct: 351 YRTLSAPIFRDEPGANIIIRYRTSLVEGVGFQIP-NNGEQLYRVRGTLDSLDQLPLEGES 409

Query: 413 GAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFWSWTHRSATPTNTIDPERITQIPLVKA 472
+YSH L HV F + D R PMFSWTHRSATPTNTIDP+ ITQIPLVKA
Sbjct: 410 SL--TEYSHRLCHVRFAQSLRNAEPLDYARVPMFSWTHRSATPTNTIDPDVITQIPLVKA 467

Query: 473 HTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYASTTNLRIYV 532
L SG TVVRGPGFTGGDILRRT+ G F VNI L QRYR RIRYAST NL+ +
Sbjct: 468 FNLHSGATVVRGPGFTGGDILRRTNAGNFGDMRVNITAPLSQRYRVIRYASTANLQFHT 527

Query: 533 TVAGERIFAGQFNKTMDTGDPLTFQSFSYATINTAFTFPMSQSSFTVGADTFSSGNEVYI 592
++ G I F TM++G+ L SF A T FTF + S+FT+GA +FSS NEVYI
Sbjct: 528 SINGRAINQANFPATMNSGENLQSGSFRVAGFTTPTFTSDALSTFTIGAFSFSNNNEVYI 587

Query: 593 DRFELIPVTAT 603
D E +P T
Sbjct: 588 DGIEFVPAEVT 598

>emb|CAA70925.1| (Y09787) delta-endotoxin [Bacillus thuringiensis]
Length = 618

Score = 519 bits (1336), Expect = e-146
Identities = 300/619 (48%), Positives = 376/619 (60%), Gaps = 20/619 (3%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLSEFVPGVGVAFLG 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGFIFGSPQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + +++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNTRQWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT H + YN GLE + G ++R W R+NQFR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTV 240

Query: 239 LDIVALEFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIV+LFPNYD RTYPI+T SQLTREIYT+ V+E+ + E +R PHLMD
Sbjct: 241 LDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQIEGSIRSPHLM 298

Query: 299 FMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADPRPF 355
+NS+ + + R+ W GH + S +G FP YG N I + +
Sbjct: 299 ILNSITIYTDARGEYWNESGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS ++ R G N VL A+ + + +R SGT+DSLDEIPPQ+N
Sbjct: 359 YRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFWSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R S RAPMFSW HRSA N I + ITQIP VK
Sbjct: 419 NVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIISDITQIPAVK 478

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGG----PFAYTIVNIN-GQLPQRYRARIRYASTT 526
+ L +G +V+ GPGFTGGD++R S G Y V I+ RYR R+RYAS T
Sbjct: 479 GNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRYASVT 537

Query: 527 NLRIYVTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTFPMSQSSFTVGADTFSS 586
+ + V IF+ T + D L F Y AFT S VG FS
Sbjct: 538 PIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT---SSLGNIVGVRNFSG 594

Query: 587 GNEVYIDRFELIPVTATLE 605
V IDRFE IPVATLE
Sbjct: 595 TAGVIIDRFEFIPVTATLE 613

>sp|Q9S515|C1AG_BACTU PESTICIDIAL CRYSTAL PROTEIN CRYIAG (INSECTICIDAL DELTA-ENDOTOXIN
CRYIA(G)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (134 KDA
CRYSTAL PROTEIN)
gb|AAD46137.1|AF081248_1 (AF081248) lepidoteran-specific toxin [Bacillus thuringiensis]
Length = 1176

Score = 515 bits (1327), Expect = e-145
Identities = 295/620 (47%), Positives = 374/620 (59%), Gaps = 24/620 (3%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFG 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIWGFIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + ++++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDYNQGLENLRGNTNQWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFR+LTLTV
Sbjct: 181 RWGFAATINSRYNDLRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFVVRPPHLM 298
LDIVALF NYD R YPI+T SQLTREIYT+ V+E+ + R E R PHLM
Sbjct: 241 LDIVALFSNYDSRRYPITVSQLTREIYTNPVLEN--FDGSFRGMAQRIEPEYRQPHLM 298

Query: 299 FMNSLFVTAETVRSQTVWGGHLVSSR--NTAGNRINFPSYGVFNPGGAIWIADDPFFY 356
+NS+ + + R W GH +++ +G FP YG + + +
Sbjct: 299 ILNSISYTDVHRGFNYWSGHQITTSFVGFSGPEFTFPLYGTYGNAAPPQRIAQTGLGIF 358

Query: 357 RTLSDPVFVR-----GGFGNPHYVLGLRGVAFOQTGTNHTRT-FRNSGTIDSLDEIPPQD 410
RTLS P++ R G +VL +F TN T +R GT+DSLID IPPQD
Sbjct: 359 RTLSSPLYRRIILGSGPNNQELFVLVDGTEFSFASLTNLPSTIYRQRTVDSLDVIPPQD 418

Query: 411 NSGAPWNDYSHVLNHVTFVRWPGEISGS-DSWRAPMF----SWTHRSATPTNTIDPERIT 465
NS P +SH L+HV + + +G+ + RA +F H + N I +IT
Sbjct: 419 NSVPPRAGFSHRLSHVPM---SQAAGAVYTLRASLFLLLVLLIHARSIFNNIIPSSQIT 475

Query: 466 QIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRIRIYAST 525
Q + S T+VV+GPGFTGGDILRR S G + VNI L QRYR RIRYA T
Sbjct: 476 Q---SFKKIISWTSVVKGPFTGGDILRRSPGLISTLRVNITAPLSQRYRVIRIYAFT 531

Query: 526 TNLRIYVTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTFPMSQSSFTVGADTFSS 585
TNL+ ++ G I G F TM +G L SF T F F S FT+ A F+
Sbjct: 532 TNLQFLTSLDGRPINQGNFYATMSSGSNLQSGSFRTVGFTTFFNFSGSSVFTLSAHVFN 591

Query: 586 SGNEVYIDRFELIPVTATLE 605
SGNEVYIDR E +P T E
Sbjct: 592 SGNEVYIDRIEFVPAEVTFE 611

>pir||A49785 parasporal crystal protein cryIA(c) - Bacillus thuringiensis subsp.
kenyae (strain HD588-2)
gb|AAA22338.1| (M35524) delta-endotoxin [Bacillus thuringiensis]
Length = 1177

Score = 514 bits (1325), Expect = e-145

Identities = 300/619 (48%), Positives = 373/619 (59%), Gaps = 21/619 (3%)

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Query: 1  MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFGL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1  MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59  FDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61  VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119  PNNAQLREDVRIRFANTDDALITAINNFTLTSTFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + +++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121  PTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179  GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT H + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181  RWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239  LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIVALFPNYD R YPI+T SQLTREIYT+ V+E+ + E +R PHLM
Sbjct: 241  LDIVALFPNYDSRRYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQGIERSIRSPHLM 298

Query: 299  FMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADEDPRPF 355
+NS+ + + R W GH + S +G FP YG N I + +
Sbjct: 299  ILNSTIYTDHRGYYWWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356  YRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS + R G N VL A+ + + +R SGT+DSLDEIPPQ+N
Sbjct: 359  YRTLSSTFYRRFPNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSCTVDSLDEIPPQNN 418

Query: 412  SGAPWNDDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R G S RAPMFSW HRSA N I + ITQIP VK
Sbjct: 419  NVPPRGQFSHRLSHVSMFR-SGSSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK 477

Query: 472  AHTLQSGTTVVRGPGFTGGDILRTSGG----PFAYTIVNIN-GQLPQRYRARIYASTT 526
+ L +G +V+ GPGFTGGD++R S G Y V I+ RYR R+RYAS T
Sbjct: 478  GNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVT 536

Query: 527  NLRIYVTVAGERIFAGQFNKMTDGTGDLTFQSFYATINTAFTFPMSSQSTVGADTFSS 586
+ + V IF+ T + D L F Y AFT S VG FS
Sbjct: 537  PIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT---SSLGNIVGVRNFGS 593

Query: 587  GNEVYIDRFELIPVTATLE 605
V IDRFE IPVTATLE
Sbjct: 594  TAGVIIDRFEFIPVTATLE 612

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>gb|AAC98807.1| (U63372) truncated Cry1Ac [synthetic construct]
Length = 613

Score = 514 bits (1325), Expect = e-145
Identities = 299/619 (48%), Positives = 374/619 (60%), Gaps = 20/619 (3%)

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Query: 1  MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFGL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1  MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59  FDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61  VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119  PNNAQLREDVRIRFANTDDALITAINNFTLTSTFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + +++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121  PTNPALREEMRIQFNDMNSALTTAIPFLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179  GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181  RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239  LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298

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LDIVALFPNYD R YPI+T SOLTREIYT+ V+E+ + E +R PHLMD
Sbjct: 241 LDIVALFPNYDSRRYPVRTVSQLTREIYTNPVLEN--FDGSFRGSAQGIERSIRSPHLMD 298

Query: 299 FMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADDEPRPF 355
+NS+ + + R W GH + S +G FP YG N I + +
Sbjct: 299 ILNSITIYTDAHRGYYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVFRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS ++ R G N VL A+ + + +R SGT+DSLDEIPPQ+N
Sbjct: 359 YRTLSSTLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R S RAPMFSW HRSA N I + ITQIP VK
Sbjct: 419 NVPPRQGFHSHLSHVSMSRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK 478

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTS GG----PFAYTIVNIN-GQLPQRYRARIRYASTT 526
+ L +G +V+ GPGETGGD++R S G Y V I+ RYR R+RYAS T
Sbjct: 479 GNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASVT 537

Query: 527 NLRIYVTVAGERIFAGQFNKMTDGTPLTFQSFSYATINTAFTFPMSSQSFVTGADTFSS 586
+ + V IF+ T + D L F Y AFT S VG FS
Sbjct: 538 PIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT---SSLGNIVGVRNFSG 594

Query: 587 GNEVYIDRFELIPVTATLE 605
V IDRFE IPVTATLE
Sbjct: 595 TAGVIIDRFEFIPVTATLE 613

>sp|P05068|C1AC BACTK Pesticidal crystal protein cryIaC (Insecticidal delta-endotoxin CryIA(c)) (Crystalline entomocidal protoxin) (133 kDa crystal protein)
pir||USBSXH parasporal crystal protein - Bacillus thuringiensis subsp. kurstaki (strain HD-73)
gb|AAA22331.1| (M11068) crystal protein [Bacillus thuringiensis]
gb|AAB46989.1| (U87793) insecticidal delta-endotoxin CryIA(c) [Bacillus thuringiensis serovar kurstaki]
gb|AAC44841.1| (U87397) crystal protein [Bacillus thuringiensis serovar kurstaki]
gb|AAB49768.1| (U89872) CryIaC delta-endotoxin [Bacillus thuringiensis]
emb|CAA05505.1| (AJ002514) insecticidal crystal protein [Bacillus thuringiensis]
Length = 1178

Score = 514 bits (1325), Expect = e-145
Identities = 299/619 (48%), Positives = 374/619 (60%), Gaps = 20/619 (3%)

Query: 1 MENNIQ-NQCVPYNCLNNEVEILNEER-STGRPLDISLSLTRLFLSEFVPGVGVAFL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLFLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLFLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + +++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNROWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSDRWRYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMD 298
LDIVALFPNYD R YPI+T SOLTREIYT+ V+E+ + E +R PHLMD
Sbjct: 241 LDIVALFPNYDSRRYPVRTVSQLTREIYTNPVLEN--FDGSFRGSAQGIERSIRSPHLMD 298

Query: 299 FMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADDEPRPF 355
+NS+ + + R W GH + S +G FP YG N I + +
Sbjct: 299 ILNSITIYTDAHRGYYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVFRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS ++ R G N VL A+ + + +R SGT+DSLDEIPPQ+N

Sbjct: 359 YRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R S RAPMFSW HRSA N I + ITQIP VK

Sbjct: 419 NVPPRQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK 478

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGG----PFAYTIVNIN-GQLPQRYRARIRYASTT 526
+ L +G +V+ GPGETGGD++R S G Y V I+ RYR R+RYAS T

Sbjct: 479 GNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVVRVYASVT 537

Query: 527 NLRIYVTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTFPMSSQSFVVGADTFSS 586
+ + V IF+ T + D L F Y AFT S VG FS

Sbjct: 538 PIHLNVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT---SSLGNIVGVRNFSG 594

Query: 587 GNEVYIDRFELIPVTATLE 605
V IDRFE IPVTATLE

Sbjct: 595 TAGVIIDRFEFIPVTATLE 613

>emb|CAA10270.1| (AJ130970) crystal toxin protein [Bacillus thuringiensis]
Length = 1178

Score = 513 bits (1320), Expect = e-144
Identities = 298/619 (48%), Positives = 372/619 (59%), Gaps = 20/619 (3%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRLPLDISLSLTRFLLSEFVPGVGVAFG 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL

Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+

Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVIRFANTDDALITAINNFTLTSTFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + +++PLLSVYVQAANLHLS+LRD FGQ

Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNQWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRRLTLTV

Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRLTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIVALFPNYD R YPI+T SQLTREIYT+ V+E+ + E +R PHLM

Sbjct: 241 LDIVALFPNYDSRRYPITVSQLTREIYTNPVLEN--FDGSFRGSAQGIERSIRSPHLM 298

Query: 299 FMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADEDPRPF 355
+NS+ + + R W GH + S +G FP YG N I + +

Sbjct: 299 ILNSITITYTDAHRGYYWWSGHQIMASPVGFSGFEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGHNHTRFRNSGTIDSLDEIPPQDN 411
YRTLS + R G N VL A+ + + +R SGT+DSLDEIPPQ+N

Sbjct: 359 YRTLSTFYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R S RAPMFSW HRSA N I + ITQIP VK

Sbjct: 419 NVPPRQGFHRLSHVSMFRSGSSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK 478

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGG----PFAYTIVNIN-GQLPQRYRARIRYASTT 526
+ L +G +V+ GPGETGGD++R S G Y V I+ RYR R+RYAS T

Sbjct: 479 GNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVVRVYASVT 537

Query: 527 NLRIYVTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTFPMSSQSFVVGADTFSS 586
+ + V IF+ T + D L F Y AFT S VG FS

Sbjct: 538 PIHLNVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT---SSLGNIVGVRNFSG 594

Query: 587 GNEVYIDRFELIPVTATLE 605
V IDRFE IPVTATLE

Sbjct: 595 TAGVIIDRFEFIPVTATLE 613

>gb|AAA73077.1| (M73249) [Bacillus thuringiensis gene, complete CDS.], gene product

Length = 1178

Score = 512 bits (1319), Expect = e-144
Identities = 298/619 (48%), Positives = 373/619 (60%), Gaps = 20/619 (3%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFLGL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + +++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLRLIGNYTDYAVRWYNTGLERVWGPDSRDWRVYNQFRRDLTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIVALFPNYD R YPI+T SQLTREIYT+ V+E+ + E +R PHLM
Sbjct: 241 LDIVALFPNYDSRRYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQGIERSIRSPHLM 298

Query: 299 FMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADDEPRPF 355
+NS+ + + R W GH + S +G FP YG N I + +
Sbjct: 299 ILNSITIYDHAHGYGYWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGTNHTTRFRNSGTIDSLDEIPPQDN 411
YRTLS ++ R G N N VL A+ + + +R SGT+DSLDEIPPQ+N
Sbjct: 359 YRTLSSTLYRRPFNIGINNQLSVDLGTETPAYGTSSNLPSAVYRKSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEGISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P P +SH L+HV+ R S RAPMFSW HRS A N I +S ITQIP VK
Sbjct: 419 NVPPRQGFHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRS AEFNNIIASDITQIPAVK 478

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGG----PFAYTIVNIN-GQLPQRYRARIRYASTT 526
+ L +G +V+ GPGFTGGD++R S G Y V I+ RYR R+RYAS T
Sbjct: 479 GNFLNG+SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVT 537

Query: 527 NLRIYVTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTFPMSSQSSFTVGADTFSS 586
+ + V IF+ T + D L F Y AFT S VG FS
Sbjct: 538 PIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFT---SSLGNIVGVNRFSG 594

Query: 587 GNEVIYDRFELIPVTATLE 605
V IDRFE IPVATLE
Sbjct: 595 TAGVIIDRFEFIPVTATLE 613

>gb|AAA22339.1| (M73248) cryIA(c)3 [Bacillus thuringiensis]
Length = 1177

Score = 512 bits (1319), Expect = e-144
Identities = 299/619 (48%), Positives = 373/619 (59%), Gaps = 21/619 (3%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFLGL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + +++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTV

Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTTLTV 240

Query: 239 LDI VALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDI VALFPNYD R YPI+T SQLTREIYT+ V+E+ + E +R PHLMD

Sbjct: 241 LDI VALFPNYDSRRYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQGIERSIRSPHLM 298

Query: 299 FMNSLFVTAETVRSQT VWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADDP RPF 355
+NS+ + + R W GH + S +G FP YG N I + +

Sbjct: 299 ILSITIYTD AHRGYYYWSGHQIMASPVGFSGP EFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS + R G N VL A+ + + +R SGT+DSLDEIPPQ+N

Sbjct: 359 YRTLSSTFYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R G S RAPMFSW HRSA N I + ITQIP VK

Sbjct: 419 NVPPRQGFSHRLSHVSMFR-SGSSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK 477

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGG----PFAYTIVNIN-GQLPQRYRARIYASTT 526
+ L +G +V+ GPGFTGGD++R S G Y V I+ RYR R+RYAS T

Sbjct: 478 GNFLENG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASVT 536

Query: 527 NLRIYVTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTFMSQSSFTVGADTFSS 586
+ + V IF+ T + D L F Y AFT S VG FS

Sbjct: 537 PIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT---SSLGNIVGVRNFSG 593

Query: 587 GNEVYIDRFELIPVTATLE 605
V IDRFE IPVATLE

Sbjct: 594 TAGVIIDRFEFIPVTATLE 612

>gb|AAD38701.1|AF148644_1 (AF148644) insecticidal protein Cry1Ac [Bacillus thuringiensis]
Length = 723

Score = 512 bits (1319), Expect = e-144
Identities = 299/619 (48%), Positives = 373/619 (59%), Gaps = 21/619 (3%)

Query: 1 MENNIQ-NQCVPYNCLNNEVEILNEER-STGRPLDISLSLTFLLSEFVPGVGVAFGL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLEFVPG G GL

Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLGL 60

Query: 59 FDLIWGITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+

Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + ++++PLLSVYVQAANLHLS+LRD FGQ

Sbjct: 121 PTNPALREEMRIQFNDMNSALTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLRGTNTRQWARFNQFRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRRLTLTLTV

Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTTLTV 240

Query: 239 LDI VALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDI VALFPNYD R YPI+T SQLTREIYT+ V+E+ + E +R PHLMD

Sbjct: 241 LDI VALFPNYDSRRYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQGIERSIRSPHLM 298

Query: 299 FMNSLFVTAETVRSQT VWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADDP RPF 355
+NS+ + + R W GH + S +G FP YG N I + +

Sbjct: 299 ILSITIYTD AHRGYYYWSGHQIMASPVGFSGP EFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS + R G N VL A+ + + +R SGT+DSLDEIPPQ+N

Sbjct: 359 YRTLSSTFYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R G S RAPMFSW HRSA N I + ITQIP VK

Sbjct: 419 NVPPRQGFSHRLSHVSMFR-SGSSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK 477

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGG----PFAYTIVNIN-GQLPQRYRARIYASTT 526

+ L +G +V+ GPGFTGGD++R S G Y V I+ RYR R+RYAS T
Sbjct: 478 GNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVT 536

Query: 527 NLRIYVTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTFPMSSQSFVVGADTFSS 586
++ V IF+ T + D L F Y AFT S VG FS

Sbjct: 537 PIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT---SSLGNIVGVRNFSG 593

Query: 587 GNEVIIDRFELIPVTATLE 605
V IDRFE IPVATLE

Sbjct: 594 TAGVIIDRFEFIPVTATLE 612

>pir||S11445 parasporal crystal protein cryIA.c - Bacillus thuringiensis
(strain BTS89A) (fragment)
emb|CAA38098.1| (X54159) cryIA(c) protein [Bacillus thuringiensis]
Length = 618

Score = 512 bits (1319), Expect = e-144
Identities = 299/619 (48%), Positives = 373/619 (59%), Gaps = 21/619 (3%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRLPLDISLSLTRFLLSEFVPGVGVAFLG 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + ++++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRDLTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHMD 298
LDIVALFPNYD R YPI+T SQLTREIYT+ V+E+ + E +R PHLMD
Sbjct: 241 LDIVALFPNYDSRRYPITVSQLTREIYTNPVLEN--FDGSFRGSAQGIERSIRSPHMD 298

Query: 299 FMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADPRPF 355
+NS+ + + R W GH + S +G FP YG N I + +
Sbjct: 299 ILNSITIYTDHARGYYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS + R G N VL A+ + + +R SGT+DSLDEIPPQ+N
Sbjct: 359 YRTLSSTFYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R G S RAPMFSW HRSA N I + ITQIP VK
Sbjct: 419 NVPPRQGFHRLSHVSMFR-SGSSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK 477

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTS GG---PFAYTIVNIN-GQLPQRYRARIYASTT 526
+ L +G +V+ GPGFTGGD++R S G Y V I+ RYR R+RYAS T
Sbjct: 478 GNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVT 536

Query: 527 NLRIYVTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTFPMSSQSFVVGADTFSS 586
++ V IF+ T + D L F Y AFT S VG FS
Sbjct: 537 PIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT---SSLGNIVGVRNFSG 593

Query: 587 GNEVIIDRFELIPVTATLE 605
V IDRFE IPVATLE

Sbjct: 594 TAGVIIDRFEFIPVTATLE 612

>pir||JC7140 protoxin - Bacillus thuringiensis
Length = 655

Score = 510 bits (1314), Expect = e-143
Identities = 298/633 (47%), Positives = 373/633 (58%), Gaps = 41/633 (6%)

Query: 1 MENNIQNQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTFLLSEFVPGVGVAFLGF 59
ME N QNQC+PYNCL+NPE +L+ ER STG +DISLSL +FL+S FVPG G GL
Sbjct: 1 MEENNQNQCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGFLVGLI 60

Query: 60 DLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANP 119
D +WG + PS W FL+QIEQLI +RI RN AI L GL +++ IY+EA +EWE +P
Sbjct: 61 DFWVGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNNFNIIYVEAFKEWEEDP 120

Query: 120 NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQG 179
NN R V RF D L I +F ++ FE+PLLSVY QAANLHL++LRD+V FG+
Sbjct: 121 NNPATRTRVIDRFRILDGLLERDIPSFRIISGFEVPLLSVYAQAANLHLAILRDSVIFGER 180

Query: 180 WGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLTLVL 239
WGL VN +YNRLI I Y HC +TYN+GL NL + + W +N+ RRDLTTLTLVL
Sbjct: 181 WGLTTINVNENYNRLIRHIDEYADHCANTYNRGLNNLPKSTYQDWITYNRLRRDLTLTLVL 240

Query: 240 DIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSP---VSANIPNGFNRAEFGVRPPHL 296
DI A FPNYD R YPIQ QLTRE+YT +I +P A +P +R PHL
Sbjct: 241 DIAAFFPNYDNRRYPIQPVGQLTREVTYDPLINFNPQLQSVAQLPTFNVMESSAIRNPHL 300

Query: 297 MDFMNSLFVTAE--TVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPGGAIWIADDP- 353
D +N+L + + +V WGGH V S G I P YG E PR
Sbjct: 301 FDILNLTIFTDWFSGVRNFYWGGRVSSIGGGNITSPIYG-----REANQEPPRS 353

Query: 354 -----PFYRTLSDP---VFVRGGFGNPHYVLGLRGVAFQQTGNHTRTFRNSGTIDSLDE 405
P +RTLS+P + + P + G+ GV F T TN + T+R GT+DSL E
Sbjct: 354 FTFNGPVFRTLSNPTLRLLQQPWPAPPFNLRGVEGVEF-STPTN-SFTYRGRGTVDLSLE 411

Query: 406 IPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERIT 465
+PP+DNS P YSH L H TFV+ G +FSWTHRSAT TNTIDPERI
Sbjct: 412 LPPEDNSVPPREGYSHRLCHATFVQRSCT---PFLTGTGVVFSWTHRSATLTNTIDPERIN 468

Query: 466 QIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYAST 525
QIPLVK + GT+V+ GPGFTGGDILRR + G F VNIN + QRYR R RYAS+
Sbjct: 469 QIPLVKGRVWGGTSVITGPGFTGGDILRRNFTGDFVSLQVNINSPIQRYRLRFYASS 528

Query: 526 TNLRIYV-TVAGERIFAGQ-----FNKMTDGDPLTFQSFSYATINTAFTFPMSSQSSFT 578
+ R+ V T A GQ KTM+ G+ LT ++F Y + F+F +
Sbjct: 529 RDARVIVLTGAASTGVGGQVSVMPLQKTMIEIGENLTSRTFRYTDFSNPFSSFRANPDIIG 588

Query: 579 V-----GADTFSSGNEVYIDREFELIPVTATLE 605
+ GA + SSG E+YID+ E+I AT E
Sbjct: 589 ISEQPLFGAGSISSG-ELYIDKIEIILADATFE 620

>emb|CAA65457.1| (X96682) delta-endotoxin [Bacillus thuringiensis]
Length = 756

Score = 510 bits (1314), Expect = e-143
Identities = 298/633 (47%), Positives = 373/633 (58%), Gaps = 41/633 (6%)

Query: 1 MENNIQNQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTFLLSEFVPGVGVAFLGF 59
ME N QNQC+PYNCL+NPE +L+ ER STG +DISLSL +FL+S FVPG G GL
Sbjct: 1 MEENNQNQCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGFLVGLI 60

Query: 60 DLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANP 119
D +WG + PS W FL+QIEQLI +RI RN AI L GL +++ IY+EA +EWE +P
Sbjct: 61 DFWVGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNNFNIIYVEAFKEWEEDP 120

Query: 120 NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQG 179
NN R V RF D L I +F ++ FE+PLLSVY QAANLHL++LRD+V FG+
Sbjct: 121 NNPATRTRVIDRFRILDGLLERDIPSFRIISGFEVPLLSVYAQAANLHLAILRDSVIFGER 180

Query: 180 WGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLTLVL 239
WGL VN +YNRLI I Y HC +TYN+GL NL + + W +N+ RRDLTTLTLVL
Sbjct: 181 WGLTTINVNENYNRLIRHIDEYADHCANTYNRGLNNLPKSTYQDWITYNRLRRDLTLTLVL 240

Query: 240 DIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSP---VSANIPNGFNRAEFGVRPPHL 296
DI A FPNYD R YPIQ QLTRE+YT +I +P A +P +R PHL
Sbjct: 241 DIAAFFPNYDNRRYPIQPVGQLTREVTYDPLINFNPQLQSVAQLPTFNVMESSAIRNPHL 300

Query: 297 MDFMNSLFVTAE--TVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPGGAIWIADDP- 353
D +N+L + + +V WGGH V S G I P YG E PR
Sbjct: 301 FDILNNLTIFTDWFVSVGRNFYWGGRHVISSLIGGNITSPIYG-----REANQEPPRS 353

Query: 354 -----PFYRTLSDP---VFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDE 405
P +RTLS+P + + P + G+ GV F T TN + T+R GT+DSL E
Sbjct: 354 FTFNGPVPFRTLSNPTLRLLQQPWPAPPFNLRGVEGVEF-STPTN-SFTYRGRGTVDLSLE 411

Query: 406 IPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERIT 465
+PP+DNS P YSH L H TFV+ G +FSWTHRSAT TNTIDPERI
Sbjct: 412 LPPEDNSVPPREGYSHRLCHATFVQSRGT---PFLTGTGVVFSWTHRSATLTNTIDPERIN 468

Query: 466 QIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYAST 525
+PP+DNS P YSH L H TFV+ G +FSWTHRSAT TNTIDPERI
Sbjct: 469 QIPLVK + GT+V+ GPGFTGGDILRR + G F VNIN + QRYR R RYAS+ 528

Query: 526 TNLRIYV-TVAGERIFAGQ-----FNKTMDDTGDPLTFQSFYSATINTAFTFPMSSSFT 578
+ R+ V T A GQ KTM+ G+ LT ++F Y + F+F +
Sbjct: 529 RDARVIVLTGAASTGVGGQVSVNMLPQKTMEIGENLTSTRFRYTFDSNPFSTRANPDIIG 588

Query: 579 V-----GADTFSSGNEVYIDRFELIPVTATLE 605
+ GA + SSG E+YID+ E+I AT E
Sbjct: 589 ISEQPLFGAGSISSG-ELYIDKIEIILADATFE 620

>sp|P05518|C1CA BACTE Pesticidal crystal protein cryIc (Insecticidal delta-endotoxin
CryIc(a)) (Crystalline entomocidal protoxin) (134 kDa
crystal protein)
gb|AAL79362.1| (AY078160) delta-endotoxin [Bacillus thuringiensis]
gb|AAM00264.1|AF362020_1 (AF362020) insecticidal protein CryIc [Bacillus thuringiensis]
Length = 1189

Score = 510 bits (1314), Expect = e-143
Identities = 298/633 (47%), Positives = 373/633 (58%), Gaps = 41/633 (6%)

Query: 1 MENNIQNCQVPYNCLNNPEVEILNEER-STGRPLDISLSLTRLFLSEFVPGVGVAFGLF 59
ME N QNQC+PYNCL+NPE +L+ ER STG +DISLSL +FL+S FVPG G GL
Sbjct: 1 MEENNQNCQCPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGFLVGLI 60

Query: 60 DLIWGFITPSDWSLFLQLIEQLIETLERNRAITTLRGLADSYEIIYIEALREWEANP 119
D +WG + PS W FL+QIEQLI +RI RN AI L GL +++ IY+EA +EWE +P
Sbjct: 61 DFWVGIVGPSQWDAFLVQIEQLINERIAEAFARNAATANLEGLGNFNFIYVEAFKEWEEDP 120

Query: 120 NNAQLREDVRIRFANTDDALITAINNFTLSFEIPLLSVYQAANLHLSLLRDAVSFGQG 179
NN R V RF D L I +F ++ FE+PLLSVY QAANLHL++LRD+V FG+
Sbjct: 121 NNPATRTTRVIDRFRILDGLLDRDIPSFRISSGFEVPLLSVYQAANLHLAILRDSVIFGER 180

Query: 180 WGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLTVL 239
WGL VN +YNRLI I Y HC +TYN+GL NL + + W +N+ RRDLTTLTVL
Sbjct: 181 WGLTTINVNENYNRLIRHIDEYADHCANTYNRGLNNLPKSTYQDWITYNRLRRDLTLTVL 240

Query: 240 DIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSP---VSANIPNGFNRAEFGVRPHL 296
DI A FPNYD R YPIQ QLTRE+YT +I +P A +P +R PHL
Sbjct: 241 DIAAEFFPNYDNRRYPIQPVGQLTREYVTDPLINFNPQLQSVQALPTFNVMESSAIRNPHL 300

Query: 297 MDFMNSLFVTAE--TVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPGGAIWIADDP- 353
D +N+L + + +V WGGH V S G I P YG E PR
Sbjct: 301 FDILNNLTIFTDWFVSVGRNFYWGGRHVISSLIGGNITSPIYG-----REANQEPPRS 353

Query: 354 -----PFYRTLSDP---VFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDE 405
P +RTLS+P + + P + G+ GV F T TN + T+R GT+DSL E
Sbjct: 354 FTFNGPVPFRTLSNPTLRLLQQPWPAPPFNLRGVEGVEF-STPTN-SFTYRGRGTVDLSLE 411

Query: 406 IPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERIT 465
+PP+DNS P YSH L H TFV+ G +FSWTHRSAT TNTIDPERI
Sbjct: 412 LPPEDNSVPPREGYSHRLCHATFVQSRGT---PFLTGTGVVFSWTHRSATLTNTIDPERIN 468

Query: 466 QIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYAST 525
QIPLVK + GT+V+ GPGFTGGDILRR + G F VNIN + QRYR R RYAS+ 528

Sbjct: 469 QIPLVKGFRVWGGSVITGPGFTGGDILRRNTFGDFVSLQVNINSPITQRYRLRFYASS 528

Query: 526 TNLRIYV-TVAGERIFAGQ-----FNKTMMDTGDPLTFQSFSYATINTAFTFPMSSSFT 578
+ R+ V T A GQ KTM+ G+ LT ++F Y + F+F +

Sbjct: 529 RDARVIVLTGAASTGVGGQSVNMPLQKTMEIGENLTSRTFRYTDFSNPFSFRANPDIIG 588

Query: 579 V-----GADTFSSGNEVYIDRFELIPVTATLE 605
+ GA + SSG E+YID+ E+I AT E

Sbjct: 589 ISEQPLFGAGSISSG-ELYIDKIEIILADATFE 620

>emb|CAA67557.1| (X99103) delta-endotoxin [synthetic construct]
Length = 630

Score = 510 bits (1314), Expect = e-143
Identities = 298/633 (47%), Positives = 373/633 (58%), Gaps = 41/633 (6%)

Query: 1 MENNIQNQCVPYNCLNNPEVEILNEER-STGRPLDISLSLRFLLSEFVPGVGVAFLG 59
ME N QNQC+PYNCL+NPE +L+ ER STG +DISLSL +FL+S FVPG G GL
Sbjct: 1 MEENNQNCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60

Query: 60 DLIWGFITPDSWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANP 119
D +WG + PS W FL+QIEQLI +RI RN AI L GL +++ IY+EA +EWE +P
Sbjct: 61 DFWVGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKEWEEDP 120

Query: 120 NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQG 179
NN R V RF D L I +F ++ FE+PLLSVY QAANLHL++LRD+V FG+
Sbjct: 121 NNPATRRVIDRFRILDGLLERRDIPSFRISGFEVPLLSVYAQAANLHLAILRDSVIFGER 180

Query: 180 WGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLTLVL 239
WGL VN +YNRLI I Y HC +TYN+GL NL + + W +N+ RRDLTTLVL
Sbjct: 181 WGLTTINVENYNRLIRHIDEYADHCANTYNRGLNNLPKSTYQDWITYNRLRRDLTLTLVL 240

Query: 240 DIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSP---VSANIPNGFNRAEFGVRPHL 296
DI A FPNYD R YPIQ QLTRE+YT +I +P A +P +R PHL
Sbjct: 241 DIAAFPNYDNRRYPIQFVGQLTREVYTDPLINFNPQLQSVACLPTFNVMESSAIRNPHL 300

Query: 297 MDFMNSLFVTAE--TVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPGGAIWIADDP- 353
D +N+L + + +V WGGH V S G I P YG E PR
Sbjct: 301 FDILNNLTIFTDWFVSGRNFYWGGRVSSLIIGGNITSPIYG-----REANQEPPRS 353

Query: 354 -----PFYRTLSDP---VFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDE 405
P +RTLS+P + + P + G+ GV F T TN + T+R GT+DSL E
Sbjct: 354 FTFNGPVFRTLSPNTLRLQLQPWPAPPFNLRGVEGVEF-STPTN-SFTYRGRGTVDLSLDE 411

Query: 406 IPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERIT 465
+PP+DNS P YSH L H TFV+ G +FSWTHRSAT TNTIDPERI
Sbjct: 412 LPPEDNSVPPREGYSHRLCHATFVQSRGT---PFLTTGVVFSWTHRSATLTNTIDPERIN 468

Query: 466 QIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYAST 525
QIPLVK + GT+V+ GPGFTGGDILRR + G F VNIN + QRYR R RYAS+
Sbjct: 469 QIPLVKGFRVWGGSVITGPGFTGGDILRRNTFGDFVSLQVNINSPITQRYRLRFYASS 528

Query: 526 TNLRIYV-TVAGERIFAGQ-----FNKTMMDTGDPLTFQSFSYATINTAFTFPMSSSFT 578
+ R+ V T A GQ KTM+ G+ LT ++F Y + F+F +
Sbjct: 529 RDARVIVLTGAASTGVGGQSVNMPLQKTMEIGENLTSRTFRYTDFSNPFSFRANPDIIG 588

Query: 579 V-----GADTFSSGNEVYIDRFELIPVTATLE 605
+ GA + SSG E+YID+ E+I AT E
Sbjct: 589 ISEQPLFGAGSISSG-ELYIDKIEIILADATFE 620

>gb|AAC63055.1| (AF023672) CryIA(c) [synthetic construct]
Length = 616

Score = 510 bits (1313), Expect = e-143
Identities = 295/610 (48%), Positives = 368/610 (59%), Gaps = 19/610 (3%)

Query: 9 CVPYNCLNNPEVEILNEER-STGRPLDISLSLRFLLSEFVPGVGVAFLGFDLIWGFIT 67
C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLEFVPG G GL D+IWG
Sbjct: 11 CIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLGLVDIIWGFIFG 70

Query: 68 PSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLRED 127
PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+P N LRE+
Sbjct: 71 PSQWDAFLVQIEQLINQRIEEFARNQAISRLGLESLNLYQIYAESFREWEADPTNPALREE 130

Query: 128 VRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATV 187
+RI+F + + AL TAI F + ++++P LLSVYVQAANLHLS+LRD FGQ WG D AT+
Sbjct: 131 MRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQWGFDAATI 190

Query: 188 NNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRRDLTLTVLIDIVALFPN 247
N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTVLIDIVALFPN
Sbjct: 191 NSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRDLTLTVLIDIVALFPN 250

Query: 248 YDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFMNSLFVTA 307
YD R YPI+T SQLTREIYT+ V+E+ + E +R PHLMD +NS+ +
Sbjct: 251 YDSRRYPIRTVSQTLTREIYTNPVLEN--FDGSRGSAQGIERSIRSPHLMDFMNSLTIYT 308

Query: 308 ETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADEDPFPFYRTLSDPVF 364
+ R W GH + S +G FP YG N I + + YRTLS ++
Sbjct: 309 DAHRGYYWVSGHQMSPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLY 368

Query: 365 VRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNSGAPWNDYS 420
R G N VL A+ + + +R SGT+DSLDEIPPQ+N+ P +S
Sbjct: 369 RPFENIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSGTVDSLDEIPPQNNNVPPRQGS 428

Query: 421 HVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
H L+HV+ R S RAPMFSW HRSA N I + ITQIP VK + L +G +
Sbjct: 429 HRLSHVSMFRSGFSNSSVSIIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNG-S 487

Query: 481 VVRGPGFTGGDILRRTSGG----PFAYTIVNIN-GQLPQRYRARIYASTTNLRIYVTA 535
V+ GPGFTGGD++R S G Y V I+ RYR R+RYAS T + + V
Sbjct: 488 VISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVVRVYASVTPIHLNVNWG 547

Query: 536 GERIFAGQFNKMTMDTGDPLTFQSFYSATINTAFTFPMSSQSFTVGADTFSSGNEVYIDRF 595
IF+ T + D L F Y AFT S V G FS V IDRF
Sbjct: 548 NSSIFSNTPATATSLDNLQSSDFGYFESANAFT---SSLGNIVGVRNFGTAGVYIDRF 604

Query: 596 ELIPVTATLE 605
E IPVTATLE
Sbjct: 605 EFIPVTATLE 614

>pir||A37829 parasporal crystal protein - Bacillus thuringiensis
Length = 1171

Score = 509 bits (1312), Expect = e-143
Identities = 290/619 (46%), Positives = 379/619 (60%), Gaps = 35/619 (5%)

Query: 4 NIQNQCVPYNCLNNPEVEILNEERSTGRPLPLDISLSLTRFLSEFVPGVGVAFLGLDLIW 63
N QNQCVPYNCLNNPE EIL+ ERS + +I+L ++R LL+ P G+ GLFD IW
Sbjct: 5 NNQNQCVPYNCLNNPENEILDIERSTVATNIALEISR-LLASATPIGGILLGLFDAIW 63

Query: 64 GFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQ 123
G I PS W LFL QIE LI+Q+IE RN+AI+ L G++ Y IY EA REWEA+P N
Sbjct: 64 GSIGPSQWDLFLEQIELLIDQKIEEFARNQAISRLGESSLYGIYTEAFREWEADPTNPA 123

Query: 124 LREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLD 183
L+E++R +F + + L+TAI F++ ++++P LSVYVQAANLHLS+LRD FGQ WG D
Sbjct: 124 LKEEMRTQFNDMNSILVTAIPLFSVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQWGFDA 183

Query: 184 IATVNNHYNRLINLIHRYTKHCLDTYNQGLENL-RGNTNRQWARFNQFRRDLTLTVLIDIV 242
IAT+N+ YN L LI YT + + YN GL+ L R R WARFNQFRR+LT++VLDI+
Sbjct: 184 IATINSRYNDLTRLIPIYTDYAVRWYNTGLDRLPRTGGLRNWARFNQFRRDLTISVLDII 243

Query: 243 ALFPNYDVRTYPIQTSSQLTREIYTSSVIE--DSPVSANIPNGFNRAEFGVRPPHLMDFM 300
+ F NYD R YPI TSSQLTRE+YT VI D V + N N A +R PHLMDF+
Sbjct: 244 SFFRNYDSRYPIPTSSQLTREYVTDVINITDYRVGPSFENIENSA---IRSPHLMDFL 300

Query: 301 NSLFTVTAETVRSQTVWGGHVLSSRNTAGNR-INFPSYGVFNPGGAIWIADEDPFP----- 354
N+L + + +R W GH V+S T ++ I P YG+ A+ +PR

Sbjct: 301 NNLTIDTDLIRGVHYWAGHRVTSHTGSSQVITTPQYGI-----TANAEPRRTIAPS 352
Query: 355 -----FYRTLSDPVFVRGGFGNPHYVLG-LRGVAFQQTGTNHTRTFRNSGTIDSLDEI 406
FYRTLS+P F R P + ++GV F Q N +R+ GT+DSL+E+
Sbjct: 353 TFPGLNLFYRTLSPFFRRSENITPTLGINVVQGVGFIQP-NNAEVLRYSRGTVDLSLNEL 411
Query: 407 PPQDMSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ 466
P + YSH L+HVT R + ++ P F WTH SAT TNTI+P+ ITQ
Sbjct: 412 PIDGENSLV--GYSHRLSHVTLTR---SLYNTNITSLEPTFVWTHSATNTNTINPDIIITQ 466
Query: 467 IPLVKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYASTT 526
IPLVK L GT+V++GPGFTGGDILRR + G F VNIN + QRYR R RYAS+
Sbjct: 467 IPLVKGFRLLGGTSSVIGKPGFTGGDILRRNTIGEFVSLQVNINSPIITQRYRLRFRYASSR 526
Query: 527 NLRIVTVAGERIFAGQFNKMTDGTGDLTTFQSFSYATINTAFTFPMSSQSFVTGADTFSS 586
+ RI V + G+ KTM+ G+ LT ++FSY + F+F + + +
Sbjct: 527 DARITVAIGGQIRVDMTLEKTMEIGESLTSRTFSYTNFSNPFSTRANPDIIIRIAEELPIR 586
Query: 587 GNEVYIDRFELIPVTATLE 605
G E+YID+ ELI AT E
Sbjct: 587 GGELYIDKIELILADATFE 605

>gb|AAA22345.1| (M73252) cryIE(a) [Bacillus thuringiensis]
gb|AAL50330.1|AF202531_1 (AF202531) Cry032 [Bacillus thuringiensis]
Length = 1171

Score = 509 bits (1312), Expect = e-143
Identities = 290/619 (46%), Positives = 379/619 (60%), Gaps = 35/619 (5%)

Query: 4 NIQNQCVPYNCLNNPEVEILNEERSTGRPLDISLSLTRLFLSEFVPGVGVAFLFDLIW 63
N QNQCVPYNCLNNPE EIL+ ERS + +I+L ++R LL+ P G+ GLFD IW
Sbjct: 5 NNQNQCVPYNCLNNPENEILDIERSTVATNIALEISR-LLASATPIGGILLGLFDAIW 63
Query: 64 GFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQ 123
G I PS W LFL QIE LI+Q+IE RN+AI+ L G++ Y IY EA REWEA+P N
Sbjct: 64 GSIGSQWDLFQIEELLIDQKIEEFARNQAISRLEGISSLYGIYTEAFREWEADPTNPA 123
Query: 124 LREDVRIRFANTDDALITAINFTLTSEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLD 183
L+E++R +F + + L+TAI F++ +++P LSVYVQAANLHLS+LRD FGQ WG D
Sbjct: 124 LKEEMRTQFNDMNSILVTAIPLESVQYQVPFLSVYVQAANLHLSVLRDVSFVGQAWGFD 183
Query: 184 IATVNNHYNRLINLIHRYTKHCLDTYNQGLENL-RGTNTRQWARFNQFRDLTLTVLDIV 242
IAT+N+ YN L LI YT + + YN GL+ L R R WARFNQFRR+LT++VLDI+
Sbjct: 184 IATINSRYNDLTRLIPIYTDYAVRWYNTGLDRLPRTGGLRNWARFNQFRRELTISVLDII 243
Query: 243 ALFPNYDVRTYPIQTSSQLTREIYTSSVIE--DSPVSANIPNGFNRAEFGVRPHLMDFM 300
+ F NYD R YPI TSSQLTRE+YT VI D V + N N A +R PHLMDF+
Sbjct: 244 SFFRNYDSRLYPIPTSSQLTREYVTDPVINITDYRVGPSFENIENSA---IRSPHLMDFL 300
Query: 301 NSLFVTAETVRSQTVWGGHLVSSRNTAGNR-INFPSYGVFNPGGAIWIADDP-- 354
N+L + + +R W GH V+S T ++ I P YG+ A+ +PR
Sbjct: 301 NNLTIDTDLIRGVHYWAGHRVTSHTGSSQVITTPQYGI-----TANAEPRRTIAPS 352
Query: 355 -----FYRTLSDPVFVRGGFGNPHYVLG-LRGVAFQQTGTNHTRTFRNSGTIDSLDEI 406
FYRTLS+P F R P + ++GV F Q N +R+ GT+DSL+E+
Sbjct: 353 TFPGLNLFYRTLSPFFRRSENITPTLGINVVQGVGFIQP-NNAEVLRYSRGTVDLSLNEL 411
Query: 407 PPQDMSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ 466
P + YSH L+HVT R + ++ P F WTH SAT TNTI+P+ ITQ
Sbjct: 412 PIDGENSLV--GYSHRLSHVTLTR---SLYNTNITSLEPTFVWTHSATNTNTINPDIIITQ 466
Query: 467 IPLVKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYASTT 526
IPLVK L GT+V++GPGFTGGDILRR + G F VNIN + QRYR R RYAS+
Sbjct: 467 IPLVKGFRLLGGTSSVIGKPGFTGGDILRRNTIGEFVSLQVNINSPIITQRYRLRFRYASSR 526
Query: 527 NLRIVTVAGERIFAGQFNKMTDGTGDLTTFQSFSYATINTAFTFPMSSQSFVTGADTFSS 586
+ RI V + G+ KTM+ G+ LT ++FSY + F+F + + +
Sbjct: 527 DARITVAIGGQIRVDMTLEKTMEIGESLTSRTFSYTNFSNPFSTRANPDIIIRIAEELPIR 586

Query: 587 GNEVYIDRFELIPVTATLE 605
G E+YID+ ELI AT E
Sbjct: 587 GGELYIDKIELILADATFE 605

>sp|Q57458|C1EA_BACTX Pesticidal crystal protein cryIEa (Insecticidal delta-endotoxin
CryIE(a)) (Crystalline entomocidal protoxin) (133 kDa
crystal protein)
pir||I40572 crystal protein - Bacillus thuringiensis
emb|CAA37933.1| (X53985) crystal protein [Bacillus thuringiensis]
emb|CAA39609.1| (X56144) crystal protein [Bacillus thuringiensis]
Length = 1171

Score = 509 bits (1312), Expect = e-143
Identities = 290/619 (46%), Positives = 379/619 (60%), Gaps = 35/619 (5%)

Query: 4 NIQNCVFPYNCLNNPEVEILNEERSTGRPLDISLSLTRLSEFVPGVGVAFLGLDLIW 63
N QNQCVPYNCLNNPE EIL+ ERS + +I+L ++R LL+ P G+ GLFD IW
Sbjct: 5 NNQNCVFPYNCLNNPENEILDIERSTVATNIALEISR-LLASATPIGGILLGLFDAIW 63

Query: 64 GFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQ 123
G I PS W LFL QIE LI+Q+IE RN+AI+ L G++ Y IY EA REWEA+P N
Sbjct: 64 GSIGPSQWDLFLEQIELLIDQKIEEFARNQAISRLEGISLYGIYTEAFREWEADPTNPA 123

Query: 124 LREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLD 183
L+E++R +F + + L+TAI F++ ++++P LSVYVQAANLHLS+LRD FGQ WG D
Sbjct: 124 LKEEMRTQFNDMNSILVTAIPLFSVQNYQVPFLSVYVQAANLHLSVLRDVSFVGQAWGFD 183

Query: 184 IATVNNHYNRLINLIHRYTKHCLDTYNQGLENL-RGTNTRQWARFNQFRDLTLTVLDIV 242
IAT+N+ YN L LI YT + + YN GL+ L R R WARFNQFR+LT++VLDI+
Sbjct: 184 IATINSRYNDLTRIPIYTDYAVRWYNTGLDRLPRTGGLRNWARFNQFRRELTISVLDII 243

Query: 243 ALFPNYDVRTYPIQTSSQLTREIYTSSVIE--DSPVSANIPNGFNRAEFGVRPPHLMDFM 300
+ F NYD R YPI TSSQLTRE+YT VI D V + N N A +R PHLMDF+
Sbjct: 244 SFFRNYDSRLYPIPTSSQLTREIYTDVINITDYRVGPSFENIENSA---IRSPHLMDFL 300

Query: 301 NSLFVTAETVRSQTVWGGHLVSSRNTAGNR-INFPSYGVFNPGGAIWADEDRP----- 354
N+L + + +R W GH V+S T ++ I P YG+ A+ +PR
Sbjct: 301 NNLITDITDLIRGVHYWAGHRVTSHFTGSSQVITTPQYGI-----TANAEPRRTIAPS 352

Query: 355 -----FYRTLSDPVFVRGGFGNPHYVLG-LRGVAFQQTGTNHTTRFRNSGTIDSLDEI 406
FYRTLS+P F R P + ++GV F Q N +R+ GT+DSL+E+
Sbjct: 353 TFPGLNLFYRTLSNPFRRSENITPTLGINVVQGVGFQIP-NNAEVLRYRSGTVDSLNEL 411

Query: 407 PPQDMSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ 466
P + YSH L+HVT R + ++ P F WTH SAT TNTI+P+ ITQ
Sbjct: 412 PIDGENSLV--GYSHRLSHVTLTR---SLYNTNITSLPTFVWTHSATNTNTINPDIITQ 466

Query: 467 IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYASTT 526
IPLVK L GT+V++GPGFTGGDILRR + G F VNIN + QRYR R RYAS+
Sbjct: 467 IPLVKGFRLLGGGTSVIKGPFTGGDILRRNTIGFVSLQVNINSPTQRYRLRFYASSR 526

Query: 527 NLRIVTVAGERIFAGQFNKMTMDTGDPLTFQSFSYATINTAFTFPMSQSSTFTVGADTFSS 586
+ RI V + G+ KTM+ G+ LT ++FSY + F+F + + +
Sbjct: 527 DARITVAIGGQIRVDMTLEKTMEIGESLTSRTFSYTNFSNPFSSFRANPDIIRIAEELPIR 586

Query: 587 GNEVYIDRFELIPVTATLE 605
G E+YID+ ELI AT E
Sbjct: 587 GGELYIDKIELILADATFE 605

>gb|AAF37224.1|AF215647_1 (AF215647) toxin CryIcA6 [Bacillus thuringiensis]
Length = 1189

Score = 509 bits (1311), Expect = e-143
Identities = 297/633 (46%), Positives = 373/633 (58%), Gaps = 41/633 (6%)

Query: 1 MENNIQNCVFPYNCLNNPEVEILNEER-STGRPLDISLSLTRLSEFVPGVGVAFLGLF 59
ME N QNQC+PYNCL+NPE +L+ ER STG +DISLSL +FL+S FVPG G GL
Sbjct: 1 MEENNQNCQIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGFLVGLI 60

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Query: 60  DLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIYIEALREWEANP 119
           D +WG + PS W FL+QIEQLI +RI   RN AI L GL +++ IY+EA +EWE +P
Sbjct: 61  DFWVGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNNFNIIYVEAFKEWEEDP 120

Query: 120 NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQG 179
           NN  R V RF  D L  I +F ++ FE+PLLSVY QAANLHL++LRD+V FG+
Sbjct: 121 NNPATRTRVIDRFRILDGLLERDIPSFRIISGFEVPLLSVYAQAANLHLAILRDSVIFGER 180

Query: 180 WGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRRDLTLTVL 239
           WG+  VN +YNRLI I Y HC +TYN+GL NL + + W +N+ RRDLTTLTVL
Sbjct: 181 WGVTTINVNENYNRLIRHIDEYADHCANTYNRGLNNLPKSTYQDWITYNRLRRDLTLTVL 240

Query: 240 DIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSP---VSANIPNGFNRAEFGVRPPHL 296
           DI A FPNYD R YPIQ  QLTRE+YT +I +P  A +P  +R PHL
Sbjct: 241 DIAAFFPNYDNRRYPIQPVGQLTREYVTDPLINFNPQLQSVAQLPTFNVMESSAIRNPHL 300

Query: 297 MDFMNSLFVTAE---TVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPGGAIWIADDP- 353
           D +N+L + + +V  WGGH V S  G I P YG  E PR
Sbjct: 301 FDILNLLTIFTDWFVSGRNFYWGGRVVISLIGGNITSPIYG-----REANQEPERS 353

Query: 354 -----PFYRTLSDP---VFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTERNSGTIDSLDE 405
           P +RTLS+P  + +  P + G+ GV F T TN + T+R GT+DSL E
Sbjct: 354 FTFNGPVFRTLSNPTLRLLQQFPWAPPFNLRGVGVF- STPTN-SFTYRGRGTVDLSLE 411

Query: 406 IPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERIT 465
           +PP+DNS P  YSH L H TFV+ G  +FSWTHRSAT TNTIDPERI
Sbjct: 412 LPPEDNSVPPREGYSHRLCHATFVQSRGT---PFLTGVVFSWTHRSATLTNTIDPERIN 468

Query: 466 QIPLVKAHTLQSGTTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYAST 525
           QIPLVK + GT+V+ GPGETGGDILRR + G F  VNIN + QRYR R RYAS+
Sbjct: 469 QIPLVKGRVWGGTSVITGPGFTGGDILRRNTFGDFVSLQVNINSPIQRYRLRFYASS 528

Query: 526 TNLRIYV-TVAGERIFAGQ-----FNKTMDTGDPLTFQSFYSATINTAFTFPMSSQSF 578
           + R+ V T A  GQ  KTM+ G+ LT ++F Y  + F+F +
Sbjct: 529 RDARVIVLTGAASTGVGGQSVNMPLQKTMEIGENLTSRTFRYTDFSNPFSSFRANPDIIG 588

Query: 579 V-----GADTFSSGNEVYIDRFELIPVTATLE 605
           +  GA + SSG E+YID+ E+I  AT E
Sbjct: 589 ISERPLFGAGSISSG-ELYIDKIEIILADATFE 620

>pir|S00944 parasporal crystal protein - Bacillus thuringiensis (strain
          entomocidus 60.5)
emb|CAA30396.1| (X07518) put. endotoxin (AA 1-1189) [Bacillus thuringiensis]
Length = 1189

Score = 508 bits (1308), Expect = e-143
Identities = 298/633 (47%), Positives = 375/633 (59%), Gaps = 41/633 (6%)

Query: 1  MENNIQNCQVPYNCLNNPEVEILNEER-STGRPLDISLSLRELLSEFVPGVGVAFGLE 59
           ME N QNQC+PYNCL+NPE +L+ ER STG +DISLSL +FL+S FVPG G GL
Sbjct: 1  MEENNQNCQIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSFVPGGGFLVGLI 60

Query: 60  DLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIYIEALREWEANP 119
           D +WG + PS W FL+QIEQLI +RI   RN AI L GL +++ IY+EA +EWE +P
Sbjct: 61  DFWVGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNNFNIIYVEAFKEWEEDP 120

Query: 120 NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQG 179
           NN + R V RF  D L  I +F ++ FE+PLLSVY QAANLHL++LRD+V FG+
Sbjct: 121 NNPETRTRVIDRFRILDGLLERDIPSFRIISGFEVPLLSVYAQAANLHLAILRDSVIFGER 180

Query: 180 WGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRRDLTLTVL 239
           WGL  VN +YNRLI I Y HC +TYN+GL NL + + W +N+ RRDLTTLTVL
Sbjct: 181 WGLTTINVNENYNRLIRHIDEYADHCANTYNRGLNNLPKSTYQDWITYNRLRRDLTLTVL 240

Query: 240 DIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPN---GFNRAEFG-VRPPHL 296
           DI A FPNYD R YPIQ  QLTRE+YT +I +P  ++  FN E  +R PHL
Sbjct: 241 DIAAFFPNYDNRRYPIQPVGQLTREYVTDPLINFNPQLQSVAQLPTFNVMESSRIIRNPHL 300

Query: 297 MDFMNSLFVTAE---TVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPGGAIWIADDP- 353

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D +N+L + + +V WGGH V S G I P YG E PR
Sbjct: 301 FDILNNLTIFTDWFVGRNFYWGGRHVISSLIGGGNITSPIYG-----REANQEPPRS 353

Query: 354 -----PFYRTLSDP---VFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDE 405
P +RTLS+P + + P + G+ GV F T TN + T+R GT+DSL E

Sbjct: 354 FTFNGPVFRTLSTNPTLRLLQQPWPAPPFNLRGVEGVEF-STPTN-SFTYRGRGTVDLSLDE 411

Query: 406 IPPQDMSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERIT 465
+PP+DNS P YSH L H TFV+ G +FSWT RSAT TNTIDPERI

Sbjct: 412 LPPEDNSVPPREGYSHRLCHATFVQSRGT---PFLTGTGVVFSWTHRSATLTNTIDPERIN 468

Query: 466 QIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYAST 525
QIPLVK + GT+V+ GPGFTGGDILRR + G F VNIN + QRYR R RYAS+

Sbjct: 469 QIPLVKGRVWGGTGVITGPGFTGGDILRRTFGDFVSLQVNINSPIQRYRLRFRYASS 528

Query: 526 TNLRIYV-TVAGERIFAGQ-----FNKTMDDTGDPLTFQSFYSATINTAFTFPMSSQSSFT 578
+ R+ V T A GQ KTM+ G+ LT ++F Y + F+F +

Sbjct: 529 RDARVIVLTGAASTGVGGQVSVNMLPQKTMEIGENLTSRTFRYTFDSNPFSTRANPDIIG 588

Query: 579 V-----GADTFSSGNEVYIDRFELIPVTATLE 605
+ GA + SSG E+YID+ E+I AT E

Sbjct: 589 ISEQPLFGAGSISSG-ELYIDKIEIILADATFE 620

>gb|AAA22343.1| (M73251) cryIC(b) [Bacillus thuringiensis]
Length = 1189

Score = 508 bits (1308), Expect = e-143
Identities = 297/633 (46%), Positives = 372/633 (57%), Gaps = 41/633 (6%)

Query: 1 MENNIQNQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRLFLSEFVPGVGVAFGLF 59
ME N QNQC+PYNCL+NPE +L+ ER STG +DISLSL +FL+S FVPG G GL

Sbjct: 1 MEENNQNCQIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGFLVGLI 60

Query: 60 DLIWGFITPSDWSLFLQLIEQLIETLERNRAITTLRGLADSYEIIYIEALREWEANP 119
D +WG + PS W FL+QIEQLI +RI RN AI L GL +++ IY+EA +EWE +P

Sbjct: 61 DFVWGVGPGSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKEWEDP 120

Query: 120 NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLSVYQAANLHLSLLRDAVSFGQG 179
NN R V RF D L I +F ++ FE+PLSVY QAANLHL++LRD+V FG+

Sbjct: 121 NNPATRTVRIDRFRILDGLLERDIPSRISGFVPLSVYQAANLHLAILRDSVIFGER 180

Query: 180 WGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRDLTLTVL 239
WGL VN +YNRLI I Y HC +TYN+GL NL + + W +N+ RRDLTTLTVL

Sbjct: 181 WGLTTINVENYNRLIRHIDEYADHCANTYNRGLNNLPKSTYQDWITYNRLRRDLTLTVL 240

Query: 240 DIVALEFPNYDVRTYPIQTSSQLTREIYTSSVIEDSP---VSANIPNGFNRAEFGVRPPLH 296
DI A FPNYD R YPIQ QLTRE+YT +I +P A +P +R PHL

Sbjct: 241 DIAAFFFNYDNRRYPIQPVGQLTREYVTDPLINFNPQLQSVQALPTFNVMESSAIRNPHL 300

Query: 297 MDFMNSLFVTAE--TVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPGGAIWADEDPR- 353
D +N+L + + +V WGGH V S G I P YG E PR

Sbjct: 301 FDILNNLTIFTDWFVGRNFYWGGRHVISSLIGGGNITSPIYG-----REANQEPPRS 353

Query: 354 -----PFYRTLSDP---VFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDE 405
P +RTLS+P + + P + G+ GV F T TN + T+R G +DSL E

Sbjct: 354 FTFNGPVFRTLSTNPTLRLLQQPWPAPPFNLRGVEGVEF-STPTN-SFTYRGRGTVDLSLDE 411

Query: 406 IPPQDMSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERIT 465
+PP+DNS P YSH L H TFV+ G +FSWTHRSAT TNTIDPERI

Sbjct: 412 LPPEDNSVPPREGYSHRLCHATFVQSRGT---PFLTGTGVVFSWTHRSATLTNTIDPERIN 468

Query: 466 QIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYAST 525
QIPLVK + GT+V+ GPGFTGGDILRR + G F VNIN + QRYR R RYAS+

Sbjct: 469 QIPLVKGRVWGGTGVITGPGFTGGDILRRTFGDFVSLQVNINSPIQRYRLRFRYASS 528

Query: 526 TNLRIYV-TVAGERIFAGQ-----FNKTMDDTGDPLTFQSFYSATINTAFTFPMSSQSSFT 578
+ R+ V T A GQ KTM+ G+ LT ++F Y + F+F +

Sbjct: 529 RDARVIVLTGAASTGVGGQVSVNMLPQKTMEIGENLTSRTFRYTFDSNPFSTRANPDIIG 588

Query: 579 V-----GADTFSSGNEVYIDRFELIPVTATLE 605
+ GA + SSG E+YID+ E+I AT E
Sbjct: 589 ISEQPLFGAGSISSG-ELYIDKIEIILADATFE 620

>pir||S04181 parasporal crystal protein - Bacillus thuringiensis (strain aizawai
7.29) (fragment)
emb|CAA31951.1| (X13620) delta-endotoxin (AA 1 - 824) (2711 is 2nd base in codon)
[Bacillus thuringiensis]
Length = 823

Score = 507 bits (1305), Expect = e-142
Identities = 299/633 (47%), Positives = 372/633 (58%), Gaps = 41/633 (6%)

Query: 1 MENNIQNCQVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFLG 59
ME N QNQC+PYNCL+NPE +L+ ER STG +DISLSL +FL+S FVPG G GL
Sbjct: 1 MEENNQNCQIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGFLVGLI 60

Query: 60 DLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANP 119
D +WG + PS W FL+QIEQLI +RI RN AI L GL +++ IY+EA +EWE +P
Sbjct: 61 DFWGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNNFNIIYVEAFKEWEEDP 120

Query: 120 NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQG 179
NN R V RF D L I +F ++ FE+PLLSVY QAANLHL++LRD+V FG+
Sbjct: 121 NNPATRTRVIDRFRILDGLLERDIPSFRISGFVPLLSVYQAANLHLAILRDSVIFGER 180

Query: 180 WGLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLRGTNTROWARFNQFRDLTLTVL 239
WGL VN +YNRLI I Y HC +TYN+GL NL + + W +N+ RDLTLTVL
Sbjct: 181 WGLTTINVENYNRLIRHIDEYADHCANTYNRGLNNLPKSTYQDWITYNRLRDLTLTVL 240

Query: 240 DIVALEFPNYDVRTYPIQTSSQLTREIYTSSVIEDSP---VSANIPNGFNRAEFGVRPPL 296
DI A FPNYD R YPIQ QLTRE+YT +I +P A +P +R PHL
Sbjct: 241 DIAAFEPNYDNRRYPIQPVGQLTREYITDPLINFNPQLQSVQALPTFNVMESSAIRNPHL 300

Query: 297 MDFMNSLFVTAE--TVRSQTVWGGHVLSSRNTAGNRINFPSYGVFNPGGAIWIADDEPR- 353
D +N+L + + +V WGGH V S G I P YG E PR
Sbjct: 301 FDILNLTIFTDWFVSGRNFYWGGRHVISSLIGGNITSPIYG-----REANQEPPRS 353

Query: 354 -----PFYRTLSDPV--FVRGGFGNPHYVL-GLRGVAFQQTGTNHTRTFRNSGTIDSLDE 405
P +RTLS P ++ H+ L G GV F T TN + T+R GT+DSL E
Sbjct: 354 FTFNGPVFRTLSTIPTLRLLQPCQRHHENLRGGEGVEF-STPTN-SFTYRGRGTVDLSLE 411

Query: 406 IPPQDMSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERIT 465
+PP+DNS P YSH L H TFV+ G +FSWTHRSAT TNTIDPERI
Sbjct: 412 LPPEDNSVPPREGYSHRLCHATFVQSRGT---PFLTTGVVFSWTHRSATLTNTIDPERIN 468

Query: 466 QIPLVKAHTLQSGTTVVRGPGFTGGDILRRSTGGPFAYTIVNINGQLPQRYRARIYAST 525
QIPLVK + GT+V+ GPGFTGGDILRR + G F VNIN + QRYR R RYAS+
Sbjct: 469 QIPLVKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVSLQVNINSPIQRYRLRFYASS 528

Query: 526 TNLRIYV-TVAGERIFAGQ-----FNKTMDDTGDPLTFQSFSYATINTAFTFPMSSQSSFT 578
+ R+ V T A GQ KTM+ G+ LT ++F Y + F+F +
Sbjct: 529 RDARVIVLTGAASTGVGGQVSVNMPLQKTMEIGENLTSRTFRYTDFSNPFSSFRANPDIIG 588

Query: 579 V-----GADTFSSGNEVYIDRFELIPVTATLE 605
+ GA + SSG E+YID+ E+I AT E
Sbjct: 589 ISEQPLFGAGSISSG-ELYIDKIEIILADATFE 620

>gb|AAB30710.1| insecticidal protein Cry I A (c) product {toxic domain} [Bacillus
thuringiensis, ssp. kurstaki HD-1, Peptide, 723 aa]
Length = 723

Score = 507 bits (1305), Expect = e-142
Identities = 297/619 (47%), Positives = 370/619 (58%), Gaps = 21/619 (3%)

Query: 1 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFLG 58
M+NN N+C+PYNCL+NPEVE+L ER G P+DISLSLT+FLLEFVPG G GL
Sbjct: 1 MDNPNINICIPYNCLSNPEVEVLGGERIEIGYTPIDISLSLTQFLLEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118

Sbjct: 61 D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + ++++PLLSVYVQAANLHLS+LRD FGQ

Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTTLTV

Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239 LDIVALEFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIVALEFPNYD R YPI+T SQL REIYT+ V+E+ + E +R PHLM

Sbjct: 241 LDIVALEFPNYDSRRYPITVSQLEPREIYTNPVLEN--FDGSGRGSAGGIERSIRSPHLM 298

Query: 299 FMNSLEVTAEVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADEDPRPF 355
+NS+ + + R W GH + S +G FP YG N I + +

Sbjct: 299 ILNSITIYTDHARGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVFVRG---GFGNPHY-VLGLRGVAFOQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS + R G N VL A+ + + +R SGT+DSLDEIPPQ+N

Sbjct: 359 YRTLSSTFYRRFPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHTVFRWVPEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R G S RAPMFSW HRSA N I + ITQIP VK

Sbjct: 419 NVPPRQGFHRLSHVSMFR-SGSSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK 477

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTS GG---PFAYTIVNIN-GQLPQRYRARIYASTT 526
+ L +G +V+ GPFTGGD++R S G Y V I+ RYR R+RYAS T

Sbjct: 478 GNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFSSTSTRYRVRYASVT 536

Query: 527 NLRIYVTVAGERIFAGQFNKTMDDTGLPLTFQSFSYATINTAFTFPMSQSSFTVGADTFSS 586
+ V IF+ T + D L F Y AET S VG FS

Sbjct: 537 PIHRNVNWNSSIFSNTVPATATSCDNLQSSDFGYFESANAFT---SSLGNIVGVNRFSG 593

Query: 587 GNEVYIDRFELIPVTATLE 605
V IDRFE IPVTATLE

Sbjct: 594 TAGVIIDRFEFIPVTATLE 612

>gb|AAD04732.1| (U94323) CryIEa4 [Bacillus thuringiensis]
Length = 1171

Score = 506 bits (1303), Expect = e-142
Identities = 288/611 (47%), Positives = 374/611 (61%), Gaps = 19/611 (3%)

Query: 4 NIQNCQVPYNCLNNPEVEILNEERSTGRPLDISLSLTRLFLSEFVPGVGVAFLGLFDLIW 63
N QNCQVPYNCLNNPE EIL+ ERS + +I+L ++R LL+ P G+ GLFD IW

Sbjct: 5 NNQNCQVPYNCLNNPENIEILDIERSNSTVATNIALEISR-LLASATPIGGILLGLFDAIW 63

Query: 64 GFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQ 123
G I PS W LFL QIE LI+Q+IE RN+AI+ L G++ Y IY EA REWEA+P N

Sbjct: 64 GSIGPSQWDLFLEQLIELLDQKIEEFARNQAISRLEGISLYGIYTEAFREWEADPTNPA 123

Query: 124 LREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLD 183
L+E++R +F + + L+TAI F++ ++++P LSVYVQAANLHLS+LRD FGQ WG D

Sbjct: 124 LKEEMRTQFNDMNSILVTAIPLFSVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQAWGFD 183

Query: 184 IATVNNHYNRLINLIHRYTKHCLDTYNQGLENL-RGNTNRQWARFNQFRRDLTLTVLDIV 242
IAT+N+ YN L LI YT + + YN GL+ L R R WARFNQFRR+LT++VLDI+

Sbjct: 184 IATINSRYNDLTRLIPIYTDYAVRWYNTGLDRLPRTGGLRNWARFNQFRRELTIISVLDII 243

Query: 243 ALFPNYDVRTYPIQTSSQLTREIYTSSVIE--DSPVSANIPNGFNRAEFGVRPPHLMDFM 300
+ F NYD R YPI TSSQLTRE+YT VI D V + N N A +R PHLMDF+

Sbjct: 244 SFFRNYDSRLYPIPTSSQLTREYVTDVINITDYRVGSPFENIENSA---IRSPHLMDFL 300

Query: 301 NSLEVTAEVRSQTVWGGHLVSSRNTAGNR-INFPSYGVFNPGGAIWIADEDPRP----F 355
N+L + + +R W GH V+S T ++ I P YG P F

Sbjct: 301 NNLTIIDTLIRGVHYWAGHRVTSHTGSSQVITTPQYGNQNAEPRRTIAPSTFPGLNLF 360

Query: 356 YRTLSDPVFVRGGFGNPHYVLG-LRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPDNSGA 414
YRTLS+P F R P + ++GV F Q N +R+ GT+DSL+E+P +
Sbjct: 361 YRTLSNPFRRSENITPTLGINVVQGVGFIQP-NNAEVLRYSRGTVDLSNELPIDGENSL 419

Query: 415 PWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHT 474
YSH L+HVT R + ++ P F WTH SAT TNTI+P+ ITQIPLVK
Sbjct: 420 V--GYSHRLSHVTLTR--SLYNTNITSLPTFVWTHHSATNTNTINPDIITQIPLVKGER 474

Query: 475 LQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTV 534
L GT+V++GPGFTGGDILRR + G F VNIN + QRYR R RYAS+ + RI V +
Sbjct: 475 LGGGTSVIKGPFTGGDILRRTTIGEFVSLQVNINSPITQRYRLRFRYASSRDARITVAI 534

Query: 535 AGERIFAGQFNKTMDTGDLTFQSFSYATINTAFTFPMSSQSSFTVGADTFSSGNEVYIDR 594
G+ KTM+ G+ LT ++FSY + F+F + + + G E+YID+
Sbjct: 535 GGQIRVDMTLEKTMIEGESLTSRTFSYTNFSNPFSSFRANPDIIRIAEELPIRGELYIDK 594

Query: 595 FELIPVTATLE 605
ELI AT E
Sbjct: 595 IELILADATFE 605

>sp|P09663|CRU_BACTK 131 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE ENTOMOCIDAL
PROTOXIN)
pir||A29838 parasporal crystal protein - Bacillus thuringiensis subsp. kurstaki
gb|AAA22613.1| (M12661) insecticidal endotoxin [Bacillus thuringiensis]
Length = 1156

Score = 504 bits (1298), Expect = e-141
Identities = 296/619 (47%), Positives = 373/619 (59%), Gaps = 20/619 (3%)

Query: 1 MENNIQ-NQCVPYNCLNNEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNPNINIECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG 60

Query: 59 FDLIWGITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGFIFGSPQWDAFLVQIEQLINQRIEEFARNQAISRLGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI F + +++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTAIPLFAVQNYQVPLSVYVQAANLHLSVLRDVSFVGL 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARENQFRDLTLTV 238
WG D AT+N+ YN L LI YT H + YN GLE + G ++R W R+NQFR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDHRVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTV 240

Query: 239 LDIVALEFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
LDIV+LFPNYD RTYPI+T SQLTREIYT+ V+E+ + E +R PHLM
Sbjct: 241 LDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSRGSAQIEGSIKSPHLM 298

Query: 299 FMNSLFVTAETVRSQTVWGGH--LVSSRNATGNRINFPSTYGVF-NPGGAIWIADDP 355
+NS+ + + R + W GH + S +G FP YG N I + +
Sbjct: 299 ILNSITITDAHRGEYYWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVFVRG---GFGNPHY--VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPD 410
YRTLS ++ R G N G R + + +DS DEIPPQ+
Sbjct: 359 YRTLSSTLYRRFPNIGINNQQLSGPDGGRICLWNLLKFGQPPYTEKAEFVDSPEIPPQN 418

Query: 411 NSGAPWNDYSH-VLNHVTFVRWPGEISGSDSWRAPM-FSWTHRSATPTNTIDPERITQIP 468
N+ P +SH L +V+ S RAP SWT+ SA + I +ITQIP
Sbjct: 419 NNVPPRQGFSHRCLAYVSMFYSGFSNSSVSVIRAPNDSSWTYCSAEFGDVIPSSQITQIP 478

Query: 469 LVKAHTLQS--GTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTT 526
L K LQS +VV+G GFTGGDIL + G + VNI L QRYR RIRYASTT
Sbjct: 479 LTK---LQSWLWNSVVKGLGFTGGDILELT-GQISTLRVNITAPLSQRYRVIRYASTT 534

Query: 527 NLRIYVTVAGERIFAGQFNKTMDTGDLTFQSFSYATINTAFTFPMSSQSSFTVGADTFSS 586
NL+ + ++ G I G F+ TM +G L SF T F F S FT+ A F+S
Sbjct: 535 NLQFHTSIDGRPINQGNFSATMSSGSLNQLSGSFRTVGTTPFNFSNGSSVFTLSAHVFNS 594

Query: 587 GNEVYIDRFELIPVTATLE 605
GNEVYIDR E +P T E
Sbjct: 595 GNEVYIDRIEFVPAEVTFE 613

>gb|AAA86266.1| (U43606) CryIA(c) [Bacillus thuringiensis]
Length = 607

Score = 503 bits (1296), Expect = e-141
Identities = 294/614 (47%), Positives = 368/614 (59%), Gaps = 21/614 (3%)

Query: 1 MENNIQ-NQCVYPYNCLNNPEVEILNEER-STGRLPLDISLSLTRFLLSEFVPGVGVAFG 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL
Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+
Sbjct: 61 VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD 120

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRDAVSFGQ 178
P N LRE++RI+F + + AL TAI + ++++PLLSVYVQAANLHLS+LRD FGQ
Sbjct: 121 PTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ 180

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRDLTLTV 238
WG D AT+N+ YN L LI YT + + YN GLE + G ++R W R+NQFRR+LTLTV
Sbjct: 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTV 240

Query: 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHMD 298
LDIVALFPNYD R YPI+T SQLTREIYT+ V+E+ + E +R PHLMD
Sbjct: 241 LDIVALFPNYDSRRYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQGIERSIRSPHMD 298

Query: 299 FMNSLEVTAEVRSQTVWGGH--LVSSRNNTAGNRINFPSYGVF-NPGGAIWIADDPDPF 355
+NS+ + + R W GH + S +G FP YG N I + +
Sbjct: 299 ILSITITTDHARGYYYWSGHQIMASPVGSGPEFTFPLYCTMGNAAPQQRIVAQLGQGV 358

Query: 356 YRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
YRTLS + R G N VL A+ + + +R SGT+DSLDEIPPQ+N
Sbjct: 359 YRTLSSTFYRRFPNIGINNQSVLDGTEFAYGTSSNLPSSAVYRKSGTVDSLDEIPPQNN 418

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ P +SH L+HV+ R G S RAPMFSW HRSA N I + ITQIP VK
Sbjct: 419 NVPPRQGFHSHLSHVMFR-SGSSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK 477

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGG---PFAYTIVNIN-GQLPQRYRARIRYASTT 526
+ L +G +V+ GPGETGGD++R S G Y V I+ RYR R+RYAS T
Sbjct: 478 GNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYVRVRYASVT 536

Query: 527 NLRIVYTVAGERIFAGQFNKTMDDTGDPLTFQSFSYATINTAFTFPMSQSSFTVGADTFSS 586
+ + V IF+ T + D L F Y AFT S VG FS
Sbjct: 537 PIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT---SSLGNIVGVNRNFSG 593

Query: 587 GNEVYIDRFELIPV 600
V IDRFE IPV
Sbjct: 594 TAGVIIDRFEFIPV 607

>sp|Q45716|C1JB_BACTU Pesticidal crystal protein cryIJB (Insecticidal delta-endotoxin
CryIJ(b)) (Crystalline entomocidal protoxin) (134 kDa
crystal protein)
Length = 1170

Score = 502 bits (1293), Expect = e-141
Identities = 287/614 (46%), Positives = 362/614 (58%), Gaps = 23/614 (3%)

Query: 1 MENNIQNCQVPYNCLNNPEVEILNEERSTGRL-PLDISLSLTRFLLSEFVPGVGVAFG 59
ME N QNQC+PYNCL+NPE +L+ ER + PL++S+SL +FLL+ FVPG G GLF
Sbjct: 1 MEINNQNQCIPYNCLSNPEEVLDDGERILPDIDPLEVSMSSLLQFLLNNFVPGGGFISGLF 60

Query: 60 DLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANP 119
D IWG + PSDW LFL QIEQLI+QRIE R +AI L GL S+++Y+EA +EWE P
Sbjct: 61 DKIWGALRPDWSLFLAQIEQLIDQRIEATVRAKAI AELEGLGRSFQLYVEAFKEWEETP 120

Query: 120 NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQG 179
+N R V RF D + I +F + FE+PLLSVY QAANLHL+LLRD+V FG+
Sbjct: 121 DNTAARSRVTERFRIIDAQIEANIPSFRIIPGFEVPLLSVYAQAANLHLALLRDSVIFGER 180

Query: 180 WGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRDLTLTVL 239
WGL VN+ YNR + IH Y+ HC+DTY LE L T+ QW +NQFRR+LTLTVL
Sbjct: 181 WGLTTTNDIYNRQVKRIHEYSDDHCVDTYKTELERLGFTSRAQWKIYNQFRRDLTLTVL 240

Query: 240 DIVALFPNYDVRTYPIQTSSQLTREIYTSSVIE--DSPVSANIPNGFNRAEFGVRPPHLM 297
DIVA+FPNYD + YPIQT S+LTREIYTS V E ++ NG + E +R PHLM
Sbjct: 241 DIVAVFPNYDGKLYPIQTKSELTREIYTSPVSEYYYGAINNNYQNGI-QTERQIRQPHLM 299

Query: 298 DFMNSLFVTAETVRSQTVWGGHLVSSRNT--AGNRINFPSYGVFNPGGAIWIADDEDPRPF 355
DF N++ + R + W G +++ T AG +++FP G +
Sbjct: 300 DFFNTMTMYTSYNRREYYWGLEMTAYFTGFAGPQVSFPLAGTRGDAAPPFNVRVNDGI 359

Query: 356 YRTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTN----HTRTFRNSGTIDSLDEIPPQDN 411
YR LS P + G VLG RG F N + +RN GT+DSL IPPQDN
Sbjct: 360 YRILSAPFYSAPFLGTS--VLGSRGEEFMALNNISPPPSARYRNPQTVDSLVSIPPQDN 417

Query: 412 SGAPWNNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
S P SH L+HVT +P+FWTHRSAT TN I+ + ITQIP+VK
Sbjct: 418 SVPPIHGRSSHRLSHVTMRN-----SSPIFWTHRSATTTNRINSDVITQIPMVK 466

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIY 531
A+ L +G TVVRGPGFTGGDILRRTS G V+ + QRYR R RYA+T+N
Sbjct: 467 AYNLHAGATVVRGPGFTGGDILRRTSNGMVVTLRVDASAVRNQRYRIRFRYAATSNFYFV 526

Query: 532 VTVAGERIFAGQFNKMTMDTGDPLTFQSFYATINTAFTFPMSSQSSFTVGADTFSSGNEVY 591
V + + KTM TG+ L SF T F F +Q + + S G EVY
Sbjct: 527 VRRGNLGVNGREIMKTMSTGEEELKSASFVLGEFITPFNEFFENQVPLQIEIQSLSPGGEVY 586

Query: 592 IDRFELIPVTATLE 605
+D+ E IP T E
Sbjct: 587 LDKIEFIPADTTFE 600

>emb|CAA70506.1| (Y09326) delta-endotoxin [Bacillus thuringiensis]
Length = 1173

Score = 501 bits (1290), Expect = e-141
Identities = 305/617 (49%), Positives = 370/617 (59%), Gaps = 30/617 (4%)

Query: 1 MENNIONQCVPNCLNPEVEILNEERSTGRPLDISLSLTRFLLSEFVPGVGVAFLGFD 60
ME + QNQ +PYNCLNPE EI N S L +S LTRFLL VP G A GLFD
Sbjct: 1 MEISDQNYIPYNCLNPESEIFNARNSNFGLVSQVSSGLTRFILLEAAVPEAGFALGLFD 60

Query: 61 LIWGFIPTSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPN 120
+IWG + WSLFL QIEQLI Q I LERNRA L GL+ SY +Y+EALREWE +PN
Sbjct: 61 IIWGALGVDQWSLFLRQIEQLIRQEITELERNRATAILIGLSSSYNLYVEALREWENDPN 120

Query: 121 NAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW 180
N +E VR RF TDDA++T + + + E+ LSVY QAANLHLSLLRDAV FG+ W
Sbjct: 121 NPASQERVTRFRRLTDDAIVTGLPTLAINRLEVNVLSVYTQAANLHLSLLRDAVYFGERW 180

Query: 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRDLTLTVLD 240
GL A + + Y RL + I Y+ HC YNQL + G + R+ F+RDLT++VLD
Sbjct: 181 GLTQANIEDLYTRLTSNIQEYSDHCAWYNQGLNEIGGIS----RRYLDFFQDRLTISVLD 236

Query: 241 IVALF-PNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDF 299
IVA F PNYD+RTYPI T SQLTREIYTS V V+ NI G + A +R PHLMDF
Sbjct: 237 IVAPFSPNYDIRTYPIPTQSQLTREIYTSPV-----VAGNINFGLSIANV-LRAPHLMDF 290

Query: 300 MNSLFVTAETVRSQTVWGGHLVSSRNTA---GNRINFPSYGV-FNPGGAIWIA----DED 351
++ + + +VRS W GH V SR T GN I FP YGV N + I ++
Sbjct: 291 IDRIVIYTNVSRSTPYWAGHEVISRRTGQAQGNIRFPLYGVAANAEPVTTIRPTGTDE 350

Query: 352 PRPFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRN--SGTIDSLDEIPPQ 409
R +YR S + R + L + VAF T + +RN D++DEIP +

Sbjct: 351 QRQWYRARS--LLSRFRSSGQDFSL-VDAVAF-LTIFSAVSIYRNGFGFNTDTIDEIPIE 406

Query: 410 DNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPL 469
P+ YSH L HV F+ I S RAP+FSWTHRSAT TNTI P+ ITQIPL

Sbjct: 407 GTD--PFTGYSHRLCHVGFLASSPFI--SQYARAPIFSWTHRSATLTNTIAPDVITQIPL 462

Query: 470 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQYRARIYASTTNLR 529
VKA L SG T+V+GPGFTGGDILRRT+ F VNI L QRYR RIRYASTT+L+

Sbjct: 463 VKAFNLHSGATIVKPGFTGGDILRRTNVRSEFRDMRVNITAPLSQRYRVRIYASTTDLQ 522

Query: 530 IYVTVAGERIFAGQFNKMTMDTGDPITFQSFYATINTAFTFMSQSSFTVGADTFSSG-N 588
Y + G I G F+ TMD+GD L + F A T FTF + +F + FS

Sbjct: 523 FYTNINGTTINIGNFSSTMDSGDDLQYGRFRVAGFTTPTFTSRCKQTFHNRSFWFSPKLT 582

Query: 589 EVYIDRFELIPVTATLE 605

EVYIDR E +P T E

Sbjct: 583 EVYIDRIEFVPAEVTFE 599

>sp|Q45715|C1KA_BACTM Pesticidal crystal protein crylKa (Insecticidal delta-endotoxin
CrylK(a)) (Crystalline entomocidal protoxin) (137 kDa
crystal protein)

gb|AAB00376.1| (U28801) CrylK [Bacillus thuringiensis]

prf|2204216A crylK gene [Bacillus thuringiensis]

Length = 1215

Score = 497 bits (1280), Expect = e-139

Identities = 288/583 (49%), Positives = 362/583 (61%), Gaps = 39/583 (6%)

Query: 49 VPGVGVAFLGFDLIWGFITPSD---WSLFLQIEQLI-EQRIETLERNRAITTLRGLADS 104
VP G + + G + PS W +F+ +EQ++ +Q+I R+ AI L GL

Sbjct: 72 VPFAQLASFLYFSLVGLWPSGRDPWEIFMEHVEQIVRQQITDSVRDTAIARLEGLGRG 131

Query: 105 YEIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAAN 164
Y Y +AL W N N+A+ R +R R+ + + TAI F++ + E+PLL VY QAAN

Sbjct: 132 YRSYQQALETWLDNRNDARSRSIIRERYIALELDITTAIPLFSIRNEEVPLLMVYAQAAN 191

Query: 165 LHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTROW 224
LHL LLRDA FG WG+ A VN +Y I Y+ HC+ YN GL LRGT W

Sbjct: 192 LHLLLLRDASLFGSEWGMSSADVNQYYQEIQIRYTEEYSNHCQWYNTGLNRLRGTTAETW 251

Query: 225 ARFNQFRRDLTLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTS-SVIEDSPVSNIPNG 283
R+NQFRRDLTL VLD+VALFP+YD RTYPI T++QLTRE+YT + + P ++ NG

Sbjct: 252 VRYNQFRRDLTLGLVLDLVALFPYSYDTRTYPIPTTAQLTREYVTDPNGVVGPNNSWFRNG 311

Query: 284 --FNRAEFGV-RPPHLMDFMNSLFVTAETVRSQT-----VWGGHLVSSRNTAGNRINFP 334
F+ E + R PHL DF+ +L T T RSQ +W GH ++ G +

Sbjct: 312 ASFSAIENAIIRQPHLYDFLTNL--TIYTRRSQVGTTIMNLWAGHRITFNRIQGGSTSEM 369

Query: 335 SYGVFNPGGAIWIADEDPRPFYRTLSDPVFVRGGFGNPHYV-LGLRGVAFQQTGTNH--- 390
YG ++ R YRT+S + GG G+ + GL V F NH

Sbjct: 370 VYGAITNPVSVSDIPFVNVDVYRTVS----LAGGLGSLSGIRYGLTRVDFDMIFRNHPDI 425

Query: 391 -TRTFRNSGTI-----DSLDEIPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWR 442
T F + G DS E+PP+ + +SH+L+H++ ++

Sbjct: 426 VTGLFYHHPGHAGIATQVKDSDELPPETTEQPNYRAFSHLLSHISMGPPTQDVP----- 479

Query: 443 APMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFA 502
P++SWTH+SA TNTI+ +RITQIPLVKAHTLQSGTTVV+GPGFTGGDILRRTSGGPFA

Sbjct: 480 -PVYSWTHQSADRNTINSRITQIPLVKAHTLQSGTTVVKPGFTGGDILRRTSGGPFA 538

Query: 503 YTIVNINGQLPQYRARIYASTTNLRIYVTVAGERIFAGQFNKMTMDTGDPITFQSFSA 562
++ VN++ L QRYRARIYASTTNLRIYVTVAGERIFAGQF+KTMD G PLTFQSFSA

Sbjct: 539 FSNVNLDFNLSQRYRARIYASTTNLRIYVTVAGERIFAGQFDKTMAGAPLTFQSFSA 598

Query: 563 TINTAFTFPMSSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605

TINTAFTFP SS T+GADTFSSGNEVY+DRFELI VTAT E

Sbjct: 599 TINTAFTFPERSSSLTIGADTFSSGNEVYDRFELIQVTATFE 641

>sp|P56953|C1CB_BACTG PESTICIDIAL CRYSTAL PROTEIN CRY1CB (INSECTICIDAL DELTA-ENDOTOXIN

CRYIC(B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (133 KDA
CRYSTAL PROTEIN)
pir|A48970 insecticidal crystal toxin CryIC(b) - *Bacillus thuringiensis*
Length = 1176

Score = 495 bits (1275), Expect = e-139
Identities = 290/623 (46%), Positives = 362/623 (57%), Gaps = 34/623 (5%)

Query: 1 MENNIQNCVPYNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVAFLGF 59
MENNIQNCVPYNCL+NPE +L+ ER STG +DISLSL + L+S FVPG G GL
Sbjct: 1 MENNIQNCVPYNCLSNPEEILLDGERISTGNSSIDISLSLVQLLVSNFVPGGFLVGLL 60

Query: 60 DLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANP 119
D +WG + PS W FL+QIEQLI +RI R+ AI+ L GL +++ IY+EA +EWEA+P
Sbjct: 61 DFVWGVGPSPWDAFLVQIEQLINERIAAYARSAASINLEGLGNNFNIIYVEAFKEWADP 120

Query: 120 NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQG 179
+N R V RF D L I +F + FE+PLLSVY QAANLHL++LRD+ FG
Sbjct: 121 DNPVTRTRVDRFRILDGLLERDIPSFRIAGFEVPLLSVYAQAANLHLAILRDSSIFGAR 180

Query: 180 WGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNRQWARFNQFRRDLTLTVL 239
WGL VN +YNRLI I Y HC DTYN+GL NL + + W +N+ RRDLTTLTVL
Sbjct: 181 WGLTTINVNENYNRLIRHIDEYANHCADTYNRGLNNLPKSTYQDWITYNRLRRDLTLTVL 240

Query: 240 DIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSNIPN--GFNRAEF-GVRPPHL 296
DI A FP+YD R YPIQ+ QLTREIYT +I +P ++ FN E +R PHL
Sbjct: 241 DIAAFFPSYDNRRIPIQSVGQLTREIYTDPLITFNPQLQSVAPLPTFNVMESNAIRTPHL 300

Query: 297 MDFMNSLFVTAE--TVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPGGAIWIADDP- 353
D +N+L + + +V WGGH V S G I P YG E PR
Sbjct: 301 FDVLNLTIFTDWFVSGRNFYWGGRHVISNRIGGGNITSPIYG-----REANQEPPRS 353

Query: 354 -----PFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTN-HTRTRNSGTIDSLDEIP 407
P +RTLS+P F P LRGV + T ++ T+R GT+DSL E+P
Sbjct: 354 FTFNGPVFRTLNSPTFRPLQQPWPAPPFNLRGVEGVFSTPLNSFTYRGRGTVDLSLTEL 413

Query: 408 PQDMSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQI 467
P+DNS P YSH L H TFV+ G P+FSWTHRSAT N I P+ I QI
Sbjct: 414 PEDNSVPPREGYSHRLCHATFVQSRGT---PFLTTPGVFSWTHRSATDRNIIYPDVINQI 470

Query: 468 PLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 527
PLVKA L SGT+VVRGPGFTGGDI+R G +N + QRYR R+RYA++
Sbjct: 471 PLVKAENLTSGTSVVRGPGFTGGDIIRTNVNGSVLSMSLNFSTTLQRYRVRVRYAASQT 530

Query: 528 LRIYVTVAGERIFAGQFNKMTMDTGDPLTFQSFYATINTAFTFMSQSSFTVGADTFSSG 587
+ + VTV G F TM LT QSF +A FP+ S+ + S
Sbjct: 531 MVMSVTVGGSTTGNQGFSTMSANGALTSQSFRFA-----EFPVGISASGSQGASISIS 584

Query: 588 NEV-----YIDRFELIPVTATLE 605
N V ++DR E +PVT+T E
Sbjct: 585 NNVGRQMFHLDRIEFLPVTSTFE 607

>sp|Q03745|C1EB_BACTA Pesticidal crystal protein cryIEb (Insecticidal delta-endotoxin
CryIE(b)) (Crystalline entomocidal protoxin) (134 kDa
crystal protein)
gb|AAA22346.1| (M73253) cryIE(b) [*Bacillus thuringiensis*]
Length = 1174.

Score = 488 bits (1256), Expect = e-137
Identities = 288/619 (46%), Positives = 369/619 (59%), Gaps = 30/619 (4%)

Query: 1 MENNIQNCVPYNCLNNPEVEILNEERSTGRPLDISLSLTRFLLSEFVPGVGVAFLGFD 60
MENNI+QNC+PYNCLNNPEVEIL ERS + +I L L+R L+S +P GLFD
Sbjct: 1 MENNIENQCIPYNCLNNPEVEILGIERSNSNVAAEIGLGLSRLLVSR-IPLGDFILGLFD 59

Query: 61 LIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANP 120
+IWG I PS W +FL QIE LI QRIE RN+AI+ L+GL++ Y IY A + WE +P
Sbjct: 60 VIWGAIGPSQWDIFLEQIELLIGQRIEEFARNQAISRLQGLSNLYRIYTNAFKNWEVDPT 119

Query: 121 NAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW 180
N LRE++RI+F + + AL TAI F++ +EIPLLSVYVQAANLHLS+LRD FGQ W
Sbjct: 120 NPALREEMRIQFNDMNSALTTAIPLFSVQGYEIPLLSVYVQAANLHLSVLRDVSFVGQRW 179

Query: 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENL-RGTNTRQWARFNQFRRDLTLTVL 239
G D+AT+N+ YN L LI YT + + YN GL L R R WARFN+FRR+LT++VL
Sbjct: 180 GFDVATINSRYNDLTRLIGEYTDYAVRWYNTGLNRLPRNEGVRGWARFNRRFRRELTISVL 239

Query: 240 DIVALFPNYDVRTYPIQTSSQLTREIYTSVIE--DSPVSANIPNGFNRAEFGVRPPLHM 297
DI++ F NYD R YPI T QLTRE+YT VI D V+ + + N A +R PHLM
Sbjct: 240 DIISFFQNYDSRLYPIPTIYQLTREYVTDPVINITDYRVTPSFESIENSA---IRSPHLM 296

Query: 298 DFMNSLFVTAETVRSQTVWGGHLVSSRNTAGNR-INFPSYGV-FNPGGAIWIADP---DP 352
DF+N++ + + +R W GH V+S T ++ I+ P YG+ N + IA
Sbjct: 297 DFLNNIIDTDLIRGVHYWAGHRVTSHTFGSSQVVISSPQYGITANAEPSTRTIAPSTFPGL 356

Query: 353 RPFYRTLSDPVFVRGGFGNPHYVLG-LRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDN 411
FYRTLSDP F R P + ++GV F Q N +R GT+DSLDE+P
Sbjct: 357 NLFYRTLSDPFFRRSDNIMPTLGINVVQGVFIQP-NGEVLRYRRGTVDLSDELDPIDG 415

Query: 412 SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ YSH L+HVT R + ++ P F WTH SAT N I P+ ITQIPLVK
Sbjct: 416 NSLV--GYSHRLSHVTLTR---SLYNTNITSLPTFWTHHSATDRNIYPDVITQIPLVK 470

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIY 531
+ +L SGT+VVRGPGFTGGDI+R G +N + QRYR R+RYA++ + +
Sbjct: 471 SFSLTSGTSVVRGPGFTGGDIIRTNVNGNVLSMSLNFSNTSLQRYRVVRVRYAASQTMVMR 530

Query: 532 VTVAGERIFAGQFNKMTDGLPTFQSFYSATINTAFTFPMSSQ-----SFTVGADTFSS 586
V V G F F TM LT QSF +A + SQ+ S G TF
Sbjct: 531 VNVGGSTTFDQGFPTMSANGSLTSQSFRFAEFPVGISTSGSQTAGISISNNPGRQTF-- 588

Query: 587 GNEVYIDRFELIPVTATLE 605
++DR E IPV AT E
Sbjct: 589 ----HLDRIEFIPVDATFE 603

>gb|AAD55947.1| (AF177675) Cry 1Ac insecticidal toxin [synthetic construct]
Length = 587

Score = 482 bits (1240), Expect = e-135
Identities = 281/589 (47%), Positives = 351/589 (58%), Gaps = 18/589 (3%)

Query: 29 TGRPLDISLSLSTRFLLSEFVPGVGVAFLFDLIWGFITPSDWSLFLQIEQLIEQRIET 88
TG P+DISLSLT+FLSEFVPG G GL D+IWG PS W FL+QIEQLI QRIE
Sbjct: 5 TGYTPIDISLSLTQFLLEFVPGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEE 64

Query: 89 LERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTL 148
RN+AI+ L GL++ Y+IY E+ REWEA+P N LRE++RI+F + + AL TAI F +
Sbjct: 65 FARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV 124

Query: 149 TSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDT 208
+++PILLSVYVQAANLHLS+LRD FGQ WG D AT+N+ YN L LI YT + +
Sbjct: 125 QNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDYAVRW 184

Query: 209 YNQGLENLRGTNTRQWARFNQFRRDLTLTVLIDIVLFPNYDVRTYPIQTSSQLTREIYTS 268
YN GLE + G ++R W R+NQFRR+LTTLTVLIDIVLFPNYD R YPI+T SQLTREIYT+
Sbjct: 185 YNTGLERVWGPDSRDWVRYNQFRRDLTLTVLIDIVLFPNYDSRRYPIRTVSQLTREIYTN 244

Query: 269 SVIEDSPVSANIPNGFNRAEFGVRPPLHMDFMNSLFVTAETVRSQTVWGGH--LVSSRNT 326
V+E+ + E +R PHLMD +NS+ + + R W GH + S
Sbjct: 245 PVLEN--FDGSFRGSAQGIERSIRSPHLMDILNSITIYTDHARGYYSWGHQIMASPVGF 302

Query: 327 AGNRINFPSYGVF-NPGGAIWIADDPFRTLSDPVFVRG---GFGNPHY-VLGLRGV 381
+G FP YG N I + + YRTLS ++ R G N VL
Sbjct: 303 SGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQLSVLDGTEF 362

Query: 382 AFQQTGTNHTRTFRNSGTIDSLDEIPPQDN SGAPWNDYSHVLNHVTFVRWPGEISGSDSW 441
A+ + + +R SGT+DSLDEIPPQ+N+ P +SH L+HV+ R S
Sbjct: 363 AYGTSNLPASVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGSSNSSVSII 422

Query: 442 RAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVVRGPGFTGGDILRRTSGG-- 499
RAPMFSW HRSA N I + ITQIP VK + L +G +V+ GPGFTGGD++R S G
Sbjct: 423 RAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNN 481

Query: 500 --PFAYTIVNIN-GQLPQRYRARIRYASTTNLRIYVTVAGERIFAGQFNKMTDGDPLTF 556
Y V I+ RYR R+RYAS T + + V IF+ T + D L
Sbjct: 482 IQNRGYIEVPIHFPSTSTRYRVVRVYASVTPIHNLNVNWNSSIFSNTVPATATSLDNLQS 541

Query: 557 QSFSYATINTAFTFPMSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
F Y AFT S VG FS V IDRFE IPVTATLE
Sbjct: 542 SDFGYFESANAFT---SSLGNIVGVNFSGTAGVIIDRFEFIPVTATLE 587

>gb|AAK14338.1| (AF327926) insecticidal crystal protein BTRX27 [Bacillus thuringiensis serovar kunthalarX27]
Length = 1118

Score = 475 bits (1223), Expect = e-133
Identities = 278/598 (46%), Positives = 352/598 (58%), Gaps = 17/598 (2%)

Query: 19 EVEILNEERSTGRPLPLDISLSLTRFLLSEFVPGVGVAFLGLFDLIWGFITPSDWSLFLQI 78
E + E TG P+DISLSLT+FLLESEFVG G GL D+IWG PS W FL QI
Sbjct: 19 EEKYCGERIETGYTPIDISLSLTQFLLSEFVPGAGFELGLVDIIWGFIPGPSQWDAFLGQI 78

Query: 79 EQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDA 138
EQLI QRIE RN+AI+ L GL++ Y+IY E+ REWEA+P N LRE++RI+F + + A
Sbjct: 79 EQLINQRIEEFARNQAISRLEGLSNLYQIYPESFREWEADPTNPALREEMRIQFNDMNSA 138

Query: 139 LITAINNFTLTSFEIPLLSVYVQAAANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLI 198
L TAI F + ++++PLLSVYVQAA + +S R + + H+ L LI
Sbjct: 139 LTTAIPLEFAVQNYQVPLLSVYVQAAAMVCVSGGRFGGPRALSSRFNALNRIHWTTLRLI 198

Query: 199 HRYTKHCLDTYNQGLENLRGTNTRQWARFNQFRDLTLTVLIDIVLFPNYDVRTYPIQTS 258
T H YN GL + G ++R W R+NQFRRLTLTLTVLDIV+LFPNYD RTYPI+T
Sbjct: 199 GNCTDHPGYWYNTGLGRVWGRDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTV 258

Query: 259 SQLTREIYTSSVIEDSPVSANIPNGFNRAEFGV----RPPHLMDFMNSLFVTAETVRSQT 314
SQLT EIYT+ V+E N F + G+ R PHLMD +NS+ + + R +
Sbjct: 259 SQLTEEIYTNPVL-----NFDGSFRGSARGIEGRFRSPHLMDILNSITIYTDHRGEY 312

Query: 315 VWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADEDPRPFYRTLSDPVFVRG---G 368
W GH + SS +G FP YG N I + + YRTLS ++ R G
Sbjct: 313 YWSGHQIMASSVGFSGFEFTFPLYGTGLGNAAPQPPIGAQTGGQVYRTLSSSTLYRRPFYIG 372

Query: 369 FGNPHY-VLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNGAPWNDYSHVLNHVT 427
N H VLG A+ + + +R GT+DSLDEIP Q+ + P +SH L+HV+
Sbjct: 373 INNQHLSVLGGVEFAYGTSSYLPSAVYRKRGTVDLSLDEIPHQNTTVKPRQGFSHRLSHVS 432

Query: 428 FVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVVRGPGF 487
R S RAPMFSW RSA N I +ITQIPL K+ L SGT+VV+GPGF
Sbjct: 433 MFRSGFSNSSVSIIRAPMFSWILRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGF 492

Query: 488 TGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYASTTNLRIYVTVAGERIFAGQFNKT 547
TGGDILRRTS G + VNI L QRYR RIRYASTTNL+ + ++ G I G ++ T
Sbjct: 493 TGGDILRRTSPGQISTLRVNITAPLSQRYRVIRYASTTNLQFHTSIDGRPINQGIYSAT 552

Query: 548 MDTGDPLTFQSFSYATINTAFTFPMSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
M +G L +F T F F S FT+ A F+SGNEVYIDR E +P T E
Sbjct: 553 MSSGSNLQSGTFRFTVGFTTPFNFSNGSSVFTLSAHVNSGNEVYIDRIEFVPAEVTFE 610

>sp|Q45709|C1IB_BACTE Pesticidal crystal protein cryIIb (Insecticidal delta-endotoxin CryII(b)) (Crystalline entomocidal protoxin) (81 kDa crystal protein)
pir||I40590 cryV465 protein - Bacillus thuringiensis
gb|AAA82114.1| (U07642) cryV465 gene product [Bacillus thuringiensis]
Length = 719

Score = 418 bits (1074), Expect = e-115
Identities = 249/595 (41%), Positives = 330/595 (54%), Gaps = 60/595 (10%)

Query: 49 VPGVGVAFLGLFDLIWGFITP---SDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSY 105
VP G L+ I G + P S W +F+ +E++I Q+I T RN+A++ LRGL D+
Sbjct: 76 VPFAGQIASLYSFLIGELWPKGKSQWEIFMEHVEEIIQKILTYARNKALSRLGLGDAL 135

Query: 106 EIIYIEALREWEANPNNAQLREDVIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANL 165
+Y E+L W N NN + R V+ ++ + + +F ++ E+PLL +Y QAANL
Sbjct: 136 AVYHESLESWVENRNNTRARSVVKQYIAELMFVQKLPFAVSGEEVPLLPIYAQAANL 195

Query: 166 HLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWA 225
HL LLRDA FG+ WGL + ++ YNR + Y+ HC+ YN GL NLRGTN + W
Sbjct: 196 HLLLLRDASIFGKEWGLSASEISTFYNRQVERTRDYSCHCKWYNTGLNNLRGTNAKSWV 255

Query: 226 RFNQFRDLTLTLVLDIVLFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSA----- 278
R+NQFR+D+TL VLD+VALFP+YD YPI+T+SQLTRE+YT ++ P A
Sbjct: 256 RYNQFRKMDTLVLDLVALFPSYDTLVYPIKTTSQLTREYVTDAGTVHPNQFAFASTTWY 315

Query: 279 -NIPNGFNRAEFGV-RPPHLMDFMN-----SLFVTAETVRSQTVWGGHLVSSRNTAGNRI 331
N F+ E V R PHL+DF+ SL + +WGGH + SR G +
Sbjct: 316 NNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMMNWGGHRLSR-PIGGAL 374

Query: 332 NFPSYGVFNPGGAIWIADDPFPFYRT-----LSDPV--FVRGGF-----G 370
N + G N R YRT L+ PV R F
Sbjct: 375 NTSTQGSTNTSINPVTLQFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFPPTLPIAS 434

Query: 371 NPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNGSAPWNDYSHVLNHVTFVR 430
+ Y LG GV Q DS +E+PP+ + YSH L+H+
Sbjct: 435 DNFFYLLGYAGVGTQLQ-----DSENELPPETTGQPNYESYSHRLSHI---- 476

Query: 431 WPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGG 490
G IS S +A ++SWTHRSA TNTI+P ITQIPLVKA L SG VVRGPGFTGG
Sbjct: 477 --GLISASHV-KALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGG 533

Query: 491 DILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTMDT 550
DILRRT+ G F VNIN QRYR RIRYASTT+L+ ++ G+ I G F+ TM+
Sbjct: 534 DILRRTNTGTFTGDIRVNINPFAQRYRVIRYASTTDLQFHTSINGKAINQGNFSATMNR 593

Query: 551 GDPLTFQSFYSATINTAFTFPMSSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
G+ L +++F T F+F QS+FT+GA FSSGNEVYIDR E +PV T E
Sbjct: 594 GEDLDYKTFRTIGFTTTPFSFSDVQSTFTIGAWNFFSSGNEVYIDRIEFVPEVETYE 648

>gb|AAK66742.1|AF373207_1 (AF373207) CryIIa [Bacillus thuringiensis]
Length = 719

Score = 416 bits (1068), Expect = e-115
Identities = 253/633 (39%), Positives = 350/633 (54%), Gaps = 42/633 (6%)

Query: 2 ENNIQNCQVPY-NCLNNPEVEILNEERSTGRPLDISLSLTRFLLSEFVPGVGVAFLGLFD 60
E +I+ Q + + +CL E E + S + I ++ + L + VP G L+
Sbjct: 29 ETDIELQNINHEDCLKMSEYENVEFPVSASTIQTGIGIA-GKILGTLGVFPFAGQVASLYS 87

Query: 61 LIWGFITP---SDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEA 117
I G + P + W +F+ +E++I Q+I T RN+A+T L+GL D+ +Y ++L W
Sbjct: 88 FILGELWPKGKNQWEIFMEHVEEIIQKISTYARNKALTDLKGGLDALAVYHDSLESWVG 147

Query: 118 NPNNALREDVIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFG 177
N NN + R V+ ++ + + +F ++ E+PLL +Y QAANLHLLRDA FG
Sbjct: 148 NNNTRARSVVKSQYIAELMFVQKLPFAVSGEEVPLLPIYAQAANLHLLLLRDASIFG 207

Query: 178 QGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRDLTLT 237
+ WGL + ++ YNR + Y+ HC+ Y+ GL NLRGTN W R+NQFRD+TL
Sbjct: 208 KEWGLSSSEISTFYNRQVERAGDYSCHCKWYSTGLNNLRGTNAESWVRYNQFRDMDTLM 267

Query: 238 VLDIVLFPNYDVRTYPIQTSSQLTREIYTSSVIEDSP-----VSANIPNGFNRAE 288
VLD+VALFP+YD + YPI+T++QLTRE+YT ++ P + N P+ F+ E
Sbjct: 268 VLDLVALFPSYDTQMPIKTTAQLTREYVTDAGTVHPHPSFTSTTWYNNNAPS-FSAIE 326

Query: 289 FG-VRPPHLMDFMN-----SLFVTAETVRSQTVWGGHLVSSRNTAGNRIINFPYGVFNPG 342
VR PHL+DF+ SL + +WGGH + R T G +N + G N

Sbjct: 327 AAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNWGGHKLEFR-TIGGTLNISTQGSTNTS 385

Query: 343 GAIWIADEDPFPFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRN----- 396
R YRT S H V G+ V F H N

Sbjct: 386 INPVTLPFTSRDVYRTES---LAGLNLFLTHPVNGVPRVDFHWKFVTHPIASDNFYYPGY 442

Query: 397 ----SGTIDSLDEIPPQDMSGAPWNDYSHVLNHVTFVRWPGGEISGSDSWRAPMFSWTHRS 452
+ DS +E+PP+ + YSH L+H+ G IS S +A ++SWTHRS

Sbjct: 443 AGIGTQLQDSENELPPEATGQPNYESYSHRLSHI-----GLISASHV-KALVYSWTHRS 495

Query: 453 ATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQL 512
A TNTI+P ITQIPLVKA L SG VVRGPGFTGGDILRRT+ G F VNIN

Sbjct: 496 ADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTNTGTFGDIRVNINPPF 555

Query: 513 PQRYRARIRYASTTNLRIYVTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTFPM 572
QRYR RIRYASTT+L+ + ++ G+ I G F+ TM+ G+ L +++F T F+F

Sbjct: 556 AQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYKTFRTVGTTPFSFLD 615

Query: 573 SQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
QS+FT+GA FSSGNEVYIDR E +PV T E

Sbjct: 616 VQSTFTIGAWNFSGNEVYIDRIEFVPEVITYE 648

>sp|Q45739|C1BB_BACTU PESTICIDIAL CRYSTAL PROTEIN CRY1BB (INSECTICIDAL DELTA-ENDOTOXIN
CRY1B(B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (140 KDA
CRYSTAL PROTEIN)
gb|AAA22344.1| (L32020) crystal protein [Bacillus thuringiensis]
Length = 1229

Score = 415 bits (1067), Expect = e-115
Identities = 255/595 (42%), Positives = 332/595 (54%), Gaps = 59/595 (9%)

Query: 49 VPGVGVAFLGLFDLIWGFITPSD---WSLFLQIEQLIEQRIETLERNRAITTLRGLADSY 105
VP G + + G + PS W +FL +EQLI Q++ RN AI L GL Y

Sbjct: 72 VPFAGQLASFYSFLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTRNTAIARLEGLGRGY 131

Query: 106 EIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANL 165
Y +AL W N N+A+ R + R+ + + TAI F + + E+PLL VY QAANL

Sbjct: 132 RSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPLFRIRNEEVPLLMVYAQAANL 191

Query: 166 HLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWA 225
HL LLRDA FG WG+ + VN +Y I Y+ HC+ YN GL NLRGTN W

Sbjct: 192 HLLLLRDASLFGSEWGMASDVNQYYQEIRYTEEYSNHCQWYNTGLNNLRGTNAESWL 251

Query: 226 RFNQFRDLTLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGF- 284
R+NQFRDLTL VLD+VALFP+YD RTYPI TS+QLTREIYT D N P+GF

Sbjct: 252 RYNQFRDLTLGLVLDLVALFPSYDTRTYPINTSAQLTREIYT-----DPIGRTNAPSGFA 306

Query: 285 -----NRAEFGV-----RPPHLMDFMNSLFVTAETVR-----SQTWVGHLVSSRNT 326
N F RPPHL+DF L + + + R W GH ++ R

Sbjct: 307 STNWFNNNAPSFSIAEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMYVVGHRLNFR-P 365

Query: 327 AGNRINFPSYGVFNPGGAIWIADE-DPRPFYRTLSD-----PV----FVRGGFGNP 372
G +N + G+ N + + R YRT S+ PV + R F NP

Sbjct: 366 IGGTLNTSTQGLTNNTSINPVTLQFTSRDVYRTESNAGTNILFTTPVNGVPWARFNFINP 425

Query: 373 HYVLGLRGVAFQQTGTNHTRTFRNSG--TIDSLDEIPPQDMSGAPWNDYSHVLNHVTFVR 430
+ +++ T +++ ++ G DS E+PP+ + YSH L+H+

Sbjct: 426 QNI-----YERGATTYSQPYQGVGIQLFDSETELPPETTERPNYESYSHRLSHI---- 474

Query: 431 WPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGG 490
G I G ++ RAP++SWTHRSA TNTI P RITQIPLVKA L SG TVV GPGFTGG

Sbjct: 475 --GLIIG-NTLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGGPGFTGG 531

Query: 491 DILRRTSGGPFAYTIVNINGQLPQRYRARIRYASTTNLRIYVTVAGERIFAGQFNKMTD 550
DILRRT+ G F +NIN L QRYR RIRYASTT+L+ + + G + G F++TM+

Sbjct: 532 DILRRTNTGTFGDIRLNINVPLSQRYRVRIRYASTTDLQFFTRINGTTVNIGNFSRTMNR 591

Query: 551 GDPLTFQSFSYATINTAFTFPMSSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
GD L ++SF A +T F F +QS+FT+GA +FS+ EVYIDR E +P T E

Sbjct: 592 GDNLEYRSFRTAGFSTPFNFLNAQSTFTLGAQSFSN-QEVYIDRVEFVPAEVTFE 645

>emb|CAA70124.1| (Y08920) Bt toxin [Bacillus thuringiensis]
Length = 719

Score = 415 bits (1067), Expect = e-115
Identities = 255/635 (40%), Positives = 353/635 (55%), Gaps = 46/635 (7%)

Query: 2 ENNIQNQCVPY-NCLNNPEVEILNEERSTGRPLDISLSLRFLLSEFVPGVGVAFLGFD 60
E +I+ Q + + +CL E E + S + I ++ + L + VP G L+
Sbjct: 29 ETDIELQNINHEDCLKMSEYENVEPFVSASTIQTGIGIA-GKILGTLGVFPFAGQVASLYS 87

Query: 61 LIWGFITP---SDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEA 117
I G + P + W +F+ +E++I Q+I T RN+A+T L+GL D+ +Y ++L W
Sbjct: 88 FILGELWPKGKNQWEIFMEHVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLESWVG 147

Query: 118 NPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFG 177
N NN + R VR ++ + + +F ++ E+PLL +Y QAANLHL LLRDA FG
Sbjct: 148 NRRNTRRSVVRSQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLRDASIFG 207

Query: 178 QGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNRQWARFNQFRRDLTLT 237
+ WGL + ++ YNR + Y+ HC+ Y+ GL NLRGTN W R+NQFRRD+TL
Sbjct: 208 KEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMLM 267

Query: 238 VLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSP-----VSANIPNGFNRAE 288
VLD+VALFP+YD + YPI+T++QLTRE+YT ++ P + N P+ F+ E
Sbjct: 268 VLDLVALFPSYDTQMPYIKTTAQLTREVTDAIGTVHPPHPSFTSTTWYNNNAPS-FSAIE 326

Query: 289 FG-VRPPHLMDFMN-----SLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPG 342
VR PHL+DF+ SL + +WGGH + R T G +N + G N
Sbjct: 327 AAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMWGGHKLEFR-TIGGTNLNISTQGSTNTS 385

Query: 343 GAIWIADEDPRPFYRT-----LSDPVFVRGGFNGPHYVLGLRGVAFQQTGTN-HTR 392
R YRT L+ PV G P + V N +
Sbjct: 386 INPVTLPFTSRDVRTESLAGLNLFLTQPV-----NGVPRVDFHWKFVTHPIASDNFYYP 440

Query: 393 TFRNSGT--IDSLDEIPPQDMSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTH 450
+ GT DS +E+PP+ + YSH L+H+ G IS S +A ++SWTH
Sbjct: 441 GYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHI-----GLISASHV-KALVYSWTH 493

Query: 451 RSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNING 510
RSA TNTI+P ITQIPLVKA L SG VVRGPGFTGGDILRRT+ G F VNIN
Sbjct: 494 RSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTFGDIRVNINP 553

Query: 511 QLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTF 570
QRYR RIRYAST+L+ + ++ G+ I G F+ TM+ G+ L +++F T F+F
Sbjct: 554 PFAQRYRVRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGFTTTPFSF 613

Query: 571 PMSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
QS+FT+GA FSSGNEVYIDR E +PV T E
Sbjct: 614 LDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVETYE 648

>sp|Q45774|C1BC_BACTM PESTICIDIAL CRYSTAL PROTEIN CRY1BC (INSECTICIDAL DELTA-ENDOTOXIN
CRY1B(C)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (140 KDA
CRYSTAL PROTEIN)
emb|CAA86568.1| (Z46442) delta-endotoxin [Bacillus thuringiensis]
Length = 1233

Score = 415 bits (1067), Expect = e-115
Identities = 255/595 (42%), Positives = 332/595 (54%), Gaps = 59/595 (9%)

Query: 49 VPGVGVAFLGFDLIWGFITPSD---WSLFLQLIEQLIEQRIETLERNRAITTLRGLADSY 105
VP G + + G + PS W +FL +EQLI Q++ RN AI L GL Y
Sbjct: 72 VPFAGQLASFYSFLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTRNTAIARLEGLGRGY 131

Query: 106 EIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANL 165
Y +AL W N N+A+ R + R+ + + TAI F + + E+PLL VY QAANL
Sbjct: 132 RSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPLFRIRNEEVPLLMVYAQAANL 191

Query: 166 HLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWA 225
HL LLRDA FG WG+ + VN +Y I Y+ HC+ YN GL NLRGTN W
Sbjct: 192 HLLLLRDASLFGSEWGMASDVNQYYQEIRYTEEYSNHCQWYNTGLNNLRGTNAESWL 251

Query: 226 RFNQFRDLTLTVLIDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGF- 284
R+NQFRDLTL VLD+VALFP+YD RTYPI TS+QLTREIYT D N P+GF
Sbjct: 252 RYNQFRDLTLGLVLDLVALFPSYDTRTYPIINTSAQLTREIYT-----DPIGRTNAPSGFA 306

Query: 285 -----NRAEFGV-----RPPHLMDFMNSLFVTAETVR-----SQTWGGHLVSSRNT 326
N F RPPHL+DF L + + + R W GH ++ R
Sbjct: 307 STNWFNNNAPSFSIAEAAIFRPPHLLDFEQLTIIYSASSRWSSTQHMMNYWVGHLNFR-P 365

Query: 327 AGNRINFPYSYGVFNPGGAIWIAD-DRPPFYRTLSD-----PV-----FVRGGFGNP 372
G +N + G+ N + + R YRT S+ PV + R F NP
Sbjct: 366 IGGTLNTSTQGLTNNTSINPVTLOFTSRDVYRTESNAGTNILFTTPVNGVPWARFNFINP 425

Query: 373 HYVLGLRGVAFQQTGTNHTRTFRNSG--TIDSLDEIPPQDNSGAPWNDYSHVLNHVTFVR 430
+ +++ T +++ ++ G DS E+PP+ + YSH L+H+
Sbjct: 426 QNI-----YERGATTYSQPYQGVGQLFDSETELPPEPPERPNYESYSHRLSHI---- 474

Query: 431 WPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVVRGPGFTGG 490
G I G ++ RAP++SWTHRSA TNTI P RITQIPLVKA L SG TVV GPGFTGG
Sbjct: 475 --GLIIG-NTLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGGPGFTGG 531

Query: 491 DILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKTMdT 550
DILRRT+ G F +NIN L QRYR RIRYASTT+L+ + + G + G F++TM+
Sbjct: 532 DILRRTNTGTFGDIRLNLINPLSQRYRVIRYASTTDLQFFTRINGTTVNIGNFSRTMNR 591

Query: 551 GDPLTFQSFSYATINTAFTFPMSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
GD L ++SF A +T F F +QS+FT+GA +FS+ EVYIDR E +P T E
Sbjct: 592 GDNLEYRSFRTAGFSTPFNFNAQSTFTLGAQSFSN-QEVYIDRVEFVPAEVTFE 645

>sp|Q45752|C1IA_BACTK Pesticidial crystal protein cryIIa (Insecticidal delta-endotoxin
CryII(a)) (Crystalline entomocidal protoxin) (81 kDa
crystal protein)
pir||I39815 insecticidal protein cryV - Bacillus thuringiensis
gb|AAA22354.1| (M98544) insecticidal protein [Bacillus thuringiensis]
Length = 719

Score = 414 bits (1064), Expect = e-114
Identities = 254/635 (40%), Positives = 353/635 (55%), Gaps = 46/635 (7%)

Query: 2 ENNIQNCVPPY-NCLNNPEVEILNEERSTGRPLDISLSLTRLSEFVPGVGVAFLGFD 60
E +I+ Q + + +CL E E + S + I ++ + L + VP G L+
Sbjct: 29 ETDIELQNINHEDCLKMEYENVEPFVASTIQTGIGIA-GKILGTLGVFPAGQVASLYS 87

Query: 61 LIWGFITP---SDWSLFLQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEA 117
I G + P K + W +F+ +E+I I Q+I T RN+A+T L+GL D+ +Y ++L W
Sbjct: 88 FILGELWPKGKNQWEIFMEHVVEIINQKISTYARNKALTDLKLGDALAVYHDSLESWVG 147

Query: 118 NPNNALREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFG 177
N NN + R V+ ++ + + +F ++ E+PLL +Y QAANLHL LLRDA FG
Sbjct: 148 NRNNTRARSVVKSQYIAELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLRDASIFG 207

Query: 178 QGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRDLTLT 237
+ WGL + ++ YNR + Y+ HC+ Y+ GL NLRGTN W R+NQFRRD+TL
Sbjct: 208 KEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRYNQFRDMLTLM 267

Query: 238 VLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSP-----VSANIPNGFNRAE 288
VLD+VALFP+YD + YPI+T++QLTRE+YT ++ P + N P+ F+ E
Sbjct: 268 VLDLVALFPSYDTQMYPIKTTAQLTREVYTDAGTVHHPSEFTSTTWYNNNAPS-FSAIE 326

Query: 289 FG-VRPPHLMDFMN-----SLEFVTAETVRSQTWGGHLVSSRNTAGNRINFPYSYGVFNPG 342
VR PHL+DF+ SL + +WGGH + R T G +N + G N
Sbjct: 327 AAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNWGGHKLFR-TIGGTLNISTQGSTNTS 385

Query: 343 GAIWIAD-DRPPFYRT-----LSDPVFVRGGFGNPHYVLGLRGVAFQQTGTN-HTR 392
R YRT L+ PV G P + V N +
Sbjct: 386 INPVTLPFTSRDVYRTESLAGLNLFLTPQV-----NGVPRVDFHWKFVTHPIASDNFYYP 440

Query: 393 TFRNSGT--IDSLDEIPPQDMSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTH 450
+ GT DS +E+PP+ + YSH L+H+ G IS S +A ++SWTH
Sbjct: 441 GYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHI-----GLISASHV-KALVYSWTH 493

Query: 451 RSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNING 510
RSA TNTI+P ITQIPLVKA L SG VVRGPGFTGGDILRRT+ G F VNIN
Sbjct: 494 RSADRTNTIEPNSITQIPLVKAFLNLSSGAAVVRGPGFTGGDILRRTNTGTFGDIRVNINP 553

Query: 511 QLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTF 570
QRYR RIRYASTT+L+ + ++ G+ I G F+ TM+ G+ L +++F T F+F
Sbjct: 554 PFAQRYRVRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGFTTFFSF 613

Query: 571 PMSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
QS+FT+GA FSSGNEVYIDR E +PV T E
Sbjct: 614 LDVQSTFTTIGAWNFFSSGNEVYIDRIEFVPEVETYE 648

>pir||S25383 parasporal crystal protein cryV - Bacillus thuringiensis
emb|CAA44633.1| (X62821) delta-endotoxin [Bacillus thuringiensis]
Length = 719

Score = 414 bits (1063), Expect = e-114
Identities = 254/635 (40%), Positives = 353/635 (55%), Gaps = 46/635 (7%)

Query: 2 ENNIQNCQVPY-NCLNNPEVEILNEERSTGRPLPLDISLSLTRFLLSEFVPGVGVAFLFD 60
E +I+ Q + + +CL E E + S + I ++ + L + VP G L+
Sbjct: 29 ETDIELQINIHEDCLKMSEYENVEPFVSASTIQTGIGIA-GKILGTGLVPPFAGQVASLYS 87

Query: 61 LIWGFITP---SDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSIEIYIEALREWEA 117
I G + P + W +F+ +E++I Q+I T RN+A+T L+GL D+ +Y ++L W
Sbjct: 88 FILGELWPKGKNQWEIFMEHVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLESWVG 147

Query: 118 NPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFG 177
N NN + R V+ ++ + + + +F ++ E+PLL +Y QAANLHL LLRDA FG
Sbjct: 148 NNRNTRARSVVKSQYIALELMFVQKLPSFAVSGEVPLLPIYAQAANLHLLLLLRDASIFG 207

Query: 178 QGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRDLTLT 237
+ WGL + ++ YNR + Y+ HC+ Y+ GL NLRGTN W R+NQFRRD+TL
Sbjct: 208 KEWGLSSSEISTFYNRQVERAGDYSYHCWKWYSTGLNNLRGTNAESWVRYNQFRDMLTLM 267

Query: 238 VLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSP-----VSANIPNGFNRAE 288
VLD+VALFP+YD + YPI+T++QLTRE+YT ++ P + N P+ F+ E
Sbjct: 268 VLDLVALFPYSYDTQMYPIKTTAQLTREYVTDAGTVHPPHPSFTSTTWYNNNAPS-FSAIE 326

Query: 289 FG-VRPPHLMDFMN-----SLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPG 342
VR PHL+DF+ SL + +WGGH + R T G +N + G N
Sbjct: 327 AAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLEFR-TIGGTNLNSTQGSTNTS 385

Query: 343 GAIWIADEDPRPFYRT-----LSDPVFVRGGFGNPHYVLGLRGVAFQQTGTN-HTR 392
R YRT L+ PV G P + V N +
Sbjct: 386 INPVTLPFTSRDVRTERSLAGLNLFLTQPV-----NGVPRVDFHWKFVTHPIASDNFYYP 440

Query: 393 TFRNSGT--IDSLDEIPPQDMSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTH 450
+ GT DS +E+PP+ + YSH L+H+ G IS S +A ++SWTH
Sbjct: 441 GYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHI-----GLISASHV-KALVYSWTH 493

Query: 451 RSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNING 510
RSA TNTI+P ITQIPLVKA L SG VVRGPGFTGGDILRRT+ G F VNIN
Sbjct: 494 RSADRTNTIEPNSITQIPLVKAFLNLSSGAAVVRGPGFTGGDILRRTNTGTFGDIRVNINP 553

Query: 511 QLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTF 570
QRYR RIRYASTT+L+ + ++ G+ I G F+ TM+ G+ L +++F T F+F
Sbjct: 554 PFAQRYRVRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGFTTFFSF 613

Query: 571 PMSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
QS+FT+GA FSSGNEVYIDR E +PV T E
Sbjct: 614 LDVQSTFTTIGAWNFFSSGNEVYIDRIEFVPEVETYE 648

>pir||I39814 insecticidal protein cryV1 - Bacillus thuringiensis

gb|AAC36999.1| (L36338) insecticidal protein [Bacillus thuringiensis]
Length = 719

Score = 414 bits (1063), Expect = e-114
Identities = 254/635 (40%), Positives = 353/635 (55%), Gaps = 46/635 (7%)

Query: 2 ENNIQNCVVPY-NCLNNPEVEILNEERSTGRPLDISLSLTRLSEFVPGVGVAFLGFD 60
E +I+ Q + + +CL E E + S + I ++ + L + VP G L+
Sbjct: 29 ETDIELQNINHEDECKMSEYENVEPFVSASTIQTGIGIA-GKILGTLGVFPAGQVASLYS 87

Query: 61 LIWGFITP---SDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEA 117
I G + P + W +F+ +E++I Q+I T RN+A+T L+GL D+ +Y ++L W
Sbjct: 88 FILGELWPKGKNQWEIFMEHVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLESWVG 147

Query: 118 NPNNAQLREDVRIRFANTDDALITAINNFTLSFEIPLLSVYVQAANLHLSLLRDAVSFG 177
N NN + R V+ ++ + + +F ++ E+PLL +Y QAANLHL LLRDA FG
Sbjct: 148 NRNNTRARSVKSQYIALELMFVQKLPFAVSGEEVPLPIYAQAANLHLLLRDASIFG 207

Query: 178 QGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLT 237
+ WGL + ++ YNR + Y+ HC+ Y+ GL NLRGTN W R+NQFRD+TL
Sbjct: 208 KEWGLSSSEISTFYNRQVERAGDYSYHCWKYSTGLNNLRGTNAESWVRYNQFRDMLTLM 267

Query: 238 VLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSP-----VSANIPNGFNRAE 288
VLD+VALFP+YD + YPI+T++QLTRE+YT ++ P + N P+ F+ E
Sbjct: 268 VLDLVALFPSTYDQMYPIKTTAQLTREYITDAIGTVHPHPSETSTTWYNNNAPS-FSAIE 326

Query: 289 FG-VRPPLHLMDFMN-----SLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPG 342
VR PHL+DF+ SL + +WGGH + R T G +N + G N
Sbjct: 327 AAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNWGGHLEFR-TIGGTNLNSTQGSTNTS 385

Query: 343 GAIWIADDEPRPFYRT-----LSDPVFVRGGFGNPHYVLGLRGVAFQQTGTN-HTR 392
R YRT L+ PV G P + V N +
Sbjct: 386 INPVTLPFTSRDVRTESLAGLNLFLTPQV-----NGVPRVDFHWKFVTHPIASDNFYYP 440

Query: 393 TFRNSGT--IDSLDEIPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTH 450
+ GT DS +E+PP+ + YSH L+H+ G IS S +A ++SWTH
Sbjct: 441 GYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHI-----GLISASHV-KALVYSWTH 493

Query: 451 RSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNING 510
RSA TNTI+P ITQIPLVKA L SG VVRGPGFTGGDILRRT+ G F VNIN
Sbjct: 494 RSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTNTGTFGDIRVNINP 553

Query: 511 QLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTMDTGDPLTFQSFYATINTAFTF 570
QRYR RIRYASTT+L+ + ++ G+ I G F+ TM+ G+ L ++F T F+F
Sbjct: 554 PFAQRYRVRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGTTPFSE 613

Query: 571 PMSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
QS+FT+GA FSSGNEVYIDR E +PV T E
Sbjct: 614 LDVQSTFTIGAWNFSSGNEVYIDRIEFPVEVTE 648

>gb|AAB00958.1| (L49391) CGCryV gene product [Bacillus thuringiensis]
Length = 719

Score = 414 bits (1063), Expect = e-114
Identities = 253/633 (39%), Positives = 351/633 (54%), Gaps = 42/633 (6%)

Query: 2 ENNIQNCVVPY-NCLNNPEVEILNEERSTGRPLDISLSLTRLSEFVPGVGVAFLGFD 60
E +I+ Q + + +CL E E + S + I ++ + L + VP G L+
Sbjct: 29 ETDIELQNINHEDECKMSEYENVEPFVSASTIQTGIGIA-GKILGTLGVFPAGQVASLYS 87

Query: 61 LIWGFITP---SDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEA 117
I G + P + W +F+ +E++I Q+I T RN+A+T L+GL D+ +Y ++L W
Sbjct: 88 FILGELWPKGKNQWEIFMEHVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLESWVG 147

Query: 118 NPNNAQLREDVRIRFANTDDALITAINNFTLSFEIPLLSVYVQAANLHLSLLRDAVSFG 177
N NN + R V+ ++ + + +F ++ E+PLL +Y QAANLHL LLRDA FG
Sbjct: 148 NRNNTRARSVKSQYIALELMFVQKLPFAVSGEEVPLPIYAQAANLHLLLRDASIFG 207

Query: 178 QGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLT 237

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+ WGL + ++ YNR +      Y+ HC+ Y+ GL NLRGTN W R+NQFRRD+TL
Sbjct: 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWVRYNQFRRDMLM 267

Query: 238 VLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSP-----VSANIPNGFNRAE 288
VLD+VALFP+YD + YPI+T++QLTRE+YT ++ P + N P+ F+ E
Sbjct: 268 VLDLVALFPSYDTQMYPIKTTAQLTREYVYTDAGTVHPPHPSFTSTTWYNNNAPS-FSAIE 326

Query: 289 FG-VRPPHLMDFMN-----SLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPG 342
VR PHL+DF+ SL + +WGGH + R T G +N + G N
Sbjct: 327 AAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWGGHKLFR-TIGGTNLNSTQGSTNTS 385

Query: 343 GAIWIADEDPRPFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTNH---TRTFRNSGT 399
R YRT S V G+ V F H + F G
Sbjct: 386 INPVTLPFTSRDVRYES---LAGLNLFLTQPVNGVPRVDFHWKFVTHPIASDNFYYPGY 442

Query: 400 I-----DSLDEIPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRS 452
+ DS +E+PP+ + YSH L+H+ G IS S +A ++SWTHRS
Sbjct: 443 VGIGTQLQDSENELPPEATGQPNYESYSHRLSHI-----GLISASHV-KALVYSWTHRS 495

Query: 453 ATPNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQL 512
A TNTI+P ITQIPLVKA L SG VVRGPGFTGGDILRRT+ G F VNIN
Sbjct: 496 ADRNTTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTNTGTFGDIRVNINPPF 555

Query: 513 PQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTDGDPLTFQSFSYATINTAFTFPM 572
QRYR RIRYASTT+L+ + ++ G+ I G F+ TM+ G+ L +++F T F+F
Sbjct: 556 AQRYRVRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGFPTTFFSFLD 615

Query: 573 SQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
QS+FT+GA FSSGNEVYIDR E +PV T E
Sbjct: 616 VQSTFTIGAWNFSGNEVYIDRIEFPVEVITYE 648

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>gb|AAC26910.1| (AF076953) insecticidal protein [Bacillus thuringiensis serovar kurstaki]
Length = 719

Score = 412 bits (1058), Expect = e-114
Identities = 253/635 (39%), Positives = 352/635 (54%), Gaps = 46/635 (7%)

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Query: 2 ENNIQNCQVPY-NCLNNPEVEILNEERSTGRPLDISLSLTRFLLSEFVPGVGVAFLFD 60
E +I+ Q + + +CL E E + S + I ++ + L + VP G L+
Sbjct: 29 ETDIELQINIHEDCLKMSEYENVEPFVSASTIQTGIGIA-GKILGTGVPFAGQVASLYS 87

Query: 61 LIWGFIPT---SDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSIEIYIEALREWEA 117
I G + P + W +F+ +E++I Q+I T RN+A+T L+GL D+ +Y ++L W
Sbjct: 88 FILGELWPKGKNQWEIFMEHVEEIIQKISTYARNKALTDLKGGLDALAVYHDSLESWVG 147

Query: 118 NPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFG 177
N NN + R V+ ++ + + + +F ++ E+PLL +Y QAANLHL LLRDA FG
Sbjct: 148 NNNTRARSVVKSQYIAELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLRDASIFG 207

Query: 178 QGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRDLTLT 237
+ WGL + ++ YNR + Y+ HC+ Y+ GL NLRGTN W R+NQFRRD+TL
Sbjct: 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWVRYNQFRRDMLM 267

Query: 238 VLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSP-----VSANIPNGFNRAE 288
VLD+VALFP+YD + YPI+T++QLTRE+YT ++ P + N P+ F+ E
Sbjct: 268 VLDLVALFPSYDTQMYPIKTTAQLTREYVYTDAGTVHPPHPSFTSTTWYNNNAPS-FSAIE 326

Query: 289 FG-VRPPHLMDFMN-----SLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPG 342
VR PHL+DF+ SL + +WGGH + R T G +N + G N
Sbjct: 327 AAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNWGGHKLFR-TIGGTNLNSTQGSTNTS 385

Query: 343 GAIWIADEDPRPFYRT-----LSDPVFVRGGFGNPHYVLGLRGVAFQQTGTN-HTR 392
R YRT L+ PV G P + V N +
Sbjct: 386 INPVTLPFTSRDVRYESLAGLNLFLTQPV-----NGVPRVDFHWKFVTHPIASDNFYYP 440

Query: 393 TFRNSGT--IDSLDEIPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTH 450
+ GT DS +E+PP+ + YSH L+H+ G IS S +A ++SWTH
Sbjct: 441 GYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHI-----GLISASHV-KALVYSWTH 493

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Query: 451 RSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNING 510
RSA TNTI+P ITQIPLVKA L SG VVRGPGFTGGDILRRT+ G F VNI
Sbjct: 494 RSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTNTGTFGDIRVNIKP 553

Query: 511 QLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTDGTPLTFQSFYATINTAFTF 570
QRYR RIRYASTT+L+ + ++ G+ I G F+ TM+ G+ L +++F T F+F
Sbjct: 554 PFAQRYRVRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGFTTPFSF 613

Query: 571 PMSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
QS+FT+GA FSSGNEVYIDR E +PV T E
Sbjct: 614 LDVQSTFTIGAWNFSGNEVYIDRIEFVPVEVTYPE 648

>sp|Q9XDL1|ClID_BACTU Pesticidial crystal protein cryII d (Insecticidal delta-endotoxin
CryII(d)) (Crystalline entomocidal protoxin) (81 kDa
crystal protein)
gb|AAD44366.1|AF047579_1 (AF047579) insecticidal crystal protein [Bacillus thuringiensis]
Length = 719

Score = 410 bits (1055), Expect = e-113
Identities = 250/622 (40%), Positives = 342/622 (54%), Gaps = 43/622 (6%)

Query: 13 NCLNNPEVEILNEERSTGRPLDISLSLTRLFLSEFVPGVGVAFLGLDIWGFITP---S 69
+CL E E + S + I ++ + L + VP G L+ I G + P S
Sbjct: 41 DCLKMSEYESVEFFVSVSTIQTGIGIA-GKILGNLGVFPAGQVASLYSFLGELWPKGKS 99

Query: 70 DWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVR 129
W +F+ +E+LI Q+I T RN+A+ L+GL D+ +Y E+L W N NN ++R V+
Sbjct: 100 QWEIFMEHVEELINQKISTYARNKALADLGLDALAVYHESLESWIENNRNTRVRSVVK 159

Query: 130 IRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNN 189
++ + + +F ++ E+PLL +Y QAANLHL LLRDA FG+ WGL + ++
Sbjct: 160 NQYIALELMFVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSESEIST 219

Query: 190 HYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLTLVDIVLFPNYD 249
YNR + Y+ +C + YN GL LRGTN W R+NQFRRD+TL VLD+VALFP+YD
Sbjct: 220 FYNRQSSQTQEYSYDCSEWYNTGLNRLRGNTNAESWVRYNQFRDMLTMVLDLVALFPSYD 279

Query: 250 VRTYPIQTSSQLTREIYTSSVIEDSPVSA-----NIPNGFNRAEFGVRPPHLMDFM 300
R YPI TS+QLTRE+YT ++ P ++ N P+ VR PHL+DF+
Sbjct: 280 TRMYPIPTSAQLTREYVYTDAGTVHPNASFASTTWYNNNAPSFEISTIEAAVVRNPHLLDFL 339

Query: 301 N-----SLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPGGAIWIADDPF 355
SL + +WGGH + R T G +N + G N R
Sbjct: 340 EQVTIYSLLSRWSNTQYMMWGGHKLEFR-TIGGTLNTSTQGSTNTSINPVTLPFTSRDV 398

Query: 356 YRT-----LSDPVFVRGGFGNPHYVLGLRGVAFQQTGTN-HTRTFRNSGT--IDSL 403
YRT L+ PV G P + V N + + GT DS
Sbjct: 399 YRTESLAGLNLFLTQPV-----NGVPRVDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSE 453

Query: 404 DEIPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPER 463
+E+PP+ + YSH L+H+ G IS S +A ++SWTHRSA TNTI+ +
Sbjct: 454 NELPPETTGQPNYESYSHRLSHI-----GLISASHV-KALVYSWTHRSADRTNTINS 506

Query: 464 ITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYA 523
ITQIPLVKA L SG +VVRGPGFTGGDIL+RT+ G F VNIN QRYR RIRYA
Sbjct: 507 ITQIPLVKAFLNPSGASVVRGPGFTGGDILQRTNTGTFGDIRVNINPPFAQRYRLRIRYA 566

Query: 524 STTNLRIYVTVAGERIFAGQFNKMTDGTPLTFQSFYATINTAFTFPMSQSSFTVGADT 583
STTNL + ++ G+ I G F+ TM+ G+ L +++F T F+F +QS+FT+GA
Sbjct: 567 STTNLEFHTSINGKAINQGNFSATMNRGEDLDYKAFRTVGFTTPFSFSAQSTFTIGAWN 626

Query: 584 FSSGNEVYIDRFELIPVTATLE 605
FS GNEVYIDR E +PV T E
Sbjct: 627 FSLGNEVYIDRIEFVPVEVTYPE 648

>gb|AAG43526.1|AF211190_1 (AF211190) CryII [Bacillus thuringiensis]
Length = 719

Score = 410 bits (1053), Expect = e-113
Identities = 245/595 (41%), Positives = 328/595 (54%), Gaps = 60/595 (10%)

Query: 49 VPGVGVAFLGLFDLIWGFITP---SDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSY 105
VP G L+ I G + P S W +F+ +E+LI+Q+I T RN A+ L+GL D+
Sbjct: 76 VPFAGQIASLYSFILGELWPKGKSQWEIFMEHVEELIDQKISTYARNIALADLKGLGDAL 135

Query: 106 EIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANL 165
+Y E+L W N NNA+ V+ ++ + + +F ++ E+PLL +Y QAANL
Sbjct: 136 AVYHESLESWIKNRNNARATSVVKSQYIALELLFVQKLPSFAVSGEEVPLLPIYAQAANL 195

Query: 166 HLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDYNQGLNLRGTNTRQWA 225
HL LLRDA FG+ WGL + ++ YNR + Y+ HC+ Y+ GL NLRGTN W
Sbjct: 196 HLLLLRDASVFGKEWGLSNSQISTFYNRQVERTSDYSDHCVKWYSTGLNNLRGTNAESWV 255

Query: 226 RFNQFRRLTLTLVLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSA----- 278
R+NQFR+D+TL VLD++ALFP+YD YPI+T+SQLTRE+YT ++ P ++
Sbjct: 256 RYNQFRKDMTLMVLDLIALFPSYDTLVYPIKTTSQLTREVTDAIGTVHPNASFASTTWY 315

Query: 279 --NIPNGFNRAEFGVRPPHLMDFMN-----SLFVTAETVRSQTVWGGHLVSSRNTAGNRI 331
N P+ VR PHL+DF+ SL + +WGGH + R T G +
Sbjct: 316 NNNAPSFSAIESAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMGHRLEFR-TIGGVL 374

Query: 332 NFPSYGVFNPGGAIWIADEDPRPFYRT-----LSDPV--FVRGGF-----G 370
N + G N R YRT L+ PV R F
Sbjct: 375 NTSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPRVDFHWKFATLPIAS 434

Query: 371 NPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNGSAPWNDYSHVLNHVTFVR 430
+ Y LG GV Q DS +E+PP+ + YSH L+H+
Sbjct: 435 DNFYYLGYAGVGTQLQ-----DSENEFPETTGQPNYESYSHRLSHI----- 476

Query: 431 WPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGG 490
G IS S +A ++SWTHRSA TNTI+P ITQIPLVKA L SG VVRGPGFTGG
Sbjct: 477 --GLISASHV-KALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGG 533

Query: 491 DILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTMDT 550
DILRRT+ G F VNIN QRYR RIRYASTT+L+ + ++ G+ I G F+ TM+
Sbjct: 534 DILRRTNTGTFGDIRVNINPPFAQRYRVRIYASTTDLQFHTSINGKAINQGNFSATMNR 593

Query: 551 GDPLTFQSFYSATINTAFTFPMSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
G+ L +++F T F+P QS+FT+GA FSSGNEVYIDR E +PV T E
Sbjct: 594 GEDLDYKTFRTVGFTHPFSFSDVQSTFTIGAWNFSGNEVYIDRIEFVPEVETYE 648

>sp|087404|C1IC_BACTU Pesticidal crystal protein cryIIc (Insecticidal delta-endotoxin
CryII(c)) (Crystalline entomocidal protoxin) (81 kDa
crystal protein)
gb|AAC62933.1| (AF056933) crystal protein toxin [Bacillus thuringiensis]
Length = 719

Score = 395 bits (1015), Expect = e-109
Identities = 239/595 (40%), Positives = 322/595 (53%), Gaps = 60/595 (10%)

Query: 49 VPGVGVAFLGLFDLIWGFITP---SDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSY 105
VP G L+ I G + P S W +F+ +E +I ++I T RN+A+T L+GL D+
Sbjct: 76 VPFPGQIASLYSFILGELWPKGKSQWEIFMEHVEAIINRKISTYARNKALPDLKGLGDAL 135

Query: 106 EIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANL 165
+Y E+L W N NN + R V+ ++ + + +F ++ E+PLL +Y QAANL
Sbjct: 136 AVYHESLESWVGNRNNRARSVVKNQYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANL 195

Query: 166 HLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDYNQGLNLRGTNTRQWA 225
HL LLRDA F + GL + ++ YNR + Y+ HC+ N GL NLR TN + W
Sbjct: 196 HLLLLRDASIFEKNGGLSASEISTFYNRQVERTRDYSYHCVKWNNNTGLNNLRATNGQSWV 255

Query: 226 RFNQFRRLTLTLVLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSA----- 278
R+NQFR+D+ L VLD+V +FP+YD YPI+T+SQLTRE+YT ++ P A
Sbjct: 256 RYNQFRKDIELMVLDLVRVFPSTYDTLVYPIKTTSQLTREVTDAIGTVDPNQAALRSTTWY 315

Query: 279 -NIPNGFNRAEFGV-RPPHLMDFMN-----SLFVTAETVRSQTVWGGHLVSSRNTAGNRI 331

N F+ E V R PHL+DF+ SL + +WGGH + SR G +
Sbjct: 316 NNNAPSFSAIEAAVIRSPHLLDFLEKVITYSLLSRWSNTQYMMNWGGHRLSR-PIGGAL 374
Query: 332 NFPSYGVFNPGGAIWIADPRPFYRT-----LSDPV--FVRGGF-----G 370
N + G N R FYRT L+ PV R F
Sbjct: 375 NTSTQGSTNTSINPVTQLQTSRDFYRTESWAGLNLFLTQPVNGVPRVDFHWKFPTLPIAS 434
Query: 371 NPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNGAPWNDYSHVLNHVTFVR 430
+ Y LG GV Q DS +E+PP+ + YSH L+H+
Sbjct: 435 DNFYYLGYAGVGTQLQ-----DSENELPPETTGQPNYESYSHRLSHI---- 476
Query: 431 WPGEISGSDSWRAPMFWSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGG 490
G ISGS +A ++SWTHRSA TNTI+P ITQIPLVKA L SG VVRGPGFTGG
Sbjct: 477 --GLISGSHV-KALVYSWTHRSADRTNTIEPNISITQIPLVKAFLNLSGAADVVRGPGFTGG 533
Query: 491 DILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTMDT 550
ILRRT G F + VNIN QRYR R+ YASTT+L+ + ++ G+ I G F+ TM+
Sbjct: 534 HILRRTKSGTFGHIRVNINPPFAQRYRVRMSYASTTDLQFHTSINGKAINQGNFSATMNR 593
Query: 551 GDPLTFQSFSYATINTAFTFPMSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
G+ L +++F T F+F QS+FT+GA FSSGNEVYI R E +PV T E
Sbjct: 594 GEDLDYKTFRTVGFTTTFPSFSDVQSTFTIGAWNFSSGNEVYIGRIEFPVEVTE 648

>emb|CAA65003.1| (X95704) crylBa2 [Bacillus thuringiensis]
gb|AAK51084.1|AF363025_1 (AF363025) delta-endotoxin CrylBa2 [Bacillus thuringiensis serovar
entomocidus]
Length = 1228

Score = 387 bits (993), Expect = e-106
Identities = 232/589 (39%), Positives = 313/589 (52%), Gaps = 47/589 (7%)

Query: 49 VPGVGVAFLGLDLIWGFITP---SDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSY 105
VP G + + G + P W +FL +EQLI Q+I RN A+ L+GL DS+
Sbjct: 67 VPFAGQLASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNALARLQGLGDSF 126
Query: 106 EIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANL 165
Y ++L +W N ++A+ R + ++ + + A+ F + + E+PLL VY QAANL
Sbjct: 127 RAYQQSLEDWLENRDDARTSVLHTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANL 186
Query: 166 HLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWA 225
HL LLRDA FG +GL + +Y R + Y+ +C++ YN GL +LRGTN W
Sbjct: 187 HLLLLRDASLFGSEFGLTSQEIQRYRERQVERTRDYSYCVWEYNTGLNSLRGTNAASWV 246
Query: 226 RFNQFRDLTLTLVDLVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSA----- 278
R+NQFRDLTL VLD+VALFP+YD RTYPI TS+QLTRE+YT ++ A
Sbjct: 247 RYNQFRDLTLGLVLDLVALFPSYDTRTYPINTSAQLTREYVYDAIGATGVNMASMNWYNN 306
Query: 279 NIPNGFNRAEFGVRPPHLMDFMNSLFVTA-----ETVRSQTVWGGHLVSSRNTAGNRINF 333
N P+ +R PHL+DF+ L + + R T W GH + SR G +N
Sbjct: 307 NAPSFSAIEAAAIRSPHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQRPIGGG-LNT 365
Query: 334 PSYGVFNPGGAIWIADPRPFYRTLS-----DPVF----VRGGFGNPHYVLGL 378
++G N R YRT S +P+ VR F NP +
Sbjct: 366 STHGATNTSINPVTLRFSRDVYRTESYAGVLLWGIYLEPIHGVPTVRFNFTNPQNISD- 424
Query: 379 RGVAFFQQTGTNHTRTFRNSG--TIDSLDEIPPQDNGAPWNDYSHVLNHVTFVRWPGEIS 436
RG A N+++ + + G DS E+PP+ + YSH L+H+ +
Sbjct: 425 RGTA-----NYSQPYESPGLQLKDSELPETTERPNYESYSHRLSHIGIIL----- 472
Query: 437 GSDSWRAPMFWSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRT 496
P++SWTHRSA TNTI P RITQIP+VKA L GTTVVRGPGFTGGDILRRT
Sbjct: 473 -QSRVNPVYSWTHRSADRTNTIGPNRITQIPMVKASELPQGTTVVRGPGFTGGDILRRT 531
Query: 497 SGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTMDTGDPLTF 556
+ G F V +NG L QRYR RYAST + +V+ G + +F +TM++GD L +
Sbjct: 532 NTGGFGPIRVTVNGPLTQRYRIGFRYASTVDFDFVSRGGTTVNNFRFLRTMNSGDELKY 591
Query: 557 QSFSYATINTAFTFPMSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
+F T FTF Q S EVYID+ E+IPVTAT E

Sbjct: 592 GNFVRRRAFTPFTFTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATFE 640

>sp|P05517|C1BA_BACTK PESTICIDIAL CRYSTAL PROTEIN CRY1BA (INSECTICIDAL DELTA-ENDOTOXIN
CRYIB(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (140 KDA
CRYSTAL PROTEIN)
pir||S00873 parasporal crystal protein - Bacillus thuringiensis subsp.
thuringiensis
emb|CAA29898.1| (X06711) delta-endotoxin (AA 1-1228) [Bacillus thuringiensis]
Length = 1228

Score = 386 bits (991), Expect = e-106
Identities = 232/589 (39%), Positives = 313/589 (52%), Gaps = 47/589 (7%)

Query: 49 VPGVGVAFLFDLIWGFITP---SDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSY 105
VP G + + G + P W +FL +EQLI Q+I RN A+ L+GL DS+
Sbjct: 67 VPFAGQLASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNALARLQGLGDSF 126

Query: 106 EIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANL 165
Y ++L +W N ++A+ R + ++ + + A+ F + + E+PLL VY QAANL
Sbjct: 127 RAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANL 186

Query: 166 HLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWA 225
HL LLRDA FG +GL + +Y R + Y+ +C++ YN GL +LRGTN W
Sbjct: 187 HLLLLRDASLFGSEFGLTSQEIQRYRQVERTRDYSYCVIEWYNTGLNSLRGTNAASWV 246

Query: 226 RFNQFRRDLTLTVLDIVALEFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSA----- 278
R+NQFRRDLTL VLD+VALEFP+YD RTYPI TS+QLTRE+YT ++ A
Sbjct: 247 RYNQFRRDLTLGVLDLVALFPSTYDTRTYPIINTSAQLTREYVTDAGATGVNMASMNWYNN 306

Query: 279 NIPNGFNRAEFGVRRPHLMDFMNSLFVTA-----ETVRSQTVWGGHLVSSRNTAGNRINF 333
N P+ +R PHL+DF+ L + + R T W GH + SR G +N
Sbjct: 307 NAPSFSIAEAAAIRSPHLLDFLEQLTIFSSASSRWSNTRHMTYWRGHTIQSRPIGGG-LNT 365

Query: 334 PSYGVFNPGGAIWIADPRPFYRTLS-----DPVF----VRGGFGNPHYVLGL 378
++G N R YRT S +P+ VR F NP +
Sbjct: 366 STHGATNTSINPVTLRFASRDVYRTESYAGVLLWGIYLEPIHGVPVTRFNFETNPQNISD- 424

Query: 379 RGVAFFQQTGTHNTRTFNRNSG--TIDSLDEIPPQDNGAPWNDYSHVLNHVTFVRWPEIS 436
RG A N+++ + + G DS E+PP+ + YSH L+H+ +
Sbjct: 425 RGTA-----NYSQPYESPGLQLKDSSETLPPETTERPNYESYSHRLSHIGIIL----- 472

Query: 437 GSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRT 496
P++SWTHRSA TNTI P RITQIP+VKA L GTTVVRGPGFTGGDILRRT
Sbjct: 473 -QSRVNVVYSWTHRSADRTNTIGPNRITQIPMVKASELPQGTTVVRGPGFTGGDILRRT 531

Query: 497 SGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKTMDDTGDPLTF 556
+ G F V +NG L QRYR RYAST + +V+ G + +F +TM++GD L +
Sbjct: 532 NTGGFGPIRVTVNGPLTQRYRIGFRYASTVDFDFVSRGGTTVNNFRFLRTMNSGDELKY 591

Query: 557 QSFYSATINTAFTFPMSQSSFTVGADTFSSGNGEVYIDRFELIPVTATLE 605
+F T FTF Q S EVYID+ E+IPVTAT E
Sbjct: 592 GNFVRRRAFTPFTFTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATFE 640

>gb|AAK63251.1|AF368257_1 (AF368257) Cry1Ba [Bacillus thuringiensis]
Length = 1228

Score = 383 bits (983), Expect = e-105
Identities = 231/589 (39%), Positives = 312/589 (52%), Gaps = 47/589 (7%)

Query: 49 VPGVGVAFLFDLIWGFITP---SDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSY 105
VP G + + G + P W +FL +EQLI Q+I RN A+ L+GL DS+
Sbjct: 67 VPFAGQLASFYSFLVGELWPRGRDQWEIFLEHVEQLINQQITENARNALARLQGLGDSF 126

Query: 106 EIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANL 165
Y ++L +W N ++A+ R + ++ + + A+ F + + E+PLL VY QAANL
Sbjct: 127 RAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANL 186

Query: 166 HLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWA 225
HL LLRDA FG +GL + +Y R + Y+ +C++ YN GL +LRGTN W

Sbjct: 187 HLLLLRDASLFGSEFGLTSQEIQRYRQVERTRDYSYCVIEWYNTGLNSLRGTNAASWV 246

Query: 226 RFNQFRRDLTLTVLIDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSA----- 278
R+NQFRRDLTL VLD+VALEFP+YD RTYPI TS+QLTRE+YT ++ A

Sbjct: 247 RYNQFRRDLTLGLVLDLVALEFPSYDTRTYPIQTSALQTLREVYTDAGATGVNMASMNWYNN 306

Query: 279 NIPNGFNRAEFGVRPPHLMDFMNSLFVTA-----ETVRSQTVWGGHLVSSRNTAGNRINF 333
N P+ +R PHL+DF+ L + + R T W G + S R G +N

Sbjct: 307 NAPSFSAIEAAAIRSPHLLDFLEQLTIFSASSRWSNTRHMTYWRGRTIQSRPIGGG-LNT 365

Query: 334 PSYGVENPGGAIWIADDEPRPFYRTLS-----DPVF----VRGGFGNPHYVLGL 378
++G N R YRT S +P+ VR F NP +

Sbjct: 366 STHGATNTSINPVTLRFASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFNFTNPQNISD- 424

Query: 379 RGVAFFQQTGTNHTRTFRNSG--TIDSLDEIPPQDNGAPWNDYSHVLNHVTFVRWPGEIS 436
RG A N+++ + + G DS E+PP+ + YSH L+H+ +

Sbjct: 425 RGTA-----NYSQPYESPLQLKDSSETLPPETTERPNYESYSHRLSHIGIIL----- 472

Query: 437 GSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRT 496
P++SWTHRSA TMTI P RITQIP+VKA L GTTVVRGPGFTGGDILRRT

Sbjct: 473 -QSRVNVVPVYSWTHRSADRTNITGNRITQIPMVKASELPQGTTVVRGPGFTGGDILRRT 531

Query: 497 SGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTDGDPLTF 556
+ G F V +NG L QRYR RYAST + +V+ G + +F +TM++GD L +

Sbjct: 532 NTGGFGPIRVTVNGPLTQRYRIGFRYASTVDFDFVSRGTTVNNFRFLRTMNSGDELKY 591

Query: 557 QSFSYATINTAFTFPMSSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
+F T FTF Q S EVYID+ E+IPVTAT E

Sbjct: 592 GNFVRRRAFTTFTFTTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATFE 640

>gb|AAK14339.1| (AF327927) insecticidal crystal protein BTRX3 [Bacillus
thuringiensis serovar kunthalanags3]
Length = 1155

Score = 375 bits (962), Expect = e-102
Identities = 254/626 (40%), Positives = 322/626 (50%), Gaps = 40/626 (6%)

Query: 1 MENNIQ-NQCVYPYNCLNNEVEILNEER-STGRPLDISLSLTFLLSEFVPGVGVAFGL 58
M+NN N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL

Sbjct: 1 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGITPSDWSLFLLOQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEAN 118
D+IWG PS W FL+QIEQLI QRIE + + S REWEA+

Sbjct: 61 VDIIWGITFGPSQWDAFLVQIEQLINQRIENSLGTPFLDWKA-KQSLSNLRRIFREWEAD 119

Query: 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ 178
P N LRE++RI+F AL TAI F + ++++PLLSVYVQAANL S R F +

Sbjct: 120 PTNPALREEMRIQFNARTSALTAIPLFAVQNYQVPLLSVYVQAANLMFSTRR-VQPFSSR 178

Query: 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRDLTLTV 238
+ V Y N K C + LE++ R + F +

Sbjct: 179 -----VVAVTPGYQSRYNF-----KRCYWGAREFLEDVGAI--RDKSNFKKEDSKQLCCY 226

Query: 239 LIDIVAL-----FPNYDVRTYPIQTSSQLT---REIYTSSVIEDSPVSANIPNGFNRAE 288
L I L + + R YPI S R +Y S + + S V + RA

Sbjct: 227 LGIFRLSSYFFKIEKFRTRVYPISESKFSPINKRNLYKPSIKKFSMV---VFEARLRAR 283

Query: 289 FGVRPPHLMDFMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVENPGGA-- 344
PHL ++N + R W GH + S FP +G N G A

Sbjct: 284 RKYWSPHLWIYLNQDNHLTDVHRGFNYWSGHQIIASPVGFQDPEFAFPLFG--NAGNAAP 341

Query: 345 -IWIADDEPRPFYRTLS-----DPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGT 399
+ I + + YRTLS + +F+R N + L + + H +R SGT

Sbjct: 342 PVRIVYQLGQGQVYRTLSSTLYEDLFIRDKVINTYLFLLAGSNLLMEPPHICHPGRYRKSQT 401

Query: 400 IDSLDEIPPQDNGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTI 459
+DSLDEIP Q+N+ P +SH L+HV+ R S RAPMFSW RSA N I

Sbjct: 402 VDSLDEIPHQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWILRSAEFNNII 461

Query: 460 DPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRAR 519
+ITQIPL K+ L SGT+VV+GPGFTGGDILRRTS G + VNI L QRYR R
Sbjct: 462 PSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVR 521

Query: 520 IRYASTTNLRIYVTVAGERIFAGQFNKMTMDTGDPLTFQSFSYATINTAFTFPMSSQSSFTV 579
IRYASTTNL+ + + G I G F+ TM +G L SF T F F S FT+
Sbjct: 522 IRYASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQASFRVTGFTTFFNFSNGSSVFTL 581

Query: 580 GADTFSSGNEVYIDRFELIPVTATLE 605
A F+SGNEVYIDR E +P T E
Sbjct: 582 SAHVFNSSGNEVYIDRIEFVPAEVTFE 607

>sp|Q45733|C9CA_BACTO Pesticidal crystal protein cry9Ca (Insecticidal delta-endotoxin
CryIXC(a)) (Crystalline entomocidal protoxin) (130 kDa
crystal protein)
pir||S49247 hypothetical protein 2 - Bacillus thuringiensis
emb|CAA85764.1| (Z37527) second open reading frame of cry9Ca1 operon [Bacillus
thuringiensis]
Length = 1157

Score = 372 bits (954), Expect = e-102
Identities = 220/573 (38%), Positives = 311/573 (53%), Gaps = 34/573 (5%)

Query: 58 LFDLIWGFITPSDWSLFLQLIEQLRIETLERNRAITTLRGLADSYEIIYIEALREWEA 117
L + +W + W F+ Q+E+L+ Q+I RN+A+ L+GL DS+ +Y +L+ W A
Sbjct: 99 LLNTLWPNVNDTAIWEAFMRQVEELVNQQITEFARNQALARLQGLGDSFNVYQRSLLQNWLA 158

Query: 118 NPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYQAANLHLSLLRDAVSFG 177
+ N+ + VR +F D + AI F + ++PLLSVY QA NLHL LL+DA FG
Sbjct: 159 DRNDTRNLSVVRAQFIALDLDFVNAIPLFAVNGQQVPLLSVYAQAVNLHLLLLKDALFG 218

Query: 178 QGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRDLTLT 237
+GWG ++ +Y+R + L +YT +C YN GL+ LRGTNT W R++QFRR++TL
Sbjct: 219 EGWGTQGEISTYYDRQLELTAKYNTNYCETWYNTGLDRLRGNTESWLRYHQFRREMTLV 278

Query: 238 VLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVS-----ANIPNGFNRAEF 289
VLD+VALFP YDVR YP ++ QLTRE+YT ++ + P + N N F+ E
Sbjct: 279 VLDVVALFPYDVRLYPTGSNPQLTREYVTDPIVFNPANVGLCRRWGNTNPYNTFSELEN 338

Query: 290 G-VRPPLHMDFMNSLFVTAE----TVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPGGA 344
+RPPHL D +NSL +++ + W GH + + + SYG+ A
Sbjct: 339 AFIRPPLHDLRLNSLTISSNRFPVSSNFMDYWSGHTLRRLSYLNDASVQEDSYGLITTTTRA 398

Query: 345 IWIADEDPRPFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGT-NHTRTRFNSG---TI 400
D R S V R +G+ +F G N T + N G
Sbjct: 399 TINPGVDGT--NRIESTAVDFRSALIG---IYGVNRASFVPGGLFNGTTSPANGGCRDLY 453

Query: 401 DSLDEIPPQDNGSAPWNDYSHVLNHVTVFVRWPGEISGS--DSWRAPMFSWTHRSATPTNT 458
D+ DE+PP +++G+ +H L+HVTF + +GS ++ P + WT R NT
Sbjct: 454 DTNDELPPDESTGSS----THRLSHVTFSSFTNQAGSIANAGSVPTYVWTRRDVDLNN 509

Query: 459 IDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRA 518
I P RITQ+PLVKA SGTTV++GPGFTGG ILRRT+ G F V +N L Q+YR
Sbjct: 510 ITPNRITQLPLVKASAPVSGTTVLKGPFTGGGILRRTTNGTFGTLRVTVNSPLTQQYRL 569

Query: 519 RIRYASTTNLRIYVTVAGERIFAGQFNKMTMDTGDPLTFQSF-----SYATINTAFTFPM 572
R+R+AST N I V G I + TM+ G LT++SF + N FTF
Sbjct: 570 RVRFASTGNFSIRVLRGGVSIGDVRLGSTMNRGQELTYESFTTREFTTTGPFPNPPFTTQ 629

Query: 573 SQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
+Q TV A+ S+G E YIDR E++PV E
Sbjct: 630 AQEILTVNAEGVSTGGEYYIDRIEIVPNPARE 662

>sp|Q9ZAZ5|C1BD_BACTZ Pesticidal crystal protein cry1Bd (Insecticidal delta-endotoxin
CryIB(d)) (Crystalline entomocidal protoxin) (140 kDa
crystal protein)
gb|AAD10292.1| (U07026) insecticidal crystal protein CryE1 [Bacillus thuringiensis
serovar wuhanensis]
Length = 1231

Score = 364 bits (934), Expect = 2e-99
Identities = 240/600 (40%), Positives = 314/600 (52%), Gaps = 67/600 (11%)

Query: 49 VPGVGVAFLGLFDLIWGFIPTSD---WSLFLQLIEQLIEQRIETLERNRAITTLRGLADSY 105
VP G + + G + PS W +FL +EQLI Q++ RN AI L GL Y
Sbjct: 72 VPFAGQLASFYSFLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTRNTAIARLEGLGRGY 131

Query: 106 EIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANL 165
Y +AL W N N+A+ R + R+ + + TAI F + + E+PLL VY QAANL
Sbjct: 132 RSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPLFRIRNEEVPLLMVYAQAANL 191

Query: 166 HLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWA 225
HL LLRDA FG WG+ + VN +Y I Y+ HC+ YN GL NLRGTN W
Sbjct: 192 HLLLLRDASLFGSEWGMASDVNQYYQEIRYTEEYSNHCQWYNTGLNNLRGTNAESWL 251

Query: 226 RFNQFRDLTLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGF- 284
R+NQFRDLTL VLD+VALFP+YD RTYPI TS+QLTREIYT D N P+GF
Sbjct: 252 RYNQFRDLTLGVLDLVALFPSYDTRYPINTSAQLTREIYT-----DPIGRTNAPSGFA 306

Query: 285 -----NRAEFGV-----RPPHLMDFMNSLFVTAETVR-----SQTWVGGLVSSRNT 326
N F RPPHL+DF L + + + R W GH ++ R
Sbjct: 307 STNWFNNNAPSFAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMMNYWVGHRNLNFR-P 365

Query: 327 AGNRINFPSYGVFNPGGAIWIAD-DRPFYRTLSD-----PV----FVRGGFGNP 372
G +N + G+ N + + R YRT S+ PV + R F NP
Sbjct: 366 IGGTLNTSTQGLTNNTSINPVTLQFTSRDVRITESNAGTNILFTTPVNGVPWARFNFINP 425

Query: 373 HYVLGLRGVAFQQTGTNHTRTFRNSG--TIDSLDEIPPQDMSGAPWNDYSHVLNHVTFVR 430
+ +++ T +++ ++ G DS E+PP+ + YSH L+H+
Sbjct: 426 QNI-----YERGATTYSQPYQGVGIQLFDSETELPETTERPNYESYSHRLSHI---- 474

Query: 431 WPGEISGSDSWRAPMFWSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGG 490
G I G ++ RAP++SWTHRSA TNTI P RITQIP VK L +G +V+ GPGFTGG
Sbjct: 475 --GLIIG-NTLRAPVYSWTHRSADRTNTIGPNRITQIPAVKGRFLFNG-SVISGPGFTGG 530

Query: 491 DILR--RTSGGPFAYTIVNINGQLPQ---RYRARIRYASTTNLRIYVTVAGERIFAGQFN 545
D++R R +G + + Q RYR R+RYAS T++ + V + IF
Sbjct: 531 DVVRLNRNNGNIQNRGYIEVPIQFTSTSTRYRVVRVYASVTSIELNVNLGNSSIFTNTLP 590

Query: 546 KTMDTGDLPLTFQSFYATINTAFTFPMSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
T + D L F Y IN AFT S + VGA FS+ EV IDRFE IPVTAT E
Sbjct: 591 ATAASLDNLQSGDFGYVEINNAFT---SATGNIVGARNFSANAEVIIDRFEFIPVTATFE 647

>sp|Q45704|C8AA_BACUK Pesticidal crystal protein cry8Aa (Insecticidal delta-endotoxin
CryVIIIA(a)) (Crystalline entomocidal protoxin) (131 kDa
crystal protein)
gb|AAA21117.1| (U04364) CryIII delta-endotoxin [Bacillus thuringiensis]
Length = 1157

Score = 353 bits (906), Expect = 3e-96
Identities = 225/620 (36%), Positives = 330/620 (52%), Gaps = 43/620 (6%)

Query: 17 NPEVEILNEERSTGRPLDISLSLTRLSEFVPGVGVAFLGLFDLIWGFIPTSD----WS 72
NPE I + TG I + + R L + VP + I G + PS W
Sbjct: 59 NPETFISSTIQTG-----IGI-VGRILGALGVFFASQIASFYSFIVGQLWPSKSVDIWG 112

Query: 73 LFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIYIEALREWEANPNNAQLREDVRIRF 132
+ ++E+L++Q+IE +++A+ L+GL ++ ++Y ++L +W N N+A+ R V +F
Sbjct: 113 EIMERVEELVDQKIEKYVKDKALAEKGLGNALDVYQQSLEDWLENRNDARTSRVVSNOF 172

Query: 133 ANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYN 192
D +++I +F ++ E+ LL+VY QA NLHL LLRDA FG+ WG ++ YN
Sbjct: 173 IALDLNLFVSSIPSAVSGHEVLLLA VYAQAVNLHLLLLRDASIFGEEWGFTPGETSRFYN 232

Query: 193 RLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRDLTLTVLDIVALFPNYDVRT 252
R + L Y+ +C+ Y GL+ L+GT ++ W ++QFR++TL VLD+VALFPNYD
Sbjct: 233 RQVQLTAEYSDYCVKWKYKIGLDKLGTTSKSWLNYHQFRREMTLLVLDLVALFPNYDTHM 292

Query: 253 YPIQTSSQLTREIYTSSVIEDSPVSANIPNG-----FNRAEFGV-RPPHLMDFMNSL 303
YPI+T++QLTR++YT + + S N F E V RPPHL D ++S+
Sbjct: 293 YPIETTAQLTRDVYTDPIAFNIVTSTGFENPWSTHSGILFYEVENNVI RPPHLFDILSSV 352

Query: 304 FVTAE-----TVRSQ---TVWGGHLVSSRNTAGNRINF-PSYG-VFNPGGAIWIADEDPRP 354
+ T+ + W GH + R TA + + + +YG + + + + D D
Sbjct: 353 EINTSRGGITLNNDAYINYWSGHTLKYRRTADSTVYTYTANYGRITSEKNSFALED R DIFE 412

Query: 355 FYRTLSDPV-FVRGGFGNP---HYV-LGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPP 408
T+++ + + +G P H V G HT + +S DEI P
Sbjct: 413 INSTVANLANYYQKAYGVPGSWFHMVKRGTSSTTAYLYSKTHTALQGCTQVYESSDEI-P 471

Query: 409 QDMSGAPWNDYSHVLNHVT---FVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERIT 465
D + YSH L+H+T F + GS P+F WTH SA NTI ++IT
Sbjct: 472 LDRTPVPAESYSHRLSHITSHSFSKNGSAYYGS----FPVFVWTHTSADLNNNTIYSDKIT 527

Query: 466 QIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYAST 525
QIP VK L G +VV+GPGFTGGDIL+RT+ V +NG L QRYR RIRYAST
Sbjct: 528 QIPAVKGDMLYLGGSVVQGPFTGGDILKRTNPSILGTFAVTVNGSLSQRYRVIRYAST 587

Query: 526 TNLRIYVTVAGERIFAGQFNKMTMDTGDPLTFQSFSYATINTAFTFPMSSQSSFTVGADTF 585
T+ + G+ I +FNKMTMD G LT+++F +A+ T F F +Q + FS
Sbjct: 588 TDFE-FTLYLGDITIEKNRNFNKTMDNGASLTYYETFKFASFITDFQFRETQDKILLSMGDFS 646

Query: 586 SGNEVYIDREFELIPVTATLE 605
SG EVYIDR E IPV T E
Sbjct: 647 SGQEVYIDRIEFIPVDETYE 666

>sp|085805|C1BE_BACTU Pesticidal crystal protein cry1Be (Insecticidal delta-endotoxin
Cry1B(e)) (Crystalline entomocidal protoxin) (139 kDa
crystal protein)
gb|AAC32850.1| (AF077326) Cry1Be1 delta-endotoxin [Bacillus thuringiensis]
Length = 1227

Score = 344 bits (883), Expect = 1e-93
Identities = 221/597 (37%), Positives = 303/597 (50%), Gaps = 65/597 (10%)

Query: 49 VPGVGVAFLGLFDLIWGFITP---SDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSY 105
VP G + + G + P W +FL +EQLI Q++ R+ A+ L+GL +S+
Sbjct: 72 VPIFQGIASFYSFLVGLWPRGRDPWEIFLEHVEQLIRQQVTENTRTALARLQGLNSF 131

Query: 106 EIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANL 165
Y ++L +W N ++A+ R + ++ + +A+ F + + E+PLL VY QAANL
Sbjct: 132 RAYQQSLEDWLENRDDARTRSVLYTQYIALELDLFLNAMPLFAIRNQEVPLLMVYAQAANL 191

Query: 166 HLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTNRQWA 225
HL LLRDA FG +GL + +Y R + Y+ +C YN GL NLRGTN W
Sbjct: 192 HLLLRDASLFGSEFGLTSQEIQRYRERQVEKTRREYSDYCARWYNTGLNNLRGTNAESWL 251

Query: 226 RFNQFRRDLTLTVLDI VALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGF- 284
R+NQFRRDLTL VLD+VALFP+YD R YP+ TS+QLTREIYT D N P+GF
Sbjct: 252 RYNQFRRDLTLGVLDLVALFPNYDTRVYPMNTSAQLTREIYT-----DPIGRTNAPSGFA 306

Query: 285 -----NRAEFG-----VRPPHLMDFMNSLFVTA-----ETVRSQTVWGGHLVSSRNT 326
N F +RPPHL+DF L + + + W GH + SR
Sbjct: 307 STNWFNNNAPSFSFAIEAAVIRPPHLLDFPEQLTIFSVLSRSWNTQYMNWVWGHRLSRTI 366

Query: 327 AGNRINFPSYGVFNPGGAIWIADEDPRPFYRT-----LSDPV---FVRGGFGNPH 373
G+ ++ ++G N R YRT L+ PV + R + NP
Sbjct: 367 RGS-LSTSTHGNTNTSINPVTLQFTSRDVYRTESFAGINILLTTPVNGVPWARFNWRNP- 424

Query: 374 YVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDMSGAPWNDYSHVLNHVTFVRWPG 433
+ LRG G T DS E+PP+ + YSH L+++ +
Sbjct: 425 -LNSLRGSLTYTIGYTGVT----QLFDSETELPPETTERPNYESSYSHRLSNIRLI---- 475

Query: 434 EISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDIL 493
++ RAP++SWTHRSA TNTI + ITQIPLVK+ L SGT+VV GPGFTGGDI+
Sbjct: 476 ---SGNTRLAPVYSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVSVSGPGFTGGDII 532

Query: 494 RRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTDGDGP 553
R G +N N QRYR R+RYA++ + + VTV G F F TM +
Sbjct: 533 RTNVNGSVLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGSGSTTFDQGFSTMSANES 592

Query: 554 LTFQSFSYATINTAFTFPMSQS-----SFTVGADTFSSGNEVYIDRFELIPVTATLE 605
LT QSF +A + SQ+ S G TF + D+ E IP+TAT E
Sbjct: 593 LTSQSFRFAEFPGVISASGSQTAGISISNNAGRQTF-----HFDKIEFIPITATFE 643

>sp|Q45705|C8BA_BACUK Pesticidal crystal protein cry8Ba (Insecticidal delta-endotoxin
CryVIIIB(a)) (Crystalline entomocidal protoxin) (134 kDa
crystal protein)
gb|AAA21118.1| (U04365) CryIII delta-endotoxin [Bacillus thuringiensis]
Length = 1169

Score = 344 bits (882), Expect = 2e-93
Identities = 219/618 (35%), Positives = 325/618 (52%), Gaps = 49/618 (7%)

Query: 21 EILNEERSTGRPLPLDISLSLTFRELLSEFV-PGVGVAFGLFDLIWGFIPTSDWSLFLQIE 79
E+ E+ + +DI L L FV P V + L D++W S W +F+ Q+E
Sbjct: 61 EVFLSEQDAVKAIDIVGKLLTGLGVFPVGPVSLYTQLIDILWPSKQKSQWEIFMEQVE 120

Query: 80 QLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDAL 139
+LI Q+I RN+A++ L GL ++Y++Y+ AL EW+ NPN ++ DVR RF D
Sbjct: 121 ELINQKIAEYARNKALSELEGLGNNYQLYLTALAEWKENPNGSRALRDVRNREFEILDSLF 180

Query: 140 ITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQWGLDIATVNNHYNRLINLIH 199
+ +F +T+FE+P L+VY AANLHL LLRDA FG+ WGL +T+NN+YNR + L
Sbjct: 181 TOYMPFSFRVTNFEVFPFLTVYTMAANLHLLLRDASIFGEEWGLSTSTINNYNRQMKLTA 240

Query: 200 RYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLTVLDIVALFPNYDVRTYPIQTSS 259
Y+ HC+ Y GL L+G++ +QW +NQFRR++TLTVLD+VALF NYD RTYP+ T++
Sbjct: 241 EYSDHCVKWYETGLAKLKSSAKQWIDYNQFRREMTLVLDVVALFSNYDTRTYPLATTA 300

Query: 260 QLTREIYTSSV-IEDSPVSANIPNGFNRA-----EFGVRPPHLMDFMNSLFVTAE--- 308
QLTRE+YT + D P NI + +++A + +RPPH+ D++ L V +
Sbjct: 301 QLTREVYTDPLGAVDVP---NIGSWYDKAPSFSEIEKAAIRPHVFDYITGLTVYTKKRS 357

Query: 309 --TVRSQTVWGGHLVSSRNTAGNRINFPFSGVFNPGGAIWIADSDPRPFYRTLSD----- 361
+ R W GH +S ++ + YG + D Y+TLS+
Sbjct: 358 FTSDRYMRYWAGHQISYKHIGTSSTFTQMYGTNQNLOSTSNFDFNTYDIYKTLNNGAVLL 417

Query: 362 ----PVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSG-----TIDSLDEIPPQDN 411
P + FG P + Q T T T++ + T DS E+PP+ +
Sbjct: 418 DIVYPGYTYTFFGMPETEFFF---VNQLNNTKTLTYKPASKDIIDRTDSELELPPETS 474

Query: 412 SGAPWNVDYSHVLNHVTVFRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
+ YSH L H+TF+ S S S P+FSWTHRSA TNT+ ITQIP K
Sbjct: 475 GQPNYESYSHRLGHITFI-----YSSSTSTYVPVFSWTHRSADLTNTVKSGEITQIPGGK 529

Query: 472 AHTLQSGTTVVVRGPGFTGGDILRRTSG-GPFAYTIVNINGQLPQRYRARIYASTTNLRI 530
+ T+ T +++G G+TGGD++ T G + ++ QR+R RIRYAS N
Sbjct: 530 SSTIGRNTYIIKGRGYTGGDLVALTDRIGSCFQMIFPES---QRFRIRIRYAS--NETS 584

Query: 531 YVTVAG-ERIFAGQFNKMTD--TGDPLTFQSFSYATINTAFTFPMSQSSFTVGADTFSSG 587
Y+++ G + +FN+T + LT+ F Y + S + + ++
Sbjct: 585 YISLYGLNQSGTLKFNQYTSNKNENDLTYNDFKYIEYPRVISVNASSNIQRLSIGIQTNT 644

Query: 588 NEVYIDRFELIPVTATLE 605
N +DR E IPV T E
Sbjct: 645 NLFILDRIEFIPVDETYE 662

>gb|AAC63366.1| (AF093107) delta-endotoxin [Bacillus thuringiensis]
Length = 638

Score = 339 bits (869), Expect = 6e-92
Identities = 207/559 (37%), Positives = 296/559 (52%), Gaps = 33/559 (5%)

Query: 58 LFDLIWGFIPTSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEA 117
L + +W + W F+ QIE+LI+QRI A+ L G+ D Y Y+ AL EW

Sbjct: 90 LLNQLWPTNNNAVWEAFMAQIEELIDQRISQVVRNALDALTGIHDYNYEYLAALAEWLE 149

Query: 118 NPNNALREDVIRFANTDDALITAINNFTLSFE----IPLLSVYVQAANLHLSLLRDA 173
PN A+ + RF N ++ + +F + LL+VY QAANLHL LL+DA

Sbjct: 150 RPNGARANLAFQ-RFENLHQLFVSQMPFSGSGPGERDAVALLTVYAQAANLHLLLLKDA 208

Query: 174 VSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRD 233
+G WGL+ +N ++N + YT HC+ TYN+GLENLRGTNT W ++QFR+

Sbjct: 209 EIYGARWGLNQGQINLYFNAQQDRTQIYTNHC VATYNRGLENLRGTNTESWYNYHQFRRE 268

Query: 234 LTLTVLIDVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEF---- 289
+TL +D+VALFP Y++R YP + QLTREIYT V+ + P + + + +

Sbjct: 269 MTLMDLVALFPYNYLRQYPNGANQLTREIYTDPVVFNPANQGLCRRWRNNPYMTFS 328

Query: 290 -----GVRPPLHMDFMNSLFVTAET-----TVRSQTVWGGHLVSSRNTAGNRINFP SYGVFN 340
+RPPHL D +NSL + + + W GH + + + SYG

Sbjct: 329 ELENFTIRPPLHFDRLNSLTINSHRFPISSNFMDYWAGHTLRRSYMNSAVQEDSYGATT 388

Query: 341 PGGAIWIADEDPRPFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGT-NHTRTFRNSG- 398
+ R S V R G V G+ +F G N T + N+G

Sbjct: 389 STRV--TINTGVNGTNRIESTAVDFRSGLLG---VYGVHRASFVPGGLFNGTISPANAGC 443

Query: 399 --TIDSLDEIPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGS--DSWRAPMFSWTHRSAT 454
D+ DE+P ++N+G+P SH L+HVT+ + + +GS +S P++ W +

Sbjct: 444 RNLHDTRDELPLEENNGSP----SHRLSHVTFLSFLTDQAGSIRNSGAVPLYVWARQDID 499

Query: 455 PTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQ 514
NTI RITQ+PLVKA + +GTTVVRGPGFTGGDILRRTS G VN+N L Q

Sbjct: 500 LNNITANRITQLPLVKASEIAAGTTVVRGPGFTGGDILRRTSAGTLGTIRVNVNSPLTQ 559

Query: 515 RYRARIRYASTTNLRIYVTVAGERIFAGQFNKMTDGTPLTFQSFYSATINTAFTFPM SQ 574
RYR R RYASTT+ +V G + F +TM++G ++S+ +T+F F Q

Sbjct: 560 RYRVRFYASTTDFNFFVIRGGTTVNNTFPRTMNSGQESRYESYVTFEFTSFNLFQIQ 619

Query: 575 SSFTVGADTFSSGNEVYID 593
+ + +FSSG +VY+D

Sbjct: 620 DTLRLTVQSFSSGQVYVD 638

>pdb|1JI6|A Chain A, Crystal Structure Of The Insecticidal Bacterial Del
Endotoxin Cry3bb1 Bacillus Thuringiensis
Length = 589

Score = 337 bits (864), Expect = 2e-91
Identities = 200/578 (34%), Positives = 305/578 (52%), Gaps = 35/578 (6%)

Query: 49 VPGVGVAFLGFDLIWGFITPSD---WSLFLQIEQLIEQRIETLERNRAITTLRGLADSY 105
VP G + I PSD W F+ Q+E LI+++IE +++A+ L+GL +++

Sbjct: 19 VPFAGALTSFYQSFLNTIWPSDADPWKAQFMAQVEVLIDKKIEEYAKSKALAELOGLQNNF 78

Query: 106 EIYIEALREWEANP---NNAQLREDVIRFANTDDALITAINNFTLSFEIPLLSVYVQA 162
E Y+ AL W+ P + + ++ +R F+ + ++ +F ++ FE+ L Y QA

Sbjct: 79 EDYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQA 138

Query: 163 ANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTR 222
AN HL LL+DA FG+ WG V Y+R + L +YT HC++ YN GL LR+G

Sbjct: 139 ANTHLLLLKDAQVFGEWGYSSDVAEFYHRQLKLTQQYTDHCVNWNVGLNGLRGSTYD 198

Query: 223 QWARFNQFRRLTLTLTVLIDVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPN 282
W +FN+FR++TLTVLD++ LFP YD+R Y ++LTR+I+T + + + P

Sbjct: 199 AWFKNFRFRREMTLTVLDLIVLFPFYDIRLYSKGVKTELTRDIPTDPIFSLNLTQEQYPT 258

Query: 283 GFNRAEFGVRPPLHMDFMNSLFVTAET-----VRSQTVWGGHLVSSRNTAGN--RINFP 334
F E +R PHL D++ + S W G+ V +R + G+ I P

Sbjct: 259 -FLSIENSIRKPLFDYLQGIEFHTRLQPGYFGKDSFNWYSGNYVETRPSIGSSKITITSP 317

Query: 335 SYGVFNPGGAIWIADEDPRPFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGT-----TG 387
YG + D + YRT+++ + N LG+ V F Q T

Sbjct: 318 FYG-DKSTEPVQKLSFDGQVYRTIANTDV--AAWPNGKVYLGVTKVDFSQYDDQKNETS 374

Query: 388 TNHTRTRFNRSGTI---DSLDEIPPQDNGSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAP 444
T + RN+G + DS+D++PP+ YSH LN+ + P
Sbjct: 375 TQTYDSKRNNGHVSAQDSIDQLPPEETDEPLEKAYSHQLNYAECF-----LMQDRRGITP 429

Query: 445 MFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDI--LRRTSGGPFA 502
F+WTHRS NTID E+ITQ+P+VKA+ L SG +++ GPGFTGG++ L+ +S
Sbjct: 430 FFTWTHRSVDFNTIDAEEKITQLPVVKAYALSSGASIEGPGFTGGNLLFLKESNSIAK 489

Query: 503 YTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTMDTGDPDPLTFQSFSYA 562
+ + + L QRYR RIRYASTTNLR++V + NKTm+ D LT+Q+F A
Sbjct: 490 FKVTLSAALLQRYRVRIYASTTNLRLVQNSNNDLFVIYINKTMNKDDDLTYQTFDLA 549

Query: 563 TINTAFTFPMSSQSSFTVGADTFSSGNEVYIDRFELIPV 600
T N+ F ++ +GA++F S ++YID+ E IPV
Sbjct: 550 TTNSNMGFSGDKNELIIGAESFVSNEKIYIDKIEFIPV 587

>sp|Q06117|C3BB_BACTU Pesticidal crystal protein cry3Bb (Insecticidal delta-endotoxin
CryIIIB(b)) (Crystalline entomocidal protoxin) (74 kDa
crystal protein)
pir||I39811 gene cryIIIB2 protein - Bacillus thuringiensis
gb|AAA22334.1| (M89794) cryIIIB2 [Bacillus thuringiensis]
Length = 652

Score = 337 bits (864), Expect = 2e-91
Identities = 200/578 (34%), Positives = 305/578 (52%), Gaps = 35/578 (6%)

Query: 49 VPGVGVAFLGLFDLIWGFIPTSD---WSLFLQLIEQLIEQRIETLERNRAITTLRGLADSY 105
VP G + I PSD W F+ Q+E LI+++IE +++A+ L+GL +++
Sbjct: 82 VPFAGALTSFYQSFLNTIWPSDADPWKAFMAQVEVLIDKKIEEYAKSKALAEQLQNNF 141

Query: 106 EIYIEALREWEANP---NNAQLREDVRIRFANTDDALITAINNETLTSFEIPLLSVYVQA 162
E Y+ AL W+ P + + ++ +R F+ + ++ +F ++ FE+ L Y QA
Sbjct: 142 EDYVNALNSWKKTPSLRSKRSDRIELFSQAESHFRNSMPSFAVSKFEVLFLPTYQA 201

Query: 163 ANLHLSLLRDAVSFGQWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTR 222
AN HL LL+DA FG+ WG V Y+R + L +YT HC++ YN GL LRG+
Sbjct: 202 ANTHLLLKDAQVFGEEWGYSSSEDVAEFYHRQLKLTQQYTDHCVNWNVGLNGLRGSTYD 261

Query: 223 QWARFNQFRRDLTLTVLDIVALEFNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPN 282
W +FN+FR++TLTVD++ LFP YD+R Y ++LTR+I+T + + + P
Sbjct: 262 AWWKFNRRFRREMTLTVLDLIVLFFPYDIRLYSGVKTELTRDIFTDPIFSLNTLQYEGPT 321

Query: 283 GFNRAEFGVRPPHLMDFMNSLFVTAET-----VRSQTVWGGLVSSRNTAGN--RINFP 334
F E +R PHL D++ + S W G+ V +R + G+ I P
Sbjct: 322 -FLSIENSIRKPHLFDYLQIEFHTRLQPGYFGKDSFNYWSGNYVETRPSIGSSKITSP 380

Query: 335 SYGVFNPGGAIWIADPRPFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQ-----TG 387
YG + D + YRT+++ + N LG+ V F Q T
Sbjct: 381 FYG-DKSTEPVQKLSFDGQKVYRTIANTDV--AAWPNGKVYLGVTKVDFSQYDDQKNETS 437

Query: 388 TNHTRTRFNRSGTI---DSLDEIPPQDNGSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAP 444
T + RN+G + DS+D++PP+ YSH LN+ + P
Sbjct: 438 TQTYDSKRNNGHVSAQDSIDQLPPEETDEPLEKAYSHQLNYAECF-----LMQDRRGITP 492

Query: 445 MFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDI--LRRTSGGPFA 502
F+WTHRS NTID E+ITQ+P+VKA+ L SG +++ GPGFTGG++ L+ +S
Sbjct: 493 FFTWTHRSVDFNTIDAEEKITQLPVVKAYALSSGASIEGPGFTGGNLLFLKESNSIAK 552

Query: 503 YTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTMDTGDPDPLTFQSFSYA 562
+ + + L QRYR RIRYASTTNLR++V + NKTm+ D LT+Q+F A
Sbjct: 553 FKVTLSAALLQRYRVRIYASTTNLRLVQNSNNDLFVIYINKTMNKDDDLTYQTFDLA 612

Query: 563 TINTAFTFPMSSQSSFTVGADTFSSGNEVYIDRFELIPV 600
T N+ F ++ +GA++F S ++YID+ E IPV
Sbjct: 613 TTNSNMGFSGDKNELIIGAESFVSNEKIYIDKIEFIPV 650

>sp|P17969|C3BA_BACTO PESTICIDIAL CRYSTAL PROTEIN CRY3BA (INSECTICIDAL DELTA-ENDOTOXIN
CRYIIIB(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (75 KDA
CRYSTAL PROTEIN)

pir||S10228 parasporal crystal protein, coleopteran-active - *Bacillus thuringiensis* (fragment)
emb|CAA34983.1| (X17123) coleopteran-active delta-endotoxin open reading frame
(659 AA) [*Bacillus thuringiensis*]
Length = 659

Score = 335 bits (860), Expect = 6e-91
Identities = 203/580 (35%), Positives = 305/580 (52%), Gaps = 39/580 (6%)

Query: 49 VPGVGVAFLGFDLIWGFITPSD---WSLFLQLIEQLIEQRIETLERNRAITTLRGLADSY 105
VP G + I PSD W F+ Q+E LI+++IE +++A+ L+GL +++
Sbjct: 90 VPFAGALTSFYQSFLNAIWPSDADPWKAFMAQVEVLIDKKIEEYAKSKALAEQLQGLQNNF 149

Query: 106 EIYIEALREWEANPNNAQLRED---VRIRFANTDDALITAINNFTLTSFEIPLLSVYVQA 162
E Y+ AL W+ P N+ R +R F+ + ++ +F ++ FE+ L Y QA
Sbjct: 150 EDYVNALDSWKKAPVNLRSRRSQDRIRLFSQAESHFRNSMPSFAVSKFEVLFLPTYAQA 209

Query: 163 ANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNR 222
AN HL LL+DA FG+ WG + Y R+ L +YT HC++ YN GL +LRG+
Sbjct: 210 ANTHLLLLKDAQVFGEEWGYSSEDIAEFYQRLKLTQQYTDHCVNWNVGLNSLRGSTYD 269

Query: 223 QWARFNQFRRDLTLTVLDIVLFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPN 282
W +FN+FRR++TLTVLD++ LFP YDVR Y ++LTR+I+T + + + P
Sbjct: 270 AWWKFNRFRRREMTLTVLDLIVLFPFYDVRLYSKGVKTELTRDIFTDPIFTLNALQEYQPT 329

Query: 283 GENRAEFQVRPHLMDFMNSL-FVTA-----ETVRSQTVWGGHLVSSRNTAGNR--INFP 334
F+ E +R PHL D++ + F T S W G+ V +R+ G+ I P
Sbjct: 330 -FSSIENSIRKPHLFDYLRGIEFHTRLRPGYSGKDSFNWWSGNYVETRPSIGSNDTITSP 388

Query: 335 SYG---VFNPGGAIWIADEDPRPFYRTLSDPVFVRGGFGNPHYVLGLRGVAF----QQTGT 388
YG P I D+ YRT+++ F + G+ V F Q
Sbjct: 389 FYGDKSIEP---IQKLSFDGQKVYRTIANTDI--AAFPGDKIYFGVTKVDFSQYDDQKNE 443

Query: 389 NHTRTFRNS-----GTIDSLDEIPPQDNGSAPWNDYSHVLNHVTFVRWPGEISGSDSWR 442
T+T+ + G DS+D++PP+ YSH LN+ +
Sbjct: 444 TSTQTYDSKRYNGYLGAQDSIDQLPPEPTTDEPLEKAYSHQLNYAECF-----LMQDRRG 498

Query: 443 APMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDI--LRRTSGGP 500
P F+WTHRS NTID E+ITQ+P+VKA+ L SG +++ GPGFTGG++ L+ +S
Sbjct: 499 IPFFTWTTHRSVDFNTIDAEEKITQLPVVKAYALSSGASIIIEGPGFTGGNLLFLKESNSI 558

Query: 501 FAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTDGDPLTFQSFS 560
+ + + L QRYR RIRYASTTNLR++V + NKTMT+ LT+Q+F
Sbjct: 559 AKFKVTLNSAALLQRYRVRIYASTTNLRLEFVQNSNNDLVIYINKTMNIDGLTYQTFD 618

Query: 561 YATINTAFTFPMSQSSFTVGADTFSSGNEVYIDRFELIPV 600
+AT N+ F + F +GA++F S ++YID+ E IPV
Sbjct: 619 FATSNSNMGFSGDTNDFIIGAESFVSNEKIYIDKIEFIPV 658

>gb|AAA74198.1| (U31633) Cry3Bb2 [*Bacillus thuringiensis*]
Length = 652

Score = 335 bits (859), Expect = 8e-91
Identities = 202/578 (34%), Positives = 305/578 (51%), Gaps = 35/578 (6%)

Query: 49 VPGVGVAFLGFDLIWGFITPSD---WSLFLQLIEQLIEQRIETLERNRAITTLRGLADSY 105
VP G + I PSD W F+ Q+E LI+++IE +++A+ L+GL +++
Sbjct: 82 VPFAGALTSFYQSFLDTIWPSDADPWKAFMAQVEVLIDKKIEEYAKSKALAEQLQGLQNNF 141

Query: 106 EIYIEALREWEANP---NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQA 162
E Y+ AL W+ P + + + +R F+ + ++ +F ++ FE+ L Y QA
Sbjct: 142 EDYVNALNSWKKTPLSLRSKRSQDRIRLFSQAESHFRNSMPSFAVSKFEVLFLPTYAQA 201

Query: 163 ANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNR 222
AN HL LL+DA FG+ WG V Y+R+ L +YT HC++ YN GL LRG+
Sbjct: 202 ANTHLLLLKDAQVFGEEWGYSSEDIAEFYHRLKLTQQYTDHCVNWNVGLNGLRGSTYD 261

Query: 223 QWARFNQFRRDLTLTVLDIVLFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPN 282
W +FN+FRR++TLTVLD++ LFP YDVR Y ++LTR+I+T + + + P

Sbjct: 262 AWWKFNRRFRREMTTLVLDLIVLFPFYDVRLYSKGVKTELTRDIFTDPIFSLNTLQEYGP 321

Query: 283 GENRAEFGVRPPHLMDFMNSL-FVTA-----ETVRSQTVWGGHLVSSRNTAGN--RINFP 334
F E +R PHL D++ + F T S W G+ V +R + G+ I P

Sbjct: 322 -FLSIENSIRKPHLFDYLQGIEFHTRLQPGYSGKDSFNYWSGNYVETRPSIGSSKITITSP 380

Query: 335 SYGVFNPGGAIWAIEDPRPFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQ-----TG 387
YG + D + YRT+++ + N G+ V F Q T

Sbjct: 381 FYG-DKSTEPVQKLSFDGQKVYRTIANTDV--AAWPNGKIYFGVTKVDFSQYDDQKNETS 437

Query: 388 TNHTRTFRNSGTI---DSLDEIPPQDNGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAP 444
T + RN+G + DS+D++PP+ YSH LN+ + P

Sbjct: 438 TQTYDSKRNGHVGAQDSIDQLPPEITDEPLEKAYSHQLNYAECF-----LMQDRRTIP 492

Query: 445 MFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDI--LRRTSGGPFA 502
F+WTHRS NTID E+ITQ+P+VKA+ L SG +++ GPGFTGG++ L+ +S

Sbjct: 493 FETWTHRSVDFNTIDAEEKITQLPVVKAYALSSGASIEGPGFTGGNLLFLKESSNSIAK 552

Query: 503 YTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTDGDPLTFQSFSYA 562
+ + + L QRYR RIRYASTTNLR++V + NKT+ D LT+Q+F A

Sbjct: 553 FKVTLSAALLQRYRVRIRYASTTNLRLFVQNSNNDFIVYINKTMNIDDDLTQTFDLA 612

Query: 563 TINTAFTFPMSSQSSFTVGADTFSSGNEVYIDRFELIPV 600
T N+ F + +GA++F S ++YID+ E IPV

Sbjct: 613 TTNSNMGFSGDTNELIIGAESFVSNEKIYIDKIEFIPV 650

>pir||S39536 parasporal crystal protein-related protein - Bacillus thuringiensis
Length = 1154

Score = 333 bits (853), Expect = 4e-90

Identities = 221/602 (36%), Positives = 312/602 (51%), Gaps = 61/602 (10%)

Query: 50 PGVGVAFLFDLIWGFITPSD---WSLFLQLIEQLIEQRIETLERNRAITTLRGLADSY 105
P G+ G ++GF+ PS+ W F+ Q+E+LIEQRI A+ L G+ + Y

Sbjct: 72 PVGGILTGFSLTFLGFLWPSNDQAVWEAFIEQMEELIEQRIQSDQVVRTALDDLTGIQNY 131

Query: 106 EIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTL---TSFEIPLLSVYVQ 161
Y+ AL+EWE PN + ++ RF ++++ +F F+ LL VY Q

Sbjct: 132 NQYLIALKEWEERPNGVRANLVQ-RFEILHALFVSSMPFSGSGPGSQRFQAQLLVVYAQ 190

Query: 162 AANLHLSLLRDAVSFGQGWGLDIATVNN-HYNRLINLIHRYTKHCLDTYNQGLNLRGTN 220
AANLHL LL DA +G WGL + + N ++N L YT HC++ YN GL LRGT+

Sbjct: 191 AANLHLLLLADAKEYGARWGLRESQIGNLYFNELOTRTRDYTNHCVNAYNNGLAGLRGTS 250

Query: 221 TRQWARENQFRDLTLTLVDLIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANI 280
W +++QFRR+ TL +D++ALFP Y+ R YPI + QLTRE+YT + S S+

Sbjct: 251 AESWLKYHQFRREATLMAMDLIALFPYNTTRRYPIAVNPQLTREYVTDPLGVPSEESSLF 310

Query: 281 PN-----GFNRAEFGV-RPPHLMDFMNSLFTVTAET---VRSQTV--WGGHLV 321
P F+ E + PHL D +N+L + + + +Q + W GH V

Sbjct: 311 PELRCLRWQETSAMTFNLENAISSPHLFDITNNLMIYTGFSFVHLTNQLIEGWIGHSV 370

Query: 322 SS-----RNTAGNRINFPSYGVFNPGGAIWAIEDPRPFYRTLSDPVFVRGGFG 370
+S R G+ + +Y FN R Y+ ++ GF

Sbjct: 371 TSSLLASGPTTVLRNRYGSTTSIVNYFSFND-----RDVYQ-INTRSHITGLGFQ 418

Query: 371 NPHYVLGLRGVAFQQTGTNHTTRFRNSGTID---SLDEIPPQDNGAPWNDYSHVLNHV 426
N + G+ F GT ++ T RN+ T + S+DE+P D + YSH L+H+

Sbjct: 419 NAP-LFGITRAQFYPPGGT-YSVTQRNALTCQYNSIDELPSLDPNPISRSYSYHRLSHI 476

Query: 427 T-FVRWPGEISGSD--SWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVR 483
T ++ I G + S P + WTHR TNTI +RITQ+PLVK+ + +GTTVVR

Sbjct: 477 TSYLHRVLTIDGINIYSGNLPTYVWTHRDVLTNTITADRTQLPLVKSFEIPAGTTVVR 536

Query: 484 GPGFTGGDILRRTSGGPFAITIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQ 543
GPGFTGGDILRRT G F V L QRYR R R+ASTTNL I + V ++

Sbjct: 537 GPGFTGGDILRRTGVGTFTIRVTTAPLTQRYRIRFRFASTTNLFIGIRVGDQVNYFD 596

Query: 544 FNKMTDGDPLTFQSFSYATINTAFTFPMSSQSSFTVGADTFSSGNEVYIDRFELIPVTAT 603

F +TM+ GD L ++SF+ T F F Q +V A+ FS+G EVY DR E+IPV
Sbjct: 597 FGRTMNRGDELRYESFATREFTTDFNFRQPQELISVFANAFSAGQEVYFDRIEIIIPVNP 656

Query: 604 LE 605

E

Sbjct: 657 RE 658

>emb|CAA52927.1| (X75019) delta-endotoxin [Bacillus thuringiensis]
Length = 1144

Score = 333 bits (853), Expect = 4e-90

Identities = 221/602 (36%), Positives = 312/602 (51%), Gaps = 61/602 (10%)

Query: 50 PGVGVAFLGFLDLIWGFITPSD---WSLFLQIEQLIEQRIETLERNRAITTLRGLADSY 105

P G+ G ++GF+ PS+ W F+ Q+E+LIEQRI A+ L G+ + Y

Sbjct: 62 PVGGILTGFSLTLFGFLWPSNDQAVWEAFIEQMEELIEQRISDQVVRTALDDLTGIQNY 121

Query: 106 EIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTL---TSFEIPLLSVYVQ 161

Y+ AL+EWE PN + ++ RF +++++F F+ LL VY Q

Sbjct: 122 NQYLIALKEWEERPNGVRANLVLQ-RFEILHALFVSSMPFSGSGPGSQRFQAQLLVYQA 180

Query: 162 AANLHLSLLRDAVSFGQWGLDIATVNN-HYNRLINLIHRYTKHCLDTYNQGLNLRGTN 220

AANLHL LL DA +G WGL + + N ++N L YT HC++ YN GL LRGT+

Sbjct: 181 AANLHLLLADAKEYGARWGLRESQIGNLYFNELQTRTRDTYNHCVNAYNGLAGLRGTS 240

Query: 221 TRQWARFNQFRDLTLTLVLDIVALEFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANI 280

W +++QFRR+ TL +D++ALEP Y+ R YPI + QLTRE+YT + S S+

Sbjct: 241 AESWLKYHQFRREATLMAMDIALFPYYNTRRYPIAVNPQLTREVTDPGLGVPSEESSLF 300

Query: 281 PN-----GENRAEFGV-RPPHLMDFMNSLFVTAET----VRSQTV--WGGLHV 321

P F+ E + PHL D +N+L + + + +Q + W GH V

Sbjct: 301 PELRCLRWQETSAMTFFSNLENAISSPHLFDITNNLMIYTGFSFVHLTNQLIEGWIGHSV 360

Query: 322 SS-----RNTAGNRINFPSYGVFNPGGAIWIADEDPRPFYRTLSDPVFVRGGFG 370

+S R G+ + +Y FN R Y+ ++ GF

Sbjct: 361 TSSLLASGPTTVLRRNYGSTTSIVNYFSFND-----RDVYQ-INTRSHITGLGFQ 408

Query: 371 NPHYVLGLRGVAFQQTGTNHTRTFRNSGTID----SLDEIPPQDMSGAPWNDYSHVLNHV 426

N + G+ F GT ++ T RN+ T + S+DE+P D + YSH L+H+

Sbjct: 409 NAP-LFGITRAQFYPGGT-YSVTQRNALTCEQNYNSIDELPSLDNPEISRSYSHRLSHI 466

Query: 427 T-FVRWPGEISGSD--SWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVR 483

T ++ I G + S P + WTHR TNTI +RITQ+PLVK+ + +GTTVVR

Sbjct: 467 TSYLHRVLTIDGINIYSGNLPTYVWTHRDVLTNTITADRITQLPLVKSFEPAGTTVVR 526

Query: 484 GPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQ 543

GPGFTGGDILRRT G F V L QRYR R R+ASTTNL I + V ++

Sbjct: 527 GPGFTGGDILRRTVGTFGTIRVRTTAPLTQRYRIRFRFASTTNLFIGIRVGDRQVNYFD 586

Query: 544 FNKTMDTGDPLTFQSFYSATINTAFTFPMSSQSFSTVGADTFSSGNEVYIDRFELIPVTAT 603

F +TM+ GD L ++SF+ T F F Q +V A+ FS+G EVY DR E+IPV

Sbjct: 587 FGRTMNRGDELRYESFATREFTTDFNFRQPQELISVFANAFSAGQEVYFDRIEIIIPVNP 646

Query: 604 LE 605

E

Sbjct: 647 RE 648

>sp|O06014|C9DA_BACTP PESTICIDIAL CRYSTAL PROTEIN CRY9DA (INSECTICIDAL DELTA-ENDOTOXIN
CRYIXD(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (132 KDA
CRYSTAL PROTEIN)

dbj|BAA19948.1| (D85560) cry9Da1 [Bacillus thuringiensis]

Length = 1169

Score = 325 bits (834), Expect = 7e-88

Identities = 216/632 (34%), Positives = 311/632 (49%), Gaps = 57/632 (9%)

Query: 15 LNNPEVEILNEERSTGRPLDISLSLTFLLSEF-----VPGVGVAFLGFLDLIWGFITPS 69

L NP + + +G+ + + +++ LLS F V V L + +W S

Sbjct: 57 LINPNLSV-----SGKDVIQVGINIVGRLLSFFGFPPSSQWVTYTYLLNSLWPDDENS 110

Query: 70 DWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVR 129
W F+ ++E+LI+Q+I + RA+ L GL +Y +Y+EAL EW PN A+ V
Sbjct: 111 VWDAFMERVEELIDQKISEAVKGRALDDLTGLQYNYNLYVEALDEWLNRPNGARASL-VS 169

Query: 130 IRFANTDDALITAINNFTL----TSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIA 185
RF D + +F ++ LL VY QAANLHL LL+DA +G WGL+
Sbjct: 170 QRFNILDSFLTQFMPSPGSGPSONYATILLPVYAQAANLHLLLLKDADIYGARWGLNQT 229

Query: 186 TVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRRDLTLTVLDIVLAF 245
++ ++R +L YT HC+ YN GL LRGT W ++NQ+RR++TLT +D+VALF
Sbjct: 230 QIDQFHSRQQSLTQTYTNHCVTAYNDGLAELRGTTAESWFKYNQYRREMTLTAMDVLAF 289

Query: 246 PNYDVRTYPIQTSSQLTREIYTSSVIED-----SPVSANIPNGFNRAEFG 290
P Y++R YP T+ QLTRE+YT + D +P N N
Sbjct: 290 PYYNLRQYPDTGNPQLTREYVTDPIAFDPLEQPTTQLCRSWYINPAFRNHLNFSVLENSL 349

Query: 291 VRPPHLMDFMNSLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNP--GGAIWIA 348
+RPPHL ++++L + + + W G V + I SYG+ + G I +
Sbjct: 350 IRPPHLFERLSLQILVNYQTNNGSAWRGSRVRYHYLHSSIIQEKSYGLLSDPVGANINVQ 409

Query: 349 DEDPRPFYRTLSDPVFVRGGFGNPH-----YVLGLRGVAFQQTGTNHTRTFRN 396
+ D Y+ +S G+ + V G+ G + Q G +
Sbjct: 410 NND---IYQIISQVSNFASPVGSSYSVWDTNLYLSSGQVSGISG--YTQQGIPAVCLQQR 464

Query: 397 SGTIDSLDEIPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSW---RAPMFSWTHRSA 453
+ T DE+P + G +YSH L+H+T R+ SGS S P WTHR
Sbjct: 465 NST----DELPSLNPEGDIIRNYSHRLSHITQYRFQATQSGSPSTVSANLPTCVWTHRDV 520

Query: 454 TPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLP 513
NTI +ITQ+PLVKA+ L SG TVV+GPGFTGGD++RRT+ G F V++ G L
Sbjct: 521 DLDNTITANQITQLPLVKAYELSSGATVVKGPFTGGDVIRRTNTGGFGAIRVSVTGPLT 580

Query: 514 QRYRARIRYASTTNLRIYVTVAGERIFAGQFNKTMDTGDPLTFQSFSYATINTAFTFPMS 573
QRYR R RYAST + +VT G I +F +TM+ G ++S+ T F F S
Sbjct: 581 QRYRIRERYASTIDFDFVTRGTTINNFRFTRTMNRGQESRYESYRTVEFTTFFNFQTS 640

Query: 574 QSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
Q S EVY+DR E+IPV E
Sbjct: 641 QDIIRTSIQGLSGNGEVYLDRIEIIIPVNPARE 672

>sp|Q45708|C7AB_BACUK Pesticidial crystal protein cry7Ab (Insecticidal delta-endotoxin
CryVIIA(b)) (Crystalline entomocidal protoxin) (130 kDa
crystal protein)
gb|AAA21121.1| (U04368) CryIII delta-endotoxin [Bacillus thuringiensis]
Length = 1138

Score = 323 bits (828), Expect = 3e-87
Identities = 207/609 (33%), Positives = 311/609 (50%), Gaps = 55/609 (9%)

Query: 25 EERSTGRLPLDISLSLTRFLLSEF-VPGVGVAFLFDLIWGFITPSD---WSLFLQIEQ 80
E ++G ++ +S+T LS VPG + I G + P D W F+ ++E
Sbjct: 50 EALASGNTAINTVSVTGATLSALGVPASFITNFYFKITGLLWPHDKNIWDEFMTEVET 109

Query: 81 LIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDALI 140
LIEQ+IE RN+A+ L GL ++ IY +AL +W NP++ V RF D
Sbjct: 110 LIEQKIEQYARNKALAELEGLGNNLTIIYQQALEDWLNPNDDPATITRVIDRFRILDALFE 169

Query: 141 TAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHR 200
+ + +F + +EIPLL+VY QAANLHL+LLRD+ +G W + +YNR I
Sbjct: 170 SYMPSFRVAGYEIPLLTVYAQAANLHLALLRDSTLYGDKWEFTQNNIEENYNRQKKHISE 229

Query: 201 YTKHCLDTYNQGLENLRGNTNRQWARFNQFRRDLTLTVLDIVLAFPNYDVRTYPIQTSSQ 260
Y+ HC+ YN GL L G+ QW +N+FRR++ L VLDI A+FP YD R Y ++TS+Q
Sbjct: 230 YSNHCVKWYNSGLSRLNGSTYEQWINYNRFRREMILMVLDAAVFPIYDPRMYSMETSTQ 289

Query: 261 LTREIYTSSVIEDSPVSANIPN-----GFNRAE-FGVRPPHLMDFMNSLFVTAETVRSQT 314
LTRE+YT P+S +I N F++ E +R PHL+D+++ L++ ++ +
Sbjct: 290 LTREYVT-----DPISLSISNPGIGSPFSQMENTAIRPHLVLDYLDLYIYTSKYKAFS 343

Query: 315 -----VWGGHLVSSRNTAGNRINFPSYGVFN-----PGGAIWIADDPFPFYRTLS 360
W H VS + + + N + G++ GA D YRTL+

Sbjct: 344 HEIQPDLFYWSAHKVSFKQS--EQSNLYTTGIYGKTSYIISGAYSFRGND---IYRTLA 398

Query: 361 DPVVRGGFGNPHYV-----LGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDMSGAP 415
P V + + V G++G + + T+ DS+D++PP G P

Sbjct: 399 APSVVVYPYQNYGVEQVEFYGVKGHVHYRGDNKYDLTY-----DSIDQLPP---DGEP 449

Query: 416 WND-YSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHT 474
++ Y+H L H T + D+ P+FSWTHRSA N I P +IT+IP VK +

Sbjct: 450 IHEKYTHRLCHATAI--SKSTPDYDNATIPIFSWTHRSAEYNNRIYPNKITKIPAVKMYK 507

Query: 475 LQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTV 534
L +TVV+GPGFTGGD++R S G +N L Q YR R+RYA+ + + V +

Sbjct: 508 LGDTSTVVKGPGFTGGDLVKRGSNGYIGDIKATVNSPLSQNYRVRYATNVSGQFVYI 567

Query: 535 AGERIFAGQFNKTMdT---GDPLTFQSFYSATINTAFTFPMSQSSFTVGADTFSSGNEVY 591
+ +F T++T G LT+ SF Y +T FP T+ S+ + Y

Sbjct: 568 NDKITLQRKQNTVETIGEGKDLTYGSFGYIEYSTTIQFPDKHKPITLHLSLNNSSFY 627

Query: 592 IDRFELIPV 600
+D E IPV

Sbjct: 628 VDSIEFIPV 636

>sp|Q9ZNL9|C9EA_BACTA Pesticidal crystal protein cry9Ea (Insecticidal delta-endotoxin
CryIXE(a)) (Crystalline entomocidal protoxin) (130 kDa
crystal protein)
dbj|BAA34908.1| (AB011496) Cry9 like protein [Bacillus thuringiensis serovar
aizawai]
Length = 1150

Score = 322 bits (825), Expect = 7e-87
Identities = 213/578 (36%), Positives = 300/578 (51%), Gaps = 51/578 (8%)

Query: 58 LFDLIWGFITPSDWSLELLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEA 117
L + +W + W F+ QIE+LI+Q+I A+ L GL D YE Y+ AL EW

Sbjct: 99 LLNQWLPTNDNAVWEAFMAQIEELIDQKISAQVVRNALDDLTGLHDYEEYLAALAEWLE 158

Query: 118 NPNNALREDVRIRFANTDDALITAINNFTLSFE----IPLLSVYVQAANLHLSLLRDA 173
PN A+ V RF N A +T + +F + LL+VY QAANLHL LL+DA

Sbjct: 159 RPNGARANL-VTQRFENLHTAFVTRMPSFGTGPQSQRDAVALLTVYAQAANLHLLLLKDA 217

Query: 174 VSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRD 233
+G WGL +N ++N YT HC++TYN+GLE++RGNT W +++FRR+

Sbjct: 218 EIYGARWGLQGGQINLYFNAQQERTRIYTNHCVETYNRGLEDVRGTNTESWLNHYHFRRE 277

Query: 234 LTLTVLDIVLFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANI-----PNGFN 285
+TL +D+VALFP Y+VR YP + QLTREIYT ++ + P + I N F+

Sbjct: 278 MTLAMDLVALFPFYNVRQYPNGANPQLTREIYTDPIVYNPPANQGICRRWGNNPYNTFS 337

Query: 286 RAEFG-VRPPLMDFMNSLFV-----TAETVRS-QTVWGGHLVSSRNTAGNRINFPSYGV 338
E +RPPHL + +N L + TA T S W GH + S++ SYG

Sbjct: 338 ELENAFIRPPLHFERLNRLTISRNRYTAPTNSFLDYWSGHTLQSQHANNPTTYETSYGQ 397

Query: 339 FNPGGAIWIADDPFPFYRTLSDPVVRGGFGNPHYVL-GLRGVAFQQTG-----TNHTR 392
++ R + FGN + L G+ + TG TN

Sbjct: 398 ITSNTLRLNTNGARAIDSARN-----FGNLYANLYGVSSLNIFPTGVMSEITNAAN 450

Query: 393 TFRNSGTIDSLDEIPPQDMSGAPWNDYSHVLNHVTFVRWPGEISG--SDSWRAPMFSWTH 450
T R + + +E+P ++N+ ++L+HVTF+R+ G + P + WT

Sbjct: 451 TCRQD--LTTEELPLENN-----FNLLSHVTFLRFNTTQGGPLATLGFVPTYVWTR 501

Query: 451 RSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNING 510
TNTI +RITQ+P VKA + GTTVV+GPGFTGGDILRRT GG N+N

Sbjct: 502 EDVDTTNTITADRITQLPWVKASEIGGTTVVKGPGFTGGDILRRTDGGAVGTIRANVNA 561

Query: 511 QLPQRYRARIYASTTNLRIYVTVAGERIFAG-QFNKTMdTGDPLTFQSFYSATINTAFT 569
L Q+YR R+RYASTT+ + + V AG TM LT++SF+ T+ T

Sbjct: 562 PLTQQYRIRLRVASTTSFVVNLVFNNSA--AGFTLPSTMAQNGSLTYESFN--TLEVHT 617

Query: 570 FPMSQSSFTVGADTFS--SGNEVYIDRFELIPVTATLE 605

SQS T+ + F SG EVY+D+ E++P+ T E

Sbjct: 618 IRFSQSDTTLRNIFPSISGQEVYVDKLEIVPINPTRE 655

>sp|Q45707|C7AB_BACUA Pesticidal crystal protein cry7Ab (Insecticidal delta-endotoxin CryVIIA(b)) (Crystalline entomocidal protoxin) (130 kDa crystal protein)

gb|AAA21120.1| (U04367) CryIII delta-endotoxin [Bacillus thuringiensis]
Length = 1138

Score = 319 bits (818), Expect = 5e-86

Identities = 207/609 (33%), Positives = 311/609 (50%), Gaps = 55/609 (9%)

Query: 25 EERSTGRPLDISLSLTRLSEF-VPGVGVAFLFDLIWGFITPSD---WSLFLQLIEQ 80

E ++G ++ +S+T LS VPG + I G + P + W F+ ++E

Sbjct: 50 EALASGNTAINTVSVTGATLSALGVPGASFITNFYKITGLLWPHNKNIWDEFMTEVET 109

Query: 81 LIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDALI 140

LIEQ+IE RN+A+ L GL ++ IY +AL +W NP++ V RF D

Sbjct: 110 LIEQKIEQYARNKALAELEGLGNNLTIIYQQALEDWLNNDPATITRVIDRFRILDALFE 169

Query: 141 TAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHR 200

+ + +F + +EIPLL+VY QAANLHL+LLRD+ +G WG + +YNR I

Sbjct: 170 SYMPSFRVAGYEIPLLTVYAQAANLHLALLRDSTLYGDKWGFTQNNIEENYNRQKKHISE 229

Query: 201 YTKHCLDTYNQGLNLRGTNRQWARFNQFRDLTLTVLDIVAFPNYDVRTYPIQTSSQ 260

Y+ HC+ YN GL L G+ QW +N+FRR++ L VLDI A+FP YD R Y ++TS+Q

Sbjct: 230 YSNHCVKWYNSGLSRLNGSTYEQWINYRFRREMILMVLDAVFPYIDPRMYSMETSTQ 289

Query: 261 LTREIYTSSVIEDSPVSANIPN-----GFNRAE-FGVRPPHLMDFMNSLFVTAETVRSQT 314

LTRE+YT P+S +I N F++ E R PHL+D+++ L++ ++ +

Sbjct: 290 LTREYVT-----DPISLSISNPDIGSFSQMENTAFRTPHLVDYLDLYIYTSKYKAFS 343

Query: 315 -----VWGHLVSSRNTAGNRINFPYGVFN-----PGGAIWIADDPREFYRTLS 360

W H VS + + + N + G++ GA D YRTL+

Sbjct: 344 HEIQPDLFYVCVHKVSFKKS--EQSNLYTTGIYGKTSYISGAYSFRGND---IYRTLA 398

Query: 361 DPVFVRGGFGNPHYV-----LGLRGVAFQOTGTNHTRTFRNSGTIDSLEIPPQDNSGAP 415

P V + + V G++G + + T+ DS+D++PP G P

Sbjct: 399 APSVVVYPYTQNYGVEQVEFYGVKGHVHYRGDNKYDLTY-----DSIDQLPP---DGEP 449

Query: 416 WND-YSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHT 474

++ Y+H L H T + D+ P+FSWTHRSA N I P +I +IP VK +

Sbjct: 450 IHEKYTHRLCHATAI--SKSTPDYDNATIPIFSWTHRSAEYNNRIYPNKKIKIPAVKMYK 507

Query: 475 LQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYASTTNLRIYVTV 534

L +TVV+GPGFTGGD+++R S G +N L Q+YR R+RYA++ V +

Sbjct: 508 LDDLSTVVGKPGFTGGDLVKRGSNGYIGDIKATVNSPLSQKYRVRVRYATSVSGLFNFI 567

Query: 535 AGERIFAGQFNKTMDT---GDPLTFQSFYSATINTAFTFPMSQSSFTVGADTFSSGNEVY 591

E F T++T G LT+ SF Y +T FP T+ + S+ + Y

Sbjct: 568 NDEIALQKNFQSTVETIGEGKDLTYGSEFYIEYSTTIQFPNEHPKITLHLNHLNNSNPFY 627

Query: 592 IDRFELIPV 600

+D E IPV

Sbjct: 628 VDSIEFIPV 636

>sp|P07130|C3AA_BACTT Pesticidal crystal protein cry3Aa precursor (Insecticidal delta-endotoxin CryIIIA(a)) (Crystalline entomocidal protoxin) (73 kDa crystal protein)

pir||I39812 crystal protein cryC - Bacillus thuringiensis

emb|CAA68482.1| (Y00420) crystal protein (AA 1-644) [Bacillus thuringiensis]

gb|AAA50255.1| (M37207) crystal protein [Bacillus thuringiensis serovar morrisoni]

gb|AAA22541.1| (J02978) insecticidal crystal protein [Bacillus thuringiensis]

gb|AAC43266.1| (U10985) CryIIIA [Bacillus thuringiensis]

prf||1312401a insecticidal crystal protein [Bacillus thuringiensis]

prf||1402204a coleopteran specific protein [Bacillus thuringiensis]

Length = 644

Score = 319 bits (817), Expect = 6e-86
Identities = 205/625 (32%), Positives = 324/625 (51%), Gaps = 56/625 (8%)

Query: 17 NPEVEILNEERSTGRPLD-----ISLSLTRLLESEFVPGVGVAFLGLFDLIWG----- 64
NP +E LN + R+ D + S T+ ++ + + VG G+ +G
Sbjct: 34 NPTLEDLNYKEFL-RMTADNNTEALDSSTTKDVIQKGISVVGDLGLGVGFPFGGALVSFY 92

Query: 65 -----FITPSD--WSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEA 117
I PS+ W F+ Q+E L++Q+I +N+A+ L+GL ++ E Y+ AL W+
Sbjct: 93 TNFLNTIWPSEDPWKAFMEQVEALMDQKIADYAKNKALAEQLQNNVEDYVSALSSWQK 152

Query: 118 NP---NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV 174
NP N + +R F+ + ++ +F ++ +E+ L+ Y QAAN HL LL+DA
Sbjct: 153 NPVSSRNPHSQGRIELFSQAESHFRNSMPSFAISGYEVLFLTTYQAANTHLFLLKDAQ 212

Query: 175 SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNROWARFNQFRDL 234
+G+ WG + + Y R + L Y T HC+ YN GL+ LRG++ W FN++RR++
Sbjct: 213 IYGEWGYEKEDIAEFYKRQLKLTQEYTDHCVKYNVGLDKLRGSSYESWVNFNRYRREM 272

Query: 235 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPP 294
TLTVLD++ALFP YDVR YP + ++LTR++ T ++ + + F+ E +R P
Sbjct: 273 TLTVDLIALFPLYDVRLYPKEVKTELTRDVLTDPIVGVNNL-RGYGTTFSNIENYIRKP 331

Query: 295 HLMDFMNSLFVTAETV-----RSQTVWGGHLVSSRNTAGNR--INFPSYGVFNPGGAIW 346
HL D+++ + S W G+ VS+R + G+ I P YG +
Sbjct: 332 HLFYDLHRIQFHTRFQPGYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYG-NKSSEPVQ 390

Query: 347 IADEDPRPFYRTLSD-----PVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTF---RNS 397
+ + YR +++ P V G + QT T+T+ RN
Sbjct: 391 NLEFNGEKYRAVANTNLAVWPASVYSGVTKVEF-----SQYNDQTDEASTQTYDSKRN 445

Query: 398 GTI--DSLDEIPPQDMSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATP 455
G + DS+D++PPP+ YSH LN+V G P+ +WTH+S
Sbjct: 446 GAVSWDSIDQLPPLVTKYKQSGASVVGPRFTGGDIIQCTENGSAATYVTPDVSYSQK 500

Query: 456 TNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQR 515
N ID ++ITQ+PLVKA+ LQSG +VV GP FTGGDI++ T G A V + Q+
Sbjct: 501 FNMIDSKKITQLPLVKAYKLQSGASVVGPRFTGGDIIQCTENGSAATYVTPDVSYSQK 560

Query: 516 YRARIRYASTTNLRIYVTVAGERIFAGQFNKTMGTGDPLTFQSFSYATINTAFTFPMSQS 575
YRARI YAST+ + +++ G F+KT++ GD LT+ SF+ A+ +T F +S +
Sbjct: 561 YRARIRYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLTYNFNLASFST--PFELSGN 618

Query: 576 SFTVGADTFSSGNEVYIDRFELIPV 600
+ +G S+G++VYID+ E IPV
Sbjct: 619 NLQIGVTGLSAGDKVYIDKIEFIPV 643

>pir||A27323 parasporal crystal protein CryIIIA - Bacillus thuringiensis
gb|AAA22336.1| (M22472) delta-endotoxin [Bacillus thuringiensis]
emb|CAB41411.1| (AJ237900) Cry3Aa protein [Bacillus thuringiensis]
Length = 652

Score = 319 bits (817), Expect = 6e-86
Identities = 205/625 (32%), Positives = 324/625 (51%), Gaps = 56/625 (8%)

Query: 17 NPEVEILNEERSTGRPLD-----ISLSLTRLLESEFVPGVGVAFLGLFDLIWG----- 64
NP +E LN + R+ D + S T+ ++ + + VG G+ +G
Sbjct: 42 NPTLEDLNYKEFL-RMTADNNTEALDSSTTKDVIQKGISVVGDLGLGVGFPFGGALVSFY 100

Query: 65 -----FITPSD--WSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEA 117
I PS+ W F+ Q+E L++Q+I +N+A+ L+GL ++ E Y+ AL W+
Sbjct: 101 TNFLNTIWPSEDPWKAFMEQVEALMDQKIADYAKNKALAEQLQNNVEDYVSALSSWQK 160

Query: 118 NP---NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV 174
NP N + +R F+ + ++ +F ++ +E+ L+ Y QAAN HL LL+DA
Sbjct: 161 NPVSSRNPHSQGRIELFSQAESHFRNSMPSFAISGYEVLFLTTYQAANTHLFLLKDAQ 220

Query: 175 SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRRDL 234
+G+ WG + + Y R + L YT HC+ YN GL+ LRG++ W FN++RR++
Sbjct: 221 IYGEWGYEKEDIAEFYKRQLKLTQEYTDHCVKWNVGLDKLRGSSYESWVNFNRYRREM 280

Query: 235 TLTVLDAIVLFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPP 294
TLTVLD++ALFP YDVR YP + ++LTR++ T ++ + + F+ E +R P
Sbjct: 281 TLTVLDAIVLFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPP 339

Query: 295 HLMDFMNSLFVTAETV-----RSQTVWGGHLVSSRNTAGNR--INFPSYGVFNPGGAIW 346
HL D+++ + S W G+ VS+R + G+ I P YG +
Sbjct: 340 HLFDYLRHQFHTRFQPGYYGNDNFYWSGNYVSTRPSIGSNDIITSPPFYG-NKSSEPQV 398

Query: 347 IADEDPFPFYRTLS-----PVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTF---RNS 397
+ + YR +++ P V G + QT T+T+ RN
Sbjct: 399 NLEFNGEKVYRAVANTNLAVWPSAVYSGVTKVEF-----SQYNDQDEASTQTYDSKRN 453

Query: 398 GTI--DSLDEIPPQDNGSAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATP 455
G + DS+D++PP+ YSH LN+V G P+ +WTH+S
Sbjct: 454 GAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFLMQG-----SRGTIPVLTWTHKSVDF 508

Query: 456 TNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQR 515
N ID ++ITQ+PLVKA+ LQSG +VV GP FTGGDI++ T G A V + Q+
Sbjct: 509 FNMIDSKKITQLPLVKAYKLQSGASVAGPRFTGGDIQCTENGSAATYVTPDVYSQK 568

Query: 516 YRARIYASTTNLRIYVTVAGERIFAGQFNKTMGTGDLTFQSFSYATINTAFTFPMSSQS 575
YRARI YAST+ + +++ G F+KT++ GD LT+ SF+ A+ +T F +S +
Sbjct: 569 YRARIYASTSQITFTLSLDGAPFNQYFDKTIKGDITLYNSFNLASFST--PFELSGN 626

Query: 576 SFTVGADTFSSGNEVYIDRFELIPV 600
+ +G S+G++VYID+ E IPV
Sbjct: 627 NLQIGVTGLSAGDKVYIDKIEFIPV 651

>gb|AAA73184.1| (M84650) crystal toxin [synthetic construct]
emb|CAA50310.1| (X70979) cryIIIA insect control protein [synthetic construct]
Length = 597

Score = 318 bits (816), Expect = 8e-86
Identities = 192/559 (34%), Positives = 300/559 (53%), Gaps = 38/559 (6%)

Query: 66 ITPSD--WSFLLLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANP---N 120
I PS+ W F+ Q+E L++Q+I +N+A+ L+GL ++ E Y+ AL W+ NP
Sbjct: 52 IWPSEDPWKAFFMEQVEALMDQKIADYAKNKALAEQLQNNVEDYVSALSSWQKNPVSSR 111

Query: 121 NAQLREDVIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW 180
N + +R F+ + ++ +F ++ +E+ L+ Y QAAN HL LL+DA +G+ W
Sbjct: 112 NPHSQGRIREFLSQAESHFRNSMPSFAISGYEVLFLTYYAQAANTHLFLLKDAQIYGEW 171

Query: 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRRDLTLTVLD 240
G + + Y R + L YT HC+ YN GL+ LRG++ W FN++RR++TLTVLD
Sbjct: 172 GYEKEDIAEFYKRQLKLTQEYTDHCVKWNVGLDKLRGSSYESWVNFNRYRREMTLTVLD 231

Query: 241 IVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM 300
++ALFP YDVR YP + ++LTR++ T ++ + + F+ E +R PHL D++
Sbjct: 232 LIALFPLYDVRLYPKEVKTELTRDVLTDPIVGVNNL-RGYGTTFNSNIENYIRKPHLFDYL 290

Query: 301 NSLFVTAETV-----RSQTVWGGHLVSSRNTAGNR--INFPSYGVFNPGGAIWADEDP 352
+ + S W G+ VS+R + G+ I P YG + + +
Sbjct: 291 HRIQFHTRFQPGYYGNDNFYWSGNYVSTRPSIGSNDIITSPPFYG-NKSSEPQVNLNFNG 349

Query: 353 RPFYRTLS-----PVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTF---RNSGTI--D 401
YR +++ P V G + QT T+T+ RN G + D
Sbjct: 350 EKVYRAVANTNLAVWPSAVYSGVTKVEF-----SQYNDQDEASTQTYDSKRNVGAVSWD 404

Query: 402 SLDEIPPQDNGSAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDP 461
S+D++PP+ YSH LN+V G P+ +WTH+S N ID
Sbjct: 405 SIDQLPPETTDEPLEKGYSHQLNYVMCFLMQG-----SRGTIPVLTWTHKSVDFNMIDS 459

Query: 462 ERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARI 521
++ITQ+PLVKA+ LQSG +VV GP FTGGDI++ T G A V + Q+YRARI

Sbjct: 460 KKITQLPLVKAYKLSGASVVAGPRFTGGDIIQCTENGSAATIIYVTPDVSYSQKYRARIH 519

Query: 522 YASTTNLRIYVTVAGERIFAGQFNKMTDGTGDLTFQSFYSYATINTAFTFPMSQSSFTVGA 581
YAST+ + +++ G F+KT++ GD LT+ SF+ A+ +T F +S ++ +G

Sbjct: 520 YASTSQITFTLSLDGAPFNQYYFDKTIKGDILTYSNENLASFST--PFELSGNNLQIGV 577

Query: 582 DTFSSGNEVYIDRFELIPV 600
S+G++VYID+ E IPV

Sbjct: 578 TGLSAGDKVYIDKIEFIPV 596

>emb|CAA51996.1| (X73600) CryIIIA insecticidal crystal protein [synthetic construct]
Length = 610

Score = 318 bits (816), Expect = 8e-86
Identities = 192/559 (34%), Positives = 300/559 (53%), Gaps = 38/559 (6%)

Query: 66 ITPSD--WSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANP---N 120
I PS+ W F+ Q+E L++Q+I +N+A+ L+GL ++ E Y+ AL W+ NP

Sbjct: 52 IWPSEDPWKAFMEQVEALMDQKIADYAKNKALAEQLQNNVEDYVSALSSWQKNPVSSR 111

Query: 121 NAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW 180
N + +R F+ + ++ +F ++ +E+ L+ Y QAAN HL LL+DA +G+ W

Sbjct: 112 NPHSQGRIRELFSQAESHFRNSMPSFAISGYEVLFLTYYAQAANTHLFLLKDAQIYGEEW 171

Query: 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRDLTLTVLD 240
G + + Y R+ L YT HC+ YN GL+ LRG++ W FN++RR++TLTVLD

Sbjct: 172 GYEKEDIAEFYKRLKLTQEYTDHCVKWNVGLDKLRGSSYESWVNFNRYREMTTLTVLD 231

Query: 241 IVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM 300
++ALFP YDVR YP + ++LTR++ T ++ + + F+ E +R PHL D++

Sbjct: 232 LIALFPYLDVRLYPKEVKTELTRDVLTDPIGVNNL-RGYGTTFNSNIENYIRKPHLPDY 290

Query: 301 NSLFVTAETV-----RSQTVWGGHLVSSRNTAGNR--INFPSYGVFNPGGAIWIADDP 352
+ + S W G+ VS+R + G+ I P YG + + +

Sbjct: 291 HRIQFHTRFQPGYYGNDSFNWSGNYVSTRPSIGSNDIITSPFYG-NKSSEPVQNLEFNG 349

Query: 353 RPFYRTLSD-----PVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTF---RNSGTI--D 401
YR +++ P V G + QT T+T+ RN G + D

Sbjct: 350 EKVYRAVANTNLAVWPSAVYSGVTKEF-----SQYNDQTDEASTQTYDSKRNVGAVSWD 404

Query: 402 SLDEIPPQDNGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDP 461
S+D++PP+ YSH LN+V G P+ +WTH+S N ID

Sbjct: 405 SIDQLPEPETTDEPLEKGYSHQLNYVMCFLMQ-----SRGTIPVLWTHKSVDFFNMIDS 459

Query: 462 ERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARI 521
++ITQ+PLVKA+ LQSG +VV GP FTGGDI++ T G A V + Q+YRARI

Sbjct: 460 KKITQLPLVKAYKLSGASVVAGPRFTGGDIIQCTENGSAATIIYVTPDVSYSQKYRARIH 519

Query: 522 YASTTNLRIYVTVAGERIFAGQFNKMTDGTGDLTFQSFYSYATINTAFTFPMSQSSFTVGA 581
YAST+ + +++ G F+KT++ GD LT+ SF+ A+ +T F +S ++ +G

Sbjct: 520 YASTSQITFTLSLDGAPFNQYYFDKTIKGDILTYSNENLASFST--PFELSGNNLQIGV 577

Query: 582 DTFSSGNEVYIDRFELIPV 600
S+G++VYID+ E IPV

Sbjct: 578 TGLSAGDKVYIDKIEFIPV 596

>pdb|1DLC| Delta-Endotoxin CryIIia (Bt13)
Length = 584

Score = 318 bits (816), Expect = 8e-86
Identities = 192/559 (34%), Positives = 300/559 (53%), Gaps = 38/559 (6%)

Query: 66 ITPSD--WSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANP---N 120
I PS+ W F+ Q+E L++Q+I +N+A+ L+GL ++ E Y+ AL W+ NP

Sbjct: 39 IWPSEDPWKAFMEQVEALMDQKIADYAKNKALAEQLQNNVEDYVSALSSWQKNPVSSR 98

Query: 121 NAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW 180
N + +R F+ + ++ +F ++ +E+ L+ Y QAAN HL LL+DA +G+ W

Sbjct: 99 NPHSQGRIRELFSQAESHFRNSMPSFAISGYEVLFLTYYAQAANTHLFLLKDAQIYGEEW 158

Query: 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRDLTLTVLD 240
G + + Y R + L Y T H C + Y N G L + L R G + + W F N + + R R + + T L T V L D
Sbjct: 159 GYEKEDIAEFYKRQLKLTQEYTDHCVKWNVGLDKLRGSSYESWVNFNRYRREMTLTVLD 218

Query: 241 IVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM 300
++ALFP YDVR YP + ++LTR++ T ++ + + F+ E +R PHL D++
Sbjct: 219 LIALFPLYDVRLYPKEVKTELTRDVLTDPIVGNNL-RGYGTTFNSNIENYIRKPHLFDYL 277

Query: 301 NSLFVTAETV-----RSQTVWGGHLVSSRNTAGNR--INFPSYGVFNPGGAIWIADDP 352
+ + S W G + V S + R + G + I P Y G + + +
Sbjct: 278 HRIQFHTRFQPGYYGNDSEFNWWSGNVSTRPSIGSNDIITSPFYG-NKSSEPVQNLEFNG 336

Query: 353 RPFYRTLSD-----PVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTF---RNSGTI--D 401
Y R + + + P V G + + Q T T + T + R N G + D
Sbjct: 337 EKVYRAVANTNLAVWPSAVYSGVTKEVF-----SQYNDQTDEASTQTYDSKRNVGAVSWD 391

Query: 402 SLDEIPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDP 461
S+D++PP+ YSH LN+V G P+ +WTH+S N ID
Sbjct: 392 SIDQLPPETTDEPLEKGYSHQLNYVMCFLMQG-----SRGTIPVLWTHKSVDFNMIDS 446

Query: 462 ERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARI 521
++ITQ+PLVKA+ LQSG +VV GP FTGGDI++ T G A V + Q+YRARI
Sbjct: 447 KKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQCTENGSAATYVTPDVSYSQKYRARIH 506

Query: 522 YASTNLRIYVTVAGERIFAGQFNKTMGTGDLTFQSFYSATINTAFTFPMSSQSSFTVGA 581
YAST+ + + + G F+KT++ GD LT+ SF+ A+ +T F +S ++ +G
Sbjct: 507 YASTSQITFTLSLDGAPFNQYYFDKTIKGDTLTYNSFNLASFST--PFELSGNNLQIGV 564

Query: 582 DTFSSGNEVYIDRFELIPV 600
S+G++VYID+ E IPV
Sbjct: 565 TGLSAGDKVYIDKIEFIPV 583

>gb|AAA22542.1| (M30503) insect control protein [Bacillus thuringiensis]
Length = 644

Score = 317 bits (811), Expect = 3e-85
Identities = 204/625 (32%), Positives = 323/625 (51%), Gaps = 56/625 (8%)

Query: 17 NPEVEILNEERSTGRPLD-----ISLSLTRLLESEFVPGVGVAFLGLFDLIWG----- 64
NP +E LN + R+ D + S T+ ++ + + VG G+ +G
Sbjct: 34 NPTLEDLNYKEFL-RMTADNNTALDSSTTKDVIQKGISVVGDLGLGVGFPPGGALVSFY 92

Query: 65 -----FITPSD--WSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEA 117
I PS+ W F+ Q+E L++Q+I +N+A+ L+GL ++ E Y+ AL W+
Sbjct: 93 TNFLNTIWPSEDPWKAEMEQLMDQKIADYAKNKALAEQLQNNVEDYVSALSSWQK 152

Query: 118 NP---NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV 174
NP N + +R F+ + ++ +F ++ +E+ L+ Y QAAN HL LL+DA
Sbjct: 153 NPVSSRNPHSQGRIRELFSQAESHFRNSMPSFAISGYEVFLFTTYAQAANTHLFLKDAQ 212

Query: 175 SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRRDL 234
+G+ WG + + Y R + L Y T H C + Y N G L + L R G + + W F N + + R R + +
Sbjct: 213 IYGEWGYEKEDIAEFYKRQLKLTQEYTDHCVKWNVGLDKLRGSSYESWVNFNRYRREM 272

Query: 235 TLTVLIDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPP 294
TLTVLD++ALFP YDVR YP + ++LTR++ T ++ + + F+ E +R P
Sbjct: 273 TLTVLIDIALFPLYDVRLYPKEVKTELTRDVLTDPIVGNNL-RGYGTTFNSNIENYIRK 331

Query: 295 HLMDFMNSLFVTAETV-----RSQTVWGGHLVSSRNTAGNR--INFPSYGVFNPGGAIW 346
HL D+++ + S W G + V S + R + G + I P Y G +
Sbjct: 332 HLFYDLHRIQFHTRFQPGYYGNDSEFNWWSGNVSTRPSIGSNDIITSPFYG-NKSSEPVQ 390

Query: 347 IADEDPFPFYRTLSD-----PVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTF---RNS 397
+ + Y R + + + P V G + + Q T T + T + R N
Sbjct: 391 NLEFNGEKVYRAVANTNLAVWPSAVYSGVTKEVF-----SQYNDQTDEASTQTYDSKRN 445

Query: 398 GTI--DSLDEIPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATP 455
G + DS+D++PP+ YSH LN+V G P+ +WTH+S

Sbjct: 446 GAVSWDSIDQLPPETTDEPLEKGYSHQLNVMCFMQG-----SRGTIPVLTWTHKSVDF 500

Query: 456 TNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQR 515
N ID ++ITQ+PLVKA+ LQSG +VV GP FTGGDI++ T A V + Q+

Sbjct: 501 FNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQCTENASAATIIYVTPDVSYSQK 560

Query: 516 YRARIRYASTTNLRIYVTVAGERIFAGQFNKMTMDTGDPLTFQSFSYATINTAFTFPMSQS 575
YRARI YAST+ + +++ G F+KT++ GD LT+ SF+ A+ +T F +S +

Sbjct: 561 YRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLTYNFNLASFST--PFELSGN 618

Query: 576 SFTVGADTFSSGNEVYIDRFELIPV 600
+ +G S+G++VYID+ E IPV

Sbjct: 619 NLQIGVTGLSAGDKVYIDKIEFIPV 643

>sp|Q03749|C7AA BACTU PESTICIDIAL CRYSTAL PROTEIN CRY7AA (INSECTICIDAL DELTA-ENDOTOXIN
CRYVIIA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (129 KDA
CRYSTAL PROTEIN)

pir||A48944 insecticidal crystal protein CryIIIC - Bacillus thuringiensis
gb|AAA22351.1| (M64478) crystal protein [Bacillus thuringiensis]
Length = 1138

Score = 315 bits (808), Expect = 7e-85

Identities = 203/609 (33%), Positives = 310/609 (50%), Gaps = 55/609 (9%)

Query: 25 EERSTGRPLPLDISLSLTRLLESEF-VPGVGVAFLGLDLIWFITPSD---WSLFLQLIEQ 80
E ++G ++ +S+T LS VPG + I G + P + W F+ ++E

Sbjct: 50 EALASGNTAINTVSVTGTATLSALGVPGASFITNFYKLAGLLWPENGKIWDEFMTVEEA 109

Query: 81 LIEQRIETLERNRAITTLRGLADSYEYIEALREWEANPNNAQLREDVRIREFANTDDALI 140
LI+Q+IE RN+AI L GL + + Y +AL +W ++ + V F D

Sbjct: 110 LIDQKIEEYVRNKAIAELDGLGSALDKYQKALADWLKGQDDPEAILSVADEFRIIDSLFE 169

Query: 141 TAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHR 200
++ +F +T +EIPLL+VY QAANLHL+LLRD+ +G WG + +YNR I

Sbjct: 170 FSMPSFKVTGYEIPLLTVYAQAANLHLALLRDSTLYGDKWGFTQNNIEENYNRQKKRISE 229

Query: 201 YTKHCLDTYNQGLENLRGNTNRQWARFNQFRRDLTLTVLDIVALEFPNYDVRTYPIQTSSQ 260
Y+ HC YN GL L G+ QW +N+FR++ L LD+VA+FP +D R Y ++TS+Q

Sbjct: 230 YSDHCTKWYNSGLSRLNGSTYEQWINYNRFRREMILMALDLVAVFPFHDPRRYSMETSTQ 289

Query: 261 LTREIYTSSVIEDSPVSANIPN----GFNRAE-FGVRPPHLMDFMNSLFVTAETVRSQT 314
LTRE+YT PVS +I N F++ E +R PHL+D+++ L++ ++ +

Sbjct: 290 LTREYYT-----DPVSLSISNPDIGPSFSQMENTAIRTPHLVDYLDLYIYTSKYKAFS 343

Query: 315 -----VWGGHLVSSRNRTAGNRINFPSYGVFN-----PGGAIWIADDPFPRFYRTL 360
W H VS + + + N + G++ GA D YRTL+

Sbjct: 344 HEIQPDLFYWSAHKVSFKKS--EQSNLYTTGIYGKTSGYISSGAYSFHGND---IYRTLA 398

Query: 361 DPVFVRGGFGNPHYV-----LGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNSGAP 415
P V + + V G++G + + T+ DS+D++PP G P

Sbjct: 399 APSVVVYPYTQNYGVEQVEFYGVKGHVHYRGDNKYDLTY-----DSIDQLPP---DGEP 449

Query: 416 WND-YSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHT 474
++ Y+H L H T + D+ P+FSWTHRSA N I P +IT+IP VK +

Sbjct: 450 IHEKYTHRLCHATAIF--KSTPDYDNATIPIFSWTHRSAEYNNRIYPNKITKIPAVKMYK 507

Query: 475 LQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYASTTNLRIYVTV 534
L +TVV+GPGFTGGD++R S G +N L Q+YR R+RYA+ + + V +

Sbjct: 508 LDDPSTVVKGPGFTGGDLVKGSTGYIGDIKATVNSPLSQYRVRVRYATNVSGQFNVIYI 567

Query: 535 AGERIFAGQFNKMTMDT---GDPLTFQSFSYATINTAFTFPMSQSSFTVGADTFSSGNEVY 591
+ +F T++T G LT+ SF Y +T FP T+ S+ + Y

Sbjct: 568 NDKITLQTKFQNTVETIGEGKDLTYGSFGYIEYSTTIQFPDEHPKITLHLSDLSSNNSSFY 627

Query: 592 IDRFELIPV 600
+D E IPV

Sbjct: 628 VDSIEFIPV 636

>gb|AAB97923.1| (AF042733) delta-endotoxin [Bacillus thuringiensis]

Length = 645

Score = 314 bits (805), Expect = 2e-84
Identities = 210/620 (33%), Positives = 304/620 (48%), Gaps = 57/620 (9%)

Query: 15 LNNPEVEILNEERSTGRPLDISLSLTRLFLSEF-----VPGVGVAFLGLFDLIWGFITPS 69
L NP + + +G+ + + +++ LLS F V V L + +W S
Sbjct: 42 LINPNLSV-----SGKDVIQVGINIVGRLLSFFGFPFSSQWVTVYTYLLNSLWPDDENS 95

Query: 70 DWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVR 129
W F+ ++E+LI+Q+I + RA+ L GL +Y +Y+EAL EW PN A+ V
Sbjct: 96 VWDAFMERVEELIDQKISEAVKGRALDDLTGLQYNLYVEALDEWLNRPNGARASL-VS 154

Query: 130 IRFANTDDALITAINNFTL----TSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIA 185
RF D + +F ++ LL VY QAANLHL LL+DA +G WGL+
Sbjct: 155 QRFNILDLSLTQFMPSFGSGPGSQNYATILLPVYAQAANLHLLLLKADIDYGARWGLNQT 214

Query: 186 TVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRDLTLTVLDIVLF 245
++ ++R +L YT HC+ YN GL LRGT W ++NQ+RR++TLT +D+VALF
Sbjct: 215 QIDQFHSRQQLTQTYTNHCVTAYNDGLAELRGTTAESWFKYNQYRREMTLTAMDVLVF 274

Query: 246 PNYDVRTYPIQTSSQLTREIYTSSVIED-----SPVSANIPNGFNRAEFG 290
P Y++R YP T+ QLTRE+YT + D +P N N
Sbjct: 275 PYYNLRQYPDGNTNPQLTREYTDPIAFDPLEQPTTQLCRSWYINPAFRNHLNFSVLENSL 334

Query: 291 VRPPHLMDFMNSLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNP--GGAIWIA 348
+RPPHL + +++L + + + W G V + I SYG+ + G I +
Sbjct: 335 IRPPHLFERLSNLQILVNYQTNGSAWRGSRVRYHYLHSSIIQEKSYGLSDPVGANINVQ 394

Query: 349 DEDPRPFYRTLSDPVFVRGGFGNPH-----YVLGLRGVAFQQTGTNHTRTFRN 396
+ D Y+ +S G+ + V G+ G + Q G +
Sbjct: 395 NND---IYQIISQVSNFASPGSSYSVWDNTNLYLSSGQVSGISG--YTQQGIPAVCLQQR 449

Query: 397 SGTIDSLDEIPPQDNGAPWNDYSHVLNHVTFVRWPGEISGSDSW---RAPMFSWTHRSA 453
+ T DE+P + G +YSH L+H+T R+ SGS S P WTHR
Sbjct: 450 NST---DELPSLNPEGDIIRNYSHRLSHITQYRFQATQSGSPSTVSANLPTCVWTHRDV 505

Query: 454 TPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLP 513
NTI +ITQ+PLVKA+ L SG TVV+GPGFTGGD++RRT+ G F V++ G L
Sbjct: 506 DLDNTITANQITQLPLVKAYELSSGATVVKGPFTGGDVIRRTNTGGFGAIRVSVTGPLT 565

Query: 514 QRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTMDTGDPLTFQSFYATINTAFTFPMS 573
QRYR R RYAST +VT G I +F +TM+ G ++S+ T F F S
Sbjct: 566 QRYRIRFRYASTIDFDFVTRGGTTINNFRTRTMNRQESRYESYRTVEFTTFFNFQTS 625

Query: 574 QSSFTVGADTFSSGNEVYID 593
Q S EVY+D
Sbjct: 626 QDIIRTSIQGLSGNGEYVLD 645

>sp|Q9X597|CQAA BACTF Pesticidial crystal protein cry26Aa (Insecticidal delta-endotoxin
CryXXVIA(a)) (Crystalline entomocidal protoxin) (131 kDa
crystal protein)
gb|AAD25075.1|AF122897_1 (AF122897) Cry26Aa1 protein [Bacillus thuringiensis serovar
finitimus]
Length = 1163

Score = 303 bits (775), Expect = 5e-81
Identities = 195/592 (32%), Positives = 307/592 (50%), Gaps = 49/592 (8%)

Query: 49 VPGVGVAFLGLFDLIWGFITPSD----WSLFLQLIEQLIEQRIETLERNRAITTLRGLADS 104
VP G + ++GF+ P++ W F+ Q+E LI+++I RN+AI+ L+GL ++
Sbjct: 84 VPFAGALTTFYQKLFGLFPPNNNTKQWEEFMKQVEALIDEKISDAVRNKAISELQGLVNN 143

Query: 105 YEIIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAAN 164
+Y EAL EW N N +R+ V R+ D + +F + FE+ LL VY QAAN
Sbjct: 144 ITLYTEALEELENKENPAVRDRVLQWRILDGFFEQQMPFAVKGFVLLLVVYTQAAN 203

Query: 165 LHLSSLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQW 224
LHL LRDA +G WGL ++ ++ RL+ YT HC++ YN GL+ L ++ + W

Sbjct: 204 LHLSSLRDAYIYGAEWGLTPTNIDQNHTRLLRHS AEYTDHCVNWN YNTGLKQLENSDAKSW 263

Query: 225 ARFNQFRRDLTLTVL DIALFPNYDVRTYPIQTSSQLTREIYTSSV-----IEDSPVSA 278
++N+FR++TL+VLD++ALFP YDV+ YPI T+ QLTRE+YT + D SA

Sbjct: 264 FQYNRFRREMTLSVLDVIALFPAYDVKMYPIPTNFQLTREVYTDVIGKIGRNSDHWYSA 323

Query: 279 NIPNGFNRAEFGVRPPHLMDFMNSLFVTAETVRSQTV-----WGGHLVSSRNTAGNRIN 332
N P+ N +R PH++D++ L + TV + W GH++S T+ N

Sbjct: 324 NAPSFSNLESTLIRTPHVVDYIKKLIFYATVDYGIYGRSGKWVGHIITSA-TSANTTE 382

Query: 333 FPSYGVFNPGGAIWIADEDPRPFYRTLSDPVFV---RGFGNPHYVLGLRGVAFQQTGTN 389
+YG ++ + E + Y+T S P V + G+ P Y + R V F +

Sbjct: 383 TRNYGTIVNHDSVELNFEG-KNIYKTGSLPQGVPPYQIGYVTPIYFI-TRAVNFTVSGS 440

Query: 390 HTRTFRNSGTID-----SLDEIPPQDNGSAPWNDYSHVLNHVTFVRWPGEI 435
T + D S +++PP + YSH L HVTFF+ +

Sbjct: 441 KTSVEKYYSKKDRYSEGLPEEQGVFSTEQLPPNSIAEPEHIAYSHRLCHVTFI----SV 496

Query: 436 SGSDSWR--APMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDIL 493
S + + P+FSWTH S N + P +ITQ+P K + + ++V+ PGF GGDI

Sbjct: 497 SNGNKYSKDLPLFSWTHSSVDFDNVYPTKITQLPATKGYNV----SIVKEPGFIGGDI- 551

Query: 494 RRTSGGPFAYTIVNINGQLPQRYRARIRYASTTNLRIYVTVAGERIFAGQFNKMTMDTGP 553
+ +G VN+ + Q+YR R+RYA+ T + + + G + Q+ KT GDP

Sbjct: 552 GKNNQILKGYKVNVE-DVSQKYRFRVRYATETEGELGIKIDGRTVNLYQYKKTAPGDP 610

Query: 554 LTFQSFSYATINTAFTFPMSSQSFVTGADTFSSGNEVYIDRFELIPVTATLE 605
LT+++F Y + +T F + S+ + +SG Y+ E+IPV + E

Sbjct: 611 LTYKAFDYLFSFSTPVKFNNASSTIELFLQNKTSKT-FYLAGIEIIPVKSNEY 661

>sp|Q45744|C3CA_BACTK PESTICIDIAL CRYSTAL PROTEIN CRY3CA (INSECTICIDAL DELTA-ENDOTOXIN
CRYIIIC(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (73 KDA
CRYSTAL PROTEIN)

pir||JH0261 parasporal crystal protein cryIIID - Bacillus thuringiensis subsp.
kurstaki (strain BT1109P)

emb|CAA42469.1| (X59797) CryIIID [Bacillus thuringiensis]
Length = 649

Score = 289 bits (740), Expect = 5e-77

Identities = 202/642 (31%), Positives = 318/642 (49%), Gaps = 55/642 (8%)

Query: 3 NNIQNQCVPYNCLNPEVEILNEE----RSTGRPLDISLSLTRLFLSEFVPGVGVAFLG 58
N + N Y + P +E LN + R+T + S T+ + + + +G G+

Sbjct: 18 NEVSNHAQYPLADPTLEELNYKEFLRRRTDNNVEALDSSTTKDAIQKGISIIGDLLGV 77

Query: 59 FDLIWG-----FITPSDWL--FLLQIEQLIEQRIETLERNRAITTLRGLADS 104
+G I P + L F+ Q+E LI+Q+I +++A L+GL +

Sbjct: 78 VGFPYGGALVSFYTNLLNTIWPGEDPLKAFMQQVEALIDQKIADYAKDKATAELQGLKNV 137

Query: 105 YEIYIEALREWEANF---NNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQ 161
++ Y+ AL W+ P + + + +R F+ + ++ +F ++ +E+ L Y Q

Sbjct: 138 FKDYVSALDSWDKTPLTLLRDGRSQGRIRELFSQAESHFRSMPSFAVSGYEVLFLEPTYAQ 197

Query: 162 AANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNT 221
AAN HL LL+DA +G WG +N + + +L YT HC Y GL+ LRG+

Sbjct: 198 AANTHLLLLKDAQIYGTDWGYSTDDLNEFHTKQKDLTIEYTNHCAKWKAGLDKLRGSTY 257

Query: 222 RQWARFNQFRRDLTLTVL DIALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSA NIP 281
+W +FN++RR++TLTVLD++ LFP YDVRTY ++LTR++ T D V+ N

Sbjct: 258 EEWKFNRYRREMTLTVLDLITLFLYDVRTYTKGVKTELTRDVL T-----DPIVAVNNM 312

Query: 282 NG----FNRAEFGVRPPHLMDFMNSLFVTAET-----VRSQTVWGGHLVSSRNTAGNR- 330
NG F+ E +R PHL D++++ + S W G+ VS+R++ G+

Sbjct: 313 NGYGTTFNSNIENYIRKPHLEFDYLHAIQFHSRLQPGYFGTDSFNYWSGNYVSTRSSIGSDE 372

Query: 331 -INFPSYGVFNPGGAIWIADEDPRPFYRTLSDPVFV-RGGFGNPHYVLGLRGVAFQQTGT 388
I P YG + + + F + + V G G G+ V F Q

Sbjct: 373 IIRSPFYGNKSTLDVQNLEFNKEGVFRVANGNLAVWPVGTGGTKIHSGVTKVQFSQYND 432

Query: 389 N----HTRTF---RNSGTI--DSLDEIPPQDMSGAPWNDYSHVLNHVTFVRWPGEISGSD 439
T+T+ RN G I DS+D++PP + YSH LN+V G
Sbjct: 433 RKDEVRTQTYDSKRNVGGIVFDSIDQLPPITDESLEKAYSHQLNYVRCFLLQG-----G 487

Query: 440 SWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSG- 498
P+F+WTH+S NT+D E+ITQIP VKA L + T+VV GPGFTGGDI++ T+G
Sbjct: 488 RGIIPVFTWTHKSVDYNTLDSEKITQIPFVKAFILVNSTSVVAGPGFTGGDIKCTNGS 547

Query: 499 GPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKMTMDTGDPDLTFQS 558
G Y + + Y+ RIRYAST+ +R + + F+KTMD G+ LT+ S
Sbjct: 548 GLTLVYTPAPDLTYSKYKIRIRYASTSQVRFGIDLGSYTHSISYFDKTMKGNLTLYNS 607

Query: 559 FSYATINTAFTFPMSSSFTVGADTFSSGNEVYIDRFELIPV 600
F+ ++++ + V SG+EYVID+ E IP+
Sbjct: 608 FNLSSVSRPIEI-SGGNKIGVSVGGIGSGDEVYIDKIEFIPM 648

>sp|Q45706|C8CA_BACTP PESTICIDIAL CRYSTAL PROTEIN CRY8CA (INSECTICIDAL DELTA-ENDOTOXIN
CRYVIIIC(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (130 KDA
CRYSTAL PROTEIN)
pir||I40589 cryIII delta-endotoxin - Bacillus thuringiensis
gb|AAA21119.1| (U04366) CryIII delta-endotoxin [Bacillus thuringiensis]
prf||2112230A delta-endotoxin [Bacillus thuringiensis]
Length = 1160

Score = 246 bits (629), Expect = 4e-64
Identities = 184/598 (30%), Positives = 288/598 (47%), Gaps = 61/598 (10%)

Query: 49 VPGVGVAFLGLFDLIWGFITPSD----WSLFLQLIEQLIEQRIETLERNRAITTLRGLADS 104
+P +G F + + G + PS+ W +F+ ++E+LI+Q+I R+RAI L +
Sbjct: 86 IPVLGEVFSILGSLIGLLWPSNNENVWQIFMNRVEELIDQKILDSVRSRAIADLANSRIA 145

Query: 105 YEIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAAN 164
E Y AL +W NP++ + V+ RF N + L T + +F+ T++E PLL Y QAA+
Sbjct: 146 VEYYQNALEDWRKNPHSTRSAAVKEFRGNAEAILRTNMGSFSQNTYETPLLPTYAQAAS 205

Query: 165 LHLSLRLDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQW 224
LHL ++RD +G+ WG ++ Y ++ RY+ HC+ YN GL LRGT +QW
Sbjct: 206 LHLLVMRDVQIYGKEWGYPNQNDIDLFYKEQVSYTARYSDHCVQWYNAGLNKLRGTGAKQW 265

Query: 225 ARFNQFRRDLTLTVLDIVALFPNYDVRTYPIQTSSQLTREIYT----SSVIEDSP----- 275
+N+FR++ + VLD+VALFPNYD R YP++T++LTREI+T S V S
Sbjct: 266 VDYNRFRRENMVMVLDLVALFPNYDARIYPLETNAELTREIFTDPVGSYVTGQSSTLISW 325

Query: 276 ---VSANIPNGFNRAEFGVRPHLMDFMNSL-----FVTAETVRSQTVWGGHLVSSRNTA 327
+ A +P+ F+ E +R P + + F T+ WGG ++
Sbjct: 326 YDMIPAAALPS-FSTLENLLRKPDFFTLQEIIRMYTSFRQNGTIEYYNYWGGQRLTLYIY 384

Query: 328 GNRINFPSYGVFNPGGAIWIADEDPRPFYRTLSDPVFVRGGFGNPHYVLGLRGVAF---- 383
G+ N S GV GA I YR + + G + N +LG+ V F
Sbjct: 385 GSSFNKYS-GVL--AGAEDIIPVGQNDIYRVVWTYI---GRYTNS--LLGVNPVTIFYFSN 436

Query: 384 --QQTGTNHTRTFRNSGTIDSLDEIPPQDMSGAPWNDYSHVLNHVTFVRWPGEISGSDSW 441
Q+T + + TIDS +E+ ++ + YSH +++T G+
Sbjct: 437 NTQKTYSKPKQFAGGIKTIDSGEELTYEN-----YQSYSHRVSYITSFEIK-STGGTVLG 490

Query: 442 RAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPG-FTGGDILRRTSGGP 500
P+F WTH SA+ N I +I+QIP+ KA G G + GG.+++ + G
Sbjct: 491 VVPIFGWTHSSASRNFIYATKISQIPINKASRTSGGAVWNFQEGLYNGGPMKLSGSGS 550

Query: 501 FAYTIVNIN-----GQLPQRYRARIYASTTNLRIYVTVAGERIFAG-----QFNKMTMDT 550
++N+ QRYR RIRYAS + ++ A + TM T
Sbjct: 551 ---QVINLRVATDAKGASQRYRIRIRYASDRAGKFTISSRSPENPATYSASIAYTNTMST 607

Query: 551 GDPLTFQSFSYA---TINTAFTFPMSSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
LT+ +F+YA IN + S +F + + +YIDR E IPV E
Sbjct: 608 NASLTYSTFAYAESGPINLGIS--GSSRTFDISITKEAGANLYIDRIEFIPVNTLFE 663

>sp|Q99031|C9AA_BACTG PESTICIDIAL CRYSTAL PROTEIN CRY9AA PRECURSOR (INSECTICIDAL
DELTA-ENDOTOXIN CRYIXA(A)) (CRYSTALLINE ENTOMOCIDAL

PROTOXIN) (130 KDA CRYSTAL PROTEIN)
pir||S19306 parasporal crystal protein - Bacillus thuringiensis
emb|CAA41122.1| (X58120) delta-endotoxin CryIG protoxin [Bacillus thuringiensis]
prf||1802272A delta endotoxin [Bacillus thuringiensis serovar galleriae]
Length = 1156

Score = 236 bits (603), Expect = 4e-61
Identities = 191/648 (29%), Positives = 298/648 (45%), Gaps = 56/648 (8%)

Query: 1 MENNIQNQCVPYN-CLNNPEVEILNEERSTGRPLDISLSLRFLLSEFVPG-VGVAFGL 58
+ NN + + N C N+ + +N + + I ++ + + + G + + + L
Sbjct: 26 LANNPYSSALNLSNCQSSILNWINIIGDAAKEAVSIGTTIVSLITAPSLTGLISIVYDL 85

Query: 59 FDLIWGFITPSDWS-LFLLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEA 117
+ G + S L + + +I+ R+ N I G Y Y+EAL W
Sbjct: 86 IGKVLGGSSGQSISDLSICDLLSIIDLRSQSVLNDGIADFNQSVLLYRNYLEALDSWNK 145

Query: 118 NPNNAQLREDVRIRFANTDDALITAINNFTLTS-----FEIPLLSVYVQAANLHLSL 169
NPN+A E++R RF D + +LT+ +I LL + AA HL L
Sbjct: 146 NPNSASA-EELRTRFRIADSEFDRILTRGSLTNGGSLARQNAQILLPSFASAAFFHLLL 204

Query: 170 LRDAVSFGQWGLDIAT-VNNHYNRLINLIHRYTKHCLDTYNQGLLENLR--GTNTRQWAR 226
LRDA +G WGL AT N+ ++L+ LI YT +C+ YN+G LR GT+ W
Sbjct: 205 LRDATRYGTNWGLYNATPFINYQSKLVELIELYTDYCVHWYNRGFNELRQRGTSATAWLE 264

Query: 227 FNQFRDLTLTVLDIVAFPNYDVRTYPIQTSSQLTREIYT-----SSVIEDSPVSA 278
F+++RR++TL VLDIVA F + D+ YPI+T QL+R IYT SS+ +S S
Sbjct: 265 FHRYRREMTLMVLDIVASFSSLDITNYPIETDFQLSRVIYTDPIGFVHRSSSLRGESWFSF 324

Query: 279 NIPNGFNRAEFGVRPPLMDFMNSLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGV 338
F+ E + P F+N++ ++ ++ L S +T R+ + S
Sbjct: 325 VNRRANSELENAIPNRPSPWFLNNMIISTGSLT-----LPVSPSTDRAVRVWYGSRRDR 376

Query: 339 FNPGGAIWIADDEPRPFYRTLSDPVFVRGGFGNPHYVLGL-----RGVAFQQTGTNH 390
+P + +I E +T + + R F L R V +
Sbjct: 377 ISPANSQFIT-ELISQHTTATQTILGRNIFRVDSQACNLNDTTYGVNRAVYHDASEGS 435

Query: 391 TRT-----FRNSG-----TIDSLDEIPPQDMSGAPW-NDYSHVLNHVTFVRWPG---EISG 437
R+ + +G + + + + + P +NS P DY+H+L+ T + G + + +
Sbjct: 436 QRSVYEGYIRTTGIDNPRVQNTINTYLPGENSDIPTPEDYTHLS--TTINLTGGLRQVAS 493

Query: 438 SDSWRAPMFWSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTS 497
+ M+ WTH+S NTI+P+RITQIPL K T +G + V PGF GG +L+RT
Sbjct: 494 NRRSSLVMYGWTHKSLARNNTINPDRTIQLTKVDTRGTGVSYNDEPGFIGGALLQRTD 553

Query: 498 GGPFAITIVNINGQLPQYRARIYASTTNLRIYVTVAGERIFAGQFNKMTMDTGDLPTFQ 557
G V L Q+YR R+RYASTTN+R+ V + I + TM G+ L +
Sbjct: 554 HGSLGVLRVQFPLHLRQQYRIRVRYASTTNIRLSVNGSFGTI-SQNLPSSTMRLGEDLRYG 612

Query: 558 SFSYATINTAFTFPMSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
SF+ NT+ S + + EVY+DR E IPV T E
Sbjct: 613 SFAIREFNTSIRPTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRE 660

>emb|CAA41425.1| (X58534) crystal protein [Bacillus thuringiensis]
Length = 1151

Score = 236 bits (603), Expect = 4e-61
Identities = 191/648 (29%), Positives = 298/648 (45%), Gaps = 56/648 (8%)

Query: 1 MENNIQNQCVPYN-CLNNPEVEILNEERSTGRPLDISLSLRFLLSEFVPG-VGVAFGL 58
+ NN + + N C N+ + +N + + I ++ + + + G + + + L
Sbjct: 26 LANNPYSSALNLSNCQSSILNWINIIGDAAKEAVSIGTTIVSLITAPSLTGLISIVYDL 85

Query: 59 FDLIWGFITPSDWS-LFLLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEA 117
+ G + S L + + +I+ R+ N I G Y Y+EAL W
Sbjct: 86 IGKVLGGSSGQSISDLSICDLLSIIDLRSQSVLNDGIADFNQSVLLYRNYLEALDSWNK 145

Query: 118 NPNNAQLREDVRIRFANTDDALITAINNFTLTS-----FEIPLLSVYVQAANLHLSL 169
NPN+A E++R RF D + +LT+ +I LL + AA HL L

Sbjct: 146 NPNSASA-EELRTRFRIADSEFDRILTRGSLTNGGSLARQNAQILLPSFASAAFFHLL 204

Query: 170 LRDAVSFGQGWGLDIAT-VNNHYNRLINLIHRYTKHCLDTYNQGLENLR--GTNTRQWAR 226
LRDA +G WGL AT N+ ++L+ LI YT +C+ YN+G LR GT+ W

Sbjct: 205 LRDATRYGTNWGLYNATPFINYQSKLVELIELYTDYCVHWYNRGFNELRQRGTSATAWLE 264

Query: 227 FNQFRDLTLTLVLDIVAFPNYDVRTYPIQTSSQLTREIYT-----SSVIEDSPVSA 278
F+++RR++TL VLDIVA F + D+ YPI+T QL+R IYT SS+ +S S

Sbjct: 265 FHRYRREMTLMVLDIVASFSSLDITNYPIETDFQLSRVIYTDPIGFVHRSSLRGESWFSF 324

Query: 279 NIPNGFNRAEFGVRPPHLMDFMNSLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGV 338
F+ E + P F+N++ ++ ++ L S +T R+ + S

Sbjct: 325 VNRAFNSDLENAIPNRPSPWFLNNMIISTGSLT-----LPVSPSTDRAVRVYGSRRDR 376

Query: 339 FNPGGAIWIADDEPRPFYRTLSDPVFVRGGFGNPHYVLGL-----RGVAFQQTGTNH 390
+P + +I E + T + + R F L R V +

Sbjct: 377 ISPANSQFIT-ELISGQHTTATQTILGRNIFRVDSQACNLNDTTYGVNRAVYHDASEGS 435

Query: 391 TRT-----FRNSG----TIDSLDEIPPQDNGSAPW-NDYSHVLNHVTFVRWPG---EISG 437
R+ R +G + +++ P +NS P DY+H+L+ T + G +++

Sbjct: 436 QRSVYEGYIRTTGIDNPRVQNTYLPGENSDIPTEDYTHILS--TTINLTGGLRQVAS 493

Query: 438 SDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTS 497
+ M+ WTH+S NTI+P+RITQIPL K T +G + V PGF GG +L+RT

Sbjct: 494 NRRSSSLVMYGWTHKSLARNNTINPDRTIQLTKVDTRGTGVSYVNDPGFIGGALLQRTD 553

Query: 498 GGPFAITIVNINGQLPQRYRARIRYASTTNLRIYVTVAGERIFAGQFNKMTDGDPLTFQ 557
G V L Q+YR R+RYASTTN+R+ V + I + TM G+ L +

Sbjct: 554 HGSLGVLRVQFPLHLRQQYRIRVRYASTTNIRLSVNGSFGTI-SQNLPSMTMLGEDLRYG 612

Query: 558 SFSYATINTAFTFPMSSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
SF+ NT+ S + + EVY+DR E IPV T E

Sbjct: 613 SFAIREFNTSIRPTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRE 660

>pir||B42459 hypothetical protein 2 (cryIF 3' region) - Bacillus thuringiensis
(strain aizawai) (fragment)
Length = 380

Score = 232 bits (591), Expect = 1e-59
Identities = 131/354 (37%), Positives = 197/354 (55%), Gaps = 20/354 (5%)

Query: 2 ENNIQNQCVPY-NCLNNPEVEILNEERSTGRPLDISLSLRFLLSEFVPGVGVAFLFD 60
E +I+ Q + + +CL E E + S + IS++ + L + VP G L+

Sbjct: 29 ETDIELQNINHEDCLKISEYENVEPFVSASTIQTGISIA-GKILGTLGVPFAGQVASLYS 87

Query: 61 LIWGFTIP---SDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEA 117
I G + P + W +F+ +E++I Q+I T RN+A+T L+GL D+ +Y E+L W

Sbjct: 88 FILGELWPKGNQWEIFMEHVVEIINQKISTYARNKALDCLKGLGDALAVYHESLESWVG 147

Query: 118 NPNNALREDVRIRFANTDDALITAINNFTLTSFEIPLSVYVQAANLHLSLLRDAVSFG 177
N N + R V+ ++ + + + +F++ E+PLL +Y QAANLHL LLRDA FG

Sbjct: 148 NRKNTRARSVVKSYIALELMFVQKLPSFAVSGEEVPLLPIYAQAANLHLLLRDASIFG 207

Query: 178 QGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLT 237
+ WGL + ++ YNR + Y+ HC+ Y+ GL NLRGTN W R+NQFR+D+TL

Sbjct: 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWVRYNQFRKDMTLM 267

Query: 238 VLDIVAFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSA-----NIPNGFNRAE 288
VLD+VALFP+YD YPI+T+SQLTRE+YT ++ P ++ N P+

Sbjct: 268 VLDLVALFPSTYTLVPIKTTSQLTREYVYTDAGTVHPNASFASTTWYNNNAPSFTIES 327

Query: 289 FGVRRPHLMDFMNSLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGV 337
VR PHL+DF+ SL + +WGGH + R T G +N + G

Sbjct: 328 AVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNWGGHRLFR-TIGGMLNTSTQG 380

>gb|AAA22349.1| (M63897) ORF [Bacillus thuringiensis]
Length = 381

Score = 232 bits (591), Expect = 1e-59

Identities = 131/354 (37%), Positives = 197/354 (55%), Gaps = 20/354 (5%)

Query: 2 ENNIQNCVPY-NCLNNPEVEILNEERSTGRPLDISLSLTRLSEFVPGVGVAFLGFD 60
E +I+ Q + + +CL E E + S + IS++ + L + VP G L+

Sbjct: 29 ETDIELQINHHEDCLKISEYENVEPFVSASTIQTGISIA-GKILGTLGVFPAGQVASLYS 87

Query: 61 LIWGFITP---SDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEA 117
I G + P + W +F+ +E++I Q+I T RN+A+T L+GL D+ +Y E+L W

Sbjct: 88 FILGELWPKGKNQWEIFMEHVVEIINQKISTYARNKALTDLKGGLDALAVYHESLESWVG 147

Query: 118 NPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFG 177
N N + R V+ ++ + + +F ++ E+PLL +Y QAANLHL LLRDA FG

Sbjct: 148 NRKNTRARSVVKSQYIAELMFVQKLPSFAVSCEEVPLLPIYAQAANLHLLLRDASIFG 207

Query: 178 QGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLT 237
+ WGL + ++ YNR + Y+ HC+ Y+ GL NLRGTN W R+NQFR+D+TL

Sbjct: 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWVRYNQFRKDMTLM 267

Query: 238 VLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSA-----NIPNGFNRAE 288
VLD+VALFP+YD YPI+T+SQLTRE+YT ++ P ++ N P+

Sbjct: 268 VLDLVALFPSYDTLVYPIKTTSQLTREYVTDAGTVHPNASFASTWYNNNAPSFSSTIES 327

Query: 289 FGVRRPPLHDMFN-----SLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYG 337
VR PHL+DF+ SL + +WGGH + R T G +N + G

Sbjct: 328 AVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNWGGHRLEFR-TIGGMLNTSTQG 380

>dbj|BAB78603.1| (AB075462) crystal protein CryE6S [Bacillus thuringiensis]
Length = 1280

Score = 222 bits (565), Expect = 1e-56
Identities = 188/633 (29%), Positives = 295/633 (45%), Gaps = 61/633 (9%)

Query: 13 NCLNNPEVEILNEERSTGRPLDISLSLTRLSEFVPGVGVAFLGFDLIWGFITPSD-- 70
NC +VE+ + +T R L + + LLS P G+ ++ + PS

Sbjct: 44 NCTLKEQVELFRDSTTVRDALATTAGIITALLSVSNPAAATAGIITILIPQLWPSGSD 103

Query: 71 ---WSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLRED 127
W F+ E LI+++I RN+A+T L G+ + +Y A W N N+ Q +E

Sbjct: 104 EVTWEKFMAAAEILIKQKITEAVRNKALTELEGVYRTIRYQLAAERWNQKNDPQAQES 163

Query: 128 VRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATV 187
+R +F T+ + A+ +F + FE+PLL+VY +AANL L+LLRDAV FG+ WGL V

Sbjct: 164 IRTQFRATNTIIEFAMPSFRVAGFEVPLLNVYAEANLQLALLRDAVKFGRDWGLPQDEV 223

Query: 188 NNHYN-RLINLIHRYTKHCLDTYNQGLE-----NLRGTNTRQWAR----- 226
++ Y+ +L+ I +T HC+ +N+GLE NL WA+

Sbjct: 224 DDIYSEQLLPRIAETHDHCVTYFNRGLEEAKKLANLNDYARYPWAQYINHSKIQGIENW 283

Query: 227 --FNQFRDLTLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGF 284
FN +RR++T+ VLD+VAL+P YD R Y + T S+LTRE+YTS + + F

Sbjct: 284 NLFNDYRRNMTILVLDLVALWPTYDPRYSMTKSELTRELYTSVRGAFYGHNNNDYQNF 343

Query: 285 NRAEFG-VRPPLHDMFNLSLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPGG 343
E + PPHL+ + + V + + G + + + P GV

Sbjct: 344 EEIERNIISPHLVTPINFVTYQNDYYPMAGLQHKFNYTESIVSLESPTVGTGTSN 403

Query: 344 AIWIADDEPRPFYRTLSDPVFVRGGFGNPHYVLGLRGVAF-QQTGT-NHTRTFR--NSGT 399
I DP T+ GFG LG+ ++F +++G+ +H

Sbjct: 404 LINFVTADPFILAVTII-----GFGQLGTSLGIYAMSFGRKSGSISHVGDIEIGTDDY 456

Query: 400 IDSLDEIPPDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSW-RAPMFSWTHRSATPTNT 458
+D +D IP D++ N +++ GS ++ + ++W H S N

Sbjct: 457 LDIVDRIPVGDSTP-----NKLSWMSAAPTTLGSTTFLQYVSYAWRHPSVDSNNR 506

Query: 459 IDPERITQIPLVKAHTLQSG-TTVVRPGFTGGDILRRTSGGPFAYTIVNING-QLPQRY 516
I ++ITQIP VKA + V++GPG TGGD++ + G V I G L Y

Sbjct: 507 ISIDKITQIPAVKAFFIDDNHVKVIKGPGSTGGDLVAFSREGYGLSISVFIPGSDLVSFY 566

Query: 517 RARIRYASTNLRIYVTVAG---ERIFAGQFNKTMDTGDPLTFQSFYSATINT-AFTFPM 572

R RIRYAS+ + ++ + G E F T G+ LT+ SF Y INT A
Sbjct: 567 RVRIRYASSQSAKVTMGFGGVEESESKEFNFPATYSNGN-LTYNSFGY--INTLAIASQS 623

Query: 573 SQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
+ + V + E +D+ E IP+ +LE

Sbjct: 624 TAQTIEVYFRQYEEA-EFIVDKLEFIPMEMSLE 655

>dbj|BAB72016.2| (AB074413) insecticidal crystal protein bun2 [Bacillus thuringiensis]
Length = 660

Score = 221 bits (563), Expect = 2e-56
Identities = 179/592 (30%), Positives = 275/592 (46%), Gaps = 44/592 (7%)

Query: 36 ISLSLSTRFLLSEFVPGVGVAFLGLFDLIWGFIPTSD-----WSLFLQLIEQLIEQRIETL 89
+S L+ F + G+ + G D+W SD W + IE+L+++R+ET
Sbjct: 71 LSTILSLFGIPLIGEGIDLLGAADFLW---PESDGGHQYTWEEDLMNHIEELMDERLETE 127

Query: 90 ERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINN-FTL 148
+R A+ LRGL ++ +A WE N N+ + V F+ + + + F+
Sbjct: 128 KRTTALDDLRLGLKALLGLFRDAFDSWEKNQNDPIAKNRVGGYFEDVHTHFVKDMASIFSA 187

Query: 149 TSFEIPLLSVYVQAANLHLSLRDAVSFGQWGLDIATVNNHYNRLINLIHRYTKHCLDT 208
T+++E LL VY QAANLHL LLR+ V +G WG+ A + ++++L+ Y HC+
Sbjct: 188 TNYEVL LLPVYAQAANLHLLLLREGVIYGSRWGIAPAA-DFYHDQLLKYTAIYANHCVTW 246

Query: 209 YNQGLLENLRG--TNTRQWARFNQFRDLTLTVLDIVAFPNYDVRTYPIQTSSQLTREIY 266
YN GL + + W RFN +RRD+T+TVLDI+ALFP YD R Y ++LTREIY
Sbjct: 247 YNGLAQKELFAKSPNWNRFNAYRRDMTITVLDIIFPTYDARLYTKPIKTEL TREIY 306

Query: 267 TSSVIEDSPVSANIPNGFNRAEFGVRPHLMDFMNSL-FVTAETVRSQTVWGGHLVSSRN 325
+ + D N A F R PHL+ + F T GH
Sbjct: 307 SDVLNLDVYGQQOTDLNKNEAAF-TRSPHLVTRLRGDFEYTRTKYAYWRYLAGHTNYFSF 365

Query: 326 TAGNRINFPSYGVFNPGGAI--WIADEDPRPFYRTLSDPVFVRGGFGNPHYVLGLRGVAF 383
T I S+ + I D Y+ + + +P +G+ + F
Sbjct: 366 TGNGTIYSSSFNNWYDMDTKSTINIPDYANIYKLWTKSYTNISPYTDP---VGISQM QF 422

Query: 384 QQTGTNHTRTFRNSG-----TIDSLDEIPPQDNGAPWNDYSHVLNHVTFVRWPGEISGS 438
T N T+ + ++ EIPP D + +YSH+L+++T + G
Sbjct: 423 SLT-NNQQLTYTGTSAPKYPVRETFFEIPTDEKPLTYENYSHILSYMTSAQHFG----- 476

Query: 439 DSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSG 498
D F+W H S N +DP++ITQIP VK LQ G V +GPG TGGD++
Sbjct: 477 DKKIGYTFAMMHESVDFDNRPDPKITQIPAVKGDYLYQG-YVKQGPCHTGGDLVSMIRT 535

Query: 499 GPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKTMD---TGDPLT 555
+N+ P YR RIRY++++N +Y+ +I +D T DP+
Sbjct: 536 DRLG---INVYFPQPLDYRIRIRYSTSSNGYLYIYSPNTKIVYLPPTTLVDGQPTFDPM 592

Query: 556 FQSFYATINTAFTFPMS-QSSFTVGADTFSSGNEVYIDRFELIP-VTATLE 605
F +F + +F ++ +FT+ A VYID+ E IP T TLE
Sbjct: 593 FSAFRVVEVPASFRASVAGYTNFTIEA---GFGPVYIDKIEFIPDNNTTLE 640

>gb|AAG36711.1| (AY008143) crystal protein [Bacillus thuringiensis serovar yunnanensis]
Length = 1236

Score = 219 bits (558), Expect = 7e-56
Identities = 161/526 (30%), Positives = 261/526 (49%), Gaps = 44/526 (8%)

Query: 31 RLPLDISLSLSTRFLLSEFV---PGVGVAFLGLFDLIWGFIPTSD-----WSLFLQLIEQ 80
R L ++ S+ +LS+ P V F+ + F+ P + W + E+
Sbjct: 58 RAALFVANSIIGIMLSKIPIVGPIVSTPFFQIMGVALPFLWPPNAPEPQFSWESLMTAAEE 117

Query: 81 LIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDALI 140
+ +++I+ R A L G+ ++ +Y +A+ +W+ +P NAQL+E +RI++ T+ +
Sbjct: 118 IADKKIDAQVRANANAELEGVHNARLYQDAVCDWKQDPTNAQLKEQLRIQYIATNTVIF 177

Query: 141 TAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHR 200
++ +F+ FE+PLLS YVQAANLHL L+D V FG+ WG+D ATV+ Y+ L+ I
Sbjct: 178 SRMPSFRVRGFEVPLLSTYVQAANLHLIHLKDGVOFGEEWGMDSATVDRFYSLKSDIEI 237

Query: 201 YTKHCLDTYNQGL-ENLRGTNT-RQWARFNQFRDLTLTLVLDIVAFPNYDVRTYPIQTS 258
YT +C+D YN+GL +++ T W FN FRRD+TL VLD+V+++P YD R YP+ T
Sbjct: 238 YTNICIDWYNKGLSDSIESEPTWNGWNTFNNFRDMTLMVLDLVSIWPTYDPRRYPLPTK 297

Query: 259 SQLTREIYTSSVIEDSPVSANIP-----NGFNRAEFGVR-----PPHLMDFMNSLFVTAE 308
SQLTRE+YT ++ V +P EF +R F T +
Sbjct: 298 SQLTRELYTQAIGSYKSVEPLPPSPFRWLREIEFFLRDSQDEAEQFAGFQQGYQYTLD 357

Query: 309 TVRSQTVWGGHLVSSRNTAGNRI-----NFPSYGVFNPGGAIWIADDPFPFYRTLSDP 362
T T++ +V +R + + I + Y + N W + FY T S+
Sbjct: 358 T----TIYRPPVVGTRTSLVDSIAMGLGSDDVYRIKNISHNGWYPKK--LDFYYTPSER 411

Query: 363 VFVRGGF-GNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNGAPWNDYSH 421
V G + + ++ G+ + T + TID+++ DN N YSH
Sbjct: 412 VESVGEIRTDANNMIDYIGLCRAKVTEPCDPTTCTIDTVNTTASCDNP----NLYSH 467

Query: 422 VLNHVT-FVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
L+ + +PG+ +G S+ + WTH S N I + ITQIP VKA+ +
Sbjct: 468 RLSSINSPAPYPGQ-NGMLSF---CYGWTHFSVDDNNLIAADSITQIPAVKAYRIGGYGK 523

Query: 481 VVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQYRARIYASTT 526
V++GPG+TGGD++ G + + + R RAR+ T+
Sbjct: 524 VMKGPYTGGLMVFGAGEINWRLTIPDTTKAYRVRARVATIPTS 569

>sp|O87905|COAA_BACTJ Pesticidal crystal protein cry24Aa (Insecticidal delta-endotoxin
CryXXIVA(a)) (Crystalline entomocidal protoxin) (Crystal
protein) (Insecticidal protein Jeg72)
gb|AAC61891.1| (U88188) insecticidal protein Jeg72 [Bacillus thuringiensis serovar
jgathesan]
Length = 674

Score = 214 bits (544), Expect = 3e-54
Identities = 185/636 (29%), Positives = 295/636 (46%), Gaps = 69/636 (10%)

Query: 7 NQCVPYNCLNNEVEILNEERSTGRLPLDISLSLTRLLEFVPGVGVAFLGLFDLIWGF 66
N+C N +P I T++ + +L + + S + + G+ I
Sbjct: 46 NECEGSNISPSAAI-----TSKIVSIVLKTAKAVASSLADSIKSSLGISKTI---- 95

Query: 67 TPSDWS-LFLLQIEQLIEQRIETLERNRAITTLRGLADSYEI-YIEALREWEANPNNAQL 124
T ++ S + ++Q+ +RI+ ++L GL Y Y+ AL W N +N
Sbjct: 96 TENNVQSQVSMVQVHQIINRRIQETIIDLGESSLNGLVAIYNRDYLGAEAWNKNKNIN 155

Query: 125 REDVRIRFANTDDALITAINN-FTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLD 183
+ +V F + T + +S +I LL + QAANLHLS+LRDAV + +GW L
Sbjct: 156 QTNVAEAFKTVEREFTKLKGIYRTSSQITLLPTFQAANLHLSMLRDAVMYQEGWNLO 215

Query: 184 IATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNQWARFNQFRDLTLTLVLDIVA 243
N+ L + + YT +C++ Y +GL LRG+ W FN FRRD+TL VLD+VA
Sbjct: 216 SHI--NYSKELDDALEDYTNVCVEVYTKGLNALRGSTAIDWLEFNSFRDMTLMVLDLVA 273

Query: 244 LFPNYDVRTYPIQTSSQLTREIYTSSV-IEDSPVSANIPN-GFNRAEFGVRPPHLMDFMN 301
+FPNY+ YP+ T L+R+IYT V DSP + N G A F + D +
Sbjct: 274 IFPNYNPVRYPLSTKISLSRKIYTDVPGRTDPSFGDWTNTGRTLANFNDLEREVTSPS 333

Query: 302 SLFVTAETVRSQTVWGGHLVSSRNTA-GNRINFPSYGVFNPGGAIWIADDPFPFYRTLS 360
+ + T++ G + S R T+ G+RI YG N A + +R
Sbjct: 334 ----LVKWLGDMTIYTGADISYRPTSPGDRIGV-WYGNIN---AFYHTGRTDVMFRQTG 385

Query: 361 D-----PVFVRGGFGNPHYVLGLRGVAFQQT-----GTNHTRTFRNSG----- 398
D F+ + Y L LR A G + +R F G
Sbjct: 386 DTAYEDPSTFISNIIYKLDLRAAAVSTIQGAMDTTFGVSSSRFFDIRGNQLYQSN 445

Query: 399 ----TIDSLDEIPPQDNGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSS--WTHRS 452
++ P +++S NDYSH+L V ++ + S R+ + S WTH S
Sbjct: 446 KPYPSPITITFPGEESSEGNANDYSHLLCDVKILQ--EDSSNICEGRSSLLSHAWTHAS 503

Query: 453 ATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQL 512
NTI P+ ITQIP V A+ L+ ++VV GPG TGGD+++ + +++ +
Sbjct: 504 LDRNNTILPDEITQIPAVTAYELRGSSVVGPGSTGGDLVKMSYHSVWSFKVYCSE--- 560

Query: 513 PQRYRARIRYASTTNLRIYV-----TVAGERIFAGQFNKMTDGTGDLTFQSFYATINTA 567
+ YR RIRYAS N + + T R +A + N + + +++F Y I
Sbjct: 561 LKNYRVIRYASHGNCQFLMKRWPSTGVAPQWA-RHNVQGTFSNSMRYEAFKYLDI--- 616

Query: 568 FTFPMSQSSFTVGADTFSSGNEVYIDRFELIPVTAT 603
FT +++F D SG +++ID+ E IPV+ +
Sbjct: 617 FTITPEENNFAFTID-LESGGDLFIDKIEFIPVSGS 651

>sp|032307|CJAA_BACTJ Pesticidal crystal protein cry19Aa (Insecticidal delta-endotoxin
CryXIXA(a)) (Crystalline entomocidal protoxin) (75 kDa
crystal protein)
emb|CAA68875.1| (Y07603) mosquitocidal toxin [Bacillus thuringiensis]
Length = 648

Score = 206 bits (523), Expect = 8e-52
Identities = 162/573 (28%), Positives = 265/573 (45%), Gaps = 42/573 (7%)

Query: 52 VGVAFLGLFDLIWGFITPSD-----WSLFLQIEQLIEQRIETLERNRAITTLRGLADSY 105
+G+ + + +L+W P D W + +E LI++RI + R AI TL L
Sbjct: 91 IGLFYQISELLW----PEDDTQQYTQWQDIMNHVEDLIDKRITFVIRGNAIRTLADLQGV 146

Query: 106 EIYIEALREWEANPNNAQLREDVRIRFANTD---DALITAINNFTLSFEIPLLSVYVQA 162
+ Y L++W+ +P + + +F D + I +NN +E+ LL VY Q
Sbjct: 147 DDYNWLKWKDDPKSTGNLSTLVTKFTALDSDFNGAIRTVNQGSFGYELLLPVYAQI 206

Query: 163 ANLHLSLLRDAVSFGQWGLDIATV--NNHYNRLINLIHRYTKHCLDTYNQGLENLRGNT 221
ANLHL LLRDA +G W A +N+Y + YT++C++ YN+GL + R
Sbjct: 207 ANLHLLLLRDAQIYGDKWWSARANARDNYYQIQLEKTEKEYTEYCINWYNGKLNDFRTAG- 265

Query: 222 RQWARFNQFRDLTLTLVLDIVAFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIP 281
QW FN++RR++TLTVLDI+++FP YD R YP + ++LTREIY S VI P
Sbjct: 266 -QWVNFNRYRREMTLTVLDIISMFPYDARLYPTEVKTELREIY-SDVINGEYIYGLMTP 323

Query: 282 N-GFNRAE-FGVRPPHLMDFMNSLFVTAETVRSQTVWGG---HLVSSRNTAGNRINFPSY 336
F +AE R PHL ++ ++ T G + N++ N +F
Sbjct: 324 YFSFEKAESLYTRAPHLFTWLKGFREVNTNSISYWTFLSGGQNKYSYTNSSINEGSFRGQ 383

Query: 337 GVFNPGGAIWIADPRPFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTR---- 392
G + I Y ++ +G+P + + + F T N ++
Sbjct: 384 DTDYGGTSSSTINIPNSYVYNLWTENYEIYPWGD---VNITKMNFSVTDNNSSKELIY 440

Query: 393 -TFRNSGTIDSLDEIPPQDMSG---APWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSW 448
R + + D + G A +NDY+H+L+++ GE G F++
Sbjct: 441 GAHRTNKPVVRTDFDLTNKEGTTELAKYNDYNHILSYMLI---NGETFGQKR-HGYSAF 496

Query: 449 THRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNI 508
TH S P NTI +ITQIP+VKA ++ ++ +GPGFTGGD+++ + T+
Sbjct: 497 THSSVDPNNTIAANKITQIPVVKASSINGSISIEKPGFTGGDLVKMRADS--GLTMRFK 554

Query: 509 NGQLPQRYRARIRYASTTNLRIYVTV-AGERIFAGQFNKMTDGTGDLTF-QSFYATINT 566
L ++YR RIRY + ++ + GE Q + T ++ +SF+ T
Sbjct: 555 AELLDDKKYRVIRYKCNYSKLLLRKWKGEYIQQQIHNSPTYGAFSYLESFTITTEN 614

Query: 567 AFTFPMSQSSFTVGADTFSSGNEVYIDRFELIP 599
F M + ++ G + +D+ E +P
Sbjct: 615 IFDLTM-EVTPYGRQFVEDIPSLILDKIEFLP 646

>sp|086170|CJBA_BACUH Pesticidal crystal protein cry19Ba (Insecticidal delta-endotoxin
CryXIXB(a)) (Crystalline entomocidal protoxin) (78 kDa
crystal protein)
dbj|BAA32397.1| (D88381) insecticidal protein [Bacillus thuringiensis]
Length = 682

Score = 191 bits (486), Expect = 1e-47

Identities = 170/581 (29%), Positives = 262/581 (44%), Gaps = 43/581 (7%)

Query: 49 VPGVGVAFG-LFDLIWGFITPSD--WSLFLQIEQLIEQRIETLERNRAITTLRGLADSY 105
+P VG + L W I + W + + L++Q + NRA + L GL +S
Sbjct: 79 IPEVGPLLSWMVSLFWPTIEKNTVWEDMIKYVANLLKQELTNDTLNRATSNLSGLNESL 138

Query: 106 EIIYEALREWEANPNNAQLREDVRIREFANTDDALITAI--NNFTLTSFEIPLLSVYVQAA 163
IY AL W+ N NN E +R + N L T ++F+L +E LL Y AA
Sbjct: 139 NIYNRALAAWKQNKNNFASGELIR-SYINDLHILFTRDIQSDFSLGGYETVLLPSYASAA 197

Query: 164 NLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQ 223
NLHL LLRD +G+ G V +YN +Y+ +C++TY GLE+ +
Sbjct: 198 NLHLLLLRDAVAIYGKELGYPSTDFEYFYNEQKYTEKYSNYCVNTYKSGLESKKQIG--- 254

Query: 224 WARFNQFRRLDTLTVDIVALEFPNYDVRTYP-----IQTSSQLTREIYTSSVIEDSPVSA 278
W+ FN++RR++TL+VLDIVALEFP YD YP I ++LTREIY S VI D
Sbjct: 255 WSDFNRYRREMTLSVLDIVALEFPDYDTGLYPSKDGKIHKVKAELTREIY--SDVINDHVYGL 313

Query: 279 NIPN-GENRAE-FGVRPPHLMDFMNSLFVTAETVRSQTVW--GGHLVSSRNTAGNRINFP 334
+P F AE R PH ++ ++ S T G + + G N P
Sbjct: 314 MYPYISFEHAESLYTRRPHAFITLWKGFRFVNTSINSWTFSLGGENRYFLTHGEGTIYNGP 373

Query: 335 SYGVFNP--GGAIIWADEDPRPFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTNHT- 391
G G + +I + Y + + +P + + + F T +++
Sbjct: 374 FLGQDTEYGGTSSYIDISNNSIYNLWTKNYEWIYPWTD---VNITKINFSTIDNSNSS 430

Query: 392 -----RTFRNSGTIDSLDEIPPQDNGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAP 444
R + + D + N +NDY+H+L+++ GE G
Sbjct: 431 ESIYGAERNMKPTVRTDFNELLNRAGNPPTYNDYNHILSYMLI---NGETFGQKR-HGY 486

Query: 445 MFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT 504
F++TH S NTI P++I QIP VK + + G +++GPG TGGD+L+ +
Sbjct: 487 SFAFTHSSVDRYNTIVPDKIVQIPAVKTNLV--GANIKPGHTGGDLLKLEYE---RFL 541

Query: 505 IVNINGQLPQRYRARIYASTNLRIYVTVAGER-IFAGQFNKMTMDTGDPLTFQSFSYAT 563
+ I +R RIRYAS + + + + + + T L F+ F
Sbjct: 542 SLRIKLIASMTFRIRIRYASNISGQMMINIGYQNPTYFNIPTTSRDYTELKFEDFQLVD 601

Query: 564 INTAFTFPMSSQSFVTGADTFSSGNEVYIDREFELIPVTATL 604
+ ++ S SS T+ D FS+G V ID+ E IP+ TL
Sbjct: 602 TSYIYSGGPSISSNTLWLDNFSNG-PVIIDKIEFIPLGITL 641

>dbj|BAB78602.1| (AB075461) crystal protein CryE6Q [Bacillus thuringiensis]
Length = 1254

Score = 189 bits (480), Expect = 7e-47
Identities = 170/589 (28%), Positives = 262/589 (43%), Gaps = 94/589 (15%)

Query: 71 WSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYEALREWEANPNNAQLREDVRI 130
W + ++E LIE++I+ N AI L GL + +Y E+ W + N+ +L+EDVR+
Sbjct: 112 WKELIGRVEILIEEKIDREAYNAAIGRLSGLKRALSLYQESFETWIDDENDPELQEDVRM 171

Query: 131 RFANTDDALITAINFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNH 190
RF +T L+T I F + E+ LL+V+VQAA+ HL LL+ V +G WG D TV++
Sbjct: 172 RFTSTLFELVTIETFKYSQELNLLTVFVQAADFHLMLLQQGVMYGVRWGFQRTVDSEF 231

Query: 191 YNR-----LINLIHRYTKHCLDTYNQGLE-----NLRGTNTRQ--- 223
Y L NL+ +Y+ +C Y+QGL NL + Q
Sbjct: 232 YQNDRGEGLKNLLPKYSDYCTYWDYQGLNRAKNLKANLSDTVRYPWAANLENMSVLQELE 291

Query: 224 -WARFNQFRRLDTLTVDIVALEFPNYDVRTYP---IQTSSQLTREIYTSSVIEDSPVSAN 279
W +N +RRD+T+ VLDLVA++P YD+ Y S+LTR IY+ +V V
Sbjct: 292 DWNLYNDYRRDMTILVLDLVAWPTYDLHYDNGNYGVQSELTRSIYSQAV---GNVMGT 348

Query: 280 IPNGFNRAEFG---VRPPLHLMDFMNSLFVTAETVR-----SQTVWGGHLVSSRNTAGNRI 331
+ F + ++ VRPPL+ ++ +F+ T+ G L S + N +
Sbjct: 349 V---FTKEQYEVSVFVRPPLVTVLEKMFQIRPTEQCAPIDATMAGVSLYYSYSGWDNTV 405

Query: 332 N-----FPSYG-----VFNPAGAIWADEDPRPFYRTLSDPVFVRGGFGNPHYVLGLRGV 381

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+      +P+Y      V +      I      E R Y T      H L R V
Sbjct: 406 DDILGYPTYSSSEIRVLSKSKVIVQDQEKNAIYNT-----DLQHDKLVDRFV 454
Query: 382 AFQQTGTNHTRTFRNSGTIDSLDEIPPDNSGAPWN-DYSHVLNHVTFVRWPGEISGSDS 440
      +Q      NSG ++      P      W+ D ++ + +T++ P
Sbjct: 455 FYQ-----NSGEVNYAGRDNPSYKTFAWDTDITNYSSQMTWINGPVPNEGHEFGY 503
Query: 441 WRAPMFSWTHRSATP-TNTIDPER-ITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSG 498
      +A      W      S P N +D E ITQIP VKA L+ G V++G G TGGD++
Sbjct: 504 IQAYAPEWIPASCEPNNIVDAEDVITQIPAVKARELYGARVIKGVGNTGGDLVSIAPH 563
Query: 499 GPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKTM-----TGDPLT 555
      G      +      N + +RY+ RI YA      +I + +      R      + T+      +G LT
Sbjct: 564 GLCELYVSFPN--VVRRYQVRIHYACQDPTKINLNIGDSR-----HDITLPSTYSGGALT 616
Query: 556 FQSFSYATINTAFTFPM-----SQSSFTVGADTFSSGNEVYIDRFELIPV 600
      + SF YAT ++ F      +      +G      S +V ID+ E IPV
Sbjct: 617 YDSFGYATSEYSYLFYADFYDEKQIVRLGNSFDISQDVIIDKIEFIPV 665

>sp|P16479|CRYU_BACTI 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE ENTOMOCIDAL
PROTOXIN)
dbj|BAA00178.1| (D00247) 130 kDa insecticidal protein (ISRH3) [Bacillus
thuringiensis serovar israelensis]
prf||1405201A insecticidal protein ISRH3 [Bacillus thuringiensis]
Length = 1135

Score = 179 bits (454), Expect = 8e-44
Identities = 162/606 (26%), Positives = 259/606 (42%), Gaps = 93/606 (15%)

Query: 54 VAFGLFDLIWGFITPSD---WSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIE 110
      V + ++W TP+      W+ F+      LI+Q +      R A      + + D + Y
Sbjct: 69 VLSAVLPILWPTNTPTPERVWDFMTNTGNLIDQTVTAYVRTDANAKMTVVKDYLDQYTT 128

Query: 111 ALREWEANPNNAQLREDVRIEFANTDDALI-TAINNFTLTSFEIPLLSVYVQAANLHLSL 169
      W+ PNN R V +F T L TA+      L +E+ LL +Y Q AN +L L
Sbjct: 129 KFTWKREPNNQSYRTAVITQFNLTSAKLRETAVYFSNLVGYELLLLPIYAQVANFNLLL 188

Query: 170 LRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARENQ 229
      +RD +      Q W L A + YN ++      Y H +      YN+GL+ LR +      QW FN
Sbjct: 189 IRDGLINAEWLSLAC-DQLYNTMYQYTKYIAHSITWYNKGLDLVRNKSNGQWITFND 247

Query: 230 FRRDLTLTVLDIVALFPNYDVRTYPIQ-----TSSQLTREIYTSSVIEDSPVSANIPN 282
      ++R++T+ VLDI+ALF +YD R P      + ++ TREIYT+ V +SP S +I
Sbjct: 248 YKREMTIQVLDILALFASYDPRRLPADKIDNTKLSKTEFTREIYTALV--ESPSSKSI- 304

Query: 283 GFNRAEFGVRPPHLMDFMNSLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSY----- 336
      A      R HL ++ ++      T+      R + N+I F SY
Sbjct: 305 ALEAAL--TRDVHLEFVWLKRVYFWTNTIYQDL-----RFLSANKIGF-SYTNSSAM 352

Query: 337 ---GVFNPGGAIWIADDEPRPFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRT 393
      G++ G      F      L+ + +      Y      +      +
Sbjct: 353 QESGIYGSSG-----FGSNLTHQIQLNSNV----YKTSITDTSSPSNRVTKMDF 397

Query: 394 FRNSGTIDSLD-EIPP-----QDNSGAP----WNDYSHVLNHVTFVRWPGEIS 436
      ++ GT+ S + I P      N P      NDY+H+L+++      ++
Sbjct: 398 YKIDGTLASYNSTPTPEGLRTTFFGFSTNENTPNQPTVNDYTHILSYI-----KTDVI 452

Query: 437 GSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRT 496
      +S R      F+WTH+      P N I + ITQ+P VK++ L +      V++GPG TGGD++ T
Sbjct: 453 DYNSTNRV-SFAWTHKIVDPNNQIYTDAITQVPAVKSNFLNATAKVIKGPHTGGDLVALT 511

Query: 497 SGGPFAYTI-----VNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAGQFNKTM----- 550
      S G + +      +I      + Y RIRYA+ + + + V+ + + G      T T
Sbjct: 512 SNGTLSGRMEIQCKTSIFNDPTRSYGLRIRYAANSPIVLNVSVYLVQVSRGTISTESTF 571

Query: 551 -----GDPLTFQSFSYATINTAFTFPMSSQSS-----FTVGADTFSSGNEVYIDRFELI 598
      L ++ F Y      A      PM SS      +      +S N+V IDR E+I
Sbjct: 572 SRPNNIPTDLKYHEFRYKDPFDAIV-PMRLSSNQLITIAIQPLNMTSNNQVIIDRIEII 630

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Query: 599 PVTATL 604
P+T ++
Sbjct: 631 PITQSV 636

>gb|AAG00235.1|AF285775_1 (AF285775) parasporal inclusion protein Cry [Bacillus thuringiensis serovar finitimus]
Length = 1128

Score = 179 bits (454), Expect = 8e-44
Identities = 171/626 (27%), Positives = 282/626 (44%), Gaps = 70/626 (11%)

Query: 17 NPEVEILNEERSTGRPLDISLSLRFLLSEFV-PGVG-VAFG-LFDLIWGFITPSD--- 70
NPEV+ + + LT F + FV PGV ++FG L ++W P +
Sbjct: 23 NPEVDSSDTVAVVSAGIVVVGITLTAFA--ASFVNPVVLISFGTLAPVLWP--DPEEDPK 78

Query: 71 --WSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANP--NNAQLRE 126
WS F+ E L+ Q I T + A+ L G D Y A +W+ NP N A+L
Sbjct: 79 KIWSQFMKHGEDLLNQTISTAVKEIALAHLNGFKDVLTYERAFNDWKRNP SANTARL-- 136

Query: 127 DVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLD--- 183
V RF N ++ + L +++ LLS Y +AANLHL+LL V F W D
Sbjct: 137 -VSQRFENAHFNFSNMPQLQLPTYDTLLLSCTEAAANLHLNLLHQVQFADQWNADQPH 195

Query: 184 ---IATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRDRLTLTVLD 240
+ + +Y+ L+ I +Y +C TY++GL +L+ + W +N +RR++TL VLD
Sbjct: 196 SPMLKSSGTYDELLVYIEKYINYCTKTYHKGLNHLKESEKITWDAYNTYREMTLIVLD 255

Query: 241 IVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSAN-IPN-GENRAEFGV-RPPHLM 297
+VA FP YD+R +P +LTRE+YTS ++ ++A IP F+ E + RPP L
Sbjct: 256 LVATFPFYDIRRFPGRVELELTREVYTS--LDPPGLNAGPIEIDFSYLEDHLTRPPGLF 313

Query: 298 DFMNSLFTVAETVRSQTVMGGHLVSSRNTAGNRINFPSYGVFNPGGAI--WIADEDPRPF 355
+++ + + E+V G + S+ GN+ F ++ + + P F
Sbjct: 314 TWLSDIELYTESVAEGDYLSG-IRESKYITGNQF-FTMKNIYGNTNRLSKQLITLLPGEF 371

Query: 356 YRTLSDPVFRGGFG-----NPHYVLGRGVAFQQTGTNHTRTFRNSGTIDSLDEIP--- 407
LS + GF N Y L ++ + F T + ++ + +++ +E
Sbjct: 372 ITHLS----INRGFQTIAGINKLYSL-IQKIVF--TTFKNDNEYQKNFNVNNQNEPQETT 424

Query: 408 --PQDMSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFS--WTHRSATPTNTIDPER 463
P D G+ + H L+H + E + + +F+ WTH S N I
Sbjct: 425 NYPNDYGGNSQKFKHNLSHFPLIIHQVEFA---EYFHSIFALGWTHNSVNSQNLISESV 481

Query: 464 ITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYA 523
TQIPLVKA+ + + +V+RGPGFTGGD++ + ++Y + YA
Sbjct: 482 STQIPLVKAYEVTT-NSVIRGPGFTGGDLIELRD-----KCSIKCKASSLKKY AISLFYA 535

Query: 524 STTNLRIYVTVAG-----ERIFAGQFNKMTMDTGDPLTFQSFSYATINTAFTFPMQS- 575
+ + + + V + F+ + N D L ++ F Y T+ P S+
Sbjct: 536 ANNAIAVSIDVGDSGAGVLLQPTFSRKGNNNFTIQD-LNYKDFQYHTLLVDIELPESEEI 594

Query: 576 -SFTVGADTFSSGNEVYIDREFELIPV 600
D + G + ID+ E P+
Sbjct: 595 HIHLKREDDYEEGVILLIDKLEFKPI 620

>pir||A26858 130K delta-endotoxin - Bacillus thuringiensis subsp. israelensis
emb|CAA68485.1| (Y00423) endotoxin (AA 1-1180) [Bacillus thuringiensis]
Length = 1180

Score = 179 bits (453), Expect = 1e-43
Identities = 167/584 (28%), Positives = 256/584 (43%), Gaps = 66/584 (11%)

Query: 71 WSLFLLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRI 130
WS F+ Q + +I++ I + + A L + Y L+ WE NPN Q +DVR
Sbjct: 114 WSDFITQTKNIKKIASTYISNANKILNRSFNVISTYHNLKTTWENPNP-PQNTQDVRT 172

Query: 131 R-----FANTDDALITAI--NNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ--- 178
+ F N L+ + N + I +LS Y QAANLHL++L AV F
Sbjct: 173 QIQLVHYHFQNVIPLELVNSCPPNPSCDYNNILVLSSYAQAANLHLTVLNQAVKFEAYLK 232

Query: 179 -----GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRG-----NTRQWARF 227
+ + T ++Y L I YT +C+ TY +GL ++ T W +
Sbjct: 233 NNRQFDYLEPLPTAIDYYPVLTKAIEDYTNVCVTTYKKGLNLIKTPDSNLDGNINWNTY 292

Query: 228 NQFRDLTLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRA 287
N +R +T VLD+VALFPNYDV YPI S+LTREIY E+SP F
Sbjct: 293 NTYRTKMTTAVLDVVALFPNYDVGVKPIGVQSELTREIYQVLNFEESPYKY---YDFQYQ 349

Query: 288 EFGV-RPPHLMDFMNSL-FVTAETVRSQTVMGGHLVSSRNTAGNRIN----FPSYGVFNP 341
E + R PHL +++SL F + H T N F ++ V +
Sbjct: 350 EDSLTRRPHLFTWLDLNLNFEYKAQTTNNFFTSHYNMFHYTLDNISQKSSVFGNHNVTDK 409

Query: 342 GGAIWIADPRPFYRTLSDPVFRGGFGNPHYVL-----GLRGVAFQQTGTNHTR 392
++ +A Y L + + + + N + + G R + + T +
Sbjct: 410 LKSLGLATN----IYIFLLNVISLDNKYLNNDYNNISKMDFFITNGTRLLEKELTAGSGQI 465

Query: 393 TFRNSGTIDSLDEIPQDNSGAP-----WNDYSHVLNHVTFVRWPGEISGSDSWRAPMFS 447
T+ + I L + ++N G P +++YSH+L+ + + I + + F+
Sbjct: 466 TYDVNKNIFGLPILKRRENQNPFLFTYDNYSHILSFIKSL----SIPATYKTQVYTF 521

Query: 448 WTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVN 507
WTH S P NTI TQIP VKA++L + + VV+GPG TGGD++ F T +
Sbjct: 522 WTHSSVDPKNTIYTHLTQIPAVKANSLGTASKVQVQPGHTGGDLI--DFKDHFKITCQH 579

Query: 508 INGQLPQRYRARIYAS----TTNLRIYVTVAGERIFAGQFNKMTMDTG--PLTFQSFYS 561
N Q Q Y RIRYAS T I +++ G N T D L ++ F Y
Sbjct: 580 SNFQ--QSYFIRIRYASNGSANTRAVINLSIPGVAELGMALNPTFSGTDYTNLKYKDFQY 637

Query: 562 ATINTAFTFPMQS-SFTVGADTFSSGNEVYIDRFELIPVTATL 604
+ F +Q+ S + V ID+ E +P+T ++
Sbjct: 638 LEFSNEVKFAPNQNISLVFNRSVDYNTTTVLIDKIEFLPITRSI 681

>sp|P16480|C4AA_BACTI PESTICIDIAL CRYSTAL PROTEIN CRY4AA (INSECTICIDAL DELTA-ENDOTOXIN
CRYIVA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (135 KDA
CRYSTAL PROTEIN)
pir||I39870 insecticidal protein ISRH4 - Bacillus thuringiensis
dbj|BAA00179.1| (D00248) 130 kDa insecticidal protein (ISRH4) [Bacillus
thuringiensis serovar israelensis]
prf||1405201B insecticidal protein ISRH4 [Bacillus thuringiensis]
Length = 1180

Score = 178 bits (452), Expect = 1e-43
Identities = 167/584 (28%), Positives = 256/584 (43%), Gaps = 66/584 (11%)

Query: 71 WSLFLLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRI 130
WS F+ Q + +I++ I + + A L + Y L+ WE NPN Q +DVR
Sbjct: 114 WSDFITQTKNIIKKEIASTYISNANKILNRSFNVISTYHNHLKTWENNPN-PQNTQDVRT 172

Query: 131 R-----FANTDDALITAI--NNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQ--- 178
+ F N L+ + N + I +LS Y QAANLHL++L AV F
Sbjct: 173 QIQLVHYHFQNVIPLEVNSCPNNPSCDYYNVLSSYAQAANLHLTVLNQAVKFEAYLK 232

Query: 179 -----GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRG-----NTRQWARF 227
+ + T ++Y L I YT +C+ TY +GL ++ T W +
Sbjct: 233 NNRQFDYLEPLPTAIDYYPVLTKAIEDYTNVCVTTYKKGLNLIKTPDSNLDGNINWNTY 292

Query: 228 NQFRDLTLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRA 287
N +R +T VLD+VALFPNYDV YPI S+LTREIY E+SP F
Sbjct: 293 NTYRTKMTTAVLDLVALFPNYDVGVKPIGVQSELTREIYQVLNFEESPYKY---YDFQYQ 349

Query: 288 EFGV-RPPHLMDFMNSL-FVTAETVRSQTVMGGHLVSSRNTAGNRIN----FPSYGVFNP 341
E + R PHL +++SL F + H T N F ++ V +
Sbjct: 350 EDSLTRRPHLFTWLDLNLNFEYKAQTTNNFFTSHYNMFHYTLDNISQKSSVFGNHNVTDK 409

Query: 342 GGAIWIADPRPFYRTLSDPVFRGGFGNPHYVL-----GLRGVAFQQTGTNHTR 392
++ +A Y L + + + + N + + G R + + T +
Sbjct: 410 LKSLGLATN----IYIFLLNVISLDNKYLNNDYNNISKMDFFITNGTRLLEKELTAGSGQI 465

Query: 393 TFRNSGTIDSLDEIPPQDNSGAP-----WNDYSHVLNHVTFVRWPGEISGSDSWRAPMFS 447
T+ + I L + ++N G P +++YSH+L+ + + I + + F+
Sbjct: 466 TYDVNKNIFGLPILKRRENQNPFTLFTYDNYSHILSFIKSL----SIPATYKTQVYTF 521

Query: 448 WTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVN 507
WTH S P NTI TQIP VKA++L + + VV+GPG TGGD++ F T +
Sbjct: 522 WTHSSVDPKNTIYTHLTQIPAVKANS LGTAS KVVQPGHTGGDLI--DFKDHFKITCQH 579

Query: 508 INGQLPQRYRARIYAS----TTNLRIYVTVAGERIFAGQFNKMTMDTG--PLTFQSFSY 561
N Q Q Y RIRYAS T I +++ G N T D L ++ F Y
Sbjct: 580 SNFQ--QSYFIRIRYASNGSANTRIVNLSIPGVAELGMALNPFTSGTDYTNLKYKDFQY 637

Query: 562 ATINTAFTFPMSSS--SFTVGADTFSSGNEVYIDRFELIPVTATL 604
+ F +Q+ S + V ID+ E +P+T ++
Sbjct: 638 LEFSNEVKFAPNQNISLVFNRSVDVYTNNTTVLIDKIEFLPITRSI 681

>sp|Q9X682|CSAA BACTF Pesticidal crystal protein cry28Aa (Insecticidal delta-endotoxin
CryXXVIIIa(a)) (Crystalline entomocidal protoxin) (126
kDa crystal protein)
gb|AAD24189.1|AF132928_1 (AF132928) Cry28Aa1 delta-endotoxin [Bacillus thuringiensis serovar
finitimus]
Length = 1109

Score = 178 bits (451), Expect = 2e-43
Identities = 165/626 (26%), Positives = 270/626 (42%), Gaps = 89/626 (14%)

Query: 17 NPEVEILNEERSTGRPLDISLSLRFLLSEFV-PGVG-VAFG-LFDLIWGFITPSD--- 70
NPEV+ + + + LT F + FV PGV ++FG L ++W P +
Sbjct: 23 NPEVDSSDTAVVSAGIVVVGITLTAFA--ASFVNPVGVVLISFGTLAPVLWP--DPEEDPK 78

Query: 71 --WSFLQLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANP--NNAQLRE 126
WS F+ E L+ Q I T + A+ L G D Y A +W+ NP N A+L
Sbjct: 79 KIWSQFMKHGEDLLNQITISTAVKEIALAHLNGFKDVLTYIERAFNDWKRNP SANTARL-- 136

Query: 127 DVRIREFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLD--- 183
V RF N ++ + L +++ LLS Y +AANLHL+LL V F W D
Sbjct: 137 -VSQRFENAHFNFSVSNMPQLQLPTYDTLLSCYTEANLHLNLLHQGVQFADQWNADQPH 195

Query: 184 ---IATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARENQFRDRLTLTVLD 240
+ + +Y+ L+ I +Y +C TY++GL +L+ + W +N +RR++TL VLD
Sbjct: 196 SPMLKSSGTYTYDELLVYIEKYINYCTKYHKLNLKESEKITWDAYNTYRREMTLTVLD 255

Query: 241 IVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM 300
+VA FP YD+R +P +LTRE+YTS + RPP L ++
Sbjct: 256 LVATFPFYDIRRFPRGVELELTREYVTS-----LDHLTRPPGLFTWL 297

Query: 301 NSLFVTAETV-----RSQTWVGHLVSSRNTAGNRINFPSYGVFNPGGAIWIAD 350
+ + + E+V S+ G + +N GN + G
Sbjct: 298 SDIELYTESVAEGDYLSGIRESKYITGNQFFTMKNIYGNTRNLRSKQLITLLPGEFMTHLS 357

Query: 351 DPRPFYRTLSDPVFRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIP--- 407
RPF +T++ N Y L ++ + F T + ++ + ++ +E
Sbjct: 358 INRPF-QTIAGI-----NKLYSL-IQKIVF--TTFKNDNEYQKNFNVNNQNEPQETT 405

Query: 408 --PQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFS--WTHRSATPTNTIDPER 463
P D G+ + H L+H + E + + +F+ WTH S N I
Sbjct: 406 NYPNDYGGSNSQKFKHNLSHFPLIIHKLEFA---EYFHSIFALGWNHNSVNSQNLISESV 462

Query: 464 ITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYA 523
TQIPLVKA+ + + +V+RGPGFTGGD++ + ++Y + YA
Sbjct: 463 STQIPLVKAYEV-TNNSVIRGPGFTGGDLIELRD-----KCSIKCKASSLKKYAISLFYA 516

Query: 524 STTNLRIYVTVAG-----ERIFAGQFNKMTMDTGDLPLTFQSFSYATINTAFTFPMSSS- 575
+ + + + V + F+ + N D L ++ F Y T+ P S+
Sbjct: 517 ANNAIAVSDVGDGAGVLLQPTFSRKGNNTFTIQD-LNYKDFQYHTLLVDIELPESEEI 575

Query: 576 -SFTVGADTFSSGNEVYIDRFELIPV 600
D + G + ID+ E P+

Sbjct: 576 HIHLKREDDYEEGVILLIDKLEFKPI 601

>emb|CAA34382.1| (X16315) delta-endotoxin (AA 429-726) [Bacillus thuringiensis]
Length = 297

Score = 175 bits (444), Expect = 1e-42
Identities = 95/183 (51%), Positives = 112/183 (60%)

Query: 423 LNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVV 482
L+HV+ R S RAPMFSW HRSA N I +ITQIPL K+ L SGT+VV
Sbjct: 2 LSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVV 61

Query: 483 RGPFGTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAG 542
+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+++ ++ G I G
Sbjct: 62 KGPFGTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIYASTTNLQLHTSIDGRIINQG 121

Query: 543 QFNKMTDGTGDLTFQSFYATINTAFTFPMSSQSFVTGADTFSSGNEVYIDRFELIPVTA 602
F+ TM +G L SF T F F S FT+ A F+SGNEVYIDR E +P
Sbjct: 122 NFSATMSSGSNLQSGSFRIVGFTTPFNFSNGSSVFTLSAHVFNSSGNEVYIDRIEFVPAEV 181

Query: 603 TLE 605
T E
Sbjct: 182 TFE 184

>pir||S04994 Parasporal crystal protein - Bacillus thuringiensis (strain aizawai
IC1) (fragment)
Length = 296

Score = 175 bits (444), Expect = 1e-42
Identities = 95/183 (51%), Positives = 112/183 (60%)

Query: 423 LNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVV 482
L+HV+ R S RAPMFSW HRSA N I +ITQIPL K+ L SGT+VV
Sbjct: 2 LSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVV 61

Query: 483 RGPFGTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVTVAGERIFAG 542
+GPGFTGGDILRRTS G + VNI L QRYR RIRYASTTNL+++ ++ G I G
Sbjct: 62 KGPFGTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIYASTTNLQLHTSIDGRIINQG 121

Query: 543 QFNKMTDGTGDLTFQSFYATINTAFTFPMSSQSFVTGADTFSSGNEVYIDRFELIPVTA 602
F+ TM +G L SF T F F S FT+ A F+SGNEVYIDR E +P
Sbjct: 122 NFSATMSSGSNLQSGSFRIVGFTTPFNFSNGSSVFTLSAHVFNSSGNEVYIDRIEFVPAEV 181

Query: 603 TLE 605
T E
Sbjct: 182 TFE 184

>sp|O32321|CKAA_BACUF Pesticidial crystal protein cry20Aa (Insecticidal delta-endotoxin
CryXXA(a)) (Crystalline entomocidal protoxin) (86 kDa
crystal protein)
gb|AAB93476.1| (U82518) mosquitocidal toxin [Bacillus thuringiensis]
Length = 753

Score = 173 bits (438), Expect = 5e-42
Identities = 161/563 (28%), Positives = 247/563 (43%), Gaps = 49/563 (8%)

Query: 64 GFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQ 123
GFI + L+ +EQLI+Q + T R+ A + G++ SY+ Y+ R+WE N +
Sbjct: 89 GFIRNGTGNELLIHVEQLIQQTTLATQYRSAATGAIYGISRSYDNYLMFFRQWERN-RTRE 147

Query: 124 LREDVRIRFANTDDALITAIN---NFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGW 180
+ V F + I A+ + + FE LL Y AAN HL LLRDAV + W
Sbjct: 148 NGQQVESAFTTINTLCINALAPQASLSRRGFETLLLPNYAMAANFHLLLLRDAVLYRNQW 207

Query: 181 -GLDIATVNNHYNRLNLIHRYTKHCLDTYNOGLENLRGT---NTRQWARFNQFRDLTL 236
I+T N + N L I+ Y HC Y GL + N +W RFN +RRD+TL
Sbjct: 208 LSNSISTANVNLNLRRAINEYITHCTRWYQDGLNRFDRSSRANMNEWRRFNAYRRDML 267

Query: 237 TVLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPPHL 296

+VLD +FP YD +P T+ +LTR +YT ++ +A IP GF R E V
Sbjct: 268 SVLDFATVFPTYDPVLFPAATNVELTRVVYTDPIVMAGGRTA-IP-GFTRMENLVNSASR 325
Query: 297 MDFMNSLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPGGAIWIADDPFPFY 356
+ F+N + + + H + +GN+ NF S G N ++ D R +
Sbjct: 326 VSFLNQM-----NIYTSFYFRPHNIPRYWWSGNQ-NFLSNGTSN----LYGYRSDGRTTF 375
Query: 357 RTLSDPVF-----VRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLD----- 404
+ +F + G F + + L T N + S I S
Sbjct: 376 NVSNIDIFRVNMTTHIGGAFTDDYRGLHRAEFIGANTQNNQRTSLLYSVEIPSSHFRFEN 435
Query: 405 ---EIPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMF--SWTHRSATPTNTI 459
+P + +Y+H L + E+S + + R +F +WTHRS TN +
Sbjct: 436 HTVFLPGESGLEPNERNYTHRL-----FQMMNEVSVNPNARGRVFLHAWTHRSRLRRTNGL 490
Query: 460 DPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYR 519
+I QIP VK + VV G + T+G + T V+ R+ R
Sbjct: 491 RSDQILQIPAVKTISNGGDRAVVLNYGENIMKLDNLTGLSYKLTAVDSEAS-NTRFIVR 549
Query: 520 IRYASTTNLRIYVTVAGERIFAGQFNKMTMDTGDPLT---FQSFSYATINTAFTFPMSSQS 576
+RYAS N ++ + + G +I + T+ G LT + +F YAT A F M S
Sbjct: 550 VRYASMNNKLNVLNGAQIASLNVHEHTVQRGGSLLTDLQYGNFKYATF--AGNFKMGSQS 607
Query: 577 FTVGADTFSSGNEVYIDRFELIP 599
+G + +D+ ELIP
Sbjct: 608 I-LGIFKEIPNIDFVLDKIELIP 629

>gb|AAF01213.1| (AF182196) endotoxin [Bacillus thuringiensis]
Length = 140

Score = 171 bits (432), Expect = 3e-41
Identities = 85/137 (62%), Positives = 102/137 (74%), Gaps = 3/137 (2%)

Query: 8 QCVYPYNCLNPEVEILNEERSTGRLP---LDISLSLTRFLLSEFVPGVGVAFGFLDLIWG 64
QCVYPYNCL+NPE EIL+ E + R +ISL LTRFLL +PG F LFD+IWG
Sbjct: 1 QCVYPYNCLSNPENEILDIESLSSRSREQVAEISLGLTRFLLSLLPGASFGFALFDIIWG 60
Query: 65 FITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQL 124
I P W+LFL QIEQLI+QRIE RN+AI+ L GL DSYE+YIE+LREWE +PNN L
Sbjct: 61 VIGPDQWNLFLAQIEQLIDQRIEAHVNRQAISRLLEGLGDSYEVYIESLREWEGSPNNEGL 120
Query: 125 REDVRIRFANTDDALIT 141
++DVR RF+NTD+ALIT
Sbjct: 121 QQDVRNRFSNTDNALIT 137

>sp|087906|CPAA_BACTJ Pesticidal crystal protein cry25Aa (Insecticidal delta-endotoxin
CryXXVA(a)) (Crystalline entomocidal protoxin) (76 kDa
crystal protein) (Insecticidal protein Jeg74)
gb|AAC61892.1| (U88189) insecticidal protein Jeg74 [Bacillus thuringiensis serovar
jegathesan]
Length = 675

Score = 164 bits (416), Expect = 2e-39
Identities = 163/606 (26%), Positives = 264/606 (42%), Gaps = 80/606 (13%)

Query: 50 PGVGVAFGFLDLIWGFI--TPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYE- 106
P +G AF L I + T + + L + + +LI + ++ NRA GL D+Y
Sbjct: 76 PSIGDAFALVSSIGYWPETKTSFPLSVADVNRLIREALDQNAINRATGKFNGLMDTYNT 135
Query: 107 IYIEALREW-----EANPN-NAQLREDVRIRFANTDDALITAI--NNFTLTSFEIPLLSVY 159
+Y++ L++W ANP ++QLRE R + A+ F +I LL +Y
Sbjct: 136 VYLKLNQDWDYDTRIPANPQGSQLEAARRSLEEIERDFRKALAGEFAEAGSQIVLPIY 195
Query: 160 VQAANLHLSLLRDAVSFGQGWGL-----DIATVNNHYNRLINLIHRYTKHCLDTYNQ 211
QAAN+HL +L+DA+ F GL + + + + I +YT HC+ Y+
Sbjct: 196 AQAANIHLILKDKAMQFRTDLGLIRPVGVPITTSAPDPESEFLLRIKKYTDHCISYYDD 255
Query: 212 GLENLR--GTNTRQWARFNQFRRDLTLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSS 269
GL +R G++ W FN+FRR++TLTVLD+VAL+P ++++ YPI T ++L+R +YT

Sbjct: 256 GLAKIRSRGSDGETWWEFNKFRREMTLTVLDLVALYPHTNIKLYPIPTQTELSRVVYTD 315

Query: 270 VIEDSPVSANIPNGFNRAEFG-----VRPPHLMDFMNSLFVTAETVR----- 311
V ++I F+R F RP +++NS+ + A TV

Sbjct: 316 VGCGFNKRSDI---FSRLNFDYLENRLTRPREPFNYLNSVQLFASTVSNNSNNGEVLGRNL 372

Query: 312 SQTVMGGHLVSSRNAGNRINFP-----SYGVFNPGGAIWIADEDPRPFYRTLSDPVFV 365
++ ++ G +SR+ G P SYG W PR Y ++

Sbjct: 373 NKIMFEGGWATASRGDGVTTGTPTFSTMDWSYG-----W---GYPRKHAEITSRSQA 421

Query: 366 RGGFGNP-HYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDMSGAPWNDYSHVLN 424
G N H ++G+ G TF G D D Q N + + H ++

Sbjct: 422 LPGLNNSIHVIVGIDSFRAIGPGGQGDHTFSLPGG-DMYDCGKVQINPLEDYRNSDHWIS 480

Query: 425 HVTFVRWPGGEISGSD----SWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
+ + +++ + ++ A W H SA N ++ITQIP K T++

Sbjct: 481 DMMTINQSVQLASNPTQTFAFSALSLGWHSSAGNRNVYVDKITQIPATK--TVRE-HP 537

Query: 481 VVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQR-----YRARIRYASTTNLRIYVTV 534
+++GPGFTGGD+ +S ++ R +R RIR AS I V

Sbjct: 538 MIKGPFTGGDLADLSSNSDILQ--YDLRSDYDDRLTEDVPFRIRIRCASIGVSTISVDN 595

Query: 535 AGERIFAGQFNKMTDGTDLTFQSFYATINTAFTFMSQSSTVGADTFSSGNEVYIDR 594
G T + D L ++SF Y +I + F + + +DR

Sbjct: 596 WGSSSPQVTVASTAASLDTLKYESFQYVSIPGNYYFDSAPR-----IRLLRQPGRLLVDR 650

Query: 595 FELIPV 600
E+IPV

Sbjct: 651 IEIIPV 656

>sp|P09662|CAAA_BACTI PESTICIDIAL CRYSTAL PROTEIN CRY10AA (INSECTICIDAL DELTA-ENDOTOXIN
CRYXA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (78 KDA
CRYSTAL PROTEIN)
gb|AAA22614.1| (M12662) insecticidal endotoxin (put.); putative [Bacillus
thuringiensis]
Length = 675

Score = 160 bits (405), Expect = 4e-38
Identities = 162/586 (27%), Positives = 247/586 (41%), Gaps = 64/586 (10%)

Query: 54 VAFG-LFDLIWGFITPSDWSLFLQLIEQLRIETLERNRAITTLRGLADSYEIIYEA 112
++FG L + W P++ LL I Q I+ N + + + + Y E

Sbjct: 97 ISFGTLPIFWQGSDPANVWQDLLNIGGRPIQEIDKNIINVLTSIVTPIKNQLDKYQEFF 156

Query: 113 REWEANPN--NAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLL 170
+WE NA+ D+ D + + N S+ IP L Y Q A HL+LL

Sbjct: 157 DKWEPARTHANAKAVHDLFTTLEPIIDKDLMLKNN--SYRIPTLPAYAQIATWHLNLL 214

Query: 171 RDAVSFGQGW----GLDIATVN--NHYNRLINL-IHRYTKHCLDTYNQGLNLRGTNTRQ 223
+ A ++ W G++ +T N N+Y + I YT +C+ TYN GL +R

Sbjct: 215 KHAATYYNIWLQNQGINPSTFNSSNYQGYLKRKIQEYTDYCIQTYNAGLTMIRTNAT 274

Query: 224 WARFNQFRRDLTLTVLDIVLFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNG 283
W +N +R ++TLTVLD++A+FPNYD YPI S+L RE+YT+ + + NG

Sbjct: 275 WNMNYTYRLEMTLTVLDLIAIFPNYDPEKYPGVKSELIREVYTNVNSDTFRITTELENG 334

Query: 284 -----FNRAEFGVR-----PPHLMDFM-NSLFVTAETVRSQTVWGGHLVSSRN 325
N+ F R P + F N + T +WG

Sbjct: 335 LTRNPTLFTWINQGRFYTRNSRDILDYDIFSTGNQMAFTHTNDDRNIWGA----- 387

Query: 326 TAGNRINFPYSGVFNPGGAIWIADEDPRPFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQ 385
GN I+ + VF P D+ +R SD ++ F N V R +

Sbjct: 388 VHGNIIQDTSKVF-PFYRNKPIDKVEIVRHREYSIDIYEMIFFSNSSEV--FRYSSNST 444

Query: 386 TGTNHTRTFRNSGTIDSLDEIPPQDMSGAPWNDYSHVLNHVTFVRWPGGEISGSDSWRAPM 445
N+ RT DS IP Q +Y H L+++ + S R

Sbjct: 445 IENNYKRT-----DSY-MIPKQTWKN---EEYGHLSYIKTDNY--IFSVMRERRRVA 491

Query: 446 FSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTI 505

FSWTH S NTID + ITQI +KA + S + +V+GPG TGGD++ F
Sbjct: 492 FSWHTSVDFQNTIDLDNITQIHALKALKVSSDSKIVKPGHTGGDLVILKDSMDFR--- 548

Query: 506 VNINGQLPQRYRARIRYASTTNLRIYVTVAGERIFAGQFNKMTMDTGDP----LTFQSFSY 561
V + ++Y+ RIRYA T + V + G + + T +P LT+ F Y

Sbjct: 549 VRFLKNVSRQYQVRIRYA-TNAPKTTVFLTGIDTISVELPSTTSRQNPATDLTYADFGY 607

Query: 562 ATINTAFTFPMSSQSFVTGADTFSSGN---EVYIDRFELIPVTATL 604
T + T+ + + N +YID+ E IP+T ++

Sbjct: 608 VTFPRTVPNKTFEGEDTLLMTLYGTPNHSYNIYIDKIEFIPITQSV 653

>pir||B29838 parasporal crystal protein - Bacillus thuringiensis subsp.
israelensis (fragment)
Length = 934

Score = 160 bits (405), Expect = 4e-38
Identities = 162/586 (27%), Positives = 247/586 (41%), Gaps = 64/586 (10%)

Query: 54 VAFG-LFDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEAL 112
++FG L + W P++ LL I Q I+ N + + + + Y E

Sbjct: 97 ISFGTLLPIFWQGS DPANVWQDLLNIGGRPIQEIDKNIINVLTSIVTPIKNQLDKYQEFF 156

Query: 113 REWEANPN--NAQLREDVRIRFANTDDALITAINNFTLTSFEIPLSVYVQAANLHLSLL 170
+WE NA+ D+ D + + N S+ IP L Y Q A HL+LL

Sbjct: 157 DKWEPARTHANAKAVHDLFTTLEPIIDKDLMLKNN--SYRIPTLPAYAQIATWHLNLL 214

Query: 171 RDAVSFGQGW----GLDIATVN--NHYNRLINL-IHRYTKHCLDTYNQGLNLRGTNTRQ 223
+ A ++ W G++ +T N N+Y + I YT +C+ TYN GL +R

Sbjct: 215 KHAATYYNIWLQNQGINPSTFNSSYYQGYLKRKIQEYTDYCIQTYNAGLTMIRTNTNAT 274

Query: 224 WARFNQFRRDLTLTVLDIVAFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNG 283
W +N +R ++TLTVLD++A+FPNYD YPI S+L RE+YT+ + + NG

Sbjct: 275 WNMNTYRLEMTLTVLDLIAIFPNYDPEKYPGVKSELIREVYTNVNSDTFRTITELENG 334

Query: 284 -----FNRAEFGVR-----PPLHMDFM-NSLFVTAETVRSQTVWGGHLVSSRN 325
N+ F R P + F N + T +WG

Sbjct: 335 LTRNPTLFTWINQGREYTRNSRDILDYDIFSTGNQMAFTHTNDNRNIWGA----- 387

Query: 326 TAGNRINFPSSYGVFNPGGAIWADEDPRPFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQO 385
GN I+ + VF P D+ +R SD ++ F N V R +

Sbjct: 388 VHGNIIQDTSKVF-PFYRNKPIDKVEIVRHREYSDIYEMIFFSNSSEV--FRYSSNST 444

Query: 386 TGTNHTRTFRNSGTIDSLDEIPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPM 445
N+ RT DS IP Q +Y H L+++ + S R

Sbjct: 445 IENNYKRT-----DSY-MIPKQTWKN---EEYGHLSYIKTDNY--IFSVVRERRRVA 491

Query: 446 FSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTI 505
FSWTH S NTID + ITQI +KA + S + +V+GPG TGGD++ F

Sbjct: 492 FSWHTSVDFQNTIDLDNITQIHALKALKVSSDSKIVKPGHTGGDLVILKDSMDFR--- 548

Query: 506 VNINGQLPQRYRARIRYASTTNLRIYVTVAGERIFAGQFNKMTMDTGDP----LTFQSFSY 561
V + ++Y+ RIRYA T + V + G + + T +P LT+ F Y

Sbjct: 549 VRFLKNVSRQYQVRIRYA-TNAPKTTVFLTGIDTISVELPSTTSRQNPATDLTYADFGY 607

Query: 562 ATINTAFTFPMSSQSFVTGADTFSSGN---EVYIDRFELIPVTATL 604
T + T+ + + N +YID+ E IP+T ++

Sbjct: 608 VTFPRTVPNKTFEGEDTLLMTLYGTPNHSYNIYIDKIEFIPITQSV 653

>emb|CAC80986.1| (AJ251978) Cry30Aa protein [Bacillus thuringiensis serovar
medellin]
Length = 688

Score = 155 bits (392), Expect = 1e-36
Identities = 177/693 (25%), Positives = 278/693 (39%), Gaps = 129/693 (18%)

Query: 3 NNIONQCVYPYNCLNPEVEILNEERSTGR-----LPLDISLSLTRFLLS----- 46
+N+ N+ Y NNP+V + N P+D L +

Sbjct: 20 SNMSNRYSKYPLTNNPKVPLQNTNYKDWNMCQTITPLCTPIDTDSKLVATAIKVIGAIF 79

Query: 47 EFVPGVGVAFL-----FDLIWGFITPSD-----WSLFLQLIEQLIEQRIETLERNRAITTL 98
+ +PG G A GL F I + P+D W F Q QL + +
Sbjct: 80 KSMPPGGAAGVLVLSFSSTIIPILWPNDKTPWKEFTKQGLQLFRPELGRDAIEIIGNDV 139

Query: 99 RGLADSYEIIIEALRE----WEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIP 154
+ +S EI + WE+N A V F+ + +I F + P
Sbjct: 140 QAEYNSLEIMMRDFENKFANWESNRTRANAIA-VTTAFSTVNTQIIRLKERFLIAPENRP 198

Query: 155 -LLSVYVQAANLHLSLLRDAVSFGQGWGLDIA-----TVNNHYNRLINLIHRYTKHCL 206
L++Y Q AN+ L L + +G W DI + ++Y L I YT +C
Sbjct: 199 AFLNLQAQTANIDLILYQRGSVYGDKWVADINNRSTSPFSSKDYQSLKGKIKDYTNCA 258

Query: 207 DTYNQGLLENLRTNTQWARFNQFRDLTLTVLDIVLFPNYDVRTYPIQTSSQLTREIY 266
+TY L L+ QW +N++RR+ L LD+VALFPNYD+ YP QT ++LTR++Y
Sbjct: 259 ETYRNSLTILKNKPHIQWDIYNRYRREAILGALDLVALFPNYDICIYPTQTRTELTRKVY 318

Query: 267 TSSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFMNSLFVTAETVRSQTVW-----GGHLV 321
S + +I N+ PP L ++N L + R V G
Sbjct: 319 MPSFYLAQALQRDIETVENQL---THPPSLFTWLNELNLYTIRERFNPVLQVASLSGLQA 375

Query: 322 SSRNTAGN-----RINFPYSYGVF-----NPGGAIWIADIEDPRPFY 356
+SR T +I+ +Y ++ +P + I+ + FY
Sbjct: 376 TSRYTQNTTTISNPVQGPVREGTPTKISLANYIYKLFMSQYRHPNDCLPISGINEMSFY 435

Query: 357 RTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQD---NSG 413
R+ + GG HY G ++ TN +T+ N PQ+ ++
Sbjct: 436 RS---DYYGAGGPAPVHYSAG-----ESPTNVIKTYMNG-----PQNALISND 475

Query: 414 APWNDYSHVLNHV--TFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVK 471
N+ SH+L+ + + R G D + F+WTH S P N I P RITQIP VK
Sbjct: 476 ISINETSHILSDIKMNSRTGGVYPLYDFGYS--FAWTHTSVDPDNLIVPNRITQIPAVK 533

Query: 472 AHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIV-----NINGQLPQRYRARIYA-- 523
A++L S V+ GPG TGGD++ + G + T+ + G ++Y R+RYA
Sbjct: 534 AYSLTSPARVIVGPGHTGGDLVALLNSGTQSGTMQIQCKTGSFTGP-SRQYGLMRMYAAN 592

Query: 524 STTNLRIYVTVAGER-----IFAGQFNKTM-DTGDPLTFQSFY-----ATINTA 567
S + + T+ G+ + F+++ + L ++ F Y NT
Sbjct: 593 SAFTVSLSYTLGQTRGTSFVTENTFSRSNNIIPDLYKEEFKYKDYLIITMTLPANTI 652

Query: 568 FTFPMSQSSFTVGADTFSSGNEVYIDRFELIPV 600
T M Q+ T N++ IDR E P+
Sbjct: 653 ITISMQQA-----TGLLNQLIIDRIEFYPM 678

>dbj|BAB72018.1| (AB074414) insecticidal crystal protein bun3 [Bacillus
thuringiensis]
Length = 666

Score = 155 bits (391), Expect = 2e-36
Identities = 167/622 (26%), Positives = 257/622 (40%), Gaps = 91/622 (14%)

Query: 36 ISLSLTRLFLSEFVPGVGVAFLFDLIWGFITPSDWSLFLQLIEQLIEQRIETLERNRAI 95
I + L FL+ + G+ F + + S +L + + +I + + + AI
Sbjct: 59 IGIDLIEFLMEPSLGGINTLFSIIGKLIPTNHQSVSALSICDLSIIRKEVADSVLSDAI 118

Query: 96 TT-LRGLADSY-EIYIEALREW--EANP----NNAQLREDVRIRFANTDDALITAINNET 147
L G +Y E Y+ L W + P NN+ + + V+ + D +
Sbjct: 119 CRFLDGKLNKYREYYLPYLEAWLKDGPLOKTNNSDGLVKYFELSERDFNEILGGSIA 178

Query: 148 LTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVN-----NHY 191
+ +I LL + + L LLRAV + + W ++ N ++Y
Sbjct: 179 RNNAQILLLPYFCASCKQLLLLRDAVQYEEQWFPFLSAENVRSELISPNSGCDFTGDY 238

Query: 192 NRLINLIHRYTKHCLDTYNQGLLENLR--GTNTRQWARFNQFRDLTLTVLDIVLFPNYD 249
RL I YT +C Y GL ++ GT WA+FN+FR++TLTVLDI+A+F YD
Sbjct: 239 ERLKCKIAEYTDYCEYWYQAGLNQIKAGTGADTWAKFNKFRREMTLTVLDIIAIFQTYD 298

Query: 250 VRTYPIQTSSQLTREIYTSSVIEDSPVSANI---PNGFNRAEF-GVRPPHLMDFMNSLFV 305
+ YP+ T +LTREIYT V S + + FN E G R P L+ ++ S+ +

Sbjct: 299 FKKYPLPTHVELTREIYTDVPGYSSGTYSWLKYWTGAFNTLEANGTRGPGLVTLWLSIGI 358

Query: 306 TAEV-RSQTVWGGHLVSSRNTAGN-----RINFPSYGVFN-PGGAIW-- 346
E V R + W G T GN I+FP+ +F AI

Sbjct: 359 YNEYVSRYFSGWVGTRHYEDYTTGNGNFQRMSTNSDLRDISFPNSDIFKIESKAIMNL 418

Query: 347 IADEDPFPFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSG--TIDSLD 404
+ + + RP YR R + T + NSG ++

Sbjct: 419 VGEINARPEYRV-----SRAEFSESTAFIYLYDAGNSGLSSMTITS 459

Query: 405 EIPPQDNSGAPWNDYSHVLNHVTVFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERI 464
++P N + DYSH L++ V G+ + R ++ WTH S + N I P++I

Sbjct: 460 KLPGIKNPEPSYRDYSHRLSNAACV-----GAGNSRINVYGWHTSMSKYNLIYPDKI 512

Query: 465 TQIPLVKAHTLQ--SGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRY 522
TQIP VKA + V+ GPG TGG+++ + I + Y R+RY

Sbjct: 513 TQIPAVKAFDISDTGPGQVIAGPGHTGGNVVSLPYYSRLKIRL--IPASTNKNYLVRVRY 570

Query: 523 ASTTNLRIYVTVAGERIFAGQFNKMTDGTGDLTFQSFSA-TINTAFTFPMSSQSSFTVGA 581
ST+N R+ V + TG SF Y T+ T F P

Sbjct: 571 TSTSNRLLVERWSPSSIINSYFFLPSTGPG--DSFGYVDTLVTTFNQP-GVEIIQNQL 626

Query: 582 DTFSSGNEVYIDRFELIPVTAT 603
DT + +D+ E IPV +T

Sbjct: 627 DT-----PINVDKVEFIPVNST 643

>sp|Q9S597|CRAA_BACUH Pesticidal crystal protein cry27Aa (Insecticidal delta-endotoxin
CryXXVIIA(a)) (Crystalline entomocidal protoxin) (94 kDa
crystal protein)
dbj|BAA82796.1| (AB023293) 94kDa mosquitocidal toxin [Bacillus thuringiensis]
Length = 826

Score = 154 bits (389), Expect = 3e-36
Identities = 161/620 (25%), Positives = 262/620 (41%), Gaps = 86/620 (13%)

Query: 38 LSLTRFLLSEFVPGVGVAFLFDLIWGFITPSDWSLFLQLIEQLRIETLERNRAITT 97
+S+T L++ G + G+ LIW T + ++ E L+ + I R A T

Sbjct: 92 VSVTAGLITVLGAGAALLAGITPLIWPATDNTFNKITDATEVLLNKEISEFVRKTANTK 151

Query: 98 LRGLADSIEYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLS 157
+ L Y AL W+ NPN++ R V RF + + A+ ++ +E+ L

Sbjct: 152 IDSLLQLIYQQNALENWKNPNDSAAARNTVSTRFQIVNAFFVEAMPALSMPGYEVVQLG 211

Query: 158 VYVQAANLHLSLLRDAVSFGQGWGLD----IATVNNHYNRLINLIHRYTKHCLDTYNQGL 213
Y QAANLHL LLR+ +++ W L A + HY ++ ++Y HC YN+G

Sbjct: 212 AYAQAANLHLILLREGIAYADQWNLARDPMHAAGDLHYKEFLDYRNQYINHCSTWYNEGQ 271

Query: 214 E--NLRGTNTRQWARFNQFRDLTLTVLIDVAFPNYDVRTY--PIQTSSQLTREIYTSS 269
NL+ ++R +TL VLD++A+F YD R Y PI+T LTR IYT

Sbjct: 272 NEANLKNNGL-----VYQRTMTLFLVDLIAMFSTYDPRLYTMPKTEI-LTRTIYTDG 323

Query: 270 VIEDSPVSANIPNGFNRAEFGVRPPLHMDFMNSLFVTAETVRSQTVWGGHLV----- 321
V + P S + P F R E H+ ++ + F++ +++ H +

Sbjct: 324 VNRNEPKSIHNPGLFRRLE--QMKLHIYEQGAQFLSGHQNIFRSMNYNHPLIYGPVQGY 381

Query: 322 SSRNTAGNRINFPSYGVFNPGGAIWIADEDPFPFYRTLSDPVFVRGGFGNPHYVLGLRGV 381
SS N N+I + G ++ +I + T D + G F N+++ +

Sbjct: 382 SSSNI--NKITTINLGDYDKIYSINTESRNLVQGSTTFDKINFYGAF-NENWLFSV--- 435

Query: 382 AFQQTGTNHTRTFRNSGTIDSLDEIPPQD--NSGAPWNDYSHVLNHVTVFVRWPGEISGSD 439
+ +G I IP D ++G +++Y+H L++ F S D

Sbjct: 436 -----YQNGPIIKHSNIPGIDAPSTGLNYSNYTHYLSNCIFQSNRNGGSAPD 483

Query: 440 -SWRAPMFSWTHRSATPT-----NTIDPE-----RITQIPLVKAHTLQSGTTVVR 483
+ ++ +F W H + PT N PE +I+Q+P VKA + + VV

Sbjct: 484 YNTQSYVFGWNHYTIDPTGNYVTDAFEVKNLPESTRYVPQISQVPAVKASDIFNPGRVVN 543

Query: 484 -----GPGFTGGDIL---RRTSGGPFAYTIVNINGQLPQRYRA-----RIRYASTTNLRI 530
GP FTGGD++ + G A T++ +P+RYRA R+ YA+ ++

Sbjct: 544 AKVESGPYFTGGDVIIVSKAQLDGSGGLARTLITF-PIIPKRYRASGFRVVMYYAANHTGQV 602

Query: 531 YVTVAGERIFA-GQFNKTMDDTGD--PLTFQSFYSYATINTAFTFPMSSQ-----SFTVG 580
VA F KT D + + F Y +T F+ S +

Sbjct: 603 SYGVANINTTGYANFQKTFDGEYFRARHEHFKYIEFDTTTSLRNSGQLEEHLLHIYPN 662

Query: 581 ADTFSSGNEVYIDRFELIPV 600
S + ID+ E IPV

Sbjct: 663 TTKISGDQLLIIDKIEFIPV 682

>emb|CAC80985.1| (AJ251977) Cry29Aa protein [Bacillus thuringiensis serovar medellin]
Length = 650

Score = 142 bits (358), Expect = 1e-32
Identities = 153/608 (25%), Positives = 250/608 (40%), Gaps = 131/608 (21%)

Query: 51 GVGVAFLGLFDLIWG-----FITPSDWSLFLQLIEQLRIETLERNRAITTLRGL 101
G +A + +W + S+ +L+ Q +QR+ R A+T L L

Sbjct: 98 GTAIAAAIIPILWPSQENNLDPKLLAISEATLYSFQ-----DQRV---REDALTRLESL 148

Query: 102 ADSYEIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQ 161
DS + + A W NPN+ VR RF + + ++ F ++E LLS Y Q

Sbjct: 149 KDSVKYFENAFTFWINPNSTNTTT-VRERFQEVNGRFVGSMAFFRAKNYEPILLSTYAQ 207

Query: 162 AANLHLSLLRDAVSFGQGWGL----DIATVNNHYNRLINLIHRYTKHCLDTYNQGLENL 217
AA LHL LRD +++ + W L D + Y + Y +HC+ YN+ L L+

Sbjct: 208 AARLHLLHLDGITYAEKNWLSRQGDMPGDLLEYKEFNKYCNEYIEHCWKYNESLSLLK 267

Query: 218 GTNTRQWARFNQFRDLTLTVLIDVALFPNYDVRTYPIQTSSQ-LTREIYTSSVIEDSPV 276
W +NQ+R LT +VLD+++LF +YD R Y + S + LTR++YT + +

Sbjct: 268 SVGA-NWLEYNQYRTFLTASVLDVISLSSYDPRLYKERLSVEILTRKLYTDPINYHRGI 326

Query: 277 SANIPNGFNRAEFGVRPPHLMDFMNSLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSY 336
S + +++ + P +LF T+ + + + NT

Sbjct: 327 SLEA---DESKYTLEP-----TLFTQLYTLTFYSNIFYNYMGHTNT----- 364

Query: 337 GVFNPGGAIWIADEDPRPFYRTLS-DPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFR 395
YR LS D +F FG +

Sbjct: 365 -----YRYSKPKIFAERSFG-----K 381

Query: 396 NSGTIDSLDEIPPQDN---SGAPWNDYSHVLNHVTFVRWPGE-----ISGSDSWRAPMF 446
S ID + IP + +++++ + N + F W GE I G S +

Sbjct: 382 QSSYIDKVPVPNDKSIYKIRAYDNHGLFNVMYFGFWDGEKDQIKIIGGSSTEIYIK 441

Query: 447 SWTHRSA-----TPT-----NTIDPERITQIPLVKAHTLQSGTTVVR 483
+ THR A T T N I + ITQIP VKA+ L + V++

Sbjct: 442 NCTHRLADVISHDLDEKNKCYSAWSTTISLENEIKNDIITQIPAVKAYQLGVQSQVIK 501

Query: 484 GPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLR----IYTVAGERI 539
GPG TGGD++ S + +++ + ++Y RIRYA+ +L I +T+ G

Sbjct: 502 GPGHTGGDLINLKSNDYLRISCQHLN-NVTKKYFVRIRYATNGSLNTRPIINITIPGMTP 560

Query: 540 FAGQFNKTMDD-TG-DPLTFQSFYSYATINTAFTFPMSSQ-SFTVGADTFSSGNEVYIDRFE 596
+ T TG L +Q+F Y T +QS S T+ +S + + +DR E

Sbjct: 561 QGMVLNDFSGTGYNSLEYQNGFYKEFLKEVTLNPNQSIISLTNRSQNSNSILLDDRIE 620

Query: 597 LIPVTATL 604
+P+T ++

Sbjct: 621 FLPIITPSI 628

>sp|Q45882|CGAA_CLOBI Pesticidal crystal-like protein cry16Aa (Insecticidal toxin CryXVIA(a)) (Cbm71 mosquitocidal toxin)
pir||JC6033 mosquitocidal protein Cbm71 - Clostridium bifermentans
emb|CAA63860.1| (X94146) cbm71 mosquitocidal toxin [Clostridium bifermentans]
Length = 613

Score = 142 bits (357), Expect = 1e-32
Identities = 129/547 (23%), Positives = 229/547 (41%), Gaps = 46/547 (8%)

Query: 58 LFDLIWGFITPSDWSLFLQIEQ---LIEQRIETLERNRAITTLRGLADSYEIIYIEALRE 114
+ ++W P++ +F IE + + + + + ++ Y A R
Sbjct: 48 ILSILWE--DPNENEIFSSMIEDGETITNKNLSAQTKEGLLNSNSFGLKFKYNNAFRS 105

Query: 115 WEANPNNAQLREDVIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV 174
W N N + +DV RF + + IN F + ++E+ +L +Y+Q ANLHL LLRD +
Sbjct: 106 WIDNYPNTSI-DDVYRFRKDVNSICENNINEFKVKNYEVTVLPYMQIANLHLLLLRDGM 164

Query: 175 SFGQGWG----LDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQF 230
+G W L + ++ YN +++ Y CL+ YN GL NL+ W ++
Sbjct: 165 IYGDAWNLYRELGFSDQDSFYNHVLDKTKFYINDCLNYYNTGLSNLKLDPNNSWIDITRY 224

Query: 231 RRDLTTLTVLIDIVALFPNYDVRTYPIQTSSQ-LTREIYTSSVIEDSPVSANIPNGFNRAEF 289
R +T +LD++++ P YD + Y + Q LTR++Y+ V + + NIP +
Sbjct: 225 CRFMFTFYILDMSICPIYDTKVYDKPINMQTLTRKVYSDPV---NFIDENIPISEYKMY 281

Query: 290 GVRPPHLMDFMNSLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSYGVFNPG--GAIWI 347
+ P + F T ++ GH+ G +N+ + G G+ +
Sbjct: 282 NISPELFSTLFSISFYTNKS--GNKFLNGHV---NRHVGTDLNYNGLRETHYGNYSNYE 336

Query: 348 ADEDPRPFFYRTLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTF--RNSGTIDSLDE 405
+ + S+ F NP +++ F T N + +S ID
Sbjct: 337 VESMAFDDIKAYSNNYFNNTQNNNP---TSVKSIFLITKNDEWIYGEPSNNIDFTRN 393

Query: 406 IPPQDNSGAPWNDYSHVLNHVTFVRWPGGEISGSDSWRAPMFSWTHRSATPTNTIDPERIT 465
I S Y+H L+ + D+ + +SW ++ TN I + I
Sbjct: 394 IQGY-LSNLNNSYTHSLSDMILANNDKIQINIDTPHSYSYSWIYKGIETNYISDKLIN 452

Query: 466 QIPLVKAHTLQ----SGTTVVRGPGFTGGDIL-----RRTSGGPFAY----TIVNINGQL 512
QIPLVK L+ S +V++GPGFTGGD++ + + P Y + I +
Sbjct: 453 QIPLVKEVKLKSRYHSEISVIKPGPGFTGGDLILSKVHKPANQIPAQYMKNKITIPKTKF 512

Query: 513 P---QRYRARIRYASTTNLRIYVTVAGERIFAGQFNKMTMDTGD---PLTFQSFSYATINT 566
P Q ++ R+ YAS ++ + +AG + +T +T + L + F Y N
Sbjct: 513 PAGSQDFKVRLCYASNHDIGLIRLIAGSKYITTNIQQTFTNTENNPSLIYDDFKYFNENE 572

Query: 567 AFTFPMS 573
+ S
Sbjct: 573 TLSITSS 579

>sp|P05519|C4BA_BACTI PESTICIDIAL CRYSTAL PROTEIN CRY4BA (INSECTICIDAL DELTA-ENDOTOXIN
CRYIVB(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (128 KDA
CRYSTAL PROTEIN)
pir||USBS8I parasporal crystal protein Bt8 - Bacillus thuringiensis subsp.
israelensis
emb|CAA30312.1| (X07423) Bt8 endotoxin (AA 1 - 1136) [Bacillus thuringiensis]
Length = 1136

Score = 128 bits (322), Expect = 2e-28
Identities = 78/238 (32%), Positives = 119/238 (49%), Gaps = 13/238 (5%)

Query: 54 VAFGLFDLIWGFITPSD---WSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIE 110
V + ++W TP+ W+ F+ LI+Q + R A + + D + Y
Sbjct: 69 VLSAVLPILWPTNTPTPERVWDFMTNTGNLIDQTVTAYVRTDANAKMTVVKDYLQYTT 128

Query: 111 ALREWEANPNNAQLREDVIRFANTDDALI-TAINNFTLTSFEIPLLSVYVQAANLHLSL 169
W+ PNN R V +F T L TA+ L +E+ LL +Y Q AN +L L
Sbjct: 129 KFNTWKREPNNQSYRTAVITQFNLTSAKLRETAVYFSNLVGYELLLLPIYAQVANFNLLL 188

Query: 170 LRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQ 229
+RD + Q W L + + YN ++ Y H + YN+GL+ LR + QW FN
Sbjct: 189 IRDGLINAQEWSLARSAGDQLYNTMVQYTKYIAHSITWYNKGLDVLNRKNSNGQWITFND 248

Query: 230 FRRDLTTLTVLIDIVALFPNYDVRTYPIQ-----TSSQLTREIYTSSVIEDSPVSANI 280
++R++T+ VLDI+ALF +YD R YP + ++ TREIYT+ V +SP S +I
Sbjct: 249 YKREMTIQVLDILALFASYDPERRYADKIDNTKLSKTEFTREIYTALV--ESPSSKSI 304

Score = 84.3 bits (207), Expect = 3e-15
Identities = 61/206 (29%), Positives = 100/206 (47%), Gaps = 25/206 (12%)

Query: 417 NDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQ 476
NDY+H+L+++ ++ +S R F+WTH+ P N I + ITQ+P VK++ L
Sbjct: 439 NDYTHILSYIKT-----DVIDYNSNRVS-FAWTHKIVDPNNQIYTDAITQVPAVKSNFLN 492

Query: 477 SGTTVVRGPGFTGGDILRRTSGGPFAYTI-----VNINGQLPQRYRARIRYASTTNLRIY 531
+ V++GPG TGGD++ TS G + + +I + Y RIRYA+ + + +
Sbjct: 493 ATAKVIKGP GHTGGDLVALTSNGTSLGRMEIQCKTSIFNDPTRSYGLRIRYAANSPIVLN 552

Query: 532 VTVAGERIFAGQFNKTMDT-----GDPLTFQSFSYATINTAFTFPMSSQSS-----FT 578
V+ + + G T T L ++ F Y A PM SS
Sbjct: 553 VSYVLQGVSRGTTISTESTFSRPNNIIPDLKYEEFRYKDPFDAIV-PMRLSSNQLITIA 611

Query: 579 VGADTFSSGNEVYIDRFELIPVTATL 604
+ +S N+V IDR E+IP+T ++
Sbjct: 612 IQPLNMTSNNQVIIDRIEIIIPITQSV 637

>emb|CAA30114.1| (X07082) delta-endotoxin (AA 1 - 1136) [Bacillus thuringiensis]
Length = 1136

Score = 128 bits (321), Expect = 2e-28
Identities = 78/238 (32%), Positives = 119/238 (49%), Gaps = 13/238 (5%)

Query: 54 VAFGLFDLIWGFITPSD---WSLFLQIEQLIEQRIETLERNRAITTLRGLADS YEIYIE 110
V + ++W TP+ W+ F+ LI+Q + R A + + D + Y
Sbjct: 69 VLSAVLPILWPTNTPTPERVWNDFMTNTGNLIDQTVTAYVRTDANAKMTVVKDYLDQYTT 128

Query: 111 ALREWEANPNNAQLREDVRIEFANTDDALI-TAINNFTLTSFEIPLLSVYVQAANLHLSL 169
W+ PNN R V +F T L TA+ L +E+ LL +Y Q AN +L L
Sbjct: 129 KFNTWKREPNNQSYRTAVITQFNLTSAKLRETAVYFSNLVGYELLLLPIYAQVANFNLLL 188

Query: 170 LRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARENQ 229
+RD + Q W L + + YN ++ Y H + YN+GL+ LR + QW FN
Sbjct: 189 IRDGLINAQEWSLARSGDQLYNTMVQYTKYIAHSITWYNKGLDVLNRKSNQGOWITFND 248

Query: 230 FRRDLTLTVLIDIVALFPNYDVRTYPIQ-----TSSQLTREIYTSSVIEDSPVSANI 280
++R++T+ VLDI+ALF +YD R YP + ++ TREIYT+ V +SP S +I
Sbjct: 249 YKREMTIQVLDILALFASYDPRRYPADKIDNTKLSKTEFTREIYTALV--ESPSSKSI 304

Score = 84.3 bits (207), Expect = 3e-15
Identities = 61/206 (29%), Positives = 100/206 (47%), Gaps = 25/206 (12%)

Query: 417 NDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQ 476
NDY+H+L+++ ++ +S R F+WTH+ P N I + ITQ+P VK++ L
Sbjct: 439 NDYTHILSYIKT-----DVIDYNSNRVS-FAWTHKIVDPNNQIYTDAITQVPAVKSNFLN 492

Query: 477 SGTTVVRGPGFTGGDILRRTSGGPFAYTI-----VNINGQLPQRYRARIRYASTTNLRIY 531
+ V++GPG TGGD++ TS G + + +I + Y RIRYA+ + + +
Sbjct: 493 ATAKVIKGP GHTGGDLVALTSNGTSLGRMEIQCKTSIFNDPTRSYGLRIRYAANSPIVLN 552

Query: 532 VTVAGERIFAGQFNKTMDT-----GDPLTFQSFSYATINTAFTFPMSSQSS-----FT 578
V+ + + G T T L ++ F Y A PM SS
Sbjct: 553 VSYVLQGVSRGTTISTESTFSRPNNIIPDLKYEEFRYKDPFDAIV-PMRLSSNQLITIA 611

Query: 579 VGADTFSSGNEVYIDRFELIPVTATL 604
+ +S N+V IDR E+IP+T ++
Sbjct: 612 IQPLNMTSNNQVIIDRIEIIIPITQSV 637

>gb|AAC60477.1| (S72313) delta-endotoxin CryIAb7 [Bacillus thuringiensis]
Length = 91

Score = 122 bits (306), Expect = 1e-26
Identities = 60/89 (67%), Positives = 70/89 (78%), Gaps = 2/89 (2%)

Query: 1 MENNIQ-NQCVYPNCLNNPEVEILNEER-STGRLPLDISLSLTRFLLSEFVPGVGVAFLG 58
M+NN + N+C+PYNCL+NPEVE+L ER TG P+DISLSLT+FLLSEFVPG G GL

Sbjct: 1 MDNNPKINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL 60

Query: 59 FDLIWGFITPSDWSLFLQIEQLIEQRIE 87
DLIW F+ PS W FL+QIEQLI QRIE

Sbjct: 61 IDLIWCFVGPSQWDAFLVQIEQLISQRIE 89

>dbj|BAB78601.1| (AB075460) crystal protein CryE6L [Bacillus thuringiensis]
Length = 1270

Score = 115 bits (287), Expect = 2e-24

Identities = 72/237 (30%), Positives = 120/237 (50%), Gaps = 21/237 (8%)

Query: 52 VGVAFLFDLIWGFITPSD-----WSLFLQIEQLIEQRIETLERNRAITTLRGLA 102
V AF + + + + P W+ F E+++++I + A+ LR +

Sbjct: 98 VAGAFAIISMFFDVLWPESENNTNSQVWVADFADAAAEEMMDEKIADEIKAEAVLQLRIVQ 157

Query: 103 DSYEYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQA 162
Y +A ++++PNN + +R F + DDAL + F+ +E LL YVQA

Sbjct: 158 SRLRDYQQACNFQSDPNNESYKALLRDAFDDADDALKEVMILFSREGYEQLLLFYVQA 217

Query: 163 ANLHLSLLRDAVSFGQGWGLDIATVNNHYNR-----LINLIHRYTKHCLDTYNQGLE 214
ANLHL LL+D V FG GWG V +Y+ ++ L+ +YT + +G+E

Sbjct: 218 ANLHLLLLKDVVRFGVGVGFPPGRVEQYYSNPTNLGNPGMVQLLAKYTNYSTSLCWKGIE 277

Query: 215 NLRGTNTRQWARFNQ----FRRDLTLTVLDIVALEFPNYDVRTYPIQTSSQLTREIYT 267
+ ++ N+ +R ++T+ VLD+VAL+P YD YP T+ +LTREIY+

Sbjct: 278 ERKWMVESEYRSNNEEYAYRSNMTMMVLDMLWPTYDPVKYPYATAVELTREIYS 334

Score = 51.6 bits (122), Expect = 2e-05

Identities = 45/168 (26%), Positives = 73/168 (42%), Gaps = 11/168 (6%)

Query: 446 FSWTHRSA-TPTNTIDPERITQIPLVKAHTL-QSGTTVVRGPGFTGGDILRRTSGGPFAY 503
F+W + T N I +I QIP VK + L QSG++VVR G TGGD++R G

Sbjct: 531 FAWRSTTCDFRYNLIIPANKIGQIPAVKGNWLGQSGSSVVRTSGNTGGDVVRLYEFGNLGM 590

Query: 504 TIVNINGQLPQRYRARIYASTT---NLRIYVTVAGERIFAGQFNKMTMDTGDPALT---FQ 557
T + + Y R+RYA+ N+ + V GE + + + + T F+

Sbjct: 591 T---VRFSENRSYIIRLYATVADDLNIIVRVQRGELEYESELPLNQTSNNSTQWKFE 647

Query: 558 SFSYATINTAFTFPMSQSSFTVGADTFSSGNEVYIDRFELIPVTATLE 605
+ Y + + + + + ID+ E IP+ +LE

Sbjct: 648 DYGQYEVGGFYPQVGEEYELWFSFVGTLSHMDIDKIEFIPMETSLE 695

>sp|P11782|CRYT_BACTI 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE ENTOMOCIDAL
PROTOXIN)

gb|AAA22337.1| (M20242) mosquitocidal protein [Bacillus thuringiensis]
Length = 1135

Score = 114 bits (286), Expect = 2e-24

Identities = 75/238 (31%), Positives = 116/238 (48%), Gaps = 14/238 (5%)

Query: 54 VAFGLFDLIWGFITPSD---WSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEYIE 110
V + ++W TP+ W+ F+ LI+Q + R A + + D + Y

Sbjct: 69 VLSAVLPILWPTNTPTPERVWDFMTNTGNLIDQTVTAYVRTDANAKMTVVVKDYLDQYTT 128

Query: 111 ALREWEANPNNAQLREDVRIRFANTDDALI-TAINNFTLTSFEIPLLSVYVQAANLHLSL 169
W+ PNN R V +F T L TA+ L +E+ LL +Y Q AN +L L

Sbjct: 129 KFNTWKREPNNQSYRTAVITQFNLTSAKLRETAVYFSNLVGYELLLPIYAQVANFNLLL 188

Query: 170 LRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNTRQWARFNQ 229
+RD + + + YN ++ Y H + YN+GL+ LR + QW FN

Sbjct: 189 IRDGPHKCTRM-VYARSCDQLYNTMVQYTKYIAHSITWYNKGLDVLRNKSNQWITFND 247

Query: 230 FRRDLTLTVLDIVALEFPNYDVRTYPIQ-----TSSQLTREIYTSSVIEDSPVSANI 280
++R++T+ VLDI+ALF +YD R YP + ++ TREIYT+ V +SP S +I

Sbjct: 248 YKREMTIQVLDILALFASYDPRRYPADKIDNTKLSKTEFTREIYTALV--ESPSSKSI 303

Score = 81.6 bits (200), Expect = 2e-14
Identities = 64/207 (30%), Positives = 100/207 (47%), Gaps = 26/207 (12%)

Query: 417 NDYSHVLNHVTFVRWPGGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQ 476
NDY+H+L+++ ++ +S R F+WTH P N I + ITQ+P VK++ L
Sbjct: 438 NDYTHILSYIKT-----DVIDYNSNRVS-FAWTHNIVDPNNQIYTDAITQVPAVKSNFLN 491

Query: 477 SGTTVVRGPGFTGGDILRRSTGGPFAYTIVNINGQL-----PQR-YRARIRYASTTNLRI 530
+ V++GPG TGGD++ TS G + + I + P R Y RIRYA+ + + I
Sbjct: 492 ATARVIKPGHTGGDLVALTSNGTSLGGRMEIQCKTSIFNDPTRSYGLRIRYAANSPIVI 551

Query: 531 -----YVTVAGERIFAGQFNKMTDGTDP--LTFQSFSYATINTAFTFPMSQSS-----F 577
Y E+ + + P L ++ F Y N A PM SS
Sbjct: 552 ECDHMYKFELEQLRVQNYVSRPNNIIPDLKYEEFRYKDPNDAIV-PMRLSSNQLITI 610

Query: 578 TVGADTFSSGNEVYIDRFELIPVTATL 604
+ +S N+V IDR E+IP+T ++
Sbjct: 611 AIQPLNMTSNNQVIIDRIETIPITQSV 637

>sp|O05102|CHAA_CLOBI Pesticidal crystal-like protein cry17Aa (Insecticidal toxin
CryXVIIA(a)) (Cbm72 mosquitocidal toxin)
emb|CAA67841.1| (X99478) cbm72 mosquitocidal toxin [Clostridium bifermentans]
Length = 618

Score = 103 bits (257), Expect = 5e-21
Identities = 82/273 (30%), Positives = 131/273 (47%), Gaps = 16/273 (5%)

Query: 6 QNQCVPYNC---LNNPEVEILNEERSTGRPLDISLSLTRFLLSEFVPGVGVAFG----L 58
QN+ V YN + E+ LN TG +S+ L + VP VG G L
Sbjct: 8 QNKIVEYNSNLDIQPRELNTLNGLVFTGAT---VSIILPLIGTTAVVPVVGGVIGIIAAL 64

Query: 59 FDLIWGFITPSDWSLF---LLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREW 115
+IW T S+ +LF + E ++++I N A+T L L + + Y + W
Sbjct: 65 LPVIWPAGTSSNDNLFDAVMKDTMIMDEKISEYVVNDAMTRLESYLNILDYRLSKDFW 124

Query: 116 EANPNNAQLREDVRIREFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVS 175
E N ++ +++ RF+ I ++ F ++E+ LL Y AANLHL LLR+ +
Sbjct: 125 EKNKDDPLAIAELKERFSKLHSQFIESMAYFKRANYEVLLLPAAYANAANLHLLLLREGLL 184

Query: 176 FGQGWGLDIATVNNHYNRLNLIHRYTKHCLDTYNQGLNLRGTNTROWARFNQFRRLDT 235
+ + T HY Y HC YN+GLEN++ TR + + N++ +
Sbjct: 185 LNKVID-NFITEGLHYEEFKTRSTYIAHCSTWYNKGLENIKN-KTRDFNKINKYDAYMN 242

Query: 236 LTVLDIVALFPNYDVRTYPIQTSSQ-LTREIYT 267
L+VLDI++LF +YD Y T Q LTR +++
Sbjct: 243 LSVLDIISLFLSYDPYQYDKATKLQTLTRTVFS 275

Score = 49.3 bits (116), Expect = 1e-04
Identities = 44/189 (23%), Positives = 78/189 (40%), Gaps = 35/189 (18%)

Query: 445 MFSWTHRSATPTNTI-----DPERITQIPLVKAHTLQS-----GTTTVVRGPGFTGGDILR 494
+F W H+S +P N + D ITQIP +KA L + ++GP FTGG+++
Sbjct: 429 LFQWIHQSI SPENYLFDKDKDDNYIITQIPAIKASELSNLGELSQAIGKPRFTGGNVIL 488

Query: 495 RT-----SGGPFAYTIVNINGQLPQRYRARIRYASTTN-----LRIYVTVAGERI 539
+ GG ++ +++ RI YA+ N + +T+ + +
Sbjct: 489 SSVSKIDNNDPLYGGTIKIPLLTAFNN-TSKFKIRIYYAANHNHNDYIGALLTINSQHV 547

Query: 540 FAGQFNKMTDGTGD--PLTFQSFSYATINTAFTFPMSQSSFTVGADTF-----SSGNEV 590
+F +T D L++ ++ + + FP + S T+ F V
Sbjct: 548 ANFKFKQTFSGEDYSNLSYNNYQFDYLVQTVAFPPQNTSDVTLNLQFFYDPKFLNDYKQIV 607

Query: 591 YIDRFELIP 599
ID+ E IP
Sbjct: 608 IIDKIEFIP 616

>sp|Q9RMG3|C2AD_BACTU Pesticidal crystal protein cry2Ad (Insecticidal delta-endotoxin
CryIIA(d)) (Crystalline entomocidal protoxin) (71 kDa

crystal protein)
gb|AAF09583.1|AF200816_1 (AF200816) crystal protein [Bacillus thuringiensis]
Length = 633

Score = 80.9 bits (198), Expect = 4e-14
Identities = 48/187 (25%), Positives = 90/187 (47%), Gaps = 5/187 (2%)

Query: 75 LLQIEQLIEQRIETLERNRAITTLRGLADSYEIYIEALREWEANPNNAQLREDVRIRFAN 134
L + E+ + Q++ T +R L GL + E + + + NPN + +
Sbjct: 94 LRETEKFLNQLNTDTLSRVNAELTGLQANVEEFNRQVDNF-LNPNRNAVPLSITSSVNT 152

Query: 135 TDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNRL 194
+ ++ F + +++ LL ++ QAANLHLS +RD + + WG+ AT+ + N L
Sbjct: 153 MQQLFLNRLSQFQMGYQLLLPLFAQAANLHLSFIRDVILNAEEWGISAATLRITYQNH 212

Query: 195 INLIHRYTKHCLDITYNQGLENLRGNTNRQWARFNQFRDLTLTVLIDIVALFPNYDVRTYP 254
N Y+ +C+DTY RG NTR +ER + L V + V+++ + ++
Sbjct: 213 RNYTRDYSNYCIDTYQTA---FRGLNTRLHDMLEFRITYMFLNVFEYVSIWSLFKYQSL 268

Query: 255 IQTSSQL 261
+ + + L
Sbjct: 269 VSSGANL 275

>sp|Q45754|CCAA_BACTU Pesticidal crystal protein cry12Aa (Insecticidal delta-endotoxin
CryXIIA(a)) (Crystalline entomocidal protoxin) (142 kDa
crystal protein)
gb|AAA22355.1| (L07027) delta-endotoxin [Bacillus thuringiensis]
Length = 1257

Score = 79.3 bits (194), Expect = 1e-13
Identities = 120/553 (21%), Positives = 204/553 (36%), Gaps = 85/553 (15%)

Query: 77 QIEQLIEQRIETLERNRAITTLRGLADSYEIYIEALREWEANPNNAQLREDVRIRFANTD 136
QIE LI+Q I + L + +Y A+ NN + ++ N +
Sbjct: 119 QIEALIQQDITNYQDAINQKKFDSLQKTINLYTVAI-----DNNDYVTAKTQLE--NLN 170

Query: 137 DALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLIN 196
L + I+ F +E L Y AN H+ LLRDA+ + G V+ H +
Sbjct: 171 SILTSDISIFIPEGYETGGLPYAMVANAHLILLRDAIVNAEKLGFSDKEVDTHKKYIKM 230

Query: 197 LIHRYTKHCLDITYNQGLENLRGNTNRQWARFNQFRDLTLTVLIDIVALFPNYDVRTYPIQ 256
IH +T+ + + GL+ + + + + +T VLD+VAL+P +D Y +
Sbjct: 231 TIHNHTEAVIKAFNLGLDKFKSLDVNSYNKKANYIKGMTMVLDLVALWPTFDPDHYQKE 290

Query: 257 TSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRPHLMDFMNSLFVTAETVRSQTVW 316
+ TR I SP+ +P + P L + L + R+
Sbjct: 291 VEIEFTRTI-----SSPIYQPVKPNMONTSSSIVPSDLFHYQGDVLKLEFSTRTPDNDG 343

Query: 317 GGHLVSS-RNTAGNRIN-FPSYGV---FNPGGAIWIADPRPFYRTLSDPVF---VRGG 368
+ + RNT N +Y V +N + I+ P L++P+ +R
Sbjct: 344 LAKIFTGIRNTFYKSPNTHETVHVDFTSYNTQSSGNISRGSSNPIPIDLNNPIISTCIRNS 403

Query: 369 FGNP-----HYVLGLRGVAFQ--TGTNHTRTFRNSGTIDSLDEIPPQDNSGAPWND 418
F ++ G +G AF Q TG +F S GAP
Sbjct: 404 FYKAIAGSSVLVNFKDGTQGYAFAQAAPTGGAWDHSFIES-----DGAP--- 446

Query: 419 YSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSG 478
H LN++ S D+ R + +T S N + E+I P K + G
Sbjct: 447 EGHKLNYI-----YTSPGDTLRDFINVTLISTPTINELSTEKIKGFPKGYIKNQ 499

Query: 479 TTVVRG-PGFTGGDILRRTSGGPFAITIVNINGQLPQRYRIRYASTTNLRIYVTVAGE 537
G P + G + + I + +Y RIRYAST + Y + +
Sbjct: 500 IMKYYGKPEYING--AQPVNLENQQTILIFEHASKTAQYTRIRYASTQGTGKYFRLDNQ 557

Query: 538 RIFAGQFNKMTDGTGDLTFQSFYATINTAFTFPMSSFTVGADTFSSGNE----- 589
+ +T++ + Y T N + + +T+G+ T + GN
Sbjct: 558 EL-----QTLN----IPTSHNGYVTGNIGENYDL----YTIGSYTITEGNHTLQIQHND 603

Query: 590 ---VYIDRFELIP 599

+ +DR E +P
Sbjct: 604 KNGMVLDRIEFVP 616

>emb|CAA10670.2| (AJ132463) Cry2A protein [Bacillus thuringiensis]
Length = 551

Score = 76.3 bits (186), Expect = 9e-13
Identities = 56/229 (24%), Positives = 104/229 (44%), Gaps = 15/229 (6%)

Query: 39 SLTRFLLSEFVPGVGVAFG--LFDLIWGFITPSDWSLFLQLI----EQLIEQRIETLERN 92
+++ FLL + VG G + +WG I PS + + I EQ + QR+ T
Sbjct: 56 TVSSFLKK----VGS�IGKRISELWGIIFPSSTNMQDILRETEQFLNQLRLNTDTLA 111

Query: 93 RAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFE 152
R L GL + + + + + NP + + + + F + ++
Sbjct: 112 RVNAELIGLQANIREFNQQVDNF-LNPTQNPVPLSITSSVNTMQQLFLNRLPQFQIQGYQ 170

Query: 153 IPLL SVYVQAANHLSSLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQG 212
+ LL ++ QAAN+HLS +RD + WG+ AT+ + + L N Y+ +C++TY
Sbjct: 171 LLLLPLFAQAANMHLSFIRDVILNADEWGISAATLRTYRDYLRNYTRDYSNYCINTYQTA 230

Query: 213 LENLRGTNTRQWARFNQFRDLTTLVLDIVALFPNYDVRTYPIQTSSQL 261
RG NTR +FR + L V + V+++ + ++ + + + L
Sbjct: 231 ---FRGLNTRLHDML-EFRTYMFLNVFEYVSIWSLFKYQSLMVSSGANL 275

>emb|CAA10671.1| (AJ132464) Cry2Aa protein [Bacillus thuringiensis]
Length = 633

Score = 76.3 bits (186), Expect = 9e-13
Identities = 56/229 (24%), Positives = 104/229 (44%), Gaps = 15/229 (6%)

Query: 39 SLTRFLLSEFVPGVGVAFG--LFDLIWGFITPSDWSLFLQLI----EQLIEQRIETLERN 92
+++ FLL + VG G + +WG I PS + + I EQ + QR+ T
Sbjct: 56 TVSSFLKK----VGS�IGKRISELWGIIFPSSTNMQDILRETEQFLNQLRLNTDTLA 111

Query: 93 RAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFE 152
R L GL + + + + + NP + + + + F + ++
Sbjct: 112 RVNAELIGLQANIREFNQQVDNF-LNPTQNPVPLSITSSVNTMQQLFLNRLPQFQIQGYQ 170

Query: 153 IPLL SVYVQAANHLSSLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQG 212
+ LL ++ QAAN+HLS +RD + WG+ AT+ + + L N Y+ +C++TY
Sbjct: 171 LLLLPLFAQAANMHLSFIRDVILNADEWGISAATLRTYRDYLRNYTRDYSNYCINTYQTA 230

Query: 213 LENLRGTNTRQWARFNQFRDLTTLVLDIVALFPNYDVRTYPIQTSSQL 261
RG NTR +FR + L V + V+++ + ++ + + + L
Sbjct: 231 ---FRGLNTRLHDML-EFRTYMFLNVFEYVSIWSLFKYQSLMVSSGANL 275

>pdb|1I5P|A Chain A, Insecticidal Crystal Protein Cry2aa
Length = 633

Score = 75.9 bits (185), Expect = 1e-12
Identities = 56/229 (24%), Positives = 104/229 (44%), Gaps = 15/229 (6%)

Query: 39 SLTRFLLSEFVPGVGVAFG--LFDLIWGFITPSDWSLFLQLI----EQLIEQRIETLERN 92
+++ FLL + VG G + +WG I PS + + I EQ + QR+ T
Sbjct: 56 TVSSFLKK----VGS�IGKRISELWGIIFPSSTNMQDILRETEQFLNQLRLNTDTLA 111

Query: 93 RAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFE 152
R L GL + + + + + NP + + + + F + ++
Sbjct: 112 RVNAELIGLQANIREFNQQVDNF-LNPTQNPVPLSITSSVNTMQQLFLNRLPQFQIQGYQ 170

Query: 153 IPLL SVYVQAANHLSSLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQG 212
+ LL ++ QAAN+HLS +RD + WG+ AT+ + + L N Y+ +C++TY
Sbjct: 171 LLLLPLFAQAANMHLSFIRDVILNADEWGISAATLRTYRDYLRNYTRDYSNYCINTYQTA 230

Query: 213 LENLRGTNTRQWARFNQFRDLTTLVLDIVALFPNYDVRTYPIQTSSQL 261
RG NTR +FR + L V + V+++ + ++ + + + L
Sbjct: 231 ---FRGLNTRLHDML-EFRTYMFLNVFEYVSIWSLFKYQSLMVSSGANL 275

>gb|AAC04867.1| (AF047038) insecticidal crystal protein [Bacillus thuringiensis]
Length = 633

Score = 75.9 bits (185), Expect = 1e-12
Identities = 56/229 (24%), Positives = 104/229 (44%), Gaps = 15/229 (6%)

Query: 39 SLTRFLLSEFVPGVGVAFG--LFDLIWGFIPTSDWSLFLQLI----EQLEQRIETLERN 92
+++ FLL + VG G + +WG I PS + + I EQ + QR+ T
Sbjct: 56 TVSSFLLKK---VGLIGKRILSELWGIIFFPSGSTNMQDILRETEQFLNQLRLNTDTLA 111

Query: 93 RAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFE 152
R L GL + + + + NP + + + + F + ++
Sbjct: 112 RVNAELIGLQANIREFNQQVDNF-LNPTQNPVPLSITSSVNTMQQLFLNRLPQFQIQGYQ 170

Query: 153 IPLLVSYYVQAANHLSSLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQG 212
+ LL ++ QAAN+HLS +RD + WG+ AT+ + + L N Y+ +C++TY
Sbjct: 171 LLLLPLFAQAANMHLSFIRDVILNADEWGISAAATLRTYRDYLRNYTRDYSNYCINTYQTA 230

Query: 213 LENLRGTNTRQWARFNQFRRDLTLTVLIDIVALFPNYDVRTYPIQTSSQL 261
RG NTR +FR + L V + V+++ + ++ + + + L
Sbjct: 231 ---FRGLNTRLHDML-EFRTYMFLNVFEYVSIWSLFKYQSLMVSSGANL 275

>sp|P21253|C2AA_BACTK Pesticidal crystal protein cry2Aa (Insecticidal delta-endotoxin
CryIIA(a)) (Crystalline entomocidal protoxin) (71 kDa
crystal protein) (P2 crystal protein) (Mosquito factor)
pir||C32053 parasporal crystal protein B1 - Bacillus thuringiensis subsp.
kurstaki
gb|AAA22335.1| (M31738) P2 crystal protein [Bacillus thuringiensis]
gb|AAA83516.1| (M23723) insecticidal crystal protein [Bacillus thuringiensis]
Length = 633

Score = 75.9 bits (185), Expect = 1e-12
Identities = 56/229 (24%), Positives = 104/229 (44%), Gaps = 15/229 (6%)

Query: 39 SLTRFLLSEFVPGVGVAFG--LFDLIWGFIPTSDWSLFLQLI----EQLEQRIETLERN 92
+++ FLL + VG G + +WG I PS + + I EQ + QR+ T
Sbjct: 56 TVSSFLLKK---VGLIGKRILSELWGIIFFPSGSTNMQDILRETEQFLNQLRLNTDTLA 111

Query: 93 RAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFE 152
R L GL + + + + NP + + + + F + ++
Sbjct: 112 RVNAELIGLQANIREFNQQVDNF-LNPTQNPVPLSITSSVNTMQQLFLNRLPQFQIQGYQ 170

Query: 153 IPLLVSYYVQAANHLSSLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQG 212
+ LL ++ QAAN+HLS +RD + WG+ AT+ + + L N Y+ +C++TY
Sbjct: 171 LLLLPLFAQAANMHLSFIRDVILNADEWGISAAATLRTYRDYLRNYTRDYSNYCINTYQTA 230

Query: 213 LENLRGTNTRQWARFNQFRRDLTLTVLIDIVALFPNYDVRTYPIQTSSQL 261
RG NTR +FR + L V + V+++ + ++ + + + L
Sbjct: 231 ---FRGLNTRLHDML-EFRTYMFLNVFEYVSIWSLFKYQSLMVSSGANL 275

>pir||A29913 parasporal crystal protein P2 - Bacillus thuringiensis subsp.
kurstaki
Length = 590

Score = 75.9 bits (185), Expect = 1e-12
Identities = 56/229 (24%), Positives = 104/229 (44%), Gaps = 15/229 (6%)

Query: 39 SLTRFLLSEFVPGVGVAFG--LFDLIWGFIPTSDWSLFLQLI----EQLEQRIETLERN 92
+++ FLL + VG G + +WG I PS + + I EQ + QR+ T
Sbjct: 56 TVSSFLLKK---VGLIGKRILSELWGIIFFPSGSTNMQDILRETEQFLNQLRLNTDTLA 111

Query: 93 RAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFE 152
R L GL + + + + NP + + + + F + ++
Sbjct: 112 RVNAELIGLQANIREFNQQVDNF-LNPTQNPVPLSITSSVNTMQQLFLNRLPQFQIQGYQ 170

Query: 153 IPLLVSYYVQAANHLSSLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQG 212
+ LL ++ QAAN+HLS +RD + WG+ AT+ + + L N Y+ +C++TY
Sbjct: 171 LLLLPLFAQAANMHLSFIRDVILNADEWGISAAATLRTYRDYLRNYTRDYSNYCINTYQTA 230

Query: 213 LENLRGTNTQWARFNQFRDLTLTLVLDIVALFPNYDVRTYPIQTSSQL 261
RG NTR +FR + L V + V+++ + ++ + + + L
Sbjct: 231 ---FRGLNTRLHDMLEFRTYMFLNVFEYVSIWSLFKYQSLMVSSGANL 275

>emb|CAA10672.1| (AJ132465) Cry2Aa protein [Bacillus thuringiensis]
Length = 633

Score = 75.1 bits (183), Expect = 2e-12
Identities = 56/229 (24%), Positives = 103/229 (44%), Gaps = 15/229 (6%)

Query: 39 SLTRFLLSEFVPGVGVAFG--LFDLIWGFITPSDWSLFLQI----EQLIEQRIETLERN 92
+++ FLL + VG G + +WG I PS + + I EQ + QR+ T
Sbjct: 56 TVSSFLKK----VGLIGKRILSELWGIIFPSGSTNLMQDILRETEQFLNQRLNTDTLA 111

Query: 93 RAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFE 152
R L GL + + + + + NP + + + F + ++
Sbjct: 112 RVNAELIGLQANIREFNQQVDNF-LNPTQNPAPLSITSSVNTMQQLFLNRLPQFQIQGYQ 170

Query: 153 IPLLSEVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQG 212
+ LL ++ QAAN+HLS +RD + WG+ AT+ + + L N Y+ +C++TY
Sbjct: 171 LLLLPLFAQAANMHLSFIRDVILNADEWGISAATLRTRYDYLRNYTRDYSNYCINTYQTA 230

Query: 213 LENLRGTNTQWARFNQFRDLTLTLVLDIVALFPNYDVRTYPIQTSSQL 261
RG NTR +FR + L V + V+++ + ++ + + + L
Sbjct: 231 ---FRGLNTRLHDMLEFRTYMFLNVFEYVSIWSLFKYQSLMVSSGANL 275

>sp|P21254|C2AB BACTK Pesticidal crystal protein cry2Ab (Insecticidal delta-endotoxin
CryIIA(b)) (Crystalline entomocidal protoxin) (71 kDa
crystal protein)
pir||D32053 parasporal crystal protein B2 - Bacillus thuringiensis subsp.
kurstaki
emb|CAA39075.1| (X55416) crystal protein CryIIB [Bacillus thuringiensis]
gb|AAA22342.1| (M23724) crystal protein B2 [Bacillus thuringiensis]
gb|AAG36762.1| (AF164666) Cry2Ab [Bacillus thuringiensis]
Length = 633

Score = 73.2 bits (178), Expect = 8e-12
Identities = 46/187 (24%), Positives = 87/187 (45%), Gaps = 5/187 (2%)

Query: 75 LLQIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFAN 134
L + E+ + QR+ T R L GL + E + + + NPN + +
Sbjct: 94 LRETEKFLNQRLNTDTLARVNAELTGLQANVEEFNRQVDNF-LNPNRNPVPLSITSSVNT 152

Query: 135 TDDALITAINNFTLTSFEIPLLSEVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNRL 194
+ + F + +++ LL ++ QAANLHLS +RD + WG+ AT+ + + L
Sbjct: 153 MQQLFLNRLPQFQMGYQLLLLPLFAQAANLHLSFIRDVILNADEWGISAATLRTRYDYLR 212

Query: 195 INLIHRYTKHCLDTYNQGLENLRGNTQWARFNQFRDLTLTLVLDIVALFPNYDVRTYP 254
N Y+ +C++TY +G NTR +FR + L V + V+++ + ++
Sbjct: 213 KNYTRDYSNYCINTYQSA---FKGLNTRLHDMLEFRTYMFLNVFEYVSIWSLFKYQSLL 268

Query: 255 IQTSSQL 261
+ + + L
Sbjct: 269 VSSGANL 275

>pir||A25140 parasporal crystal protein - Bacillus thuringiensis (fragments)
Length = 262

Score = 67.8 bits (164), Expect = 3e-10
Identities = 67/245 (27%), Positives = 88/245 (35%), Gaps = 113/245 (46%)

Query: 29 TGRPLDLISLSLTRFLLSEFVPGVGVAFGFLDLIWGFITPSDWSLFLQIEQRIET 88
TG P+ ISLSLT+F L+ F PG G IE
Sbjct: 3 TGYTPIXISLSLTQFTLNPFXPGAGFV-----IEE 32

Query: 89 LERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDALITAINNFTL 148
RN+AI+ L GL++ Y+IY EA R P N LRE++R + N LI ++ +
Sbjct: 33 FARNQAISRLEGLSNLYQIYAEAFR-----PTNPALREEMRGQRYNDLRLIGTYTDYAV 87

Query: 149 TSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDT 208
+ L V WG D
Sbjct: 88 RWYNTGLERV-----WGPD----- 101

Query: 209 YNQGLLENLRTNTRQWARFNQFRRDLTLTLVDIVALEFPNYDVRTYPIQTSSQLTREIYTS 268
+R W R+NQF RTYPI+T SQLTREIYT+
Sbjct: 102 -----SRDWVRYNQF-----RTYPIRTVSQLTREIYTN 129

Query: 269 SVIED 273
V+E+
Sbjct: 130 PVLEN 134

Score = 66.6 bits (161), Expect = 7e-10
Identities = 46/108 (42%), Positives = 51/108 (46%), Gaps = 27/108 (25%)

Query: 419 YSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSG 478
+SH L+HV+ R S RAPMFS H T +N
Sbjct: 182 FSHRLSHVSMFRSGFSNSSVSIIRAPMFSGQH---TRSNEF----- 219

Query: 479 TTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTT 526
GPGFTGGDILRRTS G + VNI L QRYR R RYASTT
Sbjct: 220 -----GPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRYRYASTT 262

>sp|P57091|CIBA_PAEPP Parasporal crystal protein cryl8Ba (Parasporal delta-endotoxin
CryXVIIIIB(a)) (Crystalline parasporal protoxin) (76 kDa
crystal protein)
gb|AAF89667.1|AF169250_2 (AF169250) parasporal crystal protein Cryl8Ba1 [Paenibacillus
popilliae]
Length = 675

Score = 67.4 bits (163), Expect = 4e-10
Identities = 45/184 (24%), Positives = 86/184 (46%), Gaps = 4/184 (2%)

Query: 79 EQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVIRFANT-DD 137
EQ +++++T+ NR L GL ++ + + + N ++ I NT
Sbjct: 126 EQYVQEQLDVTWNRVSQELEGKNNLRTFNDQIDDFLQN--RVEISPTAMIDSINTMQQ 183

Query: 138 ALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINL 197
+ + F L+ +++ LL ++ Q A LHL+ +RD + W + A +N L
Sbjct: 184 VFNRLPQFQLSDYQLLLLPLFAQGATLHLTFIRDIIINAGEWNIPEAQLNTCKRYLKQY 243

Query: 198 IHRYTKHCLDTYNQGLLENLRTNTRQWARFNQFRRDLTLTLVDIVALEFPNYDVRTYPIQT 257
+ +Y+ + L TY +G R QF+ +TL VLD+V+++ I T
Sbjct: 244 VAQYSNYALSTY-EGAFRRARYPRATLENMLQFKTFMTNLVLDLVSISLLKYMNLVIST 302

Query: 258 SSQL 261
S+ L
Sbjct: 303 SANL 306

>sp|Q45358|CIAA_PAEPP Parasporal crystal protein cryl8Aa (Parasporal delta-endotoxin
CryXVIIIA(a)) (Crystalline parasporal protoxin) (79 kDa
crystal protein)
emb|CAA67506.1| (X99049) parasporal crystal protein [Paenibacillus popilliae]
Length = 706

Score = 67.0 bits (162), Expect = 6e-10
Identities = 53/214 (24%), Positives = 98/214 (45%), Gaps = 18/214 (8%)

Query: 58 LFDLIWGFIPTSDWSLFLQLI----EQLIEQRIETLERNRAITTLRGLADSYEIIYIEALR 113
L + + P++ SL + +I EQ +++R++T NR L GL ++ + + +
Sbjct: 143 LLKTLTDLFLPNSSLTMEILRATEQYVQERLDTDTANRVSQELVGLKNNLTTFNDQVE 202

Query: 114 EWEANPNNAQLREDVIRFANTDDAL-ITAINNFTLTSFEIPLLSVYVQAANLHLSLLRD 172
++ N + I NT L + + F ++ +++ LL ++ QAA LHL+ LRD
Sbjct: 203 DFLQN--RVGISPLAIDSINTMQQLFVNRLPQFQVSGYQVLLLPLFAQAATLHLTLFLRD 260

Query: 173 AVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLLENLRTNTRQWAR-----F 227

+ W + A + N + I Y + + L TY + G TR + R
Sbjct: 261 VIINADEWNIPTAQLNTYTRYFKEYIAEYSNYALSTYDDGF-----RTRFYPRNTLEDM 314

Query: 228 NQFRDLTLTVLDIVLFPNYDVRTYPIQTSSQL 261

QF+ +TL LD+V+++ + TS+ L

Sbjct: 315 LQFKTFMTLNALDLVSIWSLLKYVNLVYSTSANL 348

>sp|P57092|CICA_PAEPP Parasporal crystal protein cry18Ca (Parasporal delta-endotoxin
CryXVIIIC(a)) (Crystalline parasporal protoxin) (78 kDa
crystal protein)
gb|AAF89668.1|AF169251_1 (AF169251) parasporal crystal protein Cry18Ca1 [Paenibacillus
popilliae]
Length = 695

Score = 62.0 bits (149), Expect = 2e-08
Identities = 49/210 (23%), Positives = 95/210 (44%), Gaps = 6/210 (2%)

Query: 54 VAFGLFDLIWGFITPSDWSLFLQLIEQRIETLERNRAITTLRGLADSYEIIYIEALR 113

V L + L + + S L EQ I + + + + T + NR L GL + + + +

Sbjct: 117 VLMSLTNLLFPNNSTSTMEILRATEQYIQQLDVTWNRVSQELEGKNDLRTFNDQID 176

Query: 114 EWEANPNNAQLREDVRIRFANTDDAL-ITAINNFTLTSFEIPLLSVYVQAANLHLSLLRD 172

++ N + I NT L + + F ++ ++ LL ++ QA LHL+ +RD

Sbjct: 177 DFLQN--RVGISPLAIDSINTMQQLFVNRLPQFQVSDQVLLPLFAQAVTLHLTFVRD 234

Query: 173 AVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLE-NLRGTNTRQWARFNQFR 231

+ W + A + N + L + + Y + + L TY + NT + + F +

Sbjct: 235 IIINADEWNIPEAQLNTYKRYLKQYVAQYSNYALSTYEEAFRRFYPRNTVE--NMLEFK 292

Query: 232 RDLTLTVLDIVLFPNYDVRTYPIQTSSQL 261

+TL VLD+V+++ + TS+ L

Sbjct: 293 TFMTLNVLDLVSMWSLLKYVNLVYSTSANL 322

>gb|AAM06002.1| (AE010957) hypothetical protein [Methanosarcina acetivorans str.
C2A]
Length = 171

Score = 58.9 bits (141), Expect = 2e-07
Identities = 35/124 (28%), Positives = 63/124 (50%), Gaps = 7/124 (5%)

Query: 165 LHLSSLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRG- 219

+HL+LLRD +G WG + + + + + I Y ++ TY+ GL++ +

Sbjct: 1 MHLTLRLDGLYGFSGWGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60

Query: 220 -NTRQWARFNQFRDLTLTVLDIVLFPNYDVRTYPIQTSSQLTREIYTSSV-IEDSPVS 277

T + N++ R++TL VLD ++ +D YP L+REIY+ +V D+ +

Sbjct: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEYVLSREIYSDAVGTADNSGA 120

Query: 278 ANIP 281

N P

Sbjct: 121 LNFP 124

>sp|Q45743|C2AC_BACTU Pesticidal crystal protein cry2Ac (Insecticidal delta-endotoxin
CryIIA(c)) (Crystalline entomocidal protoxin) (70 kDa
crystal protein)
pir||S17402 parasporal crystal protein cryIIC - Bacillus thuringiensis plasmid
emb|CAA40536.1| (X57252) CryIIC delta-endotoxin [Bacillus thuringiensis]
prf||1802281A delta endotoxin [Bacillus thuringiensis]
Length = 622

Score = 57.0 bits (136), Expect = 6e-07
Identities = 41/183 (22%), Positives = 79/183 (42%), Gaps = 5/183 (2%)

Query: 79 EQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDA 138

EQ I QR+ R L GL + + + + NPN + +

Sbjct: 98 EQFINQRLNADTLGRVNAELAGLQANVAEFNRQVDNF-LNPNQNPVPLAIDSNTLQQL 156

Query: 139 LITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLI 198

++ + F + +++ LL ++ QAAN +LS +R + WG+ ATV + + L

Sbjct: 157 FLSRLPQFQIQGYQLLLLPLFAQAANFNLSFIRGVILNADEWGISAATVVRTYRDHLRKFH 216

Query: 199 HRYTKHCLDTYNQGLENLRGNTNTRQWARFNQFRDLTLTVLIDIVALFPNYDVRTYPIQTS 258
Y+ +C++ Y RG N R +FR + L V + V+++ + ++ + +

Sbjct: 217 RDYSNYCINPYQTA---FRGLNHR-LPDMLEFRTYMFLNVFEYVSIWSLFKYQSLLVSSG 272

Query: 259 SQL 261
+ L

Sbjct: 273 ANL 275

>sp|Q45753|C5AB_BACUD Pesticidal crystal protein cry5Ab (Insecticidal delta-endotoxin
CryVA(b)) (Crystalline entomocidal protoxin) (142 kDa
crystal protein)

pir||T18212 delta-endotoxin - Bacillus thuringiensis (fragment)

gb|AAA67693.1| (L07026) delta-endotoxin [Bacillus thuringiensis]

Length = 1289

Score = 55.5 bits (132), Expect = 2e-06

Identities = 132/631 (20%), Positives = 237/631 (36%), Gaps = 95/631 (15%)

Query: 34 LDISLSLTRLFLSE---FVPGVGVAFLGLFDLIWGFITPSDWSLFLQ---IEQLIEQRIE 87
++I LSL + E F P +G+ F + P+ +F I+++I++ +

Sbjct: 78 VNIGLSLITLAVPEIGIFTFFIGLFFAALNKHDAPPPNAKDIFEAMKPAIQEMIDRTLT 137

Query: 88 TLER---NRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDALITAIN 144
E+ N I+ L+ LA Y+ ++ ++ + + D + TD+ L ++N

Sbjct: 138 ADEQTFNLGEISGLQNLAAARYQSTMDDIQS-----HGGFNKVDSGLIKKFTDEVL--SLN 190

Query: 145 NFTLTSFEIPL-----LSVYVQAANLHLSLLRDAVSFGQGWGLDI----ATVNN 189
+F + + L Y A++HL LLRD ++ G W I +++

Sbjct: 191 SFYTDRLPVFITDNTADRTLGLPYAILASMHLMLLRDIITKGPTWDSKINFTPDIDS 250

Query: 190 HYNRLINLIHRYTKHCLDTYNQGLENL-RGTNTRQWARFNQFRDLTLTVLIDIVALFPNY 248
+ N I Y+K D + +GL + ++ +A+ ++ +T LD LFP +

Sbjct: 251 FKTDIKNNIKLYSKTIYDVQKGLASYGTPSDLESFAKKQKYIEIMTTHCLDFARLFPTF 310

Query: 249 DVRTYPI---QTSSQLTREIY-----TSSVIEDSPVSANIPNGFNRAEFGVRPPHMD 298
D YP S Q TR I T+ + + S + N N P+ +

Sbjct: 311 DPDLIPTGSGDISLQKTRRLSPFIPIRTADGLTLNNTSIDTSNWPNYENGNGAFPNPKE 370

Query: 299 FMNSLFVTAETVRSQTVWGGHL-----VSSRNTAGNRINFPSYGVFNPGGAIWIADDP 352
+ F + R+ +GG L + +++ R+ V G +++ +

Sbjct: 371 RILKQFKLYPSWRA-AQYGGLLQPYLWAIQVQDSVETRLYQLPAVDPQAGPNYVSIDS 429

Query: 353 RPFYR---TLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPP 408
P + T P G+ + G++F Q G D++ +P

Sbjct: 430 NPIQINMDTWKTPPQGASGWNTNLMRGSVSGLSFLQRDGTRLSAGMGGFADTIYSLPA 489

Query: 409 QDN----SGAPWNDYSHVLNHVTFVRWPGFISGSDSWRAPMFSWTHRSATPTNTI-DPER 463
G P+ + HV G + G T + AT N I P+

Sbjct: 490 THYLSYLYGTPYQTSNYSGHV-----GALVGV-----TPQEATLPNIIGQPDE 534

Query: 464 ITQI-----PLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRA 518
+ P KA G TVV+ G + ++ + G I N+ Y+

Sbjct: 535 QGNVSTMGFPFEKA---SYGGTVVK-EWLNAGANAMKLSPGQSIGIPITNVTS---GEYQI 587

Query: 519 RIRYASTTNLRIYVTV---AGERIFAG-QFNKTMDT-----GDPLTFQSFSYATINTAFT 569
R RYAS N ++ V IF F T+D G + S AT + +FT

Sbjct: 588 RCRYASNDNTNVFFNVDTGGANPIFQQINFASVDNNTGVQGANGVYVVKSIATTDNSFT 647

Query: 570 FPMSQSSFTVGADTFSSGNEVYIDREFELIPV 600
+ + V T ++V++DR E +P+

Sbjct: 648 VKIPAKTINVHL-TNQGSSDVFLDRIEFVPI 677

>sp|Q45710|CEAA_BACTS Pesticidal crystal protein cry14Aa (Insecticidal delta-endotoxin
CryXIVA(a)) (Crystalline entomocidal protoxin) (132 kDa
crystal protein)

pir||T18210 delta endotoxin - Bacillus thuringiensis

gb|AAA21516.1| (U13955) delta endotoxin [Bacillus thuringiensis]

Length = 1186

Score = 53.1 bits (126), Expect = 8e-06
Identities = 54/260 (20%), Positives = 109/260 (41%), Gaps = 34/260 (13%)

Query: 44 LLSEFVPGVGVAFLFDLIWGFITP-----SDWSLFLQLIEQLIEQRIETL----ERNRA 94
L FVPG + +++ G++ P +D + I++ I++++ +RN
Sbjct: 75 LAGSFVPGGTFVAPIVNMVIGWLWPHKNKTADTENLIKLIIDEIQKQLNKALLDQDRNNW 134

Query: 95 ITTLRGLADSYEIIYIEAL--REWEANPNNAQLRE-----DVRIRFANTDDALITAI 143
+ L + D+ A+ +W + ++ +V +F + D ++IT
Sbjct: 135 TSFLESIFDTSATVSNALIDAQWSGTVDTTNRQQKTPPTSDYLNVVVGKFDSDSSIIITNE 194

Query: 144 NNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNR----- 193
N +F++ +V A L LSL + F W + N N
Sbjct: 195 NQIMNGNFDVAAPYFVIGATRLRLSLYQSYIKFCNSWIDAVGFSTNDANTQKANLARTKL 254

Query: 194 -LINLIHRYTKHCLDTYNQGLNLR--GTNTRQWARFNQFRRDLTLTVLDIVAFPNYDV 250
+ I+ YT+ + + +N+ GTN +N + + +TL VLD+VA++ +
Sbjct: 255 TMRTTINEYTRQVMKVFKDS-KNMPITGTNKFSDAYNVYVKGMTLNVLDMAIWSLYP 313

Query: 251 RTYPIQTSSQLTREIYTSSV 270
Y QT+ + TR +++ V
Sbjct: 314 NDYTSQTAIEQTRVTFSNMV 333

>sp|Q45712|C5BA_BACTU Pesticidal crystal protein cry5Ba (Insecticidal delta-endotoxin
CryVB(a)) (Crystalline entomocidal protoxin) (140 kDa
crystal protein)
pir||T18211 delta endotoxin - Bacillus thuringiensis (fragment)
gb|AAA68598.1| (U19725) delta endotoxin [Bacillus thuringiensis]
Length = 1245

Score = 53.1 bits (126), Expect = 8e-06
Identities = 44/149 (29%), Positives = 64/149 (42%), Gaps = 13/149 (8%)

Query: 146 FTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGL-DIATVNNHYNRLINLIHRYTKH 204
F TS E+ L +Y A LHL L + F W + +NN L LIH Y++
Sbjct: 224 FKRTSVELTL-PMYTTVATLHLLYEGYIEFMTKWNFNHNEQYLNKLKVELQQLHSYSET 282

Query: 205 CLDTYNQGLNLRGTNTRQWARFNQFRRDLTLTVLDIVAFPNYDVRTYPIQTSSQLTR- 263
++ Q L L + +N++ R++T+ LDI A +P +D Y LTR
Sbjct: 283 VRTSFLQFLPTLNNRSKSSVNAYNRYVRNMTVNCLEAATWPTFDTHNYHQGGKLDLTRI 342

Query: 264 -----EIYTSSVIEDSPVSANI-PN 282
E YT+ P +NI PN
Sbjct: 343 ILSDTAGPIEYTTGDKTSGPEHSNITPN 371

Score = 29.6 bits (65), Expect = 98
Identities = 25/97 (25%), Positives = 42/97 (42%), Gaps = 5/97 (5%)

Query: 506 VNINGQLPQRYRARIYASTTNLRIYVTV-AGERIFAG--QFNKTMGTGDLTFQSFSYA 562
+ I Q Q+Y R RYAS + +Y V E F F T + + ++ Y
Sbjct: 601 IQITNQTKQKYEIRCRYASKGDNVYFNVLDLSENPFRNSISFGSTESSVVGQENGKY- 659

Query: 563 TINTAFTFPMSQSSFTVGADTFSSGNEVYIDRFELIP 599
+ + T + SF V T +++++DR E +P
Sbjct: 660 ILKSITTVEIPAGSFYVHI-TNQSSDLFLDRIEFVP 695

>sp|Q45760|C5AA_BACUD Pesticidal crystal protein cry5Aa (Insecticidal delta-endotoxin
CryVA(a)) (Crystalline entomocidal protoxin) (152 kDa
crystal protein)
pir||T18213 delta-endotoxin - Bacillus thuringiensis (fragment)
gb|AAA67694.1| (L07025) delta-endotoxin [Bacillus thuringiensis]
Length = 1385

Score = 51.6 bits (122), Expect = 2e-05
Identities = 134/637 (21%), Positives = 239/637 (37%), Gaps = 100/637 (15%)

Query: 34 LDISLSLTRFLLSE---FVPGVGVAFLGLFDLIWGFITPSDWSLFLQ---IEQLIEQRIE 87
++I LSL + E F P +G+ F + P+ +F I+++I++ +
Sbjct: 78 VNIGLSLITLAVPEIGIFTFFIGLFFAALNKHDAPPPNAKDI FEAMKPAIQEMIDRTLT 137

Query: 88 TLER---NRAITTLRGLADSYEIIYEALREWEANPNNAQLREDVRIRFANTDDALITAIN 144
E+ N I+ L+ LA Y+ ++ ++ + + D + TD+ L ++N
Sbjct: 138 ADEQTFNLGEISGLQNLAAARYQSTMDDIQS-----HGGFNKVD SGLIKKFTDEVL--SLN 190

Query: 145 NFTLTSFEIPL-----LSVYVQAANLHLSLLRDAVSFGQGWGLDI---ATVNN 189
+F + + L Y A++HL LLRD ++ G W I +++
Sbjct: 191 SFYTDRLPVFITDNTADRTLGLPYAILASMHMLLRDIITKGPTWDSKINFPTDAIDS 250

Query: 190 HYNRLINLIHRYTKHCLDTYNQGLENL-RGTNTRQWARFNQFRRDLTLTVLIDIVALFPNY 248
+ N I Y+K D + +GL + ++ +A+ ++ +T LD LFP +
Sbjct: 251 FKTDIKNNIKLYSKTIYDVFKGLASYGTPSDLESFAKKQKYIEIMTTHCLDFARLPTF 310

Query: 249 DVRTYPI---QTSSQLTREIY-----TSSVIEDSPVSANIPNGFNRAEFGVRPPHLM 298
D YP S Q TR I T+ + + S + N N P+ +
Sbjct: 311 DPDLYPTGSGDISLQKTRRLSPFPIRTADGLTLNNTSIDTSNWPNYENGNGAFNPKE 370

Query: 299 FMNSLFVTAETVRSQTVWGGHL-----VSSRNTAGNRINFPSYGVFNPGGAIWIADDP 352
+ F + R+ +GG L + +++ R+ V G +++ +
Sbjct: 371 RILKQFKLYPSWRAGQ-YGGLLQPYLWAEVQDSVETRLYGQLPAVDPPQAGPNYVSIDSS 429

Query: 353 RPFYR-----TSDPVEFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPP 408
P + T P G+ + G++F Q G D++ +P
Sbjct: 430 NPPIQINMDTWKTPPQAGSGWNTNLMRGSVSGLSFLQRDGTLSAGMGGGFADTIYSLPA 489

Query: 409 QDN-----SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTI-DPER 463
G P+ + HV G + G T + AT N I P+
Sbjct: 490 THYLSYLYGTPYQTSNDYSGHV-----GALVGVS-----TPQEATLPNIIGQPDE 534

Query: 464 ITQI-----PLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRA 518
+ P KA G TVV+ G + ++ + G I N+ Y+
Sbjct: 535 QGNVSTMGPFPEKA---SYGGTVVK-EWLNKANAMKLSPGQSIGIPITNVTS---GEYQI 587

Query: 519 RIRYASTTNLRIYVTV---AGERIFAG-QFNKMTDGDPLTFQSFYSATINTAFTFPM 574
R RYAS N ++ V IF F T+D + + Y + A T
Sbjct: 588 RCRYASNDNTNVFFNVDTGGANPIFQQINFASVDNNTGVQGANVYVVKSIATT-----D 643

Query: 575 SSFT-VGADTFS-----SGNEVYIDRFELIPVTATL 604
+SFT + A T + ++V++DR E IP + L
Sbjct: 644 NSFTEIPAKTINVHLTNQGSDDVFLDRIEFIPFSLPL 680

>dbj|BAB11757.1| (AB031065) 81-kDa leukemia toxin [Bacillus thuringiensis]
Length = 723

Score = 51.6 bits (122), Expect = 2e-05
Identities = 46/181 (25%), Positives = 77/181 (42%), Gaps = 29/181 (16%)

Query: 151 FEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYN 210
+ + L + QA +HL LL+DA + G +D +N + LI LI YT TYN
Sbjct: 269 YPVLTLPLRAQACVMHMLLLKDATTSVWGQQIDSQQLNGYKAELIRLIKVYTNDVNNTYN 328

Query: 211 QGLE-----NLRGTNTRQ---WARFNQFRRDLTLTVLIDIVAL 244
QGLE ++ +N ++ W R +++R + ++ L + AL
Sbjct: 329 QGLELEKAKPLNYSDPPEEYLQAGRPDISVLRSNFKEVMKWNRVAKYKRGMAMSALSAL 388

Query: 245 FPNYDVRTYPIQTSSQL-TREIYTSSV-IEDSPVSANIPNGFNRAEFGVRPPHLMDFMNS 302
FP + YP Q + +R+I+ + I S + F F V+ +D +
Sbjct: 389 FPTFG-PNYPKQALKVVQSRQIFAPVIGIPGGITSQDHSFTGSMRFDVKTYDQIDALRR 447

Query: 303 L 303
L
Sbjct: 448 L 448

>sp|P56955|C5AC_BACTU Pesticidal crystal protein cry5Ac (Insecticidal delta-endotoxin
CryVA(c)) (Crystalline entomocidal protoxin) (135 kDa
crystal protein)

Length = 1220

Score = 49.7 bits (117), Expect = 9e-05
Identities = 128/625 (20%), Positives = 237/625 (37%), Gaps = 91/625 (14%)

Query: 34 LDISLSLTRLFLSE---FVPGVGVAFLGLFDLIWGFITPSDWSLFLQ---IEQLIEQRIE 87
++I LSL + E F P +G+ F + P+ +F I+++I++ +
Sbjct: 78 VNIGLSLITLAVPEIGFTPFIFGLFFAALNKHDA PPPNAKDIFEAMKPAIQEMIDRTLT 137

Query: 88 TLER---NRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDALITAIN 144
E+ N I+ L+ LA Y+ ++ ++ + + D + TD+ L ++N
Sbjct: 138 ADEQTFNLGEISGLQNLAAARYQSTMDDIQS-----HGGFNKVDSGLIKKFTDEVL--SLN 190

Query: 145 NFTLTSFEIPL-----LSVYVQAANLHLSLLRDAVSFGQGWGLDI----ATVNN 189
+F + + L Y A++HL LLRD ++ G W I +++
Sbjct: 191 SFYTDRLPVFITDNTADRTLLGLPYAILASMHMLLRDIITKGTWDSKINFPTDAIDS 250

Query: 190 HYNRLINLIHRYTKHCLDTYNQGLENL-RGTNTRQWARFNQFRDLTLTVLDIVALEFPNY 248
+ N I Y+K D + +GL + ++ +A+ ++ +T LD LFP +
Sbjct: 251 FKTDIKNNIKLYSKTIYDVQKGLASGTPSDLESFAKKKKYIEIMTTHCLDFARLFPTF 310

Query: 249 DVRTYPI---QTSSQLTREIY-----TSSVIEDSPVSANIPNGFNRAEFGVRPPLMD 298
D YP S Q TR I T+ + + S + N N P+ +
Sbjct: 311 DPDLIPTGSGDISLQKTRRLSPFPIRTADGLTLNNTSIDTSNWPNYENGNGAFNPKE 370

Query: 299 FMNSLFVTAETVRSQTVWGHL-----VSSRNTAGNRINFPSYGVFNPGGAIWIADDP 352
+ F + R+ +GG L + +++ R+ V G +++ +
Sbjct: 371 RILKQFKLYPSWRAGQ-YGGLLQPYLWAEVQDSVETRLYGQLPAVDPPQAGPNYVSIDSS 429

Query: 353 RPFYR----TLSDPVFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPP 408
P + T P G+ + G++F Q G D++ +P
Sbjct: 430 NPIIQINMDTWKTPPQAGSCWNTNLMRGSVSGLSFLQDGTRLSAGMGGGFADTIYSLPA 489

Query: 409 QDN----SGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTI-DPER 463
G P+ + HV G + G T + AT N I P+
Sbjct: 490 THYLSYLYGTPYQTSNDNYSCHV-----GALVGV-----TPQEATLPNIIGQPDE 534

Query: 464 ITQI-----PLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRA 518
+ P KA G TVV+ G + ++ + G I N+ Y+
Sbjct: 535 QGNVSTMGFFFEKA---SYGGTVVK-EWLNANAMKLSPGQSIGIPITNVT---KHNYQV 587

Query: 519 RIRYASTNLRIYVTV---AGERIFAG-QFNKMTDGDPLTFQSFSYATINTAFTFMSQ 574
R RYAS ++ ++ V IF F T+D+ + ++ Y + + T +
Sbjct: 588 RCRYASNSDNPFVFNVDTGANPIFQQINFASVDSNMGVKEENGVI-VVKSITVEIPA 646

Query: 575 SSFTVGADTFSSGNEVYIDRFELIP 599
SF V T +++++DR E +P
Sbjct: 647 GSFYVHV-TNQGSSDLFLDRIEFVP 670

>sp|Q45730|CBBA_BACTJ Pesticidal crystal protein cry11Ba (Insecticidal delta-endotoxin
CryXIB(a)) (Crystalline entomocidal protoxin) (81 kDa
crystal protein)
emb|CAA60504.1| (X86902) mosquitocidal toxin [Bacillus thuringiensis]
Length = 724

Score = 47.8 bits (112), Expect = 3e-04
Identities = 33/164 (20%), Positives = 69/164 (41%), Gaps = 12/164 (7%)

Query: 67 TPSDWSLFLQLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLRE 126
TP+ ++++ L++QR++ +G+ D +++ + + + + A
Sbjct: 67 TPATMDKVRIEVQTLQRLQDDRVKILEGEYKGIIDVSKVFTDYVNQSKFETGTANRL- 125

Query: 127 DVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGL---D 183
F +T + LI+ + F + +E +S++ Q HL LL+D + G WG D
Sbjct: 126 -----FFDTSNQLISRLPQFEIAGYEGVSISLFTQMCTFHLGLLKDGILAGSDWGFAPAD 180

Query: 184 IATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGTNTRQWARF 227
+ +NR +N Y + Y++ L N + F
Sbjct: 181 KDALICQFNRFVN---EYNTRLMLVLYSKEFGRLLAKNLNEALNF 221

>sp|P21256|CBAA_BACTI Pesticidal crystal protein cry11Aa (Insecticidal delta-endotoxin CryXIA(a)) (Crystalline entomocidal protoxin) (72 kDa crystal protein)
pir||A43647 72K crystal protein - Bacillus thuringiensis subsp. israelensis
gb|AAA22352.1| (M31737) mosquito-toxic crystal protein [Bacillus thuringiensis]
Length = 643

Score = 47.0 bits (110), Expect = 6e-04
Identities = 32/154 (20%), Positives = 65/154 (41%), Gaps = 6/154 (3%)

Query: 58 LFDLIWGFITPSDWSLFLQLQIEQLQRIETLERNRAITTLRGLADSYEIYIEALREWEA 117
+ LI+ P+ ++E LI Q++ N RG+ + +++ +++
Sbjct: 58 VLSLIFPGSQPATMEKVRTEVETLINQKLSQDRVNILNAEYRGIIIEVSDVFDAYIKQPGF 117

Query: 118 NPNNAQLREDVVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFG 177
P A + F N A+I + F + ++E ++++ Q LHL+LL+D + G
Sbjct: 118 TPATA-----KGYFLNLGAI IQRLPQFEVQTYEGVSIALFTQMCTLHLTLKDGILAG 171

Query: 178 QGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQ 211
WG A V++ + Y + Y +
Sbjct: 172 SAWGFTQADVDSFIKLFNQKVLDRTRLMRMYTE 205

>sp|P56956|CLAA_BACTU Pesticidal crystal protein cry21Aa (Insecticidal delta-endotoxin CryXXIA(a)) (Crystalline entomocidal protoxin) (132 kDa crystal protein)
Length = 1167

Score = 45.8 bits (107), Expect = 0.001
Identities = 90/447 (20%), Positives = 167/447 (37%), Gaps = 76/447 (17%)

Query: 156 LSVYVQAANLHLSLLRDAVSFGQGW---GLDIATVNNHYNRLINLIHRYTKHCLDTYNQG 212
L +Y A L+L L + + F + W D + +N L I Y+ T+ +
Sbjct: 231 LPMYTTGATLNLILHQGYIQFAERWKSVMNYDESFINQTKVDLQRRIQDYSTTVSTTFEKF 290

Query: 213 LENLRGTNTRQWARENQFRDLTLTVLDIVAFPNYDVRTYPIQTSSQL--TREIY---- 266
L +N ++N++ R +TL LDI A +P D YP QL TR ++
Sbjct: 291 KPTLNPSNKESVNKNRYVRSMTLQSLDIAATWPTLDNVNYPNSVDIQLDQTRLVFSDDVA 350

Query: 267 -----TSSVIED-SPVSANIPNGFNRAEFGVRPPHLMDFMNSLFVTAETVRSQTV- 315
TS++I+ +P++ I GF + + + + S+ + V S++V
Sbjct: 351 GPWEGNDNITSNIIDVLTPIGTGI--GFQESSDLRKFTYPRIELQSMQFHGQYVNSKSVE 408

Query: 316 ---WGGHLVSSRN---TAG-----NRINFPSYGVFNPGGAIWIADDPREFYRTLSDP 362
G ++ +N TAG N+ N +YG I Y L+
Sbjct: 409 HCYSDDLKLNKYNKNTITAGVSNIDESNQNNKHNYGPVINSPTIDINVNSQNSQYLDLNS- 467

Query: 363 VFVRGGFGNPHYVLGLRGVAFQQTGTNHTRTFRNSGTIDSLDEIPPQDNNGAPWNDYSHV 422
V V GG V G ++ N + I S+ + + + ++
Sbjct: 468 VMVNGG----QKVTGCSPLSSNGNSNNAALPNQKINVIYSVQSNKPEKHADTYRKWGYM 523

Query: 423 LNHVTFVRWPGEISGSDSWRAPMFWSWTHRSATPTNTIDPERITQIPLVKAHTLQSG---T 479
+H+ + P + G IDP+ L+K + G +
Sbjct: 524 SSHIPYDLVPENVIGD-----IDPDTKQPSLLLKGFPKAEKGYGDS 563

Query: 480 TVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRIRIRYASTTNLRIYVTVAGERI 539
G + ++ TS + + + Q Q+YR RIRYA+ G+
Sbjct: 564 IAYVSEPLNGANAVKLTS---YQVLQMEVTNQTTQKYRIRIRYAT-----GGDTA 610

Query: 540 FAGQFNKTMDTGDPLTFQSFSYATINT 566
+ F+ +G+ LT + ++++++
Sbjct: 611 ASIWFHIIIGPSGNDLTNEGHNFSVSS 637

>sp|Q45755|CDAA_BACTU Pesticidal crystal protein cry13Aa (Insecticidal delta-endotoxin CryXIIIA(a)) (Crystalline entomocidal protoxin) (88 kDa crystal protein)
gb|AAA22356.1| (L07023) delta-endotoxin [Bacillus thuringiensis]
Length = 803

Score = 44.3 bits (103), Expect = 0.004
Identities = 63/278 (22%), Positives = 108/278 (38%), Gaps = 42/278 (15%)

Query: 45 LSEFVPGVGVAFLGLDIWG-----FITPSDWSLFLQLQIEQLQRIETLERN 92
L +PGV VA L ++ G IT D + + E+L+Q I+ L +
Sbjct: 92 LGAAIPGVSVAVPLISMLVGFWPKGTNNQENLITVIDKEVQRILDEKLSQLIKLNAD 151

Query: 93 -RAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANTDDA-----LITAIN 144
A T L + E+ I+A E N+ + + + + D A L ++
Sbjct: 152 LNAFTDL--VTRLEEVIIDATFE----NHKPVQLVSKSNYMKVDSAYFSTGGILTGLMS 204

Query: 145 NFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNRLINL----- 197
+F ++ +YV A + LS + FG W + +++ + ++
Sbjct: 205 DFLTDYTSKLTFFLYVLGATMKLSAYHSYIQFGNTWLNKVYDLSSDEGKTMSQALARAKQ 264

Query: 198 -----IHRYSKHCLDTYNQGLNLRGTNRQWARFNQFRDLTLTVLDIVAFPNYDVRT 252
I YT L+ + L +L +N +N + R + L LDIVA +P
Sbjct: 265 HMRQDIAFYTSQALNMFMTGNLPSL--SSNKYAINDYNVYTRAMVLNGLDIVATWPTLYPDD 323

Query: 253 YPIQTSSQLTREIYTSSV--IEDSPVSNIPNGFNRAE 288
Y Q + TR I++ V E S I N F+ +
Sbjct: 324 YSSQIKLEKTRVIFSDMVGQSES RDGSVTIKNIFDNTD 361

>sp|Q9ZIU5|CBBB_BACTV Pesticidal crystal protein cry11Bb (Insecticidal delta-endotoxin
CryXIB(b)) (Crystalline entomocidal protoxin) (84 kDa
crystal protein)
gb|AAC97162.1| (AF017416) d-endotoxin [Bacillus thuringiensis]
Length = 750

Score = 43.9 bits (102), Expect = 0.005
Identities = 32/155 (20%), Positives = 62/155 (39%), Gaps = 12/155 (7%)

Query: 76 LQIEQLQRIETLERNRAITTLRGLADSYEIIYIEALREWEANPNNAQLREDVRIRFANT 135
L+++ ++ Q ++T G +++ + + + P A + F N
Sbjct: 76 LEVQITLNLQTLQDRVATLKAIEYEGFIHLGKVFTDYVSQSTFTPAT-----KTHFLNM 129

Query: 136 DDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGL---DIATVNNHYN 192
+ LI + F + +E +S++ Q LHL LL+D + G WG D ++ +N
Sbjct: 130 SNLLIQLRQPFEIAGYEGVSISLFTQMCTLHLGLLKGILAGSDWGFPTPEKDSLICQFN 189

Query: 193 RLINLIHRYTKHCLDTYNQGLNLRGTNRQWARF 227
R +N Y + Y+ L N + F
Sbjct: 190 RYVN---EYNTRMMGLYSIEFGRLLAKNLNEALNF 221

>emb|CAA98839.1| (Z74314) ORF YDR017c [Saccharomyces cerevisiae]
Length = 658

Score = 40.0 bits (92), Expect = 0.073
Identities = 34/161 (21%), Positives = 71/161 (43%), Gaps = 12/161 (7%)

Query: 134 NTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNR 193
N D L +++++F L++ E P + N H++ + GQG G DIA +H +
Sbjct: 109 NNPDTLSSSLSSFILSNHEEPAIK-----PNKHVAHRNNITETGQSGEDIKQSQHQPQ 163

Query: 194 LINLIHRYTKHCLDTYNQGLNLRGTNRQWARFNQFRDLTLTVLDIVAFPNYDVRTY 253
+++ H+ + + ++G + + T + DTL + +P+
Sbjct: 164 VLH--HQTSLKPIQNVDEGCISPKSTYQES---LHGISEDLTLPVSSATYYPHKSADS 218

Query: 254 PIQTSSQLTREIYT--SSVIEDSPVSNIPNGFNRAEFGVR 292
+ ++ +I T + I + A +P+ +NR F V+
Sbjct: 219 GYEEKDKMENDIDTIQPATINCASGIATLPSSYNRHTEFKVK 259

>ref|NP_010300.1| (NC_001136) Shows homology to basic leucine zipper family of
transcription factors; Kcs1p [Saccharomyces cerevisiae]
pir||S54640 KCS1 protein - yeast (Saccharomyces cerevisiae)
emb|CAA89842.1| (Z49770) unknown [Saccharomyces cerevisiae]
emb|CAA65208.1| (X95966) orf:PZF1050 [Saccharomyces cerevisiae]
emb|CAA98837.1| (Z74313) ORF YDR017c [Saccharomyces cerevisiae]
gb|AAB36234.1| (S81651) Kcs1 [Saccharomyces cerevisiae]

Length = 1050

Score = 40.0 bits (92), Expect = 0.073
Identities = 34/161 (21%), Positives = 71/161 (43%), Gaps = 12/161 (7%)

Query: 134 NTDDALITAINNFTLTSTFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNR 193
N D L +++++F L++ E P + N H++ + GQG G DIA +H +
Sbjct: 109 NNPDTLSSSLSSFILSNHEEPAIK-----PNKHVAHRNNITETGQGSGEDIAKQSQHQPPQ 163

Query: 194 LINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDLTLTVLDIVLFPNYDVRTY 253
+++ H+ + + ++G + + T + DLT L + +P+
Sbjct: 164 VLH--HQTSKPIQNVDGECISPKSTYQES---LHGISEDLTLPVSSATYYPHKSKADS 218

Query: 254 PIQTSSQLTREIYT--SSVIEDSPVSANIPNGFNRAEFGVR 292
+ ++ +I T + I + A +P+ +NR F V+
Sbjct: 219 GYEEKDKMENDIDTIQPATINCASGIATLPSSYNRHTFKVK 259

>ref|NP_437949.1| (NC_003078) putative regulatory protein, possibly two-component
response regulator [Sinorhizobium meliloti]
emb|CAC49809.1| (AL603647) putative regulatory protein, possibly two-component
response regulator [Sinorhizobium meliloti]
Length = 554

Score = 37.0 bits (84), Expect = 0.62
Identities = 43/162 (26%), Positives = 71/162 (43%), Gaps = 18/162 (11%)

Query: 294 PHLMDFMNSLFVTAETVRS-----QTVWGGHLVSSRNTAGNRINFPSYGVFNPGGAIWIA 348
P + D + L T + V S Q VWGG +V S +T + IN + + GG +
Sbjct: 51 PQVFDLLHLVGTDRVRVSKDELLQAVWGGGRIV-SESTITSHINAVRKAIGDTGGEQRLI 109

Query: 349 DEDPRPFYRTLSDPVFVR-GGFGNPHYVLGLRGVAFQQT-GTNHTRTFRNSGTIDSLDEI 406
R +R + D +R GG G +G G A Q + G+ T + S+ +
Sbjct: 110 RTVARKGFRFVG---IRIGGIGEVVRQPGV-PGAALQASGGSGETASALVLPDKPSITVL 165

Query: 407 PPQDMSGAPWNDY-----SHVLNHVTFVRWPGEISGSDSWR 442
P Q+ SG P +Y ++ ++ +RW I+ + S+R
Sbjct: 166 PFQNLSGDPEQEYFADGIVEDITALSRIKRWLFVIARNSSFR 207

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: Apr 9, 2002 12:51 PM
Number of letters in database: 288,098,425
Number of sequences in database: 919,193

Lambda	K	H
0.321	0.137	0.417

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 364,451,623

Number of Sequences: 919193

Number of extensions: 16231924

Number of successful extensions: 31053

Number of sequences better than 100.0: 244

Number of HSP's better than 100.0 without gapping: 185

Number of HSP's successfully gapped in prelim test: 60

Number of HSP's that attempted gapping in prelim test: 30119

Number of HSP's gapped (non-prelim): 347

length of query: 605

length of database: 288,098,425

effective HSP length: 126

effective length of query: 479

effective length of database: 172,280,107

effective search space: 82522171253
effective search space used: 82522171253
T: 11
A: 40
X1: 16 (7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.8 bits)
S2: 65 (29.6 bits)

FIGURE 3: Blastp results of accession AAM06002.1 against the NCBI Protein nr database.

BLASTP 2.2.3 [Apr-24-2002]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, 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.

RID: 1020211656-026968-16488

Query=

(171 letters)

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

925,521 sequences; 290,391,215 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Sequences producing significant alignments:

	Score (bits)	E Value
gi 20091447 ref NP_617522.1 (NC_003552) hypothetical prote...	343	6e-94
gi 15721993 gb AAG36711.1 (AY008143) crystal protein [Baci...	76	2e-13
gi 1261624 gb AAB00958.1 (L49391) CGCryV gene product [Bac...	68	5e-11
gi 14537812 gb AAK66742.1 AF373207_1 (AF373207) Cry1Ia [Bac...	68	5e-11
gi 1621216 emb CAA70124.1 (Y08920) Bt toxin [Bacillus thur...	68	5e-11
gi 8469149 sp Q45752 C1IA_BACTK Pesticidial crystal protein...	68	5e-11
gi 3329593 gb AAC26910.1 (AF076953) insecticidal protein [...]	68	5e-11
gi 8927997 sp Q9XDL1 C1ID_BACTU Pesticidial crystal protein...	67	9e-11
gi 8469137 sp Q03745 C1EB_BACTA Pesticidial crystal protein...	67	1e-10
gi 8928012 sp O87905 COAA_BACTJ Pesticidial crystal protein...	66	1e-10
gi 2119864 pir I39814 insecticidal protein cryV1 - Bacillu...	66	1e-10
gi 282462 pir S25383 parasporal crystal protein cryV - Bac...	66	1e-10
gi 142759 gb AAA22349.1 (M63897) ORF [Bacillus thuringiensis]	66	1e-10
gi 98516 pir B42459 hypothetical protein 2 (cryIF 3' regio...	66	1e-10
gi 1345842 sp P05517 C1BA_BACTK PESTICIDIAL CRYSTAL PROTEIN...	64	4e-10
gi 14486714 gb AAK63251.1 AF368257_1 (AF368257) Cry1Ba [Bac...	64	4e-10
gi 1200002 emb CAA65003.1 (X95704) cry1Ba2 [Bacillus thuri...	64	4e-10
gi 8928008 sp O32321 CKAA_BACUF Pesticidial crystal protein...	64	6e-10
gi 12003323 gb AAG43526.1 AF211190_1 (AF211190) Cry1I [Baci...	64	7e-10
gi 8469133 sp O66377 C1FB_BACTM PESTICIDIAL CRYSTAL PROTEIN...	64	7e-10
gi 2982744 dbj BAA25298.1 (AB012288) CryINA67-1 [Bacillus ...]	64	7e-10
gi 421541 pir S32649 parasporal crystal protein - Bacillus...	64	7e-10
gi 8469157 sp O06014 C9DA_BACTP PESTICIDIAL CRYSTAL PROTEIN...	64	9e-10
gi 48880 emb CAA41425.1 (X58534) crystal protein [Bacillus...	64	9e-10
gi 8469164 sp Q99031 C9AA_BACTG PESTICIDIAL CRYSTAL PROTEIN...	63	1e-09
gi 8469160 sp Q45733 C9CA_BACTO Pesticidial crystal protein...	63	1e-09
gi 8927979 sp O85805 C1BE_BACTU Pesticidial crystal protein...	63	1e-09
gi 2815886 gb AAB97923.1 (AF042733) delta-endotoxin [Bacil...	63	1e-09
gi 8469153 sp Q9ZAZ5 C1BD_BACTZ Pesticidial crystal protein...	62	2e-09
gi 8928007 sp O32307 CJAA_BACTJ Pesticidial crystal protein...	62	2e-09
gi 8469150 sp Q45774 C1BC_BACTM PESTICIDIAL CRYSTAL PROTEIN...	62	2e-09
gi 8469145 sp Q45739 C1BB_BACTU PESTICIDIAL CRYSTAL PROTEIN...	62	2e-09
gi 8469158 sp Q03749 C7AA_BACTU PESTICIDIAL CRYSTAL PROTEIN...	62	3e-09
gi 8928039 sp Q9X597 CQAA_BACTF Pesticidial crystal protein...	62	3e-09
gi 117534 sp P09665 CRYS_BACTS 130 KD CRYSTAL PROTEIN (DELT...	62	3e-09
gi 5901703 gb AAD55382.1 AF154676_1 (AF154676) 135 kDa inse...	62	3e-09
gi 1171233 gb AAA86265.1 (U43605) CryIA(a) [Bacillus thuri...	62	3e-09
gi 743635 prf I2013214A lepidopteran-specific protoxin [Bac...	62	3e-09

gi 80448 pir A22617 parasporal crystal protein - Bacillus ...	62	3e-09
gi 117531 sp P09664 CRYS_BACTE 133 KD CRYSTAL PROTEIN (DELT...	62	3e-09
gi 117540 sp P16478 CRYU_BACTA 135 KD CRYSTAL PROTEIN (DELT...	62	3e-09
gi 226053 prf 1409195A 135kd insecticidal protein [Bacillu...	62	3e-09
gi 5669035 gb AAD46139.1 AF081790_1 (AF081790) insecticidal...	62	3e-09
gi 6687073 emb CAA70856.1 (Y09663) delta-endotoxin [Bacill...	62	3e-09
gi 625548 pir JC2219 lepidopteran-specific protoxin - Baci...	62	3e-09
gi 4666284 dbj BAA77213.1 (AB026261) BtT84A1 crystal prote...	62	4e-09
gi 8469152 sp Q9S515 C1AG_BACTU PESTICIDIAL CRYSTAL PROTEIN...	61	4e-09
gi 1942525 pdb 1CIY Insecticidal Toxin: Structure And Cha...	61	4e-09
gi 4090435 gb AAC98807.1 (U63372) truncated CryIAc [synthe...	61	4e-09
gi 2555147 gb AAC63055.1 (AF023672) CryIA(c) [synthetic co...	61	4e-09
gi 1171235 gb AAA86266.1 (U43606) CryIA(c) [Bacillus thuri...	61	4e-09
gi 98533 pir S11445 parasporal crystal protein cryIA.c - B...	61	4e-09
gi 8469141 sp Q45715 C1KA_BACTM Pesticidal crystal protein...	61	5e-09
gi 5052774 gb AAD38701.1 AF148644_1 (AF148644) insecticidal...	61	5e-09
gi 5916230 gb AAD55947.1 (AF177675) Cry IAc insecticidal t...	61	5e-09
gi 117547 sp P05068 C1AC_BACTK Pesticidal crystal protein ...	61	5e-09
gi 143126 gb AAA73077.1 (M73249) [Bacillus thuringiensis g...	61	5e-09
gi 142742 gb AAA22339.1 (M73248) cryIA(c)3 [Bacillus thuri...	61	5e-09
gi 3979717 emb CAA10270.1 (AJ130970) crystal toxin protein...	61	5e-09
gi 8469140 sp Q45709 C1IB_BACTE Pesticidal crystal protein...	61	5e-09
gi 9087134 sp Q45707 C7AB_BACUA Pesticidal crystal protein...	60	7e-09
gi 13173240 gb AAK14337.1 (AF327925) insecticidal crystal ...	60	7e-09
gi 546641 gb AAB30710.1 insecticidal protein Cry I A (c) p...	60	8e-09
gi 3719431 gb AAC63366.1 (AF093107) delta-endotoxin [Bacil...	60	8e-09
gi 8469136 sp Q03744 C1AD_BACTA Pesticidal crystal protein...	60	9e-09
gi 225472 prf 1304168B endotoxin delta 1 [Bacillus thuring...	60	1e-08
gi 8469134 sp P56953 C1CB_BACTG PESTICIDIAL CRYSTAL PROTEIN...	59	1e-08
gi 8928019 sp Q45705 C8BA_BACUK Pesticidal crystal protein...	59	2e-08
gi 477639 pir A49785 parasporal crystal protein cryIA(c) -...	59	2e-08
gi 8469138 sp Q03746 C1FA_BACTA Pesticidal crystal protein...	59	2e-08
gi 8469139 sp Q03748 C1AE_BACTL PESTICIDIAL CRYSTAL PROTEIN...	59	2e-08
gi 13173238 gb AAK14336.1 (AF327924) insecticidal crystal ...	59	2e-08
gi 2414156 emb CAA70925.1 (Y09787) delta-endotoxin [Bacill...	59	3e-08
gi 8469151 sp Q57458 C1EA_BACTX Pesticidal crystal protein...	58	3e-08
gi 142752 gb AAA22345.1 (M73252) cryIE(a) [Bacillus thurin...	58	3e-08
gi 1946622 gb AAD04732.1 (U94323) CryIEa4 [Bacillus thurin...	58	3e-08
gi 538624 pir A37829 parasporal crystal protein - Bacillus...	58	3e-08
gi 80457 pir A26461 parasporal crystal protein Bt2 - Bacil...	58	4e-08
gi 208155 gb AAA72985.1 (M60856) cryIA(a) [synthetic const...	58	4e-08
gi 117536 sp P09666 CRYT_BACTA 130 KD CRYSTAL PROTEIN (DELT...	58	4e-08
gi 117539 sp P21257 CRYT_BACTK 130 KD CRYSTAL PROTEIN (DELT...	58	4e-08
gi 117543 sp P09667 CRYV_BACTA 130 KD CRYSTAL PROTEIN (DELT...	58	4e-08
gi 80474 pir A29125 parasporal crystal protein - Bacillus ...	58	4e-08
gi 117533 sp P06578 C1AB_BACTK PESTICIDIAL CRYSTAL PROTEIN ...	58	4e-08
gi 10440886 gb AAG16877.1 (U94191) delta endotoxin [Bacill...	58	4e-08
gi 8469147 sp Q45747 C1DB_BACTU PESTICIDIAL CRYSTAL PROTEIN...	58	4e-08
gi 8469154 sp Q9ZA26 C1GB_BACTZ Pesticidal crystal protein...	58	4e-08
gi 1769867 emb CAA67557.1 (X99103) delta-endotoxin [synthe...	58	4e-08
gi 13899010 gb AAK48937.1 AF358862_2 (AF358862) insecticida...	58	4e-08
gi 80451 pir S04181 parasporal crystal protein - Bacillus ...	58	4e-08
gi 11277639 pir JC7140 protoxin - Bacillus thuringiensis	58	4e-08
gi 1234884 emb CAA65457.1 (X96682) delta-endotoxin [Bacill...	58	5e-08
gi 142750 gb AAA22343.1 (M73251) cryIC(b) [Bacillus thurin...	58	5e-08
gi 8488968 sp P05518 C1CA_BACTE Pesticidal crystal protein...	58	5e-08
gi 16945772 dbj BAB72018.1 (AB074414) insecticidal crystal...	57	5e-08
gi 80452 pir S00944 parasporal crystal protein - Bacillus ...	57	5e-08
gi 117542 sp P09663 CRYU_BACTK 131 KD CRYSTAL PROTEIN (DELT...	57	6e-08
gi 8928043 sp Q9ZNL9 C9EA_BACTA Pesticidal crystal protein...	57	6e-08
gi 9087135 sp Q45708 C7AB_BACUK Pesticidal crystal protein...	57	6e-08
gi 7141141 gb AAF37224.1 AF215647_1 (AF215647) toxin CryICa...	57	7e-08
gi 14190061 gb AAK55546.1 AF375608_1 (AF375608) crystal pro...	57	7e-08
gi 17385650 dbj BAB78603.1 (AB075462) crystal protein CryE...	57	9e-08
gi 471281 emb CAA51996.1 (X73600) CryIIIA insecticidal cry...	57	1e-07
gi 640362 pdb 1DLC Delta-Endotoxin CryIIIA (Bt13)	56	1e-07
gi 208153 gb AAA73184.1 (M84650) crystal toxin [synthetic ...	56	1e-07
gi 80453 pir A27323 parasporal crystal protein CryIIIA - B...	56	1e-07
gi 143084 gb AAA22542.1 (M30503) insect control protein [B...	56	1e-07

gi 117325 sp P07130 C3AA_BACTT	Pesticidial crystal protein ...	56	1e-07
gi 117529 sp P19415 C1DA_BACTA	PESTICIDIAL CRYSTAL PROTEIN ...	55	2e-07
gi 19386614 dbj BAB72016.2	(AB074413) insecticidal crystal...	54	5e-07
gi 8469146 sp Q45746 C1GA_BACTU	PESTICIDIAL CRYSTAL PROTEIN...	54	5e-07
gi 8928011 sp Q86170 CJBA_BACUH	Pesticidial crystal protein...	54	6e-07
gi 8469161 sp Q45744 C3CA_BACTK	PESTICIDIAL CRYSTAL PROTEIN...	54	6e-07
gi 9828610 gb AAG00235.1 AF285775_1	(AF285775) parasporal i...	54	8e-07
gi 8469159 sp Q45706 C8CA_BACTP	PESTICIDIAL CRYSTAL PROTEIN...	54	1e-06
gi 8928018 sp Q45704 C8AA_BACUK	Pesticidial crystal protein...	53	1e-06
gi 17385646 dbj BAB78601.1	(AB075460) crystal protein CryE...	53	1e-06
gi 8928040 sp Q9X682 CSAA_BACTF	Pesticidial crystal protein...	53	1e-06
gi 17385648 dbj BAB78602.1	(AB075461) crystal protein CryE...	52	2e-06
gi 8469148 sp Q45748 C1HA_BACTU	PESTICIDIAL CRYSTAL PROTEIN...	52	3e-06
gi 80469 pir B29838	parasporal crystal protein - Bacillus ...	51	5e-06
gi 117329 sp P09662 CAAA_BACTI	PESTICIDIAL CRYSTAL PROTEIN ...	51	6e-06
gi 10719937 sp Q45882 CGAA_CLOBI	Pesticidial crystal-like p...	50	8e-06
gi 117324 sp P17969 C3BA_BACTO	PESTICIDIAL CRYSTAL PROTEIN ...	50	1e-05
gi 8469142 sp Q45716 C1JB_BACTU	Pesticidial crystal protein...	50	1e-05
gi 8469143 sp Q45718 C1HB_BACTM	Pesticidial crystal protein...	50	1e-05
gi 940200 gb AAA74198.1	(U31633) Cry3Bb2 [Bacillus thuring...	49	3e-05
gi 15988322 pdb 1JI6 A	Chain A, Crystal Structure Of The In...	49	3e-05
gi 8469155 sp Q06117 C3BB_BACTU	Pesticidial crystal protein...	48	3e-05
gi 1669651 emb CAA70506.1	(Y09326) delta-endotoxin [Bacill...	48	4e-05
gi 8928014 sp P56956 CLAA_BACTU	Pesticidial crystal protein...	47	7e-05
gi 8928013 sp Q87906 CPAA_BACTJ	Pesticidial crystal protein...	47	1e-04
gi 8488969 sp P05519 C4BA_BACTI	PESTICIDIAL CRYSTAL PROTEIN...	46	1e-04
gi 8927981 sp Q87404 C1IC_BACTU	Pesticidial crystal protein...	46	1e-04
gi 40310 emb CAA30114.1	(X07082) delta-endotoxin (AA 1 - 1...	46	2e-04
gi 629164 pir S39536	parasporal crystal protein-related pr...	45	2e-04
gi 1334252 emb CAA52927.1	(X75019) delta-endotoxin [Bacill...	45	2e-04
gi 8469144 sp Q45738 C1JA_BACTU	PESTICIDIAL CRYSTAL PROTEIN...	45	3e-04
gi 117544 sp P16480 C4AA_BACTI	PESTICIDIAL CRYSTAL PROTEIN ...	45	4e-04
gi 8928021 sp Q45712 C5BA_BACTU	Pesticidial crystal protein...	44	5e-04
gi 80463 pir A26858	130K delta-endotoxin - Bacillus thurin...	44	5e-04
gi 8928024 sp Q45754 CCAA_BACTU	Pesticidial crystal protein...	43	0.001
gi 8927987 sp P56955 C5AC_BACTU	Pesticidial crystal protein...	42	0.002
gi 8469135 sp P96315 C1AF_BACTU	Pesticidial crystal protein...	42	0.003
gi 8927991 sp Q45760 C5AA_BACUD	Pesticidial crystal protein...	41	0.004
gi 8928030 sp Q9S597 CRAA_BACUH	Pesticidial crystal protein...	41	0.005
gi 8927990 sp Q45753 C5AB_BACUD	Pesticidial crystal protein...	40	0.008
gi 8928020 sp Q45710 CEAA_BACTS	Pesticidial crystal protein...	40	0.012
gi 117541 sp P16479 CRYU_BACTI	130 KD CRYSTAL PROTEIN (DELT...	39	0.023
gi 117538 sp P11782 CRYT_BACTI	130 KD CRYSTAL PROTEIN (DELT...	39	0.029
gi 17977981 emb CAC80986.1	(AJ251978) Cry30Aa protein [Bac...	38	0.053
gi 9798640 dbj BAB11757.1	(AB031065) 81-kDa leukemia toxin...	37	0.12
gi 8469165 sp Q45755 CDAA_BACTU	Pesticidial crystal protein...	35	0.23
gi 13173242 gb AAK14338.1	(AF327926) insecticidal crystal ...	35	0.45
gi 17977979 emb CAC80985.1	(AJ251977) Cry29Aa protein [Bac...	33	0.98

Alignments

>gi|20091447|ref|NP_617522.1| (NC_003552) hypothetical protein [Methanosarcina acetivorans str. C2A]
gi|19916590|gb|AAM06002.1| (AE010957) hypothetical protein [Methanosarcina acetivorans str. C2A]
Length = 171

Score = 343 bits (879), Expect = 6e-94
Identities = 171/171 (100%), Positives = 171/171 (100%)

Query: 1 MHLTLLRDGALYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
MHLTLLRDGALYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK
Sbjct: 1 MHLTLLRDGALYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNSGA 120
HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNSGA
Sbjct: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNSGA 120

Query: 121 LNFPQHPKRSRQKWKSGPGTGLMPVRLLTRTTEGQYLRKHYGKKNLMPGVD 171

LNFPQHPSKRSQKWKSGPGTGLMPVRLLTRTTEGQYLRKHGKKNLMPGVD
Sbjct: 121 LNFPQHPSKRSQKWKSGPGTGLMPVRLLTRTTEGQYLRKHGKKNLMPGVD 171

>gi|15721993|gb|AAG36711.1| (AY008143) crystal protein [Bacillus thuringiensis serovar yunnanensis]
Length = 1236

Score = 75.9 bits (185), Expect = 2e-13
Identities = 41/127 (32%), Positives = 64/127 (50%), Gaps = 4/127 (3%)

Query: 1 MHLTLLRDGALYGFSWGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS 60
+HL L+DG +G WG + + I Y Y Y+ GL D+ ++ P+
Sbjct: 202 LHLHLKDGVOFGEEWGMDSATVDRFYSYLKSDIEIYTNICIDWYNKGLSDSIESEPTWN 261

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNSGA 120
+ NT N + R+MTL VLD +W +DP +YP P + L+RE+Y+ A+G+ +
Sbjct: 262 GW----NTFNNFRDMLMVLVLSIWPTYDPRRYPLPTKSQLTRELYTQAIGSYKSVEP 317

Query: 121 LNFPQHP 127
L P P
Sbjct: 318 LLPPFPSP 324

>gi|1261624|gb|AAB00958.1| (L49391) CGCryV gene product [Bacillus thuringiensis]
Length = 719

Score = 67.8 bits (164), Expect = 5e-11
Identities = 47/136 (34%), Positives = 67/136 (48%), Gaps = 18/136 (13%)

Query: 1 MHLTLLRDGALYGFSWGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 58
+HL LLRD +++G WG + EI Q V+ G Y ++ K YS GL + + NA S
Sbjct: 195 LHLLLRDASIFGKEWGLSSSEISTFYNRQ-VERAGDYSDDHCVKWTGLNNLRGTNAES 253

Query: 59 NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNS 118
Y N++ R+MTL VLD ++ +D YP L+RE+Y+DA+GT
Sbjct: 254 WVRY-----NQFRDMLMVLVLDLVALFPSYDTQMPIKTAAQLTREVTDAIGTVH-- 304

Query: 119 GALNFPQHPSKRSQKW 134
HP S W
Sbjct: 305 -----PHPSFTSTTW 314

>gi|14537812|gb|AAK66742.1|AF373207_1 (AF373207) CryIIa [Bacillus thuringiensis]
Length = 719

Score = 67.8 bits (164), Expect = 5e-11
Identities = 47/136 (34%), Positives = 67/136 (48%), Gaps = 18/136 (13%)

Query: 1 MHLTLLRDGALYGFSWGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 58
+HL LLRD +++G WG + EI Q V+ G Y ++ K YS GL + + NA S
Sbjct: 195 LHLLLRDASIFGKEWGLSSSEISTFYNRQ-VERAGDYSDDHCVKWTGLNNLRGTNAES 253

Query: 59 NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNS 118
Y N++ R+MTL VLD ++ +D YP L+RE+Y+DA+GT
Sbjct: 254 WVRY-----NQFRDMLMVLVLDLVALFPSYDTQMPIKTAAQLTREVTDAIGTVH-- 304

Query: 119 GALNFPQHPSKRSQKW 134
HP S W
Sbjct: 305 -----PHPSFTSTTW 314

>gi|1621216|emb|CAA70124.1| (Y08920) Bt toxin [Bacillus thuringiensis]
Length = 719

Score = 67.8 bits (164), Expect = 5e-11
Identities = 47/136 (34%), Positives = 67/136 (48%), Gaps = 18/136 (13%)

Query: 1 MHLTLLRDGALYGFSWGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 58
+HL LLRD +++G WG + EI Q V+ G Y ++ K YS GL + + NA S
Sbjct: 195 LHLLLRDASIFGKEWGLSSSEISTFYNRQ-VERAGDYSDDHCVKWTGLNNLRGTNAES 253

Query: 59 NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNS 118

Y N++ R+MTL VLD ++ +D YP L+RE+Y+DA+GT
Sbjct: 254 WVRV-----NQFRDRTLMLVLDLVALFPSYDTQMYPIKTTAQLTREVTDAIGTVH-- 304

Query: 119 GALNFPQHPKRSRSQKW 134

HP S W

Sbjct: 305 -----PHPSFTSTTW 314

>gi|8469149|sp|Q45752|C1IA_BACTK Pesticidal crystal protein cryIIa (Insecticidal delta-endotoxin

CryII(a)) (Crystalline entomocidal protoxin) (81 kDa
crystal protein)

gi|2119868|pir||I39815 insecticidal protein cryV - Bacillus thuringiensis

gi|142768|gb|AAA22354.1| (M98544) insecticidal protein [Bacillus thuringiensis]

Length = 719

Score = 67.8 bits (164), Expect = 5e-11

Identities = 47/136 (34%), Positives = 67/136 (48%), Gaps = 18/136 (13%)

Query: 1 MHLTLLRDGALYGFSWGW-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 58

+HL LLRD +++G WG +EI Q V+ G Y ++ K YS GL + + NA S

Sbjct: 195 LHLLLLRDASIFGKEWGLSSSEISTFYNRQ-VERAGDYSCHVKWYSTGLNNLRGTNAES 253

Query: 59 NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNS 118

Y N++ R+MTL VLD ++ +D YP L+RE+Y+DA+GT

Sbjct: 254 WVRV-----NQFRDRTLMLVLDLVALFPSYDTQMYPIKTTAQLTREVTDAIGTVH-- 304

Query: 119 GALNFPQHPKRSRSQKW 134

HP S W

Sbjct: 305 -----PHPSFTSTTW 314

>gi|3329593|gb|AAC26910.1| (AF076953) insecticidal protein [Bacillus thuringiensis serovar kurstaki]

Length = 719

Score = 67.8 bits (164), Expect = 5e-11

Identities = 47/136 (34%), Positives = 67/136 (48%), Gaps = 18/136 (13%)

Query: 1 MHLTLLRDGALYGFSWGW-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 58

+HL LLRD +++G WG +EI Q V+ G Y ++ K YS GL + + NA S

Sbjct: 195 LHLLLLRDASIFGKEWGLSSSEISTFYNRQ-VERAGDYSCHVKWYSTGLNNLRGTNAES 253

Query: 59 NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNS 118

Y N++ R+MTL VLD ++ +D YP L+RE+Y+DA+GT

Sbjct: 254 WVRV-----NQFRDRTLMLVLDLVALFPSYDTQMYPIKTTAQLTREVTDAIGTVH-- 304

Query: 119 GALNFPQHPKRSRSQKW 134

HP S W

Sbjct: 305 -----PHPSFTSTTW 314

>gi|8927997|sp|Q9XDL1|C1ID_BACTU Pesticidal crystal protein cryIIId (Insecticidal delta-endotoxin

CryII(d)) (Crystalline entomocidal protoxin) (81 kDa
crystal protein)

gi|5531642|gb|AAD44366.1|AF047579_1 (AF047579) insecticidal crystal protein [Bacillus thuringiensis]

Length = 719

Score = 66.6 bits (161), Expect = 9e-11

Identities = 43/116 (37%), Positives = 62/116 (53%), Gaps = 10/116 (8%)

Query: 1 MHLTLLRDGALYGFSWGWNE-EIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 58

+HL LLRD +++G WG +E EI Q T Y +Y + Y+ GL + NA S

Sbjct: 195 LHLLLLRDASIFGKEWGLSESEISTFYNRQSSQT-QEYSDYCEWYNTGLNRLRGTTNAES 253

Query: 59 NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGT 114

Y N++ R+MTL VLD ++ +D YP P L+RE+Y+DA+GT

Sbjct: 254 WVRV-----NQFRDRTLMLVLDLVALFPSYDTRMYPIPTSAQLTREVTDAIGT 302

>gi|8469137|sp|Q03745|C1EB_BACTA Pesticidal crystal protein cryIEb (Insecticidal delta-endotoxin

CryIE(b)) (Crystalline entomocidal protoxin) (134 kDa crystal protein)

gi|142754|gb|AAA22346.1| (M73253) cryIE(b) [Bacillus thuringiensis]
Length = 1174

Score = 66.6 bits (161), Expect = 1e-10
Identities = 35/112 (31%), Positives = 57/112 (50%), Gaps = 5/112 (4%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL++LRD +++G WG++ + IG Y +Y + Y+ GL +N
Sbjct: 164 LHLVLRDVSFVGQWGFVDVATINSRYNDLTRLIGEYTDYAVRWYNTGLNRLPRNEG--- 220

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ NR+ RE+T+ VLD +Q +D YP P L+RE+Y+D V
Sbjct: 221 --VRGWARFNRFRELITISVLDIISFFQNYDSRLYPIPTIYQLTREYVTDVPV 270

>gi|8928012|sp|O87905|COAA_BACTJ Pesticidal crystal protein cry24Aa (Insecticidal delta-endotoxin

CryXXIVA(a)) (Crystalline entomocidal protoxin) (Crystal protein) (Insecticidal protein Jeg72)

gi|3668333|gb|AAC61891.1| (U88188) insecticidal protein Jeg72 [Bacillus thuringiensis serovar jegathesan]
Length = 674

Score = 66.2 bits (160), Expect = 1e-10
Identities = 36/117 (30%), Positives = 64/117 (53%), Gaps = 8/117 (6%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL++LRD +Y GWN + + +++ D + Y Y + Y+ GL + + +
Sbjct: 197 LHLMLRDAVMY--QEGWNLQSHINYSKELDDALEDYTNVCVEVYTKGLNALRGSTAD- 253

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADN 117
+ N + R+MTL VLD ++ ++PV+YP ++ LSR+IY+D VG D+
Sbjct: 254 -----WLEFNSFRDMLMVLDLVAIFPNYNPVRYPLSTKISLSRKIYTDVPVGRDTS 305

>gi|2119864|pir||I39814 insecticidal protein cryV1 - Bacillus thuringiensis
gi|540282|gb|AAC36999.1| (L36338) insecticidal protein [Bacillus thuringiensis]
Length = 719

Score = 66.2 bits (160), Expect = 1e-10
Identities = 47/136 (34%), Positives = 66/136 (47%), Gaps = 18/136 (13%)

Query: 1 MHLTLRLDGLYGFSGW-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 58
+HL LRLD +++G WG + EI Q V+ G Y + K YS GL + + NA S
Sbjct: 195 LHLLLRLDASIFGKEWGLSSSEISTFYNRQ-VERAGDYSYHCVKWKYSTGLNNLRGTNAES 253

Query: 59 NKHYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNS 118
Y N++ R+MTL VLD ++ +D YP L+RE+Y+DA+GT
Sbjct: 254 WVRY-----NQFRDMLMVLDLVALFPSYDTQMYPIKTTAQLTREYVTDAGTVH-- 304

Query: 119 GALNFPQHPKRSRSQKW 134
HP S W
Sbjct: 305 -----PHPSFTSTTW 314

>gi|282462|pir||S25383 parasporal crystal protein cryV - Bacillus thuringiensis
gi|40290|emb|CAA44633.1| (X62821) delta-endotoxin [Bacillus thuringiensis]
Length = 719

Score = 66.2 bits (160), Expect = 1e-10
Identities = 47/136 (34%), Positives = 66/136 (47%), Gaps = 18/136 (13%)

Query: 1 MHLTLRLDGLYGFSGW-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 58
+HL LRLD +++G WG + EI Q V+ G Y + K YS GL + + NA S
Sbjct: 195 LHLLLRLDASIFGKEWGLSSSEISTFYNRQ-VERAGDYSYHCVKWKYSTGLNNLRGTNAES 253

Query: 59 NKHYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNS 118
Y N++ R+MTL VLD ++ +D YP L+RE+Y+DA+GT

Sbjct: 254 WVRV-----NQFRDMTLMVLDLVALFPSYDTQMPIKTTAQLTREVTDAIGTVH-- 304

Query: 119 GALNFPQHPSKRSQKW 134

HP S W

Sbjct: 305 -----PHPSFTSTTW 314

>gi|142759|gb|AAA22349.1| (M63897) ORF [Bacillus thuringiensis]
Length = 381

Score = 66.2 bits (160), Expect = 1e-10
Identities = 42/116 (36%), Positives = 64/116 (54%), Gaps = 10/116 (8%)

Query: 1 MHLTLLRDGALYGFSGWG-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 58

+HL LLRD +++G WG + EI Q V+ G Y ++ K YS GL + + NA S

Sbjct: 195 LHLLLLRDASIFGKEWGLSSSEISTFYNRQ-VERAGDYSCHVKWYSTGLNNLRGTNAES 253

Query: 59 NKHYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAVGT 114

Y N++ ++MTL VLD ++ +D + YP L+RE+Y+DA+GT

Sbjct: 254 WVRV-----NQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVTDAIGT 302

>gi|98516|pir|B42459 hypothetical protein 2 (cryIF 3' region) - Bacillus thuringiensis
(strain aizawai) (fragment)
Length = 380

Score = 66.2 bits (160), Expect = 1e-10
Identities = 42/116 (36%), Positives = 64/116 (54%), Gaps = 10/116 (8%)

Query: 1 MHLTLLRDGALYGFSGWG-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 58

+HL LLRD +++G WG + EI Q V+ G Y ++ K YS GL + + NA S

Sbjct: 195 LHLLLLRDASIFGKEWGLSSSEISTFYNRQ-VERAGDYSCHVKWYSTGLNNLRGTNAES 253

Query: 59 NKHYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAVGT 114

Y N++ ++MTL VLD ++ +D + YP L+RE+Y+DA+GT

Sbjct: 254 WVRV-----NQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVTDAIGT 302

>gi|1345842|sp|P05517|C1BA_BACTK PESTICIDIAL CRYSTAL PROTEIN CRY1BA (INSECTICIDAL DELTA-
ENDOTOXIN

CRYIB(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (140 KDA

CRYSTAL PROTEIN)

gi|80480|pir|S00873 parasporal crystal protein - Bacillus thuringiensis subsp.
thuringiensis

gi|580949|emb|CAA29898.1| (X06711) delta-endotoxin (AA 1-1228) [Bacillus thuringiensis]
Length = 1228

Score = 64.3 bits (155), Expect = 4e-10
Identities = 41/125 (32%), Positives = 66/125 (52%), Gaps = 9/125 (7%)

Query: 1 MHLTLLRDGALYGFSGWGNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 59

+HL LLRD +L+G +G + Q E+ V+ Y +Y + Y+ GL + NA S

Sbjct: 186 LHLLLLRDASLFGSEFGLTSQEIQRYRQVERTRDYSYCVIEWYNTGLNSLRGTNAASW 245

Query: 60 KHYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAVG-TADNS 118

Y N++ R++TL VLD ++ +D YP L+RE+Y+DA+G T N

Sbjct: 246 VRY-----NQFRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVTDAIGATGVNM 298

Query: 119 GALNF 123

++N+

Sbjct: 299 ASMNW 303

>gi|14486714|gb|AAK63251.1|AF368257_1 (AF368257) Cry1Ba [Bacillus thuringiensis]
Length = 1228

Score = 64.3 bits (155), Expect = 4e-10
Identities = 41/125 (32%), Positives = 66/125 (52%), Gaps = 9/125 (7%)

Query: 1 MHLTLLRDGALYGFSGWGNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 59

+HL LLRD +L+G +G + Q E+ V+ Y +Y + Y+ GL + NA S

Sbjct: 186 LHLLLLRDASLFGSEFGLTSQEIQRYRQVERTRDYSYCVIEWYNTGLNSLRGTNAASW 245

Query: 60 KHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVG-TADNS 118
Y N++ R++TL VLD ++ +D YP L+RE+Y+DA+G T N
Sbjct: 246 VRY-----NQFRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVTDAIGATGVNM 298

Query: 119 GALNF 123
++N+
Sbjct: 299 ASMNW 303

>gi|1200002|emb|CAA65003.1| (X95704) cry1Ba2 [Bacillus thuringiensis]
gi|13959051|gb|AAK51084.1|AF363025_1 (AF363025) delta-endotoxin Cry1Ba2 [Bacillus thuringiensis
serovar
entomocidus]
Length = 1228

Score = 64.3 bits (155), Expect = 4e-10
Identities = 41/125 (32%), Positives = 66/125 (52%), Gaps = 9/125 (7%)

Query: 1 MHLTLRDGALYGFSWGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 59
+HL LLRD +L+G +G + Q E+ V+ Y +Y + Y+ GL + NA S
Sbjct: 186 LLLLLLRDASLFGSEFGLTSQEIQRYYERQVERTRDYSYCVIEWYNTGLNSLRGTNAASW 245

Query: 60 KHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVG-TADNS 118
Y N++ R++TL VLD ++ +D YP L+RE+Y+DA+G T N
Sbjct: 246 VRY-----NQFRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREVTDAIGATGVNM 298

Query: 119 GALNF 123
++N+
Sbjct: 299 ASMNW 303

>gi|8928008|sp|O32321|CKAA_BACUF Pesticidal crystal protein cry20Aa (Insecticidal delta-
endotoxin
CryXXA(a)) (Crystalline entomocidal protoxin) (86 kDa
crystal protein)
gi|2228580|gb|AAB93476.1| (U82518) mosquitocidal toxin [Bacillus thuringiensis]
Length = 753

Score = 63.9 bits (154), Expect = 6e-10
Identities = 41/121 (33%), Positives = 60/121 (48%), Gaps = 4/121 (3%)

Query: 2 HLTLLRDGALYGFSWGWNEEIQQHTREQIVD-TIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
HL LLRD LY W N + I+ I YI + + Y DGL +++ +N
Sbjct: 193 LLLLLRDAVLYRNQWLSNSISTANVNLNLRRAINEYITHCTRWYQDGLNRFDRSSRAM 252

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNSGA 120
+ FN Y R+MTL VLD + + +DPV +P V L+R +Y+D + A A
Sbjct: 253 NEWRRFNA---YRRDMLSVLDFATVFPTYDPLFPAATNVELTRVVYTDPIVMAGGRTA 309

Query: 121 L 121
+
Sbjct: 310 I 310

>gi|12003323|gb|AAG43526.1|AF211190_1 (AF211190) CryII [Bacillus thuringiensis]
Length = 719

Score = 63.9 bits (154), Expect = 7e-10
Identities = 41/116 (35%), Positives = 63/116 (53%), Gaps = 10/116 (8%)

Query: 1 MHLTLRDGALYGFSWGW-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 58
+HL LLRD +++G WG N +I Q V+ Y ++ K YS GL + + NA S
Sbjct: 195 LLLLLLRDASVFGKEWGLSNSQISTFYNRQ-VERTSDYSDHCVKWYSTGLNNLRGTNAES 253

Query: 59 NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGT 114
Y N++ ++MTL VLD ++ +D + YP L+RE+Y+DA+GT
Sbjct: 254 WVRY-----NQFRKDMTMLVLDLIALFPSYDTLVYPIKTTSQLTREVTDAIGT 302

>gi|8469133|sp|O66377|C1FB_BACTM PESTICIDIAL CRYSTAL PROTEIN CRY1FB (INSECTICIDAL DELTA-
ENDOTOXIN
CRYIF(B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (132 KDA
CRYSTAL PROTEIN)

gi|6650206|gb|AAF21767.1|AF062350_1 (AF062350) crystal protein Cry1Fb [Bacillus thuringiensis serovar

morrisoni]
Length = 1169

Score = 63.9 bits (154), Expect = 7e-10
Identities = 37/124 (29%), Positives = 64/124 (50%), Gaps = 7/124 (5%)

Query: 1 MHLTLLRDGALYGFSWGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL+LLRD +G WG + + ++++ I Y E+ TY+ GL++ +
Sbjct: 165 LHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTEHCLDTYNQGLENLRGTN---- 220

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNSGA 120
T ++ N++ RE+TL VLD ++ +D YP L+REIY+ +V D+ +
Sbjct: 221 --TRQWSRFNQFRRELTTLTVLDIVALFPNYDARAYPIQTSSQLTREIYTSSV-IEDSPVS 277

Query: 121 LNFP 124
N P
Sbjct: 278 ANIP 281

>gi|2982744|dbj|BAA25298.1| (AB012288) CryINA67-1 [Bacillus thuringiensis]
Length = 1168

Score = 63.9 bits (154), Expect = 7e-10
Identities = 37/124 (29%), Positives = 64/124 (50%), Gaps = 7/124 (5%)

Query: 1 MHLTLLRDGALYGFSWGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL+LLRD +G WG + + ++++ I Y E+ TY+ GL++ +
Sbjct: 165 LHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTEHCLDTYNQGLENLRGTN---- 220

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNSGA 120
T ++ N++ RE+TL VLD ++ +D YP L+REIY+ +V D+ +
Sbjct: 221 --TRQWSRFNQFRRELTTLTVLDIVALFPNYDARAYPIQTSSQLTREIYTSSV-IEDSPVS 277

Query: 121 LNFP 124
N P
Sbjct: 278 ANIP 281

>gi|421541|pir||S32649 parasporal crystal protein - Bacillus thuringiensis
gi|295866|emb|CAA80235.1| (Z22512) crystal protein [Bacillus thuringiensis]
Length = 1174

Score = 63.5 bits (153), Expect = 7e-10
Identities = 37/124 (29%), Positives = 64/124 (50%), Gaps = 7/124 (5%)

Query: 1 MHLTLLRDGALYGFSWGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL+LLRD +G WG + + ++++ I Y E+ TY+ GL++ +
Sbjct: 165 LHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTEHCLDTYNQGLENLRGTN---- 220

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNSGA 120
T ++ N++ RE+TL VLD ++ +D YP L+REIY+ +V D+ +
Sbjct: 221 --TRQWSRFNQFRRELTTLTVLDIVALFPNYDARAYPIQTSSQLTREIYTSSV-IEDSPVS 277

Query: 121 LNFP 124
N P
Sbjct: 278 ANIP 281

>gi|8469157|sp|O06014|C9DA_BACTP PESTICIDIAL CRYSTAL PROTEIN CRY9DA (INSECTICIDAL DELTA-
ENDOTOXIN

CRYIXD(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (132 KDA
CRYSTAL PROTEIN)

gi|2102642|dbj|BAA19948.1| (D85560) cry9Da1 [Bacillus thuringiensis]
Length = 1169

Score = 63.5 bits (153), Expect = 9e-10
Identities = 37/114 (32%), Positives = 62/114 (53%), Gaps = 10/114 (8%)

Query: 1 MHLTLLRDGALYGFSWGWNE-EIQQ-HTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS 58
+HL LL+D +YG WG N+ +I Q H+R+Q + +Y + Y+DGL + +

Sbjct: 209 LLLLLLLKDADIYGARWGLNQTDQFHSRQQSLTQ--TYTNHCVTAYNDGLAELRGTT-- 264

Query: 59 NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
E + N+Y REMTL +D ++ Y++ +YP L+RE+Y+D +

Sbjct: 265 ----AESWFKYNQYRREMTLTAMDVLALFPYVNLQYDPGTNPQLTREVTYTDPI 314

>gi|48880|emb|CAA41425.1| (X58534) crystal protein [Bacillus thuringiensis]
Length = 1151

Score = 63.5 bits (153), Expect = 9e-10
Identities = 40/118 (33%), Positives = 58/118 (48%), Gaps = 5/118 (4%)

Query: 2 HLTLLRDGALYGFSWG-WNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
HL LLRD YG +WG +N + + ++V+ I Y +Y Y+ G + ++ S
Sbjct: 201 HLLLLRDATRYGTNWGLYNATPFINYQSKLVELIELYTDYCVHWYNRGNELRQRGTSAT 260

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNS 118
+ E +RY REMTL VLD + D YP + LSR IY+D +G S
Sbjct: 261 AWLE----FHYRREMTLMVLDIVASFSSLDITNYPIETDFQLSRVIYTDPIGFVHRS 314

>gi|8469164|sp|Q99031|C9AA_BACTG PESTICIDIAL CRYSTAL PROTEIN CRY9AA PRECURSOR (INSECTICIDAL
DELTA-ENDOTOXIN CRYIXA(A)) (CRYSTALLINE ENTOMOCIDAL
PROTOXIN) (130 KDA CRYSTAL PROTEIN)
gi|80462|pir|S19306 parasporal crystal protein - Bacillus thuringiensis
gi|40271|emb|CAA41122.1| (X58120) delta-endotoxin CryIG protoxin [Bacillus thuringiensis]
gi|228273|prf|1802272A delta endotoxin [Bacillus thuringiensis serovar galleriae]
Length = 1156

Score = 63.2 bits (152), Expect = 1e-09
Identities = 40/118 (33%), Positives = 58/118 (48%), Gaps = 5/118 (4%)

Query: 2 HLTLLRDGALYGFSWG-WNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
HL LLRD YG +WG +N + + ++V+ I Y +Y Y+ G + ++ S
Sbjct: 201 HLLLLRDATRYGTNWGLYNATPFINYQSKLVELIELYTDYCVHWYNRGNELRQRGTSAT 260

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNS 118
+ E +RY REMTL VLD + D YP + LSR IY+D +G S
Sbjct: 261 AWLE----FHYRREMTLMVLDIVASFSSLDITNYPIETDFQLSRVIYTDPIGFVHRS 314

>gi|8469160|sp|Q45733|C9CA_BACTO Pesticidal crystal protein cry9Ca (Insecticidal delta-
endotoxin
CryIXC(a)) (Crystalline entomocidal protoxin) (130 kDa
crystal protein)
gi|1075948|pir|S49247 hypothetical protein 2 - Bacillus thuringiensis
gi|547556|emb|CAA85764.1| (Z37527) second open reading frame of cry9Ca1 operon [Bacillus
thuringiensis]
Length = 1157

Score = 63.2 bits (152), Expect = 1e-09
Identities = 38/113 (33%), Positives = 61/113 (53%), Gaps = 8/113 (7%)

Query: 1 MHLTLLRDGALYGFSWGWNE-EIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSN 59
+HL LL+D +L+G WG+ + EI + Q+ + Y Y E Y+ GL +
Sbjct: 206 LLLLLLLKASLFEGEGWGFTQGEISTYYDRQL-ELTAKYTNYCETWYNTGLDRLRGTN--- 261

Query: 60 KHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
TE + +++ REMTL VLD ++ Y+D YPT + L+RE+Y+D +
Sbjct: 262 ---TESWLRYHQFRREMTLVLDVVALFPYVDVRLYPTGSNPQLTREVTYTDPI 311

>gi|8927979|sp|O85805|C1BE_BACTU Pesticidal crystal protein cry1Be (Insecticidal delta-
endotoxin
CryIB(e)) (Crystalline entomocidal protoxin) (139 kDa
crystal protein)
gi|3360519|gb|AAC32850.1| (AF077326) Cry1Be1 delta-endotoxin [Bacillus thuringiensis]
Length = 1227

Score = 62.8 bits (151), Expect = 1e-09
Identities = 38/114 (33%), Positives = 60/114 (52%), Gaps = 8/114 (7%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPSN 59
+HL LLRD +L+G +G + Q E+ V+ Y +Y + Y+ GL + + NA S
Sbjct: 191 LHLLLLRDASLFGSEFGLTSQEIQRYYERQVEKTREYSDYCARWYNTGLNNLRGTNAESW 250

Query: 60 KHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVG 113
Y N++ R++TL VLD ++ +D YP L+REIY+D +G
Sbjct: 251 LRY-----NQFRDLTLGVLDLVALFSPYDTRVPMNTSAQLTREIYTDPIG 297

>gi|2815886|gb|AAB97923.1| (AF042733) delta-endotoxin [Bacillus thuringiensis]
Length = 645

Score = 62.8 bits (151), Expect = 1e-09
Identities = 37/114 (32%), Positives = 62/114 (53%), Gaps = 10/114 (8%)

Query: 1 MHLTLRLDGLYGFSGWNE-EIQQ-HTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS 58
+HL LL+D +YG WG N+ +I Q H+R+Q + +Y + Y+DGL + +
Sbjct: 194 LHLLLLKDADIYGARWGLNQTQIDQFHSRQQSLTQ--TYTNHCVTAYNDGLAELRGTT-- 249

Query: 59 NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
E + N+Y REMTL +D ++ Y++ +YP L+RE+Y+D +
Sbjct: 250 ----AESWFKYNQYRREMTLTAMDVLALFPYINLRQYPDGTPNQLTREIYTDPI 299

>gi|8469153|sp|Q9ZAZ5|C1BD_BACTZ Pesticidal crystal protein cryIbD (Insecticidal delta-endotoxin
CryIB(d)) (Crystalline entomocidal protoxin) (140 kDa
crystal protein)
gi|4097878|gb|AAD10292.1| (U70726) insecticidal crystal protein CryEI [Bacillus thuringiensis
serovar wuhanensis]
Length = 1231

Score = 62.4 bits (150), Expect = 2e-09
Identities = 40/115 (34%), Positives = 63/115 (54%), Gaps = 10/115 (8%)

Query: 1 MHLTLRLDGLYGFSGW-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 58
+HL LLRD +L+G WG + ++ Q+ +EQI T Y + + Y+ GL + + NA S
Sbjct: 191 LHLLLLRDASLFGSEWGMASDVNQYQEQIRYT-EEYSNHCVQWYNTGLNNLRGTNAES 249

Query: 59 NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVG 113
Y N++ R++TL VLD ++ +D YP L+REIY+D +G
Sbjct: 250 WLRY-----NQFRDLTLGVLDLVALFSPYDTRYPINTSAQLTREIYTDPIG 297

>gi|8928007|sp|O32307|CJAA_BACTJ Pesticidal crystal protein cryI9Aa (Insecticidal delta-endotoxin
CryXIXA(a)) (Crystalline entomocidal protoxin) (75 kDa
crystal protein)
gi|2624005|emb|CAA68875.1| (Y07603) mosquitocidal toxin [Bacillus thuringiensis]
Length = 648

Score = 62.4 bits (150), Expect = 2e-09
Identities = 41/113 (36%), Positives = 54/113 (47%), Gaps = 9/113 (7%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQI-VDTIGSYIEYTEKTYSDGLQDTQKNAPSN 59
+HL LLRD +YG W + QI ++ Y EY Y+ GL D +
Sbjct: 209 LHLLLLRDAQIYGDKWWSARANARDNYYQIQLEKTKEYTEYCINWYNKGLNDFRTAG--- 265

Query: 60 KHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ NRY REMTL VLD M+ +D YPT + L+REIYSD +
Sbjct: 266 -----QWVNFNRYRREMTLTVLDIISMFPYDARLYPTEVKTELREIYSDVI 313

>gi|8469150|sp|Q45774|C1BC_BACTM PESTICIDIAL CRYSTAL PROTEIN CRY1BC (INSECTICIDAL DELTA-ENDOTOXIN
CRYIB(C)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (140 KDA
CRYSTAL PROTEIN)
gi|565394|emb|CAA86568.1| (Z46442) delta-endotoxin [Bacillus thuringiensis]
Length = 1233

Score = 62.0 bits (149), Expect = 2e-09
Identities = 40/115 (34%), Positives = 63/115 (54%), Gaps = 10/115 (8%)

Query: 1 MHLTLRLDGLYGFSGWG-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 58
+HL LLRD +L+G WG + ++ Q+ +EQI T Y + + Y+ GL + + NA S
Sbjct: 191 LHLALLRDASLFGSEWGMASDVNQYYQEIRYT-EEYSNHCVQWYNTGLNNLRGTNAES 249

Query: 59 NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVG 113
Y N++ R++TL VLD ++ +D YP L+REIY+D +G
Sbjct: 250 WLRY-----NQFRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIG 297

>gi|8469145|sp|Q45739|C1BB_BACTU PESTICIDIAL CRYSTAL PROTEIN CRY1BB (INSECTICIDAL DELTA-
ENDOTOXIN

CRYIB(B)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (140 KDA
CRYSTAL PROTEIN)
gi|474894|gb|AAA22344.1| (L32020) crystal protein [Bacillus thuringiensis]
Length = 1229

Score = 62.0 bits (149), Expect = 2e-09
Identities = 40/115 (34%), Positives = 63/115 (54%), Gaps = 10/115 (8%)

Query: 1 MHLTLRLDGLYGFSGWG-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 58
+HL LLRD +L+G WG + ++ Q+ +EQI T Y + + Y+ GL + + NA S
Sbjct: 191 LHLALLRDASLFGSEWGMASDVNQYYQEIRYT-EEYSNHCVQWYNTGLNNLRGTNAES 249

Query: 59 NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVG 113
Y N++ R++TL VLD ++ +D YP L+REIY+D +G
Sbjct: 250 WLRY-----NQFRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREIYTDPIG 297

>gi|8469158|sp|Q03749|C7AA_BACTU PESTICIDIAL CRYSTAL PROTEIN CRY7AA (INSECTICIDAL DELTA-
ENDOTOXIN

CRYVIA(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (129 KDA
CRYSTAL PROTEIN)
gi|477378|pir||A48944 insecticidal crystal protein CryIIIC - Bacillus thuringiensis
gi|142761|gb|AAA22351.1| (M64478) crystal protein [Bacillus thuringiensis]
Length = 1138

Score = 62.0 bits (149), Expect = 3e-09
Identities = 36/112 (32%), Positives = 53/112 (47%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL LLRD LYG WG+ + + I Y ++ K Y+ GL N
Sbjct: 194 LHLALLRDSTLYGDKWGFQNNIEENYNRQKKRISEYSDHCTKWYNSGLSRL-----NG 247

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
E + NR+ REM L LD ++ + DP +Y L+RE+Y+D V
Sbjct: 248 STYEQWINYNRFRREMILMALDLVAVFPFHDPRYSMETSTQLTREIYTDPIV 299

>gi|8928039|sp|Q9X597|CQAA_BACTF Pesticidal crystal protein cry26Aa (Insecticidal delta-
endotoxin

CryXXVIA(a)) (Crystalline entomocidal protoxin) (131 kDa
crystal protein)
gi|4583416|gb|AAD25075.1|AF122897_1 (AF122897) Cry26Aa protein [Bacillus thuringiensis serovar
finitimus]
Length = 1163

Score = 62.0 bits (149), Expect = 3e-09
Identities = 40/116 (34%), Positives = 58/116 (49%), Gaps = 12/116 (10%)

Query: 1 MHLTLRLDGLYGFSGWNEE--IQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQK-NAP 57
+HL LRD +YG WG Q HTR ++ Y ++ Y+ GL+ + +A
Sbjct: 204 LHLALLRDASLFGSEWGLTPTNIDQNHTR--LLRHSAEYTDHCVNWNWYNTGLKQLENSDAK 261

Query: 58 SNKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVG 113
S Y NR+ REMTL VLD ++ +D YP P L+RE+Y+D +G
Sbjct: 262 SWFQY-----NRFRREMTLSVLDVIALFPAYDVKMYPIPTNFQLTREIYTDPIG 310

>gi|117534|sp|P09665|CRYS_BACTS 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALINE ENTOMOCIDAL
PROTOXIN)

gi|80449|pir||A22798 parasporal crystal protein - Bacillus thuringiensis
gi|551713|gb|AAA22552.1| (M10917) insecticidal crystal protein [Bacillus thuringiensis]
gi|224474|prf||1106181A protein,insecticidal crystal [Bacillus thuringiensis serovar sotto]

Length = 934

Score = 61.6 bits (148), Expect = 3e-09
 Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
 +HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
 Sbjct: 167 LHLVLRDVSFVGQRWGFDAATINSRYNDLRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
 + N++ RE+TL VLD ++ +D +YP L+REIY++ V
 Sbjct: 225 DWVR----YNQFRRELTLTVLIDVALFSNYDSRRYPPIRTVSQLTREIYTNPV 272

>gi|5901703|gb|AAD55382.1|AF154676_1 (AF154676) 135 kDa insecticidal protein [Bacillus thuringiensis serovar kurstaki]
 Length = 1176

Score = 61.6 bits (148), Expect = 3e-09
 Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
 +HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
 Sbjct: 167 LHLVLRDVSFVGQRWGFDAATINSRYNDLRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
 + N++ RE+TL VLD ++ +D +YP L+REIY++ V
 Sbjct: 225 DWVR----YNQFRRELTLTVLIDVALFSNYDSRRYPPIRTVSQLTREIYTNPV 272

>gi|1171233|gb|AAA86265.1| (U43605) CryIA(a) [Bacillus thuringiensis]
 Length = 620

Score = 61.6 bits (148), Expect = 3e-09
 Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
 +HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
 Sbjct: 167 LHLVLRDVSFVGQRWGFDAATINSRYNDLRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
 + N++ RE+TL VLD ++ +D +YP L+REIY++ V
 Sbjct: 225 DWVR----YNQFRRELTLTVLIDVALFSNYDSRRYPPIRTVSQLTREIYTNPV 272

>gi|743635|prf||2013214A lepidopteran-specific protoxin [Bacillus thuringiensis]
 Length = 1176

Score = 61.6 bits (148), Expect = 3e-09
 Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
 +HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
 Sbjct: 167 LHLVLRDVSFVGQRWGFDAATINSRYNDLRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
 + N++ RE+TL VLD ++ +D +YP L+REIY++ V
 Sbjct: 225 DWVR----YNQFRRELTLTVLIDVALFSNYDSRRYPPIRTVSQLTREIYTNPV 272

>gi|80448|pir||A22617 parasporal crystal protein - Bacillus thuringiensis
 gi|142765|gb|AAA22353.1| (M11250) crystal protein [Bacillus thuringiensis]
 Length = 1176

Score = 61.6 bits (148), Expect = 3e-09
 Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
 +HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
 Sbjct: 167 LHLVLRDVSFVGQRWGFDAATINSRYNDLRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112

+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLIDVAFSNDYDSSRRYPRTVSQLTREIYTNPV 272

>gi|117531|sp|P09664|CRYS_BACTE 133 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALINE ENTOMOCIDAL PROTOXIN)
gi|8488967|sp|P02965|C1AA_BACTK PESTICIDIAL CRYSTAL PROTEIN CRY1AA (INSECTICIDAL DELTA-ENDOTOXIN
CRYIA(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (133 KDA
CRYSTAL PROTEIN)
gi|80446|pir||S02215 parasporal crystal protein (clone pMP36) - Bacillus thuringiensis
(strain entomocidus)
gi|40267|emb|CAA31886.1| (X13535) parasporal crystal toxin (AA 1-1176) [Bacillus
thuringiensis]
Length = 1176

Score = 61.6 bits (148), Expect = 3e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLVLRDVSVFGQRWGFDATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLIDVAFSNDYDSSRRYPRTVSQLTREIYTNPV 272

>gi|117540|sp|P16478|CRYU_BACTA 135 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALINE ENTOMOCIDAL PROTOXIN)
gi|80456|pir||JT0241 parasporal crystal protein - Bacillus thuringiensis (strain aizawai
IPL7)
gi|216284|dbj|BAA00257.1| (D00348) 135 kDa insecticidal protein [Bacillus thuringiensis]
Length = 1176

Score = 61.6 bits (148), Expect = 3e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLVLRDVSVFGQRWGFDATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLIDVAFSNDYDSSRRYPRTVSQLTREIYTNPV 272

>gi|226053|prf||1409195A 135kD insecticidal protein [Bacillus thuringiensis]
Length = 1176

Score = 61.6 bits (148), Expect = 3e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLVLRDVSVFGQRWGFDATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLIDVAFSNDYDSSRRYPRTVSQLTREIYTNPV 272

>gi|5669035|gb|AAD46139.1|AF081790_1 (AF081790) insecticidal crystal protein [Bacillus
thuringiensis]
Length = 1176

Score = 61.6 bits (148), Expect = 3e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLVLRDVSVFGQRWGFDATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLDIVALFSNYDSRRYPPIRTVSQLTREIYTNPV 272

>gi|6687073|emb|CAA70856.1| (Y09663) delta-endotoxin [Bacillus thuringiensis]
Length = 1176

Score = 61.6 bits (148), Expect = 3e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLDIVALFSNYDSRRYPPIRTVSQLTREIYTNPV 272

>gi|25548|pir|JC2219 lepidopteran-specific protoxin - Bacillus thuringiensis
gi|535781|dbj|BAA04468.1| (D17518) insecticidal crystal protein [Bacillus thuringiensis]
Length = 1176

Score = 61.6 bits (148), Expect = 3e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLDIVALFSNYDSRRYPPIRTVSQLTREIYTNPV 272

>gi|4666284|dbj|BAA77213.1| (AB026261) Bt84A1 crystal protein [Bacillus thuringiensis]
Length = 1180

Score = 61.6 bits (148), Expect = 4e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLDIVALFSNYDSRRYPPIRTVSQLTREIYTNPV 272

>gi|8469152|sp|Q9S515|C1AG_BACTU PESTICIDIAL CRYSTAL PROTEIN CRY1AG (INSECTICIDAL DELTA-
ENDOTOXIN

CRYIA(G)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (134 KDA
CRYSTAL PROTEIN)

gi|5669019|gb|AAD46137.1|AF081248_1 (AF081248) lepidoteran-specific toxin [Bacillus
thuringiensis]
Length = 1176

Score = 61.2 bits (147), Expect = 4e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLDIVALFSNYDSRRYPPIRTVSQLTREIYTNPV 272

>gi|1942525|pdb|1CIY| Insecticidal Toxin: Structure And Channel Formation
Length = 590

Score = 61.2 bits (147), Expect = 4e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 139 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 196

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 197 DWVR----YNQFRRELTLTVLDIVLFSNYDSRRYPPIRTVSQTLTREIYTNPV 244

>gi|4090435|gb|AAC98807.1| (U63372) truncated CryIaC [synthetic construct]
Length = 613

Score = 61.2 bits (147), Expect = 4e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLDIVLFPNYDSRRYPPIRTVSQTLTREIYTNPV 272

>gi|2555147|gb|AAC63055.1| (AF023672) CryIA(c) [synthetic construct]
Length = 616

Score = 61.2 bits (147), Expect = 4e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 168 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 225

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 226 DWVR----YNQFRRELTLTVLDIVLFPNYDSRRYPPIRTVSQTLTREIYTNPV 273

>gi|1171235|gb|AAA86266.1| (U43606) CryIA(c) [Bacillus thuringiensis]
Length = 607

Score = 61.2 bits (147), Expect = 4e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLDIVLFPNYDSRRYPPIRTVSQTLTREIYTNPV 272

>gi|98533|pir||S11445 parasporal crystal protein cryIA.c - Bacillus thuringiensis
(strain BTS89A) (fragment)
gi|40275|emb|CAA38098.1| (X54159) cryIA(c) protein [Bacillus thuringiensis]
Length = 618

Score = 61.2 bits (147), Expect = 4e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLDIVLFPNYDSRRYPPIRTVSQTLTREIYTNPV 272

>gi|8469141|sp|Q45715|C1KA_BACTM Pesticidal crystal protein crylKa (Insecticidal delta-endotoxin

CryIK(a)) (Crystalline entomocidal protoxin) (137 kDa
crystal protein)
gi|1022696|gb|AAB00376.1| (U28801) CrylK [Bacillus thuringiensis]
gi|1586492|prf|2204216A crylK gene [Bacillus thuringiensis]
Length = 1215

Score = 61.2 bits (147), Expect = 5e-09
Identities = 37/114 (32%), Positives = 60/114 (52%), Gaps = 8/114 (7%)

Query: 1 MHLTLLRDGALYGFSGWNE-EIQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSN 59
+HL LLRD +L+G WG + ++ Q+ +EQI T Y + + Y+ GL +
Sbjct: 192 LHLTLLRDASLFGSEWGMSSADVNQYYQEIQIRYT-EEYSNHCQVWYNTGLNRLRGTT--- 247

Query: 60 KHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVG 113
E + N++ R++TL VLD ++ +D YP P L+RE+Y+D G
Sbjct: 248 ---AETWVRYNQFRDLTLGVLDLVALFPSYDTRTYPIPTTAQLTREYVTDPNG 298

>gi|5052774|gb|AAD38701.1|AF148644_1 (AF148644) insecticidal protein CrylAc [Bacillus thuringiensis]
Length = 723

Score = 61.2 bits (147), Expect = 5e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLLRDGALYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLDIVLFPNYDSRRYPPIRTVSQLTREIYTNPV 272

>gi|5916230|gb|AAD55947.1| (AF177675) Cry lAc insecticidal toxin [synthetic construct]
Length = 587

Score = 61.2 bits (147), Expect = 5e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLLRDGALYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 141 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 198

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 199 DWVR----YNQFRRELTLTVLDIVLFPNYDSRRYPPIRTVSQLTREIYTNPV 246

>gi|117547|sp|P05068|C1AC_BACTK Pesticidal crystal protein crylAc (Insecticidal delta-endotoxin
CryIA(c)) (Crystalline entomocidal protoxin) (133 kDa
crystal protein)

gi|72770|pir|USBSXH parasporal crystal protein - Bacillus thuringiensis subsp. kurstaki
(strain HD-73)
gi|142722|gb|AAA22331.1| (M11068) crystal protein [Bacillus thuringiensis]
gi|1839246|gb|AAB46989.1| (U87793) insecticidal delta-endotoxin CryIA(c) [Bacillus
thuringiensis serovar kurstaki]
gi|1842095|gb|AAC44841.1| (U87397) crystal protein [Bacillus thuringiensis serovar kurstaki]
gi|1888559|gb|AAB49768.1| (U89872) CrylAc delta-endotoxin [Bacillus thuringiensis]
gi|2584729|emb|CAA05505.1| (AJ002514) insecticidal crystal protein [Bacillus thuringiensis]
Length = 1178

Score = 60.8 bits (146), Expect = 5e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLLRDGALYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112

+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLIDIVALFPNYDSRRYPPIRTVSQLTREIYTNPV 272

>gi|143126|gb|AAA73077.1| (M73249) [Bacillus thuringiensis gene, complete CDS.], gene product
Length = 1178

Score = 60.8 bits (146), Expect = 5e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLVLRLDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERLV--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLIDIVALFPNYDSRRYPPIRTVSQLTREIYTNPV 272

>gi|142742|gb|AAA22339.1| (M73248) cryIA(c)3 [Bacillus thuringiensis]
Length = 1177

Score = 60.8 bits (146), Expect = 5e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLVLRLDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERLV--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLIDIVALFPNYDSRRYPPIRTVSQLTREIYTNPV 272

>gi|3979717|emb|CAA10270.1| (AJ130970) crystal toxin protein [Bacillus thuringiensis]
Length = 1178

Score = 60.8 bits (146), Expect = 5e-09
Identities = 33/112 (29%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLVLRLDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERLV--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLIDIVALFPNYDSRRYPPIRTVSQLTREIYTNPV 272

>gi|8469140|sp|Q45709|C1IB_BACTE Pesticidal crystal protein cryIIb (Insecticidal delta-endotoxin

CryII(b)) (Crystalline entomocidal protoxin) (81 kDa
crystal protein)

gi|2119867|pir||I40590 cryV465 protein - Bacillus thuringiensis
gi|467235|gb|AAA82114.1| (U07642) cryV465 gene product [Bacillus thuringiensis]
Length = 719

Score = 60.8 bits (146), Expect = 5e-09
Identities = 40/116 (34%), Positives = 63/116 (53%), Gaps = 10/116 (8%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 58
+HL LLRD +++G WG + EI Q V+ Y ++ K Y+ GL + + NA S
Sbjct: 195 LHLLLRLDASIFGKEWGLSASEISTFYNRQ-VERTRDYS DHCIK WYNTGLNNLRGTNAKS 253

Query: 59 NKHYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAVGT 114
Y N++ ++MTL VLD ++ +D + YP L+RE+Y+DA+GT
Sbjct: 254 WVRY-----NQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAIGT 302

>gi|9087134|sp|Q45707|C7AB_BACUA Pesticidal crystal protein cry7Ab (Insecticidal delta-endotoxin

CryVIIA(b)) (Crystalline entomocidal protoxin) (130 kDa
crystal protein)

gi|436839|gb|AAA21120.1| (U04367) CryIII delta-endotoxin [Bacillus thuringiensis]

Length = 1138

Score = 60.5 bits (145), Expect = 7e-09
Identities = 36/112 (32%), Positives = 52/112 (46%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL LLRD LYG WG+ + + + I Y + K Y+ GL N
Sbjct: 194 LHLALLRDSTLYGDKWGFQNNIEENYNRQKKHISEYSNHCVKWYNSGLSRL-----NG 247

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
E + NR+ REM L VLD ++ +DP Y L+RE+Y+D +
Sbjct: 248 STYEQWINYNRFRREMILMVLDAIAVFPYIDPRMYMETSTQLTREYVTDPI 299

>gi|13173240|gb|AAK14337.1| (AF327925) insecticidal crystal protein BTRX28 [Bacillus thuringiensis serovar kunthalaRX28]
Length = 1118

Score = 60.5 bits (145), Expect = 7e-09
Identities = 33/112 (29%), Positives = 59/112 (52%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRREITLTVLDAIFPNYDSRTYPIRTVSQLTREIYTNPV 272

>gi|546641|gb|AAB30710.1| insecticidal protein Cry I A (c) product {toxic domain} [Bacillus thuringiensis, ssp. kurstaki HD-1, Peptide, 723 aa]
Length = 723

Score = 60.5 bits (145), Expect = 8e-09
Identities = 33/112 (29%), Positives = 59/112 (52%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLDAIFPNYDSRRYPPIRTVSQLPREIYTNPV 272

>gi|3719431|gb|AAC63366.1| (AF093107) delta-endotoxin [Bacillus thuringiensis]
Length = 638

Score = 60.1 bits (144), Expect = 8e-09
Identities = 41/139 (29%), Positives = 70/139 (49%), Gaps = 16/139 (11%)

Query: 1 MHLTLRLDGLYGFSGWNE-EIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSN 59
+HL LL+D +YG WG N+ +I + Q D Y + TY+ GL++ +
Sbjct: 200 LHLALLKDAEYIGARWGLNQQQINLYFNAQ-QDRTQIYTNHCVATYNRGLENLRGTN--- 255

Query: 60 KHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNSG 119
TE + +++ REMTL +D ++ Y++ +YP A L+REIY+D V
Sbjct: 256 ---TESWYNYHQFRREMTLMAMDVLALFPYINLRQYPNGANPQLTREIYTDPV----- 305

Query: 120 ALNFPQHPKRSRSQKWKSGP 138
N P + + ++W++ P
Sbjct: 306 VFNPPAN-QGLCRRWRNNP 323

>gi|8469136|sp|Q03744|C1AD_BACTA Pesticidal crystal protein cryIAd (Insecticidal delta-endotoxin
CryIA(d)) (Crystalline entomocidal protoxin) (133 kDa
crystal protein)
gi|142744|gb|AAA22340.1| (M73250) cryIA(d) [Bacillus thuringiensis]
Length = 1179

Score = 60.1 bits (144), Expect = 9e-09

Identities = 33/112 (29%), Positives = 59/112 (52%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y +Y + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGTYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLTDIVSLFPNYDSRTYPIRTVSQTLREIYTNPV 272

>gi|225472|prf|l1304168B endotoxin delta 1 [Bacillus thuringiensis]
Length = 1176

Score = 59.7 bits (143), Expect = 1e-08
Identities = 32/112 (28%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y ++ + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V
Sbjct: 225 DWVR----YNQFRRELTLTVLDIVLFSNYDSRRYPIRTVSQTLREIYTNPV 272

>gi|8469134|sp|P56953|C1CB_BACTG PESTICIDIAL CRYSTAL PROTEIN CRY1CB (INSECTICIDAL DELTA-
ENDOTOXIN

CRYIC(B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (133 KDA
CRYSTAL PROTEIN)
gi|477402|pir|A48970 insecticidal crystal toxin CryIC(b) - Bacillus thuringiensis
Length = 1176

Score = 59.3 bits (142), Expect = 1e-08
Identities = 35/114 (30%), Positives = 58/114 (50%), Gaps = 6/114 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL +LRD +++G WG +++ I Y + TY+ GL N P +
Sbjct: 166 LHLAILRDSSIFGARWGLTTINNVNENYRLIRHIDEYANHCADTYNRGLN----NLPKST 221

Query: 61 HYTEPNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAVGT 114
+ + + T NR R++TL VLD + +D +YP + L+REIY+D + T
Sbjct: 222 Y--QDWITYNRLRRDLTLTVLDIAAFFPSYDNRRYPIQSVGQLTREIYTDPLIT 273

>gi|8928019|sp|Q45705|C8BA_BACUK Pesticidal crystal protein cry8Ba (Insecticidal delta-
endotoxin

CryVIIIB(a)) (Crystalline entomocidal protoxin) (134 kDa
crystal protein)
gi|436835|gb|AAA21118.1| (U04365) CryIII delta-endotoxin [Bacillus thuringiensis]
Length = 1169

Score = 58.9 bits (141), Expect = 2e-08
Identities = 35/116 (30%), Positives = 57/116 (48%), Gaps = 6/116 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL LLRD +++G WG + + + Y ++ K Y GL + S K
Sbjct: 206 LHLLLLRDASIFGEEWGLSTSTINNYNRQMKLTAEYSDHCVKQWYETGL--AKLKGSSAK 263

Query: 61 HYTEPNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTAD 116
+ + N++ REMTL VLD ++ +D YP L+RE+Y+D +G D
Sbjct: 264 QWID----YNQFRREMTLTVLDDVVALFSNYDTRTYPLATTAQLTREIYTDPLGAVD 315

>gi|477639|pir|A49785 parasporal crystal protein cryIA(c) - Bacillus thuringiensis subsp.
kenyae (strain HD588-2)
gi|142740|gb|AAA22338.1| (M35524) delta-endotoxin [Bacillus thuringiensis]
Length = 1177

Score = 58.9 bits (141), Expect = 2e-08
Identities = 32/112 (28%), Positives = 60/112 (53%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60

+HL++LRD +++G WG++ + IG+Y ++ + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D +YP L+REIY++ V

Sbjct: 225 DWVR---YNQFRRELTLTVLDIVLFPNYDSRRYPITVSQLTREIYTNPV 272

>gi|8469138|sp|Q03746|C1FA_BACTA Pesticidal crystal protein cryIa (Insecticidal delta-endotoxin)

CryIF(a) (Crystalline entomocidal protoxin) (134 kDa
crystal protein)
gi|98519|pir|A42459 insecticidal crystal protein CryIF - Bacillus thuringiensis
(strain aizawai)
gi|142756|gb|AAA22347.1| (M73254) cryIF [Bacillus thuringiensis]
gi|142758|gb|AAA22348.1| (M63897) insecticidal crystal protein [Bacillus thuringiensis]
Length = 1174

Score = 58.9 bits (141), Expect = 2e-08
Identities = 35/124 (28%), Positives = 63/124 (50%), Gaps = 7/124 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL+LLRD +G WG + + + + + I Y ++ TY+ GL++ +

Sbjct: 165 LHLSLLRDAVSFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGTN---- 220

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNSGA 120
T + N++ R++TL VLD ++ +D YP L+REIY+ +V D+ +

Sbjct: 221 --TRQWARFNQFRRLTLTVLDIVLFPNYDVRTYPIQTSSQLTREIYTSSV-IEDSPVS 277

Query: 121 LNFP 124
N P

Sbjct: 278 ANIP 281

>gi|8469139|sp|Q03748|C1AE_BACTL PESTICIDIAL CRYSTAL PROTEIN CRYIAE (INSECTICIDAL DELTA-ENDOTOXIN)

CRYIA(E) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (134 KDA
CRYSTAL PROTEIN)
gi|98532|pir|A41052 parasporal crystal protein - Bacillus thuringiensis (strain alesti)
gi|142875|gb|AAA22410.1| (M65252) delta-endotoxin [Bacillus thuringiensis]
Length = 1181

Score = 58.9 bits (141), Expect = 2e-08
Identities = 33/112 (29%), Positives = 58/112 (51%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL++LRD +++G WG + + IG+Y +Y + Y+ GL+ P ++

Sbjct: 167 LHLSVLRDVSFVGQRWGLDVATINSRYNDLTRLIGITYTDYAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D YP L+REIY++ V

Sbjct: 225 DWVR---YNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV 272

>gi|13173238|gb|AAK14336.1| (AF327924) insecticidal crystal protein BTRX24 [Bacillus thuringiensis serovar kunthalarX24]
Length = 1118

Score = 58.9 bits (141), Expect = 2e-08
Identities = 32/112 (28%), Positives = 59/112 (52%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL++LRD +++G WG++ + IG+Y ++ + Y+ GL+ P ++

Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D YP L+REIY++ V

Sbjct: 225 DWIR---YNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV 272

>gi|2414156|emb|CAA70925.1| (Y09787) delta-endotoxin [Bacillus thuringiensis]
Length = 618

Score = 58.5 bits (140), Expect = 3e-08
Identities = 32/112 (28%), Positives = 59/112 (52%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL++LRD +++G WG++ + IG+Y ++ + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERLVW--GPDSR 224

Query: 61 HYTEPNTVNRVYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D YP L+REIY++ V
Sbjct: 225 DWIR----YNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPV 272

>gi|8469151|sp|Q57458|C1EA_BACTX Pesticidal crystal protein cryIEa (Insecticidal delta-endotoxin)

CryIE(a)) (Crystalline entomocidal protoxin) (133 kDa
crystal protein)
gi|2119865|pir||I40572 crystal protein - Bacillus thuringiensis
gi|40257|emb|CAA37933.1| (X53985) crystal protein [Bacillus thuringiensis]
gi|40282|emb|CAA39609.1| (X56144) crystal protein [Bacillus thuringiensis]
Length = 1171

Score = 58.2 bits (139), Expect = 3e-08
Identities = 31/112 (27%), Positives = 56/112 (49%), Gaps = 5/112 (4%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL++LRD +++G +WG++ + I Y +Y + Y+ GL +
Sbjct: 165 LHLSVLRDVSFVGQAWGFDAATINSRYNDLTRLIPIYTDYAVRWYNTGLDRLPRTGGLRN 224

Query: 61 HYTEPNTVNRVYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+T+ VLD ++ +D YP P L+RE+Y+D V
Sbjct: 225 -----WARFNQFRRELTLISVLDIISFFRNYDSRLYPIPTSSQLTREVTDPV 271

>gi|142752|gb|AAA22345.1| (M73252) cryIE(a) [Bacillus thuringiensis]
gi|17979619|gb|AAL50330.1|AF202531_1 (AF202531) Cry032 [Bacillus thuringiensis]
Length = 1171

Score = 58.2 bits (139), Expect = 3e-08
Identities = 31/112 (27%), Positives = 56/112 (49%), Gaps = 5/112 (4%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL++LRD +++G +WG++ + I Y +Y + Y+ GL +
Sbjct: 165 LHLSVLRDVSFVGQAWGFDAATINSRYNDLTRLIPIYTDYAVRWYNTGLDRLPRTGGLRN 224

Query: 61 HYTEPNTVNRVYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+T+ VLD ++ +D YP P L+RE+Y+D V
Sbjct: 225 -----WARFNQFRRELTLISVLDIISFFRNYDSRLYPIPTSSQLTREVTDPV 271

>gi|1946622|gb|AAD04732.1| (U94323) CryIEa4 [Bacillus thuringiensis]
Length = 1171

Score = 58.2 bits (139), Expect = 3e-08
Identities = 31/112 (27%), Positives = 56/112 (49%), Gaps = 5/112 (4%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL++LRD +++G +WG++ + I Y +Y + Y+ GL +
Sbjct: 165 LHLSVLRDVSFVGQAWGFDAATINSRYNDLTRLIPIYTDYAVRWYNTGLDRLPRTGGLRN 224

Query: 61 HYTEPNTVNRVYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+T+ VLD ++ +D YP P L+RE+Y+D V
Sbjct: 225 -----WARFNQFRRELTLISVLDIISFFRNYDSRLYPIPTSSQLTREVTDPV 271

>gi|538624|pir||A37829 parasporal crystal protein - Bacillus thuringiensis
Length = 1171

Score = 58.2 bits (139), Expect = 3e-08
Identities = 31/112 (27%), Positives = 56/112 (49%), Gaps = 5/112 (4%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL++LRD +++G +WG++ + I Y +Y + Y+ GL +
Sbjct: 165 LHLSVLRDVSFVGQAWGFDAATINSRYNDLTRLIPIYTDYAVRWYNTGLDRLPRTGGLRN 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+T+ VLD ++ +D YP P L+RE+Y+D V
Sbjct: 225 -----WARFNQFRRELTISVLDIISFFRNYSRLYPIPTSSQLTREYVYTDPV 271

>gi|80457|pir||A26461 parasporal crystal protein Bt2 - Bacillus thuringiensis (strain
berliner 1715)
gi|40255|emb|CAA28405.1| (X04698) delta endotoxin (AA 1-1155) [Bacillus thuringiensis]
Length = 1155

Score = 58.2 bits (139), Expect = 4e-08
Identities = 32/112 (28%), Positives = 59/112 (52%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNNK 60
+HL++LRD +++G WG++ + IG+Y ++ + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D YP L+REIY++ V
Sbjct: 225 DWIR----YNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV 272

>gi|208155|gb|AAA72985.1| (M60856) cryIA(a) [synthetic construct]
Length = 615

Score = 58.2 bits (139), Expect = 4e-08
Identities = 32/112 (28%), Positives = 59/112 (52%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNNK 60
+HL++LRD +++G WG++ + IG+Y ++ + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D YP L+REIY++ V
Sbjct: 225 DWIR----YNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV 272

>gi|117536|sp|P09666|CRYT_BACTA 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE ENTOMOCIDAL
PROTOXIN)
gi|98529|pir||S02134 parasporal crystal protein - Bacillus thuringiensis (strain aizawai
IC1)
gi|40278|emb|CAA31620.1| (X13233) delta-endotoxin [Bacillus thuringiensis]
Length = 1155

Score = 58.2 bits (139), Expect = 4e-08
Identities = 32/112 (28%), Positives = 59/112 (52%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNNK 60
+HL++LRD +++G WG++ + IG+Y ++ + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D YP L+REIY++ V
Sbjct: 225 DWIR----YNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV 272

>gi|117539|sp|P21257|CRYT_BACTK 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE ENTOMOCIDAL
PROTOXIN) (5.3 CLASS)
gi|2119866|pir||I39838 delta-endotoxin (5.3 class) - Bacillus thuringiensis
gi|142886|gb|AAA22420.1| (M37263) 5.3 class delta endotoxin [Bacillus thuringiensis]
Length = 1155

Score = 58.2 bits (139), Expect = 4e-08
Identities = 32/112 (28%), Positives = 59/112 (52%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNNK 60
+HL++LRD +++G WG++ + IG+Y ++ + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D YP L+REIY++ V
Sbjct: 225 DWIR----YNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV 272

>gi|117543|sp|P09667|CRYV_BACTA 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE ENTOMOCIDAL PROTOXIN)
gi|98531|pir|A26513 parasporal crystal protein - Bacillus thuringiensis (strain aizawai)
gi|143099|gb|AAA22551.1| (M16463) insecticidal protein [Bacillus thuringiensis]
Length = 1155

Score = 58.2 bits (139), Expect = 4e-08
Identities = 32/112 (28%), Positives = 59/112 (52%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y ++ + Y+ GL+ P ++
Sbjct: 167 LHLVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D YP L+REIY++ V
Sbjct: 225 DWIR----YNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPV 272

>gi|80474|pir|A29125 parasporal crystal protein - Bacillus thuringiensis subsp. kurstaki (strain HD-1)
gi|225669|prf|1310234A insect control protein [Bacillus thuringiensis]
Length = 1156

Score = 58.2 bits (139), Expect = 4e-08
Identities = 32/112 (28%), Positives = 59/112 (52%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y ++ + Y+ GL+ P ++
Sbjct: 167 LHLVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D YP L+REIY++ V
Sbjct: 225 DWIR----YNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPV 272

>gi|117533|sp|P06578|C1AB_BACTK PESTICIDIAL CRYSTAL PROTEIN CRY1AB (INSECTICIDAL DELTA-ENDOTOXIN CRYIA(B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (130 KDA CRYSTAL PROTEIN)
gi|80447|pir|JD0002 parasporal crystal protein Bt2 - Bacillus thuringiensis
gi|40273|emb|CAA38701.1| (X54939) unnamed protein product [Bacillus thuringiensis]
gi|142720|gb|AAA22330.1| (M13898) entomocidal protoxin [Bacillus thuringiensis]
gi|143124|gb|AAA22561.1| (M15271) crystal protein precursor [Bacillus thuringiensis]
gi|216280|dbj|BAA00071.1| (D00117) delta-endotoxin [Bacillus thuringiensis]
gi|3746545|gb|AAC64003.1| (AF059670) crystal protein [Bacillus thuringiensis serovar kurstaki]
gi|225471|prf|1304168A endotoxin delta 2 [Bacillus thuringiensis]
Length = 1155

Score = 58.2 bits (139), Expect = 4e-08
Identities = 32/112 (28%), Positives = 59/112 (52%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y ++ + Y+ GL+ P ++
Sbjct: 167 LHLVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D YP L+REIY++ V
Sbjct: 225 DWIR----YNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPV 272

>gi|10440886|gb|AAG16877.1| (U94191) delta endotoxin [Bacillus thuringiensis]
Length = 1155

Score = 58.2 bits (139), Expect = 4e-08
Identities = 32/112 (28%), Positives = 59/112 (52%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD +++G WG++ + IG+Y ++ + Y+ GL+ P ++
Sbjct: 167 LHLVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D YP L+REIY++ V
Sbjct: 225 DWIR----YNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV 272

>gi|8469147|sp|Q45747|C1DB_BACTU PESTICIDIAL CRYSTAL PROTEIN CRY1DB (INSECTICIDAL DELTA-
ENDOTOXIN

CRYID(B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (131 KDA
CRYSTAL PROTEIN)
gi|421540|pir||S32647 parasporal crystal protein - Bacillus thuringiensis
gi|295864|emb|CAA80234.1| (Z22511) crystal protein [Bacillus thuringiensis]
Length = 1160

Score = 58.2 bits (139), Expect = 4e-08
Identities = 32/110 (29%), Positives = 56/110 (50%), Gaps = 6/110 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD ++YG WG++ + I Y ++ TY+DGL++ + + S+
Sbjct: 166 LHLVLRDVSVMYQQRWGFDPATVNSRYSDLTRLIHVYTDHCVDTYNDGLKNLEGSRLSD- 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSD 110
+ NR+ R +T+ VLD + +D YP L+RE+Y D
Sbjct: 225 -----WVVYNRFRRLTISVLDIIAFFPNYDIEAYPIQTASQLTREYVLD 269

>gi|8469154|sp|Q9ZAZ6|C1GB_BACTZ Pesticidal crystal protein cry1Gb (Insecticidal delta-
endotoxin
CryIG(b)) (Crystalline entomocidal protoxin) (133 kDa
crystal protein)
gi|4097876|gb|AAD10291.1| (U70725) insecticidal crystal protein CryH2 [Bacillus thuringiensis
serovar wuhanensis]
Length = 1169

Score = 57.8 bits (138), Expect = 4e-08
Identities = 33/112 (29%), Positives = 56/112 (49%), Gaps = 10/112 (8%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL LLRD +G WG + ++ ++I Y + + Y+ GL + P +
Sbjct: 165 LHLALLRDAVFFGERWGLTQTININDLYSRLKNSIRDYTNHCVRFYNIGLGNLNVIRP--E 222

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+Y R+ RE+T+ VLD ++ +D YP P + L+REIY+D +
Sbjct: 223 YY-----RFQRELTLISVLDLVALFPNYDIRTYPIPTKSQLTREIYTDPI 266

>gi|1769867|emb|CAA67557.1| (X99103) delta-endotoxin [synthetic construct]
Length = 630

Score = 57.8 bits (138), Expect = 4e-08
Identities = 33/110 (30%), Positives = 55/110 (50%), Gaps = 6/110 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL +LRD ++G WG +++ I Y ++ TY+ GL N P +
Sbjct: 166 LHLAILRDSVIFGERWGLTTINVNENYNRLIRHIDEYADHCANTYNRGLN----NLPKST 221

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSD 110
+ + + T NR R++TL VLD + +D +YP L+RE+Y+D
Sbjct: 222 Y--QDWITYNRLRRDLTLTVLDIAAFFPNYDNRYPPIQPVGQLTREYVTD 269

>gi|13899010|gb|AAK48937.1|AF358862_2 (AF358862) insecticidal crystal protein [Bacillus
thuringiensis]
Length = 1160

Score = 57.8 bits (138), Expect = 4e-08
Identities = 32/110 (29%), Positives = 56/110 (50%), Gaps = 6/110 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD ++YG WG++ + I Y ++ TY+DGL++ + + S+
Sbjct: 166 LHLVLRDVSVMYQQRWGFDPATVNSRYSDLTRLIHVYTDHCVDTYNDGLKNLEGSRLSD- 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSD 110
+ NR+ R +T+ VLD + +D YP L+RE+Y D

Sbjct: 225 -----WVVYNRFRRLTISVLDIIAFFPNYDIEAYPIQTASQLTREYVLD 269

>gi|80451|pir||S04181 parasporal crystal protein - Bacillus thuringiensis (strain aizawai
7.29) (fragment)
gi|40356|emb|CAA31951.1| (X13620) delta-endotoxin (AA 1 - 824) (2711 is 2nd base in codon)
[Bacillus thuringiensis]
Length = 823

Score = 57.8 bits (138), Expect = 4e-08
Identities = 33/110 (30%), Positives = 55/110 (50%), Gaps = 6/110 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL +LRD ++G WG +++ I Y ++ TY+ GL NP +
Sbjct: 166 LHLAILRDSVIFGERWGLTTINVNENYRLIRHIDEYADHCANTYNRGLN----NLPKST 221

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSD 110
+ + + T NR R++TL VLD + +D +YP L+RE+Y+D
Sbjct: 222 Y--QDWITYNRLRRDLTLTVLDIAAFFPNYDNRYPPIQPVGQLTREYVTD 269

>gi|11277639|pir||JC7140 protoxin - Bacillus thuringiensis
Length = 655

Score = 57.8 bits (138), Expect = 4e-08
Identities = 33/110 (30%), Positives = 55/110 (50%), Gaps = 6/110 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL +LRD ++G WG +++ I Y ++ TY+ GL NP +
Sbjct: 166 LHLAILRDSVIFGERWGLTTINVNENYRLIRHIDEYADHCANTYNRGLN----NLPKST 221

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSD 110
+ + + T NR R++TL VLD + +D +YP L+RE+Y+D
Sbjct: 222 Y--QDWITYNRLRRDLTLTVLDIAAFFPNYDNRYPPIQPVGQLTREYVTD 269

>gi|1234884|emb|CAA65457.1| (X96682) delta-endotoxin [Bacillus thuringiensis]
Length = 756

Score = 57.8 bits (138), Expect = 5e-08
Identities = 33/110 (30%), Positives = 55/110 (50%), Gaps = 6/110 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL +LRD ++G WG +++ I Y ++ TY+ GL NP +
Sbjct: 166 LHLAILRDSVIFGERWGLTTINVNENYRLIRHIDEYADHCANTYNRGLN----NLPKST 221

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSD 110
+ + + T NR R++TL VLD + +D +YP L+RE+Y+D
Sbjct: 222 Y--QDWITYNRLRRDLTLTVLDIAAFFPNYDNRYPPIQPVGQLTREYVTD 269

>gi|142750|gb|AAA22343.1| (M73251) cryIC(b) [Bacillus thuringiensis]
Length = 1189

Score = 57.8 bits (138), Expect = 5e-08
Identities = 33/110 (30%), Positives = 55/110 (50%), Gaps = 6/110 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL +LRD ++G WG +++ I Y ++ TY+ GL NP +
Sbjct: 166 LHLAILRDSVIFGERWGLTTINVNENYRLIRHIDEYADHCANTYNRGLN----NLPKST 221

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSD 110
+ + + T NR R++TL VLD + +D +YP L+RE+Y+D
Sbjct: 222 Y--QDWITYNRLRRDLTLTVLDIAAFFPNYDNRYPPIQPVGQLTREYVTD 269

>gi|8488968|sp|P05518|C1CA_BACTE Pesticidal crystal protein cry1Ca (Insecticidal delta-
endotoxin

CryIC(a)) (Crystalline entomocidal protoxin) (134 kDa
crystal protein)
gi|18913153|gb|AAL79362.1| (AY078160) delta-endotoxin [Bacillus thuringiensis]
gi|19880135|gb|AAM00264.1|AF362020_1 (AF362020) insecticidal protein Cry1Ca [Bacillus
thuringiensis]
Length = 1189

Score = 57.8 bits (138), Expect = 5e-08
Identities = 33/110 (30%), Positives = 55/110 (50%), Gaps = 6/110 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL +LRD ++G WG +++ I Y ++ TY+ GL N P +
Sbjct: 166 LHLAILRDSVIFGERWGLTTINVENYNNRLIRHIDEYADHCANTYNRGLN----NLPKST 221

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSD 110
+ + + T NR R++TL VLD + +D +YP L+RE+Y+D
Sbjct: 222 Y--QDWITYNNRLRRDLTLTVLDIAAFFPNYDNRRIPIQPVGQLTREYVTD 269

>gi|16945772|dbj|BAB72018.1| (AB074414) insecticidal crystal protein bun3 [Bacillus thuringiensis]
Length = 666

Score = 57.4 bits (137), Expect = 5e-08
Identities = 32/86 (37%), Positives = 46/86 (53%), Gaps = 4/86 (4%)

Query: 28 EQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NKHYTEPFNTVNRYVREMTLDVDFKDMW 87
E++ I Y +Y E Y GL ++ + + N++ REMTL VLD ++
Sbjct: 239 ERLCKIAEYTDYCEYWYQAGLNQIKQAGTG----ADTWAKFNKFRREMTLTVLDDIAIF 294

Query: 88 QYFDPVKYPTPAEVYLSREIYSDAVG 113
Q +D KYP P V L+REIY+D VG
Sbjct: 295 QTYDFKKYPLPTHVELTREIYTDVPV 320

>gi|80452|pir||S00944 parasporal crystal protein - Bacillus thuringiensis (strain entomocidus 60.5)
gi|40294|emb|CAA30396.1| (X07518) put. endotoxin (AA 1-1189) [Bacillus thuringiensis]
Length = 1189

Score = 57.4 bits (137), Expect = 5e-08
Identities = 33/110 (30%), Positives = 55/110 (50%), Gaps = 6/110 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL +LRD ++G WG +++ I Y ++ TY+ GL N P +
Sbjct: 166 LHLAILRDSVIFGERWGLTTINVENYNNRLIRHIDEYADHCANTYNRGLN----NLPKST 221

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSD 110
+ + + T NR R++TL VLD + +D +YP L+RE+Y+D
Sbjct: 222 Y--QDWITYNNRLRRDLTLTVLDIAAFFPNYDNRRIPIQPVGQLTREYVTD 269

>gi|117542|sp|P09663|CRYU_BACTK 131 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE ENTOMOCIDAL PROTOXIN)
gi|80475|pir||A29838 parasporal crystal protein - Bacillus thuringiensis subsp. kurstaki
gi|143227|gb|AA22613.1| (M12661) insecticidal endotoxin [Bacillus thuringiensis]
Length = 1156

Score = 57.4 bits (137), Expect = 6e-08
Identities = 32/112 (28%), Positives = 59/112 (52%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL++LRD +++G WG++ + IG+Y ++ + Y+ GL+ P ++
Sbjct: 167 LHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHRVVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D YP L+REIY++ V
Sbjct: 225 DWIR---YNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV 272

>gi|8928043|sp|Q9ZNL9|C9EA_BACTA Pesticidal crystal protein cry9Ea (Insecticidal delta-endotoxin
CryIXE(a)) (Crystalline entomocidal protoxin) (130 kDa
crystal protein)
gi|3986086|dbj|BAA34908.1| (AB011496) Cry9 like protein [Bacillus thuringiensis serovar aizawai]
Length = 1150

Score = 57.4 bits (137), Expect = 6e-08

Identities = 36/113 (31%), Positives = 60/113 (52%), Gaps = 8/113 (7%)

Query: 1 MHLTLRLDGLYGFSGWNE-EIQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSN 59
+HL LL+D +YG WG + +I + Q T Y + +TY+ GL+D +
Sbjct: 209 LHLLLKDAEYIGARWGLQQGQINLYFNAQQERT-RIYTNHCVETYNRGLEDVRGTN--- 264

Query: 60 KHYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
TE + +R+ REMTL +D ++ +++ +YP A L+REIY+D +
Sbjct: 265 ---TESWLNHYHRFRREMTLMAMDVLALFPFYNVQRYPNGANPQLTREIYTDPI 314

>gi|9087135|sp|Q45708|C7AB_BACUK Pesticidal crystal protein cry7Ab (Insecticidal delta-endotoxin

CryVIIA(b)) (Crystalline entomocidal protoxin) (130 kDa
crystal protein)

gi|436841|gb|AAA21121.1| (U04368) CryIII delta-endotoxin [Bacillus thuringiensis]
Length = 1138

Score = 57.4 bits (137), Expect = 6e-08
Identities = 35/112 (31%), Positives = 51/112 (45%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL LRLD LYG W + + + + I Y + K Y+ GL N
Sbjct: 194 LHLALRLDSTLYGDKWEFTQNNIEENYNRQKKHISEYSNHCVKWYNSGLSRL-----NG 247

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
E + NR+ REM L VLD ++ +DP Y L+RE+Y+D +
Sbjct: 248 STYEQWINYNRFRREMILMVLDAIAVFPIYDPRMYSMETSTQLTREIYTDPI 299

>gi|7141141|gb|AAF37224.1|AF215647_1 (AF215647) toxin CryIc6 [Bacillus thuringiensis]
Length = 1189

Score = 57.0 bits (136), Expect = 7e-08
Identities = 33/110 (30%), Positives = 55/110 (50%), Gaps = 6/110 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL +LRD ++G WG +++ I Y ++ TY+ GL N P +
Sbjct: 166 LHLAILRDSVIFGERWGVTTINVNENYRNLIRHIDEYADHCANTYNRGLN----NLPKST 221

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSD 110
+ + + T NR R++TL VLD + +D +YP L+RE+Y+D
Sbjct: 222 Y--QDWITYNRLRRDLTLTVLDIAAFFPNYDNRYPPIQPVGQLTREIYTD 269

>gi|14190061|gb|AAK55546.1|AF375608_1 (AF375608) crystal protein CryIAb16 [Bacillus thuringiensis serovar israelensis]
Length = 1155

Score = 57.0 bits (136), Expect = 7e-08
Identities = 32/112 (28%), Positives = 58/112 (51%), Gaps = 6/112 (5%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL++LRD ++G WG++ + IG+Y ++ + Y+ GL+ P ++
Sbjct: 167 LHLVLRLDVLFVGRWGFDAATINSRYNDLRLIGNYTHAVRWYNTGLERVW--GPDSR 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D YP L+REIY++ V
Sbjct: 225 DWIR----YNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPV 272

>gi|17385650|dbj|BAB78603.1| (AB075462) crystal protein CryE6S [Bacillus thuringiensis]
Length = 1280

Score = 56.6 bits (135), Expect = 9e-08
Identities = 35/130 (26%), Positives = 59/130 (44%), Gaps = 17/130 (13%)

Query: 1 MHLTLRLDGLYGFSGW-NEEIQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSN 59
+ L LRLD +G WG +E+ EQ++ I + ++ ++ GL++ +K +
Sbjct: 201 LQLALLRDAVKFGRDWGLPQDEVDDIYSEQLLPRIAEHTDHCVTYFNRGLEEAKKLKANL 260

Query: 60 KHYT-----EPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYL 103

Y E +N N Y R MT+ VLD +W +DP +Y + L
Sbjct: 261 NDYARYPWAQYINHSKIQGIENWNLFNDYRRNMTILVLDLVALWPTYDPRRYSMTKSEL 320

Query: 104 SREIYSDAVG 113

+RE+Y+ G

Sbjct: 321 TRELYTSVRG 330

>gi|471281|emb|CAA51996.1| (X73600) CryIIIA insecticidal crystal protein [synthetic construct]
Length = 610

Score = 56.6 bits (135), Expect = 1e-07
Identities = 37/117 (31%), Positives = 61/117 (51%), Gaps = 8/117 (6%)

Query: 2 HLTLLRDGALYGFSWGW-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60

HL LL+D +YG WG+ E+I + + Q+ T Y ++ K Y+ GL + ++

Sbjct: 157 HLFLKDAQIYGEEWGYEKEDIAEFYKRQLKLT-QEYTDHCVKWNVGLDKLRGSS---- 211

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADN 117

E + NRY REMTL VLD ++ +D YP + L+R++ +D + +N

Sbjct: 212 --YESWVNFNRYRREMTLTVDLIALFPLYDVRLYPKEVKTELTRDVLTDPIVGNN 266

>gi|640362|pdb|1DLC| Delta-Endotoxin CryIIIA (Bt13)
Length = 584

Score = 56.2 bits (134), Expect = 1e-07
Identities = 37/117 (31%), Positives = 61/117 (51%), Gaps = 8/117 (6%)

Query: 2 HLTLLRDGALYGFSWGW-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60

HL LL+D +YG WG+ E+I + + Q+ T Y ++ K Y+ GL + ++

Sbjct: 144 HLFLKDAQIYGEEWGYEKEDIAEFYKRQLKLT-QEYTDHCVKWNVGLDKLRGSS---- 198

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADN 117

E + NRY REMTL VLD ++ +D YP + L+R++ +D + +N

Sbjct: 199 --YESWVNFNRYRREMTLTVDLIALFPLYDVRLYPKEVKTELTRDVLTDPIVGNN 253

>gi|208153|gb|AAA73184.1| (M84650) crystal toxin [synthetic construct]
gi|312848|emb|CAA50310.1| (X70979) cryIIIA insect control protein [synthetic construct]
Length = 597

Score = 56.2 bits (134), Expect = 1e-07
Identities = 37/117 (31%), Positives = 61/117 (51%), Gaps = 8/117 (6%)

Query: 2 HLTLLRDGALYGFSWGW-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60

HL LL+D +YG WG+ E+I + + Q+ T Y ++ K Y+ GL + ++

Sbjct: 157 HLFLKDAQIYGEEWGYEKEDIAEFYKRQLKLT-QEYTDHCVKWNVGLDKLRGSS---- 211

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADN 117

E + NRY REMTL VLD ++ +D YP + L+R++ +D + +N

Sbjct: 212 --YESWVNFNRYRREMTLTVDLIALFPLYDVRLYPKEVKTELTRDVLTDPIVGNN 266

>gi|80453|pir||A27323 parasporal crystal protein CryIIIA - Bacillus thuringiensis
gi|142734|gb|AAA22336.1| (M22472) delta-endotoxin [Bacillus thuringiensis]
gi|4688623|emb|CAB41411.1| (AJ237900) Cry3Aa protein [Bacillus thuringiensis]
Length = 652

Score = 56.2 bits (134), Expect = 1e-07
Identities = 37/117 (31%), Positives = 61/117 (51%), Gaps = 8/117 (6%)

Query: 2 HLTLLRDGALYGFSWGW-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60

HL LL+D +YG WG+ E+I + + Q+ T Y ++ K Y+ GL + ++

Sbjct: 212 HLFLKDAQIYGEEWGYEKEDIAEFYKRQLKLT-QEYTDHCVKWNVGLDKLRGSS---- 266

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADN 117

E + NRY REMTL VLD ++ +D YP + L+R++ +D + +N

Sbjct: 267 --YESWVNFNRYRREMTLTVDLIALFPLYDVRLYPKEVKTELTRDVLTDPIVGNN 321

>gi|143084|gb|AAA22542.1| (M30503) insect control protein [Bacillus thuringiensis]
Length = 644

Score = 56.2 bits (134), Expect = 1e-07
Identities = 37/117 (31%), Positives = 61/117 (51%), Gaps = 8/117 (6%)

Query: 2 HLTLLRDGALYGFSGW-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
HL LL+D +YG WG+ E+I + + Q+ T Y ++ K Y+ GL + ++
Sbjct: 204 HLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLT-QEYTDHCVKWNVGLDKLRGSS---- 258

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADN 117
E + NRY REMTL VLD ++ +D YP + L+R++ +D + +N
Sbjct: 259 --YESWVNFNRYRREMTLTVDLIALFPLYDVRLYPKEVKTELTRDVLTDPIVGVNN 313

>gi|117325|sp|P07130|C3AA_BACTT Pesticidal crystal protein cry3Aa precursor (Insecticidal delta-endotoxin CryIIIA(a)) (Crystalline entomocidal protoxin) (73 kDa crystal protein)
gi|2127277|pir|I39812 crystal protein cryC - Bacillus thuringiensis
gi|40253|emb|CAA68482.1| (Y00420) crystal protein (AA 1-644) [Bacillus thuringiensis]
gi|142736|gb|AAA50255.1| (M37207) crystal protein [Bacillus thuringiensis serovar morrisoni]
gi|143082|gb|AAA22541.1| (J02978) insecticidal crystal protein [Bacillus thuringiensis]
gi|514312|gb|AAC43266.1| (U10985) CryIIIA [Bacillus thuringiensis]
gi|225760|prf|1312401A insecticidal crystal protein [Bacillus thuringiensis]
gi|225866|prf|1402204A coleopteran specific protein [Bacillus thuringiensis]
Length = 644

Score = 56.2 bits (134), Expect = 1e-07
Identities = 37/117 (31%), Positives = 61/117 (51%), Gaps = 8/117 (6%)

Query: 2 HLTLLRDGALYGFSGW-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
HL LL+D +YG WG+ E+I + + Q+ T Y ++ K Y+ GL + ++
Sbjct: 204 HLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLT-QEYTDHCVKWNVGLDKLRGSS---- 258

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADN 117
E + NRY REMTL VLD ++ +D YP + L+R++ +D + +N
Sbjct: 259 --YESWVNFNRYRREMTLTVDLIALFPLYDVRLYPKEVKTELTRDVLTDPIVGVNN 313

>gi|117529|sp|P19415|C1DA_BACTA PESTICIDIAL CRYSTAL PROTEIN CRYIDA (INSECTICIDAL DELTA-ENDOTOXIN CRYID(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (132 KDA CRYSTAL PROTEIN)
gi|98534|pir|S11446 parasporal crystal protein cryID - Bacillus thuringiensis
gi|40280|emb|CAA38099.1| (X54160) cryID protein [Bacillus thuringiensis]
Length = 1165

Score = 55.5 bits (132), Expect = 2e-07
Identities = 34/132 (25%), Positives = 62/132 (46%), Gaps = 7/132 (5%)

Query: 1 MHLTLLRDGALYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL++LRD +++G WG++ + + I Y + TY+ GL+ +
Sbjct: 166 LHL SILRDVSVFGERWGYDTATINNRYSDLTSLIHVYTNHCVDTYNQGLRRLE-----G 219

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADN-SG 119
+ + NR+ R++T+ VLD + +D YP L+RE+Y D +N S
Sbjct: 220 RFLSDWIVYNRFRRLTISVLDIVAFFPNYDIRTYPIQTATQLTREYVLDLPFINENLSP 279

Query: 120 ALNFPQHPKRS 131
A ++P + S
Sbjct: 280 AASYPTFSAAES 291

>gi|19386614|dbj|BAB72016.2| (AB074413) insecticidal crystal protein bun2 [Bacillus thuringiensis]
Length = 660

Score = 54.3 bits (129), Expect = 5e-07
Identities = 34/112 (30%), Positives = 57/112 (50%), Gaps = 5/112 (4%)

Query: 1 MHLTLLRDGALYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL LLR+G +YG WG + +Q++ Y + Y++GL ++ +
Sbjct: 204 LHL LLLREGVYGSRWGIAPADFY-HDQLLKYTAIYANHCVTWYNNGLAQQKELFAKSP 262

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
++ N N Y R+MT+ VLD ++ +D Y P + L+REIYSD +

Sbjct: 263 NW----NRFNAYRRDMTITVLDIIALFPTYDARLYTKPIKTEL TREIYSDVL 310

>gi|8469146|sp|Q45746|C1GA_BACTU PESTICIDIAL CRYSTAL PROTEIN CRY1GA (INSECTICIDAL DELTA-ENDOTOXIN

CRYIG(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (132 KDA
CRYSTAL PROTEIN)

gi|421539|pir||S32645 parasporal crystal protein - Bacillus thuringiensis
gi|295862|emb|CAA80233.1| (Z22510) crystal protein [Bacillus thuringiensis]
Length = 1166

Score = 54.3 bits (129), Expect = 5e-07
Identities = 33/123 (26%), Positives = 60/123 (47%), Gaps = 14/123 (11%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL+LLRD +G WG + + ++ I Y ++ + Y+ GL + ++
Sbjct: 165 LHLSLLRDVAVYFGERWGLTQANIEDLYTRLTSNIQEYSDHRCARWYNQGLNEI---GGISR 221

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNSGA 120
Y + + R++T+ VLD ++ +D YP P + L+REIY+ V +G
Sbjct: 222 RYLD-----FQRLTISVLDIVALFPNYDIRTYPIPTQSQLTREIYTSPV----VAGN 270

Query: 121 LNF 123
+NF
Sbjct: 271 INF 273

>gi|8928011|sp|O86170|CJBA_BACUH Pesticidal crystal protein cry19Ba (Insecticidal delta-endotoxin

CryXIXB(a)) (Crystalline entomocidal protoxin) (78 kDa
crystal protein)

gi|3426160|dbj|BAA32397.1| (D88381) insecticidal protein [Bacillus thuringiensis]
Length = 682

Score = 53.9 bits (128), Expect = 6e-07
Identities = 41/118 (34%), Positives = 60/118 (50%), Gaps = 16/118 (13%)

Query: 1 MHLTLRLDGLYGFSGW-NEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSN 59
+HL LLRD A+YG G+ + +++ + EQ T Y Y TY GL+ ++ S+
Sbjct: 199 LLLLLLLRDVAIYGKELGYPSTDFEYFYNEQKYTT-EKYSNYCVNTYKSGLESKKQIGWSD 257

Query: 60 KHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTP-----AEVYLSREIYSDAV 112
NRY REMTL VLD ++ +D YP+ + L+REIYSD +
Sbjct: 258 -----FNRYRREMTLSVLDIVALFPLYDTGLYPSKDGKIHVKAELTREIYSDVI 306

>gi|8469161|sp|Q45744|C3CA_BACTK PESTICIDIAL CRYSTAL PROTEIN CRY3CA (INSECTICIDAL DELTA-ENDOTOXIN

CRYIIIC(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (73 KDA
CRYSTAL PROTEIN)

gi|80470|pir||JH0261 parasporal crystal protein cryIIID - Bacillus thuringiensis subsp.
kurstaki (strain BT1109P)
gi|40288|emb|CAA42469.1| (X59797) CryIIID [Bacillus thuringiensis]
Length = 649

Score = 53.9 bits (128), Expect = 6e-07
Identities = 33/116 (28%), Positives = 53/116 (45%), Gaps = 6/116 (5%)

Query: 2 HLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNKH 61
HL LL+D +YG WG++ + + D Y + K Y GL + +
Sbjct: 202 HLLLLKDAQIYGTDWGYSTDDLNEFHKTQKDLTIEYTNHCAKWKAGLDKLRGST----- 256

Query: 62 YTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADN 117
E + NRY REMTL VLD ++ +D Y + L+R++ +D + +N
Sbjct: 257 -YEEWVKFNRYRREMTLTVDLITLFLYDVRTYTKGVKTELTRDVLTDPIAVNN 311

>gi|9828610|gb|AAG00235.1|AF285775_1 (AF285775) parasporal inclusion protein Cry [Bacillus thuringiensis
serovar finitimus]
Length = 1128

Score = 53.5 bits (127), Expect = 8e-07

Identities = 37/127 (29%), Positives = 61/127 (47%), Gaps = 12/127 (9%)

Query: 1 MHLTLLRDGALYGFSWGWNEEQHTR-----EQIVDTIGSYIEYTEKTYSDGLQDTQK 54
+HL LL G + W ++ + +++ I YI Y KTY GL ++
Sbjct: 174 LHLNLLHQGVQFADQWNADQPHSPMLKSSGTYDELLVYIEKYINYCTKYHKGLNHLKE 233

Query: 55 NAPS NKHYTEPNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGT 114
S K + +NT Y REMTL VLD + ++D ++P E+ L+RE+Y+
Sbjct: 234 ---SEKITWDAYNT---YRREMTLIVLDLVATFPFYDIRRFPRGVELELTREYVTSLDPP 287

Query: 115 ADNSGAL 121
N+G +
Sbjct: 288 GLNAGPI 294

>gi|8469159|sp|Q45706|C8CA_BACTP PESTICIDIAL CRYSTAL PROTEIN CRY8CA (INSECTICIDAL DELTA-
ENDOTOXIN
CRYVIIIC(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (130 KDA
CRYSTAL PROTEIN)
gi|2127275|pir|I40589 cryIII delta-endotoxin - Bacillus thuringiensis
gi|532524|gb|AAA21119.1| (U04366) CryIII delta-endotoxin [Bacillus thuringiensis]
gi|1096647|prf|2112230A delta-endotoxin [Bacillus thuringiensis]
Length = 1160

Score = 53.5 bits (127), Expect = 1e-06
Identities = 35/115 (30%), Positives = 60/115 (51%), Gaps = 8/115 (6%)

Query: 1 MHLTLLRDGALYGFSWGWNE-EIQHTRREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS 59
+HL ++RD +YG WG+ + +I +EQ+ T Y ++ + Y+ GL +
Sbjct: 206 LHLVLRDQVQYIGKEWGYQNDIDLFYKEQVSYT-ARYSDHCVQWYNAGLNKLRTGA-- 262

Query: 60 KHYTEPNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGT 114
K + + NR+ REM + VLD ++ +D YP L+REI++D VG+
Sbjct: 263 KQWVD----YNRFRREMNMVLDLVALFPNYDARIYPLETNAELTREIFTDPVGS 313

>gi|8928018|sp|Q45704|C8AA_BACUK Pesticidal crystal protein cry8Aa (Insecticidal delta-
endotoxin
CryVIIIA(a)) (Crystalline entomocidal protoxin) (131 kDa
crystal protein)
gi|436833|gb|AAA21117.1| (U04364) CryIII delta-endotoxin [Bacillus thuringiensis]
Length = 1157

Score = 53.1 bits (126), Expect = 1e-06
Identities = 37/113 (32%), Positives = 57/113 (49%), Gaps = 8/113 (7%)

Query: 1 MHLTLLRDGALYGFSWGWNE-EIQHTRREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS 59
+HL LLRD +++G WG+ EI + Q V Y +Y K Y GL D K S
Sbjct: 205 LHLNLLRDASIFGEWGFTPGEISRFYNRQ-VQLTAEYSDYCVKWKIGL-DKLGKTT- 261

Query: 60 KHYTEPNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ + +++ REMTL VLD ++ +D YP L+R++Y+D +
Sbjct: 262 ---KSWLNHYQFRREMTLLVLDLVALFPNYDTHMYPIETTAQLTRDVYTDPI 310

>gi|17385646|dbj|BAB78601.1| (AB075460) crystal protein CryE6L [Bacillus thuringiensis]
Length = 1270

Score = 53.1 bits (126), Expect = 1e-06
Identities = 36/121 (29%), Positives = 54/121 (43%), Gaps = 10/121 (8%)

Query: 1 MHLTLLRDGALYGFSWGWNE-EIQHTRREQ-----IVDTIGSYIEYTEKTYSDGLQDT 52
+HL LL+D +G WG+ ++Q+ +V + Y Y+ G+++
Sbjct: 220 LHLNLLKDVVRFGVGVGFPPGRVEQYYSNPTNLGNPGMVQLLAKYTNYSTSLCWKGIEER 279

Query: 53 QKNAPS NKHYTEPNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ S Y Y MT+ VLD +W +DPVKYP V L+REIYS
Sbjct: 280 KWMVES--EYRSNNEEYAYRSNMTMMVLDLVALWPTYDPVKYPYATAVELTREIYSLIA 337

Query: 113 G 113
G
Sbjct: 338 G 338

>gi|8928040|sp|Q9X682|CSAA_BACTF Pesticidal crystal protein cry28Aa (Insecticidal delta-endotoxin
CryXXVIII(a)) (Crystalline entomocidal protoxin) (126
kDa crystal protein)
gi|4574730|gb|AAD24189.1|AF132928_1 (AF132928) Cry28Aa delta-endotoxin [Bacillus thuringiensis
serovar
finitimus]
Length = 1109

Score = 52.8 bits (125), Expect = 1e-06
Identities = 35/115 (30%), Positives = 57/115 (49%), Gaps = 12/115 (10%)

Query: 1 MHLTLLRDGALYGFSGWNEEIQQHTR-----EQIVDTIGSYIEYTEKTYSDGLQDTQK 54
+HL LL G + W ++ + +++++ I YI Y KTY GL ++
Sbjct: 174 LHLNLLHQGVQFADQWNADQPHSPMLKSSGTYDELLVYIEKYINYCTKTYHKGLNHLKE 233
Query: 55 NAPS NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYS 109
S K + +NT Y REMTL VLD + ++D ++P E+ L+RE+Y+
Sbjct: 234 ---SEKITWDAYNT---YRREMTLIVLDLVATFPFYDIRRFRPGVELELTREYVT 282

>gi|17385648|dbj|BAB78602.1| (AB075461) crystal protein CryE6Q [Bacillus thuringiensis]
Length = 1254

Score = 52.0 bits (123), Expect = 2e-06
Identities = 43/140 (30%), Positives = 61/140 (42%), Gaps = 31/140 (22%)

Query: 2 HLTLLRDGALYGFSGWNEEI-----QQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNA 56
HL LL+ G +YG WG+++ Q E + + + Y +Y Y GL + KN
Sbjct: 207 HLMLLQQGVMYGVRWGFQDQRTVDSFYQNDREGELKNLLPKYSDYCTYWDQGL-NRAKNL 265
Query: 57 PSNKHYT-----EPFNTVNRYVREMTLDVLDKDMW-----QYFDPV 93
+N T E +N N Y R+MT+ VLD +W Y+D
Sbjct: 266 KANLSDTVRYPWAAENLENMSVLQELEWDNLYNDYRRDMTILVLDLVAVWPTYDLHYDNG 325
Query: 94 KYPTPAEVYLSREIYSDAVG 113
Y +E L+R IYS AVG
Sbjct: 326 NYGVQSE--LTRSIYSQAVG 343

>gi|8469148|sp|Q45748|C1HA_BACTU PESTICIDIAL CRYSTAL PROTEIN CRY1HA (INSECTICIDAL DELTA-ENDOTOXIN
CRYIH(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (133 KDA
CRYSTAL PROTEIN)
gi|421542|pir||S32689 parasporal crystal protein - Bacillus thuringiensis
gi|296087|emb|CAA80236.1| (Z22513) crystal protein [Bacillus thuringiensis]
Length = 1172

Score = 52.0 bits (123), Expect = 3e-06
Identities = 36/134 (26%), Positives = 65/134 (47%), Gaps = 21/134 (15%)

Query: 1 MHLTLLRDGALYGFSGWNEEIQQHTRREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL+LLRD +G WG + + +++++ I +Y ++ + ++ GL +
Sbjct: 169 LHLSSLRDAVYFGQRWGLDVTVNHNHYNRLINLINTYSDHCAQWFNRGLDN----- 219
Query: 61 HYTEPFNTVN-RYV---REMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV---G 113
F V+ RY+ RE+T+ VLD ++ +D YP + L+REIY+ V G
Sbjct: 220 -----FGGVSARYLDFQREVTISVLDIVALFPNYDIRTYPISTQSQTREIYTSPVAEPG 274
Query: 114 TADNSGALNFPQHP 127
+ N+ N + P
Sbjct: 275 ASLNANLQNILREP 288

>gi|80469|pir||B29838 parasporal crystal protein - Bacillus thuringiensis subsp.
israelensis (fragment)
Length = 934

Score = 50.8 bits (120), Expect = 5e-06
Identities = 37/116 (31%), Positives = 54/116 (45%), Gaps = 13/116 (11%)

Query: 2 HLTLLRDGALYGFSWGWNEEIQQHT-----REQIVDTIGSYIEYTEKTYSDGLQDTQK 54
HL LL+ A Y W N+ I T + + I Y +Y +TY+ GL +
Sbjct: 210 HLNLLKHAATYYNIWLQNQGINPSTFNSSNYYQGYLKRKIQEYTDYCIQTYNAGLTMIRT 269

Query: 55 NAPS NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSD 110
N + +N N Y EMTL VLD ++ +DP KYP + L RE+Y++
Sbjct: 270 NTNAT-----WNMYNTYRLEMTLTVLDLIAIFPNYDPEKYPIGVKSELIREVYTN 319

>gi|117329|sp|P09662|CAAA_BACTI PESTICIDIAL CRYSTAL PROTEIN CRY10AA (INSECTICIDAL DELTA-
ENDOTOXIN

CRYXA(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (78 KDA
CRYSTAL PROTEIN)
gi|143229|gb|AAA22614.1| (M12662) insecticidal endotoxin (put.); putative [Bacillus
thuringiensis]
Length = 675

Score = 50.8 bits (120), Expect = 6e-06
Identities = 37/116 (31%), Positives = 54/116 (45%), Gaps = 13/116 (11%)

Query: 2 HLTLLRDGALYGFSWGWNEEIQQHT-----REQIVDTIGSYIEYTEKTYSDGLQDTQK 54
HL LL+ A Y W N+ I T + + I Y +Y +TY+ GL +
Sbjct: 210 HLNLLKHAATYYNIWLQNQGINPSTFNSSNYYQGYLKRKIQEYTDYCIQTYNAGLTMIRT 269

Query: 55 NAPS NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSD 110
N + +N N Y EMTL VLD ++ +DP KYP + L RE+Y++
Sbjct: 270 NTNAT-----WNMYNTYRLEMTLTVLDLIAIFPNYDPEKYPIGVKSELIREVYTN 319

>gi|10719937|sp|Q45882|CGAA_CLOBI Pesticidal crystal-like protein cryl6Aa (Insecticidal toxin
CryXVIA(a)) (Cbm71 mosquitocidal toxin)
gi|2127309|pir||JC6033 mosquitocidal protein Cbm71 - Clostridium bifermentans
gi|1246432|emb|CAA63860.1| (X94146) cbm71 mosquitocidal toxin [Clostridium bifermentans]
Length = 613

Score = 50.4 bits (119), Expect = 8e-06
Identities = 37/123 (30%), Positives = 58/123 (47%), Gaps = 11/123 (8%)

Query: 1 MHLTLLRDGALYGFSWGWNEEI----QQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNA 56
+HL LLRDG +YG +W E+ Q ++D YI Y+ GL + + +
Sbjct: 155 LHLLLRDGMIYGDawnLYRELGFSDQDSFYNHVLDKTKFYINDCLNYYNTGLSNLKLd- 213

Query: 57 PSNKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVY-LSREIYSDAVGTA 115
P+N + + RY R MT +LD + +D Y P + L+R++YSD V
Sbjct: 214 PNNS-----WIDITRYCRFMTFYILDMISICPIYDVKYDPINMQTLTRKVYSDPVNFI 268

Query: 116 DNS 118
D +
Sbjct: 269 DEN 271

>gi|117324|sp|P17969|C3BA_BACTO PESTICIDIAL CRYSTAL PROTEIN CRY3BA (INSECTICIDAL DELTA-ENDOTOXIN
CRYIIIIB(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (75 KDA
CRYSTAL PROTEIN)

gi|98537|pir||S10228 parasporal crystal protein, coleopteran-active - Bacillus
thuringiensis (fragment)
gi|40259|emb|CAA34983.1| (X17123) coleopteran-active delta-endotoxin open reading frame
(659 AA) [Bacillus thuringiensis]
Length = 659

Score = 50.1 bits (118), Expect = 1e-05
Identities = 30/113 (26%), Positives = 56/113 (49%), Gaps = 6/113 (5%)

Query: 2 HLTLLRDGALYGFSWGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NKH 61
HL LL+D ++G WG++ E ++ + Y ++ Y+ GL + +
Sbjct: 213 HLLLLKDAQVFGEEWGYSSEDIAEFYQRQLKLTQQYTDHCVNWNVGLNSLRGST----- 267

Query: 62 YTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGT 114
+ + NR+ REMTL VLD ++ ++D Y + L+R+I++D + T
Sbjct: 268 -YDAWVKFNRFREMTLTVLDLIVLFPFYDVRLYSKGVKTELTRDIFTDPIFT 319

>gi|8469142|sp|Q45716|C1JB_BACTU Pesticidal crystal protein cry1Jb (Insecticidal delta-endotoxin

CryIJ(b)) (Crystalline entomocidal protoxin) (134 kDa
crystal protein)
Length = 1170

Score = 49.7 bits (117), Expect = 1e-05
Identities = 35/114 (30%), Positives = 53/114 (45%), Gaps = 10/114 (8%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL LLRD ++G WG T + D ++ + YSD DT K
Sbjct: 166 LHLALLRDSVIFGERWGL-----TTTNVNDIYNRQVKRIHE-YSDHCVDTYKTELERL 217

Query: 61 HYTE--PFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+T + N++ RE+TL VLD ++ +D YP + L+REIY+ V
Sbjct: 218 GFTSRAQWKIYNQFRRELTTLVLDIVAVFPNYDGKLYPIQTKSELTREIYTSVPV 271

>gi|8469143|sp|Q45718|C1HB_BACTM Pesticidal crystal protein cry1Hb (Insecticidal delta-endotoxin

CryIH(b)) (Crystalline entomocidal protoxin) (131 kDa
crystal protein)
gi|1022728|gb|AAA79694.1| (U35780) crystal toxin [Bacillus thuringiensis]
Length = 1155

Score = 49.7 bits (117), Expect = 1e-05
Identities = 35/126 (27%), Positives = 61/126 (47%), Gaps = 20/126 (15%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNK 60
+HL+LLRD +G WG + + ++++ I +Y ++ + ++ GL +
Sbjct: 168 LHLALLRDAVYFGQRWGLDTATVNNHYNRLINLINTYSDHCAQWFNRGLDN----- 218

Query: 61 HYTEPFNTVN-RYV---REMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTAD 116
F V RY+ RE+T+ VLD ++ +D YP L+REIY+ V A+
Sbjct: 219 -----FGVVTARYLDFQREVTISVLDIVALFPNYDIRTYPIQTLSQLTREIYTSVPV--AE 271

Query: 117 NSGALN 122
+LN
Sbjct: 272 PGASLN 277

>gi|940200|gb|AAA74198.1| (U31633) Cry3Bb2 [Bacillus thuringiensis]
Length = 652

Score = 48.5 bits (114), Expect = 3e-05
Identities = 29/111 (26%), Positives = 54/111 (48%), Gaps = 6/111 (5%)

Query: 2 HLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNKH 61
HL LL+D ++G WG++ E + + Y ++ Y+ GL + +
Sbjct: 205 HLLLLKDAQVFGEWGYSSDVAEFYHRQLKLTQQYTDHCVNWNVGLNGLRGST----- 259

Query: 62 YTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ + NR+ REMTL VLD ++ ++D Y + L+R+I++D +
Sbjct: 260 -YDAWVKFNRFREMTLTVDLIVLFPFYDVRLYSGVKTELTRDIFTDPI 309

>gi|15988322|pdb|1JI6|A Chain A, Crystal Structure Of The Insecticidal Bacterial Del
Endotoxin Cry3bb1 Bacillus Thuringiensis
Length = 589

Score = 48.5 bits (114), Expect = 3e-05
Identities = 29/111 (26%), Positives = 54/111 (48%), Gaps = 6/111 (5%)

Query: 2 HLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNKH 61
HL LL+D ++G WG++ E + + Y ++ Y+ GL + +
Sbjct: 142 HLLLLKDAQVFGEWGYSSDVAEFYHRQLKLTQQYTDHCVNWNVGLNGLRGST----- 196

Query: 62 YTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ + NR+ REMTL VLD ++ ++D Y + L+R+I++D +
Sbjct: 197 -YDAWVKFNRFREMTLTVDLIVLFPFYDIRLYSGVKTELTRDIFTDPI 246

>gi|8469155|sp|Q06117|C3BB_BACTU Pesticidal crystal protein cry3Bb (Insecticidal delta-endotoxin

CryIIIB(b)) (Crystalline entomocidal protoxin) (74 kDa
crystal protein)

gi|2127279|pir||I39811 gene cryIIIB2 protein - Bacillus thuringiensis
gi|142730|gb|AAA22334.1| (M89794) cryIIIB2 [Bacillus thuringiensis]
Length = 652

Score = 48.1 bits (113), Expect = 3e-05
Identities = 29/111 (26%), Positives = 54/111 (48%), Gaps = 6/111 (5%)

Query: 2 HLTLLRDGALYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NKH 61
HL LL+D ++G WG++ E + + Y ++ Y+ GL + +
Sbjct: 205 HLLLLKDAQVFGEWGYSSDVAEFYHRQLKLTQQYTDHCVNWNVGLNGLRGST----- 259

Query: 62 YTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ + NR+ REMTL VLD ++ ++D Y + L+R+I++D +
Sbjct: 260 -YDAWVKFNRRREMTLTVLDLIVLFFPYDIRLYSKGVKTELTRDIFTDPI 309

>gi|1669651|emb|CAA70506.1| (Y09326) delta-endotoxin [Bacillus thuringiensis]
Length = 1173

Score = 48.1 bits (113), Expect = 4e-05
Identities = 33/124 (26%), Positives = 59/124 (46%), Gaps = 15/124 (12%)

Query: 1 MHLTLLRDGALYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NK 60
+HL+LLRD +G WG + + ++ I Y ++ + Y+ GL + ++
Sbjct: 165 LHLSSLRDVAVYFGERWGLTQANIEDLYTRLTSNIQEYSDHRCARWYNQGLNEI---GGISR 221

Query: 61 HYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNSG 119
Y + + R++T+ VLD + +D YP P + L+REIY+ V +G
Sbjct: 222 RYLD-----FQDLTISVLDIVAPFSPNYDIRTYPIPTQSQLTREIYTSPV----VAG 270

Query: 120 ALNF 123
+NF
Sbjct: 271 NINF 274

>gi|8928014|sp|P56956|CLAA_BACTU Pesticidal crystal protein cry21Aa (Insecticidal delta-endotoxin

CryXXIA(a)) (Crystalline entomocidal protoxin) (132 kDa
crystal protein)
Length = 1167

Score = 47.4 bits (111), Expect = 7e-05
Identities = 26/59 (44%), Positives = 32/59 (54%), Gaps = 5/59 (8%)

Query: 57 PSNKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYL--SREIYSDAVG 113
PSNK E N NRYVR MTL LD W D V YP+ ++ L +R ++SD G
Sbjct: 296 PSNK---ESVNKYNRYVRSMTLQSLDIAATWPTLDNVNYPNSNVDIQLDQTRLVFSVDVAG 351

>gi|8928013|sp|O87906|CPAA_BACTJ Pesticidal crystal protein cry25Aa (Insecticidal delta-endotoxin

CryXXVA(a)) (Crystalline entomocidal protoxin) (76 kDa
crystal protein) (Insecticidal protein Jeg74)

gi|3668335|gb|AAC61892.1| (U88189) insecticidal protein Jeg74 [Bacillus thuringiensis serovar
jegathesan]
Length = 675

Score = 46.6 bits (109), Expect = 1e-04
Identities = 27/84 (32%), Positives = 40/84 (47%), Gaps = 4/84 (4%)

Query: 34 IGSYIEYTEKTYSDGLQDTQKNAPS NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPV 93
I Y ++ Y DGL + + + E N++ REMTL VLD ++ +
Sbjct: 242 IKKYTDHCISYDDGLAKIRSRGSDGETWWE----FNKFRREMTLTVLDLVALYPTHNIK 297

Query: 94 KYPTPAEVYLSREIYSDAVGTADN 117
YP P + LSR +Y+D VG N
Sbjct: 298 LYPIPTQTELSRVVYTDVPVGCFCN 321

>gi|8488969|sp|P05519|C4BA_BACTI PESTICIDIAL CRYSTAL PROTEIN CRY4BA (INSECTICIDAL DELTA-ENDOTOXIN

CRYIVB(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (128 KDA
CRYSTAL PROTEIN)

gi|72769|pir||USBS8I parasporal crystal protein Bt8 - Bacillus thuringiensis subsp.
israelensis
gi|40354|emb|CAA30312.1| (X07423) Bt8 endotoxin (AA 1 - 1136) [Bacillus thuringiensis]
Length = 1136

Score = 46.2 bits (108), Expect = 1e-04
Identities = 35/118 (29%), Positives = 53/118 (44%), Gaps = 13/118 (11%)

Query: 2 HLTLLRDGALYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NKH 61
+L L+RDG + W +V YI ++ Y+ GL D +N SN
Sbjct: 185 NLLLRDGLINAQEWLSARSAGDQLYNTMVQYTKYIAHSITWYNKGL-DVLRNK-SNGQ 242

Query: 62 YTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTP-----AEVYLSREIYSDAV 112
+ T N Y REMT+ VLD ++ +DP +YP ++ +REIY+ V
Sbjct: 243 WI----TFNDYKREMTIQVLDILALFASYDPRYPADKIDNTKLSKTEFTREIYTALV 296

>gi|8927981|sp|O87404|C1IC_BACTU Pesticidal crystal protein cryIIc (Insecticidal delta-endotoxin

CryII(c)) (Crystalline entomocidal protoxin) (81 kDa
crystal protein)

gi|3702807|gb|AAC62933.1| (AF056933) crystal protein toxin [Bacillus thuringiensis]
Length = 719

Score = 46.2 bits (108), Expect = 1e-04
Identities = 37/123 (30%), Positives = 62/123 (50%), Gaps = 10/123 (8%)

Query: 1 MHLTLLRDGALYGFSGWNE-EIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQ-KNAPS 58
+HL LLRD +++ + G + EI Q V+ Y + K + GL + + N S
Sbjct: 195 LHLLLLRDASIFEKNGGLSASEISTFYNRQ-VERTRDYSYHCVKWNNTGLNNLRATNGQS 253

Query: 59 NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNS 118
Y N++ +++ L VLD ++ +D + YP L+RE+Y+DA+GT D +
Sbjct: 254 WVRV-----NQFRKDIELMVLDLVRVFPSTYDLVYPIKTTSQLTREVTDAIGTVDPN 306

Query: 119 GAL 121
AL
Sbjct: 307 QAL 309

>gi|40310|emb|CAA30114.1| (X07082) delta-endotoxin (AA 1 - 1136) [Bacillus thuringiensis]
Length = 1136

Score = 45.8 bits (107), Expect = 2e-04
Identities = 35/118 (29%), Positives = 53/118 (44%), Gaps = 13/118 (11%)

Query: 2 HLTLLRDGALYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPS NKH 61
+L L+RDG + W +V YI ++ Y+ GL D +N SN
Sbjct: 185 NLLLRDGLINAQEWLSARSRGDQLYNTMVQYTKYIAHSITWYNKGL-DVLRNK-SNGQ 242

Query: 62 YTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTP-----AEVYLSREIYSDAV 112
+ T N Y REMT+ VLD ++ +DP +YP ++ +REIY+ V
Sbjct: 243 WI----TFNDYKREMTIQVLDILALFASYDPRYPADKIDNTKLSKTEFTREIYTALV 296

>gi|629164|pir||S39536 parasporal crystal protein-related protein - Bacillus thuringiensis
Length = 1154

Score = 45.4 bits (106), Expect = 2e-04
Identities = 37/144 (25%), Positives = 63/144 (43%), Gaps = 27/144 (18%)

Query: 1 MHLTLLRDGALYGFSGWNE-----EIQQHTREQIVDTIGSYIEYTEKTYSDGLQD 51
+HL LL D YG WGL E E+Q TR+ Y + Y++GL
Sbjct: 194 LHLLLLADAKEYGARWGLRESQIGNLYFNLQTRTRD-----YTNHCVNAYNNGLAG 245

Query: 52 TQKNAPS NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDA 111
+ + E + ++ RE TL +D ++ Y++ +YP L+RE+Y+D
Sbjct: 246 LRGT-----AESWLKYHQFRREATLMAMDIALFPYNTRRYPIAVNPQLTREVTDP 299

Query: 112 VGTADNSGALNFPQHPKRSRSQKWK 135
+G +L P+ R +W+
Sbjct: 300 LGVPSEESSL----FPELRCLRWQ 319

>gi|1334252|emb|CAA52927.1| (X75019) delta-endotoxin [Bacillus thuringiensis]
Length = 1144

Score = 45.4 bits (106), Expect = 2e-04
Identities = 37/144 (25%), Positives = 63/144 (43%), Gaps = 27/144 (18%)

Query: 1 MHLTLLRDGALYGFSGWNE-----EIQQHTREQIVDTIGSYIEYTEKTSYDGLQD 51
+HL LL D YG WG E E+Q TR+ Y + Y++GL
Sbjct: 184 LHLALLADAKEYGARWGLRESQIGNLYFNEQLTRTRD-----YTNHCVNAYNNGLAG 235

Query: 52 TQKNAPSNNKHYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDA 111
+ + E + +++ RE TL +D ++ Y++ +YP L+RE+Y+D
Sbjct: 236 LRGS-----AESWLKYHQFRREATLMAMDIALFPYNTTRYPIAVNPQLTREYVYTD 289

Query: 112 VGTADNSGALNFPQHPKRSRSQKWK 135
+G +L P+ R +W+
Sbjct: 290 LGVPSEESSL----FPELRCLRWQ 309

>gi|8469144|sp|Q45738|C1JA_BACTU PESTICIDIAL CRYSTAL PROTEIN CRY1JA (INSECTICIDAL DELTA-ENDOTOXIN
CRYIJ(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (133 KDA
CRYSTAL PROTEIN)
gi|474892|gb|AAA22341.1| (L32019) crystal protein [Bacillus thuringiensis]
Length = 1167

Score = 45.1 bits (105), Expect = 3e-04
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 6/112 (5%)

Query: 1 MHLTLLRDGALYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTSYDGLQDTQKNAPSNNK 60
+HL LLRD ++G WG + + + I Y + TY+ L+ + +
Sbjct: 166 LHLALLRDSVIFGERWGLTTKNVNDIYNRQIREIHEYSNHCVDYNTLEERLGRSIAQ- 224

Query: 61 HYTEPFNTVNRYVREMTLDVDFKDMWQYFDPVKYPTPAEVYLSREIYSDAV 112
+ N++ RE+TL VLD ++ +D YP L+REI + V
Sbjct: 225 -----WRIYNQFRRELTLTVLDIVLFPNYDSRLYPITQFSQLTREIVTSPV 271

>gi|117544|sp|P16480|C4AA_BACTI PESTICIDIAL CRYSTAL PROTEIN CRY4AA (INSECTICIDAL DELTA-ENDOTOXIN
CRYIVA(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (135 KDA
CRYSTAL PROTEIN)
gi|2119863|pir||I39870 insecticidal protein ISRH4 - Bacillus thuringiensis
gi|216290|dbj|BAA00179.1| (D00248) 130 kDa insecticidal protein (ISRH4) [Bacillus
thuringiensis serovar israelensis]
gi|225983|prf||1405201B insecticidal protein ISRH4 [Bacillus thuringiensis]
Length = 1180

Score = 44.7 bits (104), Expect = 4e-04
Identities = 31/98 (31%), Positives = 41/98 (41%), Gaps = 10/98 (10%)

Query: 30 IVDTIGSYIEYTEKTSYDGLQDTQKNAPSNNKHYTEPFNTVNRYVREMTLDVDFKDMWQY 89
+ I Y Y TY GL + SN +NT N Y +MT VLD ++
Sbjct: 253 LTKAIEDYTNVCVTTYKKGLNLIKTTTPDSNLDGNINWNTYNTYRTKMTTAVLDLVALFPN 312

Query: 90 FDPVKYPTPAEVYLSREIYSDAVGTADNSGALNFPQHP 127
+D KYP + L+REIY LNF + P
Sbjct: 313 YDVGKYPIGVQSELTREIYQ-----VLNFEESP 340

>gi|8928021|sp|Q45712|C5BA_BACTU Pesticidal crystal protein cry5Ba (Insecticidal delta-endotoxin
CryVB(a)) (Crystaline entomocidal protoxin) (140 kDa
crystal protein)
gi|7475985|pir||T18211 delta endotoxin - Bacillus thuringiensis (fragment)
gi|862637|gb|AAA68598.1| (U19725) delta endotoxin [Bacillus thuringiensis]
Length = 1245

Score = 44.3 bits (103), Expect = 5e-04
Identities = 32/114 (28%), Positives = 49/114 (42%), Gaps = 7/114 (6%)

Query: 1 MHLTLRLDGLYGFSGW-NNEIIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSN 59
+HL L + W + NE+ + + + I SY E ++ L + S+
Sbjct: 242 LHLLLYEGYIEFMTKWNFHNEQYLNNLKVELQQLIHSYSETVRTSLQFLPTLNNRSKSS 301

Query: 60 KHYTEPFNTVNRVYREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVG 113
N NRYVR MT++ LD W FD Y ++ L+R I SD G
Sbjct: 302 -----VNAYNRYVRNMTVNCLDIAATWPTFDTHNYHQGGKLDLTRIILSDTAG 349

>gi|80463|pir||A26858 130K delta-endotoxin - Bacillus thuringiensis subsp. israelensis
gi|40352|emb|CAA68485.1| (Y00423) endotoxin (AA 1-1180) [Bacillus thuringiensis]
Length = 1180

Score = 44.3 bits (103), Expect = 5e-04
Identities = 31/98 (31%), Positives = 41/98 (41%), Gaps = 10/98 (10%)

Query: 30 IVDTIGSYIEYTEKTYSDGLQDTQKNAPSNKHYTEPFNTVNRVYREMTLDVLDKDMWQY 89
+ I Y Y TY GL + SN +NT N Y +MT VLD ++
Sbjct: 253 LTKAIEDYTYNCVTTYKKGLNLIKTTPDSNLDGNINWNTYNTYRTKMTTAVLDVVALFPN 312

Query: 90 FDPVKYPTPAEVYLSREIYSDAVGTADNSGALNFPQHP 127
+D KYP + L+REIY LNF + P
Sbjct: 313 YDVGKYPIGVQSELTREIYQ-----VLNFEESP 340

>gi|8928024|sp|Q45754|CCAA_BACTU Pesticidal crystal protein cry12Aa (Insecticidal delta-endotoxin
CryXIIA(a)) (Crystalline entomocidal protoxin) (142 kDa
crystal protein)
gi|142772|gb|AAA22355.1| (L07027) delta-endotoxin [Bacillus thuringiensis]
Length = 1257

Score = 43.1 bits (100), Expect = 0.001
Identities = 32/108 (29%), Positives = 51/108 (46%), Gaps = 6/108 (5%)

Query: 2 HLTLRLDGLYGFSGWNEEIIQQHTREQIVDTIGSYIEYTEKTYSDGLQDTQKNAPSNKH 61
H+ LLRD + G++++ ++ I TI ++ E K + +GL D K+ N
Sbjct: 200 HILLRLDAIVNAEKLGFSDKEVDTHKKYIKMTIHNHTEAVIKAFNLGL-DKFKSLDVNS- 257

Query: 62 YTEPFNTVNRVYREMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYS 109
+N Y++ MT VLD +W FDP Y E+ +R I S
Sbjct: 258 ----YNNKANYIKGTEMVLDLVALWPTFDPDHYQKEVEIEFTRTISS 301

>gi|8927987|sp|P56955|C5AC_BACTU Pesticidal crystal protein cry5Ac (Insecticidal delta-endotoxin
CryVA(c)) (Crystalline entomocidal protoxin) (135 kDa
crystal protein)
Length = 1220

Score = 42.0 bits (97), Expect = 0.002
Identities = 54/201 (26%), Positives = 79/201 (38%), Gaps = 36/201 (17%)

Query: 1 MHLTLRLDGLYGFSGWNEEIIQQHTREQIVDTIGSYIEYTEKTYSDGLQD--TQKNAPS 58
MHL LLRD G +W + I + I+ KT D Q PS
Sbjct: 222 MHLMLLRDIITKGPTWDSKINFPTDAIDSFKTDIKNNIKLYSKTIYDVVFQKGLASYGTPS 281

Query: 59 NKHYTEPFNTVNRVYREMTLDVLDKDMWQYFDPVKYPTPA---EVYLSREIYSD--AVG 113
+ E F +Y+ MT LDF ++ FDP YPT + + +R I S +
Sbjct: 282 D---LESFAKKKKYIEIMTTHCLDFARLFPTFDPDLYPTGSGDISLQKTRRILSPFIPR 338

Query: 114 TAD----NSGAL---NFPQH-----PKSRSQK-----WKS GPGTGLMPVRLTR 150
TAD N+ ++ N+P + PK R K W++G GL+ L
Sbjct: 339 TADGLTLNNTSIDTSNWPNYENGNGAFPNPKERILKQFKLYPSWRAGQYGGLLQPYLWAI 398

Query: 151 TTEGQYLRKHYGKKNLMPGVD 171
+ + YG+ +P VD
Sbjct: 399 EVQDSVETRLYGQ---LPAVD 416

>gi|8469135|sp|P96315|C1AF_BACTU Pesticidal crystal protein cry1Af (Insecticidal delta-endotoxin

CryIA(f)) (Crystalline entomocidal protoxin)
gi|1850365|gb|AAB82749.1| (U82003) insecticidal crystal protein [Bacillus thuringiensis]
Length = 911

Score = 41.6 bits (96), Expect = 0.003
Identities = 24/79 (30%), Positives = 42/79 (52%), Gaps = 6/79 (7%)

Query: 34 IGSYIEYTEKTYSDGLQDTQKNAPSNKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPV 93
IG+Y ++ + Y+ GL+ P ++ + N++ RE+TL VLD ++ +D
Sbjct: 197 IGNYTDHAVRWYNTGLERVW--GPDSRDWIR----YNQFRRELTTLVLDIVSLFPNYDSR 250

Query: 94 KYPTPAEVYLSREIYSDAV 112
YP L+REIY++ V
Sbjct: 251 TYPIRTVSQLTREIYTNPV 269

>gi|8927991|sp|Q45760|C5AA_BACUD Pesticidal crystal protein cry5Aa (Insecticidal delta-endotoxin

CryVA(a)) (Crystalline entomocidal protoxin) (152 kDa
crystal protein)
gi|7475987|pir||T18213 delta-endotoxin - Bacillus thuringiensis (fragment)
gi|142869|gb|AAA67694.1| (L07025) delta-endotoxin [Bacillus thuringiensis]
Length = 1385

Score = 41.2 bits (95), Expect = 0.004
Identities = 54/201 (26%), Positives = 79/201 (38%), Gaps = 36/201 (17%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQHTREQIVDTIGSYIEYTEKTYSDGLQD--TQKNAPS 58
MHL LLRD G +W + I + I+ KT D Q PS
Sbjct: 222 MHLMLLRDIITKGPTWDSKINFPTDAIDSFKTDIKNNIKLYSKTIYDVFQKGLASYGTPS 281

Query: 59 NKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPA---EVYLSREIYSD--AVG 113
+ E F +Y+ MT LDF ++ FDP YPT + + +R I S +
Sbjct: 282 D---LESFAKKQKYIEIMTTHCLDFARLFPTFDPDLYPTGSGDISLQKTRRILSPFIPIR 338

Query: 114 TAD----NSGAL---NFPQH-----PKSRSQK-----WKSQPGTGLMPVRLTR 150
TAD N+ ++ N+P + PK R K W++G GL+ L
Sbjct: 339 TADGLTLNNTSIDTSNWPNYENGNGAFNPKEKILKQFKLYPSWRAGQYGGLLPYLWAI 398

Query: 151 TTEGQYLRKHGKKNLMPGVD 171
+ + YG+ +P VD
Sbjct: 399 EVQDSVETRLYGQ---LPAMD 416

>gi|8928030|sp|Q9S597|CRAA_BACUH Pesticidal crystal protein cry27Aa (Insecticidal delta-endotoxin

CryXXVIIA(a)) (Crystalline entomocidal protoxin) (94 kDa
crystal protein)
gi|5689049|dbj|BAA82796.1| (AB023293) 94kDa mosquitocidal toxin [Bacillus thuringiensis]
Length = 826

Score = 40.8 bits (94), Expect = 0.005
Identities = 36/118 (30%), Positives = 51/118 (42%), Gaps = 18/118 (15%)

Query: 1 MHLTLRLDGLYGFSGWNEEIQQ-----HTREQIVDTIGSYIEYTEKTYSDGLQDTQKN 55
+HL LLR+G Y W + H +E +D YI + Y++G + N
Sbjct: 219 LHLILLREGIAYADQWNLARDPMHAAGDLHYKE-FLDYRNQYINHCSTWYNeg--QNEAN 275

Query: 56 APSNKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEV-YLSREIYSDAV 112
+N Y R MTL VLD M+ +DP Y P + L+R IY+D V
Sbjct: 276 LKNNGLV-----YQRTMTLFVLDLIAMFSTYDPRLYTMPIKTEILTRTIYTDGV 324

>gi|8927990|sp|Q45753|C5AB_BACUD Pesticidal crystal protein cry5Ab (Insecticidal delta-endotoxin

CryVA(b)) (Crystalline entomocidal protoxin) (142 kDa
crystal protein)
gi|7475986|pir||T18212 delta-endotoxin - Bacillus thuringiensis (fragment)
gi|142770|gb|AAA67693.1| (L07026) delta-endotoxin [Bacillus thuringiensis]
Length = 1289

Query: 57 PSNKHYTEPFNTVNRYVREMTLDVLDKDMWQYFDPVKYPTPAEV-YLSREIYSDAV 112
+ Y N+Y +T VLD ++ +DP Y V L+R++Y+D +
Sbjct: 271 ANWLEY-----NQYRTFLTASVLDVISLFSSYDPRLYKERLSVEILTRKLYTDPI 320

>gi|2367611|gb|AAC53328.1| (AF016181) putative pheromone receptor [Rattus norvegicus]
Length = 866

Score = 31.6 bits (70), Expect = 3.3
Identities = 16/52 (30%), Positives = 27/52 (51%)

Query: 74 REMTLDVLDKDMWQYFDPVKYPTPAEVYLSREIYSDAVGTADNSGALNFPQ 125
+ MT +L F +W F PV + T +V ++ EI+S +A G + P+
Sbjct: 788 KSMTFMSLVFCSVWVTFLPVYHGKTKGKVMVAVEIFSTLASSAGMLGCI FAPK 839

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: Apr 29, 2002 3:56 AM
Number of letters in database: 290,391,215
Number of sequences in database: 925,521

Lambda	K	H
0.315	0.134	0.412

Gapped Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 113,935,926
Number of Sequences: 925521
Number of extensions: 4929458
Number of successful extensions: 7397
Number of sequences better than 10.0: 171
Number of HSP's better than 10.0 without gapping: 153
Number of HSP's successfully gapped in prelim test: 18
Number of HSP's that attempted gapping in prelim test: 7100
Number of HSP's gapped (non-prelim): 176
length of query: 171
length of database: 290,391,215
effective HSP length: 112
effective length of query: 59
effective length of database: 186,732,863
effective search space: 11017238917
effective search space used: 11017238917
T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 42 (22.0 bits)
S2: 67 (30.4 bits)

FIGURE 4: Blastp results of accession CAA98839.1 against the NCBI Protein nr database.

BLASTP 2.2.3 [Apr-24-2002]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, 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.

RID: 1020211532-024818-31972

Query=

(658 letters)

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF

925,521 sequences; 290,391,215 total letters

If you have any problems or questions with the results of this search
please refer to the BLAST FAQs

Taxonomy reports

Sequences producing significant alignments:	Score (bits)	E Value
gi 6320220 ref NP_010300.1 (NC_001136) Shows homology to b...	1158	0.0
gi 1903296 emb CAA98839.1 (Z74314) ORF YDR017c [Saccharomy...	1093	0.0
gi 19075347 ref NP_587847.1 (NC_003421) putative b-zip tra...	114	4e-24
gi 18376053 emb CAD21059.1 (AL669986) related to transcrip...	79	2e-13
gi 14736134 ref XP_030060.1 (XM_030060) mammalian inositol...	58	3e-07
gi 7305195 ref NP_038813.1 (NM_013785) inositol hexaphosph...	58	3e-07
gi 6683115 dbj BAA13393.2 (D87452) KIAA0263 protein [Homo ...	58	3e-07
gi 7705553 ref NP_057375.1 (NM_016291) mammalian inositol ...	58	3e-07
gi 15277917 gb AAH12944.1 AAH12944 (BC012944) Unknown (prot...	58	4e-07
gi 10280996 dbj BAB13737.1 (AB049151) inositol hexakisphos...	57	4e-07
gi 18565021 ref XP_084209.1 (XM_084209) inositol hexakisph...	57	9e-07
gi 12804837 gb AAH01864.1 AAH01864 (BC001864) Similar to ma...	55	3e-06
gi 1872498 gb AAB49289.1 (U74297) PiUS [Oryctolagus cunicu...	54	4e-06
gi 11360184 pir T46275 hypothetical protein DKFZp564L0678....	54	5e-06
gi 16305265 gb AAL17053.1 AF393812_1 (AF393812) inositol he...	54	5e-06
gi 7291313 gb AAF46743.1 (AE003454) CG10082 gene product [...	39	0.23
gi 8469138 sp Q03746 ClFA_BACTA Pesticidal crystal protein...	37	0.74

Alignments

>gi|6320220|ref|NP_010300.1| (NC_001136) Shows homology to basic leucine zipper family of
transcription factors; Kcslp [Saccharomyces cerevisiae]
gi|1078508|pir|S54640 KCS1 protein - yeast (Saccharomyces cerevisiae)
gi|840870|emb|CAA89842.1| (Z49770) unknown [Saccharomyces cerevisiae]
gi|1216223|emb|CAA65208.1| (X95966) orf:PZF1050 [Saccharomyces cerevisiae]
gi|1431442|emb|CAA98837.1| (Z74313) ORF YDR017c [Saccharomyces cerevisiae]
gi|1478442|gb|AAB36234.1| (S81651) Kcs1 [Saccharomyces cerevisiae]
Length = 1050

Score = 1158 bits (2996), Expect = 0.0

Identities = 658/658 (100%), Positives = 658/658 (100%)

Query: 1 MDTSHEIHDKIPDTLREQQQLRQKESEGCITTLKDLNVPETKKLSSVLHGRKASTYLRI 60
MDTSHEIHDKIPDTLREQQQLRQKESEGCITTLKDLNVPETKKLSSVLHGRKASTYLRI
Sbjct: 1 MDTSHEIHDKIPDTLREQQQLRQKESEGCITTLKDLNVPETKKLSSVLHGRKASTYLRI 60

Query: 61 FRDDECLADNNGVDSNNGGSVTCADKITRSEATPKSVPEGLQVSEKKNPDTLSSSLSS 120
FRDDECLADNNGVDSNNGGSVTCADKITRSEATPKSVPEGLQVSEKKNPDTLSSSLSS

Sbjct: 61 FRDDECLADNNGVDSNNGGSVTCADKITSSEATPKSVPEGLQVSEKKNPDTLSSSLSS 120

Query: 121 FILSNHEEPAIKPNKHVAHRNNITETGQGSGEDIAKQOSHQPQVLHHQTSKPIQNVDEG 180
FILSNHEEPAIKPNKHVAHRNNITETGQGSGEDIAKQOSHQPQVLHHQTSKPIQNVDEG

Sbjct: 121 FILSNHEEPAIKPNKHVAHRNNITETGQGSGEDIAKQOSHQPQVLHHQTSKPIQNVDEG 180

Query: 181 CISPSTYQESLHGISEDLTLPVSSATYYPHKSKADSGYEEKDKMENDIDTIQPATINC 240
CISPSTYQESLHGISEDLTLPVSSATYYPHKSKADSGYEEKDKMENDIDTIQPATINC

Sbjct: 181 CISPSTYQESLHGISEDLTLPVSSATYYPHKSKADSGYEEKDKMENDIDTIQPATINC 240

Query: 241 ASGIATLPSSYNRHTFKVKTYSTLSQSLRQENVNRRSNEKKPQQFVPHSESIKEKPNTFE 300
ASGIATLPSSYNRHTFKVKTYSTLSQSLRQENVNRRSNEKKPQQFVPHSESIKEKPNTFE

Sbjct: 241 ASGIATLPSSYNRHTFKVKTYSTLSQSLRQENVNRRSNEKKPQQFVPHSESIKEKPNTFE 300

Query: 301 QDKEGEQADEEEDEGDNEHREYPLAVELKPFNTNRVGGHTAIFRFSKRAVCKALVNRENRW 360
QDKEGEQADEEEDEGDNEHREYPLAVELKPFNTNRVGGHTAIFRFSKRAVCKALVNRENRW

Sbjct: 301 QDKEGEQADEEEDEGDNEHREYPLAVELKPFNTNRVGGHTAIFRFSKRAVCKALVNRENRW 360

Query: 361 YENIELCHKELLQFMPRIYIGVLNVRQHFQSKDDFLSDLDQENNGKNDTSNENKDIEVNHN 420
YENIELCHKELLQFMPRIYIGVLNVRQHFQSKDDFLSDLDQENNGKNDTSNENKDIEVNHN

Sbjct: 361 YENIELCHKELLQFMPRIYIGVLNVRQHFQSKDDFLSDLDQENNGKNDTSNENKDIEVNHN 420

Query: 421 NNDDIALNTEPTGTPLTHISFPLEHSSRQVLEKEHPEIESVHHPVKRSLSSSNQPSLLP 480
NNDDIALNTEPTGTPLTHISFPLEHSSRQVLEKEHPEIESVHHPVKRSLSSSNQPSLLP

Sbjct: 421 NNDDIALNTEPTGTPLTHISFPLEHSSRQVLEKEHPEIESVHHPVKRSLSSSNQPSLLP 480

Query: 481 EVVLNDRNRIIPESLWYKSDSPNSAPNDYFSSSSSHNSCSFGERGNTNKLKRRDSGST 540
EVVLNDRNRIIPESLWYKSDSPNSAPNDYFSSSSSHNSCSFGERGNTNKLKRRDSGST

Sbjct: 481 EVVLNDRNRIIPESLWYKSDSPNSAPNDYFSSSSSHNSCSFGERGNTNKLKRRDSGST 540

Query: 541 MINTELKNLVIREVFAPKCFRRKRNSNTTGMNHNARLGSSPSFLTQKSRASSHDASNTS 600
MINTELKNLVIREVFAPKCFRRKRNSNTTGMNHNARLGSSPSFLTQKSRASSHDASNTS

Sbjct: 541 MINTELKNLVIREVFAPKCFRRKRNSNTTGMNHNARLGSSPSFLTQKSRASSHDASNTS 600

Query: 601 MKTLGDSSSQASLQMDDSKVNPNLQDPFLKKSLEHESISNALDGSHSVMDLKQFHKNEQ 658
MKTLGDSSSQASLQMDDSKVNPNLQDPFLKKSLEHESISNALDGSHSVMDLKQFHKNEQ

Sbjct: 601 MKTLGDSSSQASLQMDDSKVNPNLQDPFLKKSLEHESISNALDGSHSVMDLKQFHKNEQ 658

>gi|1903296|emb|CAA98839.1| (Z74314) ORF YDR017c [Saccharomyces cerevisiae]
Length = 658

Score = 1093 bits (2826), Expect = 0.0
Identities = 658/658 (100%), Positives = 658/658 (100%)

Query: 1 MDTSHIHDKIPDTLREQQQHLRQKESEGCITTLKDLNVPETKKLSSVLHGRKASTYLRI 60
MDTSHIHDKIPDTLREQQQHLRQKESEGCITTLKDLNVPETKKLSSVLHGRKASTYLRI

Sbjct: 1 MDTSHIHDKIPDTLREQQQHLRQKESEGCITTLKDLNVPETKKLSSVLHGRKASTYLRI 60

Query: 61 FRDDECLADNNGVDSNNGGSVTCADKITSSEATPKSVPEGLQVSEKKNPDTLSSSLSS 120
FRDDECLADNNGVDSNNGGSVTCADKITSSEATPKSVPEGLQVSEKKNPDTLSSSLSS

Sbjct: 61 FRDDECLADNNGVDSNNGGSVTCADKITSSEATPKSVPEGLQVSEKKNPDTLSSSLSS 120

Query: 121 FILSNHEEPAIKPNKHVAHRNNITETGQGSGEDIAKQOSHQPQVLHHQTSKPIQNVDEG 180
FILSNHEEPAIKPNKHVAHRNNITETGQGSGEDIAKQOSHQPQVLHHQTSKPIQNVDEG

Sbjct: 121 FILSNHEEPAIKPNKHVAHRNNITETGQGSGEDIAKQOSHQPQVLHHQTSKPIQNVDEG 180

Query: 181 CISPSTYQESLHGISEDLTLPVSSATYYPHKSKADSGYEEKDKMENDIDTIQPATINC 240
CISPSTYQESLHGISEDLTLPVSSATYYPHKSKADSGYEEKDKMENDIDTIQPATINC

Sbjct: 181 CISPSTYQESLHGISEDLTLPVSSATYYPHKSKADSGYEEKDKMENDIDTIQPATINC 240

Query: 241 ASGIATLPSSYNRHTFKVKTYSTLSQSLRQENVNRRSNEKKPQQFVPHSESIKEKPNTFE 300
ASGIATLPSSYNRHTFKVKTYSTLSQSLRQENVNRRSNEKKPQQFVPHSESIKEKPNTFE

Sbjct: 241 ASGIATLPSSYNRHTFKVKTYSTLSQSLRQENVNRRSNEKKPQQFVPHSESIKEKPNTFE 300

Query: 301 QDKEGEQADEEEDEGDNEHREYPLAVELKPFNTNRVGGHTAIFRFSKRAVCKALVNRENRW 360
QDKEGEQADEEEDEGDNEHREYPLAVELKPFNTNRVGGHTAIFRFSKRAVCKALVNRENRW

Sbjct: 301 QDKEGEQADEEEDEGDNEHREYPLAVELKPFNTNRVGGHTAIFRFSKRAVCKALVNRENRW 360

Query: 361 YENIELCHKELLQFMPRIYIGVLNVRQHFQSKDDFLSDLDQENNGKNDTSNENKDIEVNHN 420

Sbjct: 361 YENIELCHKELLQFMPRYIGVLNVRQHFQSKDDFLSDLDQENNGKNDTSNENKDIEVNHN 420

Query: 421 NNDDIALNTEPTGTPPLTHIHSFPLEHSSRQVLEKEHPEIESVHPHVKRSLSSSNQPSLLP 480
NNDDIALNTEPTGTPPLTHIHSFPLEHSSRQVLEKEHPEIESVHPHVKRSLSSSNQPSLLP

Sbjct: 421 NNDDIALNTEPTGTPPLTHIHSFPLEHSSRQVLEKEHPEIESVHPHVKRSLSSSNQPSLLP 480

Query: 481 EVVLNDNRHIIPESLWYKYS DSPNSAPND SYFSSSSSHNSCSFGERGNTNKLKRRDSGST 540
EVVLNDNRHIIPESLWYKYS DSPNSAPND SYFSSSSSHNSCSFGERGNTNKLKRRDSGST

Sbjct: 481 EVVLNDNRHIIPESLWYKYS DSPNSAPND SYFSSSSSHNSCSFGERGNTNKLKRRDSGST 540

Query: 541 MINTELKNLVIREVFAPKCFRRKRNSNTTTMGNNHARLGSSPSFLTQKSRASSHDASNTS 600
MINTELKNLVIREVFAPKCFRRKRNSNTTTMGNNHARLGSSPSFLTQKSRASSHDASNTS

Sbjct: 541 MINTELKNLVIREVFAPKCFRRKRNSNTTTMGNNHARLGSSPSFLTQKSRASSHDASNTS 600

Query: 601 MKTLGDSSSQASLQMDSDKVNPNLQDPFLKKS LHEKISNALDGSHSVMDLKQFHKNEQ 658
MKTLGDSSSQASLQMDSDKVNPNLQDPFLKKS LHEKISNALDGSHSVMDLKQFHKNEQ

Sbjct: 601 MKTLGDSSSQASLQMDSDKVNPNLQDPFLKKS LHEKISNALDGSHSVMDLKQFHKNEQ 658

>gi|19075347|ref|NP_587847.1| (NC_003421) putative b-zip transcription factor
{Schizosaccharomyces pombe}
gi|7492426|pir|T41672 probable b-zip transcription factor - fission yeast
(Schizosaccharomyces pombe)
gi|3560233|emb|CAA20701.1| (AL031530) putative b-zip transcription factor [Schizosaccharomyces
pombe]
Length = 967

Score = 114 bits (284), Expect = 4e-24
Identities = 96/289 (33%), Positives = 128/289 (44%), Gaps = 70/289 (24%)

Query: 321 EYPLAVELKPFNTNRVGHTAIFRFSKRAVCKALVNRENWYENIELCHKELLQFMPRYIG 380
+YP+ V L+PF ++VGGHTA FRFSKRAVCK L EN +YE IE CH ELL F+P+YIG

Sbjct: 306 DYPVTVRLEPFKHQVGHTAIFRFSKRAVCKPLTRNENTFYETIEACHPELLPFIPKYIG 365

Query: 381 VLNVRQHFQSKDDFLSDLDQENNGKNDTSNENKDIEVNHNNDIALNTEPTG-TPLTHI 439
VLNV ++ ND++ E +NTE + TP H

Sbjct: 366 VLVNTHITITKTEE-----NDSTTE-----YVNTESSTKTPAPHK 399

Query: 440 HSFPLEHSSRQVLEKEHPEIESVHPHVKRSLSSSNQPSLLPEVVLNDNRHIIPESLWYKY 499
H+F S +PEV + NRHI PE +

Sbjct: 400 HTF-----NSCYQKKDGYIPEVSVEQNRHIFPEWML--- 431

Query: 500 SDSPNSAPND SYFSSSSSHNSCSFGERGNTNKL-----KRRDSGSTMINTELKNLVIREV 554
P+ + S H S S GER + + G+T+IN +L+ V+REV

Sbjct: 432 ---PDKRSHSYGSPKSLHHKSSSAGERPVSPTFVADIPKTPWGTTLINRKLREEVLREV 488

Query: 555 FAPKCFRRKRNSNTTTMGNNHARLGSSPSFLTQKSRASSH-DASNTSMK 602
FAPK RR+ + + +H PS S A D NTS +

Sbjct: 489 FAPKHARRRLGTRFHSRSSHR-----PSVFRDNSVAFGLDNGNTSSR 531

>gi|18376053|emb|CAD21059.1| (AL669986) related to transcription factor KCS1 [Neurospora crassa]
Length = 1466

Score = 79.0 bits (193), Expect = 2e-13
Identities = 129/530 (24%), Positives = 211/530 (39%), Gaps = 98/530 (18%)

Query: 119 SSFILSNHEEPAIKPNKHVAHRNNITETGQSGGEDIAKQ--QSHQ-PQVLHHQTSLKPIQ 175
SS L EP K + + ++ E + E I+ HQ P+ + S P

Sbjct: 547 SSPSLDRKPEPRKSDASIEGGSHTEEGEESGEEKISSAVFLPHQGPPEAEHEHSDVP-- 604

Query: 176 NVDEGCISPKSTYQESLHGISEDLTLPVSSATYYPHKSADSGYEEKDKMEN--DIDTI 233
G S ++ H +ED H +G E + ++ D++

Sbjct: 605 ----GAASSRTALPSRTHSRAEDF-----HSWLKAGEPEVECLDECPDVEKT 648

Query: 234 QPATINCASGIATLPSSYNRHTFKVKYTYSTLSQSLRQENVNNSNEKKPQQFVPHSESIK 293
A AT+P + ++ T ++ E +KP Q + H

Sbjct: 649 HRPAPKAADSAATVPFVGS----QIDTGKVNPAVADEIETGVPPPQKPFQSIHHSRHH 704

Query: 294 EKPNTFEQDKGEQADEEEDGNEHREYPL-AVELKPFTNRVGHTAIFRFSKRAVCKA 352

Sbjct: 705 + + + E D + + + E PL A+EL P+ ++VGGHT ++RFS+RAVCK
DHHHHHHRHPEEAIHDHQGEPEKE---EQPLDAIELIPYKHQVGGHTTLWRFSRRAVCKQ 760

Query: 353 LVNRENRWYENIELCHKELLQFMPRYIGVLNV-----RQHFQSKDDFLSDLDQENNGK 405
L NREN +YE IE H++LL F+PRYIGVLNV R+ KD+ + L+ G+

Sbjct: 761 LNNRENEFYEKIERYHRDLLAFLPRYIGVLNVTFQKKPRKSVHKKDEAAAALEAPTAGQ 820

Query: 406 NDTSENKNDIEVNHNNNDIALNTEPTGTPLTHHSFPLEHSSRQVLEKEHPEIESVHPH 465
+ E T + + + P H + + PE

Sbjct: 821 D-----EATSSGVKGDEAAPTTHGA----QPAQPE----- 846

Query: 466 VKRSLSSSNQPSL--LPEVVLNDNRHIIPESLWYKYS DSPNSAPNDSYFSSSSSHNSCSF 523
+R +S S Q L +P V DN+HI+P SL S +S SS+S H

Sbjct: 847 -QRMISQSLQOPLGQIPTVTFVDNQHILPRSLIQPALASSSSFTRLRSASSASLHGRRIM 905

Query: 524 GERGNTN-----KLKRRDS---GSTMINTLKNLVIREVFAPKCFRRKRNSNTTGMGN 573
+ N +L+ R + G+TM+N L+N V + F + +

Sbjct: 906 NGQCAENPSHMLRPRLEDHRANSWGATMVNKLRLNEVFND AFLKQ-----PVAV 954

Query: 574 HNRALGSSPSFLTQKSRAS-SHDASNTSMKTLGDSSSQASLQMDSDSKVNP 622
H + G F + + H S+ ++ D+ +AS ++S++ P

Sbjct: 955 HRHKKGHQRPFSRSLQPVLRHTESDPNLDVAQDAKPRASSAGEESRLKP 1004

>gi|14736134|ref|XP_030060.1| (XM_030060) mammalian inositol hexakisphosphate kinase 2 [Homo sapiens]
gi|9955981|gb|AAG01984.1| (AY007091) similar to Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA with GenBank
Accession Number AF177145
gi|18043111|gb|AAH19694.1|AAH19694 (BC019694) Unknown (protein for MGC:24971) [Homo sapiens]
Length = 426

Score = 58.2 bits (139), Expect = 3e-07
Identities = 28/68 (41%), Positives = 47/68 (68%), Gaps = 5/68 (7%)

Query: 326 VELKPFTNRVGGHTAIFRFSKRAVCKALVNRENRWYENIELCHKELLQFMPRYIGVLNVR 385
V L+PF ++VGGH+ + RF++ +CK LV RE+++YE + E+ +F P+Y GV++VR

Sbjct: 17 VLLEPFVHVQGGHSCVLRFNETTLCPLVPREHQFYETLP---AEMRKFTPQYKGVVSVR 73

Query: 386 QHFQSKDD 393
F+ +D

Sbjct: 74 --FEEDED 79

>gi|7305195|ref|NP_038813.1| (NM_013785) inositol hexaphosphate kinase 1; inositol hexakisphosphate kinase 6 [Mus musculus]
gi|6524024|gb|AAF15056.1|AF177144_1 (AF177144) mammalian inositol hexakisphosphate kinase 1 [Mus musculus]
Length = 433

Score = 58.2 bits (139), Expect = 3e-07
Identities = 30/78 (38%), Positives = 46/78 (58%), Gaps = 3/78 (3%)

Query: 307 QADEEEDEGDNEHREYPLAVELKPFTNRVGGHTAIFRFSKRAVCKALVNRENRWYENIEL 366
Q E G N R V L+PF ++VGGH+++ R+ VCK L++RE R+YE++

Sbjct: 5 QTMEVGQYGNASRAGDRGVLEPFIHQVGGHSSMMRYDDHTVCKPLISREQRFYESLP- 63

Query: 367 CHKELLQFMPRYIGVLNV 384
E+ +F P Y GV++V

Sbjct: 64 --PEMKEFTPEYKGVVSV 79

>gi|6683115|dbj|BAA13393.2| (D87452) KIAA0263 protein [Homo sapiens]
Length = 462

Score = 58.2 bits (139), Expect = 3e-07
Identities = 30/78 (38%), Positives = 46/78 (58%), Gaps = 3/78 (3%)

Query: 307 QADEEEDEGDNEHREYPLAVELKPFTNRVGGHTAIFRFSKRAVCKALVNRENRWYENIEL 366
Q E G N R V L+PF ++VGGH+++ R+ VCK L++RE R+YE++

Sbjct: 26 QTMEVGQYGNASRAGDRGVLEPFIHQVGGHSSMMRYDDHTVCKPLISREQRFYESLP- 84

Query: 367 CHKELLQFMPRYIGVLNV 384
E+ +F P Y GV++V
Sbjct: 85 --PEMKFTPEYKGVSV 100

>gi|7705553|ref|NP_057375.1| (NM_016291) mammalian inositol hexakisphosphate kinase 2 [Homo sapiens]
gi|6524026|gb|AAF15057.1|AF177145_1 (AF177145) mammalian inositol hexakisphosphate kinase 2 [Homo sapiens]
Length = 426

Score = 58.2 bits (139), Expect = 3e-07
Identities = 28/68 (41%), Positives = 47/68 (68%), Gaps = 5/68 (7%)

Query: 326 VELKPFTNRVGGHTAIFRFSKRAVCKALVNRENRWYENIELCHKELLQFMPRYIGVLNVR 385
V L+PF ++VGGH+ + RF++ +CK LV RE+++YE + E+ +F P+Y GV++VR
Sbjct: 17 VLLEPFVHQVGGHSCVLRFNETTLCKPLVPREHQFYETLP---AEMRKFTPQYKGVSVR 73

Query: 386 QHFQSKDD 393
F+ +D
Sbjct: 74 --FEEDED 79

>gi|15277917|gb|AAH12944.1|AAH12944 (BC012944) Unknown (protein for MGC:9925) [Homo sapiens]
Length = 441

Score = 57.8 bits (138), Expect = 4e-07
Identities = 30/78 (38%), Positives = 46/78 (58%), Gaps = 3/78 (3%)

Query: 307 QADEEEDEGDNEHREYPLAVELKPFTNRVGGHTAIFRFSKRAVCKALVNRENRWYENIEL 366
Q E G N R V L+PF ++VGGH+++ R+ VCK L++RE R+YE++
Sbjct: 5 QTMEVGQYGNASRAGDRGVLEPFVHQVGGHSSMMRYDDHTVCKPLISREQRFYESLP- 63

Query: 367 CHKELLQFMPRYIGVLNV 384
E+ +F P Y GV++V
Sbjct: 64 --PEMKFTPEYKGVSV 79

>gi|10280996|dbj|BAB13737.1| (AB049151) inositol hexakisphosphate kinase [Rattus norvegicus]
Length = 433

Score = 57.4 bits (137), Expect = 4e-07
Identities = 30/78 (38%), Positives = 46/78 (58%), Gaps = 3/78 (3%)

Query: 307 QADEEEDEGDNEHREYPLAVELKPFTNRVGGHTAIFRFSKRAVCKALVNRENRWYENIEL 366
Q E G N R V L+PF ++VGGH+++ R+ VCK L++RE R+YE++
Sbjct: 5 QTMEVGQYGNASRAGDRGVLEPFVHQVGGHSSMMRYDDHTVCKPLISREQRFYESLP- 63

Query: 367 CHKELLQFMPRYIGVLNV 384
E+ +F P Y GV++V
Sbjct: 64 --PEMKFTPEYKGVSV 79

>gi|18565021|ref|XP_084209.1| (XM_084209) inositol hexakisphosphate kinase 3 [Homo sapiens]
Length = 410

Score = 56.6 bits (135), Expect = 9e-07
Identities = 25/59 (42%), Positives = 41/59 (69%), Gaps = 3/59 (5%)

Query: 326 VELKPFTNRVGGHTAIFRFSKRAVCKALVNRENRWYENIELCHKELLQFMPRYIGVLNV 384
V+L+PF ++VGGH ++ ++ + VCK LV+RE R+YE++ L K +F P+Y G + V
Sbjct: 16 VQLEPFVHQVGGHSMVMKYDEHTVCKPLVSREQRFYESLPLAMK---RFTPQYKGTVTV 71

>gi|12804837|gb|AAH01864.1|AAH01864 (BC001864) Similar to mammalian inositol hexakisphosphate kinase 2
[Homo sapiens]
Length = 70

Score = 55.1 bits (131), Expect = 3e-06
Identities = 24/56 (42%), Positives = 39/56 (68%), Gaps = 3/56 (5%)

Query: 326 VELKPFTNRVGGHTAIFRFSKRAVCKALVNRENRWYENIELCHKELLQFMPRYIGV 381
V L+PF ++VGGH+ + RF++ +CK LV RE+++YE + E+ +F P+Y GV
Sbjct: 17 VLLEPFVHQVGGHSCVLRFNETTLCKPLVPREHQFYETLP---AEMRKFTPQYKGV 69

>gi|1872498|gb|AAB49289.1| (U74297) PiUS [Oryctolagus cuniculus]
Length = 425

Score = 54.3 bits (129), Expect = 4e-06
Identities = 23/57 (40%), Positives = 41/57 (71%), Gaps = 3/57 (5%)

Query: 328 LKPFTNRVGGHTAIFRFSKRAVCKALVNRENRWYENIELCHKELLQFMPRYIGVLNV 384
L+PF ++VGGH+ + RF++ +CK L+ RE+++YE + E+ +F P+Y GV++V
Sbjct: 19 LEFVHQVGGHSCVLRFNETTLCKPLIPREHQFYETLP---AEMRKFTPQYKGVSV 72

>gi|11360184|pir||T46275 hypothetical protein DKFZp564L0678.1 - human
gi|6808172|emb|CAB70780.1| (AL137514) hypothetical protein [Homo sapiens]
Length = 97

Score = 53.9 bits (128), Expect = 5e-06
Identities = 23/55 (41%), Positives = 38/55 (68%), Gaps = 3/55 (5%)

Query: 326 VELKPFTNRVGGHTAIFRFSKRAVCKALVNRENRWYENIELCHKELLQFMPRYIG 380
V L+PF ++VGGH+ + RF++ +CK LV RE+++YE + E+ +F P+Y G
Sbjct: 17 VLLEPFVHQVGGHSCVLRFNETTLCKPLVPREHQFYETLP---AEMRKFTPQYKG 68

>gi|16305265|gb|AAL17053.1|AF393812_1 (AF393812) inositol hexakisphosphate kinase 3 [Homo sapiens]
Length = 410

Score = 53.9 bits (128), Expect = 5e-06
Identities = 24/59 (40%), Positives = 40/59 (67%), Gaps = 3/59 (5%)

Query: 326 VELKPFTNRVGGHTAIFRFSKRAVCKALVNRENRWYENIELCHKELLQFMPRYIGVLNV 384
V+L+PF ++VGGH ++ ++ + VCK LV+RE R+YE++ K +F P+Y G + V
Sbjct: 16 VQLEPFLHQVGGHMSVMKYDEHTVCKPLVSREQRFYESLPQAMK---RFTPQYKGTVTV 71

>gi|7291313|gb|AAF46743.1| (AE003454) CG10082 gene product [Drosophila melanogaster]
Length = 893

Score = 38.5 bits (88), Expect = 0.23
Identities = 36/131 (27%), Positives = 58/131 (43%), Gaps = 8/131 (6%)

Query: 252 NRHTFKVKTYSTLSQSLRQENVNNSNEKKPQQFVPHSESIKEKPNTFEQDKEGEQADEE 311
N V + + S S + + + KPQ+ P K +
Sbjct: 103 NLQQLSVSSSNASSSSNNNSASGCNTPTKPKQKPLLLPEAAASTATAVGKSSKNPQLS 162

Query: 312 EDEGDNEHREYPLAVELKPFTNRVGGHTAIFRFSKRAVCKALVNRENRWYENIELCHKEL 371
+D DNE V L P +N+VGGH + ++ V K L RE +Y+NI +++
Sbjct: 163 KDLLDNEDE-----VALHPLSNQVGGHTRLNLLNQSTVIKPLNLRELDYQNIPI---QDI 214

Query: 372 LQFMPRYIGVL 382
L+F+P+Y GV+
Sbjct: 215 LKFVPKYKGV 225

>gi|8469138|sp|Q03746|C1FA_BACTA Pesticidal crystal protein cryIFa (Insecticidal delta-endotoxin

CryIF(a)) (Crystalline entomocidal protoxin) (134 kDa
crystal protein)

gi|98519|pir||A42459 insecticidal crystal protein CryIF - Bacillus thuringiensis
(strain aizawai)

gi|142756|gb|AAA22347.1| (M73254) cryIF [Bacillus thuringiensis]

gi|142758|gb|AAA22348.1| (M63897) insecticidal crystal protein [Bacillus thuringiensis]
Length = 1174

Score = 37.0 bits (84), Expect = 0.74
Identities = 34/161 (21%), Positives = 71/161 (43%), Gaps = 12/161 (7%)

Query: 109 NNPDTLSSSLSSFILSNHEEPAIK-----PNKHVAHRNNITETGQSGEDIKQOSHQPQ 163
N D L +++++F L++ E P + N H++ + GQG G DIA +H +

Sbjct: 134 NTDDALITAINNFTLTSTFEIPLLSVYVQAANLHLSLLRDAVSFGQGWGLDIATVNNHYNR 193

Query: 164 VLH--HQTSCLKPIQNVDEGCISPKSTYQES---LHGISEDLTLPVSSATYYPHKSADS 218
+++ H+ + + ++G + + T + DLT + +P+

Sbjct: 194 LINLIHRYTKHCLDTYNQGLENLRGTNTRQWARFNQFRDLTLTVLDIVLFPNYDVRTY 253

Query: 219 GYEEKDKMENDIDTIQPATINCASGIATLPSSYNRHTFKVK 259
+ ++ +I T + I + A +P+ +NR F V+

Sbjct: 254 PIQTSSQLTREIYT--SSVIEDSPVSANIPNGFNRAEFGVR 292

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: Apr 29, 2002 3:56 AM
Number of letters in database: 290,391,215
Number of sequences in database: 925,521

Lambda	K	H
0.308	0.126	0.354

Gapped		
Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 393,824,463

Number of Sequences: 925521

Number of extensions: 17796636

Number of successful extensions: 87807

Number of sequences better than 10.0: 547

Number of HSP's better than 10.0 without gapping: 77

Number of HSP's successfully gapped in prelim test: 491

Number of HSP's that attempted gapping in prelim test: 78619

Number of HSP's gapped (non-prelim): 4152

length of query: 658

length of database: 290,391,215

effective HSP length: 127

effective length of query: 531

effective length of database: 172,850,048

effective search space: 91783375488

effective search space used: 91783375488

T: 11

A: 40

X1: 16 (7.1 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 42 (21.7 bits)

S2: 74 (33.1 bits)

FIGURE 5: Blastp results of accession NP_010300.1 against the NCBI Protein nr database.

BLASTP 2.2.3 [Apr-24-2002]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, 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.

RID: 1020211572-025569-14496

Query=

(1050 letters)

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

925,521 sequences; 290,391,215 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Sequences producing significant alignments:		Score (bits)	E Value
gi 6320220 ref NP_010300.1	(NC_001136) Shows homology to b...	1935	0.0
gi 1903296 emb CAA98839.1	(Z74314) ORF YDR017c [Saccharomy...	1144	0.0
gi 19075347 ref NP_587847.1	(NC_003421) putative b-zip tra...	260	5e-68
gi 18376053 emb CAD21059.1	(AL669986) related to transcrip...	220	7e-56
gi 16305265 gb AAL17053.1	AF393812.1 (AF393812) inositol he...	110	6e-23
gi 18565021 ref XP_084209.1	(XM_084209) inositol hexakisph...	110	7e-23
gi 16905371 ref NP_473452.1	(NM_054111) inositol hexakisph...	110	1e-22
gi 7305195 ref NP_038813.1	(NM_013785) inositol hexaphosph...	105	3e-21
gi 10280996 dbj BAB13737.1	(AB049151) inositol hexakisphos...	104	5e-21
gi 14722051 ref XP_028610.1	(XM_028610) KIAA0263 gene prod...	103	1e-20
gi 6683115 dbj BAA13393.2	(D87452) KIAA0263 protein [Homo ...	102	2e-20
gi 15277917 gb AAH12944.1	AAH12944 (BC012944) Unknown (prot...	102	3e-20
gi 18485446 ref XP_079965.1	(XM_079965) CG10082 [Drosophil...	99	2e-19
gi 7291313 gb AAF46743.1	(AE003454) CG10082 gene product [...	99	3e-19
gi 7705553 ref NP_057375.1	(NM_016291) mammalian inositol ...	99	3e-19
gi 14736134 ref XP_030060.1	(XM_030060) mammalian inositol...	99	3e-19
gi 1872498 gb AAB49289.1	(U74297) PiUS [Oryctolagus cunicu...	99	4e-19
gi 7512923 pir T17246	hypothetical protein DKFZp586M0617.1...	97	1e-18
gi 11067377 ref NP_067692.1	(NM_021660) PiUS protein [Ratt...	96	2e-18
gi 17507001 ref NP_492519.1	(NM_060118) F30A10.3.p [Caenor...	96	3e-18
gi 17555592 ref NP_497443.1	(NM_065042) Y22D7AR.6.p [Caeno...	79	2e-13
gi 8744998 emb CAB95220.1	(AL359773) hypothetical protein ...	77	8e-13
gi 19114505 ref NP_593593.1	(NC_003424) putative arginine ...	59	3e-07
gi 19705555 ref NP_599244.1	(NM_134417) inositol polyphosp...	57	1e-06
gi 12804837 gb AAH01864.1	AAH01864 (BC001864) Similar to ma...	56	2e-06
gi 7296185 gb AAF51477.1	(AE003589) CG13688 gene product [...	55	5e-06
gi 11360184 pir T46275	hypothetical protein DKFZp564L0678....	55	5e-06
gi 17569885 ref NP_510724.1	(NM_078323) T20F7.3.p [Caenorh...	54	1e-05
gi 13509208 emb CAC35322.1	(AJ310150) hypothetical protein...	46	0.002
gi 12846033 dbj BAB27004.1	(AK010523) evidence:NAS-hypothe...	46	0.002
gi 6320378 ref NP_010458.1	(NC_001136) Regulator of argini...	45	0.003
gi 4200312 emb CAA09965.1	(AJ012219) ip3ka [Gallus gallus]	43	0.024
gi 14028614 gb AAK52432.1	(AF282731) Mf1 protein [Schistos...	40	0.20
gi 17544638 ref NP_502402.1	(NM_070001) ZK795.1.p [Caenorh...	39	0.37
gi 13509210 emb CAC35324.1	(AJ310150) hypothetical protein...	38	0.47

Alignments

>gi|6320220|ref|NP_010300.1| (NC_001136) Shows homology to basic leucine zipper family of transcription factors; Kcs1p [Saccharomyces cerevisiae]
gi|1078508|pir|S54640 KCS1 protein - yeast (Saccharomyces cerevisiae)
gi|840870|emb|CAA89842.1| (Z49770) unknown [Saccharomyces cerevisiae]
gi|1216223|emb|CAA65208.1| (X95966) orf:PZF1050 [Saccharomyces cerevisiae]
gi|1431442|emb|CAA98837.1| (Z74313) ORF YDR017c [Saccharomyces cerevisiae]
gi|1478442|gb|AAB36234.1| (S81651) Kcs1 [Saccharomyces cerevisiae]
Length = 1050

Score = 1935 bits (5012), Expect = 0.0
Identities = 1050/1050 (100%), Positives = 1050/1050 (100%)

Query: 1 MDTSH EIHDKIPDTLREQQHLRQKESEGCITTLKDLNVPETKKLSSVLHGRKASTYLRI 60
Sbjct: 1 MDTSH EIHDKIPDTLREQQHLRQKESEGCITTLKDLNVPETKKLSSVLHGRKASTYLRI 60

Query: 61 FRDDECLADNNNGVDSNNGGSVTCADKITRSEATPKSVPEGLQVSEKKNPDTLSSSLSS 120
Sbjct: 61 FRDDECLADNNNGVDSNNGGSVTCADKITRSEATPKSVPEGLQVSEKKNPDTLSSSLSS 120

Query: 121 FILSNHEEPAIKPNKHVAHRNNITETGQSGGEDIAKQOSHQPQVLHHQTSLKPIQNVDEG 180
Sbjct: 121 FILSNHEEPAIKPNKHVAHRNNITETGQSGGEDIAKQOSHQPQVLHHQTSLKPIQNVDEG 180

Query: 181 CISPSTYQESLHGISEDLTLPVSSATYYPHKSKADSGYEEKDKMENDIDTIQPATINC 240
Sbjct: 181 CISPSTYQESLHGISEDLTLPVSSATYYPHKSKADSGYEEKDKMENDIDTIQPATINC 240

Query: 241 ASGIATLPSSYNRHTFKVKTYSTLSQSLRQENVNRSNEKKPQQFVPHSESIKEKPNTFE 300
Sbjct: 241 ASGIATLPSSYNRHTFKVKTYSTLSQSLRQENVNRSNEKKPQQFVPHSESIKEKPNTFE 300

Query: 301 QDKEGEQADEEEDGDNHREYPLAVELKPFTRNVGGHTAIFRFSKRAVCKALVNRENRW 360
Sbjct: 301 QDKEGEQADEEEDGDNHREYPLAVELKPFTRNVGGHTAIFRFSKRAVCKALVNRENRW 360

Query: 361 YENIELCHKELLQFMPRYIGVLNVRQHFQSKDDFLSDLQENNGKNDTSNENKDIEVNHN 420
Sbjct: 361 YENIELCHKELLQFMPRYIGVLNVRQHFQSKDDFLSDLQENNGKNDTSNENKDIEVNHN 420

Query: 421 NNDDIALNTEPTGTPLTHIHSFPLEHSSRQVLEKEHPEIESVHPHVKRSLSNQPSSLP 480
Sbjct: 421 NNDDIALNTEPTGTPLTHIHSFPLEHSSRQVLEKEHPEIESVHPHVKRSLSNQPSSLP 480

Query: 481 EVVLNDRHIIPESLWYKYS DSPNSAPNDSYFSSSSSHNSCSFGERGNTNKLKRRDSGST 540
Sbjct: 481 EVVLNDRHIIPESLWYKYS DSPNSAPNDSYFSSSSSHNSCSFGERGNTNKLKRRDSGST 540

Query: 541 MINTELKNLVIREVFAPKCFRRKRNSNTTTMGNNHARLGSSPSFLTQKSRASSHDASNTS 600
Sbjct: 541 MINTELKNLVIREVFAPKCFRRKRNSNTTTMGNNHARLGSSPSFLTQKSRASSHDASNTS 600

Query: 601 MKTLGSSSQASLQMDDSKVNPNLQDPFLKKSLEKISNALDGSHSVMDLKQFHKNEQIK 660
Sbjct: 601 MKTLGSSSQASLQMDDSKVNPNLQDPFLKKSLEKISNALDGSHSVMDLKQFHKNEQIK 660

Query: 661 HKNSFCNSLSPILTATNSRDDGEFATSPNYISNAQDGVFDMDEDTGNETINMDNHGCHLD 720
Sbjct: 661 HKNSFCNSLSPILTATNSRDDGEFATSPNYISNAQDGVFDMDEDTGNETINMDNHGCHLD 720

Query: 721 SGKNMIKSLAYNVSN DYSHHDIESITFEETSHTIVSKFILLEDLTRNMNKP CALDLKMG 780
Sbjct: 721 SGKNMIKSLAYNVSN DYSHHDIESITFEETSHTIVSKFILLEDLTRNMNKP CALDLKMG 780

Query: 781 TRQYGVDAKRAKQLSQRAKCLKTTSRRLGVRICGLKVWNKDYITRDKYFGRRVKVGWQF 840
Sbjct: 781 TRQYGVDAKRAKQLSQRAKCLKTTSRRLGVRICGLKVWNKDYITRDKYFGRRVKVGWQF 840

Query: 841 ARVLARFLYDGKTIESLIRQIPRLIKQLDTLYSEIFNLKGYRLYGASLLL MYDGDANKSN 900

Sbjct: 841 ARVLARFLYDGKTIESLIRQIPRLIKQLDLYSEIFNLKGYRLYGASLLMYDGDANKSN 900
Query: 901 SKRKAANVKVNLIDFARCVTKEDAMECMDKFRIPPKSPNIEDKGFLRGVKSRLRFYLLLI 960
Sbjct: 901 SKRKAANVKVNLIDFARCVTKEDAMECMDKFRIPPKSPNIEDKGFLRGVKSRLRFYLLLI 960
Query: 961 WNYLTSDMPLIFDEVEMNDMISEEADSNSTSATGSKINFNSKWDWLDEFDKEDEEMYND 1020
Sbjct: 961 WNYLTSDMPLIFDEVEMNDMISEEADSNSTSATGSKINFNSKWDWLDEFDKEDEEMYND 1020
Query: 1021 PNSKLRQKWRKYELIFDAEPRYNDDAQVSD 1050
Sbjct: 1021 PNSKLRQKWRKYELIFDAEPRYNDDAQVSD 1050

>gi|1903296|emb|CAA98839.1| (Z74314) ORF YDR017c [Saccharomyces cerevisiae]
Length = 658

Score = 1144 bits (2958), Expect = 0.0
Identities = 658/658 (100%), Positives = 658/658 (100%)

Query: 1 MDTSHIEHDKIPDTLREQQHLRQKESEGCITTLKDLNVPETKKLSSVLHGRKASTYLRI 60
Sbjct: 1 MDTSHIEHDKIPDTLREQQHLRQKESEGCITTLKDLNVPETKKLSSVLHGRKASTYLRI 60
Query: 61 FRDDECLADNNGGVSNNNGSVTCADKIRSEATPKSVPEGLQVSEKKNPDTLSSSLSS 120
Sbjct: 61 FRDDECLADNNGGVSNNNGSVTCADKIRSEATPKSVPEGLQVSEKKNPDTLSSSLSS 120
Query: 121 FILSNHEEPAIKPNKHVAHRNNITETGQSGGEDIAKQOSHQPQVLHHQTSKPIQNVDEG 180
Sbjct: 121 FILSNHEEPAIKPNKHVAHRNNITETGQSGGEDIAKQOSHQPQVLHHQTSKPIQNVDEG 180
Query: 181 CISPKSTYQESLHGISEDLTLPVSSATYYPHKSKADSGYEEKDKMENDIDTIQPATINC 240
Sbjct: 181 CISPKSTYQESLHGISEDLTLPVSSATYYPHKSKADSGYEEKDKMENDIDTIQPATINC 240
Query: 241 ASGIATLPSSYNRHTFKVKTYSTLSQSLRQENVNRSNEKKPQQFVPHSESIKEKPNTFE 300
Sbjct: 241 ASGIATLPSSYNRHTFKVKTYSTLSQSLRQENVNRSNEKKPQQFVPHSESIKEKPNTFE 300
Query: 301 QDKEGEQADEEEDEGDNEHREYPLAVELKPFTRNVGGHTAIFRFSKRAVCKALVNRENRW 360
Sbjct: 301 QDKEGEQADEEEDEGDNEHREYPLAVELKPFTRNVGGHTAIFRFSKRAVCKALVNRENRW 360
Query: 361 YENIELCHKELLQFMPRYIGVLNVRQHFQSKDDFLSDLDQENNGKNDTSNENKDIEVNHN 420
Sbjct: 361 YENIELCHKELLQFMPRYIGVLNVRQHFQSKDDFLSDLDQENNGKNDTSNENKDIEVNHN 420
Query: 421 NNDDIALNTEPTGTPLTHIHSFPLEHSSRQVLEKEHPEIESVHPPVKRSLSSSNQPSLLP 480
Sbjct: 421 NNDDIALNTEPTGTPLTHIHSFPLEHSSRQVLEKEHPEIESVHPPVKRSLSSSNQPSLLP 480
Query: 481 EVVLNDRNHIIPESLWYKYS DSPNSAPND SYFSSSSSHNSCSFGERGNTNKLKRRDSGST 540
Sbjct: 481 EVVLNDRNHIIPESLWYKYS DSPNSAPND SYFSSSSSHNSCSFGERGNTNKLKRRDSGST 540
Query: 541 MINTELKNLVIREVFAPKCFRRKRNSNTTTMGNNHARLGSSPSFLTQKSRASSHDASNTS 600
Sbjct: 541 MINTELKNLVIREVFAPKCFRRKRNSNTTTMGNNHARLGSSPSFLTQKSRASSHDASNTS 600
Query: 601 MKTLGDSSSQASLQMDSDSKVNPNLQDPFLKKS LHEKISNALDGSHSVMDLKQFHKNEQ 658
Sbjct: 601 MKTLGDSSSQASLQMDSDSKVNPNLQDPFLKKS LHEKISNALDGSHSVMDLKQFHKNEQ 658

>gi|19075347|ref|NP_587847.1| (NC_003421) putative b-zip transcription factor
[Schizosaccharomyces pombe]
gi|7492426|pir||T41672 probable b-zip transcription factor - fission yeast
(Schizosaccharomyces pombe)

gi|3560233|emb|CAA20701.1| (AL031530) putative b-zip transcription factor [Schizosaccharomyces pombe]
Length = 967

Score = 260 bits (665), Expect = 5e-68
Identities = 223/699 (31%), Positives = 322/699 (45%), Gaps = 137/699 (19%)

Query: 321 EYPLAVELKPFNTNRVGGHTAIFRFSKRAVCKALVNRENWYENIELCHKELLQFMPRYIG 380
+YP+ V L+PF ++VGGHTA FRFSKRAVCK L EN +YE IE CH ELL F+P+YIG
Sbjct: 306 DYPVTVRLEPFKHQVGGHTAFFRFSKRAVCKPLTRNENTFYETIEACHPELLPFIPKYIG 365

Query: 381 VLNVQRHFQSKDDFLSDLDQENNGKNDTSNENKDIEVNHNNNDIALNTEPTG-TPLTHI 439
VLNV ++ ND++ E +NTE + TP H
Sbjct: 366 VLNVTHITITKEE-----NDSTTE-----YVNTSSSKTPAPHK 399

Query: 440 HSFPLEHSSRQVLEKEHPEIESVHPHVKRSLSNQPSSLPEVVLNDRHIIPESLWYKY 499
H+F S +PEV + NRHI PE +
Sbjct: 400 HTF-----NSCYQKKDYGYPEVSVEQNRHIFPEWML--- 431

Query: 500 SDSPNSAPNDYFSSSSSHNSCSFGERGNTNKL----KRRDSGSTMINTELKNLVIREV 554
P+ + S H S S GER + + G+T+IN +L+ V+REV
Sbjct: 432 ---PDKRSHSYGSPKSLHHKSSSAGERPVSPFTVADIPKTPWGTTLINRKLREEVLREV 488

Query: 555 FAPKCFRRKRNSNTTGMGNHNRALGSSPSFLTQKSRSSH-DASNTSMKTL---GDSSSQ 610
FAPK RR+ + + +H PS S A D NTS + D +
Sbjct: 489 FAPKHARRRLGTRFHSRSSHR-----PSVFRDNSVAFGQLDNGNTSSRARDKDADPNKS 542

Query: 611 ASLQMDSDKVNPNLQDPFLKKSLEHKISNALDGSHSVMDLKQFHKNEQIKHKNSFCNS-- 668
S ++D + LH + A + +L N Q K F +
Sbjct: 543 LSCSVEDKHYD-----LHSAV--AEENEVDEELNVPNNQKSYRRFSSDAV 589

Query: 669 -----LSPILTATNSRDD-----GEFATSPN-YISNAQDGVFDMDEDTGNE--- 708
+S + +SR+ E ++PN + + D +F MD + +E
Sbjct: 590 WEEPESNEFPVSGTMDYDSRESTGHTIKELRSTPNSHGTVPDDSI FAMDNEENSELPP 649

Query: 709 TINMDNHGCHLDGSKN-MIIKSLAYNSNDYSHHDIES-----ITFEETSH- 753
+ G S + + SL + S D H S E+ H
Sbjct: 650 PLEPAEIGDPFRSVNDPRRVLSPHMASADEHRIPASDNQNNNNNDANALAENSESQHS 709

Query: 754 TIVSKFILLEDLTRNMNKPCLDLKMGTQYGVDAKRAKQLSQRACKLKTTSRRLGVRIC 813
T + ++I++EDLT M +PC LD+KMGTQYG+ A K+ SQ KC TTSR LGVRIC
Sbjct: 710 TQIERIVIEDLTSGMKRCPVLVDVKMGTRQYGIMATEKKKASQTKKCAMTTSRVLGVRIC 769

Query: 814 GLKVWNK--DYIYTRDKYFGRRVKVGWQFARVLARFLYDGKTIES-----LIRQIPRLI 865
G++VW+ Y DKY GR +K G +F L R+L GKT + L+ IP +I
Sbjct: 770 GMQVWHPWLQSYTFEDKYVGRDIKAGEEFQHALMRYL--GKTDDDEDNSHLLVHHIPTII 827

Query: 866 KQLDTLYSEIFNLKGYRLYGASLLLMYDGD---ANKSNSKRKKAANVKVNLIDFARCVTK 922
++L+ L + LKG RLY +SLL +YDG+ ++KS+ ++ K + + ++DFA CV
Sbjct: 828 RKLEQLEQIVRFLKGSRLYASSLLFLYDGEPPPSDKSKEKVKPREIDIRIVDFANCVFA 887

Query: 923 EDAMECMDKFRIPPKSPNIEDKGFLRGVKSRLRFYLLLIW 961
ED E + K PP+ + D+G++RG++LR Y L IW
Sbjct: 888 EDK-ELLAKATCPPQHKTIDYRGYVRGLRTLRLYFLKIW 925

>gi|18376053|emb|CAD21059.1| (AL669986) related to transcription factor KCS1 [Neurospora crassa]
Length = 1466

Score = 220 bits (560), Expect = 7e-56
Identities = 261/958 (27%), Positives = 405/958 (42%), Gaps = 195/958 (20%)

Query: 119 SSFILSNHEEPAIKPNKHVAHRNNITETGQSGEDIAKQ--QSHQ-PQVLHHQTSCLKPIQ 175
SS L EP K + + ++ E + E I+ HQ P+ + S P
Sbjct: 547 SSPSLDRKPEPRRKSASIEGSGHTEEGESGEEKISSAVFLPHQGPPEEAEEHSDVP-- 604

Query: 176 NVDEGCISPKSTYQESLHGISDRTLKPVSATYYPHKSKADSGYEEKDKMEN--DIDTI 233
G S ++ H +ED H +G E + ++ D++
Sbjct: 605 ----GAASSRTALPSRTHSRAEDF-----HSWLVKAGEPEVECLDECPDVEKT 648

Query: 234 QPATINCASGIATLPSSYNRHTFKVKTYSTLSQSLRQENVNRSNEKKPQQFVP----- 287
A AT+P + ++ T ++ E +KP Q +
Sbjct: 649 HRPAPKAADSAAATVFFVGS----QIDTGKVNPAVADEIETGVPPPQKPFQSIHHSRHH 704

Query: 288 -HSESIKEKPNTEFQDKEGEQADEEDEDEGDNHREYPL-AVELKPFNTNRVGGHTAIFRFS 345
H P D +GE +E+ PL A+EL P+ ++VGGHT ++RFS
Sbjct: 705 DHHHHHHRRHPPEAIHDHQGEPEEQ-----PLDAIELIPYKHQVGGHTTLWRFS 753

Query: 346 KRAVCKALVNRENRYENIELCHKELLQFMPRYIGVLNV-----RQHFQSKDDFLSDL 398
+RAVCK L NREN +YE IE H++LL F+PRYIGVLNV R+ KD+ + L
Sbjct: 754 RRAVCKQLNNRENEFYEKIERYHRDLLAFLPRYIGVLNVTFQKKPRKSVHKKDEAAAAAL 813

Query: 399 DQENNGKNDTSNENKDIEVNHNNNDIALNTEPTGTPLTHHSFPLEHSSRQVLEKEHPE 458
+ G++ E T + + + P H + + PE
Sbjct: 814 EAPTAGQD-----EATSSGVKGDEAAPTTHGA----QPAQPE 846

Query: 459 IESVHPHVKRSLSSSNQPSL--LPEVVLNDNRHIIPESLWKYSDSPNSAPNDSYFSSSS 516
+R +S S Q L +P V DN+HI+P SL S +S SS+S
Sbjct: 847 -----QRMISQSLQQLGQIPTVTFVDNQHILPRSLIQPALASSSSSFTRLRSASSAS 898

Query: 517 SHNSCSFGERGNTN-----KLKRRDS---GSTMINTLKNLVIREVFAPKCFRRKRNS 566
H + N +L+ R + G+TM+N L+N V + F +
Sbjct: 899 LHGRRIMNGQCAENPSHMLRPRLEDHRANSWGATMVNKRRLRNEVFNDALFKQ----- 950

Query: 567 NTTTTMGNNHARLGSSPSFLTQKSRAS-SHDASNTSMKTLGDSSSQASLQMDDSKVNPN--- 622
+ H + G F + + H S+ ++ D+ +AS ++S++ P
Sbjct: 951 ---PVAVHRHKKGHQRPFSRRSLQPVLRHTESDPNLDVAQDAKPRASSAGEESRLKPCDL 1007

Query: 623 -----NLQD---PFLKKSLEHKISNALDGSHSV-DLKQFHKNEQIKHKNSFCNS--LSP 671
NL F ++ + + + G+ + ++ + Q K K + +
Sbjct: 1008 VRSEENLATRPRSFREEGVEDDGPKDVTGTSAPPEILKDASPAQPKKKRRYSGTGLRRK 1067

Query: 672 ILTATNSRDDGEF---ATSPNYISNAQDGVFDMDEDTG---NETINMDNHGCHLDGSKNM 725
+SR D ++ A S Y ++ ++ VF+ G E+I + + +G N
Sbjct: 1068 PKDVEDSRGDLQYFEEADSAPYKADNEEPVFESGGVPGVPAEESIGPLDTTHNGTNGTNG 1127

Query: 726 IIKSL-AYNVSNDSYSHHDIESI-----TFEETSHTIVSKFILLEDLTRNMNKPALDL 777
+ S+ +++ H++I I + + + V F+LLEDLT M +PC +DL
Sbjct: 1128 VDASVNTDDLAPSSPHNEIAKIPRPINPKEAQTQDSRVEYFLLLEDLTAGMKRPMCIMDL 1187

Query: 778 KMGTRQYGVDAKRAKQLSQRACKLKTTSRRLGVRICGLKVVN--KDYYITRDKYFGRRVK 835
KMGTRQYGV+A KQ SQ+ KC KTTSR LGVR+CGL+VW+ Y+ +DKY+GR +K
Sbjct: 1188 KMGTRQYGEASPKKQKSQQGKCAKTTRELGVRCGLQVWDVATQSYVFKDKYYGRDLK 1247

Query: 836 VGWQFARVLARFLYDGKTIESLIRQIPRLIKQLDTLYSEIFNLKGYRLYGASLLMYDG- 894
G +F L RFLY+G S++R IP +++L L I LKGYR Y ASLL+ YDG
Sbjct: 1248 AGQEFQDALTRFLYNGVDRASILRHPTVLQKLAELEVIIRRLKGYRFYAASLLMFYDGE 1307

Query: 895 -----DANKSNSKRKKAANV----- 909
D + + S + + N
Sbjct: 1308 PLPPPAPPTPTSTTHSEYDTAMEDYYSTDFATDNDDAVSIKHRIDNTLNGSSSGGGGKKK 1367

Query: 910 -KVNLIIDF-----ARCVTKED-AMECMDKFRIPPKSPNIEDKGFLRGVKSIRFYLLLI 960
+ IDF A CVT ED A ++ PP+ P D GFLRG++SLR Y L I
Sbjct: 1368 KDKHEIDFKMADFANCVTAEDLAANGIEGKPCPPRYQEPDNGFLRGLRSLRRYFLRI 1425

>gi|16305265|gb|AAL17053.1|AF393812_1 (AF393812) inositol hexakisphosphate kinase 3 [Homo sapiens]

Length = 410

Score = 110 bits (276), Expect = 6e-23
Identities = 58/139 (41%), Positives = 88/139 (62%), Gaps = 5/139 (3%)

Query: 758 KFILLEDLTRNMNKPALDLKMGTRQYGVDAKRAKQLSQRACKLKTTSRRLGVRICGLKV 817
+F+LLE++ PC LDLKMGTRQ+G DA K+ KC ++TS LGVRICG++V
Sbjct: 197 RFLLENVVSQYTHPCVLDLKMGTROHGDDASEEKKARHMRKCAQSTSACLGVRICGMQV 256

Query: 818 WNKD--YYITRDKYFGRRVKVGWQFARVLARFLYDGKTIESLIRQIPRLIKQLDTLYSEI 875
+ D Y++ +DKY+GR++ V F + L +FL++G + + + ++ QL L S I

Sbjct: 257 YQTDKKYFLCKDKYYGRKLSVE-GFRQALYQFLHNGSHLRREL--LEPILHQLRALLSVI 313

Query: 876 FNLKGYRLYGASLLLMYDG 894
+ YR Y +SLL++YDG

Sbjct: 314 RSQSSYRFYSSSLLVIYDG 332

Score = 55.1 bits (131), Expect = 4e-06
Identities = 24/59 (40%), Positives = 40/59 (67%), Gaps = 3/59 (5%)

Query: 326 VELKPFTNRVGGHTAIFRFSKRAVCKALVNRENRWYENIELCHKELLQFMPRYIGVLNV 384
V+L+PF ++VGGH ++ ++ + VCK LV+RE R+YE++ K +F P+Y G + V
Sbjct: 16 VQLEPFLHQVGGHMSVMKYDEHTVCKPLVSREQRFYESLPQAMK---RFTPQYKGTVTV 71

>gi|18565021|ref|XP_084209.1| (XM_084209) inositol hexakisphosphate kinase 3 [Homo sapiens]
Length = 410

Score = 110 bits (276), Expect = 7e-23
Identities = 58/139 (41%), Positives = 88/139 (62%), Gaps = 5/139 (3%)

Query: 758 KFILLEDLTRNMNKPALDLKMGTRQYGVDAKRAKQLSQRACKLKTTSRRLGVRICGLKV 817
+F+LLE++ PC LDLKMGTRQ+G DA K+ KC ++TS LGVRICG++V
Sbjct: 197 RFLLENVVSQYTHPCVLDLKMGTQHGDDASEEKKARHMRKCAQSTSACLGVRICGMQV 256

Query: 818 WNKD--YYITRDKYFGRRVKVGWQFARVLARFLYDGKTIESLIRQIPRLIKQLDLYSEI 875
+ D Y++ +DKY+GR++ V F + L +FL++G + + + ++ QL L S I
Sbjct: 257 YQTDKKYFLCKDKYYGRKLSVE-GFRQALYQFLHNGSHLRREL--LEPILHQLRALLSVI 313

Query: 876 FNLKGYRLYGASLLLMYDG 894
+ YR Y +SLL++YDG
Sbjct: 314 RSQSSYRFYSSSLLVIYDG 332

Score = 57.4 bits (137), Expect = 8e-07
Identities = 25/59 (42%), Positives = 41/59 (69%), Gaps = 3/59 (5%)

Query: 326 VELKPFTNRVGGHTAIFRFSKRAVCKALVNRENRWYENIELCHKELLQFMPRYIGVLNV 384
V+L+PF ++VGGH ++ ++ + VCK LV+RE R+YE++ L K +F P+Y G + V
Sbjct: 16 VQLEPFLHQVGGHMSVMKYDEHTVCKPLVSREQRFYESLPLAMK---RFTPQYKGTVTV 71

>gi|16905371|ref|NP_473452.1| (NM_054111) inositol hexakisphosphate kinase 3 [Homo sapiens]
gi|16552031|dbj|BAB71225.1| (AK056586) unnamed protein product [Homo sapiens]
Length = 293

Score = 110 bits (274), Expect = 1e-22
Identities = 60/139 (43%), Positives = 89/139 (63%), Gaps = 5/139 (3%)

Query: 758 KFILLEDLTRNMNKPALDLKMGTRQYGVDAKRAKQLSQRACKLKTTSRRLGVRICGLKV 817
+F+LLE++ PC LDLKMGTRQ+G DA K+ KC ++TS LGVRICG++V
Sbjct: 80 RFLLENVVSQYTHPCVLDLKMGTQHGDDASEEKKARHMRKCAQSTSACLGVRICGMQV 139

Query: 818 WNKD--YYITRDKYFGRRVKVGWQFARVLARFLYDGKTIESLIRQIPRLIKQLDLYSEI 875
+ D Y++ +DKY+GR++ V F + L +FL++G + + + P L+ QL L S I
Sbjct: 140 YQTDKKYFLCKDKYYGRKLSVE-GFRQALYQFLHNGSHLRRELLE-PILL-QLRALLSII 196

Query: 876 FNLKGYRLYGASLLLMYDG 894
+ YR Y +SLL++YDG
Sbjct: 197 RSQSSYRFYSSSLLVIYDG 215

>gi|7305195|ref|NP_038813.1| (NM_013785) inositol hexaphosphate kinase 1; inositol
hexakisphosphate kinase 6 [Mus musculus]
gi|6524024|gb|AAE15056.1|AF177144_1 (AF177144) mammalian inositol hexakisphosphate kinase 1
[Mus
musculus]
Length = 433

Score = 105 bits (262), Expect = 3e-21
Identities = 78/266 (29%), Positives = 127/266 (47%), Gaps = 42/266 (15%)

Query: 719 LDSGKNMIIKSLAYNVSNDSYSHHDIESITFEETSHTIVSKFILLEDLTRNMNKPALDLK 778
LDS + + ++YN + H S E+ + KF+LLE++ + PC LDLK
Sbjct: 167 LDSNSGLSSEKISYNPWSLRCHKQQLSRMRSESKDRKLYKFLLENVHHFKYPCVLDLK 226

Query: 779 MGTRQYGVDAKRAKQLSQRACKLKTTSRRLGVRICGLKVWNKD--YYITRDKYFGRRVKV 836
MGTRQ+G DA K Q KC ++TS LGVR+CG++V+ D +Y+ R+KY+GR + +
Sbjct: 227 MGTRQHGDASA EKAARQMRKCEQSTSATLGVRVCGMQVYQLDTGHYLCRNKYYGRGLSI 286

Query: 837 GWQFARVLARFLYDGKTIESLIRQIPRLIKQLDTLYSEIFNLKGYRLYGASLLLMYDGDA 896
F L ++L++G + + + ++ +L L + + YR Y +SLL++YDG
Sbjct: 287 E-GFRNALYQYLHNGLDLRRDLFE--PILSKLRGLKAVLERQASYRFYSSSLLVIYDGKE 343

Query: 897 NKSNSKRKKA-----ANVKVNLIDFARCVTKEDAME 927
+S + K V V +IDFA K
Sbjct: 344 CRSELRLKHVDMGLPEVPPPCGPSTSPSSTSLEAGPSSPPKVDVRMIDFAHSTFK----- 398

Query: 928 CMDKFRIPPKSPNIEDKGFLRGVKS 953
FR P + D+G++ G++L
Sbjct: 399 ---GFRDDPTVHDGPDGRGYVFGLENL 421

Score = 58.9 bits (141), Expect = 3e-07
Identities = 30/78 (38%), Positives = 46/78 (58%), Gaps = 3/78 (3%)

Query: 307 QADEEEDEGDNHREYPLAVELKPFNTNRVGGHTAIFRFSKRAVCKALVNRENRYENIEL 366
Q E G N R V L+PF ++VGGH+++ R+ VCK L++RE R+YE++
Sbjct: 5 QTMEVGQYGNASRAGDRGVLLPEFIHQVGGHSSMMRYDDHTVCKPLISREQRFYESLP- 63

Query: 367 CHKELLQFMPRYIGVLNV 384
E+ +F P Y GV++V
Sbjct: 64 --PEMKEFTPEYKGVVSV 79

>gi|10280996|dbj|BAB13737.1| (AB049151) inositol hexakisphosphate kinase [Rattus norvegicus]
Length = 433

Score = 104 bits (260), Expect = 5e-21
Identities = 78/266 (29%), Positives = 127/266 (47%), Gaps = 42/266 (15%)

Query: 719 LDSGKNMIIKSLAYNVSNDSYSHHDIESITFEETSHTIVSKFILLEDLTRNMNKPALDLK 778
LDS + + ++YN + H S E+ + KF+LLE++ + PC LDLK
Sbjct: 167 LDSNSGLSSEKISYNPWSLRCHKQQLSRMRSESKDRKLYKFLLENVHHFKYPCVLDLK 226

Query: 779 MGTRQYGVDAKRAKQLSQRACKLKTTSRRLGVRICGLKVWNKD--YYITRDKYFGRRVKV 836
MGTRQ+G DA K Q KC ++TS LGVR+CG++V+ D +Y+ R+KY+GR + +
Sbjct: 227 MGTRQHGDASA EKAARQMRKCEQSTSASLGVRVCGMQVYQLDTGHYLCRNKYYGRGLSI 286

Query: 837 GWQFARVLARFLYDGKTIESLIRQIPRLIKQLDTLYSEIFNLKGYRLYGASLLLMYDGDA 896
F L ++L++G + + + ++ +L L + + YR Y +SLL++YDG
Sbjct: 287 E-GFRNALYQYLHNGLDLRRDLFE--PILSKLRGLKAVLERQASYRFYSSSLLVIYDGKE 343

Query: 897 NKSNSKRKKA-----ANVKVNLIDFARCVTKEDAME 927
+S + K V V +IDFA K
Sbjct: 344 CRSELRLKHVDMGLPEVPPPCGPSTSPSNTSLEAGPSSPPKVDVRMIDFAHSTFK----- 398

Query: 928 CMDKFRIPPKSPNIEDKGFLRGVKS 953
FR P + D+G++ G++L
Sbjct: 399 ---GFRDDPTVHDGPDGRGYVFGLENL 421

Score = 58.5 bits (140), Expect = 4e-07
Identities = 30/78 (38%), Positives = 46/78 (58%), Gaps = 3/78 (3%)

Query: 307 QADEEEDEGDNHREYPLAVELKPFNTNRVGGHTAIFRFSKRAVCKALVNRENRYENIEL 366
Q E G N R V L+PF ++VGGH+++ R+ VCK L++RE R+YE++
Sbjct: 5 QTMEVGQYGNASRAGDRGVLLPEFIHQVGGHSSMMRYDDHTVCKPLISREQRFYESLP- 63

Query: 367 CHKELLQFMPRYIGVLNV 384
E+ +F P Y GV++V
Sbjct: 64 --PEMKEFTPEYKGVVSV 79

>gi|14722051|ref|XP_028610.1| (XM_028610) KIAA0263 gene product [Homo sapiens]
Length = 276

Score = 103 bits (256), Expect = 1e-20
Identities = 66/212 (31%), Positives = 114/212 (53%), Gaps = 8/212 (3%)

Query: 719 LD SGKNMIIKSLAYNVSN DYSHHDIESITFEETSHTIVSKFILLEDLTRNMNKP CALDLK 778
LD + + +++N + H S E+ + KF+LLE++ + PC LDLK
Sbjct: 2 LDGNSGLSSEKISHNPWSLRCHKQQLSRMRSESKDRKLYKFLLENV VHHFKYPCVLDLK 61

Query: 779 MGTRQYGVDAKRAKQLSQR AKCLKTTSRR LGVRICGLKVWNKD--YYITRD KYFGRRVKV 836
MGTRQ+G DA K Q KC ++TS LGVR+CG++V+ D +Y+ R+KY+GR + +
Sbjct: 62 MGTRQHGD DASA EKAARQMRKEQSTSATLGVRVCGMQVYQLDTGHYLCRNKY YGRGLSI 121

Query: 837 GWQFARVLARFLYDGKTIESLRQIPRLIKQLDTLYSEIFNLKGYRLYGASLLL MYDGDA 896
F L ++L++G + + + ++ +L L + + YR Y +SLL++YDG
Sbjct: 122 E-GFRNALYQYLHNGLDLRRDLFE--PILSKLRGLKAVLERQASYRFYSSSLLVIYDGKE 178

Query: 897 NKSNSKRKKAANVKVNLIDFARCVTKEDAMEC 928
++ S + + +++ +D V E A C
Sbjct: 179 CRAESCLDRRSEMRLKHLDM---VLPEVASSC 207

>gi|6683115|dbj|BAA13393.2| (D87452) KIAA0263 protein [Homo sapiens]
Length = 462

Score = 102 bits (255), Expect = 2e-20
Identities = 66/212 (31%), Positives = 114/212 (53%), Gaps = 8/212 (3%)

Query: 719 LD SGKNMIIKSLAYNVSN DYSHHDIESITFEETSHTIVSKFILLEDLTRNMNKP CALDLK 778
LD + + +++N + H S E+ + KF+LLE++ + PC LDLK
Sbjct: 188 LDGNSGLSSEKISHNPWSLRCHKQQLSRMRSESKDRKLYKFLLENV VHHFKYPCVLDLK 247

Query: 779 MGTRQYGVDAKRAKQLSQR AKCLKTTSRR LGVRICGLKVWNKD--YYITRD KYFGRRVKV 836
MGTRQ+G DA K Q KC ++TS LGVR+CG++V+ D +Y+ R+KY+GR + +
Sbjct: 248 MGTRQHGD DASA EKAARQMRKEQSTSATLGVRVCGMQVYQLDTGHYLCRNKY YGRGLSI 307

Query: 837 GWQFARVLARFLYDGKTIESLRQIPRLIKQLDTLYSEIFNLKGYRLYGASLLL MYDGDA 896
F L ++L++G + + + ++ +L L + + YR Y +SLL++YDG
Sbjct: 308 E-GFRNALYQYLHNGLDLRRDLFE--PILSKLRGLKAVLERQASYRFYSSSLLVIYDGKE 364

Query: 897 NKSNSKRKKAANVKVNLIDFARCVTKEDAMEC 928
++ S + + +++ +D V E A C
Sbjct: 365 CRAESCLDRRSEMRLKHLDM---VLPEVASSC 393

Score = 58.9 bits (141), Expect = 3e-07
Identities = 30/78 (38%), Positives = 46/78 (58%), Gaps = 3/78 (3%)

Query: 307 QADEEEDEGDNEHREYPLAVELKPFTNRVGGHTAIFRF SKRAVCKALVNREN R WYENIEL 366
Q E G N R V L+PF ++VGGH+++ R+ VCK L++RE R+YE++
Sbjct: 26 QTMEVGQYGNASRAGDRGVLLPEFPIHQVGGHSSMMRYDDHTVCKPLISREQRFYESLP- 84

Query: 367 CHKELLQFMPRYIGVLNV 384
E+ +F P Y GV++V
Sbjct: 85 --PEMKEFTPEYKGVSV 100

>gi|15277917|gb|AAH12944.1|AAH12944 (BC012944) Unknown (protein for MGC:9925) [Homo sapiens]
Length = 441

Score = 102 bits (253), Expect = 3e-20
Identities = 66/212 (31%), Positives = 114/212 (53%), Gaps = 8/212 (3%)

Query: 719 LD SGKNMIIKSLAYNVSN DYSHHDIESITFEETSHTIVSKFILLEDLTRNMNKP CALDLK 778
LD + + +++N + H S E+ + KF+LLE++ + PC LDLK
Sbjct: 167 LDGNSGLSSEKISHNPWSLRCHKQQLSRMRSESKDRKLYKFLLENV VHHFKYPCVLDLK 226

Query: 779 MGTRQYGVDAKRAKQLSQR AKCLKTTSRR LGVRICGLKVWNKD--YYITRD KYFGRRVKV 836
MGTRQ+G DA K Q KC ++TS LGVR+CG++V+ D +Y+ R+KY+GR + +

Sbjct: 227 MGTRQHGDASA EKAARQMRKCEQSTSATLGVRVCGMQVYQLDTGHYLCRNKYYGRGLSI 286

Query: 837 GWQFARVLARFLYDGKTIESLIRQIPRLIKQLDTLYSEIFNLKGYRLYGASLLLMYDGD 896
F L ++L++G + + + ++ +L L + + YR Y +SLL++YDG

Sbjct: 287 E-GFRNALYQYLHNGLDLRRDLFE--PILSKLRGLKAVLERQASRYFYSSLLVIYDGKE 343

Query: 897 NKSNSKRKKAANVKVNLIDFARCVTKEDAMEC 928
++ S + + +++ +D V E A C

Sbjct: 344 CRAESCLDRRSEMRKHLDM--VLPEVASSC 372

Score = 58.5 bits (140), Expect = 4e-07
Identities = 30/78 (38%), Positives = 46/78 (58%), Gaps = 3/78 (3%)

Query: 307 QADEEEDGNEHREYPLAVELKPFTRNVGHTAIFRFSKRAVCKALVNRENRWYENIEL 366
Q E G N R V L+PF ++VGGH+++ R+ VCK L++RE R+YE++

Sbjct: 5 QTMEVGQYKGNASRAGDRGVLLPEFIHQVGGHSSMMRYDDHTVCKPLISREQRFYESLP- 63

Query: 367 CHKELLQFMPRYIGVLNV 384
E+ +F P Y GV++V

Sbjct: 64 --PEMKEFTPEYKGVVSV 79

>gi|18485446|ref|XP_079965.1| (XM_079965) CG10082 [Drosophila melanogaster]
gi|19922696|ref|NP_611595.1| (NM_137751) CG10082 gene product [Drosophila melanogaster]
gi|15010388|gb|AAK77242.1| (AY047510) GH01729p [Drosophila melanogaster]
Length = 672

Score = 99.4 bits (246), Expect = 2e-19
Identities = 59/150 (39%), Positives = 86/150 (57%), Gaps = 5/150 (3%)

Query: 747 TFEETSHTIVSKFILLEDLTRNMNKPICALDLKMGTRQYGVDAKRAKQLSQRACKLKTTSR 806
+ + +T F++LE++T PC LDLKMGTRQ+G DA K+ Q AKC +TS

Sbjct: 61 SISQLDNTNKQYFLMLENITSQFRNPCILDLMGTRQHGDASA EKRKQMAKCAASTSG 120

Query: 807 RLGVRICGLVWNKDY--YITRDKYFGRRVKVGWQFARVLARFLYDGKTIESLIRQIPRL 864
LGVR+CG++ + D Y RDKY+GR + G F L F ++G + IR I ++

Sbjct: 121 SLGVRICGMQTYLADLEQYAKRDKYWGRELNEG-GFKTALHDFHNGYRLR--IRVIRKI 177

Query: 865 IKQLDTLYSEIFNLKGYRLYGASLLLMYDG 894
+++L L I YR Y SLL++Y+G

Sbjct: 178 LQRLQLRRVIEKQSSYRFYSCSLIVYEG 207

>gi|7291313|gb|AAF46743.1| (AE003454) CG10082 gene product [Drosophila melanogaster]
Length = 893

Score = 99.0 bits (245), Expect = 3e-19
Identities = 59/150 (39%), Positives = 86/150 (57%), Gaps = 5/150 (3%)

Query: 747 TFEETSHTIVSKFILLEDLTRNMNKPICALDLKMGTRQYGVDAKRAKQLSQRACKLKTTSR 806
+ + +T F++LE++T PC LDLKMGTRQ+G DA K+ Q AKC +TS

Sbjct: 282 SISQLDNTNKQYFLMLENITSQFRNPCILDLMGTRQHGDASA EKRKQMAKCAASTSG 341

Query: 807 RLGVRICGLVWNKDY--YITRDKYFGRRVKVGWQFARVLARFLYDGKTIESLIRQIPRL 864
LGVR+CG++ + D Y RDKY+GR + G F L F ++G + IR I ++

Sbjct: 342 SLGVRICGMQTYLADLEQYAKRDKYWGRELNEG-GFKTALHDFHNGYRLR--IRVIRKI 398

Query: 865 IKQLDTLYSEIFNLKGYRLYGASLLLMYDG 894
+++L L I YR Y SLL++Y+G

Sbjct: 399 LQRLQLRRVIEKQSSYRFYSCSLIVYEG 428

Score = 39.7 bits (91), Expect = 0.18
Identities = 36/131 (27%), Positives = 58/131 (43%), Gaps = 8/131 (6%)

Query: 252 NRHTFKVKTSTLSQSLRQENVNNSRNEKKPQQFVPHSESIKEKPNTEQDKEGEQADEE 311
N V + + S S + + + KPQ+ P K +

Sbjct: 103 NLQQLSVSSSNASSSSNNNSASGCNTPTKPQKQKPLLLPEAAASTATAVGSSKNPQLS 162

Query: 312 EDEGDNEHREYPLAVELKPFTRNVGHTAIFRFSKRAVCKALVNRENRWYENIELCHKEL 371

+D DNE V L P +N+VGGHT + ++ V K L RE +Y+NI +++
Sbjct: 163 KDLLDNEDE-----VALHPLSNQVGGHTRLLLLNQSTVIKPLNLRELDYQNIPI---QDI 214

Query: 372 LQFMPRYIGVL 382

L+F+P+Y GV+

Sbjct: 215 LKFVPKYKGV 225

>gi|7705553|ref|NP_057375.1| (NM_016291) mammalian inositol hexakisphosphate kinase 2 [Homo sapiens]

gi|6524026|gb|AAF15057.1|AF177145_1 (AF177145) mammalian inositol hexakisphosphate kinase 2 [Homo sapiens]

Length = 426

Score = 98.6 bits (244), Expect = 3e-19

Identities = 57/148 (38%), Positives = 87/148 (58%), Gaps = 5/148 (3%)

Query: 749 EETSHTIVSKFILLEDLTRNMNKPCLDLKMGTRQYGVDAKRAKQLSQRACLKTTSRRL 808

E H KFILLE+LT PC LDLKMGTRQ+G DA K +Q KC ++TS +

Sbjct: 193 ENAKHRNQYKFILLENLTSRYEVPCVLDLKMGTQHGDDASEEKAANQIRKCQSTSAVI 252

Query: 809 GVRICGLKVWN--KDYITRDKYFGRRVKGWQFARVLARFLYDGKTIESLIRQIPRLIK 866

GVR+CG++V+ + +KY GR++ V F L +F ++G+ + + + ++K

Sbjct: 253 GVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQ-GFKEALFQFFHNGRYLRREL--LGPVLK 309

Query: 867 QLDTLYSEIFNLKGYRLYGASLLMYDG 894

+L L + + + YR Y +SLL++YDG

Sbjct: 310 KLTELKAVLERQESYRFYSSSLLVIYDG 337

Score = 58.5 bits (140), Expect = 4e-07

Identities = 28/68 (41%), Positives = 47/68 (68%), Gaps = 5/68 (7%)

Query: 326 VELKPFTNRVGGHTAIFRSKRAVCKALVNRENRWYENIELCHKELLQFMPRYIGVLNVR 385

V L+PF ++VGGH+ + RE++ +CK LV RE+++YE + E+ +F P+Y GV++VR

Sbjct: 17 VLLEPFVHQVGGHSCVLRFNETTLCKPLVPREHQFYETLP---AEMRKFTPQYKGVSVR 73

Query: 386 QHFQSKDD 393

F+ +D

Sbjct: 74 --FEDEED 79

>gi|14736134|ref|XP_030060.1| (XM_030060) mammalian inositol hexakisphosphate kinase 2 [Homo sapiens]

gi|9955981|gb|AAG01984.1| (AY007091) similar to Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA with GenBank

Accession Number AF177145

gi|18043111|gb|AAH19694.1|AAH19694 (BC019694) Unknown (protein for MGC:24971) [Homo sapiens]

Length = 426

Score = 98.6 bits (244), Expect = 3e-19

Identities = 57/148 (38%), Positives = 87/148 (58%), Gaps = 5/148 (3%)

Query: 749 EETSHTIVSKFILLEDLTRNMNKPCLDLKMGTRQYGVDAKRAKQLSQRACLKTTSRRL 808

E H KFILLE+LT PC LDLKMGTRQ+G DA K +Q KC ++TS +

Sbjct: 193 ENAKHRNQYKFILLENLTSRYEVPCVLDLKMGTQHGDDASEEKAANQIRKCQSTSAVI 252

Query: 809 GVRICGLKVWN--KDYITRDKYFGRRVKGWQFARVLARFLYDGKTIESLIRQIPRLIK 866

GVR+CG++V+ + +KY GR++ V F L +F ++G+ + + + ++K

Sbjct: 253 GVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQ-GFKEALFQFFHNGRYLRREL--LGPVLK 309

Query: 867 QLDTLYSEIFNLKGYRLYGASLLMYDG 894

+L L + + + YR Y +SLL++YDG

Sbjct: 310 KLTELKAVLERQESYRFYSSSLLVIYDG 337

Score = 58.5 bits (140), Expect = 4e-07

Identities = 28/68 (41%), Positives = 47/68 (68%), Gaps = 5/68 (7%)

Query: 326 VELKPFTNRVGGHTAIFRSKRAVCKALVNRENRWYENIELCHKELLQFMPRYIGVLNVR 385

Sbjct: 17 V L+PF ++VGGH+ + RF++ +CK LV RE+++YE + E+ +F P+Y GV++VR
VLLEPFVHQVGGHSCVLRFNETTLCPLVPREHQFYETLP---AEMRKFTPQYKGVSVR 73

Query: 386 QHFQSKDD 393

F+ +D

Sbjct: 74 --FEEDED 79

>gi|1872498|gb|AAB49289.1| (U74297) PiUS [Oryctolagus cuniculus]
Length = 425

Score = 98.6 bits (244), Expect = 4e-19
Identities = 62/173 (35%), Positives = 96/173 (54%), Gaps = 14/173 (8%)

Query: 733 NVSNDYSHHDIESITF-----EETSHTIVSKFILLEDLTRNMNKPICALDLKMGTRQ 783

NVS+ H++ S+ E H KFILLE+LT PC LDLKMGTRQ
Sbjct: 167 NVSSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFILLENLTSRYEVPVLDLKMGTRO 226

Query: 784 YGVDAKRAKQLSQRACCLKTTSRRLGVRICGLKVWN--KDYIITRDKYFGRRVKVGWQFA 841

+G DA K +Q KC ++TS +GVR+CG++V+ + +KY GR++ V F
Sbjct: 227 HGDDASEEKAANQIRKCCQSTSAVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQ-GFK 285

Query: 842 RVLARFLYDGKTIESLIRQIPRLIKQLDLYSEIFNLKGYRLYGASLLLMYDG 894

L +F ++G+ + + + ++K+L L + + + YR Y +SLL++YDG
Sbjct: 286 EALFQFFHNGRYLRREL--LGPVLKLAELKAVLERQESYRFYSSSLLVIYDG 336

Score = 54.7 bits (130), Expect = 6e-06
Identities = 23/57 (40%), Positives = 41/57 (71%), Gaps = 3/57 (5%)

Query: 328 LKPFTRNVGHTAIFRFSKRAVCKALVNRENRYENIELCHKELLQFMPRYIGVLNV 384

L+PF ++VGGH+ + RF++ +CK L+ RE+++YE + E+ +F P+Y GV++V
Sbjct: 19 LEFVHQVGGHSCVLRFNETTLCPLIPREHQFYETLP---AEMRKFTPQYKGVSV 72

>gi|7512923|pir||T17246 hypothetical protein DKFZp586M0617.1 - human (fragment)
gi|5911911|emb|CAB55936.1| (AL117458) hypothetical protein [Homo sapiens]
Length = 351

Score = 97.1 bits (240), Expect = 1e-18
Identities = 57/148 (38%), Positives = 87/148 (58%), Gaps = 5/148 (3%)

Query: 749 EETSHTIVSKFILLEDLTRNMNKPICALDLKMGTRQYGVDAKRAKQLSQRACCLKTTSRRL 808

E H KFILLE+LT PC LDLKMGTRQ+G DA K +Q KC ++TS +
Sbjct: 118 ENAKHRNQYKFILLENLTSRYEVPVLDLKMGTROHGDDASEEKAANQIRKCCQSTSAVI 177

Query: 809 GVRICGLKVWN--KDYIITRDKYFGRRVKVGWQFARVLARFLYDGKTIESLIRQIPRLIK 866

GVR+CG++V+ + +KY GR++ V F L +F ++G+ + + + ++K
Sbjct: 178 GVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQ-GFKEALFQFFHNGRYLRREL--LGPVLK 234

Query: 867 QLDLYSEIFNLKGYRLYGASLLLMYDG 894

+L L + + + YR Y +SLL++YDG
Sbjct: 235 KLTELKAVLERQESYRFYSSSLLVIYDG 262

>gi|11067377|ref|NP_067692.1| (NM_021660) PiUS protein [Rattus norvegicus]
gi|6484372|dbj|BAA87611.1| (AB015723) PiUS [Rattus norvegicus]
Length = 424

Score = 96.3 bits (238), Expect = 2e-18
Identities = 57/148 (38%), Positives = 87/148 (58%), Gaps = 5/148 (3%)

Query: 749 EETSHTIVSKFILLEDLTRNMNKPICALDLKMGTRQYGVDAKRAKQLSQRACCLKTTSRRL 808

E H KFILLE+LT PC LDLKMGTRQ+G DA K +Q KC ++TS +
Sbjct: 191 ENAKHRNQYKFILLENLTCRYEVPVLDLKMGTROHGDDASEEKAANQIRKCCQSTSAVI 250

Query: 809 GVRICGLKVWN--KDYIITRDKYFGRRVKVGWQFARVLARFLYDGKTIESLIRQIPRLIK 866

GVR+CG++V+ + +KY GR++ V F L +F ++G+ + + + ++K
Sbjct: 251 GVRVCGMQVYQAGTQQLMFMNKYHGRKLSVQ-GFKEALFQFFHNGRYLRRELLGL--VLK 307

Query: 867 QLDLYSEIFNLKGYRLYGASLLLMYDG 894

+L L + + + YR Y +SLL++YDG

Sbjct: 308 KLTELKAVLERQESYRFYSSSLVIYDG 335

>gi|17507001|ref|NP_492519.1| (NM_060118) F30A10.3.p [Caenorhabditis elegans]
gi|7500181|pir||T21569 hypothetical protein F30A10.3 - Caenorhabditis elegans
gi|3876555|emb|CAB03023.1| (Z81072) cDNA EST EMBL:Z14598 comes from this gene [Caenorhabditis elegans]
Length = 323

Score = 95.5 bits (236), Expect = 3e-18
Identities = 60/162 (37%), Positives = 93/162 (57%), Gaps = 14/162 (8%)

Query: 759 FILLEDLTRNMNKPICALDLKMGTRQYGVDAKRAKQLSQRACKLTTSRRLGVRICGLKVV 818
F+LLE++ + +PC LDLK+GTRQ+G DA +K+ Q KC +TS LGVR+ G++++
Sbjct: 132 FLLLENVVAHYTRPCVLDLKGITRQHGDDASESKRHRQLMKCRHSTSATLGVRVVGMLY 191

Query: 819 NKDY--YITRDKYFGRRVKVGWQFARVLARFLY-DGKTIESLIRQIPRLIKQLDTLYSEI 875
+ Y +K GRR+ F + RF+ G++ + IRQ +L L S +
Sbjct: 192 EAETKSYSYVEKQEGRRIDAA-GFRGYVKRFKCCGRSRAAIRQ-----KLSKLSLL 244

Query: 876 FNLKGYRLYGASLLMYDGDANKSNSKRKKAANVKVNLIDFA 917
+GYR + AS+L+ +D +A S+S VKV +IDFA
Sbjct: 245 AEFEGYRFFSASILIAFDAEADSSSDDA----VKVCIIDFA 282

>gi|17555592|ref|NP_497443.1| (NM_065042) Y22D7AR.6.p [Caenorhabditis elegans]
gi|13559660|gb|AAK29869.1| (AC084154) Hypothetical protein Y22D7AR.6 [Caenorhabditis elegans]
Length = 323

Score = 79.3 bits (194), Expect = 2e-13
Identities = 64/208 (30%), Positives = 95/208 (44%), Gaps = 39/208 (18%)

Query: 740 HHDIESTFEET-----SHTIVSKFILLEDLTRNMNKPICALDLKMGTRQYGVDAKRA 791
HH +E++ E+ + FI+L DLT M P LDLK+GTRQ+G A +
Sbjct: 90 HHQLENVVIPESIEGSPILNKRKLSKNFIVLSDLTYRMKSPRILDLKLGTRQHGDAQTVS 149

Query: 792 KQLSQRACKLTTSRRLGVRICGLKV-----WNKDYITRDKY 829
K AKC TTS LG+R+CG+K+ + I+ +KY
Sbjct: 150 KIACMTAKCQATTSATLGIRLCGMKIPFLEQNSQNFAPNFAPNSAAPNFAPKSEISINKY 209

Query: 830 FGRRVKVGWQFARVLARFLYDGKTIESLIRQIPRLIKQLDTLYSEIFNLKGYRLYGASLL 889
GR + F V F +E + R RL+ D L G RL+GASLL
Sbjct: 210 MGRSMKDTDLFLAVKQFFDVPEAVLEEVER---RLLGIRDVLCGA----DGVRLFGASLL 262

Query: 890 LMYDGDANKSNSKRKKAANVKVNLIDFA 917
++ ++N S+S+ V++ ++DFA
Sbjct: 263 IVI--ESNFSDSLPIIDNLVRIKVVDFDA 288

>gi|8744998|emb|CAB95220.1| (AL359773) hypothetical protein P1295.12 [Leishmania major]
Length = 1086

Score = 77.4 bits (189), Expect = 8e-13
Identities = 54/200 (27%), Positives = 92/200 (46%), Gaps = 22/200 (11%)

Query: 756 VSKFILLEDLTRNMNKPICALDLKMGTRQYGVDAKRAKQLSQRACKLTTSRRLGVRICGL 815
+ I+LE + +PC +D+KMG+RQYG+ K+ S+ K +TS R G+R+ G
Sbjct: 902 ICHMIMLEYVCYFRFRPCVMDIKMGSRQYGLHPSAEKKRSKERKARLSTSARYGIRLAGY 961

Query: 816 KVWNKD--YYITRDKYFGRRVKVGWQFARVLARFLYDGKTIESLIRQIPRLIKQLDTLYS 873
+ WN D Y R K R + + + ++ FL + +E + R +QL L
Sbjct: 962 RRWNADEGRYNCRSKLQCRCLSLN-EVKSEMSTFLLHSREMEQVFR-----RQLQRLRV 1014

Query: 874 EIFNLKGYRLYGASLLMYDGDANKSNSKRKKAANVKVNLIDFARCVTKEDAMECMDKFR 933
+R Y +SLL +YD D +V ++DFA ++ ++ D
Sbjct: 1015 AFSQQTIFRFTYSSLLFVYDAD-----DPLKTARVTMVDFAITYTESKELLQGGD--- 1063

Query: 934 IPPKSPNIEDKGFLRGVKS 953
P + D G+L+ + +L
Sbjct: 1064 --PDADFVDYDVGYLKALDTL 1081

>gi|19114505|ref|NP_593593.1| (NC_003424) putative arginine metabolism transcriptional control

protein [Schizosaccharomyces pombe]
gi|11359225|pir|T50224 probable arginine metabolism transcription control protein
[imported] - fission yeast (Schizosaccharomyces pombe)
gi|6624600|emb|CAB63791.1| (AL135751) putative arginine metabolism transcriptional control
protein [Schizosaccharomyces pombe]
Length = 268

Score = 58.9 bits (141), Expect = 3e-07
Identities = 54/188 (28%), Positives = 84/188 (43%), Gaps = 19/188 (10%)

Query: 739 SHHDIESIT--FEETSHTIVSKFILEDLTRNMNKPALDLKMGTRQYGVDAKRAKQLSQ 796
S DIE I E + ++ K I+LE++ M PC +D+K+G + + DA K+

Sbjct: 60 SSRDIEGINPIAESVAFSLTGKAIILENILEYQMETPCVMDIKLGKQLWADDAPLEKRRRL 119

Query: 797 RAKCLKTTSRRLGVRICGLKVWNK--DYYITRDKYFGRR-----VKVGWQFARVLARFLY 849
A TTS LG RI G+ W++ + YI R +G+ V G V

Sbjct: 120 DAVSRSTTSGSLGFRITGILSWDRNTNTYIKRSTAWGKTLTDSDDVEGLNDFVSCSLSQ 179

Query: 850 DGKTIESLIRQIPRLIKQLDLYSEIFNLKGYRLYGASLLMYDGDANKSNSKRKKAANV 909
+ +ES + L+K + SE + L +S+L +Y D + N +NV

Sbjct: 180 KARLVESFL----NLLKLFVEVDLSESY----IELKSSSILFVY--DYSSLNPTYHCESNV 229

Query: 910 KVNLIIDFA 917
+ LID A

Sbjct: 230 VLKLIIDLA 237

>gi|19705555|ref|NP_599244.1| (NM_134417) inositol polyphosphate multikinase [Rattus
norvegicus]

gi|13162658|gb|AAG42923.1| (AY014898) inositol polyphosphate multikinase [Rattus norvegicus]
Length = 396

Score = 57.0 bits (136), Expect = 1e-06
Identities = 42/178 (23%), Positives = 85/178 (47%), Gaps = 9/178 (5%)

Query: 759 FILLEDLTRNMNKPALDLKMGTRQYGVDAKRAKQLSQRAKCLKTTSRRLGVRICGLKVW 818
++ LED+T NKPC +D+K+G + Y A K Q +K +G + G++V+

Sbjct: 110 YLKLEVDVTHKFNKPCIMDVKIGRKSYPFASAEKIQQVSK--YPLMEEIGFLVLGMRVY 167

Query: 819 --NKDYYITRDKYFGRRVKVGWQFARVLARFLYDGKTIESLIRQIPRLIKQLDLYSEIF 876
+ D Y T++++GR + +++F ++G + + I++++ +

Sbjct: 168 HLHSDSYETQNHYGRGL-TKETLKEGVSKFFHNGFCLRK--DAVAASIQKVEKILQWFE 224

Query: 877 NLKGYRLYGASLLMYDGDANKSNSKRKKAANVKNLIDFARCVTKEDAMECMDKFRI 934
N K Y +SLL +Y+G + + +K L A ++ D +EC + F +

Sbjct: 225 NQKQLNFYASSLLFVYEGSSQPATTKSNDRTLGRFLSKGA--LSDADVLECNNNFHL 280

>gi|12804837|gb|AAH01864.1|AAH01864 (BC001864) Similar to mammalian inositol hexakisphosphate
kinase 2

[Homo sapiens]
Length = 70

Score = 56.2 bits (134), Expect = 2e-06
Identities = 24/56 (42%), Positives = 39/56 (68%), Gaps = 3/56 (5%)

Query: 326 VELKPFTNRVGGHTAIFRFSKRAVCKALVNRENRWYENIELCHKELLQFMPRYIGV 381
V L+PF ++VGGH+ + RF++ +CK LV RE+++YE + E+ +F P+Y GV

Sbjct: 17 VLLEPFVHQVGGHSCVLRNFNETTLCKPLVPREHQFYETLP---AEMRKFTPQYKGV 69

>gi|7296185|gb|AAF51477.1| (AE003589) CG13688 gene product [Drosophila melanogaster]
Length = 291

Score = 54.7 bits (130), Expect = 5e-06
Identities = 55/218 (25%), Positives = 101/218 (46%), Gaps = 41/218 (18%)

Query: 759 FILLEDLTRNMNKPALDLKMGTRQYGVDAKRAKQLSQRAKCLKTTSRRLGVRICGLKVW 818
F+ LEDLTR+ KPC +D+KMG R + ++ K+ + AK + ++LG+ + G +V+

Sbjct: 82 FLRLLEDLTRSYPKPCVMDVKMGKRTWDPESSPNKRKVEEAKYV-MCKQKLGCLPGFQVY 140

Query: 819 -----NKDYYITRD-KYFGRRVKVGWQFARVLARFLYDGKTIESLIRQ-----IPRLI 865

```

++ I R K +G+ + V F + +A F ++ T +S R+ + ++
Sbjct: 141 LPKEEHTQETTLRHGKDYGKSLNVE-GFKQTMALF-FNASTSDSKSRRAGCELLLKEVL 198

Query: 866 KQLDTLYSEIFNLKGYRLYGASLLLMYD----GDANKS-----NSKRKKAANVKVNLID 915
+QL + + + Y +SLL+ YD D K + A V+V +ID
Sbjct: 199 RQLQEILAWFQRQRLLFYASSLLICYDYSLRADPPKPLINGYHQNDDDPATWVRVKMID 258

Query: 916 FARCVTKEAMECMDKFRIPPKSPNIEDKGFLRGVKS 953
FA + P + D+ ++ G++SL
Sbjct: 259 FA-----HVYPAEQGLPDENYMFGLQSL 281

>gi|11360184|pir||T46275 hypothetical protein DKFZp564L0678.1 - human
gi|6808172|emb|CAB70780.1| (AL137514) hypothetical protein [Homo sapiens]
Length = 97

Score = 54.7 bits (130), Expect = 5e-06
Identities = 23/55 (41%), Positives = 38/55 (68%), Gaps = 3/55 (5%)

Query: 326 VELKPFNTNRVGHTAIFRSKRAVCKALVNRENRWYENIELCHKELLQFMPRIYIG 380
V L+PF ++VGGH+ + RF++ +CK LV RE+++YE + E+ +F P+Y G
Sbjct: 17 VLLEPFVHQVGGHSCVLRFNETTLCPLVPREHQFYETLP---AEMRKFTPYQKG 68

>gi|17569885|ref|NP_510724.1| (NM_078323) T20F7.3.p [Caenorhabditis elegans]
gi|7508077|pir||T25898 hypothetical protein T20F7.3 - Caenorhabditis elegans
gi|13325009|gb|AAK18979.1| (U97550) Hypothetical protein T20F7.3 [Caenorhabditis elegans]
Length = 280

Score = 53.5 bits (127), Expect = 1e-05
Identities = 44/165 (26%), Positives = 77/165 (46%), Gaps = 15/165 (9%)

Query: 759 FILLEDLTRNMNKPICALDLKMGTROYGVDAKRAKQLSQRACLKTTSRRLGVRICGLKVV 818
++L++D P LDLK+GTR + K+++ K L TT+ LG+R+ G
Sbjct: 106 YLLMKDEAHAASPRILDLKLGRTRTHSDYISEEKKINHIKSLSTTTAVLGLRLSGASFG 165

Query: 819 NKDYYITRDKYFGRRVKVGVQFARVLARFLYDGKTIESLIRQIPRLIKQLDTLYSEIFNL 878
+ T++ G+R+ F R + F + ++ + +QL + + + +
Sbjct: 166 RGEVKTKE--GKRMAE-TFKRAMKHFFDVSQPKNAK-----RQLLKIKASLKS 216

Query: 879 KGYRLYGASLLLMYDGDANKSNSKRKKAANVKVNLIDFARCVTKE 923
+ R +G+SLL++ D D A+VKV LIDFA E
Sbjct: 217 ENTRFFGSSLLVIIDDDVESPE-----ASVKVKLIDFASMARSE 255

>gi|13509208|emb|CAC35322.1| (AJ310150) hypothetical protein [Linum usitatissimum]
Length = 300

Score = 46.2 bits (108), Expect = 0.002
Identities = 27/81 (33%), Positives = 46/81 (56%), Gaps = 2/81 (2%)

Query: 741 HDIESITFEETSHTIVSKFILLEDLTRNMNKPICALDLKMGTROYGVDAKRAKQLSQRAC 800
H +SI E + + + ++LEDLT PC +D+K+G+R + +A +A K
Sbjct: 67 HGTQSI--EASDGSLHPLHILEDLTSTRLHPCVMDIKIGSRTWYPEASQAYIEKCLKKD 124

Query: 801 LKTTSRRLGVRICGLKVWNKD 821
++++S LG RI GL+V+ D
Sbjct: 125 VESSSPFLGFRISGLQVYGND 145

>gi|12846033|dbj|BAB27004.1| (AK010523) evidence:NAS-hypothetical protein-putative [Mus musculus]
Length = 216

Score = 46.2 bits (108), Expect = 0.002
Identities = 24/76 (31%), Positives = 43/76 (56%), Gaps = 4/76 (5%)

Query: 759 FILLEDLTRNMNKPICALDLKMGTROYGVDAKRAKQLSQRACLKTTSRRLGVRICGLKVV 818
++ LED+T NKPC +D+K+G + Y A K Q +K +G + G++V+
Sbjct: 110 YLKLEDVTHKFNKPCIMDVKIGRKSYPFASSEKIQQVSK--YPLMEEIGFLVLGMRVY 167

Query: 819 --NKDYYITRDKYFGR 832
+ D Y T+++++GR

```

Sbjct: 168 HLHSDSYETQNHQHYGR 183

>gi|6320378|ref|NP_010458.1| (NC_001136) Regulator of arginine-responsive genes with ARG80 and ARG81; Arg82p [Saccharomyces cerevisiae]
gi|114134|sp|P07250|ARG3_YEAST ARGININE METABOLISM REGULATION PROTEIN III
gi|73242|pir|RGBYR3 regulatory protein ARG82 - yeast (Saccharomyces cerevisiae)
gi|3376|emb|CAA28945.1| (X05328) ARGRIII protein (AA 1-355) [Saccharomyces cerevisiae]
gi|1289288|emb|CAA86678.1| (Z46727) Argr3p [Saccharomyces cerevisiae]
Length = 355

Score = 45.4 bits (106), Expect = 0.003
Identities = 44/203 (21%), Positives = 89/203 (43%), Gaps = 25/203 (12%)

Query: 714 NHGCHLDSGKNMIKSLAYNVSNDSYSHHDIESITFEETSHTIVSKFILLEDLTRNMNKP 773
N G ++ + + + +S+ + D + E++ ++++LE+L +KP
Sbjct: 74 NEGAKIEQSGDAALLKIDERLSDSTDNLDSPVKSEK-----KQYLVLENLLYGFSKPN 128

Query: 774 ALDLKMGTRQYGVDAKRAKQLSQRACKLKTTSRRLGVRICGLKVWNK-----DY-- 822
LD+K+G Y A K+ + TTS LG RICG+K+ +Y
Sbjct: 129 ILDIKLGKTLYDSKASLEKRERMKRVSSETTSGSLGFRICGMKIQKNPSVLNQLSLEYE 188

Query: 823 -----YITRDKYFGRRVKVGWQFARVLARFLYDGKTIESLIRQIPR-LIKQLDTLYSEI 875
YI +K +GR + + + + + ++ Q+ + +K+L Y+ +
Sbjct: 189 EEADSDYIFINKLYGRS-RTDQNVSDAIELYFNNPHLS DARKHQLKKTFLKRLQLFYNTM 247

Query: 876 FNLKGYRLYGASLLLMYDGDANK 898
+ R+ +SLL +Y+GD +
Sbjct: 248 LE-EEVRMISSLLFIYEGDPER 269

>gi|4200312|emb|CAA09965.1| (AJ012219) ip3ka [Gallus gallus]
Length = 452

Score = 42.7 bits (99), Expect = 0.024
Identities = 63/233 (27%), Positives = 96/233 (41%), Gaps = 64/233 (27%)

Query: 759 FILLEDLTRNMNKP CALDLKMGTRQY-----GVD--AKRAKQ 793
+I L+DL + PC +D KMG R Y VD A A++
Sbjct: 236 YIQLDLLTDFEGPCVMDCKMGIRTYLEEELTKAREKPKLRKDMYKKMIEVDPLAPTAE 295

Query: 794 LSQRA-----KCLKTTSRRLGVRICGLK----VWNKDYYITRDKYFGRRVKVGWQF 840
+Q A + ++S LG RI G+K N ++ T+ + Q
Sbjct: 296 NAQHAVTKPRYMQWRETISSANLGFRIEIKKADGTCNTNFKTTKTQE-----QV 346

Query: 841 ARVLARFLYDGKTIESLIRQIPRLIKQLDTLYSEIFNLKGYRLYGASLLLMYDGDANKSN 900
+V F+ TI L + + RL + L S F K + + G+SLL ++DG
Sbjct: 347 LQVFVEFIEGNTTI--LKKYLKRLQEIHIILESSDF-FKRHEVVGSSLLFVHDG----- 397

Query: 901 SKRKKAAVKNVLIDFARCVTKEDAMECMDKFRIPPKSPNIEDKGFLRGVKSL 953
+ N V LIDF + D + +D RIP + N ED G+L G+ +L
Sbjct: 398 -----SGNANVWLIDFGKTTLLPDG-QTLDH-RIPWQEGNRED-GYLLGLDNL 442

>gi|14028614|gb|AAK52432.1| (AF282731) Mf1 protein [Schistosoma japonicum]
Length = 382

Score = 39.7 bits (91), Expect = 0.20
Identities = 37/147 (25%), Positives = 69/147 (46%), Gaps = 14/147 (9%)

Query: 762 LEDLTRNMNKP CALDLKMGTRQYGVDAKRAKQLSQRACKLKTTSRRLGVRICGLKVWNKD 821
L DL N +P D KMG T Y D+ K +++K R+LG + G++V++ +
Sbjct: 78 LSDLVANFKQPNVCDFKMGTTITYFPDSSSEDKIAREQSK--YAWRRKLGFVLSGMQVYDTE 135

Query: 822 YY--ITRDKYFGRRVKVGWQFARVLARFL-----YDGKTIESLIRQIPRLIKQLDTLYSE 874
+ I K FGR + ++ + FL Y K ++ I+Q+ ++ ++
Sbjct: 136 NHCLIKFSKEFGRNLTPEQVYSVGKTFGLGSDSTYCIKLAQNYIQQLGHILNWRGIWRR 195

Query: 875 IFNLKGYRLYGASLLLMYDGDANKSNS 901
I + + +SLL++ N S +
Sbjct: 196 IVD-----VCRSSLLLIHETINNNSGN 217

>gi|17544638|ref|NP_502402.1| (NM_070001) ZK795.1.p [Caenorhabditis elegans]
gi|7511315|pir|T27999 hypothetical protein ZK795.1 - Caenorhabditis elegans
gi|3881874|emb|CAB05842.1| (Z83246) ZK795.1 [Caenorhabditis elegans]
Length = 242

Score = 38.5 bits (88), Expect = 0.37
Identities = 22/60 (36%), Positives = 32/60 (52%), Gaps = 2/60 (3%)

Query: 758 KILLEDLTRNMNKPICALDLKMGTRQYGVDAKRAKQLSQRACKLKTTSRRLGVRICGLKV 817
+F+ +ED+T +P LDLKMG Y AK K +R K ++G+RI G +V
Sbjct: 118 EFLAMEDVTIGYQRPAILDLKMGQVTDPIAKPEKIEKERIK--YPPQAKMGMRIILGYRV 175

>gi|13509210|emb|CAC35324.1| (AJ310150) hypothetical protein [Linum usitatissimum]
Length = 285

Score = 38.1 bits (87), Expect = 0.47
Identities = 20/59 (33%), Positives = 36/59 (60%)

Query: 760 ILLEDLTRNMNKPICALDLKMGTRQYGVDAKRAKQLSQRACKLKTTSRRLGVRICGLKVW 818
++LEDLT C +D+K+G+R + +A +A K +++++ LG RI GL+V+
Sbjct: 84 LILEDLTSTRHLVCMDIKIGSRTWYPEASQAYIEKCLKKDVESNPLLGFRISGLQVY 142

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: Apr 29, 2002 3:56 AM
Number of letters in database: 290,391,215
Number of sequences in database: 925,521

Lambda K H
0.312 0.129 0.371

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 618,331,593
Number of Sequences: 925521
Number of extensions: 27469963
Number of successful extensions: 107277
Number of sequences better than 10.0: 509
Number of HSP's better than 10.0 without gapping: 69
Number of HSP's successfully gapped in prelim test: 458
Number of HSP's that attempted gapping in prelim test: 98506
Number of HSP's gapped (non-prelim): 3880
length of query: 1050
length of database: 290,391,215
effective HSP length: 131
effective length of query: 919
effective length of database: 169,147,964
effective search space: 155446978916
effective search space used: 155446978916
T: 11
A: 40
X1: 16 (7.2 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 42 (21.9 bits)
S2: 76 (33.9 bits)

FIGURE 6: Blastp results of accession NP_437949.1 against the NCBI Protein nr database.

BLASTP 2.2.3 [Apr-24-2002]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, 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.

RID: 1020211615-026225-20760

Query=

(554 letters)

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

925,521 sequences; 290,391,215 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Sequences producing significant alignments:			Score (bits)	E Value
gi 16265157 ref NP_437949.1	(NC_003078)	putative regulator...	1040	0.0
gi 13471899 ref NP_103466.1	(NC_002678)	adenylate cyclase ...	396	e-109
gi 13473448 ref NP_105015.1	(NC_002678)	adenylate cyclase ...	302	7e-81
gi 13472852 ref NP_104419.1	(NC_002678)	adenylate cyclase ...	275	9e-73
gi 15965348 ref NP_385701.1	(NC_003047)	HYPOTHETICAL TRANS...	271	1e-71
gi 13473907 ref NP_105475.1	(NC_002678)	adenylate cyclase ...	257	2e-67
gi 16263314 ref NP_436107.1	(NC_003037)	CyaF5 adenylate cy...	235	1e-60
gi 13471136 ref NP_102705.1	(NC_002678)	adenylate cyclase ...	234	2e-60
gi 15965803 ref NP_386156.1	(NC_003047)	PROBABLE ADENYLATE...	231	2e-59
gi 4468712 emb CAB38103.1	(AJ225896)	adenylate cyclase cya...	228	1e-58
gi 15966747 ref NP_387100.1	(NC_003047)	PUTATIVE ADENYLATE...	203	4e-51
gi 15966522 ref NP_386875.1	(NC_003047)	PROBABLE ADENYLATE...	197	2e-49
gi 16264038 ref NP_436830.1	(NC_003078)	putative adenylate...	195	1e-48
gi 13471135 ref NP_102704.1	(NC_002678)	adenylate cyclase ...	188	1e-46
gi 13473903 ref NP_105471.1	(NC_002678)	adenylate cyclase ...	180	4e-44
gi 16264266 ref NP_437058.1	(NC_003078)	probable adenylate...	165	1e-39
gi 16262751 ref NP_435544.1	(NC_003037)	putative CyaF4 ade...	137	3e-31
gi 13471884 ref NP_103451.1	(NC_002678)	adenylate cyclase ...	135	1e-30
gi 16262767 ref NP_435560.1	(NC_003037)	conserved hypothet...	100	4e-20
gi 1439552 gb AAB17513.1	(U39409)	TfuA [Rhizobium legumino...	86	7e-16
gi 15007264 gb AAK77321.1	(AF028810)	unknown [Rhizobium le...	75	1e-12
gi 15966040 ref NP_386393.1	(NC_003047)	CONSERVED HYPOTHET...	75	2e-12
gi 16262803 ref NP_435596.1	(NC_003037)	conserved hypothet...	74	5e-12
gi 13475575 ref NP_107139.1	(NC_002678)	transcriptional re...	65	2e-09
gi 8708903 gb AAF78794.1	(U33883)	putative transmembrane t...	63	1e-08
gi 15600553 ref NP_254047.1	(NC_002516)	two-component resp...	61	3e-08
gi 16124549 ref NP_419113.1	(NC_002696)	phosphate regulon ...	60	7e-08
gi 15894977 ref NP_348326.1	(NC_003030)	Response regulator...	59	1e-07
gi 17229169 ref NP_485717.1	(NC_003272)	hypothetical prote...	59	2e-07
gi 6531667 gb AAF15533.1	(AF196490_3)	(AF196490) phosphate re...	58	2e-07
gi 2769532 emb CAA11074.1	(AJ223073)	phosphate regulatory ...	57	4e-07
gi 15640307 ref NP_229934.1	(NC_002505)	transcriptional ac...	57	6e-07
gi 16765877 ref NP_461492.1	(NC_003197)	transcriptional ac...	57	6e-07
gi 16761470 ref NP_457087.1	(NC_003198)	transcriptional ac...	57	6e-07
gi 15791723 ref NP_281546.1	(NC_002163)	two-component regu...	57	6e-07
gi 791140 emb CAA56853.1	(X80892)	iagA [Salmonella typhi]	57	8e-07
gi 16761653 ref NP_457270.1	(NC_003198)	invasion protein r...	56	1e-06
gi 13475726 ref NP_107293.1	(NC_002678)	transcriptional re...	56	1e-06
gi 2126153 pir S70817		invasion genes transcription activat...	55	1e-06

gi 15640738 ref NP_230368.1	(NC_002505)	DNA-binding respon...	55	2e-06
gi 16766182 ref NP_461797.1	(NC_003197)	invasion genes tra...	55	2e-06
gi 15891373 ref NP_357045.1	(NC_003063)	AGR_L_2522p [Agrob...	55	2e-06
gi 15645657 ref NP_207833.1	(NC_000915)	response regulator...	55	2e-06
gi 15894830 ref NP_348179.1	(NC_003030)	Response regulator...	55	2e-06
gi 13958023 gb AAK50764.1 AF360364_1	(AF360364)	lysine deca...	55	2e-06
gi 15887773 ref NP_353454.1	(NC_003062)	AGR_C_746p [Agroba...	55	3e-06
gi 17937275 ref NP_534064.1	(NC_003305)	conserved hypothet...	55	3e-06
gi 4530445 gb AAD22036.1	(AF118229)	response regulator Pnp...	54	3e-06
gi 17988267 ref NP_540901.1	(NC_003317)	PHOSPHATE REGULON ...	54	3e-06
gi 4768853 gb AAD29647.1 AF124757_7	(AF124757)	phosphate re...	54	4e-06
gi 15901898 ref NP_346502.1	(NC_003028)	response regulator...	54	4e-06
gi 3282774 gb AAC25063.1	(AF043352)	response regulator hom...	54	5e-06
gi 15611449 ref NP_223100.1	(NC_000921)	putative TRANSCRIP...	54	5e-06
gi 15964268 ref NP_384621.1	(NC_003047)	PHOSPHATE REGULON ...	54	5e-06
gi 18265910 gb AAL67383.1 AF447814_51	(AF447814)	transcript...	54	6e-06
gi 16131959 ref NP_418557.1	(NC_000913)	transcriptional ac...	54	6e-06
gi 15804726 ref NP_290767.1	(NC_002655)	transcriptional ac...	54	6e-06
gi 16123366 ref NP_406679.1	(NC_003143)	phosphate regulon ...	53	9e-06
gi 13473197 ref NP_104764.1	(NC_002678)	phosphate regulato...	53	1e-05
gi 15615719 ref NP_244023.1	(NC_002570)	two-component resp...	52	2e-05
gi 1172482 sp P45606 PHOB_SHIDY	Phosphate regulon transcrip...	52	2e-05	
gi 15893613 ref NP_346962.1	(NC_003030)	Response regulator...	51	3e-05
gi 17549263 ref NP_522603.1	(NC_003296)	PROBABLE TWO-COMPO...	51	3e-05
gi 15802560 ref NP_288587.1	(NC_002655)	transcriptional re...	51	3e-05
gi 15800125 ref NP_286137.1	(NC_002655)	positive response ...	51	3e-05
gi 8569282 pdb 1QQI A	Chain A, Solution Structure Of The Dn...	51	3e-05	
gi 15803373 ref NP_289406.1	(NC_002655)	putative invasion ...	51	3e-05
gi 16332107 ref NP_442835.1	(NC_000911)	OmpR subfamily [Sy...	51	3e-05
gi 16121054 ref NP_404367.1	(NC_003143)	putative regulator...	51	4e-05
gi 16130019 ref NP_416583.1	(NC_000913)	transcriptional re...	51	4e-05
gi 15832141 ref NP_310914.1	(NC_002695)	transcriptional re...	51	4e-05
gi 17232242 ref NP_488790.1	(NC_003272)	two-component resp...	50	5e-05
gi 94799 pir A37775	phoB protein - Pseudomonas aeruginosa	50	5e-05	
gi 7339512 emb CAB82846.1	(AJ277082)	putative response reg...	50	6e-05
gi 15641332 ref NP_230964.1	(NC_002505)	DNA-binding respon...	50	7e-05
gi 9081855 gb AAF82621.1 AF157830_2	(AF157830)	PhoP2 respon...	50	9e-05
gi 8546941 emb CAB94653.1	(AL359215)	putative two-componen...	50	9e-05
gi 15610901 ref NP_218282.1	(NC_000962)	hypothetical prote...	49	1e-04
gi 15807407 ref NP_296139.1	(NC_001263)	DNA-binding respon...	49	1e-04
gi 15644403 ref NP_229455.1	(NC_000853)	response regulator...	49	1e-04
gi 1575577 gb AAC44436.1	(U67196)	DNA-binding response reg...	49	1e-04
gi 2143952 pir I55603	reduced hepatic glutathione transpor...	49	1e-04	
gi 15614371 ref NP_242674.1	(NC_002570)	two-component resp...	49	1e-04
gi 15843385 ref NP_338422.1	(NC_002755)	DNA-binding respon...	49	1e-04
gi 15840172 ref NP_335209.1	(NC_002755)	DNA-binding respon...	49	2e-04
gi 15607897 ref NP_215271.1	(NC_000962)	phoP [Mycobacteriu...	49	2e-04
gi 16804539 ref NP_466024.1	(NC_003210)	two-component resp...	49	2e-04
gi 15596354 ref NP_249848.1	(NC_002516)	probable two-compo...	49	2e-04
gi 17230752 ref NP_487300.1	(NC_003272)	two-component resp...	49	2e-04
gi 16759374 ref NP_454991.1	(NC_003198)	phosphate regulon ...	49	2e-04
gi 17351932 gb AAL38202.1 AF319446_1	(AF319446)	putative re...	49	2e-04
gi 1172481 sp P45605 PHOB_KLEPN	Phosphate regulon transcrip...	49	2e-04	
gi 16801706 ref NP_471974.1	(NC_003212)	two-component resp...	49	2e-04
gi 15924683 ref NP_372217.1	(NC_002758)	alkaline phosphata...	49	2e-04
gi 1172483 sp P45607 PHOB_SHIFL	Phosphate regulon transcrip...	49	2e-04	
gi 1055347 gb AAB38749.1	(U38917)	response regulator PhoB ...	49	2e-04
gi 887803 gb AAA83034.1	(U28375)	ORF_o458 [Escherichia coli]	48	2e-04
gi 18034495 gb AAL57517.1 AF453441_1	(AF453441)	CadC [Esche...	48	3e-04
gi 15807237 ref NP_295967.1	(NC_001263)	phosphate regulon ...	48	3e-04
gi 16125842 ref NP_420406.1	(NC_002696)	transcriptional re...	48	3e-04
gi 15644443 ref NP_229495.1	(NC_000853)	conserved hypothet...	48	3e-04
gi 10802733 gb AAG23588.1 AF244639_1	(AF244639)	DNA-binding...	48	3e-04
gi 16803987 ref NP_465472.1	(NC_003210)	similar to two-com...	48	3e-04
gi 12642552 gb AAK00284.1 AF288536_6	(AF288536)	possible tr...	48	3e-04
gi 17231804 ref NP_488352.1	(NC_003272)	two-component syst...	48	3e-04
gi 15839182 ref NP_299870.1	(NC_002488)	two-component syst...	47	4e-04
gi 16130756 ref NP_417329.1	(NC_000913)	putative invasion ...	47	4e-04
gi 15678100 ref NP_275215.1	(NC_000916)	O-linked GlcNAc tr...	47	4e-04

gi 16077443 ref NP_388257.1	(NC_000964)	similar to two-com...	47	4e-04
gi 15991570 gb AAL12938.1 AF394228_1	(AF394228)	putative tr...	47	4e-04
gi 16119346 ref NP_396052.1	(NC_003064)	AGR_pAT_174p [Agro...	47	5e-04
gi 16765461 ref NP_461076.1	(NC_003197)	response regulator...	47	5e-04
gi 16761060 ref NP_456677.1	(NC_003198)	putative two-compo...	47	5e-04
gi 17231995 ref NP_488543.1	(NC_003272)	two-component resp...	47	6e-04
gi 15642901 ref NP_227942.1	(NC_000853)	response regulator...	47	6e-04
gi 15644015 ref NP_229064.1	(NC_000853)	phosphate regulon ...	47	6e-04
gi 17938707 ref NP_535495.1	(NC_003306)	two component resp...	47	6e-04
gi 16119348 ref NP_396054.1	(NC_003064)	AGR_pAT_177p [Agro...	47	6e-04
gi 16801128 ref NP_471396.1	(NC_003212)	similar to two-com...	47	7e-04
gi 16078390 ref NP_389208.1	(NC_000964)	similar to two-com...	47	7e-04
gi 19551981 ref NP_599983.1	(NC_003450)	COG0745:Response r...	47	8e-04
gi 13475894 ref NP_107464.1	(NC_002678)	similar to trifoli...	46	8e-04
gi 13475573 ref NP_107137.1	(NC_002678)	similar to transcr...	46	8e-04
gi 5353563 gb AAD42180.1 AF130997_1	(AF130997)	response reg...	46	0.001
gi 5759261 gb AAD51056.1 AF175293_1	(AF175293)	response reg...	46	0.001
gi 15887392 ref NP_353073.1	(NC_003062)	AGR_C_54p [Agrobac...	46	0.001
gi 18311470 ref NP_563404.1	(NC_003366)	two-component resp...	46	0.001
gi 17547783 ref NP_521185.1	(NC_003295)	PROBABLE RESPONSE ...	46	0.001
gi 17933959 ref NP_530749.1	(NC_003304)	two component resp...	46	0.001
gi 7672246 emb CAB89435.1	(AL354048)	putative two-componen...	46	0.001
gi 2145544 pir S70816	hila protein - Salmonella typhimuriu...		45	0.001
gi 2947107 gb AAC28777.1	(AF005157)	regulatory protein Bvr...	45	0.001
gi 7474358 pir T31680	bacR protein - Bacillus licheniformi...		45	0.001
gi 17988319 ref NP_540953.1	(NC_003317)	TRANSCRIPTIONAL RE...	45	0.001
gi 2944391 gb AAC33849.1	(AF049128)	response regulator Nbl...	45	0.002
gi 18309624 ref NP_561558.1	(NC_003366)	two-component resp...	45	0.002
gi 6137054 emb CAB59609.1	(AL132662)	putative response reg...	45	0.002
gi 19703920 ref NP_603482.1	(NC_003454)	Two-component resp...	45	0.002
gi 19553806 ref NP_601808.1	(NC_003450)	COG0745:Response r...	45	0.002
gi 18309439 ref NP_561373.1	(NC_003366)	two-component resp...	45	0.002
gi 16265215 ref NP_438007.1	(NC_003078)	hypothetical expor...	45	0.002
gi 15838927 ref NP_299615.1	(NC_002488)	two-component syst...	45	0.002
gi 13474249 ref NP_105817.1	(NC_002678)	two-component syst...	45	0.002
gi 16079369 ref NP_390193.1	(NC_000964)	two-component resp...	45	0.002
gi 16263704 ref NP_436497.1	(NC_003037)	probable transcrip...	45	0.002
gi 12830428 emb CAC29081.1	(AJ300267)	putative regulatory ...	45	0.002
gi 19746167 ref NP_607303.1	(NC_003485)	putative response ...	45	0.002
gi 15675198 ref NP_269372.1	(NC_002737)	putative response ...	45	0.003
gi 17545792 ref NP_519194.1	(NC_003295)	PROBABLE TWO-COMPO...	45	0.003
gi 15601325 ref NP_232956.1	(NC_002506)	transcriptional re...	45	0.003
gi 19552100 ref NP_600102.1	(NC_003450)	COG0745:Response r...	45	0.003
gi 15963797 ref NP_384150.1	(NC_003047)	TRANSCRIPTIONAL RE...	45	0.003
gi 17546253 ref NP_519655.1	(NC_003295)	PROBABLE PHOSPHATE...	45	0.003
gi 15615988 ref NP_244293.1	(NC_002570)	two-component resp...	44	0.003
gi 10303272 emb CAC10110.1	(AL442165)	putative two compone...	44	0.003
gi 281708 pir S28674	hypothetical protein 2 - Rhizobium sp...		44	0.003
gi 7799238 emb CAB90861.1	(AL355752)	putative regulatory p...	44	0.003
gi 12964068 emb CAC29256.1	(AJ302696)	putative regulatory ...	44	0.003
gi 9909919 emb CAC04498.1	(AL391588)	putative two-componen...	44	0.004
gi 17228689 ref NP_485237.1	(NC_003272)	two-component resp...	44	0.004
gi 16121116 ref NP_404429.1	(NC_003143)	putative regulator...	44	0.004
gi 15923696 ref NP_371230.1	(NC_002758)	response regulator...	44	0.004
gi 10281108 gb AAG15433.1 AF189161_1	(AF189161)	putative re...	44	0.004
gi 7799208 emb CAB90924.1	(AL355774)	putative two-componen...	44	0.004
gi 16331756 ref NP_442484.1	(NC_000911)	OmpR subfamily [Sy...	44	0.005
gi 5764628 gb AAD51348.1 AF173226_5	(AF173226)	SmeR [Stenot...	44	0.005
gi 1729783 emb CAA70931.1	(Y09798)	colR [Pseudomonas fluor...	44	0.005
gi 40056 emb CAA47908.1	(X67676)	phoP [Bacillus subtilis]	44	0.006
gi 18311314 ref NP_563248.1	(NC_003366)	two-component resp...	44	0.006
gi 6683054 dbj BAA89010.1	(AB027503)	transmembrane regulat...	44	0.006
gi 16123046 ref NP_406359.1	(NC_003143)	two-component syst...	44	0.006
gi 16331577 ref NP_442305.1	(NC_000911)	OmpR subfamily [Sy...	43	0.007
gi 11278069 pir T45446	probable two-component response reg...		43	0.007
gi 15675804 ref NP_269978.1	(NC_002737)	putative two-compo...	43	0.007
gi 886038 gb AAB36584.1	(U24659)	JadR1 [Streptomyces venez...	43	0.007
gi 16079963 ref NP_390789.1	(NC_000964)	two-component resp...	43	0.007
gi 7211008 emb CAB76988.1	(AL159178)	putative response reg...	43	0.008

gi 15826987 ref NP_301250.1	(NC_002677) putative two-compo...	43	0.009
gi 15840463 ref NP_335500.1	(NC_002755) DNA-binding respon...	43	0.011
gi 625683 pir A49903	phosphate regulatory protein ChvI - A...	43	0.011
gi 585207 sp Q05943 GLNR_STRCO	Transcriptional regulatory p...	43	0.011
gi 1705849 sp Q07783 CHVI_AGRTU	Transcriptional regulatory ...	43	0.011
gi 16123188 ref NP_406501.1	(NC_003143) putative two-compo...	43	0.011
gi 16800610 ref NP_470878.1	(NC_003212) similar to two-com...	42	0.012
gi 15608173 ref NP_215549.1	(NC_000962) hypothetical prote...	42	0.012
gi 15894147 ref NP_347496.1	(NC_003030) Two-component resp...	42	0.012
gi 19551649 ref NP_599651.1	(NC_003450) COG0745:Response r...	42	0.013
gi 12002210 gb AAG43239.1 AF123314_2	(AF123314) putative re...	42	0.013
gi 12964066 emb CAC29257.1	(AJ302695) putative regulatory ...	42	0.013
gi 3115359 gb AAC15868.1	(U77060) ToxR [Photobacterium pro...	42	0.014
gi 17549138 ref NP_522478.1	(NC_003296) PROBABLE TWO COMPO...	42	0.014
gi 6714581 dbj BAA89504.1	(AB029903) toxRS operon [Vibrio ...	42	0.014
gi 6714593 dbj BAA89512.1	(AB029907) toxRS operon [Vibrio ...	42	0.014
gi 730972 sp Q05938 TOXR_VIBPA	CHOLERA TOXIN HOMOLOG TRANSC...	42	0.014
gi 6714602 dbj BAA89518.1	(AB029910) toxRS operon [Vibrio ...	42	0.014
gi 6714596 dbj BAA89514.1	(AB029908) toxRS operon [Vibrio ...	42	0.014
gi 5726300 gb AAD48402.1 AF129010_1	(AF129010) response reg...	42	0.014
gi 417621 sp Q01473 RCAC_FREDI	RcaC protein >gi 282227 pir ...	42	0.015
gi 17510937 ref NP_491526.1	(NM_059125) Y110A7A.17.p [Caen...	42	0.015
gi 19743660 gb Q06239 VANR_ENTFC	Regulatory protein vanR >gi ...	42	0.015
gi 7242751 emb CAB77324.1	(AL160331) putative response reg...	42	0.016
gi 15601024 ref NP_232654.1	(NC_002506) transcriptional re...	42	0.016
gi 387603 gb AAA24892.1	(M95680) putative [Fremyella diplo...	42	0.016
gi 586203 sp Q06239 VANR_ENTFC	Regulatory protein vanR >gi ...	42	0.016
gi 13473757 ref NP_105325.1	(NC_002678) two-component resp...	42	0.018
gi 13892068 gb AAK39631.1	(AY032724) ColR [Pseudomonas put...	42	0.018
gi 13474926 ref NP_106496.1	(NC_002678) phosphate regulato...	42	0.018
gi 15610382 ref NP_217763.1	(NC_000962) mtrA [Mycobacteriu...	42	0.020
gi 15842835 ref NP_337872.1	(NC_002755) DNA-binding respon...	42	0.021
gi 3599371 gb AAC64935.1	(AF082668) CsrR [Streptococcus py...	42	0.021
gi 509815 gb AAB07804.1	(U01971) MtrA [Mycobacterium tuber...	42	0.021
gi 7636029 emb CAB88489.1	(AL353816) putative two-componen...	42	0.021
gi 15866137 gb AAL10207.1 AF410884_3	(AF410884) MtrA [Mycob...	42	0.021
gi 15612935 ref NP_241238.1	(NC_002570) two-component resp...	42	0.022
gi 6002654 gb AAF00081.1 AF095713_1	(AF095713) response reg...	42	0.023
gi 15895992 ref NP_349341.1	(NC_003030) Response regulator...	42	0.024
gi 12744844 gb AAK06808.1 AF324838_27	(AF324838) putative r...	42	0.025
gi 12644198 sp P30260 CC27_HUMAN	Protein CDC27Hs (Cell divi...	42	0.025
gi 15079681 gb AAH11656.1 AAH11656	(BC011656) Unknown (prot...	42	0.025
gi 16554577 ref NP_001247.2	(NM_001256) cell division cycl...	42	0.025
gi 18587728 ref XP_067035.2	(XM_067035) cell division cycl...	42	0.025
gi 2134884 pir A48792	CDC27 - human >gi 7459513 pir S5364...	42	0.025
gi 15673576 ref NP_267750.1	(NC_002662) two-component syst...	41	0.028
gi 8177554 gb AAF73970.1	(U81166) putative response regula...	41	0.028
gi 15608121 ref NP_215496.1	(NC_000962) hypothetical prote...	41	0.029
gi 17547806 ref NP_521208.1	(NC_003295) PROBABLE RESPONSE ...	41	0.029
gi 11321503 gb AAG34188.1 AF321122_7	(AF321122) Siml [Strep...	41	0.029
gi 777765 gb AAB38544.1	(L41661) srrB [Synechococcus sp.]	41	0.030
gi 19704766 ref NP_604328.1	(NC_003454) Tetratricopeptide ...	41	0.030
gi 15614143 ref NP_242446.1	(NC_002570) two-component resp...	41	0.031
gi 15827334 ref NP_301597.1	(NC_002677) putative two-compo...	41	0.031
gi 15807647 ref NP_295328.1	(NC_001263) response regulator...	41	0.031
gi 15805769 ref NP_294466.1	(NC_001263) response regulator...	41	0.034
gi 18309930 ref NP_561864.1	(NC_003366) two-component resp...	41	0.034
gi 15895700 ref NP_349049.1	(NC_003030) Response regulator...	41	0.038
gi 15613318 ref NP_241621.1	(NC_002570) two-component resp...	41	0.039
gi 4104608 gb AAD10267.1	(AF036968) putative response regu...	41	0.039
gi 17887423 gb AAL40886.1	(AY065624) transcriptional regul...	41	0.041
gi 15777925 dbj BAB68524.1	(AB042547) ToxR [Listonella ang...	41	0.041
gi 13540875 ref NP_110563.1	(NC_002689) TPR-repeat-contain...	41	0.042
gi 14324257 dbj BAB59185.1	(AP000991) hypothetical protein...	41	0.042
gi 6174678 dbj BAA85986.1	(AB024522) gcrR [Streptococcus m...	40	0.046
gi 15229253 ref NP_187074.1	(NM_111295) putative O-linked ...	40	0.048
gi 17549661 ref NP_523001.1	(NC_003296) PROBABLE TWO-COMPO...	40	0.048
gi 16079802 ref NP_390626.1	(NC_000964) similar to hypothe...	40	0.058
gi 18311081 ref NP_563015.1	(NC_003366) two-component resp...	40	0.061

gi 15599577 ref NP_253071.1	(NC_002516)	probable two-compo...	40	0.068
gi 15613383 ref NP_241686.1	(NC_002570)	two-component resp...	40	0.071
gi 16080525 ref NP_391352.1	(NC_000964)	similar to two-com...	40	0.072
gi 15805807 ref NP_294505.1	(NC_001263)	response regulator...	40	0.074
gi 9294730 gb AAF86641.1 AF162694_5	(AF162694)	response reg...	40	0.075
gi 19745448 ref NP_606584.1	(NC_003485)	CovR [Streptococcu...	40	0.078
gi 17227839 ref NP_484387.1	(NC_003272)	hypothetical prote...	40	0.081
gi 4104595 gb AAD10258.1	(AF036964)	putative response regu...	40	0.081
gi 5825487 gb AAD53266.1	(AF166120)	transmembrane transcri...	40	0.082
gi 18202894 sp Q9F868 RGX3 MYCSM	Sensory transduction prote...		40	0.085
gi 6318168 emb CAB60254.1	(AJ250862)	MrsR2 protein [Bacill...	40	0.087
gi 16212082 gb AAL27445.1 AF430807_10	(AF430807)	VanRE [Ent...	40	0.096
gi 15606362 ref NP_213741.1	(NC_000918)	hypothetical prote...	40	0.098
gi 18460982 gb AAK53981.1	(AY033089)	VanRc-2 [Enterococcus...	39	0.10
gi 15616473 ref NP_244779.1	(NC_002570)	two-component resp...	39	0.10
gi 15893581 ref NP_346930.1	(NC_003030)	Response regulator...	39	0.11
gi 141358 sp P19737 YREC_SYNP2	Hypothetical 28.7 kDa protei...		39	0.11
gi 16803547 ref NP_465032.1	(NC_003210)	similar to two-com...	39	0.12
gi 18310175 ref NP_562109.1	(NC_003366)	two-component resp...	39	0.12
gi 15640999 ref NP_230630.1	(NC_002505)	cholera toxin tran...	39	0.12
gi 79261 pir A25970	transcription activator of cholera tox...		39	0.12
gi 15825402 gb AAL09685.1	(AF414370)	ToxR [Serratia marces...	39	0.12
gi 16122893 ref NP_406206.1	(NC_003143)	two-component regu...	39	0.12
gi 143328 gb AAA22661.1	(M16775)	phoP protein (put.); puta...	39	0.13
gi 15792585 ref NP_282408.1	(NC_002163)	two-component regu...	39	0.13
gi 17229920 ref NP_486468.1	(NC_003272)	two-component hybr...	39	0.13
gi 16080375 ref NP_391202.1	(NC_000964)	similar to two-com...	39	0.14
gi 9081852 gb AAF82619.1 AF157829_2	(AF157829)	PhoP3 respon...	39	0.15
gi 13476389 ref NP_107959.1	(NC_002678)	two-component resp...	39	0.15
gi 15888321 ref NP_354002.1	(NC_003062)	AGR_C 1793p [Agrob...	39	0.16
gi 15896467 ref NP_349816.1	(NC_003030)	Response regulator...	39	0.16
gi 17549382 ref NP_522722.1	(NC_003296)	PROBABLE TWO-COMPO...	39	0.16
gi 15894784 ref NP_348133.1	(NC_003030)	Response regulator...	39	0.17
gi 16127555 ref NP_422119.1	(NC_002696)	DNA-binding respon...	39	0.17
gi 16125434 ref NP_419998.1	(NC_002696)	DNA-binding respon...	39	0.17
gi 8134654 sp O07130 RGX3 MYCBO	Sensory transduction protei...		39	0.18
gi 15902380 ref NP_357930.1	(NC_003098)	Response regulator...	39	0.18
gi 15839882 ref NP_334919.1	(NC_002755)	DNA-binding respon...	39	0.18
gi 4104605 gb AAD10265.1	(AF036967)	putative response regu...	39	0.18
gi 15607632 ref NP_215005.1	(NC_000962)	regX3 [Mycobacteri...	39	0.18
gi 15900299 ref NP_344903.1	(NC_003028)	DNA-binding respon...	39	0.18
gi 6448492 emb CAB61229.1	(Y15706)	vanr protein [Bacillus ...	39	0.18
gi 15893941 ref NP_347290.1	(NC_003030)	Response regulator...	39	0.18
gi 15896754 ref NP_350103.1	(NC_003030)	Response regulator...	39	0.19
gi 17987612 ref NP_540246.1	(NC_003317)	TWO COMPONENT RESP...	39	0.19
gi 493217 gb AAA20502.1	(L29053)	toxR [Vibrio fischeri]	39	0.20
gi 15641723 ref NP_231355.1	(NC_002505)	DNA-binding respon...	39	0.20
gi 15792551 ref NP_282374.1	(NC_002163)	putative two-compo...	39	0.21
gi 17546367 ref NP_519769.1	(NC_003295)	PROBABLE OXIDATIVE...	39	0.21
gi 15607128 ref NP_214510.1	(NC_000918)	hypothetical prote...	39	0.21
gi 15896896 ref NP_350245.1	(NC_003030)	Response regulator...	38	0.22
gi 17547886 ref NP_521288.1	(NC_003295)	HYPOTHETICAL PROTE...	38	0.23
gi 18310907 ref NP_562841.1	(NC_003366)	two-component resp...	38	0.27
gi 17231280 ref NP_487828.1	(NC_003272)	two-component resp...	38	0.27
gi 16080092 ref NP_390918.1	(NC_000964)	similar to two-com...	38	0.28
gi 15599296 ref NP_252790.1	(NC_002516)	probable two-compo...	38	0.30
gi 15964775 ref NP_385128.1	(NC_003047)	PUTATIVE TRANSCRIP...	38	0.30
gi 14140153 emb CAC39070.1	(AJ307662)	anaphase-promoting c...	38	0.31
gi 17231314 ref NP_487862.1	(NC_003272)	two-component resp...	38	0.31
gi 19705092 ref NP_602587.1	(NC_003454)	Tetratricopeptide ...	38	0.32
gi 1149660 emb CAA60222.1	(X86502)	hypC [Clostridium perfr...	38	0.32
gi 2613086 gb AAB84277.1	(AF030315)	OmpR [Enterobacter clo...	38	0.33
gi 7481652 pir T34824	probable turgor pressure regulator k...		38	0.33
gi 12483701 gb AAG53726.1 AF176556_2	(AF176556)	LlrrB [Lact...	38	0.34
gi 3288064 emb CAB09801.1	(Z97065)	RisA protein [Bordetell...	38	0.34
gi 16272824 ref NP_439045.1	(NC_000907)	aerobic respiratio...	38	0.35
gi 17545795 ref NP_519197.1	(NC_003295)	PROBABLE TWO-COMPO...	38	0.35
gi 15601292 ref NP_232923.1	(NC_002506)	DNA-binding respon...	38	0.35
gi 13122184 emb CAC32360.1	(AL583945)	putative two compone...	38	0.36

gi 16262974 ref NP_435767.1	(NC_003037) putative response ...	38	0.36
gi 5713266 gb AAD47875.1 AF170884.1	(AF170884) transmembran...	38	0.36
gi 15600078 ref NP_253572.1	(NC_002516) two-component resp...	38	0.37
gi 15839123 ref NP_299811.1	(NC_002488) two-component syst...	38	0.37
gi 15902120 ref NP_357670.1	(NC_003098) Response regulator...	37	0.38
gi 15610261 ref NP_217640.1	(NC_000962) hypothetical prote...	37	0.38
gi 15614507 ref NP_242810.1	(NC_002570) two-component resp...	37	0.38
gi 15842697 ref NP_337734.1	(NC_002755) transcriptional re...	37	0.39
gi 20090223 ref NP_616298.1	(NC_003552) O-linked GlcNAc tr...	37	0.40
gi 79118 pir S01366	regulatory protein ompR - Salmonella t...	37	0.41
gi 2108342 emb CAA70146.1	(Y08950) OmpR protein [Yersinia ...	37	0.42
gi 15892516 ref NP_360230.1	(NC_003103) petR protein [Rick...	37	0.43
gi 17942992 pdb 1KGS A	Chain A, Crystal Structure At 1.50 A...	37	0.43
gi 16264749 ref NP_437541.1	(NC_003078) putative two compo...	37	0.43
gi 15803909 ref NP_289945.1	(NC_002655) response regulator...	37	0.44
gi 2613088 gb AAB84278.1	(AF030316) OmpR [Yersinia enteroc...	37	0.44
gi 16804460 ref NP_465945.1	(NC_003210) similar to two-com...	37	0.44
gi 15602084 ref NP_245156.1	(NC_002663) ArcA [Pasteurella ...	37	0.45
gi 16764820 ref NP_460435.1	(NC_003197) response regulator...	37	0.46
gi 15900027 ref NP_344631.1	(NC_003028) DNA-binding respon...	37	0.46
gi 16760440 ref NP_456057.1	(NC_003198) putative two-compo...	37	0.46
gi 16120479 ref NP_403792.1	(NC_003143) transcriptional re...	37	0.48
gi 15828317 ref NP_302580.1	(NC_002677) probable two-compo...	37	0.48
gi 16262977 ref NP_435770.1	(NC_003037) putative response ...	37	0.49
gi 16081218 ref NP_393517.1	(NC_002578) 72K mitochondrial ...	37	0.51
gi 496695 emb CAA56022.1	(X79489) CDC27 D-618 protein [Sac...	37	0.52
gi 6319387 ref NP_009469.1	(NC_001134) Protein required fo...	37	0.52
gi 7669466 gb AAF66142.1	(U81488) putative response regula...	37	0.53
gi 2194039 pdb 1ODD	OmpR C-Terminal Domain (OmpR-C) From ...	37	0.54
gi 18311346 ref NP_563280.1	(NC_003366) two-component resp...	37	0.55
gi 6117972 gb AAF03932.1 AF139908.2	(AF139908) LisR [Lister...	37	0.55
gi 2076608 emb CAB08413.1	(Z95151) unknown [Mycobacterium ...	37	0.56
gi 17351934 gb AAL38203.1 AF319447.1	(AF319447) putative re...	37	0.56
gi 18309822 ref NP_561756.1	(NC_003366) two-component resp...	37	0.56
gi 541208 pir S41887	ompR protein - Salmonella typhi	37	0.57
gi 7481739 pir T36369	response regulator - Streptomyces co...	37	0.59
gi 15893516 ref NP_346865.1	(NC_003030) Response regulator...	37	0.61
gi 13472041 ref NP_103608.1	(NC_002678) hypothetical prote...	37	0.62
gi 15643165 ref NP_228209.1	(NC_000853) response regulator...	37	0.63
gi 16800482 ref NP_470750.1	(NC_003212) two-component resp...	37	0.64
gi 15673417 ref NP_267591.1	(NC_002662) two-component syst...	37	0.65
gi 7339508 emb CAB82844.1	(AJ277080) putative response reg...	37	0.65
gi 15613825 ref NP_242128.1	(NC_002570) BH1262-unknown con...	37	0.67
gi 17232815 ref NP_489363.1	(NC_003272) two-component tran...	37	0.68
gi 16126989 ref NP_421553.1	(NC_002696) DNA-binding respon...	37	0.71
gi 699378 gb AAA63138.1	(U15187) mtrX [Mycobacterium leprae]	37	0.74
gi 10956625 ref NP_066761.1	(NC_002576) two-component resp...	37	0.75
gi 15596996 ref NP_250490.1	(NC_002516) probable two-compo...	37	0.75
gi 3687663 gb AAC62213.1	(AF049873) LcoR [Lactococcus lactis]	37	0.78
gi 6862579 gb AAD30119.2	(AF135388) DNA binding response r...	37	0.82
gi 15790410 ref NP_280234.1	(NC_002607) Vng1389c [Halobact...	37	0.83
gi 15679902 ref NP_275211.1	(NC_000916) TPR-repeat-contain...	36	0.91
gi 15678111 ref NP_275226.1	(NC_000916) O-linked GlcNAc tr...	36	0.91
gi 18311222 ref NP_563156.1	(NC_003366) two-component resp...	36	0.93
gi 15669130 ref NP_247935.1	(NC_000909) transformation sen...	36	0.95
gi 17227939 ref NP_484487.1	(NC_003272) hypothetical prote...	36	0.96
gi 15896015 ref NP_349364.1	(NC_003030) Response regulator...	36	0.99

Alignments

>gi|16265157|ref|NP_437949.1| (NC_003078) putative regulatory protein, possibly two-component response regulator [Sinorhizobium meliloti]
gi|15141297|emb|CAC49809.1| (AL603647) putative regulatory protein, possibly two-component response regulator [Sinorhizobium meliloti]
Length = 554

Score = 1040 bits (2688), Expect = 0.0
Identities = 554/554 (100%), Positives = 554/554 (100%)

Query: 1 MPCYQILFASCPDSEGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHL 60
MPCYQILFASCPDSEGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHL
Sbjct: 1 MPCYQILFASCPDSEGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHL 60

Query: 61 VGTRDRVSKDELLQAVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFV 120
VGTRDRVSKDELLQAVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFV
Sbjct: 61 VGTRDRVSKDELLQAVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFV 120

Query: 121 GDIRIGGIGEVRRQVPGGAALQASGGSGETASALVLPDKPSITVLPFQNLSGDPEQEYFA 180
GDIRIGGIGEVRRQVPGGAALQASGGSGETASALVLPDKPSITVLPFQNLSGDPEQEYFA
Sbjct: 121 GDIRIGGIGEVRRQVPGGAALQASGGSGETASALVLPDKPSITVLPFQNLSGDPEQEYFA 180

Query: 181 DGIVEDIIITALSRIKWLFIARNSSFRYKGRAVEVKDVGRELGVRYVLEGSVRKSGNRVR 240
DGIVEDIIITALSRIKWLFIARNSSFRYKGRAVEVKDVGRELGVRYVLEGSVRKSGNRVR
Sbjct: 181 DGIVEDIIITALSRIKWLFIARNSSFRYKGRAVEVKDVGRELGVRYVLEGSVRKSGNRVR 240

Query: 241 ITGQLIDATTGTHLWAERFEGTLDDIFELQDRMAESVVGAIAPQVERAEMERAKRKPTES 300
ITGQLIDATTGTHLWAERFEGTLDDIFELQDRMAESVVGAIAPQVERAEMERAKRKPTES
Sbjct: 241 ITGQLIDATTGTHLWAERFEGTLDDIFELQDRMAESVVGAIAPQVERAEMERAKRKPTES 300

Query: 301 LDAHDYYLRGMAKLHSGTHEAIEAALPLFYRAIELDQEFASAYAGAACYFWRKLNQWV 360
LDAHDYYLRGMAKLHSGTHEAIEAALPLFYRAIELDQEFASAYAGAACYFWRKLNQWV
Sbjct: 301 LDAHDYYLRGMAKLHSGTHEAIEAALPLFYRAIELDQEFASAYAGAACYFWRKLNQWV 360

Query: 361 DRAEEIAEGARLARRAVELGRDDAVALTRSGHALGHLVGDLDGGIALIDRARLLNPNFAP 420
DRAEEIAEGARLARRAVELGRDDAVALTRSGHALGHLVGDLDGGIALIDRARLLNPNFAP
Sbjct: 361 DRAEEIAEGARLARRAVELGRDDAVALTRSGHALGHLVGDLDGGIALIDRARLLNPNFAP 420

Query: 421 AWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHHFAGRFDSALVWAE 480
AWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHHFAGRFDSALVWAE
Sbjct: 421 AWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHHFAGRFDSALVWAE 480

Query: 481 RALGNLPSLLVAVALVAASHALAGRTTEARKTMQRLRALDPSLRVSTLRDWLPIHRPEDL 540
RALGNLPSLLVAVALVAASHALAGRTTEARKTMQRLRALDPSLRVSTLRDWLPIHRPEDL
Sbjct: 481 RALGNLPSLLVAVALVAASHALAGRTTEARKTMQRLRALDPSLRVSTLRDWLPIHRPEDL 540

Query: 541 ARFADGLRLAGLPE 554
ARFADGLRLAGLPE
Sbjct: 541 ARFADGLRLAGLPE 554

>gi|13471899|ref|NP_103466.1| (NC_002678) adenylate cyclase [Mesorhizobium loti]
gi|14022643|dbj|BAB49252.1| (AP002998) adenylate cyclase [Mesorhizobium loti]
Length = 541

Score = 396 bits (1017), Expect = e-109
Identities = 237/534 (44%), Positives = 321/534 (59%), Gaps = 15/534 (2%)

Query: 20 GDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWG 79
G + + ++F D+ LD +RREL R +++V PQVFDLL +L+ R+RVVSKD+L+ AVW
Sbjct: 22 GASNLPLYLFEDFALDGRRELRRGNSLIAVEPQVFDLLQYLIRNRERVVSKDDLVDVWQ 81

Query: 80 GRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDIDIRIGGIGEVRRQVPGGA 139
GRIVS++T+ S +NA R A+ D G +QRL+RT R+GFRFVG + E PV P
Sbjct: 82 GRIVSDATLASRVNAARSALQDNQEQQRLVRTFPRRGFRFVGTVEEAGAEATAPVEPA- 140

Query: 140 ALQASGGSGETASALVLPDKPSITVLPFQNLSGDPEQEYFADGIVEDIIITALSRIKWLFI 199
L +P +PSI VLPF NLSGDP+Q+YFADG+VEDIIT LSRIKWLFI
Sbjct: 141 -----KPGLGIPARPSIAVLFFVNLSGDPDQDYFADGMVEDIITGLSRIKWLFI 189

Query: 200 IARNSSFRYKGRAVEVKDVGRELGVRYVLEGSVRKSGNRVRITGQLIDATTGTHLWAERF 259
IARNSSF YKGRAV++K VG+ELGVRYVLEGSVRK G+RVRTGQLID G HLWAER+
Sbjct: 190 IARNSSFTYKGRAVDMKQVQELGVRYVLEGSVRKSGNRVRITGQLIDTEDGGHLWAERY 249

Query: 260 EGTLLDIFELQDRMAESVVGAIAPQVERAEMERAKRKPTESLDAHDYYLRGMAKLHSGTH 319
+ L D+F LQD + SVV AI P + RAE+ER KR+ +SLDA+D +LR + +++
Sbjct: 250 DRELTDVVALQDEITISVVAIEPNLRRAEIERVKRQRPDSLDAVDLFLRALPDVYTFMP 309

Query: 320 EAIEAALPLFYRAIELDQEFASAYAGAACYFWRKLNQWVDRAEEIAEGARLARRAVEL 379
+ LPL +A+ ++ +A + AAW + + G M +AE + +R A +A+E

Sbjct: 310 QGAARGPLPLDQALAEPSYALVHGFAAWAHQTLFIRGGM--QAEHSGKASRHAHAIEH 367
Query: 380 GRDDAVALTRSGHALVGLDGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAI 439
G DA+AL +G +G + D +A L+ + A + G + G+ AI
Sbjct: 368 GSGDAMALALAGFTIGLVEHDRKLADAEAFSQALSLSASCAFYAFGCVPVAYGGDATRAI 427
Query: 440 EHIEHAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALGNLPSLLVAVALVAAS 499
+ E A RL+PLD Q +F AGR + A+ RA+ P + +AA
Sbjct: 428 DWGEQALRLNPLDAMNCVPQGMIGFGNFLAGRHEQAIAAGRRVEMNPGFSILHGWLAAP 487
Query: 500 HALAGRTEEARKTMQRLRALDPSLRVSTLRDWLPIHRPEDLARFADGLRLAGLP 553
A GR EEA+ RL ALDP + + + P + + +RLAGLP
Sbjct: 488 LARLGRIEEAKAAGSRLMALDPHTTIGRWSAAVGL-APAIIDDVTEAMRLAGLP 540

>gi|13473448|ref|NP_105015.1| (NC_002678) adenylate cyclase cya3 [Mesorhizobium loti]
gi|14024197|dbj|BAB50801.1| (AP003003) adenylate cyclase; Cya3 [Mesorhizobium loti]
Length = 581

Score = 302 bits (773), Expect = 7e-81
Identities = 176/438 (40%), Positives = 255/438 (58%), Gaps = 7/438 (1%)

Query: 116 GFRFVGDIRIGGIGEVQPVGPAALQASGGSETASALVLPDKPSITVLPFQNLSGDPE 175
GF +GD+R+ I +PV A + S A+ LP+KPSI VLPF N+SGDP+
Sbjct: 150 GFTPLGLRLKNI---ERPV--RAYRVETDASASVAAPPALPEKPSIAVLPFTNMSGDPD 204
Query: 176 QEYFADGIVEDITIALSRIRWLFVIARNSSFRYKGRAVEVKDVGRELGVRYVLEGSVRKS 235
QEYFADG+VEDIIT LSR+ FVIARNSSF YKGRAV+++ VGRELGVRYVLEGS+R++
Sbjct: 205 QEYFADGLVEDIITGLSRVNSFFVIARNSSFTYKGRAVDLRQVGRELGVRYVLEGSIRRA 264
Query: 236 GNRVRITGQLIDATTGTHLWAEFEGTLDDIFELQDRMAESVVGAIAPQVERAEMERAKR 295
G+RVRI+GQL+DA +G H+WA+RFEG L DIF+LQD++ ESUVGA+ P + E+++A+
Sbjct: 265 GSRVRISGQLVDADISGHHVWADRFEGLSDIFDLQDKVTESVVGAVEPSIRLQEIQAARM 324
Query: 296 KPTESLDAHDYYLRGMAKLHSGTHEAIEAALPLFYRAIELDQEFASAYAGAAWCYFWRKL 355
KPT+ + A+D YLR + + +S T E L A+ +D F A A+
Sbjct: 325 KPTDYISAYDLYLRALPRFYSMTREGFADVRRLTNEALSIDPGFNLAAGLGAIRSLSVS 384
Query: 356 NGWMVDRAEEIEAGARLARRAVELGRDDAVALTRSGHALVGLDGGIALIDRARLLN 415
W +++ R+AR + RDD +L + + + D + + I+R+ LLN
Sbjct: 385 QCW--HEPDDVRVAVRMAREVLAEARDDPTSLRFAAQVIAYSADYEMALGAIERSLN 442
Query: 416 PNFAPAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHFFAGRFDSA 475
PN A G++ P AIEH A RLSP+D E +G +++ R++ A
Sbjct: 443 PNSAQHTGSGWVNAHSSRPLVAIEHFHAMRLSPVDPEKGIALSGIGMSYLMLERYEEA 502
Query: 476 LVWAERALGNLPSLLVAVALVAASHALAGRTEEARKTMQRLRALDPSLRVSTLRDWLPIH 535
L W ERAL +P+ + +V + R +EA+ +RL P+ ++ R P
Sbjct: 503 LAWGERALHEMPNYGSSHRVIMALVKNRLDEAQAARRLMEAFPTYTLTLQRIQINPWL 562
Query: 536 RPEDLARFADGLRLAGLP 553
R+ + L ++G+P
Sbjct: 563 DKVFAERYVEALGISGVP 580

>gi|13472852|ref|NP_104419.1| (NC_002678) adenylate cyclase cya3 [Sinorhizobium meliloti]
[Mesorhizobium loti]
gi|14023599|dbj|BAB50205.1| (AP003001) adenylate cyclase; Cya3 [Mesorhizobium loti]
Length = 589

Score = 275 bits (703), Expect = 9e-73
Identities = 182/418 (43%), Positives = 239/418 (56%), Gaps = 7/418 (1%)

Query: 138 GAALQASGGSGETAS--ALVLPDKPSITVLPFQNLSGDPEQEYFADGIVEDITIALSRIR 195
G+A + + ETA A P K SI VLPF N+SGD EQ+YFADGI EDITIALS++
Sbjct: 174 GSAGTKAAATSETAGRPATAAPPKLSIAVLFPANMSGDAEQDYFADGISEDITIALSKLS 233
Query: 196 WLFVIARNSSFRYKGRAVEVKDVGRELGVRYVLEGSVRKSGNRVRITGQLIDATTGTHLW 255
LFVIARNSSF +KG+ V+V++VG +LGVR+VLEGSVRKSGNRVRIT QLIDA +G HLW
Sbjct: 234 QLFVIARNSSFTFKGQNVQVQEVGTKLGVHVLEGSVRKSGNRVRITQLIDAISGGHLW 293

Query: 256 AERFEGTLDDIFELQDRMAESVVGAIAPQVERAEMERAKRKPTESLDAHDYYLRGMAKLH 315
AERF+ L DIF +QD + + +VGA+A + + +R + + +A+D +LRG H
Sbjct: 294 AERFDRELTDFAVQDDVTQQIVGALALNLTEGDRQLAPEHPRNAEAYDCFLRGRELWH 353

Query: 316 SGTAEIAEALPLFYRAIELDQEFASAYAGAACYFWRKLNQWMDRAEEIAEGARLARR 375
T E AA + RAI+LD FASA+A A Y LN W E +A+ +A R
Sbjct: 354 RLTKETNVAARDVLQRAIDLDPNFASAHAFALTYVLDYLNRRWSASPPESMAQAEVATR 413

Query: 376 AVELGRDDAVALTRSGHALGHLVGDL-DGGIALIDRARLLNPNFAPAWFLGGFLRVFRGE 434
AV L DD+ A+ L DG I +RA +LNPFA + G + G
Sbjct: 414 AVAL--DDSDPWAHWALAIKLYTRRHGDAIDEAERAIVLNPFAEGHVILGEALYSGR 471

Query: 435 PESAEIEHIEHAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALGNLPSLLVAVA 494
PE A+E A L+P ++ + ALA F GR++ A+ + L V+ A
Sbjct: 472 PEEALESFARAKTLNPFYFPDV--LLHFQALAAFQLGRYEEAVDLLQLRLARNAVTDVSRA 529

Query: 495 LVAASHALAGRTEEARCTMQRLRALDPSLRVSTLRDWLPIHRPEDLARFADGLRLAGL 552
L+AA + GR EAR Q + L+P + R LP P D DGLR AG+
Sbjct: 530 LLAACYGHLGRFAEARAQEVLRNPDYSLEYRRKVLPHYKNPADFELVVDGLRKAGV 587

>gi|15965348|ref|NP_385701.1| (NC_003047) HYPOTHETICAL TRANSMEMBRANE PROTEIN [Sinorhizobium meliloti]
gi|15074528|emb|CAC46174.1| (AL591787) HYPOTHETICAL TRANSMEMBRANE PROTEIN [Sinorhizobium meliloti]
Length = 502

Score = 271 bits (693), Expect = 1e-71
Identities = 200/542 (36%), Positives = 277/542 (50%), Gaps = 56/542 (10%)

Query: 25 QFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKEDELQAVWGGGRIVS 84
+F+FG +VLD L R + V+VG + LL LVG ++ K EL+ A W GR V
Sbjct: 5 RFVFGPFVLDPGAGTLVRNDEPVAVGVRGLKLEALVGRPGEILGKAELMDAAWSGRAVE 64

Query: 85 ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDIRIGGIGEVROPVGPAAALQAS 144
E +T I +RK +G I T+ R G+RF G + G G R P
Sbjct: 65 EGNLTVQIAQLRKMLGAPPDGGEWIATIPRVGYRFTGPVEKAG-GAKRNP----- 113

Query: 145 GGSGETASALVLPDPKPSITVLPFQNLSGDPEQEYFADGIVEDIITALSRIRWLFVIARNS 204
L LPD+PSI VLPF N S DPEQE FADG+ ED+IT LSRI LFVIARNS
Sbjct: 114 -----LPLPDEPSIAVLPFVNFSSDPEQESFADGLTEDLITDLSRIYGLFVIARNS 164

Query: 205 SFRYKGRAVEVKDVGRELGVRYVLEGSVRKSGNRVRITGQLIDATTGTHLWAERFEGTLD 264
+F +KG+A +V+++ +LGVRY+LEGS R++ RVRI QL+DA +G HLWAERF+ +L+
Sbjct: 165 TFAFKGKARDVREIAEDLGVRYLLEGSARRAAGRVRINAQLVDAVSGNHLWAERFDRSLE 224

Query: 265 DIFELQD----RMAESVVGAIAPQVERAEMERAKRKPTESLDAHDYYLRGMAKLHSGTHE 320
DIF +QD ++ E+++G + PQ A R ++L+A+D +R +
Sbjct: 225 DIFAVQDEVTKIVEALLGRLRPQ-----APRNRPKNLEAYDLCVRARKLIDDSPQT 276

Query: 321 AIEAALPLFYRAIELDQEFASAYAGAACYFWRKLNQWMDRAEEI----AEGARLAR 374
A EA L + RA+ LD E+A AY W +N WM V E + + LAR
Sbjct: 277 AREAHL-MLTRAVSLDPEYAEAYR-----WLANHWMRWVHWGEPVNPNSVALELAR 328

Query: 375 RAVELGRDDAVALTRSGHALGH--LVGDLDGGIALIDRARLLNPNFAPAWFLGGFLRVFR 432
+AV + +DA + L + + D A +A L+PN A W + V
Sbjct: 329 KAVAI DPNDAGCRWVLNLLAYERSFAEADAIFA---KAIELDPNEADTWATLSDI AVL A 385

Query: 433 GEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALGNLPSLLVA 492
G E +EHI A RL+P + + G A + AG +++A+ R S +
Sbjct: 386 GRVEEGVEHIRKAFRLNPFASWYYLTLGQ--AQYAAGEYEA AVETLRRDETYRTS----S 440

Query: 493 VALVAASHALAGRTEEARCTMQRLRALDPSLRVSTLRDWLPIHRPEDLARFADGLRLAGL 552
+AAS A GR +EAR ++ +P D P LA F DG R AGL
Sbjct: 441 RRFLAASLAQLGRLEAREAEVLFVGNPHFTTRHWADTEPFRDAATLAHFVDGYRKAGL 500

Query: 553 PE 554
PE
Sbjct: 501 PE 502

>gi|13473907|ref|NP_105475.1| (NC_002678) adenylate cyclase cya3 [Mesorhizobium loti]
gi|14024658|dbj|BAB51261.1| (AP003004) adenylate cyclase; Cya3 [Mesorhizobium loti]
Length = 502

Score = 257 bits (656), Expect = 2e-67
Identities = 201/538 (37%), Positives = 268/538 (49%), Gaps = 48/538 (8%)

Query: 25 QFMFGDYVLDQERRELTRRGQVVSVPQVFDLLHLVGTDRDVRVSKDELLQAVWGGRIVS 84
+F FG +VLD L R V+VG + LL LVG ++ K EL+ A W G V
Sbjct: 5 RFAFGPFVLDPGAGTLLRNDPVAVGVRGLKLLAALVGRPGEILEKAELMDAAWPGTAVE 64

Query: 85 ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDIRIGGIGEVQPVGPGALQAS 144
E +T I +RK +G I TV R G+RF G I + R+P
Sbjct: 65 EGNLTVQIAQLRKLGPADGGEWISTVPRVGYRFTGAIEQLDRAK-RKP----- 113

Query: 145 GGSGETASALVLPDKPSITVLPFQNLSGDPEQEYFADGIVEDITALSRIWLFVIARNS 204
L LPDKPSI VLPF NLS DPEQE FADG+ ED+IT LSR LFVIARNS
Sbjct: 114 -----LPLDPKPSIAVLFPVNLNDPEQEAFAADGLTEDLITDLSRAPGLFVIARNS 164

Query: 205 SFRYKGRAVEVKDVGRELGVRYVLEGSVRKSGNRVITGQLIDATTGTHLWAERFEGTLD 264
+F YKG+A++V+ + ELGVRY+LEGS R++ RVRI QL+DA +G HLWAERF+ LD
Sbjct: 165 TFAYKKGAMDVRAIAELGVRYLLEGSARRAAGRVINAQLVDAKSGEHLWAERFDRGLD 224

Query: 265 DIFELQDRMAESVVGAIAPQVERAEMERAKRKPTESLDAHDYYLRGMAKLHSGTHEAIEA 324
DIF +QD +V A+ + R + +PT +L+A+D +R + A EA
Sbjct: 225 DIFAVQDEATAKIVEAL---LGRLRAPPPNRPT-NLEAYDLCVRARKLIEESPQTAREA 280

Query: 325 ALPLFYRAIELDQEFASAYAGAAWCYFWRKLNWMM-----VDRAEEIAEGARLARRA 376
L L RA+ LD E+A A+ W +N WM VD IA LAR+A
Sbjct: 281 HL-LTRAVSLDPEYAEHR-----WLMNHWMGVHWGEPVDPNRRIA--LELARKA 330

Query: 377 VELGRDDAVALTRSGHALGHLVGDLDGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPE 436
V + +DA G+ L + + A +A L+PN A AW + V G E
Sbjct: 331 VAIDPNDAGCRWVLGNLLAY-EHSFEESEAEFAKAFELDPNEADAWATLSDIAGVLAGRVE 389

Query: 437 SAIEHIEHAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALGNLPSLLVAVALV 496
+EHI A RL+P + + G A + A +++A+ R S + +
Sbjct: 390 EGLEHIRKAFRLNPYPASWYLTIGE--AQYAARDYEA AVETLRREETYRTS---SRRFL 444

Query: 497 AASHALAGRTEEARMTQRLRALDPSLRVSTLRDWLPIHRPEDLARFADGLRLAGLPE 554
AAS A GR +EAR ++ +P S P F DG R AGLP+
Sbjct: 445 AASLAQLGRLDDEARAEVEMFLIGNPHFTTSYVWTEPFRRDDAMRDHFVDGFRKAGLPD 502

>gi|16263314|ref|NP_436107.1| (NC_003037) CyaF5 adenylate cyclase [Sinorhizobium meliloti]
gi|17380491|sp|Q9Z3Q0|CYA3_RHIME Putative adenylate cyclase 3 (ATP pyrophosphate-lyase 3)
(Adenylyl
cyclase 3)
gi|14523994|gb|AAK65519.1| (AE007273) CyaF5 adenylate cyclase [Sinorhizobium meliloti]
Length = 587

Score = 235 bits (599), Expect = 1e-60
Identities = 155/397 (39%), Positives = 217/397 (54%), Gaps = 4/397 (1%)

Query: 156 LPDKPSITVLPFQNLSGDPEQEYFADGIVEDITALSRIWLFVIARNSSFRYKGRAVEV 215
LP KPSI VLPF N+SGDPEQ YFADGI EDIIT LS++ LFVIARNSSF YKG+ ++
Sbjct: 193 LPAKPSIAVLFPDNMSGDPEQGYFADGITEDIITLSKVSGLFVIARNSSFAYKGKTPDI 252

Query: 216 KDVGRELGVRYVLEGSVRKSGNRVITGQLIDATTGTHLWAERFEGTLDIFELQDRMAE 275
+ V RELGVRYVLEGSVR++ NR+RI Q+ID TTG HLWAER++ L+DIF +QD +
Sbjct: 253 RKVSRELGVRYVLEGSVRRANRIRINAQMIDGTTGHLWAERYDRGLEDFAVQDEVTR 312

Query: 276 SVVGAIAPQVERAEMERAKRKPTESLDAHDYYLRGMAKLHSGTHEAIEAALPLFYRAIEL 335
++V A+ ++ E ER + + +A+D +R + + A + +R +E+
Sbjct: 313 TIVNALRVKLTAGEEERRESRGKVDPEAYDLLVRSRQAILQFNALSSMEARRMLHRVLEI 372

Query: 336 DQEFASAYAGAAWCYFWRKLNWMMVDRAEEIAEGARLARRAVELGRDDAVALTRSGHALG 395
D A+A+A + +N W + + + LA+ A++ + AL
Sbjct: 373 DPGMAAAHASLSIIALTDFINQWNGATPDNLTQALGLAQEAIDTDGSEPQGHYTLALALS 432

Query: 396 HLVGDLGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEM 455
+ LD +RA L+PN A A+ G +R F+G E A+ A RL P
Sbjct: 433 WM-RRLDEAEHAAERAIELDPNSANAYTALGTIRDFQGRHEEALALYTRAHRLDPQFDLS 491

Query: 456 FRMQAGTALAHFFAGRFDSALVWAERALGNLPSLLVAVALVAASHALAGRTEEARKTMQR 515
Q G AL + GRFD A V +R L P + +A + GR EEAR +
Sbjct: 492 LHFQ-GRALLNL--GRFDEAEVAFKRRLLLAPRSDMTRFYLACLYGRTGRHEEARGYWRE 548

Query: 516 LRALDPSLRVSTLRDWLPIHRPEDLARFADGLRLAGL 552
+ ++PS V LR LP P + R +GLR AG+
Sbjct: 549 VLGVPNSFSVDHLRRLSLPYQDPHMDRLVEGLREAGV 585

>gi|13471136|ref|NP_102705.1| (NC_002678) adenylate cyclase [Mesorhizobium loti]
gi|14021880|dbj|BAB48491.1| (AP002996) adenylate cyclase [Mesorhizobium loti]
Length = 581

Score = 234 bits (597), Expect = 2e-60
Identities = 189/527 (35%), Positives = 275/527 (51%), Gaps = 34/527 (6%)

Query: 51 PQVFDLLHLVGTRDRVSKDELLQA-----VWGGRIVSEST-----ITSHIN 93
P D L V T++R+ ++ L + + G ++ + T + + +
Sbjct: 66 PSAVDALQFAVETQERITLRNTDLPSERRMAFRMGINAGEVILDETTIYGDCVNVAARLE 125

Query: 94 AVRKAIGDTGGEQRLIRTVARKGFREVV--GDIRIGGIGEVQPVGPGAALQASGGSGETA 151
V + G G + + + F+ GD + I + G QA G A
Sbjct: 126 KVSEPGGVVIGRSVYDQVSGKLPYEFIDLGDHTMKNIAGAVRAYRVGTGEQAQEGPVAIA 185

Query: 152 SA--LVLPDKPSITVLPFQNLSGDPEQEYFADGIVEDIIITALSRIRWLFVIARNSSFRYK 209
SA L LP KPS+ VLPF N+S DPEQEYF+DGI ED+IT LSR + LFVIARNSSF +K
Sbjct: 186 SANDLPLPFKPSVAVLPFANMSADPEQEYFSDGITEDLITELSRQSLEFVIARNSSSFVFK 245

Query: 210 GRAVEVKDVGRELGVRYVLEGSVRKSGNRVRITGQLIDATTGTHLWAERFEGTLDDIFEL 269
GR+V +VGR+LGVRYV+EGSVRK+G RVRIT QLI+A++G H+WAER++ ++DD+F +
Sbjct: 246 GRSVNTTEVGRKLGVRVVEGSVRKAGARVRITAQLIEASSGNHVWAERYDRSIDDLFAV 305

Query: 270 QDRMAESVVGAIAPQVERAEMERAKRKPTESLDAHYYLRGMAKLHSGTHEAIEAALPLF 329
QD + E + A+ +V AE+ RA++ T SL A+D +LRGM H T + AA+ F
Sbjct: 306 QDEVTERIAWALVGKVGTAETIARARQTKT-SLGAYDAFLRGMEAHRFTEDDTIAAIEFF 364

Query: 330 YRAIELDQEFASAYAGAAWCYFWRKLNWMMVDRAEEIAEGARLARRAVELGRDDAVALTR 389
A+ + A +A A Y L+ + D + A + A RA+ELG DA L
Sbjct: 365 KLALRGQPSARGHACLADAY--ATLSAFRADGGLK-ALAMQSALRAIELG--DASGLAE 419

Query: 390 S-GHALGHLVGDLGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARL 448
+ AL GD + RA +L P A A G++ ++ G+ A E E RL
Sbjct: 420 AVVAALYAWKGFEEAAETHGQRALVLGPTNALALNWVGYISLWDGQLARAREIGERLQRL 479

Query: 449 SPL-DQEMFRMQAGTALAHFFAGRFDSALVWAERALGNLPSLLVAVALVAASHALAGRTE 507
+PL D+++ + A T H+ G ++++L R N + A +AA GR E
Sbjct: 480 NPLEDRIHELLAFT---HYLLGDYEASLRSFRRWDNN--NYDRGFANLAACLGQLGRAE 534

Query: 508 EARKTMQRLRALDPSLRVSTLRDWLPIHRPEDLARFADGLRLAGLPE 554
EAR R P +S + P R EDL + +GLR AG+ +
Sbjct: 535 EARSAGWRCLOCKPGFTLSDYKRDSPYRRQEDLEHWLEGLRKAGIAD 581

>gi|15965803|ref|NP_386156.1| (NC_003047) PROBABLE ADENYLATE/GUANYLATE CYCLASE PROTEIN
[Sinorhizobium meliloti]
gi|15075072|emb|CAC46629.1| (AL591789) PROBABLE ADENYLATE/GUANYLATE CYCLASE PROTEIN
[Sinorhizobium meliloti]
Length = 589

Score = 231 bits (588), Expect = 2e-59
Identities = 155/424 (36%), Positives = 223/424 (52%), Gaps = 12/424 (2%)

Query: 142 QASGSGSETASALVLPD-----KPSITVLPFQNLSGDPEQEYFADGIVEDIIITALSRIR 195
Q G +GE A A D +PSI VLPF NLS EQE+F+DG E++I L+R R
Sbjct: 167 QPGGAAGEEPAPAPATDPLPGKKRPSIAVLFPVNLSSVEEQEHFSDGFTEELIATLARC 226

Query: 196 WLFVIARNSSFRYKGRAVEVKDVGRELGVRYVLEGSVRKSGNRVRITGQLIDATTGTHLW 255

WL V+ARNSSF +KG+A +V+ V +LGV+YV+EGS+R++ NR+RIT QL+ TG LW
Sbjct: 227 WLRVVARNSSFTFKGAADVRRVAEDLGVKYVIEGSIRRAANRIRITAQLLSGETGMLLW 286

Query: 256 AERFEGTLDDIFELQDRMAESVVGAIAPQVERAEMERAKRKPTESLDAHDYYLRGMAKLH 315
AER++ LDD+F LQD +A + G + P++ E + +DA + YL+G+ L+

Sbjct: 287 AERYDRMLDDFVLQDEIAGQITGTVEPELGFIEFAALRGHTATDMDAWNIIYKGLCHLY 346

Query: 316 SGTHEAIEAALPLFYRAIELDQEFASAYAGAACYFWRKLNWVMDRAEEIAEGARLARR 375
E + + LF RAI+L+ FA A+A A+ + G + +RAE IA+ LA R

Sbjct: 347 KFDLENLRISKALFERAIDLEPAFAQAHARLAYVHIQLGWYGPLDERAERIADATALAER 406

Query: 376 AVELGRDDAVALTRSGHALGHLVGDLDGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEP 435
A+ L + A G A L G GI + A L+ +FA F G + P

Sbjct: 407 AIALDDREPAALHALGRARA-LGGQPQRGIDHLRNALRLDASFAQGHFALGQALCYVCRP 465

Query: 436 ESAIEHIEHAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALGNLPSLLVAVAL 495
E I I A RLSP D ++ A+AH+ +GRF A A +L + +

Sbjct: 466 EEGIAAINEAFRLSPRPHLWTFYNNMVAIAHYQSGRFAQAAEAARASLRQENATFWPAMV 525

Query: 496 VAASHALAGRTEEARMTQRLRALDPSLRVSTLR-----DWLPIHRPEDLARFADGLRLA 550
+AAS R++EA + L P + V T R +P+ + + RF L A

Sbjct: 526 LAASLGATERSDEAGSAVANLLRRRPDMTVKTARAEFYFGSVPMPEDFIDRFVRLHRA 585

Query: 551 GLPE 554
GLP+

Sbjct: 586 GLPD 589

>gi|4468712|emb|CAB38103.1| (AJ225896) adenylate cyclase cya3 [Sinorhizobium meliloti]
Length = 586

Score = 228 bits (581), Expect = 1e-58
Identities = 152/392 (38%), Positives = 212/392 (53%), Gaps = 4/392 (1%)

Query: 161 SITVLPFQNLSGDPEQEYFADGIVEDITIALSRIRWLFVIARNSSFRYKGRAVEVKDVGR 220
SI VLPF N+SGDPEQ YFADGI EDIT LS++ LFVIARNSSF YKG+ ++ V R

Sbjct: 197 SI AVLFPDNMSGDPEQGYFADGITEDIITDLKSVSGLFVIARNSSFAKKGKTPNIRKVS 256

Query: 221 ELGVRYVLEGSVRKSGNRVRITGQLIDATTGTHLWAERFEGTLDDIFELQDRMAESVVG 280
ELGVRYVLEGSVR++ NR+RI Q+ID TTG HLWAER++ L+DIF +QD + ++V A

Sbjct: 257 ELGVRYVLEGSVRRANRIRINAQMIDGTTGGHLWAERYDRGLEDFAVQDEVTRTIVNA 316

Query: 281 IAPQVERAEMERAKRKPTESLDAHDYYLRGMAKLHSGTHEAIEAALPLFYRAIELDQEFA 340
+ ++ E ER + + +A+D +R + + A + +R +E+D A

Sbjct: 317 LRVKLTAGEEERRESRGKVDPEAYDLLVRSRQAILQFNALSSMEARRMLHRVLEIDPGMA 376

Query: 341 SAYAGAACYFWRKLNWVMDRAEEIAEGARLARRAVELGRDDAVALTRSGHALGHLVGD 400
+A+A + +N W + + + LA+ A++ + AL +

Sbjct: 377 AAHASLSIIALTDFINQWNGATPDNLTQALGLAQEAIDTDGSEPQGHYTLALALSWM-RR 435

Query: 401 LDGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQA 460
LD +RA L+PN A A+ G +R F+G E A+ A RL P Q

Sbjct: 436 LDEAEHAAERAIELDPNSANAYTALGTIRDFQGRHEEALALYTRAHRLDPQFDLSLHFQ- 494

Query: 461 GTALAHFFAGRFDSALVWAERALGNLPSLLVAVALVAASHALAGRTEEARMTQRLRALD 520
G AL + GRFD A V +R L P + +A + GR EEAR + + +D

Sbjct: 495 GRALLNL--GRFDEAEVAFKRRLLLAPRSDMTFRYLACLYGRTGRHEEARGYWREVLGVD 552

Query: 521 PSLRVSTLRDWLPIHRPEDLARFADGLRLAGL 552
PS V LR LP P + R +GLR AG+

Sbjct: 553 PSFSDHLRRSLPYQDPHMLDRLVEGLREAGV 584

>gi|15966747|ref|NP_387100.1| (NC_003047) PUTATIVE ADENYLATE CYCLASE PROTEIN [Sinorhizobium meliloti]
gi|15076019|emb|CAC47573.1| (AL591792) PUTATIVE ADENYLATE CYCLASE PROTEIN [Sinorhizobium meliloti]
Length = 590

Score = 203 bits (517), Expect = 4e-51
Identities = 172/514 (33%), Positives = 252/514 (48%), Gaps = 30/514 (5%)

Query: 35 QERRELTRRGQVSVGPQVFDLLHLVGTDRVVSKEDELLQAVWGGGRIVSESTITSHINA 94
Q+RR R G +++G +FD + G + ++ E L V GG V+ + T +
Sbjct: 88 QDRRIEFRIG--INLGDIIFD-EDDIFGDGVNIAARIEQLADV-GGICVTAAVATQVADR 143

Query: 95 VRKAIGDTGGEQRLIRTVARKGFRFVGDIRIGGIGEVQPVGPGAAALQASGGSGETASAL 154
+ I D G +++++ ++R F R+G G V P E A
Sbjct: 144 IDVPIDELG--EKMLKNISRPIHLF----RVGIEGPVLPPE-----PEATDAP 185

Query: 155 VLPDKPSITVLPFQNLSGDPEQEYFADGIVEDIIITALSRIWLFVIARNSSFRYKGRAVE 214
KPSI VLPF N+SGDP+QE+FADG+ EDIIT LSR LFVI+RNSSF YK + V
Sbjct: 186 RAISKPSIVLPFDNMSGDPDQEFFADGLTEDIITELSRHELFIISRNSSFVYKNQPVN 245

Query: 215 VKDVGRELGVRYVLEGSVRKSGNRVRITGQLIDATTGTHLWAERFEGTLDDIFELQDRMA 274
V++V +LG +Y++EGSVRK G+RVR+T QLIDA H+WA++++ LDDIF +QD +
Sbjct: 246 VREVAEKLGAQYLVLEGSVRKIGDRVRVTQQLIDAVNDAHIWADKYDRRLDDIFAIQDEVT 305

Query: 275 ESUVGAIAPQVERAEMERAKRKPTESLDAHDYLLRGMALHSGTHEAIEAALPLFYRAIE 334
++ + +VE A+ + R ++ A++ L H T E A L RA+
Sbjct: 306 AAIAATLPGRVEAAQRDLLARTKPNMAAYECALAAKVLHHRSTVADNEQAQALIDRAVA 365

Query: 335 LDQEFASAYAGAACYFWRKLNQWMDRAEEIAEGARLARRAVELGRDDAVALTRSGHAL 394
LD +A A+A A ++GW D+ AE RA+ L +DA + R A+
Sbjct: 366 LDPGYAHAAHWRACILGQAWVHGWCEDKDAVWAEIWAELDRALALDDNDA-DVHRILAAV 424

Query: 395 GHLVGDLDGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQE 454
L +RA LNP+ G L + G PE +E I A +L+P E
Sbjct: 425 NVNNNALTARYHQERALSINPNYDLVVVQQGELLTWLGRPEEGVEWIRKAMQLNPHPE 484

Query: 455 MFRMQAGTALAHFFAGRFDSALVWAERALGNLPSL-LVAVALVAASHALAGRTEEARCTM 513
F G AHF A ++ A+ A +L L V A VAA + G A M
Sbjct: 485 RFWSHLGK--AHFAARQYGEAI----EAFMHLVLDHVQHAFVAACYGWLGDIAAHAM 538

Query: 514 QRLRALDPSLRVSTLRDWLPIHRPEDLARFADGL 547
+++R L P + + DL ++GL
Sbjct: 539 EKVRTLAPDFDLDAFLATQHYVQESDLQHLSEGL 572

>gi|15966522|ref|NP_386875.1| (NC_003047) PROBABLE ADENYLATE/GUANYLATE CYCLASE PROTEIN
[Sinorhizobium meliloti]
gi|15075793|emb|CAC47348.1| (AL591791) PROBABLE ADENYLATE/GUANYLATE CYCLASE PROTEIN
[Sinorhizobium meliloti]
Length = 634

Score = 197 bits (502), Expect = 2e-49
Identities = 145/394 (36%), Positives = 201/394 (50%), Gaps = 46/394 (11%)

Query: 161 SITVLPFQNLSGDPEQEYFADGIVEDIIITALSRIWLFVIARNSSFRYKGRAVEKDVGR 220
SI VLPF N+S DPEQEYF+DGI ED+IT LS+I L V+ARN+ F YKG++V+VK +
Sbjct: 203 SIAVLPFTNMSHDPEQEYFSDGITEDVITDLSKISRLHVVARNTVFTYKGSVKVKQIAH 262

Query: 221 ELGVRYVLEGSVRKSGNRVRITGQLIDATTGTHLWAERFEGTLDDIFELQDRMAESVVG 280
ELGVR++LEGSVRK+G RVRITGQLIDA TG HLWA+R++ L DIF +QD + ++V
Sbjct: 263 ELGVRFILEGSVRKAGGRVRITGQLIDAQTGGHLWADRYDRDLTDIFAIQDEITHAIVDQ 322

Query: 281 IAPQVERAEMERAKRKPTESLDAHDYLLRGMALHSGTHEAIEAALPLFYRAIELDQEFA 340
+ ++ E + PT S++A+ YYLRG H+ T + A +F +A+ELD +A
Sbjct: 323 LKIKLLPEEKRAIESDPTTSVEAYTYLLRGRQFSHTWTRPYLLARRMFLKAVELDPNYA 382

Query: 341 SAYAGAACYFWRKLNQWMDRAEEIAEGARLARRAVELGRDDAVALTRSGHALGHLVGD 400
AYAG A C + W ++ + ++ RA+ L + A A G AL H G
Sbjct: 383 RAYAGIAECE--AIRDWH-EKEFPLESILDSARALALDPNLAEEAHASRGALALNH-DGQ 438

Query: 401 LDGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARL-----SPLD-- 452
+ +A L+P+ A G +G AI E AA + SP+
Sbjct: 439 TEEASREFLQALALDPSLYEANLYYGRFLFAQGRFREAIGFFERAAEIRSDDYFSPHLM 498

Query: 453 -----QEMFRM-----QAGTALAHFFAGRFDSALVWAE 480
Q R+ + ALAH G + A W
Sbjct: 499 GCYLSLGMETERQWRARIGIERAQSAMERNPENASPAHRGALALAHM--GEAERAKEWVS 556

Query: 481 RALGNLPSLLVAVALVAASHALAGRTEEARMTQ 514
RAL P +VA A H+L G E A + ++
Sbjct: 557 RALAIDPDDIVAQYNAACVHSLLEGGERALELLE 590

>gi|16264038|ref|NP_436830.1| (NC_003078) putative adenylate cyclase protein [Sinorhizobium meliloti]
gi|15140162|emb|CAC48690.1| (AL603642) putative adenylate cyclase protein [Sinorhizobium meliloti]
Length = 637

Score = 195 bits (495), Expect = 1e-48
Identities = 141/405 (34%), Positives = 209/405 (50%), Gaps = 15/405 (3%)

Query: 130 EVRQPVGPGGAALQASGGSGETASALVLPDKPSITVLPFQNLSGDPEQEYFADGIVEDIIT 189
EVR A A GE A A +P++ VLPF N+SGD EQ YFADG+ EDII
Sbjct: 204 EVRAVGADLAGRLARLAGGELADA-----RPTVAVLPFDNMSGDAEQSYFADGLTEDIIA 258

Query: 190 ALSRIRWLFVIARNSSFRYKGRAVEVKDVGRELGVRYVLEGSVRKSGNRVRITGQLIDAT 249
L+R L VIARNS+F +G+A +++ +G LG YV+EGS R++G+++R+ QLIDA
Sbjct: 259 NLARNPELQVIARNSTFALRGQAEDIRLIGERLGAGYVVEGSARRAGDQLRVVAQLIDAR 318

Query: 250 TGTHLWAERFEGTLDLDDIFELQDRMAESVVGAIAPQVERAEMERAKRKPTESLDAHDYYLR 309
+G HLW+ ++ ++DIF +Q + +V + V +E+ A +PTE+L A+D L+
Sbjct: 319 SGHLWSRSYDRRVEDIFAVQTELTAIEIVSHLVSYVRESEVSNAERPTENLQAYDLVLK 378

Query: 310 GMAKLHSGTH--EAIEAALPLFYRAIELDQEFASAYAGAACY---FWRKLNQWMDRAE 364
+ G+ EA+ AA L +RA+ELD +A+A A Y F + L+G
Sbjct: 379 ARDRYKHGSKDAEALIAARALLHRALELDPGYAAARANLGMTYIYDFVQNLSGRAT--TT 436

Query: 365 EIAEGARLARRAVELGRDDAVALTRSGHALGHLVGDLDGGIALIDRARLLNPNFAPAWFL 424
++ G AR+AV L + A L GD G + RA LNP +
Sbjct: 437 DVETGLSEARQAVRLDPNLAAGFQVLSFGLS-ATGDYPGAMQAAQRAVELNPNPDSLMA 495

Query: 425 GGFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALG 484
+V G + A+++ E A RL P+ E + G AL + AGR D A L
Sbjct: 496 LAKAQVRFGSYDEAVQNAERARRLHPMAPEYTYVYGQAL--YAAGRLDEADEVLRECLI 553

Query: 485 NLPSSLVAVALVAASHALAGRTEEARMTQRLRALDPSLRVSTLR 529
P + A + G E A++TM RL +DP +++ R
Sbjct: 554 RAPQEADCLLIRTAVLSQRGDVEGAQRTMARLTVDPDFSLASER 598

>gi|13471135|ref|NP_102704.1| (NC_002678) adenylate cyclase [Mesorhizobium loti]
gi|14021879|dbj|BAB48490.1| (AP002996) adenylate cyclase [Mesorhizobium loti]
Length = 626

Score = 188 bits (477), Expect = 1e-46
Identities = 145/429 (33%), Positives = 220/429 (50%), Gaps = 29/429 (6%)

Query: 127 GIGEVQPVGPGGAALQASGGSGETASALVLPDKPSITVLPFQNLSGDPEQEYFADGIVED 186
G+ +P P L + + L PD SI VLPF N+ GD EQE+F DG+ ED
Sbjct: 174 GVPTKAKPAAPAEPLVLE----KFSQPLAPPDNHSAVLPPFINMRGDSEQEFTDGLTED 229

Query: 187 IITALSRIRWLFVIARNSSFRYKGRAVEVKDVGRELGVRYVLEGSVRKSGNRVRITGQLI 246
IIT LS + FVIARNS+F YKG+ +V+ + R+LG+Y+LEGS R+S R+R+ QLI
Sbjct: 230 IITDLSNVSGFFVIARNSTFAYKGP+DVRQISRDGLGVKYLEGSARRSNKRLRVNVQLI 289

Query: 247 DA-TTGTHLWAERFEGTLDLDDIFELQDRMAESVVGAIAPQVERAEMERAKRKPTESLDAHD 305
+A G H+WAERF+ + DIF++QD + VV AI+ ++ E + R +L+A+D
Sbjct: 290 NAGEGHNHVAERFDREIADIFDVQDEVTRRVVEAISGKL--GEKKLVARSRPSNLEAYD 347

Query: 306 YYLRGMAKLHSGTHEAIEAALPLFYRAIELDQEFASAYAGAACYFWRKLNQWMDRAE 364
+R K ++ + EA L RAI++D + A++ A + GW++ +
Sbjct: 348 LCVRSRGKCNNSRSDNREACADL-ERAIQIDPNYCEAHSNLAISLLF----GWIWGEPEQ 402

Query: 365 EIAEGARL--ARRAVELGRDDAVALTRSGHALGHLVGDLDGGIALIDRARLLNPNFAPAW 422
E L A+RAVE+ DD+ A G + + D + D A LNP A A
Sbjct: 403 EPGRNALIHAQRAVEIDPDDSHARRILG-CVQLYERNWDEAKSQFDDAARLVNPNNAADAV 461

Query: 423 FLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAER- 481
G L+++ G+P++A+ A R++P + G +A +G ++ A+ R
Sbjct: 462 AWMGELQIYLGDPQAALRACGAALRINPRPPGWYFWIMG--IAQISSGHYEEAVASLSRE 519

Query: 482 ---ALGNLPSLLVAALVAASHALAGRTEEARKTMQRLRALDPSLRVSTLRDWLPIHRPE 538
G+ L+ A+ ALAGR EA++ + A +P VS L P P
Sbjct: 520 ETYGTGSREHLVPAL-----ALAGRVPEAQEEARLFLAGNPKWSVSDLVAASPFKSPS 572

Query: 539 DLARFADGL 547
D F G+
Sbjct: 573 DAQPFVAGV 581

>gi|13473903|ref|NP_105471.1| (NC_002678) adenylate cyclase cya3 [Mesorhizobium loti]
gi|14024654|dbj|BAB51257.1| (AP003004) adenylate cyclase; Cya3 [Mesorhizobium loti]
Length = 671

Score = 180 bits (456), Expect = 4e-44
Identities = 148/443 (33%), Positives = 225/443 (50%), Gaps = 20/443 (4%)

Query: 114 RKGFRFVGDIRIGGIGEVQPVG---PGAALQASGGSGETASALVLPDKPSITVLPFQNL 170
R+ +R + D R QP G P + ASG +G V P S+ V+PF +
Sbjct: 242 RQAWRSIRDQR---ASHQAQFAGLTPSHLVAASGDTGP-----VEPSHASLAVMPFVDE 293

Query: 171 SGDPEQEYFADGIVEDIIITLSRIRWLFVIARNSSFRYKGRAVEVKDVGRELGVRYVLEG 230
SG + ADG DIIT L+++R FVIAR S F +A+ ++ GR+LGV YV G
Sbjct: 294 SG--ARGGLADGFTHDIIITRLAKLRDFFVIARGSVFALAIEAIEEAGRKLGVDPYVASG 351

Query: 231 SVRKSNGNRVITGQLIDATTGTHLWAEFEGTLDIFELQDRMAESVVGAIAPQVERAEM 290
+VR R+ ++ +L++ T +WAE FE D+F + D + +S+V +I+ ++E E
Sbjct: 352 TVRSLTGRILIVSVELVEVRTARIVWAETFERPHDLFAVLDDIGDSIVSSISAEIETVER 411

Query: 291 ERAKRKPTESLDAHDYYLRGMAKLHSGTHEAIEAALPLFYRAIELDQEFASAYAGAACY 350
RA K SL+A + Y RG+ ++ T E A F +A++LD FA AYAG ++ +
Sbjct: 412 NRAMLKAPNSLNAWEAYHRGLWHMYRFTQAENEQARHFFDKALQLDPTFARAYAGLSFTH 471

Query: 351 FWRKLNQWMDRAEEIAEGARLARRAVELGRDDAVALTRSGHALGHLVGDLDGGIALIDR 410
+ W DR E A A ++ + + A G AL L G+ DG +A ++R
Sbjct: 472 WQNAFQRWG--DRRESALAYESAGHSLLVDDHNPAAHWAMGRAL-WLRGEQDGSALAELE 529

Query: 411 ARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHFFAG 470
A L+PNFA + F+ G+P++AI +H+ LSP D +F M A++H G
Sbjct: 530 AVDLSPNFALGHYALS FVHSQS GGPQAIGSSDHSRHLSPFDPLLFGLGSRAMSHVRLG 589

Query: 471 RFDSALVWAERALGNLPSLLVAALVAASHALAGRTEEARKTMQRLRALDPSLRVSTLRD 530
+F+ A WA +A + + +A+ A ALAGR +EAR +R P R D
Sbjct: 590 QFEEAAEWALKAAARPNHAHTIILAAHCLALAGRLDEARGFAAAIRKTLDPYRAD---D 646

Query: 531 WLPIHR--PEDLARFADGLRLAG 551
++ R P+ A F G R G
Sbjct: 647 FIGTFRFDPDAEALFRQGARRIG 669

>gi|16264266|ref|NP_437058.1| (NC_003078) probable adenylate cyclase protein [Sinorhizobium meliloti]
gi|15140391|emb|CAC48918.1| (AL603643) probable adenylate cyclase protein [Sinorhizobium meliloti]
Length = 624

Score = 165 bits (417), Expect = 1e-39
Identities = 130/376 (34%), Positives = 196/376 (51%), Gaps = 14/376 (3%)

Query: 158 DKPSITVLPFQNLSGDPEQEYFADGIVEDIIITLSRIRWLFVIARNSSFRYKGRAVEVKD 217
+KPSI VLPF N+SGDPEQEYF+DGI EDIIT LS+I LFV+ARN+++ YK + V+V+
Sbjct: 197 EKPSIAVLFPNNISGDPEQEYFSDGITEDIIITLSKISGLFVVARNATYTYKNKPVKVQQ 256

Query: 218 VGRELGVRYVLEGSVRKSNGNRVITGQLIDATTGTHLWAEFEGTLDIFELQDRMAESV 277
V ++L V Y+LEGSVR+ G+RVR+T QL++ G LWA+R++ L +IF LQD + ++
Sbjct: 257 VSQDLRVGYILEGSVRRVGSRRVTAQLVEGKGGPLWADRYDWDLTEIFALQDEITHTI 316

Query: 278 VGAIAPQVERAEMERAKRKPTESLDAHDYYLRGMAKLHSGTHEAIEAALPLFYRAIELDQ 337

V + ++ E + R PT + +A+ YYLRG LH + A +F A+ELD
Sbjct: 317 VDHLKVKLLPEEKDGRVPTGNFEAYAYYLRGRQFLHWSQSHYVLAKRMFAMAVELDP 376
Query: 338 EFASAYAGAAWC--YFWRKLNQWMDRAEEIAEGARLARRAVELGRDDAVALTRSGHALG 395
+A AYAG A C + + N +++ LA A L + +A + L
Sbjct: 377 LYARAYAGIADCDSEFLFLHYNA-----DVSIDGILATSALDLESGLAEEHSLGLA 429
Query: 396 -HLVGDLGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQE 454
L +A D+A L+P+ A + +G+ + A H + AA + P D +
Sbjct: 430 LSLRERHSEAMAEFDQAITLDPDLFEAHYFYARACFTQGLDEAARHFQRAADIKPDDYQ 489
Query: 455 MFRMQAGTALAHFFAGRFDSA---LVWAERALGNLPSLLVAVALVAASHALAGRTEEAR 510
+ + +A + AER L P L A A G + A+
Sbjct: 490 ALLVLINVLRSLGREQEMNTAAREGVARAERELMMRPENPRPAYLGAVGLAALGELDRAK 549
Query: 511 KTMQRLRALDPSLRVS 526
+ R A DP R++
Sbjct: 550 EWAGRALATDPDDRLA 565

>gi|16262751|ref|NP_435544.1| (NC_003037) putative CyaF4 adenylate cyclase [Sinorhizobium meliloti]
gi|14523380|gb|AAK64956.1| (AE007222) putative CyaF4 adenylate cyclase [Sinorhizobium meliloti]
Length = 629

Score = 137 bits (345), Expect = 3e-31
Identities = 122/359 (33%), Positives = 179/359 (48%), Gaps = 21/359 (5%)

Query: 135 VGPGAALQASGGSGETASALVLPD-----KPSITVLPFQNLSGDPEQEYFADGIVEDIT 189
VG G A+ A A+ P KPS+ VLPF N GD ADG+ EDIT
Sbjct: 187 VGTGTAVLALLVLGAAWQFWPTATVSGKPSVAVLPFDNYGGDEASGRADGLTEDIT 246
Query: 190 ALSRIRWLFVIARNSSFRYKGRAVEVKDVGRELGVRYVLEGSVRKSGNRVRITGQLIDAT 249
L+R VIARN+ YKG+A++V++G+ L V +V+EGS+ + +RVR+T QLID+
Sbjct: 247 DLARFPEFKVIARNSTETYKGAIDVREIGKALDVGFEVVEGSIAREADRVVRVTAQLIDSK 306
Query: 250 TGTHLWAERFEGTLDLDFELQDRMAESV---VGAIAPQVERAEMERAKRKPTESLDAHDY 306
G HLW++R++ ++F +Q +AE + +G A V+ + A RK +L+A++
Sbjct: 307 QGRHLWSQRWDRPDKEVFVQAEIAEQIANRLGGGAGLVQESGRIAAHRKVPGNLNAYEL 366
Query: 307 YLRGMAKLHSGTHEAIEAALPLFYRAIELDQEFASAYAGAAWCFWRK---LNGWMDRA 363
YL G +L +EAAL L +A++ D A W + L G ++
Sbjct: 367 YLLGTERLEQLDQANLEAALSLLTQAVQSDPGLAR-----GWVELFHTHDLGLAGLIEPE 421
Query: 364 EEIAEGARLARRAVELGRDDAVALTRSGHALGHLVGDLGGIALIDRARLLNPNFAPAW- 422
A A RA+ L D A G +LG + GD A + A + PN A
Sbjct: 422 RNRALADAAAERALTLDPSDPEAHAVYGSGLG-MRGDFARAEAEYEAALRMAPNAEILI 480
Query: 423 FLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAER 481
F G+ F G+PE + +E A +L P G LA+F AGR+ A+ ER
Sbjct: 481 FYIGWASTF-GKPERGADLVERAIQLDPNYPGWANRPFG--LAYFMAGRYPEAVTMFER 536

>gi|13471884|ref|NP_103451.1| (NC_002678) adenylate cyclase [Mesorhizobium loti]
gi|14022628|dbj|BAB49237.1| (AP002998) adenylate cyclase [Mesorhizobium loti]
Length = 485

Score = 135 bits (341), Expect = 1e-30
Identities = 113/373 (30%), Positives = 170/373 (45%), Gaps = 7/373 (1%)

Query: 131 VRQVPVGAALQASGGSGETASALVLPDKPSITVLPFQNLSGDPEQEYFADGIVEDIT 190
VR V + + + G+G + P + + P + + + FADG+ DI
Sbjct: 64 VRNKVALASHINGAIGAGMDGPPRLPGASPVLAIFPIECQTSEERWRRFADGLSSDITID 123
Query: 191 LSRIRWLFVIARNSSFRYKGRAVEVKDVGRELGVRYVLEGSVRKSGNRVRITGQLIDATT 250
L+R L VIA ++ + + G+ LG YV+ G +R RVR++ +L DA
Sbjct: 124 LARYADLPVIAFHTMKSGLGSKPADFAADGKALGATYVVGQLRADERRVRLSIELADADN 183
Query: 251 GTHLWAERFEGTLDLDFELQDRMAESVVGAIAPQ---VERAEMERAKRKPTESLDAHDY 307
G LW+ER++ ++DIF LQD + E+V+ IA + + +RKP SL A+D Y

Sbjct: 184 GVSLWSERYDRQVEDIFALQDSLTTETVINVIAGSYGALATVGRKAIRRKPPASLRAYDCY 243

Query: 308 LRGMALHSGTHEAIEAALPLFYRAIELDQEFASAYAGAACYFWRKLNQWVMDRAEEIA 367
L G + + + + I A + L F RA+ELD A+ A+ Y NG+ D I

Sbjct: 244 LLGVEQQDTFSRAGIAEIRLFSRALELDPTLVRAWTALAYAYSIEGANGFGDDAQVSIE 303

Query: 368 EGARLARRAVELGRDDAVALTRSGHALGHLVGDLDGGIALIDRARLLNPNFAPAW-FLGG 426
A+ L D+VA G G L GDL+G RA N A L G

Sbjct: 304 NWRTAVERNAILLDPMDSVACNCLGDLRGCL-GDLEGAERAYRRAFEYGSNHADTLAMLAG 362

Query: 427 FLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALGNL 486
+ G+P A+ IE A L+PL + G L F GR A+ R+ N

Sbjct: 363 SKALVAGDPAEAMPLIERAMHLNPLAPPWYFGMLGRIL--FTLGRHREAIAALCRSTLNS 420

Query: 487 PSLVAVALVAAS 499

P++L+ +AL S

Sbjct: 421 PNVLLFLALAHTS 433

>gi|16262767|ref|NP_435560.1| (NC_003037) conserved hypothetical protein [Sinorhizobium meliloti]

gi|14523397|gb|AAK64972.1| (AE007223) conserved hypothetical protein [Sinorhizobium meliloti]
Length = 767

Score = 100 bits (249), Expect = 4e-20

Identities = 130/489 (26%), Positives = 214/489 (43%), Gaps = 44/489 (8%)

Query: 78 WGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDIRIGGIGEVQPVG 137
W + +ES T AV A G +R R + G V I G + +P G

Sbjct: 286 WKEAVRAESDRT----AVPDASGPIVSARRRGRVLLTVGVVAVAAAAAILGYWTIDRP-GS 340

Query: 138 GAALQASGGSGETASALVLPDKPSITVLPFQNLSGDPEQEYFADGIVEDIITALSRI 197
++L+A S +PD P++ + PF NL P E + DG+ E+++TAL R + +

Sbjct: 341 VSSLRAGSVS-----VPDGP TLVIAPFANLGE GPNALYTDGVT EELLTALPRFKEI 392

Query: 198 FVIARNSSFRYKGRAVEVKDVGRELGVRYVLEGSVRKSGNRVRITGQLIDATTGTHLWAE 257
V R +S + V+V V ELG RY+L G VR SG+R+R+T +L+DA+ G LW+E

Sbjct: 393 KVFGRETS-KSLPPDVDSQVRDELGARYLLAGGVRVSGSRIRVTARLVDASDGAILWSE 451

Query: 258 RFEGTLD--DIFELQDRMAESVVGAI-PQVERAEMERAKRKPT-----SLDAHYYL 308
++ L D+F +Q +A V A+ A P A+ + A P + +L +DY

Sbjct: 452 DYDNQLQSRDLFAIQSDVASKVATAVAQPYGIIAQTDAAANPPPDDLGAYSCTLSFYDYRA 511

Query: 309 RGMALHSGTHEAIEAALPLFYRAIELDQEFASAYAGAACYFWRKLNQWVMDRAEEIA- 367
A+ H+ +E+A+ + +A+A+A + + + +A

Sbjct: 512 ELSAERHAKVSACLESVARY-----PGYATAWAMLSIAHLDEERFKFNPKSGAPMAM 564

Query: 368 -EGARLARRAVELGRDDAVALTRSGHALGHLVGDLDGGIALIDRARLLNPNFAPAWFLGG 426
+ ARRAV+L + L AL G + ++A +N N G

Sbjct: 565 ERALQAARRAVQLDPGNTRGLQALMTAL-FFNGQYAEAMRTGEQALAMNSNDTELMGELG 623

Query: 427 FLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALGNL 486
G+ + ++ A L+P + ALA G +A+ +A +L

Sbjct: 624 TRVAMGGQWQRGAALLDRAIALNPGGAGYY--HGTRALAAHMLGDHPAAVAGIRQA--DL 679

Query: 487 PSLVAVALVAASHALAGRTEEARKT----MQRLRALDPSLRVSTLRDWLPIHRPEDLAR 542
+ A+ + +A AG EAR+ M+R P+L+ + L +P+D R

Sbjct: 680 QKFPLFHAVASVIYAEAGMLHEARRAGETFMRRRPDFVPNLQAEFMMRNL---QPKQLR 736

Query: 543 FADGLRLAG 551

GLR AG

Sbjct: 737 LVSGLRKAG 745

>gi|1439552|gb|AAB17513.1| (U39409) TfuA [Rhizobium leguminosarum bv. trifolii]
Length = 650

Score = 86.3 bits (212), Expect = 7e-16

Identities = 104/424 (24%), Positives = 179/424 (41%), Gaps = 25/424 (5%)

Query: 140 ALQASGGSGETAS--ALVLPDKPSITVLPFQNLSGDPEQEYFADGIVEDIITALSRI 197

A QA+ G + A+ L +P I +LP +++ DP E ++ED+ LS+ R
Sbjct: 242 AAQAASGHSQPGPNLAITLLGQPRIIILPPESIFTDPLMERVGRALLEDVTIGLSQQRGF 301
Query: 198 FVIARNSSFRYKGRAVEVKDVGR---ELGVRYVLEGSVRKSGNRVRITGQLIDATTGTHL 254
VIA ++S R+++ +L Y + +++ V T +L TT +
Sbjct: 302 KVIAAHTSLEILSRSIDPSRAVSGPLDLSFDYAVYVTIQGRDEDVFATCRLTRTTTSEVI 361
Query: 255 WAERFEGTLDLDFELQDRMAESVVGAIAPQVERAEMERAKRKPTESLDAHDYLRGMAKL 314
WA + I E + +V ++A +ER E+ + S A+ YL G +
Sbjct: 362 WAIELPLVMQKISESFAHLTRRIVSSSLADTIERHELAMPIGEAPP--AYRLEYEGKRLI 419
Query: 315 HSGTHEAIEAALPLFYRAIELDQEFASAYAGAAWCYFWRKLN-GWMVD--RAEEIAEGAR 371
+ + A F ++ + F++A+AG + R L W++ R +E+ + A
Sbjct: 420 AQTDLQHLRQARKWFKSSLNRYEHFSAAHAGVS-----RALGMEWLIRGMRDKELLDEAN 474
Query: 372 LARRAVELGRDDAVALTRSGHALGHLVGDLGGIALIDRARLLNPNFAPAWFLGGFLRVF 431
A R + ++ R + D + +A+ LNP A L F
Sbjct: 475 GAARQAQQSDPNSSGRAYRELGFVALYRRRFDESLEYFQQAQDLNPNAD--ILADFDAL 532
Query: 432 R--GEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHHFFAGRFDSALVWAERALGNLPSL 489
G+ + A+E A +L+PL + + G HF ++ A+ AL + +
Sbjct: 533 SHDGFDRALSLRAAFKLNPLPPDYWNLGG--IHFMREEYEMAI----EALPVPKAK 586
Query: 490 LVAVALVAASHALAGRTEEARKTMQRLRALDPSLRVSTLRDWLPIHRPEDLARFADGLRL 549
L+AASHA+AG T +AR + + P R +R +P P GL L
Sbjct: 587 QATARLLAASHAMAGDTAKARNYARVLENFPDFRSEDIRHFVDPDRDPAYTEPLIQGLHL 646
Query: 550 AGLP 553
AGLP
Sbjct: 647 AGLP 650

>gi|15007264|gb|AAK77321.1| (AF028810) unknown [Rhizobium leguminosarum bv. viciae]
Length = 615

Score = 75.5 bits (184), Expect = 1e-12
Identities = 102/432 (23%), Positives = 188/432 (42%), Gaps = 32/432 (7%)

Query: 132 RQFVGPAA---LQASGGSETASALVLPDK-----PSITVLFPQNLSGDPEQEYFADGI 183
R P G G A + S GET + + + P + +LP + D A+ +
Sbjct: 203 RLPNGDGNARVQVTRSEAGGETTADIERSVQAPLILPRLVLLPPTSKHADAGLA-LANAL 261
Query: 184 VEDIITALSRIWLFVIARNSSFRYKGRAVEVKDVGRELGVRVLEGSVRKSGNRVRITG 243
+ED+ L +R + ++A +++ + + + V R + Y+L+ + + G +
Sbjct: 262 IEDVTIELCALRNISIVAPHTAGQIRRDSEKAAVVARH-SIAYLLDTRLSEEG----LFA 316
Query: 244 QLIDATTGTHLWAERFEGTLDLDFELQDRMAESVVGAIAPQVERAEMERAKRKPTESLDA 303
QL+ T +WA RF T D + + +A+ + ++A ++ E ER + + +A
Sbjct: 317 QLVYFPTDEI IWANRFTMTDPILPRQRRLIAQQLTMSVARELAENEEERLRFANP--EA 374
Query: 304 HDYYLRGMAKLHSGTHEAIEAALPLFYRAIELDQEFASAYAGAAWCYFWRKLN-GWMVD-- 361
+ YL G + + T I A F +++ +F+ ++ G A + + W+V
Sbjct: 375 YHAYLVGSSLSKLTLPHIRRARKAFKQSLSHKADFSPTSFTGLARTF----TSEWLVTAG 430
Query: 362 -RAEEIAEGARLARRAVELGRDDAVALTRSGHALGHL-VGDLGGIALIDRARLLNPNFA 419
E + + A RA+E RD A A + L +GD+D +A +D A L+P+FA
Sbjct: 431 GNNELHLAEQNALRAIE--RDPASAAGHRELGVTKLYLGVDVDASVAALDLAEQLSPHFA 488
Query: 420 PAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHHFFAGRFDSALVWA 479
+ V P A+ I A L+P+ + + A A A FF +++ A+ +
Sbjct: 489 DVIYSHADTLVHASRPGDALAKIRRAISLNPIAPDAYLWCA--AGASFFLEQYEEAVAYV 546
Query: 480 ERALGNLPSLLVAVALVAASHALAGRTEEARKTMQRLRALDPSLRVSTLRDWLPIHRPED 539
E P+ +A AAS A+ G + A QR +++P V +P
Sbjct: 547 EAMKDKAPAHRIA---AASCAMIGDRKRALFHRQRAESINPVFDVEKWLAIVPFKEDWQ 602
Query: 540 LARFADGLRLAG 551
+ +GL AG
Sbjct: 603 KELYREGLLKAG 614

>gi|15966040|ref|NP_386393.1| (NC_003047) CONSERVED HYPOTHETICAL PROTEIN [Sinorhizobium meliloti]
gi|15075310|emb|CAC46866.1| (AL591790) CONSERVED HYPOTHETICAL PROTEIN [Sinorhizobium meliloti]
Length = 608

Score = 75.5 bits (184), Expect = 2e-12
Identities = 103/408 (25%), Positives = 170/408 (41%), Gaps = 15/408 (3%)

Query: 144 SGGSETASALVLPDKPSITVLPFQNLSGDPEQEYFADGIVEDITALSRIKRWLFVIARN 203
+G ASA + P + +LP DP + +VEDI L R + V+A
Sbjct: 215 AGEPAEASAPPVAPAPRVALLPPAAGSDPMLHAVSVAVVEDITIGLCAQRSMVSVAPY 274
Query: 204 SSFRYKGRAVEVKDVGRELGVRYVLEGSVRKSGNRVRITGQLIDATTGTHLWAERFEGTL 263
++ R + A + + + GV Y L + + G + QLI + +WAERF +
Sbjct: 275 TAERIRDAADKAAFLKX-GVTYALDCRMSDQG----LFTQLIFLPSDAIVWAERFAISP 329
Query: 264 DDIFELQDRMAESVVGAIAPQVERAEMERAKRKPTESLDAHDYYLRGMAKLHSGTHEAIE 323
+ + + +A V A+ QVE R +A+ YL G+ L S I
Sbjct: 330 VGLLQQRQETAFHVARAVTEQVETGRAARIDY--LAHPEAYYAYLAGLRNLSSVGLPEIR 387
Query: 324 AALPLFYRAIELDQEFASAYAGAACYFWRKLNQWMDRAEEIAEGARLARRAVELGRDD 383
A F A++ +FA A +G A Y + DR E ++ A+ A+E +D
Sbjct: 388 RARGDFRAALKHKPDPFAPALSGMARTYAIEWILTARGDR-ELLSVAEHHAKGAIE-SNED 445
Query: 384 AVALTRSGHALGHLVGDLDGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIE 443
R + GDLD +A +D A L+P++A + V P A++ +
Sbjct: 446 LPGAHREFGVVKLYQGDLDESALDLAENLSPHYADVLVSHADTLVHVSRRPREALDKLG 505
Query: 444 HAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALGNLPSLLVAVALVAASHALA 503
A L+PL + + A A A +F + A+ + +R P L+AAS A+
Sbjct: 506 KALSINPLAPDITYFWSA--AGASYFLENYQDAIGYVQRMKDKSP----GDRLLAASWAML 559
Query: 504 GRTEEARKTMQRLRALDPSLRVSTLRDWLPIHRPEDLARFADGLRLAG 551
G ++AR R +P+ V +P+ + +GL+ AG
Sbjct: 560 GDQKKARAYMRALKSNPTFDVDKWLAVVPMKEQWQKDLVREGLEKAG 607

>gi|16262803|ref|NP_435596.1| (NC_003037) conserved hypothetical protein [Sinorhizobium meliloti]
gi|14523436|gb|AAK65008.1| (AE007226) conserved hypothetical protein [Sinorhizobium meliloti]
Length = 585

Score = 73.6 bits (179), Expect = 5e-12
Identities = 95/408 (23%), Positives = 170/408 (41%), Gaps = 27/408 (6%)

Query: 157 PDKPSITVLPFQNLSGDPEQEYFADGIVEDITALSRIKRWLFVIARNSSFRYKGRAVEVK 216
P+ P + V+PF++LS P+ G+ +++I+ +++ + + V+A G A
Sbjct: 190 PNIPKLMVMPFEDLSQTPQSAMITRGLTDEVISNIAKFEIVVVA-----GPAAPNP 241
Query: 217 DVGRELGVRYVLEGSVRKSGNRVRITGQLIDATTGTHLWAERFEGTLD--DIFELQDRMA 274
+ LEG VR G+++R+ +L+ + G+ +WA ++ L I ELQ A
Sbjct: 242 HSAEREYPFALEGRVRLDGDKLRLGIRLVQHSQSGSVVWANTYDEVLPQRKIIELQQNAA 301
Query: 275 ESVVG-----AIAPQVERAEMERAKRKPTESLDAHDYYLRGMAKLHSGTHEAIEAALPL 328
+V I Q R+ ++ Y L+ TH +++ L
Sbjct: 302 AAVASAIAPYQIVGIFQANATHFMRSPDDWQAYACTLAYGYRGDLNPQTHASVQECLQ- 360
Query: 329 FYRAIELDQEFASAYAGAACYFWRKLNQWMDRAEEI--AEGARLARRAVELGRDDAVA 386
A ++A+A+A + Y + ++R+ + + A RAVEL + A
Sbjct: 361 --HATTQFPDYATAWALLSLTYVDELRFYRLNRSTTVSLSHAIEAAARAVELDPQNVRA 418
Query: 387 LTRSGHALGHLVGDLDGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAA 446
L L G+++ + + RA +NPN GF G+ S + +
Sbjct: 419 LQAEMTLT-LFRGEVNAALTVGARAYAINPNDTELSGEYGFRLALSGQWRSGCDLVSKTV 477
Query: 447 RLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALGNLPSLLVAVALVAASHALAGRT 506
+P F +A A+ + + +A WA A +L + V ++ A G+
Sbjct: 478 ASNPGPVGYF--EALAVCCYIEHDYVAAERWARSA--DLHANPVYHVILLAILGKLGKM 533

Query: 507 EEARKTMQRLRALDPSLRVSTLRD-WLPIHRPEDLARFADGLRLAGLP 553
+ AR + L P + + L IHRPED F +GLR AG+P
Sbjct: 534 DLARAEREWLEINVPGFLENARNEVALRIHRPEDQKHFIIEGLRQAGVP 581

>gi|13475575|ref|NP_107139.1| (NC_002678) transcriptional regulator [Mesorhizobium loti]
gi|14026327|dbj|BAB52925.1| (AP003009) transcriptional regulator [Mesorhizobium loti]
Length = 952

Score = 65.5 bits (158), Expect = 2e-09
Identities = 37/105 (35%), Positives = 56/105 (53%)

Query: 23 EVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGGRI 82
+V FG + L R LTR G V +G + D+L+ L + V SK+EL+ VW G
Sbjct: 9 KVGISFGAFTLFAGERLLTREGVPVKLGARALDILVALTSAPNEVCSKEELMSRVWPGVT 68

Query: 83 VSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDIRIGG 127
V E ++ H+ ++RKA+GD R I T+ +G+ FV + G
Sbjct: 69 VEEGSRVRFHVASLRKALGDGKDGARFIATLPGRGYCFVAASVQAG 113

>gi|8708903|gb|AAF78794.1| (U33883) putative transmembrane transcriptional regulator protein
TtrR [Bradyrhizobium japonicum]
Length = 902

Score = 62.8 bits (151), Expect = 1e-08
Identities = 38/111 (34%), Positives = 60/111 (53%), Gaps = 1/111 (0%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGGRI VSEST 87
FG + + R +TR G + +G + FD L+ L+ + VVSK +L+ VW G V E+
Sbjct: 14 FGPFTVIPHERLVTRDGVALPLGTAKFDTLIALMSRPNEVSKWDLMALVWPGMAVEEAN 73

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDIRIGGIGEVQPVGPG 138
+ H+ A+RK +GD R I T++ +G+ FV I + R+P PG
Sbjct: 74 LRFHVAALRKVLGDGKGARYITTLSGRGYCFVAPISQTDVPAERRP-APG 123

>gi|15600553|ref|NP_254047.1| (NC_002516) two-component response regulator PhoB [Pseudomonas aeruginosa]
gi|12230950|sp|P23620|PHOB_PSEAE Phosphate regulon transcriptional regulatory protein phoB
gi|11352750|pir||C82975 two-component response regulator PhoB PA5360 [imported] -
Pseudomonas aeruginosa (strain PA01)
gi|9951681|gb|AAG08745.1|AE004948_1 (AE004948) two-component response regulator PhoB
[Pseudomonas
aeruginosa]
Length = 229

Score = 61.2 bits (147), Expect = 3e-08
Identities = 36/105 (34%), Positives = 57/105 (54%), Gaps = 3/105 (2%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQ 75
R PGD+E G +LD +T G+ +GP + LL + ++R ++ +LL
Sbjct: 123 RTGPGDSEAPIEVGGLLDPISHRVITDGKPAEMGPTEYRLLQFFMTHQERAYTRGQLLD 182

Query: 76 AVWGGRI-VSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
VWGG + V E T+ HI +RKA+G+ + L++TV G+RF
Sbjct: 183 QVWGGNVYVEERTVDVHIRRLRKALGEV--YENLVQTVRGTGYRF 225

>gi|16124549|ref|NP_419113.1| (NC_002696) phosphate regulon response regulator PhoB [Caulobacter crescentus CB15]
gi|13421435|gb|AAK22281.1| (AE005703) phosphate regulon response regulator PhoB [Caulobacter crescentus CB15]
Length = 230

Score = 59.7 bits (143), Expect = 7e-08
Identities = 38/103 (36%), Positives = 59/103 (56%), Gaps = 2/103 (1%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQ 75
R RPG A+ + GD ++D+ + R G+ + +GP F LL +L+ RV S+++LL
Sbjct: 122 RIRPGLADDRITVGDIIDRVHRVVRSGKEIHLGPTEFRLLDYLMOHPGRVFSREQLLD 181

Query: 76 AVWGGRI VSES-TITSHINAVRKAIGDTGGEQRLIRTVARKG 117

AVWG + E+ T+ HI +RKA+ T + IRTV G+
Sbjct: 182 AVWGSDVYVEARTVDVHIGRLRKALNGT-TDADPIRTVRSAGY 223

>gi|15894977|ref|NP_348326.1| (NC_003030) Response regulator (CheY-like receiver domain and DNA-binding HTH domain) [Clostridium acetobutylicum]
gi|15024664|gb|AAK79666.1|AE007679_12 (AE007679) Response regulator (CheY-like receiver domain and DNA-binding HTH domain) [Clostridium acetobutylicum]
Length = 232

Score = 58.9 bits (141), Expect = 1e-07
Identities = 30/95 (31%), Positives = 54/95 (56%), Gaps = 1/95 (1%)

Query: 26 FMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKEDELLQAVWGGRIVSE 85
F FG+ +D +R +T+ G+ V + + F+LL L+ + RV+++D LL +WG + E
Sbjct: 133 FKFGNIQIDFQRHNVTKKEGKVELTLKEFELLQVLIKNKGRVMTRDFLLDKIWGYEYIGE 192

Query: 86 S-TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
+ T+ H+ +R+ I D + I T+ G+RF
Sbjct: 193 TRTVDVHVRHLRQKIEDDDKNPKYIETIRGIGYRF 227

>gi|17229169|ref|NP_485717.1| (NC_003272) hypothetical protein [Nostoc sp. PCC 7120]
gi|17135497|dbj|BAB78043.1| (AP003586) ORF_ID:alr1677~hypothetical protein [Nostoc sp. PCC 7120]
Length = 280

Score = 58.5 bits (140), Expect = 2e-07
Identities = 47/156 (30%), Positives = 77/156 (49%), Gaps = 14/156 (8%)

Query: 295 RKPTESLDAHDYYLRGMAKLHSGTHEAIEAALPLFYRAIELDQEFASAYAGAAWCYFWRK 354
R+ T + A +Y++G + G +AA+ + +AI LD ++++AY G YF
Sbjct: 51 RRTTNSQAGQFYVQGRQHAQGDS---QAAIASYDKAIGLDPDYSAAAYRGRGLAYF--- 104

Query: 355 LNGWMVDRAEEIAEGARLARRAVELGRDDAVALTRSGHALGHLVGDLDGGIALIDRARLL 414
+ D+ + IA+ A+ L +DA A G+A L GD G I + A L
Sbjct: 105 ---DLGDKQKAIAD---YNEAIRLSPNDAEAFNSRGNARASL-GDNAGAITDYNEAIRL 156

Query: 415 NPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARLSP 450
+PN+A A+ G R +G+ + A+E A RL+P
Sbjct: 157 SPNYAEAYNNRGNARSVQGDQGALEDFNQAIRLNP 192

Score = 37.4 bits (85), Expect = 0.45
Identities = 40/145 (27%), Positives = 62/145 (42%), Gaps = 14/145 (9%)

Query: 302 DAHDYYLRGMAKLHSGTHEAIEAALPLFYRAIELDQEFASAYAGAAWCYFWRKLNWGMVD 361
DA + RG A+ G + A+ + AI L +A AY R + G
Sbjct: 126 DAEAFNSRGNARASLGDN---AGAITDYNEAIRLSPNYAEAYNNRGNA---RSVQGDQKG 179

Query: 362 RAEEIAEGARLARRAVELGRDDAVALTRSGHALGHLVGDLDGGIALIDRARLLNPNFAPA 421
E+ + RL + A+A G+A GD G I+ ++A LN NF PA
Sbjct: 180 ALEDFNQAIRLNPKY-----AIAYNNRGNARASQ-GDRQGAISDYNQAIRLNSNFPA 231

Query: 422 WFLGGFLRVFRGEPESAIEHIEHAA 446
+ G R +G+ + A+E ++ AA
Sbjct: 232 YNNRGNARAAQGDQGALEDLQKAA 256

Score = 36.2 bits (82), Expect = 1.0
Identities = 22/61 (36%), Positives = 30/61 (49%)

Query: 396 HLVGDLDGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEM 455
H GD IA D+A L+P+++ A+ G G+ + AI A RLSP D E
Sbjct: 70 HAQGSQAATIASYDKAIGLDPDYSAAAYRGRGLAYFDLGDQKAIADYNEAIRLSPNDAEA 129

Query: 456 F 456
F
Sbjct: 130 F 130

>gi|6531667|gb|AAF15533.1|AF196490_3 (AF196490) phosphate regulon response regulator PhoB
[Caulobacter
 crescentus] [Caulobacter vibrioides]
Length = 230

Score = 58.2 bits (139), Expect = 2e-07
Identities = 37/103 (35%), Positives = 58/103 (55%), Gaps = 2/103 (1%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQ 75
R RPG A+ + GD ++D+ + R G+ + +GP F LL +L+ RV S+++LL
Sbjct: 122 RIRPGLADDRITVGDIIIDRAHRVRSKGKEIHLGPTFRLLDYLMQHPGRVFSREQLLD 181

Query: 76 AVWGGRIVSES-TITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
AVWG + E+ T+ HI +RK + T + IRTV G+
Sbjct: 182 AVWGSDDVVEARTVDVHIGRLRKELNGT-TDADPIRTVRSAGY 223

>gi|2769532|emb|CAA11074.1| (AJ223073) phosphate regulatory protein [Bradyrhizobium japonicum]
Length = 235

Score = 57.4 bits (137), Expect = 4e-07
Identities = 36/103 (34%), Positives = 56/103 (53%), Gaps = 2/103 (1%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQ 75
R P +GD LD+++R + R G+ + +GP + LL + RV S+++LL
Sbjct: 122 RASPERLATVLAAGDIELDRDKRRVARSGRPIDLGPTFYRLLEFFLEHPGRVFSREQLLD 181

Query: 76 AVWGGRI-VSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
+VWG I + E T+ HI +RK + + G EQ IRTV G+
Sbjct: 182 SVWGRDIYIDERTVDVHIGRLRKLL-NLGREQDPIRTVIRGAGY 223

>gi|15640307|ref|NP_229934.1| (NC_002505) transcriptional activator CadC, putative [Vibrio
cholerae]
gi|11356005|pir|B82342 probable transcription activator CadC VC0278 [imported] - Vibrio
cholerae (group O1 strain N16961)
gi|9654689|gb|AAF93453.1| (AE004116) transcriptional activator CadC, putative [Vibrio
cholerae]
Length = 541

Score = 57.0 bits (136), Expect = 6e-07
Identities = 33/101 (32%), Positives = 58/101 (56%), Gaps = 3/101 (2%)

Query: 26 FMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGRIVSE 85
F D+VL + +L R+ + VS P++ +LL L V ++EL+Q VW G IV++
Sbjct: 28 FQINDWVLCIDENKLYRQDREVSAPRLINLLHFLAEHAGEVFGREELIQHVWDGAIVTD 87

Query: 86 STITSHINAVRKAIGDTGGEQRL--IRTVARKGFRFVGDIR 124
+T I +RK + D G E+ L + TV ++G++ V +++
Sbjct: 88 QVVTQSIFELRKLRLD-GREENLSYVVTVPKRGYKLVANVQ 127

>gi|16765877|ref|NP_461492.1| (NC_003197) transcriptional activator of cad operon (OmpR family)
[Salmonella typhimurium LT2]
gi|16421103|gb|AAL21451.1| (AE008816) transcriptional activator of cad operon (OmpR family)
[Salmonella typhimurium LT2]
Length = 514

Score = 56.6 bits (135), Expect = 6e-07
Identities = 25/96 (26%), Positives = 56/96 (58%), Gaps = 1/96 (1%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGRIVSESTI 88
G++++ ++R+G+ +++ P++ DLL++ D V+S+D ++ VW IV+ +
Sbjct: 9 GEWLVTSPVSNQISRQGRQITLPRLLIDLLMYFAHHPDEVLSRDNIIDHVMMRTIVTNHV 68

Query: 89 TSHINAVRKAIGDTG-GEQRLIRTVARKGFRFVGDI 123
T I+ +RK++ D G I TV ++G++ +
Sbjct: 69 TQSISELRKSLRDGGDSNAEYIVTVPKRGYKLTAPV 104

>gi|16761470|ref|NP_457087.1| (NC_003198) transcriptional activator cadC [Salmonella enterica,
subsp. enterica serovar Typhi]
gi|16503770|emb|CAD02760.1| (AL627275) transcriptional activator cadC [Salmonella enterica

subsp. enterica serovar Typhi]
Length = 514

Score = 56.6 bits (135), Expect = 6e-07
Identities = 25/96 (26%), Positives = 56/96 (58%), Gaps = 1/96 (1%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTDRDRVSKDELLQAVWGGGRIVSESTI 88
G++++ ++R+G+ +++ P++ DLL++ D V+S+D ++ VW IV+ +
Sbjct: 9 GEWLVTSPVNQISRQGRQITLPRLLIDLLMYFAHHPDEVLSRDNIIDHVWMRTIVTNHV 68

Query: 89 TSHINAVRKAIGDTG-GEQRLIRTVARKGFRFVGGDI 123
T I+ +RK++ D G I TV ++G++ +
Sbjct: 69 TQSISELRKSLRDGGDSNAEYIVTPKRGYKLTAPV 104

>gi|15791723|ref|NP_281546.1| (NC_002163) two-component regulator [Campylobacter jejuni]
gi|11278077|pir|B81378 two-component regulator Cj0355c [imported] - Campylobacter jejuni
(strain NCTC 11168)
gi|6967830|emb|CAB74192.1| (AL139075) two-component regulator [Campylobacter jejuni]
Length = 223

Score = 56.6 bits (135), Expect = 6e-07
Identities = 31/91 (34%), Positives = 54/91 (59%), Gaps = 2/91 (2%)

Query: 30 DYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTDRDRVSKDELLQAVWGG-RIVSESTI 88
D V+D + ++T +GQ + + + F++L HL D++VSK++LL A+W +V+ + I
Sbjct: 128 DLVIDPDEEKITYKGQDIELKGKPFVLTSLARHSDQIVSKEQLLDALWEEPELVTPNVI 187

Query: 89 TSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
IN +R+ + D I TV R+G+RF
Sbjct: 188 EVAINQIRQKM-DKPLNISTIETVRRRGYRF 217

>gi|791140|emb|CAA56853.1| (X80892) iagA [Salmonella typhi]
Length = 553

Score = 56.6 bits (135), Expect = 8e-07
Identities = 31/95 (32%), Positives = 58/95 (60%), Gaps = 2/95 (2%)

Query: 25 QFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTDRDRVSKDELLQAVWGGGRIVS 84
+F+F D++L+ + L R + V++ P+ + +L+ L+ ++VSK+ LL VWG V+
Sbjct: 13 KVFVDDFILNMD-GSLVRSEKKVNIPPKEYAVLVILLEAAGKIVSKNTLLDQVWGDAEVN 71

Query: 85 ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
E ++T I A+R+ + + E R I T+ +G+RF
Sbjct: 72 EESLTRCIYALRRILSED-KEHRYIETLYGQGYRF 105

>gi|16761653|ref|NP_457270.1| (NC_003198) invasion protein regulator [Salmonella enterica subsp.
enterica serovar Typhi]
gi|17433714|sp|P43016|IAGA_SALTI Invasion protein iagA
gi|16503954|emb|CAD05983.1| (AL627276) invasion protein regulator [Salmonella enterica subsp.
enterica serovar Typhi]
Length = 553

Score = 55.8 bits (133), Expect = 1e-06
Identities = 31/95 (32%), Positives = 58/95 (60%), Gaps = 2/95 (2%)

Query: 25 QFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTDRDRVSKDELLQAVWGGGRIVS 84
+F+F D++L+ + L R + V++ P+ + +L+ L+ ++VSK+ LL VWG V+
Sbjct: 13 KVFVDDFILNMD-GSLLRSEKKVNIPPKEYAVLVILLEAAGKIVSKNTLLDQVWGDAEVN 71

Query: 85 ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
E ++T I A+R+ + + E R I T+ +G+RF
Sbjct: 72 EESLTRCIYALRRILSED-KEHRYIETLYGQGYRF 105

>gi|13475726|ref|NP_107293.1| (NC_002678) transcriptional regulator [Mesorhizobium loti]
gi|14026482|dbj|BAB53079.1| (AP003010) transcriptional regulator [Mesorhizobium loti]
Length = 903

Score = 55.8 bits (133), Expect = 1e-06
Identities = 32/99 (32%), Positives = 55/99 (55%), Gaps = 1/99 (1%)

Query: 26 FMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVRVSKDELLQAVWGGRIVSE 85
F FG + + +E+R L R G+++ +G + FD+L LV VV +EL+ VW V+E
Sbjct: 6 FRFGPFEMHREQRRLYRDGKLLQLGSRAFDILQILVMRAGEVVRHEELIAMVWPDTFVAE 65

Query: 86 STITSHINAVRKAIGDTGG-EQRLIRTVARKGFRFVVDI 123
+ + ++ A+R+A+G G LI V +G+ F +
Sbjct: 66 NNLRVNMTALRRALGPEGSLTNGLIANVPGRGYSFTAPV 104

>gi|2126153|pir||S70817 invasion genes transcription activator hila - Salmonella
typhimurium
gi|806901|gb|AAD12579.1| (U25352) Hila [Salmonella typhimurium]
Length = 553

Score = 55.5 bits (132), Expect = 1e-06
Identities = 31/95 (32%), Positives = 57/95 (59%), Gaps = 2/95 (2%)

Query: 25 QFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVRVSKDELLQAVWGGRIVS 84
+F+F D++L+ + L R + V++ P+ + +L+ L+ +VSK+ LL VWG V+
Sbjct: 13 KVFVDDFILNMD-GSLVRSEKKVNIPPKEYAVLVILLEAAGEIVSKNTLLDQVWGDAEVN 71

Query: 85 ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
E ++T I A+R+ + + E R I T+ +G+RF
Sbjct: 72 EESLTRCIYALRRILSED-KEHRYIETLYGQGYRF 105

>gi|15640738|ref|NP_230368.1| (NC_002505) DNA-binding response regulator PhoB [Vibrio cholerae]
gi|11278053|pir||H82288 DNA-binding response regulator PhoB VC0719 [imported] - Vibrio
cholerae (group O1 strain N16961)
gi|9655162|gb|AAF93884.1| (AE004158) DNA-binding response regulator PhoB [Vibrio cholerae]
Length = 229

Score = 55.1 bits (131), Expect = 2e-06
Identities = 32/88 (36%), Positives = 50/88 (56%), Gaps = 2/88 (2%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVRVSKDELLQAVWGGRIVS-VSESTITSH 91
LD +T Q + +GP F +L + ++RV S+++LL VWG + V + T+ H
Sbjct: 139 LDPVSHRVTANDQPLDMGPTEFKMLHFFMTHQERVYSREQLNNVWGTNVYVEDRTVDVH 198

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRF 119
I +RKA+ D G +LI+TV G+RF
Sbjct: 199 IRRLRKALED-AGHDKLIQTVRGAGYRF 225

>gi|16766182|ref|NP_461797.1| (NC_003197) invasion genes transcription activator [Salmonella
typhimurium LT2]
gi|20141561|sp|P43015|IAGA_SALTY Invasion protein iagA (Protein hila)
gi|16421423|gb|AAL21756.1| (AE008831) invasion genes transcription activator [Salmonella
typhimurium LT2]
Length = 553

Score = 55.1 bits (131), Expect = 2e-06
Identities = 31/95 (32%), Positives = 57/95 (59%), Gaps = 2/95 (2%)

Query: 25 QFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVRVSKDELLQAVWGGRIVS 84
+F+F D++L+ + L R + V++ P+ + +L+ L+ +VSK+ LL VWG V+
Sbjct: 13 KVFVDDFILNMD-GSLRSEKKVNIPPKEYAVLVILLEAAGEIVSKNTLLDQVWGDAEVN 71

Query: 85 ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
E ++T I A+R+ + + E R I T+ +G+RF
Sbjct: 72 EESLTRCIYALRRILSED-KEHRYIETLYGQGYRF 105

>gi|15891373|ref|NP_357045.1| (NC_003063) AGR_L_2522p [Agrobacterium tumefaciens] [Agrobacterium
tumefaciens str. C58 (Cereon)]
gi|15159764|gb|AAK89830.1| (AE008326) AGR_L_2522p [Agrobacterium tumefaciens str. C58
(Cereon)]
Length = 650

Score = 55.1 bits (131), Expect = 2e-06
Identities = 103/406 (25%), Positives = 166/406 (40%), Gaps = 40/406 (9%)

Query: 159 KPSITVLPFQNLSGDPEQEYFADGIVEDIITALSRIKWLFIARNSSFRYKGRAVEVKDV 218
KP + + + G P VED+ +L R R V++ +S+F V+ D
Sbjct: 272 KPRVAFVRPARVDGQPVPTVI-HAFVEDVANSLVRYRTFTVLSPHSTFALAHDRVD--DS 328

Query: 219 GRELGVRYVLEGSVRKSGNRVRITGQLIDATTGTHLWAEFEGTLDDIFELQDRMAESV 278
L Y + +V R++ LI+ +G +W+ T I +++ V
Sbjct: 329 YAMLRADYRIISTVFDSD---RMSVALIEDASGEIWSLEAVLTERHIAAFRLLSKQVA 385

Query: 279 GAIAPQVERAEMERAKRKPTES---LDAHDYYLRGMAKLHSGTHEAIEAALPLFYRAIEL 335
A+A ++ER ++E + E+ L LRG L + A LF +A++L
Sbjct: 386 AALAREIERLQVEPRNHSGEAYRQLLEGQQLLRGKCDL-----PLLRARSIFRKAIDL 440

Query: 336 DQEFASAYAGAAWCYF--WRKLNG---WMVDRAEEIAEGARLARRAVELGRDDAVALTRS 390
D A A A A W L G ++ RA+ A+ +VE+ D A+ +
Sbjct: 441 DHS LAVARARVAQSLQLEWMLGNDPPLLHRAKAEADA-----SVEI--DPALGV--- 489

Query: 391 GHALGHLVG---DLGGIALIDRALLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAA 446
GH + +V D D A L PN A G+ E A + + A
Sbjct: 490 GHWMCAVVALYQRDFDISAEKFFAEALAPNSADLLQLHADALAHFGDAEIAWDKQQA 549

Query: 447 RLSPLDQEMFRMQAGTALAHEFFAGRFDSALVWAERALGNLPSLLVAVALVAASHALAGRT 506
L+PL +++ AG ++A F + +A+ R + P+L V + ASHAL G
Sbjct: 550 NLNPLAPDIY-WWAGASIA-FKRQDYGTAVELCGRMENDEPALRV---LTASHALHGDL 603

Query: 507 EEARKTMQRLRALDPSLRVSTLRDWLPIHRPEDLARFADGLRLAGL 552
AR++ RL+ P + + P P RF LRLAG+
Sbjct: 604 LAARESGSRLQENYPGMTAREISSLSPPDRPIANERFYHALRLAGI 649

>gi|15645657|ref|NP_207833.1| (NC_000915) response regulator [Helicobacter pylori 26695]
gi|7465348|pir|C64650 response regulator - Helicobacter pylori (strain 26695)
gi|2314190|gb|AAD08088.1| (AE000612) response regulator [Helicobacter pylori 26695]
Length = 223

Score = 55.1 bits (131), Expect = 2e-06
Identities = 30/92 (32%), Positives = 54/92 (58%), Gaps = 2/92 (2%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGG-RIVSEST 87
GD + + ++ +G+ V V + F++L HL RD++VSK++LL A+W +V+ +
Sbjct: 124 GDLTISPDEEKIIYKGREVEVGKGPFEVLTHLARHRDQIVSKEQLLDAIWEEFEMVTFNV 183

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
I IN +R+ + G ++ TV R+G+RF
Sbjct: 184 IEVAINQIRQKMDKPLGIS-MVETVRRRGYRF 214

>gi|15894830|ref|NP_348179.1| (NC_003030) Response regulator (CheY-like receiver domain and HTH
DNA-binding domain) [Clostridium acetobutylicum]
gi|15024503|gb|AAK79519.1|AE007665_6 (AE007665) Response regulator (CheY-like receiver domain
and HTH
DNA-binding domain) [Clostridium acetobutylicum]
Length = 227

Score = 55.1 bits (131), Expect = 2e-06
Identities = 31/97 (31%), Positives = 57/97 (57%), Gaps = 1/97 (1%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVS-EST 87
G+ + ++R + + Q +S+ P FD+L LV + RV+S+++L++ V+G + T
Sbjct: 131 GNLQICSDKRIVRIKDQQISLTPNEFDILYALVLNKGRLVLSREQLIERVFGLEDGDFDRT 190

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDIR 124
I HI +RK I + + + I TV + G++F GDI+
Sbjct: 191 IDVHIKNIRKKIEEDTKPKYIITVTKLGKFGGDIK 227

>gi|13958023|gb|AAK50764.1|AF360364_1 (AF360364) lysine decarboxylase regulator CadC [Salmonella
typhimurium]
Length = 512

Score = 54.7 bits (130), Expect = 2e-06
Identities = 26/98 (26%), Positives = 56/98 (56%), Gaps = 5/98 (5%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGGRIVSESTI 88
GD+++ ++RRG+ ++ P++ DLL++ D V+S+D ++ VW IV+ +
Sbjct: 9 GDWLTPSVNQISRRGRQITLEPRLLIDLLMYFAHHPDEVLSRDNIIDHVWMRTIVTNHV 68

Query: 89 TSHINAVRKAI---GDTGGEQRLIRTVARKGFRFVGDI 123
I+ +RK++ D+ E I TV ++G++ +
Sbjct: 69 AKAISELRKSLRRSADSNAE--YIVTPKRGYKLTAPV 104

>gi|15887773|ref|NP_353454.1| (NC_003062) AGR_C_746p [Agrobacterium tumefaciens] [Agrobacterium tumefaciens str. C58 (Cereon)]
gi|17934339|ref|NP_531129.1| (NC_003304) two component response regulator [Agrobacterium tumefaciens str. C58 (U. Washington)]
gi|15155345|gb|AAK86239.1| (AE007980) AGR_C_746p [Agrobacterium tumefaciens str. C58 (Cereon)]
gi|17738768|gb|AAL41445.1| (AE009013) two component response regulator [Agrobacterium tumefaciens str. C58 (U. Washington)]
Length = 227

Score = 54.7 bits (130), Expect = 3e-06
Identities = 38/103 (36%), Positives = 54/103 (51%), Gaps = 2/103 (1%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQ 75
R RP GD LD+E + R+ + V +GP F LL L+ + RV S+ +LL
Sbjct: 122 RARPEVLSSVLKCGDIELDRETHRVHRKSREVRGPTFEFRLLEFLMTSPGRVFSRSQLLD 181

Query: 76 AVWGGRI-VSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
VWG I V E T+ H+ +RKA+ + Q +IRTV G+
Sbjct: 182 GVWGHDIYVDERTVDVHVGRRLKAL-NFSHMQDVIRTVRGAGY 223

>gi|17937275|ref|NP_534064.1| (NC_003305) conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)]
gi|17741976|gb|AAL44380.1| (AE009286) conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)]
Length = 642

Score = 54.7 bits (130), Expect = 3e-06
Identities = 103/406 (25%), Positives = 166/406 (40%), Gaps = 40/406 (9%)

Query: 159 KPSITVLPFQNLSGDPEQEYFADGIVEDIIITALSRIRWLFVIARNSSFRYKGRAVEVKDV 218
KP + + + G P VED+ +L R R V++ +S+F V+ D
Sbjct: 264 KPRVAFVRPARVDGQVPPTVI-HAFVEDVANSLVRYRTFTVLSPHSTFALAHDRVD--DS 320

Query: 219 GRELGVRVYLEGSVRKSGNRVRITGQLIDATTGTHLWAERFEGTLDDIFELQDRMAESVV 278
L Y + +V R++ LI+ +G +W+ T I +++ V
Sbjct: 321 YAMLRADYRIISTVFDSDS---RMSVALIEDASGEIWSLEAVLTERIHAFAFRLLSKQVA 377

Query: 279 GAIAPQVERAEMERAKRKPTES---LDAHYYLRGMAKLHSGTHEAIEAALPLFYRAIEL 335
A+A ++ER ++E + E+ L LRG L + A LF +A++L
Sbjct: 378 AALAREIERLQVEPDNRHSGEAYRQLLEGQQLLRGKCDL-----PLLRARSIFRKAIDL 432

Query: 336 DQEFASAYAGAAWCYF--WRKLNG---WMVDRAEEIAEGARLARRAVELGRDDAVALTRS 390
D A A A A W L G ++ RA+ A+ +VE+ D A+ +
Sbjct: 433 DHS LAVARARVAQSLQLEWMLGGNDPPLLHRAKAEADA-----SVEI--DPALGV--- 481

Query: 391 GHALGHLVG----DLGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAA 446
GH + +V D D A L PN A G+ E A + + A
Sbjct: 482 GHWMCAVVALYQRDFDISAEKFFAEALAPNSADLLLQHADALAHFGDAEIAWDKFQQA 541

Query: 447 RLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALGNLPSLLVAVALVAASHALAGRT 506
L+PL +++ AG ++A F + +A+ R + P+L V + ASHAL G
Sbjct: 542 NLNPLAPDIY-WWAGASIA-FKRQDYSTAVELCGRMENDEPALRV----LTASHALHGD 595

Query: 507 EEARKTMQRLRALDPFLRVSTLRDWLPIHRPEDLARFADGLRLAGL 552
AR++ RL+ P + + P P RF LRLAG+
Sbjct: 596 LAARESGSRQLQENYPGMTAREISSLSPPDRDPIANERFYHALRLAGI 641

>gi|4530445|gb|AAD22036.1| (AF118229) response regulator PnpR [Streptococcus pneumoniae]
Length = 250

Score = 54.3 bits (129), Expect = 3e-06

Identities = 28/99 (28%), Positives = 57/99 (57%), Gaps = 1/99 (1%)

Query: 22 AEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSVSKDELLQAVWGG 81
A+ ++FG + ER E+ + +++S+ P+ F+LLL+L+ + ++++ LL+ +WG
Sbjct: 149 ADDSWLFGTLKVYPERHEVYKANKLLSLTPKEFELLYLMKHPNMTLTRELLERIWGYD 208

Query: 82 IVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
E+ + HI +R+ I D + IRT+ G++F
Sbjct: 209 FGQETRLVDVHIGKLREKIEDNPKAPQFIRTIRGYGYKF 247

>gi|17988267|ref|NP_540901.1| (NC_003317) PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN
PHOB [Brucella melitensis]
gi|17984036|gb|AAL53165.1| (AE009631) PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN
PHOB [Brucella melitensis]
Length = 255

Score = 54.3 bits (129), Expect = 3e-06
Identities = 36/105 (34%), Positives = 55/105 (52%), Gaps = 2/105 (1%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSVSKDELLQ 75
R P GD +LD+++ + R+ + V +GP F LL + + + RV S+ +LL
Sbjct: 151 RANPSILSHVLKVGDLLDRQQRVYRKEKEVHLGPTEFRLLLEYFMMSPGRVFSRSQLLD 210

Query: 76 AVWGGRI-VSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
VWG I V + T+ H+ +RKAI + G IRTV G+ F
Sbjct: 211 GVWGPDIYVDDRTVDVHVGRRLRKAI-NVGRAADSIRTVRGAGYSF 254

>gi|4768853|gb|AAD29647.1|AF124757_7 (AF124757) phosphate regulatory protein PhoB [Zymomonas mobilis]
Length = 231

Score = 54.3 bits (129), Expect = 4e-06
Identities = 37/103 (35%), Positives = 54/103 (51%), Gaps = 2/103 (1%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSVSKDELLQ 75
R RP ++ Q + D +D + R G VS+GP F LL HL+ RV S+++LL
Sbjct: 123 RIRPALSKEQLNYNDIEMDLVSHRVKRACTNVSIGPTEFRLLRLMEYPRRVFSREKLLD 182

Query: 76 AVWG-GRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
+WG + T+ HI +RKA+ + G LIRTV G+
Sbjct: 183 YIWGQDSIELRTVDVHIRRLRKAL-NRDGLPDLIRTVRSAGY 224

>gi|15901898|ref|NP_346502.1| (NC_003028) response regulator [Streptococcus pneumoniae TIGR4]
gi|15903934|ref|NP_359484.1| (NC_003098) Response regulator [Streptococcus pneumoniae R6]
gi|5830529|emb|CAB54572.1| (AJ006394) response regulator [Streptococcus pneumoniae]
gi|14973592|gb|AAK76142.1| (AE007497) response regulator [Streptococcus pneumoniae TIGR4]
gi|15459586|gb|AAL00695.1| (AE008553) Response regulator [Streptococcus pneumoniae R6]
Length = 235

Score = 53.9 bits (128), Expect = 4e-06
Identities = 28/99 (28%), Positives = 57/99 (57%), Gaps = 1/99 (1%)

Query: 22 AEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSVSKDELLQAVWGG 81
A+ ++FG + ER E+ + +++S+ P+ F+LLL+L+ + ++++ LL+ +WG
Sbjct: 134 ADDSWLFGTLKVYPERHEVYKANKLLSLTPKEFELLYLMKHPNMTLTRELLERIWGYD 193

Query: 82 IVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
E+ + HI +R+ I D + IRT+ G++F
Sbjct: 194 FGQETRLVDVHIGKLREKIEDNPKAPQFIRTIRGYGYKF 232

>gi|3282774|gb|AAC25063.1| (AF043352) response regulator homolog PhoB [Vibrio cholerae]
Length = 229

Score = 53.9 bits (128), Expect = 5e-06
Identities = 31/88 (35%), Positives = 49/88 (55%), Gaps = 2/88 (2%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSVSKDELLQAVWGGRI-VSESTITSH 91
LD +T Q + +GP F +L + ++RV S+++LL VWG + V + T+ H
Sbjct: 139 LDPVSHRVTANDQPLDMGPTEFKMLHFFMTHQERVYSREQLLNNVWGTVNYVEDRTVDVH 198

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRF 119
I +R A+ D G +LI+TV G+RF
Sbjct: 199 IRPLRNALED-AGHDKLIQTVRGAGYRF 225

>gi|15611449|ref|NP_223100.1| (NC_000921) putative TRANSCRIPTIONAL REGULATOR [Helicobacter pylori
J99]
gi|7465309|pir||C71937 probable transcription regulator - Helicobacter pylori (strain
J99)
gi|4154918|gb|AAD05966.1| (AE001473) putative TRANSCRIPTIONAL REGULATOR [Helicobacter pylori
J99]
Length = 223

Score = 53.5 bits (127), Expect = 5e-06
Identities = 30/92 (32%), Positives = 53/92 (57%), Gaps = 2/92 (2%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVRVSKDELLQAVWGG-RIVSEST 87
GD + + ++ +G+ V V + F++L HL RD++VSK++LL A+W +V+ +
Sbjct: 124 GDLTISPDEEKIIYKGREVEVGKPKPEVLTHLARHRDQIVSKEQLLDAIWEEPMPVTPNV 183

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
I IN +R+ + G + TV R+G+RF
Sbjct: 184 IEVAINQIRQKMDKPLGIST-VETVRRRGYRF 214

>gi|15964268|ref|NP_384621.1| (NC_003047) PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN
[Sinorhizobium meliloti]
gi|6685724|sp|Q52990|PHOB_RHIME Phosphate regulon transcriptional regulatory protein phoB
gi|152404|gb|AAB42026.1| (M96261) phosphate regulatory protein [Sinorhizobium meliloti]
gi|15073445|emb|CAC45087.1| (AL591784) PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN
[Sinorhizobium meliloti]
Length = 227

Score = 53.5 bits (127), Expect = 5e-06
Identities = 37/103 (35%), Positives = 53/103 (50%), Gaps = 2/103 (1%)

Query: 16 RGRPGDAEVQMFQGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVRVSKDELLQ 75
R +P GD LD+E + RR + V +GP F LL L+ + RV S+ +LL
Sbjct: 122 RAKPEVLSTLLRCGDIELDRHVRHRSREVRLGPTEFRLLLEFLMSSPGRVFSRSQLLD 181

Query: 76 AVWGGRI-VSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
VWG I V E T+ H+ +RKA+ + +IRTV G+
Sbjct: 182 GVWGHDIYVDERTVDVHVGLRLKAL-NFSNMPDVIRTVRGAGY 223

>gi|18265910|gb|AAL67383.1|AF447814_51 (AF447814) transcriptional activator [Escherichia coli]
Length = 512

Score = 53.5 bits (127), Expect = 6e-06
Identities = 25/93 (26%), Positives = 55/93 (58%), Gaps = 1/93 (1%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVRVSKDELLQAVWGGRIVSESTI 88
G++++ ++R G+ +++ P++ DLL+ V+S+DEL+ VW IV+ +
Sbjct: 9 GEWLVTSPINQISRNGRQLTLEPRLIDLVLFFAQHSGEVLSRDELIDNVWKRISIVTNHV 68

Query: 89 TSHINAVRKAIGDTGGEQRL-IRTVARKGFRFV 120
T I+ +RK++ D + + I TV ++G++ +
Sbjct: 69 TQSISELRKSLKDNDEDSPVYIATVPKRGYKLM 101

>gi|16131959|ref|NP_418557.1| (NC_000913) transcriptional activator of cad operon [Escherichia coli K12]
gi|115416|sp|P23890|CADC_ECOLI Transcriptional activator cadC
gi|281820|pir||C41968 transcription activator cadC - Escherichia coli
gi|145452|gb|AAA23531.1| (M67452) transcriptional activator [Escherichia coli]
gi|536978|gb|AAA97033.1| (U14003) cadC [Escherichia coli]
gi|1790576|gb|AAC77094.1| (AE000486) transcriptional activator of cad operon [Escherichia coli K12]
Length = 512

Score = 53.5 bits (127), Expect = 6e-06

Identities = 25/93 (26%), Positives = 55/93 (58%), Gaps = 1/93 (1%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRIVSESTI 88
G++++ ++R G+ +++ P++ DLL+ V+S+DEL+ VW IV+ +
Sbjct: 9 GEWLVTSPINQISRNGRQLTLEPRILIDLLVFFAQHSGEVLSRDELIDNVWKRISIVTNHVV 68

Query: 89 TSHINAVRKAIGDTGGEQRL-IRTVARKGFRFV 120
T I+ +RK++ D + + I TV ++G++ +
Sbjct: 69 TQSISELRKSLKDNDEDSPYIATVPKRGYKLM 101

>gi|15804726|ref|NP_290767.1| (NC_002655) transcriptional activator of cad operon [Escherichia coli O157:H7 EDL933]
gi|15834369|ref|NP_313142.1| (NC_002695) transcriptional activator of cad operon [Escherichia coli O157:H7]
gi|12519113|gb|AAG59333.1|AE005647_2 (AE005647) transcriptional activator of cad operon [Escherichia coli O157:H7 EDL933]
gi|13364592|dbj|BAB38538.1| (AP002568) transcriptional activator of cad operon [Escherichia coli O157:H7]
Length = 512

Score = 53.5 bits (127), Expect = 6e-06
Identities = 25/93 (26%), Positives = 55/93 (58%), Gaps = 1/93 (1%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRIVSESTI 88
G++++ ++R G+ +++ P++ DLL+ V+S+DEL+ VW IV+ +
Sbjct: 9 GEWLVTSPINQISRNGRQLTLEPRILIDLLVFFAQHSGEVLSRDELIDNVWKRISIVTNHVV 68

Query: 89 TSHINAVRKAIGDTGGEQRL-IRTVARKGFRFV 120
T I+ +RK++ D + + I TV ++G++ +
Sbjct: 69 TQSISELRKSLKDNDEDSPYIATVPKRGYKLM 101

>gi|16123366|ref|NP_406679.1| (NC_003143) phosphate regulon transcriptional regulatory protein [Yersinia pestis]
gi|15981142|emb|CAC92440.1| (AJ414155) phosphate regulon transcriptional regulatory protein [Yersinia pestis]
Length = 229

Score = 52.8 bits (125), Expect = 9e-06
Identities = 30/88 (34%), Positives = 49/88 (55%), Gaps = 2/88 (2%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRIVSESTITSH 91
LD + Q + +GP F LL + +RV S+++LL VWG + V + T+ H
Sbjct: 139 LDPSSHRVMANDQALDMGPTEFKLLHFFMTHPERVYSREQLLNYVWGTVNVYVEDRTVDVH 198

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRF 119
I +RKA+ +T G ++++TV G+RF
Sbjct: 199 IRRLRKAL-ETDGHDKMVQTVRGTYRF 225

>gi|13473197|ref|NP_104764.1| (NC_002678) phosphate regulatory protein, PhoB [Mesorhizobium loti]
gi|14023945|dbj|BAB50550.1| (AP003002) phosphate regulatory protein; PhoB [Mesorhizobium loti]
Length = 229

Score = 52.8 bits (125), Expect = 1e-05
Identities = 34/103 (33%), Positives = 53/103 (51%), Gaps = 2/103 (1%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQ 75
R +P GD VLD+E + R+ + +GP F LL ++ RV S+ +LL
Sbjct: 123 RAKPEVLSSVLKVGDIVLDRESHRVYRKKSEIRLGPTEFRLLFMMRHPGRVFSRSQLLD 182

Query: 76 AVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
VWG I + E T+ H+ +RKA+ + G +IRT+ G+
Sbjct: 183 NVWGETIYIDERTVDVHVGRRLKAV-NNGRMPDVIRTIRGAGY 224

>gi|15615719|ref|NP_244023.1| (NC_002570) two-component response regulator involved in phosphate regulation [Bacillus halodurans]
gi|10175779|dbj|BAB06876.1| (AP001517) two-component response regulator involved in phosphate regulation [Bacillus halodurans]

Length = 239

Score = 52.0 bits (123), Expect = 2e-05
Identities = 28/92 (30%), Positives = 53/92 (57%), Gaps = 1/92 (1%)

Query: 28 FG DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSEST 87
FG+ + + E+ +GQ + + P+ F+LLL+L + RV+++D+LL AVW V ++
Sbjct: 140 FGNVEIYPDNYEVYLGQPLELTPKEFELLLYLANHKGRLTRDQLLNAVWNYEFVGDTR 199

Query: 88 ITS-HINAVRKAIGDTGGEQRLIRTVARKGFR 118
I HI+ +R+ I + I+T+ G++
Sbjct: 200 IVDVHISHLREKIEPNTKKPIYIKTIRGLGYK 231

>gi|1172482|sp|P45606|PHOB_SHIDY Phosphate regulon transcriptional regulatory protein phoB
gi|280132|pir|A44753 phoB protein - Shigella dysenteriae
gi|152773|gb|AAA26535.1| (M31793) phosphate regulatory protein phoB [Shigella dysenteriae]
Length = 229

Score = 51.6 bits (122), Expect = 2e-05
Identities = 30/88 (34%), Positives = 49/88 (55%), Gaps = 2/88 (2%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSESTITSH 91
LD + + + +GP F LL + +RV S+++LL VWG + V + T+ H
Sbjct: 139 LDPTSHRVMGTGEEPLEMGPTFEKLLHFFMTHPERVYSREQLLNHVWGNTNVYVEDRTVDVH 198

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRF 119
I +RKA+ + GG R+++TV G+RF
Sbjct: 199 IRRLRKAL-EPGGHDMVQTVRGTYRF 225

>gi|15893613|ref|NP_346962.1| (NC_003030) Response regulator (CheY-like domain, HTH domain)
[Clostridium acetobutylicum]
gi|15023165|gb|AAK78302.1|AE007546_8 (AE007546) Response regulator (CheY-like domain, HTH domain)
[Clostridium acetobutylicum]
Length = 230

Score = 51.2 bits (121), Expect = 3e-05
Identities = 30/90 (33%), Positives = 45/90 (49%), Gaps = 1/90 (1%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSE-STITSH 91
+++ R++ G+ + FDLL+ L DRV SK+EL +WG E +T+T H
Sbjct: 141 INKASRKVFVNGKESQFTAKEFDLLVFLAQNPDRVFSKEELFDKIWGMDSFGEIATVTVH 200

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRFVG 121
I +R+ I I TV G+RF G
Sbjct: 201 IKKIREKIEKDTSNPEYIETVWAGYRFRG 230

>gi|17549263|ref|NP_522603.1| (NC_003296) PROBABLE TWO-COMPONENT RESPONSE REGULATOR
TRANSCRIPTION
REGULATOR PROTEIN [Ralstonia solanacearum]
gi|17431515|emb|CAD18193.1| (AL646082) PROBABLE TWO-COMPONENT RESPONSE REGULATOR TRANSCRIPTION
REGULATOR PROTEIN [Ralstonia solanacearum]
Length = 227

Score = 51.2 bits (121), Expect = 3e-05
Identities = 32/99 (32%), Positives = 56/99 (56%), Gaps = 2/99 (2%)

Query: 27 MFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVS-E 85
+ GD VLD R +TR GQ + V P+ + +L +L+ ++VS+ +L + VW +++ +
Sbjct: 127 VIGDLVLDPNARAVTRGGQALDVTPEKYAILEYLMRHAGQIVSRLQLAEHVVRADLIAID 186

Query: 86 STITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDIR 124
+ I H+ +R+ + D G+ LI TV +GFR R
Sbjct: 187 NLIDVHMKNLRRKV-DPPGQPALIHTVRGQGFRLAAPER 224

>gi|15802560|ref|NP_288587.1| (NC_002655) transcriptional response regulatory protein (sensor
Baes) [Escherichia coli O157:H7 EDL933]
gi|12516285|gb|AAG57142.1|AE005434_6 (AE005434) transcriptional response regulatory protein
(sensor)

BaeS) [Escherichia coli O157:H7 EDL933]
Length = 240

Score = 51.2 bits (121), Expect = 3e-05
Identities = 29/92 (31%), Positives = 52/92 (56%), Gaps = 1/92 (1%)

Query: 32 VLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGG-RIVSESTIT 90
++D+ R + + RG+++ + P F LL L +V S+++LL ++ R+V++ TI S
Sbjct: 144 IIDEXRFQASWRGKMLDLTPAEFRLLKTLSEHPGKVSREQLLNHLYDDYRVVTDRTIDS 203

Query: 91 HINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
HI +R+ + EQ IR V G+R+ D
Sbjct: 204 HIKNLRRKLESLDAEQSFIRAVYGVGYRWEAD 235

>gi|15800125|ref|NP_286137.1| (NC_002655) positive response regulator for pho regulon, sensor is
PhoR (or CreC) [Escherichia coli O157:H7 EDL933]
gi|15829703|ref|NP_308476.1| (NC_002695) positive response regulator for pho regulon PhoB
[Escherichia coli O157:H7]
gi|16128384|ref|NP_414933.1| (NC_000913) positive response regulator for pho regulon, sensor is
PhoR (or CreC) [Escherichia coli K12]
gi|130119|sp|P08402|PHOB_ECOLI Phosphate regulon transcriptional regulatory protein phoB
gi|73044|pir|RGECEFB transcription activator phoB - Escherichia coli
gi|42388|emb|CAA27659.1| (X04026) phoB protein (aa 1-229) [Escherichia coli]
gi|1657595|gb|AAB18123.1| (U73857) phosphate regulon transcriptional regulatory protein phoB
[Escherichia coli]
gi|1786599|gb|AAC73502.1| (AE000146) positive response regulator for pho regulon, sensor is
PhoR (or CreC) [Escherichia coli K12]
gi|12513245|gb|AAG54745.1|AE005219_1 (AE005219) positive response regulator for pho regulon,
sensor is
PhoR (or CreC) [Escherichia coli O157:H7 EDL933]
gi|13359906|dbj|BAB33872.1| (AP002551) positive response regulator for pho regulon PhoB
[Escherichia coli O157:H7]
gi|16209152|gb|AAL09901.1| (AY048733) PhoB [CRIM plasmid pAH150]
Length = 229

Score = 51.2 bits (121), Expect = 3e-05
Identities = 30/88 (34%), Positives = 49/88 (55%), Gaps = 2/88 (2%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRI-VSESTITSH 91
LD + + +GP F LL + +RV S+++LL VWG + V + T+ H
Sbjct: 139 LDPTSHRVMAGEEPLMGPTFEKLLHFFMTHPERVYSREQLLNHVWGNTNVYVEDRTVDVH 198

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRF 119
I +RKA+ + GG R+++TV G+RF
Sbjct: 199 IRRLRKAL-EPGGHDMVQTVRGTYRF 225

>gi|8569282|pdb|1QQI|A Chain A, Solution Structure Of The Dna-Binding And Transactivation
Domain Of Phob From Escherichia Coli
Length = 104

Score = 51.2 bits (121), Expect = 3e-05
Identities = 30/88 (34%), Positives = 49/88 (55%), Gaps = 2/88 (2%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRI-VSESTITSH 91
LD + + +GP F LL + +RV S+++LL VWG + V + T+ H
Sbjct: 14 LDPTSHRVMAGEEPLMGPTFEKLLHFFMTHPERVYSREQLLNHVWGNTNVYVEDRTVDVH 73

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRF 119
I +RKA+ + GG R+++TV G+RF
Sbjct: 74 IRRLRKAL-EPGGHDMVQTVRGTYRF 100

>gi|15803373|ref|NP_289406.1| (NC_002655) putative invasion protein [Escherichia coli O157:H7
EDL933]
gi|15832963|ref|NP_311736.1| (NC_002695) putative invasion protein [Escherichia coli O157:H7]
gi|12517348|gb|AAG57965.1|AE005514_2 (AE005514) putative invasion protein [Escherichia coli
O157:H7
EDL933]
gi|13363181|dbj|BAB37132.1| (AP002563) putative invasion protein [Escherichia coli O157:H7]
Length = 458

Score = 51.2 bits (121), Expect = 3e-05
Identities = 29/84 (34%), Positives = 50/84 (59%), Gaps = 1/84 (1%)

Query: 40 LTRRGQVSVSGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSESTITSHINAVRKAI 99
LT+ + V + P+ +L+ L+ + VV KD ++++VW IVS+ ++T I ++R I
Sbjct: 23 LTQGNQVYIPPELGVLLVLESAGHVVLKDMIIESVWKNIIVSDESLTRCIYSLR-CI 81

Query: 100 GDTGGEQRLIRTVARKGFRFVGDI 123
+ G R I T+ RKG+RF G +
Sbjct: 82 FEKIGYDRCIETIYRKGFRFSGQV 105

>gi|16332107|ref|NP_442835.1| (NC_000911) OmpR subfamily [Synechocystis sp. PCC 6803]
gi|7444058|pir|S76735 hypothetical protein - Synechocystis sp. (strain PCC 6803)
gi|1653736|dbj|BAA18647.1| (D90916) OmpR subfamily [Synechocystis sp. PCC 6803]
Length = 250

Score = 51.2 bits (121), Expect = 3e-05
Identities = 31/96 (32%), Positives = 48/96 (49%)

Query: 28 FGDYVLDQERRELTRRGQVSVSGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSEST 87
+G +D +R + +G V + PQ F LL L +S+ ELL+ W I + T
Sbjct: 132 YGVLIKIDLVQRRVEYQGNFVDLTPQEFSLLYVLTQAEGSALSRTTELLRRAWPEAIDNPRT 191

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDI 123
I +H+ ++RK I + LI+TV G+RF I
Sbjct: 192 IDTHVLSLRKKIETDPRQPSLIQTVRNVG YRFNSSI 227

>gi|16121054|ref|NP_404367.1| (NC_003143) putative regulatory protein [Yersinia pestis]
gi|15978819|emb|CAC89587.1| (AJ414144) putative regulatory protein [Yersinia pestis]
Length = 348

Score = 50.8 bits (120), Expect = 4e-05
Identities = 26/87 (29%), Positives = 51/87 (57%), Gaps = 6/87 (6%)

Query: 31 YVLDQERRELTRRGQVSVSGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSESTIT 90
++ QE RE R G+ ++ ++LL G ++S+DEL VW R++ +++ +
Sbjct: 27 FITHQETREKRLGE---YQLKLINVLLEHAG---EILSRDELTLNVWKKRRVIGNNSLPN 80

Query: 91 HINAVRKAIGDTGGEQRLIRTVARKGF 117
I+ +R A+GD +QR+I+T+ + G+
Sbjct: 81 AIHTLRVALGDENKQQRRIITIPKIGY 107

>gi|16130019|ref|NP_416583.1| (NC_000913) transcriptional response regulatory protein (sensor
Baes) [Escherichia coli K12]
gi|399094|sp|P30846|BAER_ECOLI Transcriptional regulatory protein baer
gi|478427|pir|JX0283 response-regulator Baer protein - Escherichia coli
gi|216533|dbj|BAA03141.1| (D14054) Baer [Escherichia coli]
gi|1736788|dbj|BAA15935.1| (D90846) Response-regulator Baer protein [Escherichia coli]
gi|1736800|dbj|BAA15946.1| (D90847) Response-regulator Baer protein [Escherichia coli]
gi|1788394|gb|AAC75140.1| (AE000297) transcriptional response regulatory protein (sensor
Baes) [Escherichia coli K12]
Length = 240

Score = 50.8 bits (120), Expect = 4e-05
Identities = 29/92 (31%), Positives = 52/92 (56%), Gaps = 1/92 (1%)

Query: 32 VLDQERRELTRRGQVSVSGPQVFDLLHLVGTRDRVSKDELLQAVWGG-RIVSESTIT 90
++D+ R + + RG+++ + P F LL L +V S+++LL ++ R+V++ TI S
Sbjct: 144 IIDEGRFQASWRGKMLDLTPAEFRLLKTLSEHPGKVFVSREQLLNHLYDDYRVVTDRTIDS 203

Query: 91 HINAVRKAIGDTGGEQRLIRTVARKGFRFVGDI 122
HI +R+ + EQ IR V G+R+ D
Sbjct: 204 HIKNLRRKLESLDAEQSFIRAVYGVGYRWEAD 235

>gi|15832141|ref|NP_310914.1| (NC_002695) transcriptional response regulatory protein
[Escherichia coli O157:H7]
gi|13362356|dbj|BAB36310.1| (AP002560) transcriptional response regulatory protein [Escherichia
coli O157:H7]

Length = 240

Score = 50.8 bits (120), Expect = 4e-05
Identities = 29/92 (31%), Positives = 52/92 (56%), Gaps = 1/92 (1%)

Query: 32 VLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGG-RIVSESTIT 90
++D+ R + + RG+++ + P F LL L +V S+++LL ++ R+V++ TI S
Sbjct: 144 IDEGRFQASWRGKMLDLTPAEFRLLKTLSEHPGKVSREQLLNHLYDDYRVVTDRTIDS 203

Query: 91 HINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
HI +R+ + EQ IR V G+R+ D
Sbjct: 204 HIKNLRRKLESLDAEQSFIRAVYGVGYRWEAD 235

>gi|17232242|ref|NP_488790.1| (NC_003272) two-component response regulator [Nostoc sp. PCC 7120]
gi|17133887|dbj|BAB76449.1| (AP003597) two-component response regulator [Nostoc sp. PCC 7120]
Length = 228

Score = 50.4 bits (119), Expect = 5e-05
Identities = 32/98 (32%), Positives = 54/98 (54%), Gaps = 2/98 (2%)

Query: 21 DAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGG 80
D Q FGD +LD R G+ V + + F+LL +L+ V+++++L+ VWG
Sbjct: 127 DTTEQLRFGDLILDLANRRVYSGRNVELTMKEFELLKYLMEHPREVLTRQILENVWGY 186

Query: 81 RIVSESTIT-HINAVRKAIGDTGGEQRLIRTVARKGF 117
+ ES + +I +R I D G++RLI+TV G+
Sbjct: 187 DFMGESNVIEVYIRYLRKIEDE-GQKRLIQTVRGVGY 223

>gi|94799|pir||A37775 phoB protein - Pseudomonas aeruginosa
Length = 229

Score = 50.4 bits (119), Expect = 5e-05
Identities = 32/105 (30%), Positives = 53/105 (50%), Gaps = 3/105 (2%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQ 75
R PG +E G +LD +T G+ +GP + LL + ++R ++ +
Sbjct: 123 RTGPGHSEAPIEVGGLLDPIHRVTIDGKPAEMGPTEYGLLOFFMTHQERAYTRGQRRD 182

Query: 76 AVWGGRI-VSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
VWGG + V E T+ I +RKA+G+ + L++TV G+RF
Sbjct: 183 QVWGGNVYVEERTVDMDIRRLRKALGEV--YENLVQTVRGTYRF 225

>gi|7339512|emb|CAB82846.1| (AJ277082) putative response regulator [Amycolatopsis mediterranei]
gi|14572576|emb|CAC42478.2| (AJ318385) response regulator protein [Amycolatopsis mediterranei]
Length = 229

Score = 50.1 bits (118), Expect = 6e-05
Identities = 33/101 (32%), Positives = 54/101 (52%), Gaps = 1/101 (0%)

Query: 20 GDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWG 79
G A + GD V+D+ E+T+RG+ VS+ P LLL L T +V S+ ++L AVW
Sbjct: 126 GPAAAEERHGDLDVIDRAALEVTKRGEFVSLTPTELKLLLELSRTPGQVYSRQILSAVWD 185

Query: 80 GRIVSEST-ITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
+ +S + + + +R I D + ++TV G+RF
Sbjct: 186 HDYLGDSRLVDACVQRLRAKIEDVPAKPEHVQTVRGFGYRF 226

>gi|15641332|ref|NP_230964.1| (NC_002505) DNA-binding response regulator [Vibrio cholerae]
gi|11278052|pir||F82213 DNA-binding response regulator VC1320 [imported] - Vibrio cholerae
(group O1 strain N16961)
gi|9655810|gb|AAF94478.1| (AE004212) DNA-binding response regulator [Vibrio cholerae]
Length = 234

Score = 50.1 bits (118), Expect = 7e-05
Identities = 34/103 (33%), Positives = 53/103 (51%), Gaps = 1/103 (0%)

Query: 21 DAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGG 80
DA FG +L+Q RR G+V+++ FDLL L D+VVS++ L +++ G
Sbjct: 130 DATHLLQFGGLLLNQSRRHCELDGEVINLSDSEFDLLWLLASAADQVVSREFLTksLRGI 189

Query: 81 RIVS-ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
+ T+ + I +RK + D + I TV KG+ FV D
Sbjct: 190 EYDGLDRTVDNKIVTLRKKLCDDSSTPKRIITVRGKGYLFVPD 232

>gi|9081855|gb|AAF82621.1|AF157830_2 (AF157830) PhoP2 response regulator [Myxococcus xanthus]
Length = 238

Score = 49.7 bits (117), Expect = 9e-05
Identities = 32/96 (33%), Positives = 54/96 (55%), Gaps = 2/96 (2%)

Query: 25 QFMFGDYVLDQERRELTRR-GQVSVGPGQVFDLLHLVGTRDRVVSKDELLQAVWGGRIV 83
Q F + LD RR+++R G VV + FDLL L+ +DR + + E+L AVWG +V
Sbjct: 137 QMGFSSTFLDLGRQVSRADGSVELTRTEFDLLAFLLRHQDRALPRGEILDVWGRDGV 196

Query: 84 SE-STITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
+ T+ + +++++K +G T I T+ G+R
Sbjct: 197 VDPRTVDNFVSSLKKKLGTSTSGFSIHTIRGVGYR 232

>gi|8546941|emb|CAB94653.1| (AL359215) putative two-component system response regulator.
[Streptomyces coelicolor A3(2)]
Length = 229

Score = 49.7 bits (117), Expect = 9e-05
Identities = 30/92 (32%), Positives = 52/92 (55%), Gaps = 1/92 (1%)

Query: 29 GDYVLDQERRELTRRQGVSVGPGQVFDLLHLVGTRDRVVSKDELLQAVWGGRIVSEST- 87
GD V+D+ +T +G+ V++GP LLL L + +V S+ +LL+AVW ++
Sbjct: 135 GDLVIDRAGLTVTHQGRPVALGPSELRLLLTLASAGQVFSRQQLLEAVWEHNYHGDARL 194

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
+ + + +R IG++ G R + TV G+RF
Sbjct: 195 VDACVKRLRSKIGESPGSPRYVHTVRGFGYRF 226

>gi|15610901|ref|NP_218282.1| (NC_000962) hypothetical protein Rv3765c [Mycobacterium tuberculosis H37Rv]
gi|7444061|pir||F70801 hypothetical protein Rv3765c - Mycobacterium tuberculosis (strain H37Rv)
gi|2960189|emb|CAA18087.1| (AL022121) hypothetical protein Rv3765c [Mycobacterium tuberculosis H37Rv]
Length = 234

Score = 49.3 bits (116), Expect = 1e-04
Identities = 32/98 (32%), Positives = 53/98 (53%), Gaps = 3/98 (3%)

Query: 21 DAEVQFMFGDYVLDQERRELTRRQGVSVGPGQVFDLLHLVGTRDRVVSKDELLQAVWGG 80
D+ Q + GD VLD++ E+ R G+ VS+ F+LL ++ RV+SK ++L VW
Sbjct: 133 DSGAQLVVGDVLVDEDSHEVMRAGEPVSLTSTEFELFRFMMHNSKRVLSKAQILDRVWSY 192

Query: 81 RIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
S I +I+ +RK I + G + +I T+ G+
Sbjct: 193 DFGGRSNIVELYIISYLRKKIDN--GREPMIHTLRGAGY 228

>gi|15807407|ref|NP_296139.1| (NC_001263) DNA-binding response regulator [Deinococcus radiodurans]
gi|7471835|pir||B75276 DNA-binding response regulator - Deinococcus radiodurans (strain R1)
gi|6460240|gb|AAF11967.1|AE002072_9 (AE002072) DNA-binding response regulator [Deinococcus radiodurans]
Length = 373

Score = 49.3 bits (116), Expect = 1e-04
Identities = 29/85 (34%), Positives = 48/85 (56%), Gaps = 2/85 (2%)

Query: 29 GDYVLDQERRELTRRQGVSVGPGQVFDLLHLVGTRDRVVSKDELLQAVWGGRIVSESTI 88
GD LD ++R +T +G+ + + P+ FD+L L+ RV S+ E+ Q +W GR+ S +
Sbjct: 129 GDLTLDPQKRLVITYKGEELRLSPKEFDILALLIRQPGRVYSRQEIGQEIWQGRLEPGSNV 188

Query: 89 TS-HINAVRKAIGDTGGEQRLIRTV 112

H+ +R + D G L+RTV
Sbjct: 189 VDVHMANLRRAKLRDLRG-YGLLRTV 212

>gi|15644403|ref|NP_229455.1| (NC_000853) response regulator DrrA [Thermotoga maritima]
gi|7444020|pir||D72228 response regulator DrrA - Thermotoga maritima (strain MSB8)
gi|4982229|gb|AAD36722.1|AE001807_13 (AE001807) response regulator DrrA [Thermotoga maritima]
Length = 247

Score = 49.3 bits (116), Expect = 1e-04
Identities = 30/91 (32%), Positives = 48/91 (51%), Gaps = 1/91 (1%)

Query: 30 DYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSKDELLQAVWGGGRIVSES-TI 88
D +D E+ E+ RG+ V++ P F+LL L +V S+D LL +WG ++ T+
Sbjct: 150 DLEIDVEKYEKVRGKKVNLTPLEFELLRFLAENEGKVFSRDVLLDKLWGYDYYGDTRTV 209

Query: 89 TSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
HI +R I + + I TV KG++F
Sbjct: 210 DVHIRRLRTKIEEDPSNPKYIITVRGKGKYKF 240

>gi|1575577|gb|AAC44436.1| (U67196) DNA-binding response regulator [Thermotoga maritima]
Length = 239

Score = 49.3 bits (116), Expect = 1e-04
Identities = 30/91 (32%), Positives = 48/91 (51%), Gaps = 1/91 (1%)

Query: 30 DYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSKDELLQAVWGGGRIVSES-TI 88
D +D E+ E+ RG+ V++ P F+LL L +V S+D LL +WG ++ T+
Sbjct: 142 DLEIDVEKYEKVRGKKVNLTPLEFELLRFLAENEGKVFSRDVLLDKLWGYDYYGDTRTV 201

Query: 89 TSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
HI +R I + + I TV KG++F
Sbjct: 202 DVHIRRLRTKIEEDPSNPKYIITVRGKGKYKF 232

>gi|2143952|pir||I55603 reduced hepatic glutathione transporter with canalicular features -
rat
Length = 835

Score = 49.3 bits (116), Expect = 1e-04
Identities = 28/84 (33%), Positives = 48/84 (56%), Gaps = 1/84 (1%)

Query: 40 LTRRGQVSVGPQVFDLLLHLVGTRDRVSKDELLQAVWGGGRIVSESTITSHINAVRKAI 99
LT+ + V + + +L+ L+ + VV KD ++++VW IVS+ + T I ++R+
Sbjct: 375 LTQNGEQVYIPQKELGVLLIVLLESAGHVVLKDMIIESVWENIIVSDESPTKSIYSLRRIF 434

Query: 100 GDTGGEQRLIRTVARKGFRFVGDI 123
G G R I T+ RKG+RF G +
Sbjct: 435 GKI-GYYRCIETIYRKGYRFSQV 457

>gi|15614371|ref|NP_242674.1| (NC_002570) two-component response regulator [Bacillus halodurans]
gi|10174426|dbj|BAB05527.1| (AP001513) two-component response regulator [Bacillus halodurans]
Length = 231

Score = 48.9 bits (115), Expect = 1e-04
Identities = 27/95 (28%), Positives = 49/95 (51%), Gaps = 1/95 (1%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSKDELLQAVWG-GRIVSES 86
FG V+ E+R++T G+ + + P+ F++L L +V S + + VWG +
Sbjct: 137 FGGLVIAPEQRKVTLTYGETIELTPKEFEILYLLASHPKKVSVENIFHQVWGEAYFEGGN 196

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVG 121
T+ H+ +RK + D + + I+TV G+ F G
Sbjct: 197 TVMVHVRTLRRKKLKDQKSKWIKTVWGVGYAFNG 231

>gi|15843385|ref|NP_338422.1| (NC_002755) DNA-binding response regulator [Mycobacterium
tuberculosis CDC1551]
gi|13883750|gb|AAK48236.1| (AE007181) DNA-binding response regulator [Mycobacterium
tuberculosis CDC1551]
Length = 286

Score = 48.9 bits (115), Expect = 1e-04
Identities = 32/98 (32%), Positives = 53/98 (53%), Gaps = 3/98 (3%)

Query: 21 DAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSVSKDELLQAVWGG 80
D+ Q + GD VLD++ E+ R G+ VS+ F+LL ++ RV+SK ++L VW
Sbjct: 185 DSGAQLVVGDLVLEDSHEVMRAGEPVSLTSTEFELLRFMMHNSKRVLSKAQILDRVWSY 244

Query: 81 RIVSESTIT-HINAVRKAIGDTGGEQRLIRTVARKGF 117
S I +I+ +RK I + G + +I T+ G+
Sbjct: 245 DFGGRSNIVELYISYLRKKIDN--GREPMIHLRGAGY 280

>gi|15840172|ref|NP_335209.1| (NC_002755) DNA-binding response regulator [Mycobacterium tuberculosis CDC1551]
gi|13880325|gb|AAK45023.1| (AE006969) DNA-binding response regulator [Mycobacterium tuberculosis CDC1551]
Length = 240

Score = 48.9 bits (115), Expect = 2e-04
Identities = 36/106 (33%), Positives = 58/106 (53%), Gaps = 9/106 (8%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSVSKDELLQ 75
+G V+ F D LD+E E+ + GQ VS+ P F LL + V V+SK ++L
Sbjct: 134 KGNKEPRNVRLTFADIELDEETHEVWKAGQPVLSPTFTLLRYFVINAGTVLSKPKILD 193

Query: 76 AVW---GGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
VW GG + + + S+++ +R+ I DT GE+RL+ T+ G+
Sbjct: 194 HVWRYDFGGDV---NVVESYVSYLRRKI-DT-GEKRLHLTLRGVGY 234

>gi|15607897|ref|NP_215271.1| (NC_000962) phoP [Mycobacterium tuberculosis H37Rv]
gi|7444063|pir||H70705 probable phoP protein - Mycobacterium tuberculosis (strain H37RV)
gi|1550635|emb|CAB02400.1| (Z80226) phoP [Mycobacterium tuberculosis H37Rv]
Length = 247

Score = 48.9 bits (115), Expect = 2e-04
Identities = 36/106 (33%), Positives = 58/106 (53%), Gaps = 9/106 (8%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSVSKDELLQ 75
+G V+ F D LD+E E+ + GQ VS+ P F LL + V V+SK ++L
Sbjct: 141 KGNKEPRNVRLTFADIELDEETHEVWKAGQPVLSPTFTLLRYFVINAGTVLSKPKILD 200

Query: 76 AVW---GGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
VW GG + + + S+++ +R+ I DT GE+RL+ T+ G+
Sbjct: 201 HVWRYDFGGDV---NVVESYVSYLRRKI-DT-GEKRLHLTLRGVGY 241

>gi|16804539|ref|NP_466024.1| (NC_003210) two-component response phosphate regulator [Listeria monocytogenes EGD-e]
gi|16411989|emb|CAD00579.1| (AL591983) two-component response phosphate regulator [Listeria monocytogenes]
Length = 236

Score = 48.9 bits (115), Expect = 2e-04
Identities = 28/99 (28%), Positives = 51/99 (51%), Gaps = 1/99 (1%)

Query: 21 DAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSVSKDELLQAVWGG 80
D E + GD + + E+ + ++ + P+ F+LLL L R +V S+D+LL VW
Sbjct: 133 DVEATILIGDLKILPDSYEVYLQDDLLDLTPKEFELLLFLANHRGKVFSRDQLLDTVWNY 192

Query: 81 RIVSESTIT-HINAVRKAIGDTGGEQRLIRTVARKGFR 118
V E+ I H++ +R I + + I+T+ G++
Sbjct: 193 DYVGETRIVDVHVSHLRDKIELDTKQPKYIKTIRGFGYK 231

>gi|15596354|ref|NP_249848.1| (NC_002516) probable two-component response regulator [Pseudomonas aeruginosa]
gi|11352318|pir||B83500 probable two-component response regulator PA1157 [imported] -
Pseudomonas aeruginosa (strain PAO1)
gi|9947080|gb|AAG04546.1|AE004546_1 (AE004546) probable two-component response regulator [Pseudomonas aeruginosa]
Length = 236

Score = 48.5 bits (114), Expect = 2e-04
Identities = 36/109 (33%), Positives = 53/109 (48%), Gaps = 1/109 (0%)

Query: 15 ERGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDRVSKDELL 74
E G P + FG V+D RE G + + FDLL L R++S++E+
Sbjct: 127 EAGAPAAADSKRLAFGRLLVIDNAMREAWLDGTTIELTSAEFDLLWLLAANAGRILSREEIF 186

Query: 75 QAVWGGRIVSES-TITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
A+ G + +I I+ +R IGD RLI+TV KG+ FVG+
Sbjct: 187 NALRGIEYDQDRSIDVRISRIKIGDDPMHPRLIKTVRSKGYLFVGE 235

>gi|17230752|ref|NP_487300.1| (NC_003272) two-component response regulator [Nostoc sp. PCC 7120]
gi|17132355|dbj|BAB74959.1| (AP003592) two-component response regulator [Nostoc sp. PCC 7120]
Length = 238

Score = 48.5 bits (114), Expect = 2e-04
Identities = 32/93 (34%), Positives = 45/93 (47%), Gaps = 1/93 (1%)

Query: 28 FG DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDRVSKDELLQAVWGGRIVSEST 87
F ++D RRE+T Q V + FDLL L RV + EL+Q VW V +
Sbjct: 134 FEKLMIDPVRREVTLSQAVPLTALEFDLLHFLASHPGRVWRRRAELIQEVWDYEVGDQR 193

Query: 88 ITS-HINAVRKAIGDTGGEQRLIRTVARKGFRF 119
+ HI +RK I + LI+TV G++F
Sbjct: 194 VVDVHIGQIRKKIEVDASQPALIQTVRGVGYKF 226

>gi|16759374|ref|NP_454991.1| (NC_003198) phosphate regulon transcriptional regulatory protein
PhoB [Salmonella enterica subsp. enterica serovar Typhi]
gi|16763777|ref|NP_459392.1| (NC_003197) response regulator in two-component regulatory system
with PhoR (or CreC), regulates pho regulon (OmpR family)
[Salmonella typhimurium LT2]
gi|16418901|gb|AAL19351.1| (AE008714) response regulator in two-component regulatory system
with PhoR (or CreC), regulates pho regulon (OmpR family)
[Salmonella typhimurium LT2]
gi|16501665|emb|CAD08852.1| (AL627266) phosphate regulon transcriptional regulatory protein
PhoB [Salmonella enterica subsp. enterica serovar Typhi]
Length = 229

Score = 48.5 bits (114), Expect = 2e-04
Identities = 27/74 (36%), Positives = 44/74 (58%), Gaps = 2/74 (2%)

Query: 47 VSVGPQVFDLLHLVGTDRDRVSKDELLQAVWGGRI-VSESTITSHINAVRKAIGDTGGE 105
+ +GP F LL + +RV S+++LL VWG + V + T+ HI +RKA+ + G
Sbjct: 153 LDMGPTEFKLLHFFMTHPERVYSREQLLNHVWGTNVYVEDRTVDVHIRRLRKAL-EHSGH 211

Query: 106 QRLIRTVARKGFRF 119
R+++TV G+RF
Sbjct: 212 DRMVQTVRGTYRF 225

>gi|17351932|gb|AAL38202.1|AF319446_1 (AF319446) putative response regulator RR62 [Listeria
monocytogenes]
Length = 240

Score = 48.5 bits (114), Expect = 2e-04
Identities = 28/99 (28%), Positives = 51/99 (51%), Gaps = 1/99 (1%)

Query: 21 DAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDRVSKDELLQAVWGG 80
D E + GD + + E+ + + + P+ F+LLL L R +V S+D+LL VW
Sbjct: 137 DVEATILIGDLKILPDSYEVYLQDDLLDLTPKEFELLFLANHRGKVFSRDQLLDTVWNY 196

Query: 81 RIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
V E+ I H++ +R I + + I+T+ G++
Sbjct: 197 DYVGETRIVDVHVSRLRDKIELDTKQPKYIKTIRGFGYK 235

>gi|1172481|sp|P45605|PHOB_KLEPN Phosphate regulon transcriptional regulatory protein phoB
gi|280103|pir||C44753 phoB protein - Klebsiella pneumoniae
gi|149295|gb|AAA25122.1| (M31794) phosphate regulatory protein phoB [Klebsiella pneumoniae]
Length = 229

Score = 48.5 bits (114), Expect = 2e-04
Identities = 29/88 (32%), Positives = 47/88 (52%), Gaps = 2/88 (2%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRI-VSESTITSH 91
LD + + +GP F LL + +RV S+++LL VWG + V + T+ H
Sbjct: 139 LDPSSHRVMTGDSPLDMGPTEFKLLHFFMTHPERVYSREQLLNHVWGTVNYVEDRTVDVH 198

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRF 119
I +RKA+ + G R+++TV G+RF
Sbjct: 199 IRRLRKAL-EHSGHDMVQTVRGTYRF 225

>gi|16801706|ref|NP_471974.1| (NC_003212) two-component response phosphate regulator [Listeria innocua]
gi|16415181|emb|CAC97871.1| (AL596173) two-component response phosphate regulator [Listeria innocua]
Length = 236

Score = 48.5 bits (114), Expect = 2e-04
Identities = 28/99 (28%), Positives = 51/99 (51%), Gaps = 1/99 (1%)

Query: 21 DAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGG 80
D E + GD + + E+ + ++ + P+ F+LLL L R +V S+D+LL VW
Sbjct: 133 DTEATILIGDLKILPDSYEVYLQDDLLDLTPKEFELLFLANHRGKVFSRDQLLDTVWNY 192

Query: 81 RIVSESTIT-HINAVRKAIGDTGGEQRLIRTVARKGFR 118
V E+ I H++ +R I + + I+T+ G++
Sbjct: 193 DYVGETRIVDVHVSRLDKIELDTKQPKYIKTIRGFGYK 231

>gi|15924683|ref|NP_372217.1| (NC_002758) alkaline phosphatase synthesis transcriptional regulatory protein [Staphylococcus aureus subsp. aureus Mu50]
gi|15927271|ref|NP_374804.1| (NC_002745) alkaline phosphatase synthesis transcriptional regulatory protein [Staphylococcus aureus subsp. aureus N315]
gi|13701489|dbj|BAB42783.1| (AP003134) alkaline phosphatase synthesis transcriptional regulatory protein [Staphylococcus aureus subsp. aureus N315]
gi|14247465|dbj|BAB57855.1| (AP003363) alkaline phosphatase synthesis transcriptional regulatory protein [Staphylococcus aureus subsp. aureus Mu50]
Length = 234

Score = 48.5 bits (114), Expect = 2e-04
Identities = 23/81 (28%), Positives = 48/81 (58%), Gaps = 1/81 (1%)

Query: 39 ELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRI-VSESTITSH-HINAVRK 97
E+ + +++ + P+ F+LLL+L+ + RV++++ +L VW +S I HI+ +R
Sbjct: 147 EVYKHNELLELTPKEFELLYLIERQGRVITREHMLNTVWNYEFAGDSRIVDVHISHLRD 206

Query: 98 AIGDTGGEQRLIRTVARKGFR 118
+ D + +LI+TV G++
Sbjct: 207 KLEDNPKKPQLIKTVRGLGYK 227

>gi|1172483|sp|P45607|PHOB_SHIFL Phosphate regulon transcriptional regulatory protein phoB
gi|2120000|pir||S61298 transcription activator phoB - Shigella flexneri
gi|531494|emb|CAA56927.1| (X81000) phoB [Shigella flexneri]
Length = 229

Score = 48.5 bits (114), Expect = 2e-04
Identities = 29/88 (32%), Positives = 48/88 (53%), Gaps = 2/88 (2%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRI-VSESTITSH 91
LD + + +GP F LL + + V S+++LL VWG + V + T+ H
Sbjct: 139 LDPTSHRVMAAGEEPLMGPTTEFKLLHFFMTHPVLVSREQLLNHVWGTVNYVEDRTVDVH 198

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRF 119
I +RKA+ + GG R+++TV G+RF
Sbjct: 199 IRRLRKAL-EPGGHDMVQTVRGTYRF 225

>gi|1055347|gb|AAB38749.1| (U38917) response regulator PhoB [Synechococcus sp. WH 7803]
Length = 234

Score = 48.5 bits (114), Expect = 2e-04
Identities = 29/92 (31%), Positives = 52/92 (56%), Gaps = 1/92 (1%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGRIVSES-T 87
G+ L + +TR G+ +++ P+ + +L L+ RV S+D+LL+ +WG V ++ T
Sbjct: 142 GNLCLYAQECRVTRDGEDLTLSPEYKILELLIRNPKRVSRDQLLERIWGIDFVGDTKT 201

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
+ HI +R+ I + + IRTV G+RF
Sbjct: 202 VDVHIRWLREKIEEEPSSPQHIRTVRGFGYRF 233

>gi|887803|gb|AAA83034.1| (U28375) ORF_o458 [Escherichia coli]
Length = 458

Score = 48.1 bits (113), Expect = 2e-04
Identities = 30/91 (32%), Positives = 51/91 (55%), Gaps = 1/91 (1%)

Query: 40 LTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGRIVSESTITSHINAVRKAI 99
LT+ + V + + +L+ L+ + VV KD ++++VW IVS+ ++T I ++R I
Sbjct: 23 LTQGNEQVYIPQKELGVLIVLLESAGHVVLKDMIIESVWKNIIVSDESLTRCIYSLR-CI 81

Query: 100 GDTGGEQRLIRTVARKGFRFVGDIRIGGIGE 130
+ G R I T+ RKG+RF G + I E
Sbjct: 82 FEKIGYDRCIETIYRKGYRFSGQVFXTKINE 112

>gi|18034495|gb|AAL57517.1|AF453441_1 (AF453441) CadC [Escherichia coli]
Length = 95

Score = 48.1 bits (113), Expect = 3e-04
Identities = 21/73 (28%), Positives = 44/73 (59%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGRIVSESTI 88
G++++ ++R G+ +++ P++ DLL+ V+S+DEL+ VW IV+ +
Sbjct: 9 GEWLVTSPINQISRNQRLTLEPRILDLLVFFAQHSGEVLSRDELIDNVWKRISIVTNHVV 68

Query: 89 TSHINAVRKAIGD 101
T I+ +RK++ D
Sbjct: 69 TQSISELRKSLKD 81

>gi|15807237|ref|NP_295967.1| (NC_001263) phosphate regulon transcriptional regulatory protein
PhoB [Deinococcus radiodurans]
gi|7473307|pir|[G75296 phosphate regulon transcription regulatory protein PhoB -
Deinococcus radiodurans (strain R1)
gi|6460051|gb|AAF11793.1|AE002057_1 (AE002057) phosphate regulon transcriptional regulatory
protein
PhoB [Deinococcus radiodurans]
Length = 238

Score = 48.1 bits (113), Expect = 3e-04
Identities = 30/91 (32%), Positives = 45/91 (48%), Gaps = 1/91 (1%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGRIV-SEST 87
G +D E G+ +++ + FDLL L RV S+ ELL VWG + E T
Sbjct: 133 GPLTVDLAAEAQLAGRTLNLTRREFDLLAFLTANAGRVYSRTELLDRVWGADFLGGERT 192

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
+ H+ +R +GD G+ + TV KG+R
Sbjct: 193 VDQHTQLRAHLGDDPGKPSFLETVRGKGYR 223

>gi|16125842|ref|NP_420406.1| (NC_002696) transcriptional regulator KdpE [Caulobacter crescentus
CB15]
gi|13422990|gb|AAK23574.1| (AE005834) transcriptional regulator KdpE [Caulobacter crescentus
CB15]
Length = 257

Score = 48.1 bits (113), Expect = 3e-04
Identities = 28/95 (29%), Positives = 49/95 (51%), Gaps = 1/95 (1%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTDRDVSVDKDELLQAVWGGGRIVSEST 87
FGD ++D + R +T+ G V + P+ F+LL L + +V++ ELL +WG ++
Sbjct: 160 FGDVIDLDLRLVTKAGAAVKLSPKEFELLARLALSPGKVLTHKELLVGIWGASHADDTQ 219

Query: 88 -ITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVG 121
+ + +R+ + D RLi T G+R G
Sbjct: 220 YLRVFGQLRQKLEDDSAHPRLILTEPGVG YRLQG 254

>gi|15644443|ref|NP_229495.1| (NC_000853) conserved hypothetical protein [Thermotoga maritima]
gi|7462092|pir|A72220 conserved hypothetical protein - Thermotoga maritima (strain MSB8)
gi|4982272|gb|AAD36762.1|AE001810_1 (AE001810) conserved hypothetical protein [Thermotoga maritima]
Length = 357

Score = 47.8 bits (112), Expect = 3e-04
Identities = 29/108 (26%), Positives = 57/108 (51%), Gaps = 3/108 (2%)

Query: 414 LNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHFFAGRFD 473
++ N+APA+ L G L V +G+ E I+ ++ A + P + + A A++ G ++
Sbjct: 126 IDENYAPAYELKGSLLVEQKIEEGIKFLDKAVEIDPW---LVQAYASLGEAYYNLGDYE 182

Query: 474 SALVWAERALGNLPSLLVAVALVAASHALAGRTEEARKTMQRLRALDP 521
A+ + ER L P+ + ++ ++ R + A KT++RL +DP
Sbjct: 183 KAIHYWERELEYNPNDKITYFMITEAYYEMNRKDLAVKTLERLLEIDP 230

>gi|10802733|gb|AAG23588.1|AF244639_1 (AF244639) DNA-binding response regulator
[Carboxydothermus hydrogenoformans]
Length = 206

Score = 47.8 bits (112), Expect = 3e-04
Identities = 32/104 (30%), Positives = 54/104 (51%), Gaps = 1/104 (0%)

Query: 17 GRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTDRDVSVDKDELLQA 76
GR G E D V+DQE+ + +G+ + P+ F+LL L +V +++ LL+
Sbjct: 98 GREGKKEGIKIKIDIVIDQEKFAVYVKGKKMDFTPKEFELLKLLASNPGKVFTREYLLK 157

Query: 77 VWGGGRIVSES-TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
+WG + ++ T+ HI +R+ I D + I TV G+RF
Sbjct: 158 IWGYEFLGDTRTVDVHIRHIRQKIEDNPADPVYIETVRGVGYRF 201

>gi|16803987|ref|NP_465472.1| (NC_003210) similar to two-component response regulator (ResD)
[Listeria monocytogenes EGD-e]
gi|16411401|emb|CAD00026.1| (AL591981) similar to two-component response regulator (ResD)
[Listeria monocytogenes]
Length = 238

Score = 47.8 bits (112), Expect = 3e-04
Identities = 32/112 (28%), Positives = 56/112 (49%), Gaps = 5/112 (4%)

Query: 10 SCPDSERGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTDRDVS 69
S +S G PGD F +D E + G+ + + P+ +DLL +L + D+V
Sbjct: 125 SSEESAGGTPGDI---ITPFLKIDNEAHRVIVDGKEIGLTPKEYDLLYYLAKSPDKVFD 181

Query: 70 KDELLQAVWGGGRIVSE-STITSHINAVRKAIGDTGGE-QRLIRTVARKGFRF 119
++ LL+ VW + TI +H+ +R+ + D + R+I TV G++F
Sbjct: 182 RESLLKEVWRYEFGDLRTIDTHVKRLREKLHDVSEDAARMIVTVWGLGYKF 233

>gi|12642552|gb|AAK00284.1|AF288536_6 (AF288536) possible transcriptional regulatory protein
[Legionella longbeachae]
Length = 230

Score = 47.8 bits (112), Expect = 3e-04
Identities = 27/97 (27%), Positives = 53/97 (53%), Gaps = 1/97 (1%)

Query: 25 QFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGGRIVS 84
QF FG++ ++ + + + +S+ F++L LV DR++S+D ++ A+ G
Sbjct: 129 QFHFGNFSINFSTKSVQLFDEEISISTSDFEMLALLVKNHDRLLSRDSIMYALSGHEYDG 188

Query: 85 -ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFV 120
+ I I+ +RKA+ D + I+T+ +KG+ FV
Sbjct: 189 VDRGIDLKISRLRKALNDNNKKPYRIKTIHKKGYIFV 225

>gi|17231804|ref|NP_488352.1| (NC_003272) two-component system response regulator [Nostoc sp. PCC

7120]
gi|17133448|dbj|BAB76011.1| (AP003596) two-component system response regulator [Nostoc sp. PCC
7120]
Length = 256

Score = 47.8 bits (112), Expect = 3e-04
Identities = 30/104 (28%), Positives = 51/104 (48%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQ 75
R R A +G +D +R + +G+ + + PQ F LL L +S+ ELL+
Sbjct: 120 RKRTFTAPAYLDYGTLDVQRRVRFQGEFIDLTPQEFSLLYVLAQAGGVPLSRSELLR 179

Query: 76 AVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
W I + TI +H+ ++RK + + LI+T+ G+RF
Sbjct: 180 RAWPDAIDNPRITIDTHVLSLRKKVELDPRQPSLIQTIRNVGYRF 223

>gi|15839182|ref|NP_299870.1| (NC_002488) two-component system, regulatory protein [Xylella fastidiosa 9a5c]
gi|11278059|pir||F82538 two-component system, regulatory protein XF2593 [imported] -
Xylella fastidiosa (strain 9a5c)
gi|9107813|gb|AAF85390.1|AE004066_4 (AE004066) two-component system, regulatory protein [Xylella fastidiosa 9a5c]
Length = 266

Score = 47.4 bits (111), Expect = 4e-04
Identities = 34/111 (30%), Positives = 53/111 (47%), Gaps = 2/111 (1%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQ 75
R R D + G +D + V +GP + LL + +RV S+ +LL
Sbjct: 157 RTRDDDEGDSVAIGKLRIIDGAAHRVYAGHVQVPIGPTEYRLLHFFMTHSERVYSRTQLLD 216

Query: 76 AVWG-GRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDRI 125
VWG G + E TI HI +R+ + + G +++TV G+RF G I+I
Sbjct: 217 HVWGSGVYIEERTIDVHIRLRRTL-EPYGLDDMVQTVRSAGYRFSGAIQI 266

>gi|16130756|ref|NP_417329.1| (NC_000913) putative invasion protein [Escherichia coli K12]
gi|2829647|sp|P76639|YGEH_ECOLI Hypothetical protein ygeH
gi|7466451|pir||E65068 hypothetical protein b2852 - Escherichia coli (strain K-12)
gi|1789216|gb|AAC75891.1| (AE000369) putative invasion protein [Escherichia coli K12]
Length = 458

Score = 47.4 bits (111), Expect = 4e-04
Identities = 28/84 (33%), Positives = 49/84 (58%), Gaps = 1/84 (1%)

Query: 40 LTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGGRIVSESTITSHINAVRKAI 99
LT+ + V + + +L+ L+ + VV KD +++VW IVS+ ++T I ++R I
Sbjct: 23 LTQGNEQVYIPQKELGVLIIVLLESAGHVVLKDMIIESVWKNIIIVSDESLTRCIYSLR-CI 81

Query: 100 GDTGGEQRLIRTVARKGFRFVGD I 123
+ G R I T+ RKG+RF G +
Sbjct: 82 FEKIGYDRCIETIYRKGYRFSQV 105

>gi|15678100|ref|NP_275215.1| (NC_000916) O-linked GlcNAc transferase [Methanothermobacter thermautotrophicus]
gi|7459510|pir||B69196 conserved hypothetical protein MTH72 - Methanobacterium thermoautotrophicum (strain Delta H)
gi|2621106|gb|AAB84576.1| (AE000798) O-linked GlcNAc transferase [Methanothermobacter thermautotrophicus]

Length = 403

Score = 47.4 bits (111), Expect = 4e-04
Identities = 34/140 (24%), Positives = 65/140 (46%), Gaps = 11/140 (7%)

Query: 323 EAALPLFYRAIELDQEFASAYAGAAWCYFWRKLNQWMDRAEEIAEGARLARRAVELGRD 382
E A + + +A+E++Q+ A A+ G +++ + E +A+E+ +
Sbjct: 237 EKAIECYEKALEINQKNAKAWN-----KGVVLEELKRYDEALECYEKALEINLE 286

Query: 383 DAVALTRSGHALGHLVGDLGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHI 442
+ G L L G + + ++A +NP FA AW G + +PE A++
Sbjct: 287 NDETWANKGVLLRKL-GKYEEALECFEKALEINPEFADAWEWKGIILEDLKKPEEALKCY 345

Query: 443 EHAARLSPLDQEMFRMQAGT 462
E A +L+P D+ ++ MQ T
Sbjct: 346 EKALKLNPDQKTLWYMQGKT 365

>gi|16077443|ref|NP_388257.1| (NC_000964) similar to two-component response regulator [YclK]
[Bacillus subtilis]
gi|7444044|pir||G69762 two-component response regulator [YclK] homolog yclJ - Bacillus
subtilis
gi|1805445|dbj|BAA09007.1| (D50453) homologue of alkaline phosphatase synthesis
transcriptional regulatory protein PhoP of B. subtilis
[Bacillus subtilis]
gi|2632676|emb|CAB12183.1| (Z99106) similar to two-component response regulator [YclK]
[Bacillus subtilis]
Length = 227

Score = 47.4 bits (111), Expect = 4e-04
Identities = 29/94 (30%), Positives = 54/94 (56%), Gaps = 4/94 (4%)

Query: 31 YVLDQERRELTRRGQVV-SVGPQVFDLLLHLVGTRDRVVSKEDELLQAVWGGGRIV-SESTI 88
+ ++++ RE+ G+ V ++ P+ FDLL +LV +V S+++LL+ VWG + E T+
Sbjct: 136 FTINKKTREVLNGEPVENLTPKEFDLLYYLVQNPRQVFSREQLLEQVWGYQFYGDERTV 195

Query: 89 TSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
HI +RK + ++ + TV G++F D
Sbjct: 196 DVHIKRLRKLASE--DKPFLYTVWGVGYKFDED 227

>gi|15991570|gb|AAL12938.1|AF394228.1 (AF394228) putative transcriptional regulator WmpR
[Pseudoalteromonas tunicata]
Length = 696

Score = 47.4 bits (111), Expect = 4e-04
Identities = 21/76 (27%), Positives = 43/76 (55%)

Query: 45 QVVSQVQVFDLLLHLVGTRDRVVSKEDELLQAVWGGGRIVSESTITSHINAVRKAIGDTGG 104
Q V + P+VFD+L + +R +S EL + +W GR VS++ + I+ +R + D
Sbjct: 8 QRVILLEPKVFDVLTIFYCQHNNRYISMTELHENIWQGRVSDAAVRRRIISKIRILMNDHDK 67

Query: 105 EQRLIRTVARKGFRFV 120
I+++ ++G++ +
Sbjct: 68 NPTYIQSLPKRGYKLI 83

>gi|16119346|ref|NP_396052.1| (NC_003064) AGR_pAT_174p [Agrobacterium tumefaciens]
[Agrobacterium
tumefaciens str. C58 (Cereon)]
gi|17938705|ref|NP_535493.1| (NC_003306) two component response regulator [Agrobacterium
tumefaciens str. C58 (Dupont)] [Agrobacterium
tumefaciens str. C58 (U. Washington)]
gi|15161866|gb|AAK90493.1| (AE007884) AGR_pAT_174p [Agrobacterium tumefaciens str. C58
(Cereon)]
gi|17743547|gb|AAL45809.1| (AE008936) two component response regulator [Agrobacterium
tumefaciens str. C58 (U. Washington)]
Length = 241

Score = 47.4 bits (111), Expect = 5e-04
Identities = 30/90 (33%), Positives = 46/90 (50%), Gaps = 2/90 (2%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGGRIVSEST 87
G+ L ER+ + G +++GP F LL HL+ RV S+DEL+ A W + V T
Sbjct: 144 GEIELWPERKRVLVSGVELTLGPIEFKLEHLLTAPGRVFSRDELITAAWPNEVYVQPRT 203

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
+ HI +R+ + G +IRT G+
Sbjct: 204 VDVHIGRIRRHLLKKAAGFD-IIRTARSSGY 232

>gi|16765461|ref|NP_461076.1| (NC_003197) response regulator in two-component regulatory system
with BaeS (OmpR family) [Salmonella typhimurium LT2]
gi|16420665|gb|AAL21035.1| (AE008794) response regulator in two-component regulatory system
with BaeS (OmpR family) [Salmonella typhimurium LT2]
Length = 240

Score = 47.0 bits (110), Expect = 5e-04
Identities = 33/113 (29%), Positives = 55/113 (48%), Gaps = 6/113 (5%)

Query: 11 CPDSEGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSK 70
C + DAE M +D+ R + + G+ + + P F LL L +V S+
Sbjct: 128 CKPQRELQQQDAESPLM-----IDESRFQASWCGKALDLTPAEFRLLKTLSEPGKVFSR 182

Query: 71 DELLQAVWGG-RIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
++LL ++ R+V++ TI SHI +R+ + EQ IR V G+R+ D
Sbjct: 183 EQLLNHLYDDYRVVTDRTIDSHIKNLRRKLESLEDAEQSFIRAVYGVGYRWEAD 235

>gi|16761060|ref|NP_456677.1| (NC_003198) putative two-component system response regulator
[Salmonella enterica subsp. enterica serovar Typhi]
gi|16503358|emb|CAD02494.1| (AL627273) putative two-component system response regulator
[Salmonella enterica subsp. enterica serovar Typhi]
Length = 240

Score = 47.0 bits (110), Expect = 5e-04
Identities = 33/113 (29%), Positives = 55/113 (48%), Gaps = 6/113 (5%)

Query: 11 CPDSEGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSK 70
C + DAE M +D+ R + + G+ + + P F LL L +V S+
Sbjct: 128 CKPQRELQQQDAESPLM-----IDESRFQASWCGKALDLTPAEFRLLKTLSEPGKVFSR 182

Query: 71 DELLQAVWGG-RIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
++LL ++ R+V++ TI SHI +R+ + EQ IR V G+R+ D
Sbjct: 183 EQLLNHLYDDYRVVTDRTIDSHIKNLRRKLESLEDAEQSFIRAVYGVGYRWEAD 235

>gi|17231995|ref|NP_488543.1| (NC_003272) two-component response regulator [Nostoc sp. PCC 7120]
gi|17133639|dbj|BAB76202.1| (AP003596) two-component response regulator [Nostoc sp. PCC 7120]
Length = 253

Score = 47.0 bits (110), Expect = 6e-04
Identities = 31/93 (33%), Positives = 47/93 (50%), Gaps = 1/93 (1%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGGRIVSEST 86
F D L+ + + RGQ V++ P+ F LL + RV S+++LL VWG V+S
Sbjct: 160 FKDVTLNPQECRVLVRGQEVNLSPKFEFRLLELFMSYARRVWSREQLLDQVWGPDFVGDGSK 219

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
T+ HI +R+ + I TV G+RF
Sbjct: 220 TVDVHIRWLREKLEQDPSPHEIYIVTVRFGFYRF 252

>gi|15642901|ref|NP_227942.1| (NC_000853) response regulator [Thermotoga maritima]
gi|7444050|pir||F72415 response regulator - Thermotoga maritima (strain MSB8)
gi|4980618|gb|AAD35220.1|AE001698_9 (AE001698) response regulator [Thermotoga maritima]
Length = 220

Score = 47.0 bits (110), Expect = 6e-04
Identities = 29/97 (29%), Positives = 50/97 (50%), Gaps = 1/97 (1%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGGRIVSEST 87
FGD +D + +G+ + + + F++LL L +VV++LL+ W VS
Sbjct: 125 FGDLEKIDATGFTVFLKKGRIHLPKKEFEILLFLAENAGKVVTREKLETFWEDP-VSPRV 183

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDIR 124
+ + I +RKAI D R I+T+ G+ F G R
Sbjct: 184 VDTVIRKIRKAIEDDPNRPRIYIKTIWGVGYMFTGGER 220

>gi|15644015|ref|NP_229064.1| (NC_000853) phosphate regulon transcriptional regulatory protein
PhoB [Thermotoga maritima]
gi|7444049|pir|F72275 phosphate regulon transcription regulator PhoB - Thermotoga
maritima (strain MSB8)
gi|4981814|gb|AAD36333.1|AE001781_4 (AE001781) phosphate regulon transcriptional regulatory
protein
PhoB [Thermotoga maritima]
Length = 229

Score = 47.0 bits (110), Expect = 6e-04
Identities = 32/102 (31%), Positives = 52/102 (50%), Gaps = 5/102 (4%)

Query: 18 RPGDAEVQFMFGDYVLDQERRELTRRGQVVSQVDFDLLLLHLVGTRDRVVSKDDELLQAV 77
R G + FG + E + G+ V + + F+LL L T ++V S++E+L V
Sbjct: 123 RMGKEQKVLRFGRLEIFPEDYIVRYDGKNVEMTAKEFELLKLLATTPNKVFSREEILNRV 182

Query: 78 WGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
WG VS+ + HI+A+R IG + I+TV G++F
Sbjct: 183 WGDDYVSDRVVDVHISAIRSKIG-----KGWIKTVRGLGYKF 219

>gi|17938707|ref|NP_535495.1| (NC_003306) two component response regulator [Agrobacterium
tumefaciens str. C58 (Düpont)] [Agrobacterium
tumefaciens str. C58 (U. Washington)]
gi|17743549|gb|AAL45811.1| (AE008936) two component response regulator [Agrobacterium
tumefaciens str. C58 (U. Washington)]
Length = 194

Score = 47.0 bits (110), Expect = 6e-04
Identities = 29/78 (37%), Positives = 44/78 (56%), Gaps = 4/78 (5%)

Query: 42 RRGQV-VSVPQVDFDLLLLHLVGTRDRVVSKDDELLQAVWGGRI-VSESTITSHINAVRKAI 99
RRG+ +S+ P F +LL+L DRVVS+DEL++ W V T+ HI +R+++
Sbjct: 115 RRGETHISLSPLHFRILLYLARNTDRVVSDELIRNCWPEDADVEPRTVDIHIGKIRRS 174

Query: 100 GDTGGEQRLIRTVARKGF 117
G +IRTV G+
Sbjct: 175 NRHG--HNVIRTVRSAGY 190

>gi|16119348|ref|NP_396054.1| (NC_003064) AGR_pAT_177p [Agrobacterium tumefaciens]
[Agrobacterium
tumefaciens str. C58 (Cereon)]
gi|15161868|gb|AAK90495.1| (AE007884) AGR_pAT_177p [Agrobacterium tumefaciens str. C58
(Cereon)]
Length = 234

Score = 47.0 bits (110), Expect = 6e-04
Identities = 29/78 (37%), Positives = 44/78 (56%), Gaps = 4/78 (5%)

Query: 42 RRGQV-VSVPQVDFDLLLLHLVGTRDRVVSKDDELLQAVWGGRI-VSESTITSHINAVRKAI 99
RRG+ +S+ P F +LL+L DRVVS+DEL++ W V T+ HI +R+++
Sbjct: 155 RRGETHISLSPLHFRILLYLARNTDRVVSDELIRNCWPEDADVEPRTVDIHIGKIRRS 214

Query: 100 GDTGGEQRLIRTVARKGF 117
G +IRTV G+
Sbjct: 215 NRHG--HNVIRTVRSAGY 230

>gi|16801128|ref|NP_471396.1| (NC_003212) similar to two-component response regulator (ResD)
[Listeria innocua]
gi|16414563|emb|CAC97292.1| (AL596170) similar to two-component response regulator (ResD)
[Listeria innocua]
Length = 238

Score = 46.6 bits (109), Expect = 7e-04
Identities = 31/112 (27%), Positives = 56/112 (49%), Gaps = 5/112 (4%)

Query: 10 SCPDSEGRGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVS 69
S ++ G PGD F +D E + G+ + + P+ +DLL +L + D+V
Sbjct: 125 SSEEAAGGTPGDI---ITFPHLKIDNEAHRVIVDGKEIGLTPKEYDLLYYLAKSPDKVFD 181

Query: 70 KDELLQAVWGGRIVSE-STITSHINAVRKAIGDTGGE-QRLIRTVARKGFRF 119
++ LL+ VW + TI +H+ +R+ + D + R+I TV G++F
Sbjct: 182 RESLLKEVWRYEFFGDLRTIDTHVKRLREKLHDVSEDAARMIVTVWGLGYKF 233

>gi|16078390|ref|NP_389208.1| (NC_000964) similar to two-component response regulator [YkoH]
[Bacillus subtilis]
gi|7444043|pir||C69859 two-component response regulator [YkoH] homolog ykoG - Bacillus
subtilis
gi|2632045|emb|CAA05604.1| (AJ002571) YkoG [Bacillus subtilis]
gi|2633679|emb|CAB13182.1| (Z99110) similar to two-component response regulator [YkoH]
[Bacillus subtilis]
Length = 228

Score = 46.6 bits (109), Expect = 7e-04
Identities = 25/95 (26%), Positives = 57/95 (59%), Gaps = 2/95 (2%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVS KDELLQAVWGGRIVSEST 87
+ D ++++ RE+ R + V + P+ FDLL++++ +V+++++L +VWG + ++
Sbjct: 135 YDDL RVNEKTREVRRGDKEVELTPREFDLLVYMLKHPQVLTREQLSSVWGFYIGDTN 194

Query: 88 ITS-HINAVRKAIGDTGGEQRLIRTVARKGFRFVG 121
+ +I +RK + D E++LI T+ G+ G
Sbjct: 195 VVDVYIRYIRKKL-DYPYEQLIHTIRGVGYAIGK 228

>gi|19551981|ref|NP_599983.1| (NC_003450) COG0745:Response regulators consisting of a CheY-like
receiver domain and a winged-helix DNA-binding domain
[Corynebacterium glutamicum]
Length = 226

Score = 46.6 bits (109), Expect = 8e-04
Identities = 28/91 (30%), Positives = 47/91 (50%), Gaps = 1/91 (1%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVS KDELLQAVWGGRIVSESTI 88
GD +D + R G +S+ P FDLLL L +V +++ELL VWG R S++ +
Sbjct: 131 GDLSIDVPAHTVKRNGAEISLTPLEFDLLLELARKPQQVFTREELLGKVWGYRHASDTRL 190

Query: 89 TS-HINAVRKAIGDTGGEQRLIRTVARKGFR 118
+ H+ +R I +++ TV G++
Sbjct: 191 VNVHVQRLRAKIEKDPENPQIVLTVRGVGYK 221

>gi|13475894|ref|NP_107464.1| (NC_002678) similar to trifolitoxin synthesis, TfuA [Mesorhizobium
loti]
gi|14026653|dbj|BAB53250.1| (AP003010) similar to trifolitoxin synthesis, TfuA [Mesorhizobium
loti]
Length = 688

Score = 46.2 bits (108), Expect = 8e-04
Identities = 62/271 (22%), Positives = 106/271 (38%), Gaps = 25/271 (9%)

Query: 120 VGDIRIGGIGEVRRQPVGPGALQASGGSG----ETASALVLPDKPSITVLPFQNLSGDPE 175
V DI++G IG + A +A G E A+ ++L V F+ +SG
Sbjct: 241 VSDIKLGTIGATRGAVTAIAAEAFGSQAQRLQEPAGVLL-----FVREFELVSGSVR 294

Query: 176 QEYFADGIVEDIIITLSRIR-WLFVIARNSSFRYKGRAVEVKDVGRELGVRYVLEGSVRK 234
+++ +L R R W + R+ A Y +E +
Sbjct: 295 ARNAVQIFRSELVASLVRFRDVAWMEWEGHPFRFTENA-----YCIEATGFI 341

Query: 235 SGNRVKITGQLIDATGTGTHLWAERFEGTLDDIFELQDRMAESVVGAIAPQVERAEMERAK 294
G +R++ L +G ++W+E+F ++ Q R+ + A+ + + +
Sbjct: 342 DGPTLRLSMTLKQLASGRYIWSEQFVIENSQWYQTQORLIRRIAVALGVSMSSERLVQIA 401

Query: 295 RKPTESLDAHDYYLRGMALHSGTHEAIEAALPLFYRAIELDQEFASAYAGAACYFWRK 354
P SL+ D +LR + E+ E A LF I FA+AYAG A R
Sbjct: 402 SIPDLSLEQFDRWLRAQELIFQWRPESEERAEALFRSIIAESPRFAAYAGLAGIINSRH 461

Query: 355 LNGWMVDRAEEI-AEGARLARRAVELGRDDA 384
L + R E AE A++A ++ D+
Sbjct: 462 LIFPGIGRRRRERHAEALTFAKQATQIDPIDS 492

>gi|13475573|ref|NP_107137.1| (NC_002678) similar to transcriptional activator [Mesorhizobium loti]
gi|14026325|dbj|BAB52923.1| (AP003009) similar to transcriptional activator [Mesorhizobium loti]
Length = 168

Score = 46.2 bits (108), Expect = 8e-04
Identities = 27/99 (27%), Positives = 51/99 (51%)

Query: 25 QFMFGDYVLDQERRELTRRGQVVSVPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVS 84
+ FG ++L ++ L + V +G + +L+ L+ +VSK EL+ VW V
Sbjct: 28 EIAFGPFLLFPKQFLLLEGDKPVPLGSRALGILIALLERPGELVSKQELMARVWPVDFV 87

Query: 85 ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVVDI 123
+ +T HI+A+R+ + D R I + +G++FV +
Sbjct: 88 PTNLTVHISALRRVLRDGRDGNRFIINIPGRGYQFVASV 126

>gi|5353563|gb|AAD42180.1|AF130997_1 (AF130997) response regulator [Enterococcus faecium]
Length = 232

Score = 46.2 bits (108), Expect = 0.001
Identities = 24/75 (32%), Positives = 42/75 (56%), Gaps = 1/75 (1%)

Query: 44 GQVVSVPQVFDLLHLVGTRDRVSKDELLQAVWGGRIV-SESTITSHINAVRKAIGDT 102
G+ + + P F +L +L + VVS +EL +AVWG R S +T+ +HI +R+ + +
Sbjct: 154 GKEIQLTPTEFSILWYLCERQGTVVSTEELEAVWGERFFDSNNTVMAHIGRLREKMKEP 213

Query: 103 GGEQRLIRTVARKGF 117
+ I+TV G+
Sbjct: 214 SRNPKFIKTVMWGVGY 228

>gi|5759261|gb|AAD51056.1|AF175293_1 (AF175293) response regulator [Enterococcus faecium]
Length = 232

Score = 46.2 bits (108), Expect = 0.001
Identities = 24/75 (32%), Positives = 42/75 (56%), Gaps = 1/75 (1%)

Query: 44 GQVVSVPQVFDLLHLVGTRDRVSKDELLQAVWGGRIV-SESTITSHINAVRKAIGDT 102
G+ + + P F +L +L + VVS +EL +AVWG R S +T+ +HI +R+ + +
Sbjct: 154 GKEIQLTPTEFSILWYLCERQGTVVSTEELEAVWGERFFDSNNTVMAHIGRLREKMKEP 213

Query: 103 GGEQRLIRTVARKGF 117
+ I+TV G+
Sbjct: 214 SRNPKFIKTVMWGVGY 228

>gi|15887392|ref|NP_353073.1| (NC_003062) AGR_C_54p [Agrobacterium tumefaciens] [Agrobacterium tumefaciens str. C58 (Cereon)]
gi|15154897|gb|AAK85858.1| (AE007946) AGR_C_54p [Agrobacterium tumefaciens str. C58 (Cereon)]
Length = 265

Score = 46.2 bits (108), Expect = 0.001
Identities = 33/93 (35%), Positives = 51/93 (54%), Gaps = 3/93 (3%)

Query: 29 GDYVLDQERRELTRRGQVVSVPQVFDLLHLVGTRDRVV-SKDELLQAVWGGRIV-VSES 86
G +DQER T +G+ V++ F L+LH + R VV S+D L+ A + ++ V +
Sbjct: 170 GQLAMDQERHTCTWKGEPTLTVTVEF-LILHSLAQRPGVVKSRDALMDAAYDEQVYVDDR 228

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
TI SHI +RK G+ +I T+ G+RF
Sbjct: 229 TIDSHIKRLRKKFKLVGDGDFMIETLYGVGYRF 261

>gi|18311470|ref|NP_563404.1| (NC_003366) two-component response regulator [Clostridium perfringens]
gi|18146154|dbj|BAB82194.1| (AP003194) two-component response regulator [Clostridium perfringens]

Length = 228

Score = 45.8 bits (107), Expect = 0.001
Identities = 28/93 (30%), Positives = 48/93 (51%), Gaps = 3/93 (3%)

Query: 28 FG DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRIVSES- 86
F +D ++ G+ V P+ F+LL +L +++V ++D+LL VWG S
Sbjct: 135 FPGLTIDANSYKVIYNGEEVKTPPKFELLHYLASNKNKVFTRDQLLCEVWGYDYPGYSR 194

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
T+ HI +R+ + GGE + TV G++F
Sbjct: 195 TVDVHIKRLREKL--NGGEDWQLETVWGVGYKF 225

>gi|17547783|ref|NP_521185.1| (NC_003295) PROBABLE RESPONSE REGULATOR TRANSCRIPTION REGULATOR
PROTEIN [Ralstonia solanacearum]
gi|17430088|emb|CAD16773.1| (AL646073) PROBABLE RESPONSE REGULATOR TRANSCRIPTION REGULATOR
PROTEIN [Ralstonia solanacearum]
Length = 243

Score = 45.8 bits (107), Expect = 0.001
Identities = 33/112 (29%), Positives = 58/112 (51%), Gaps = 3/112 (2%)

Query: 9 ASCPDSESRGPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVV 68
++ P +E P D + +FG+ + R +T RGQ V + F+LLL L V+
Sbjct: 127 SAMPAAEPATPRDDL--VFGELAISPPNRTVTWRGQPVLEKTAEFNLLILARAAGTVL 184

Query: 69 SKDELLQAVWGGRIVS-ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
S+D++L+ + G + T+ S I+ +R+ GD E I+T+ +G+ F
Sbjct: 185 SRDDILKQLRGIEFDGLDRTVDSGISRLRRRFGDASPEPHIKTIWGRGYLF 236

>gi|17933959|ref|NP_530749.1| (NC_003304) two component response regulator [Agrobacterium
tumefaciens str. C58 (U. Washington)]
gi|17738353|gb|AAL41065.1| (AE008978) two component response regulator [Agrobacterium
tumefaciens str. C58 (U. Washington)]
Length = 241

Score = 45.8 bits (107), Expect = 0.001
Identities = 33/93 (35%), Positives = 51/93 (54%), Gaps = 3/93 (3%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVV-SKDELLQAVWGGRIVS- 86
G +DQER T +G+ V++ F L+LH + R VV S+D L+ A + ++ V +
Sbjct: 146 GQLAMDQERHTCTWKGEPTVTLTVTEF-LILHSLAQRPVGVKSRDALMDAAYDEQVYVDDR 204

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
TI SHI +RK G+ +I T+ G+RF
Sbjct: 205 TIDSHIKRLRKKFKLVGDGDFMIETLYGVGYRF 237

>gi|7672246|emb|CAB89435.1| (AL354048) putative two-component system response regulator
[Streptomyces coelicolor A3(2)]
Length = 225

Score = 45.8 bits (107), Expect = 0.001
Identities = 29/67 (43%), Positives = 39/67 (57%), Gaps = 1/67 (1%)

Query: 54 FDLLHLVGTRDRVVSKDELLQAVWGGRIVSES-TITSHINAVRKAIGDTGGEQRLIRTV 112
FDLL LV RVV++D+L++ VW S + T+ HI+ +RK +GD R I TV
Sbjct: 156 FDLLRVLVRDAGRVVTRDQLMREVWDTTWWSSTKTLDMHISWLRKKLGDDAANPRYIATV 215

Query: 113 ARKGFRF 119
GFRF
Sbjct: 216 RGVGFRF 222

>gi|2145544|pir||S70816 hla protein - Salmonella typhimurium (fragment)
Length = 87

Score = 45.4 bits (106), Expect = 0.001
Identities = 26/78 (33%), Positives = 46/78 (58%), Gaps = 1/78 (1%)

Query: 42 RRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRIVSESTITSHINAVRKAIGD 101

R + V++ P+ + +L+ L+ +VSK+ LL VWG V+E ++T I A+R+ + +
Sbjct: 6 RSEKKVNIPPKEYAVLVILLEAAGEIVSKNTLLDQVWGDAEVNEESLTRCIYALRRILSE 65

Query: 102 TGGEQRLIRTVARKGFRF 119
E R I T+ +G+RF

Sbjct: 66 D-KEHRYIETLYGQGYRF 82

>gi|2947107|gb|AAC28777.1| (AF005157) regulatory protein BvrR [Brucella melitensis biovar Abortus]
Length = 237

Score = 45.4 bits (106), Expect = 0.001
Identities = 33/93 (35%), Positives = 50/93 (53%), Gaps = 3/93 (3%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVV-SKDELLQAVWGGRI-VSES 86
G V+DQER T +G+ V++ F L+LH + R VV S+D L+ A + ++ V +
Sbjct: 143 GQLVMDQERHTCTWKGEPTVTLTVTEF-LILHSLAQRPVGVKSRDALMDAAYDEQVYVDDR 201

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
TI SHI +RK +I T+ G+RF
Sbjct: 202 TIDSHIKRLRKKFKAVDDSFEMIETLYGVGYRF 234

>gi|7474358|pir||T31680 bacR protein - Bacillus licheniformis
gi|4481749|gb|AAD21216.2| (AF007865) BacR [Bacillus licheniformis]
Length = 238

Score = 45.4 bits (106), Expect = 0.001
Identities = 28/103 (27%), Positives = 51/103 (49%), Gaps = 1/103 (0%)

Query: 21 DAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGG 80
D + F +D + +T GQ +S+ + F+LL +V +K +L + W
Sbjct: 131 DEQSLIQFKGLTIDLKTYTVTAGGQEISLTAKEFELLKFFASNPGQVFTKTQLFRNAWSD 190

Query: 81 R-IVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
+ I ++T+ HI +RK I + + I+TV G++FVG+
Sbjct: 191 QYIEDNTVMVHIRLRKKIEPDSPDQFIQTVMWIGYKFVGE 233

>gi|17988319|ref|NP_540953.1| (NC_003317) TRANSCRIPTIONAL REGULATORY PROTEIN CHVI [Brucella melitensis]
gi|17984093|gb|AAL53217.1| (AE009636) TRANSCRIPTIONAL REGULATORY PROTEIN CHVI [Brucella melitensis]
Length = 239

Score = 45.4 bits (106), Expect = 0.001
Identities = 33/93 (35%), Positives = 50/93 (53%), Gaps = 3/93 (3%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVV-SKDELLQAVWGGRI-VSES 86
G V+DQER T +G+ V++ F L+LH + R VV S+D L+ A + ++ V +
Sbjct: 145 GQLVMDQERHTCTWKGEPTVTLTVTEF-LILHSLAQRPVGVKSRDALMDAAYDEQVYVDDR 203

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
TI SHI +RK +I T+ G+RF
Sbjct: 204 TIDSHIKRLRKKFKAVDDSFEMIETLYGVGYRF 236

>gi|2944391|gb|AAC33849.1| (AF049128) response regulator NblR [Synechococcus sp. PCC 7942]
Length = 228

Score = 45.4 bits (106), Expect = 0.002
Identities = 29/97 (29%), Positives = 52/97 (52%), Gaps = 2/97 (2%)

Query: 22 AEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRI 81
A+ F + LD R R G+ + + + FDLL L+ V+++++L+ VWG
Sbjct: 128 AQEHLQFSNLTLDLSTRRAARNGRQIDLTMEKFDLLRFLMEHPREVLTREQILENVWGYD 187

Query: 82 IVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
+ ES + +I +R I + GE+RL++TV G+
Sbjct: 188 FMGESNVIEVYIRYLRKI-EIEGEKRLVQTVRGVGY 223

>gi|18309624|ref|NP_561558.1| (NC_003366) two-component response regulator [Clostridium

perfringens]
gi|18144301|dbj|BAB80348.1| (AP003187) two-component response regulator [Clostridium
perfringens]
Length = 231

Score = 45.1 bits (105), Expect = 0.002
Identities = 28/96 (29%), Positives = 54/96 (56%), Gaps = 1/96 (1%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSVKDELLQAVWGGRIVSES- 86
FGD V++ + RE+T+ Q V + + F+LL L+ + +++++ LL +WG + E+
Sbjct: 135 FGDVVVNFKTREVTKGTQNVELTLKEFELLKLLIKNKGNIILTRELLDKIWGYEYIGETR 194

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
T+ HI +RK I + I+T+ G++F +
Sbjct: 195 TVDVHIRHLRKKIESDDKNPQYIQTIRGVGYKFTSN 230

>gi|6137054|emb|CAB59609.1| (AL132662) putative response regulator [Streptomyces coelicolor
A3(2)]
Length = 238

Score = 45.1 bits (105), Expect = 0.002
Identities = 26/91 (28%), Positives = 47/91 (51%)

Query: 30 DYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSVKDELLQAVWGGRIVSESTIT 89
D +D R G+ + + + FDLL +L D+V+S+ +L VW V + T+
Sbjct: 145 DLRIDPTARTAHLAGRELPLTRREFDLLAYLAHADQVMSRQRILAEVWQQPYVEDQTV 204

Query: 90 SHINAVRKAIGDTGGEQRLIRTVARKGFRFV 120
H++A+R+ +G+ + R + TV G + V
Sbjct: 205 VHLSALRRKMGEKARKPRYLHTVRGIGIKLV 235

>gi|19703920|ref|NP_603482.1| (NC_003454) Two-component response regulator czcR [Fusobacterium
nucleatum subsp. nucleatum ATCC 25586]
gi|19714090|gb|AAL94781.1| (AE010570) Two-component response regulator czcR [Fusobacterium
nucleatum subsp. nucleatum ATCC 25586]
Length = 224

Score = 45.1 bits (105), Expect = 0.002
Identities = 28/103 (27%), Positives = 53/103 (51%), Gaps = 2/103 (1%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSVKDELLQ 75
R + G+ + D ++D ++ +TR G+ + + + ++L +L+ + RV+S+D++
Sbjct: 117 RRKYNISNELQIDDLIVDTSKSVTRAGKNIELTGKEYEVLEYLIQNKGRVLSRDKIRD 176

Query: 76 AVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
VW ES I I +RK I D G + LI T G+
Sbjct: 177 GVWDYAYEGESNIIDVLIKNIRKKI-DLGDSPKPLIHTKRGLGY 218

>gi|19553806|ref|NP_601808.1| (NC_003450) COG0745:Response regulators consisting of a CheY-like
receiver domain and a winged-helix DNA-binding domain
[Corynebacterium glutamicum]
Length = 235

Score = 45.1 bits (105), Expect = 0.002
Identities = 31/101 (30%), Positives = 55/101 (53%), Gaps = 9/101 (8%)

Query: 21 DAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSVKDELLQAVW-- 78
D + D L+ E E+T+ G+++ + P F+LL +L+ + V+SK ++L VW
Sbjct: 133 DTSTSLQYADLTLDNETHEVTKAGELIDLSPTEFNLLRYLMLNAEVVLSKAKILDNVWHY 192

Query: 79 --GGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
GG + + S+I+ +R+ + DT Q LI+TV G+
Sbjct: 193 DFGG---DGNVVSYSYLRKKV-DTQDPQ-LIQTVRGVGY 228

>gi|18309439|ref|NP_561373.1| (NC_003366) two-component response regulator [Clostridium
perfringens]
gi|18144115|dbj|BAB80163.1| (AP003186) two-component response regulator [Clostridium
perfringens]
Length = 234

Score = 45.1 bits (105), Expect = 0.002
Identities = 24/93 (25%), Positives = 46/93 (48%)

Query: 26 FMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKEDELLQAVWGGRIVSE 85
+ G ++ +R+E+ G VV V P F +L L+ + RV S +E+ + VW V+
Sbjct: 138 YSIGGLEVNSDRKEVILDGDVVKVTPIEFKILQLLIKSPGRVFSAEIYERVWNENAVNT 197

Query: 86 STITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
T+ H+ +R+ I + ++ V G++
Sbjct: 198 DTMVHVVRNIREKIEIDPKNPYLVVWVGVGK 230

>gi|16265215|ref|NP_438007.1| (NC_003078) hypothetical exported protein, TonB-dependent receptor protein [Sinorhizobium meliloti]
gi|15141355|emb|CAC49867.1| (AL603647) hypothetical exported protein, TonB-dependent receptor protein [Sinorhizobium meliloti]
Length = 1200

Score = 45.1 bits (105), Expect = 0.002
Identities = 41/151 (27%), Positives = 65/151 (42%), Gaps = 6/151 (3%)

Query: 359 MVDRAEEIAEGARLARRAVELGRDDAVALTRSGHALGHLVGDLDGGIALIDRARLLNPNF 418
++D +E+ +G RA+ + DD AL H H+ DL+G +A ++RA P
Sbjct: 385 LLDDRDELDRG---VERALSIDPDPTALEARAHYRHHIDNDLEGALADLERALKTAPGS 441

Query: 419 APAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVW 478
+ W G ++ RG+ +A + A L PLD A A+ + R A
Sbjct: 442 SSIWNSLGLVQGARGDNRAEAFAFQAIALDPLDPV---SHANLAIQYMDEMRAEAKRE 498

Query: 479 AERALGNLPSLLVAVALVAASHALAGRTEEA 509
+ AL PS VA+ H G ++A
Sbjct: 499 IDAALSVDPSFDVALVARGRYHMONGEADKA 529

>gi|15838927|ref|NP_299615.1| (NC_002488) two-component system, regulatory protein [Xylella fastidiosa 9a5c]
gi|11278061|pir|C82570 two-component system, regulatory protein XF2336 [imported] -
Xylella fastidiosa (strain 9a5c)
gi|9107507|gb|AAF85135.1|AE004044_6 (AE004044) two-component system, regulatory protein [Xylella fastidiosa 9a5c]
Length = 241

Score = 45.1 bits (105), Expect = 0.002
Identities = 36/106 (33%), Positives = 52/106 (48%), Gaps = 3/106 (2%)

Query: 15 ERGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKEDELL 74
ER + G AEV D VLD TR G + + P LL L+ RVVS+ E+
Sbjct: 132 ERRQVG-AEV-LKLADLVLDVSLRATRAGTELQLSPIGLRLTLILMRESRPRVSRQEIE 189

Query: 75 QAVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFV 120
+ +WG + T+ SH+ +RK + G + L+ TV G+R V
Sbjct: 190 REIWGNCLPDSDTLRSHLYNLKRVVDKPFGR-PLLLHTVQSAGYRMV 234

>gi|13474249|ref|NP_105817.1| (NC_002678) two-component system response regulator [Mesorhizobium loti]
gi|14025001|dbj|BAB51603.1| (AP003005) two-component system response regulator [Mesorhizobium loti]
Length = 233

Score = 45.1 bits (105), Expect = 0.002
Identities = 35/113 (30%), Positives = 56/113 (48%), Gaps = 3/113 (2%)

Query: 9 ASCPDSERGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVV 68
AS ++ P G V+DQER T +G+ V++ F L+LH + R VV
Sbjct: 119 ASAREAAAKAPSQQARSLERGQLVMDQERHTCTWKGEPTTLTVTEF-LILHSLAQRPVV 177

Query: 69 -SKDELLQAVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
S+D L+ + + ++ V + TI SHI +RK + +I T+ G+RF
Sbjct: 178 KSRDALMDSAYDEQVYVDDRTIDSHIKRLKKFKAVDDDFEMETLYGVGYRF 230

>gi|16079369|ref|NP_390193.1| (NC_000964) two-component response regulator [Bacillus subtilis]
gi|466194|sp|P35163|RESB_BACSU Transcriptional regulatory protein resD
gi|629124|pir||S45559 . hypothetical protein X17 - Bacillus subtilis
gi|7429073|pir||G69691 two-component response regulator involved in aerobic and anaer resD
- Bacillus subtilis
gi|410141|gb|AAA67497.1| (L09228) ORFX17 [Bacillus subtilis]
gi|2634747|emb|CAB14244.1| (Z99116) two-component response regulator [Bacillus subtilis]
Length = 240

Score = 45.1 bits (105), Expect = 0.002
Identities = 27/95 (28%), Positives = 50/95 (52%), Gaps = 2/95 (2%)

Query: 27 MFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKEDELLQAVWGGRIVSE- 85
+F +D + +T G VS+ P+V++LL L T D+V +++LL+ VW +
Sbjct: 141 VFSLHSIDHDAHRVTADGTEVSLTPKVYELLYFLAKTPDKVYDREKLLKEVWQYEFEGDL 200

Query: 86 STITSHINAVRKAIGDTGGE-QRLIRTVARKGFRF 119
T+ +H+ +R+ + E + I TV G++F
Sbjct: 201 RTVDTHVKRLREKLNKVSPEAAKKIVTVWGVGYKF 235

>gi|16263704|ref|NP_436497.1| (NC_003037) probable transcriptional regulator [Sinorhizobium
meliloti]
gi|14524421|gb|AAK65909.1| (AE007310) probable transcriptional regulator [Sinorhizobium
meliloti]
Length = 230

Score = 45.1 bits (105), Expect = 0.002
Identities = 30/91 (32%), Positives = 46/91 (49%), Gaps = 1/91 (1%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKEDELLQAVWG-GRIVSESTITSH 91
+D +R +TR G + + P+ +DLL+ L RVV+ LL +VWG +
Sbjct: 138 IDMKRVVTRDGAALRLTPKEYDLLVMLAHAGRVVTHRTLLTSVWGLAHGEDLHYLRVF 197

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
I +R I G +++RT G+RFVGD
Sbjct: 198 IGQLRGKIERDPGNPKIVRTEPGVGYRFVGD 228

>gi|12830428|emb|CAC29081.1| (AJ300267) putative regulatory protein [Bartonella bacilliformis]
Length = 240

Score = 44.7 bits (104), Expect = 0.002
Identities = 32/96 (33%), Positives = 50/96 (51%), Gaps = 3/96 (3%)

Query: 26 FMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVV-SKDELLQAVWGGRIV- 83
F GD ++DQER T + + V + F L+L + R VV S+D L+ A + ++ V
Sbjct: 143 FKRGLIMDQERHTCTWKDRPVILTVEF-LILQTLAQRPGVVKSRLMDAAYNDQVYV 201

Query: 84 SESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
+ TI SHI +RK + +I T+ G+RF
Sbjct: 202 DDTIDSHIKRLRKKFKQVDDDFAMITLYGVGYRF 237

>gi|19746167|ref|NP_607303.1| (NC_003485) putative response regulator [Streptococcus pyogenes
MGAS8232]
gi|19748346|gb|AAL97802.1| (AE010043) putative response regulator [Streptococcus pyogenes
MGAS8232]
Length = 224

Score = 44.7 bits (104), Expect = 0.002
Identities = 27/90 (30%), Positives = 52/90 (57%), Gaps = 5/90 (5%)

Query: 22 AEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKEDELLQAVWGGR 81
A+ FG+ V+D R+E+ G+VV + + FDLL++L+ ++ ++ K ++ +WG
Sbjct: 123 ADKNISFGNLVVDLARKEVKVEGKVVVELLGKEFDLLVYLLQONQNVILPKTQIFDRLWG-- 180

Query: 82 IVSESTIT---SHINAVRKAIGDTGGEQRL 108
S++TI+ +I+ +RK + T RL
Sbjct: 181 FDSDTTISVVEVYISKIRKKLKGTRFVNRL 210

>gi|15675198|ref|NP_269372.1| (NC_002737) putative response regulator [Streptococcus pyogenes]
[Streptococcus pyogenes M1 GAS]
gi|13622364|gb|AAK34093.1| (AE006563) putative response regulator [Streptococcus pyogenes M1
GAS]
Length = 224

Score = 44.7 bits (104), Expect = 0.003
Identities = 27/90 (30%), Positives = 52/90 (57%), Gaps = 5/90 (5%)

Query: 22 AEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGR 81
A+ FG+ V+D R+E+ G+VV + + FDLL++L+ ++ ++ K ++ +WG
Sbjct: 123 ADKNISFGNLVVDLARKEVKVEGKVVELLGKEFDLLVYLLQNQNVLPKTQIFDRLWG-- 180

Query: 82 IVSESTIT---SHINAVRKAIGDTGGEQRL 108
S++TI+ +I+ +RK + T RL
Sbjct: 181 FSDTTISVVEVYISKIRKKLKGTCFVNRL 210

>gi|17545792|ref|NP_519194.1| (NC_003295) PROBABLE TWO-COMPONENT SYSTEM RESPONSE REGULATOR
TRANSCRIPTION REGULATOR PROTEIN [Ralstonia solanacearum]
gi|17428086|emb|CAD14775.1| (AL646062) PROBABLE TWO-COMPONENT SYSTEM RESPONSE REGULATOR
TRANSCRIPTION REGULATOR PROTEIN [Ralstonia solanacearum]
Length = 237

Score = 44.7 bits (104), Expect = 0.003
Identities = 28/80 (35%), Positives = 45/80 (56%), Gaps = 1/80 (1%)

Query: 18 RPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAV 77
R G++ + G Y +D R LT G V + P+ FDL L+L ++V ++ + QAV
Sbjct: 125 RTGESLERMRVGPYAVDPLGRVLT LHGLQVELSPREFDLALYLFRNVGKLVPRELIEQAV 184

Query: 78 WGRIVSES-TITSHINAVR 96
WG I +S T+ +HI+ +R
Sbjct: 185 WGRSIGPDSRTLATHISKLR 204

>gi|15601325|ref|NP_232956.1| (NC_002506) transcriptional regulator [Vibrio cholerae]
gi|11278055|pir||G82444 transcription regulator VCA0566 [imported] - Vibrio cholerae (group
O1 strain N16961)
gi|9657975|gb|AAF96468.1| (AE004387) transcriptional regulator [Vibrio cholerae]
Length = 245

Score = 44.7 bits (104), Expect = 0.003
Identities = 31/105 (29%), Positives = 52/105 (49%), Gaps = 8/105 (7%)

Query: 12 PDSERGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKD 71
PDS G + + + + +D+ RE+ G+ +++ FDLL L RV ++D
Sbjct: 145 PDS-----GQDDSKVVTSNLTIDKATREVFNGESITLRTFEFDLLFLASNLGRVFTRD 199

Query: 72 ELLQAVWG-GRIVSESTITSHINAVRKAIGDTGGEQRLIRT VARK 115
ELL VWG + T+ +H+ +R+ + G E +R V K
Sbjct: 200 ELLDHVWGYNHFPTRTVDTHVLQRLQKL--PGLEIETLRGVGYK 242

>gi|19552100|ref|NP_600102.1| (NC_003450) COG0745:Response regulators consisting of a CheY-like
receiver domain and a winged-helix DNA-binding domain
[Corynebacterium glutamicum]
gi|11526729|gb|AAG36759.1|AF119221_1 (AF119221) response regulator [Corynebacterium glutamicum]
Length = 232

Score = 44.7 bits (104), Expect = 0.003
Identities = 29/90 (32%), Positives = 50/90 (55%), Gaps = 2/90 (2%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRI-VSEST 87
GD LD E R++ R G+ +S+ F LL L+ + +V+++ ++L+ VWG S +
Sbjct: 137 GDLTLDPESDVYRNGRAISLRTFEFALLQLLKNQRKVLTRAQILEEVWGCDFTSGNA 196

Query: 88 ITSHINAVRKAIGDTGGEQRLIRT VARKGF 117
+ +I +R+ + GE RLI TV G+
Sbjct: 197 LEVYIGYLRKKT-ELEGEDRLIHTVRGVGY 225

>gi|15963797|ref|NP_384150.1| (NC_003047) TRANSCRIPTIONAL REGULATORY PROTEIN [Sinorhizobium

meliloti]
gi|1705850|sp|P50350|CHVI_RHIME Transcriptional regulatory protein chvI
gi|987505|gb|AAB07685.1| (U32941) chvI [Sinorhizobium meliloti]
gi|15072972|emb|CAC41431.1| (AL591782) TRANSCRIPTIONAL REGULATORY PROTEIN [Sinorhizobium
meliloti]
Length = 240

Score = 44.7 bits (104), Expect = 0.003
Identities = 32/93 (34%), Positives = 50/93 (53%), Gaps = 3/93 (3%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVV-SKDELLQAVWGGRI-VSES 86
G V+DQER T + + V++ F L+LH + R VV S+D L+ A + ++ V +
Sbjct: 145 GQLVMDQERHTCTWKNESVTLTVTEF-LILHALAQRPGVVKSRDALMDAAYDEQVYVDDR 203

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
TI SHI +RK + +I T+ G+RF
Sbjct: 204 TIDSHIKRLRKKFKMVDNDFMIETLYGVGYRF 236

>gi|17546253|ref|NP_519655.1| (NC_003295) PROBABLE PHOSPHATE REGULON TWO-COMPONENT RESPONSE
REGULATOR TRANSCRIPTION REGULATOR PROTEIN [Ralstonia
solanacearum]
gi|17428550|emb|CAD15236.1| (AL646065) PROBABLE PHOSPHATE REGULON TWO-COMPONENT RESPONSE
REGULATOR TRANSCRIPTION REGULATOR PROTEIN [Ralstonia
solanacearum]
Length = 237

Score = 44.7 bits (104), Expect = 0.003
Identities = 28/73 (38%), Positives = 40/73 (54%), Gaps = 2/73 (2%)

Query: 47 VSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRI-VSESTITSHINAVRKAIGDTGGE 105
+ +GP F LL L+ +RV S+ +LL VWG + V E T+ HI +R A+ GG
Sbjct: 159 LDLGPTFEFRLHFLMTHPERVHSRSQLLDQVWGDHVFVEERTVDVHIKRLRAALA-PGGY 217

Query: 106 QRLIRTVARKGFR 118
+I TV G+R
Sbjct: 218 SSMIETVRGSGYR 230

>gi|15615988|ref|NP_244293.1| (NC_002570) two-component response regulator [Bacillus halodurans]
gi|10176049|dbj|BAB07145.1| (AP001518) two-component response regulator [Bacillus halodurans]
Length = 241

Score = 44.3 bits (103), Expect = 0.003
Identities = 31/96 (32%), Positives = 51/96 (52%), Gaps = 1/96 (1%)

Query: 26 FMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWG-GRIVS 84
F F + +++ EL G+ V QVF LL + +R++SK++LL+AVWG V
Sbjct: 141 FTFDRFTVNELAGELLVDGRKVPQAVFLLLCYFCKHPNRILSKEQLLEAVWGMDSFVD 200

Query: 85 ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFV 120
++T+ HI +R+ I R + TV G++ V
Sbjct: 201 DNTVMVHIRRIRERIEIDPSHPRYLVTVRGLGYKLV 236

>gi|10303272|emb|CAC10110.1| (AL442165) putative two component system response regulator
[Streptomyces coelicolor A3(2)]
Length = 237

Score = 44.3 bits (103), Expect = 0.003
Identities = 31/105 (29%), Positives = 48/105 (45%), Gaps = 2/105 (1%)

Query: 16 RGRPGDAE--VQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDEL 73
RG P +A G +D RR+ G + + + FDLL L G VV + EL
Sbjct: 123 RGGPAEAAAPTTLRVGGTLVDPLRRQAELDGTALDLTRREFDLAFLAGRPGVVVPRKEL 182

Query: 74 LQAVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
L VW + TI H++ +R+ +G+T R + T+ G +
Sbjct: 183 LAEVWQQSYGDDQTIDVHLSWLRRKLGETAARPRYLHTLRGVGVK 227

>gi|281708|pir||S28674 hypothetical protein 2 - Rhizobium sp. (strain IC3342)
gi|152259|gb|AAA74221.1| (M38698) lcrB gene product [Rhizobium sp.]

Length = 238

Score = 44.3 bits (103), Expect = 0.003
Identities = 31/100 (31%), Positives = 50/100 (50%), Gaps = 2/100 (2%)

Query: 26 FMFGDYVLDQERRELTRR-GQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWG-GRIV 83
F F ++LD +RR+LT GQ + + FDLL+ V RV+++D LL G R
Sbjct: 135 FHF DGWMLDADRRQLTSTAGQTIELTTGEFDLLMVFTHPGRVLTDRFLDQTRGRTREA 194

Query: 84 SESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVVDI 123
+ I + +R + D G+ R I++V G+ F +
Sbjct: 195 FDRAIDVQVTRLRAKVEDDPGDPRIKSVRGAGYVFAAKV 234

>gi|7799238|emb|CAB90861.1| (AL355752) putative regulatory protein [Streptomyces coelicolor A3(2)]
Length = 193

Score = 44.3 bits (103), Expect = 0.003
Identities = 28/88 (31%), Positives = 48/88 (53%), Gaps = 3/88 (3%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWG-GRIVSESTITSH 91
+D RR T G+ + + F+LL HLV RV ++D L+ VWG G + T+ H
Sbjct: 102 IDPARRTATVDGRELDLTYLEFELLAHLVAHPRVHTRDRLVTTVWGYGHVGDGRTVDVH 161

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRF 119
+ +R+ +G ++ I+TV R G+++
Sbjct: 162 VARLRKRLG--AQHRQTIQTVRRVGYKY 187

>gi|12964068|emb|CAC29256.1| (AJ302696) putative regulatory protein [Bartonella quintana]
Length = 240

Score = 44.3 bits (103), Expect = 0.003
Identities = 32/93 (34%), Positives = 49/93 (52%), Gaps = 3/93 (3%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVV-SKDELLQAVWGGRI-VSES 86
GD V+DQER T + + V + F L+L + R VV S+D L+ A + ++ V +
Sbjct: 146 GDLVMDQERHTCTWKDKPVILTVEF-LILQTLAQRPGVVKSRLDALMDAAYSQVYVDDR 204

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
TI SHI +RK + +I T+ G+RF
Sbjct: 205 TIDSHIKRLRKKFKQVDDDFAMTIETLYGVGYRF 237

>gi|9909919|emb|CAC04498.1| (AL391588) putative two-component system response regulator [Streptomyces coelicolor A3(2)]
Length = 244

Score = 44.3 bits (103), Expect = 0.004
Identities = 32/90 (35%), Positives = 48/90 (52%), Gaps = 6/90 (6%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRI-VSES-T 87
G+ +D +R + R + V + P FDLL+ L T V+S+++LL VW S + T
Sbjct: 153 GELEIDHAQRRVRVRSSEVDHLTPTEFDLLVCLANTPRAVLSREQLLAEVWDWADASGTRT 212

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
+ SHI A+R+ IG IRTV G+
Sbjct: 213 VDSHIKALRRKIG-----AERIRTVHGVGY 237

>gi|17228689|ref|NP_485237.1| (NC_003272) two-component response regulator [Nostoc sp. PCC 7120]
gi|17130541|dbj|BAB73151.1| (AP003585) two-component response regulator [Nostoc sp. PCC 7120]
Length = 228

Score = 44.3 bits (103), Expect = 0.004
Identities = 28/91 (30%), Positives = 51/91 (55%), Gaps = 2/91 (2%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRI-VSEST 87
F D L++ RE+ R + V + + FDLL +L+ +V ++D++L+ VWG + +S
Sbjct: 131 FEDLSLNRRTREVFRGNRAVELTAKEFDLLEYLLSYPRQVFTRDQILEKVGWYDFMGDSN 190

Query: 88 ITS-HINAVRKAIGDTGGEQRLIRTVARKGF 117

I +I +R + + E+RL+ TV G+
Sbjct: 191 IIEVYIRYLRKLK-L-EENNEKRLVHTVRGVGY 220

>gi|16121116|ref|NP_404429.1| (NC_003143) putative regulatory membrane protein [Yersinia pestis]
gi|15978881|emb|CAC89653.1| (AJ414144) putative regulatory membrane protein [Yersinia pestis]
Length = 238

Score = 44.3 bits (103), Expect = 0.004
Identities = 24/92 (26%), Positives = 50/92 (54%), Gaps = 2/92 (2%)

Query: 27 MFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGRIVSES 86
+ D ++R + R G+V + + +LL L +S++++ + +W G V+++
Sbjct: 5 VINDVFFTPQKRTIDRNGKVTKIRNKESELLSLLCEYYPEPISREDIEKRLWEGSYVTDN 64

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
T+T I+ +R A+ D E L+ T+ +KG+R
Sbjct: 65 TLTQTISNLRHALDDKKHE--LVVTIPKKGYR 94

>gi|15923696|ref|NP_371230.1| (NC_002758) response regulator [Staphylococcus aureus subsp. aureus
Mu50]

gi|15926383|ref|NP_373916.1| (NC_002745) response regulator [Staphylococcus aureus subsp. aureus
N315]

gi|13700597|dbj|BAB41894.1| (AP003131) response regulator [Staphylococcus aureus subsp. aureus
N315]

gi|14246475|dbj|BAB56868.1| (AP003360) response regulator [Staphylococcus aureus subsp. aureus
Mu50]

Length = 228

Score = 43.9 bits (102), Expect = 0.004
Identities = 28/96 (29%), Positives = 47/96 (48%), Gaps = 1/96 (1%)

Query: 25 QFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGRIVS 84
Q F + L + +T G V + + F+LL +L + V+SK ELL+ VWG
Sbjct: 129 QLSFDELTILNLSKVVTVNGHEVPMRIKEFELLWYLASRENEVISKSELLEKVVWGYDYDE 188

Query: 85 ES-TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
++ T+ HI+ +R+ + I TV G++F
Sbjct: 189 DANTVNVHHRIREKLEKESFTTYTITTWGLGYKF 224

>gi|10281108|gb|AAG15433.1|AF189161_1 (AF189161) putative response regulator [Streptomyces
coelicolor]
Length = 228

Score = 43.9 bits (102), Expect = 0.004
Identities = 27/98 (27%), Positives = 51/98 (51%), Gaps = 1/98 (1%)

Query: 22 AEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGR 81
A Q GD V+D + R GQ +++ P FDLL+ L +V +++ LL+ VWG R
Sbjct: 127 APEQLAIGDLVIDVAGHSVKRDGQSIALTPLEFDLLVALARKPWQVFTREVILLEQVWGYR 186

Query: 82 IVSESTIT-HINAVRKAIGDTGGEQRLIRTVARKGFR 118
+++ + + H+ +R + + ++ TV G++
Sbjct: 187 HAADTRLNVVHVQRLRSKVEKDPEKPEIVVTVRGVGYK 224

>gi|7799208|emb|CAB90924.1| (AL355774) putative two-component system response regulator
[Streptomyces coelicolor A3(2)]
Length = 229

Score = 43.9 bits (102), Expect = 0.004
Identities = 27/98 (27%), Positives = 51/98 (51%), Gaps = 1/98 (1%)

Query: 22 AEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGR 81
A Q GD V+D + R GQ +++ P FDLL+ L +V +++ LL+ VWG R
Sbjct: 128 APEQLAIGDLVIDVAGHSVKRDGQSIALTPLEFDLLVALARKPWQVFTREVILLEQVWGYR 187

Query: 82 IVSESTIT-HINAVRKAIGDTGGEQRLIRTVARKGFR 118
+++ + + H+ +R + + ++ TV G++

Sbjct: 188 HAADTRLNVNHVQRLRSKVEKDPEKPEIVTVRGVGYK 225

>gi|16331756|ref|NP_442484.1| (NC_000911) OmpR subfamily [Synechocystis sp. PCC 6803]
gi|7429068|pir||S76610 hypothetical protein - Synechocystis sp. (strain PCC 6803)
gi|1001717|dbj|BAA10554.1| (D64004) OmpR subfamily [Synechocystis sp. PCC 6803]
Length = 262

Score = 43.9 bits (102), Expect = 0.005
Identities = 28/93 (30%), Positives = 49/93 (52%), Gaps = 1/93 (1%)

Query: 28 FG DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSES- 86
F D VL + + RG+ VS+ P+ F LL + RV S+++L++ +WG + +S
Sbjct: 169 FRDLVLYPQECRVLMRGEEVSLAPKEFRLLLELFMSYPRRVWSREQLEHIGIDFMGDSK 228

Query: 87 TITSHINAVRKAIGDTGGEQRLIRT VARKGFRF 119
T+ HI +R+ + + + TV G+RF
Sbjct: 229 TVDVHIRWLREKLEQDPSQPEYLVTVRGFGYRF 261

>gi|5764628|gb|AAD51348.1|AF173226_5 (AF173226) SmeR [Stenotrophomonas maltophilia]
Length = 229

Score = 43.5 bits (101), Expect = 0.005
Identities = 27/92 (29%), Positives = 49/92 (52%), Gaps = 1/92 (1%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVW-GGRIVSEST 87
G +D+ T G+ + + P + LL L+ T R+ ++DELL ++ R+V + T
Sbjct: 136 GGLHIDEPAARATWNGKGLDLPVEYRLLRTLATPGRIWARDELDRLYLDHRVVVDRT 195

Query: 88 ITSHINAVRKAIGDTGGEQRLIRT VARKGFRF 119
+ SH+ +R+ + D G E IR+V G+ +
Sbjct: 196 VDSHVNRLLRKLADAGMEGEPIRSVMGYSY 227

>gi|1729783|emb|CAA70931.1| (Y09798) colR [Pseudomonas fluorescens]
Length = 227

Score = 43.5 bits (101), Expect = 0.005
Identities = 28/103 (27%), Positives = 50/103 (48%), Gaps = 1/103 (0%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQ 75
R G GD D + E+TR G+++ + P LL L+ V+ ++ L +
Sbjct: 118 RRSQGGRRALQVGDLSYDLDTLEVTREGKLLKLPVGLKLLAVLMQKSPHVLRRILEE 177

Query: 76 AVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRT VARKGFR 118
A+WG ++ SH++ +R+ I D ++ L+ TV G+R
Sbjct: 178 ALWGDDCPDSDSLRSHVQLRQVI-DKRS DKPLLHTVHGVGYR 219

>gi|40056|emb|CAA47908.1| (X67676) phoP [Bacillus subtilis]
Length = 240

Score = 43.5 bits (101), Expect = 0.006
Identities = 30/110 (27%), Positives = 56/110 (50%), Gaps = 2/110 (1%)

Query: 10 SCPDSEGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVS 69
+ P SE + + E Q + GD + + E + + + P+ F+LLL+L + RV++
Sbjct: 124 AAPSSEM-KNDEMEGQIVIGDLKILPDHYEAYFKESQLELTPKEFELLYLGRHKGRVLT 182

Query: 70 KDELQAVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRT VARKGFR 118
+D LL AVW ++ I HI+ +R I + + I+T+ G++
Sbjct: 183 RDLILLSAVWNYDFAGDTRIVDVHISHLRDKIENNTKKPIYIKTIRGLGYK 232

>gi|18311314|ref|NP_563248.1| (NC_003366) two-component response regulator [Clostridium perfringens]
gi|18145997|dbj|BAB82038.1| (AP003193) two-component response regulator [Clostridium perfringens]
Length = 230

Score = 43.5 bits (101), Expect = 0.006
Identities = 29/112 (25%), Positives = 58/112 (50%), Gaps = 6/112 (5%)

Query: 11 CPDSERGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSK 70
CP+ G + F G+ ++ + RE+ R +++++ F++LL L ++ ++
Sbjct: 121 CPNE-----GSDILVFNNELKINVDTRVWVRDELITLTSTEFNILLCLSSYPKKIFTR 175

Query: 71 DELLQAVWGGRIVS-ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVG 121
DE+++ V G + S + I SHI +R I + + + I TV G++F G
Sbjct: 176 DEIIELVLGDKSDSFDRVIDSHIKNLRGKIEENTRKPKFIVTVYGVGYKFEG 227

>gi|6683054|dbj|BAA89010.1| (AB027503) transmembrane regulatory protein ToxR [Vibrio hollisae]
Length = 292

Score = 43.5 bits (101), Expect = 0.006
Identities = 30/134 (22%), Positives = 61/134 (45%), Gaps = 9/134 (6%)

Query: 34 DQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVW--GGRIVSESTITSH 91
D +L ++ +G +L+ L+ +V+++ + VW G V +S++T
Sbjct: 20 DSSLIDLYLENDLIRLGSNECRVLMVLIEEPHAIVTRNRIHDFVWRKQGFEVDDSSLTQS 79

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRFVGDIRIGGIGEVQPVGPGALQASGGSGE-- 149
I+ +RK++ D+ ++TV ++G++ V + + EV P + + + E
Sbjct: 80 ISTLRKSLKDSTKSPMFVKTVPKRGYQVVCSEVYNEQVELPEPAASVIDETAAKTEPE 139

Query: 150 -----TASALVLPD 158
TA L LPD
Sbjct: 140 LLSDNATAQTLPLPD 153

>gi|16123046|ref|NP_406359.1| (NC_003143) two-component system response regulator [Yersinia pestis]
gi|15980821|emb|CAC92104.1| (AJ414154) two-component system response regulator [Yersinia pestis]
Length = 239

Score = 43.5 bits (101), Expect = 0.006
Identities = 25/93 (26%), Positives = 52/93 (55%), Gaps = 1/93 (1%)

Query: 32 VLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGG-RIVSESTIT 90
++++ R + + +G ++ + P F LL L V S+++LL ++ R+V++ TI S
Sbjct: 143 LINESRFQASYQGHMLELTPAEFRLLKILASQPGHVFSREQLLNLYDDYRVVTDRTIDS 202

Query: 91 HINAVRKAIGDTGGEQRLIRTVARKGFRFVGDI 123
HI +++ + GE+ IR V G+R+ ++
Sbjct: 203 HIKNLQRKLELLDGEKPFIRAVYGMGYRWEAEM 235

>gi|16331577|ref|NP_442305.1| (NC_000911) OmpR subfamily [Synechocystis sp. PCC 6803]
gi|7429067|pir||S76529 hypothetical protein - Synechocystis sp. (strain PCC 6803)
gi|1001644|dbj|BAA10375.1| (D64002) OmpR subfamily [Synechocystis sp. PCC 6803]
Length = 224

Score = 43.1 bits (100), Expect = 0.007
Identities = 26/91 (28%), Positives = 53/91 (57%), Gaps = 2/91 (2%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSEST 87
F D ++ RE+ R +++ + + F+LL +L+ +V+++++L+ VWG + +S
Sbjct: 131 FADLRFNRSTREIQRGDRILDLTAKFELLDYLLSHARQVLTREQILERVWGYDFMGDSN 190

Query: 88 ITS-HINAVRKAIGDTGGEQRLIRTVARKGF 117
I +I +R + + GE RLI+TV G+
Sbjct: 191 IIEVYIRYLRKL- EAAGEPRLIQTVRGVGY 220

>gi|11278069|pir||T45446 probable two-component response regulator [imported] -
Mycobacterium leprae
gi|4455703|emb|CAB36688.1| (AL035500) putative two-component response regulator [Mycobacterium leprae]
Length = 253

Score = 43.1 bits (100), Expect = 0.007
Identities = 33/105 (31%), Positives = 52/105 (49%), Gaps = 4/105 (3%)

Query: 16 RGRPGDA--EVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDEL 73

R + P DA V F D LD RE+ R + +S+ F LL L+ RV+++ +
Sbjct: 143 RTKPDDAAESVAMSFSDLTLDPVTRVARGQRWISLTRTEFALLEMLIANPRRVLTSRRI 202

Query: 74 LQAVWGGRI-VSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
L+ VWG S + + ++ +R+ + GE RLI TV G+

Sbjct: 203 LEEVWGFDFPTSGNALEVYVGYLRRKT-EADGESRLIHTVRGVGY 246

>gi|15675804|ref|NP_269978.1| (NC_002737) putative two-component response regulator
[Streptococcus pyogenes] [Streptococcus pyogenes M1 GAS]
gi|19746916|ref|NP_608052.1| (NC_003485) putative two-component response regulator
[Streptococcus pyogenes MGAS8232]
gi|13623031|gb|AAK34699.1| (AE006624) putative two-component response regulator [Streptococcus
pyogenes M1 GAS]
gi|19749163|gb|AAL98551.1| (AE010111) putative two-component response regulator [Streptococcus
pyogenes MGAS8232]
Length = 217

Score = 43.1 bits (100), Expect = 0.007
Identities = 21/92 (22%), Positives = 46/92 (49%), Gaps = 10/92 (10%)

Query: 6 ILFASCPDSEGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRD 65
+L S PD +R GD ++D+ + +G +V + + +D++ +L
Sbjct: 115 VLRVSTPDEKR-----QIGDLLVDETEHSVWQGTLVKLTKEYDIDYLAKRHQ 164

Query: 66 RVVSKDELLQAVWGGGRIVSESTITSHINAVRK 97
++V++D+L+ +WG + + +HI +RK
Sbjct: 165 KIVTRDQLMDDIWGYSELDTRVLDNHIKRLRK 196

>gi|886038|gb|AAB36584.1| (U24659) JadR1 [Streptomyces venezuelae]
Length = 234

Score = 43.1 bits (100), Expect = 0.007
Identities = 29/91 (31%), Positives = 48/91 (51%), Gaps = 5/91 (5%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSKDELLQAVWGGGRIVSESTI 88
G +D R++T GQ V + + FDLL L D V+ + +L+Q VWG S T+
Sbjct: 146 GPLHIDAAARQVTLGQDVLDLTKREFDLLYLLASHPDTVIPRKQLMQQVWGDSW-SRRTV 204

Query: 89 TSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
+H++++R +G + + T+ GFRF
Sbjct: 205 DTHVSSLRNKLGASD----WVITIRGVGFRF 231

>gi|16079963|ref|NP_390789.1| (NC_000964) two-component response regulator [Bacillus subtilis]
gi|7404414|sp|P13792|PHOP_BACSU Alkaline phosphatase synthesis transcriptional regulatory
protein

phoP
gi|7429064|pir|RGBSAP phosphate response regulator protein phoP - Bacillus subtilis
gi|2293270|gb|AAC00348.1| (AF008220) signal transduction regulator [Bacillus subtilis]
gi|2635376|emb|CAB14871.1| (Z99118) two-component response regulator [Bacillus subtilis]
Length = 240

Score = 43.1 bits (100), Expect = 0.007
Identities = 30/108 (27%), Positives = 55/108 (50%), Gaps = 2/108 (1%)

Query: 12 PDSEGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSKD 71
P SE + + E Q + GD + + E + + + P+ F+LLL+L + RV+++D
Sbjct: 126 PSSEM-KNDEMEGQIVIGDLKILPDHYEAYFKESQLELTPKEFELLYLGRHKGRVLTRD 184

Query: 72 ELLQAVWGGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
LL AVW ++ I HI+ +R I + + I+T+ G++
Sbjct: 185 LLLSAVWNYDFAGDTRIVDVHISHLRDKIENNTKKPIYIKTIRGLGYK 232

>gi|7211008|emb|CAB76988.1| (AL159178) putative response regulator [Streptomyces coelicolor
A3(2)]
Length = 256

Score = 43.1 bits (100), Expect = 0.008
Identities = 32/104 (30%), Positives = 49/104 (46%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQ 75
R RP A D R T+ G +++ + FDLL + R +++EL++
Sbjct: 145 RTRPAPAPRPPSAAGLTADPAARRATKDGAEALALTREFDLLAFFLRHPGRAFAREELMR 204

Query: 76 AVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
VWG ST+T H+ +R + D RLI+TV G+RF
Sbjct: 205 EVWGWDFGDLSTVTVHVRLRGKVEDDPARPLIQTVMWGVGYRF 248

>gi|15826987|ref|NP_301250.1| (NC_002677) putative two-component response regulator
[Mycobacterium leprae]
gi|13092534|emb|CAC29682.1| (AL583917) putative two-component response regulator [Mycobacterium
leprae]
Length = 228

Score = 42.7 bits (99), Expect = 0.009
Identities = 33/105 (31%), Positives = 52/105 (49%), Gaps = 4/105 (3%)

Query: 16 RGRPGDA--EVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDEL 73
R +P DA V F D LD RE+ R + +S+ F LL L+ RV+++ +
Sbjct: 118 RTKPDAAESVAMSFSDLTLDPVTREVARQQRWISLTRTEFALLEMLIANPRRVLTSRRI 177

Query: 74 LQAVWGGRI-VSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
L+ VWG S + + ++ +R+ + GE RLI TV G+
Sbjct: 178 LEEVWGFDFPTSGNALEVYVGYLRRKT-EADGESRLIHTVRGVGY 221

>gi|15840463|ref|NP_335500.1| (NC_002755) DNA-binding response regulator TrcR [Mycobacterium
tuberculosis CDC1551]
gi|13880635|gb|AAK45314.1| (AE006988) DNA-binding response regulator TrcR [Mycobacterium
tuberculosis CDC1551]
Length = 276

Score = 42.7 bits (99), Expect = 0.011
Identities = 32/101 (31%), Positives = 50/101 (48%), Gaps = 5/101 (4%)

Query: 18 RPDGAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAV 77
RP D ++ GD LD RE+TR G +S+ F+LL L+ R +S+ E+L V
Sbjct: 174 RPADEALR--VGDLTLDGASREVTRDGTPISSLSTEFELLRLMRNPRRALSRTIELDRV 231

Query: 78 WGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
W ++I +I+ +RK I + +I TV G+
Sbjct: 232 WNYDFAGRTSIVDLYISYLRKKIDS--REPMIHTVRGIGY 270

>gi|625683|pir||A49903 phosphate regulatory protein ChvI - Agrobacterium tumefaciens
Length = 241

Score = 42.7 bits (99), Expect = 0.011
Identities = 29/92 (31%), Positives = 46/92 (49%), Gaps = 1/92 (1%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRI-VSEST 87
G +DQER T +G+ V++ F +L L R +D L+ A + ++ V + T
Sbjct: 146 GQLAMDQERHTCTWKGEPTVTLTVTEFLILHSLAPAAGRGEKRDALMDAAYDEQVYVDDRT 205

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
I SHI +RK G+ +I T+ G+RF
Sbjct: 206 IDSHIKRLRKKFKLVDGDFMIETLYGVGYRF 237

>gi|585207|sp|Q05943|GLNR_STRCO Transcriptional regulatory protein glnR
gi|478299|pir||JN0831 GlnR protein - Streptomyces coelicolor
gi|153283|gb|AAA02838.1| (L03213) glnR [Streptomyces coelicolor A3(2)]
gi|7636032|emb|CAB88492.1| (AL353816) transcriptional regulatory protein [Streptomyces
coelicolor A3(2)]
Length = 267

Score = 42.7 bits (99), Expect = 0.011
Identities = 30/101 (29%), Positives = 52/101 (50%), Gaps = 3/101 (2%)

Query: 21 DAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGG 80
D+ ++ GD +D+ +G+V+ + + F+LL +L RV ++ +LLQ VWG
Sbjct: 122 DSPMEIRNGDLSVDEATYSAKLKGRVLDLTFKEFELLKYLAQHPGRVFTRAQLLEQVWGY 181

Query: 81 RIVSES-TITSHINAVRKAIGDTGGEQRLIRTVARKGFRFV 120
+ T+ H+ +R +G + LI TV G+RFV
Sbjct: 182 DYFGGTRTVDVHVRLRAKLGPE--HESLIGTVRNVGYRFV 220

>gi|1705849|sp|Q07783|CHVI_AGRTU Transcriptional regulatory protein chvi
gi|304125|gb|AAA03553.1| (L19166) putative [Agrobacterium tumefaciens]
Length = 241

Score = 42.7 bits (99), Expect = 0.011
Identities = 29/92 (31%), Positives = 46/92 (49%), Gaps = 1/92 (1%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSVSKDELLQAVWGGRI-VSEST 87
G +DQER T +G+ V++ F +L L R +D L+ A + ++ V + T
Sbjct: 146 GQLAMDQERHTCTWKGEPTLTVTETFLILHSLAPAAGRGEKRDALMDAAYDEQVYVDRT 205

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
I SHI +RK G+ +I T+ G+RF
Sbjct: 206 IDSHIKRLRKFKFLVDGDFMIETLYGVGYRF 237

>gi|16123188|ref|NP_406501.1| (NC_003143) putative two-component response regulator [Yersinia
pestis]
gi|15980963|emb|CAC92252.1| (AJ414154) putative two-component response regulator [Yersinia
pestis]
Length = 235

Score = 42.7 bits (99), Expect = 0.011
Identities = 31/97 (31%), Positives = 49/97 (49%), Gaps = 1/97 (1%)

Query: 26 FMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSVSKDELLQAVWGGRI-VSE 85
F FGD ++ R + + + ++L +L + RVV++D L AVWG + +
Sbjct: 132 FPFGLMVPFNLCAIRGETRLELSREVNIIRYLYQHKGRRVTRDMLFDAVWGYDHLPO 191

Query: 86 S-TITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVG 121
S T+ HI+ +RK I LIRT V G+R+ G
Sbjct: 192 SRTLDQHISKLRKTIELDPVHPVLIRTVHGAGYRYQG 228

>gi|16800610|ref|NP_470878.1| (NC_003212) similar to two-component response regulators [Listeria
innocua]
gi|16414015|emb|CAC96773.1| (AL596168) similar to two-component response regulators [Listeria
innocua]
Length = 228

Score = 42.4 bits (98), Expect = 0.012
Identities = 28/92 (30%), Positives = 53/92 (57%), Gaps = 6/92 (6%)

Query: 31 YVLDQERRELTRRGQVV-SVGPQVFDLLHLVGTRDRVSVSKDELLQAVWGGRI-VSESTI 88
+ + + RE+ +G+++ ++ P+ FDL L+ +V S+++LL+ VWG + E T+
Sbjct: 136 FKISKRTREIFYQGEELDALTPKEFDLLYFLMQHPRQVFSREQLLEQVWGYQFYGDERTV 195

Query: 89 TSHINAVRKAIG-DTGGEQRLIRTVARKGFRF 119
HI +R+ I DT + + TV G++F
Sbjct: 196 DVHIKRLRQKIATDT---KPFLHTVWGVGYKF 224

>gi|15608173|ref|NP_215549.1| (NC_000962) hypothetical protein Rv1033c [Mycobacterium
tuberculosis H37Rv]
gi|7444047|pir|D70624 probable two-component regulatory protein - Mycobacterium
tuberculosis (strain H37RV)
gi|1869995|emb|CAB06846.1| (Z92539) hypothetical protein Rv1033c [Mycobacterium tuberculosis
H37Rv]
gi|2979514|gb|AAC06144.1| (U88959) response regulator homolog TrcR [Mycobacterium
tuberculosis]
Length = 257

Score = 42.4 bits (98), Expect = 0.012
Identities = 32/101 (31%), Positives = 50/101 (48%), Gaps = 5/101 (4%)

Query: 18 RPDGAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSVSKDELLQAV 77
RP D ++ GD LD RE+TR G +S+ F+LL L+ R +S+ E+L V

Sbjct: 155 RPADEALR--VGDLTLDGASREVTRDGTPISSLSTEFELLRFLMRNPRRALSRTILDRV 212

Query: 78 WGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117

W ++I +I+ +RK I + +I TV G+

Sbjct: 213 WNYDFAGRTSIVDLYISYLRKKIDSD--REPMIHTVRGIGY 251

>gi|15894147|ref|NP_347496.1| (NC_003030) Two-component response regulator [Clostridium acetobutylicum]

gi|15023754|gb|AAK78836.1|AE007601_7 (AE007601) Two-component response regulator [Clostridium acetobutylicum]

Length = 231

Score = 42.4 bits (98), Expect = 0.012

Identities = 27/103 (26%), Positives = 51/103 (49%), Gaps = 1/103 (0%)

Query: 17 GRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQA 76

G+ + +F D +LD E+ GQ +S+ + F +L L+ + +V SK L ++

Sbjct: 126 GKDESFSNKIVFKDMILDSVAMEVIVNGQRMSTLNREFKILEVLLNKRKVFSSKANLFES 185

Query: 77 VWGGRIV-SESTITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118

VW + ++T+ HI+ +R + ++ I TV G+R

Sbjct: 186 VWEDTYMGDDNTLNVHISNLRNKLKANSKEEYIETVWGMGYR 228

>gi|19551649|ref|NP_599651.1| (NC_003450) COG0745:Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain

[Corynebacterium glutamicum]

Length = 232

Score = 42.4 bits (98), Expect = 0.013

Identities = 25/88 (28%), Positives = 48/88 (54%), Gaps = 1/88 (1%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGRIVSES-TITSH 91

+D + +T G+ VS+ + FDL +L+ RV+++ +L+ +WG V ++ T+ H

Sbjct: 143 MDVDSHTVTVGGEPVSMPLKEFDLLEYLLRNAGRVLTGRQLIDRIWGADYVGDTKTLDVH 202

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRF 119

+ +R I + R + TV G++F

Sbjct: 203 VKRLRSKIEEESRPRYLTVRGLGYKF 230

>gi|12002210|gb|AAG43239.1|AF123314_2 (AF123314) putative response regulator rr [Corynebacterium glutamicum]

Length = 232

Score = 42.4 bits (98), Expect = 0.013

Identities = 25/88 (28%), Positives = 48/88 (54%), Gaps = 1/88 (1%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGRIVSES-TITSH 91

+D + +T G+ VS+ + FDL +L+ RV+++ +L+ +WG V ++ T+ H

Sbjct: 143 MDVDSHTVTVGGEPVSMPLKEFDLLEYLLRNAGRVLTGRQLIDRIWGADYVGDTKTLDVH 202

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRF 119

+ +R I + R + TV G++F

Sbjct: 203 VKRLRSKIEEESRPRYLTVRGLGYKF 230

>gi|12964066|emb|CAC29257.1| (AJ302695) putative regulatory protein [Bartonella taylorii]

Length = 240

Score = 42.4 bits (98), Expect = 0.013

Identities = 32/93 (34%), Positives = 48/93 (51%), Gaps = 3/93 (3%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVV-SKDELLQAVWGGRI-VSES 86

GD V+DQER T + + V + F L+L + R VV S+D L+ A + ++ V +

Sbjct: 146 GDLVMDQERHTCTWKDKPVILTVTEF-LILQTLAQRPGVVKSRDALMDAAYSQVYVDDR 204

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119

TI SHI +RK + +I T+ G RF

Sbjct: 205 TIDSHIKRLRKKFKQVDDDFAMIEPLYGVGHRF 237

>gi|3115359|gb|AAC15868.1| (U77060) ToxR [Photobacterium profundum]

Length = 290

Score = 42.4 bits (98), Expect = 0.014
Identities = 31/105 (29%), Positives = 56/105 (52%), Gaps = 12/105 (11%)

Query: 25 QFMFGDY---VLDQ-ERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKEDELLQAVW-- 78
+F+F Y ++DQ E ELTR G S + LL+ G +++++ L VW
Sbjct: 13 RFLDFPYDNLSDQHEDELTRLGSNES---RALGLLIEDPGA---IITRNLRLHDHVWRE 66

Query: 79 GGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDI 123
G V +S++T I+ +RKA+ D+ I+TV ++G++ + +
Sbjct: 67 QGFEVDDSSLTQAISTLRKALKDSTKSPEFIKTVPKRGYQMIAPV 111

>gi|17549138|ref|NP_522478.1| (NC_003296) PROBABLE TWO COMPONENT RESPONSE REGULATOR
TRANSCRIPTION
REGULATOR PROTEIN [Ralstonia solanacearum]
gi|17431389|emb|CAD18068.1| (AL646081) PROBABLE TWO COMPONENT RESPONSE REGULATOR TRANSCRIPTION
REGULATOR PROTEIN [Ralstonia solanacearum]
Length = 259

Score = 42.4 bits (98), Expect = 0.014
Identities = 32/110 (29%), Positives = 55/110 (49%), Gaps = 3/110 (2%)

Query: 9 ASCPDSEGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVV 68
++ P +E P D + +FG+ + R +T RGQ V + F+LLL L V+
Sbjct: 127 SAMPAAEPATPRDDTL--VFGELAISPPNRTVTWRGQPVLEKTAEFNLLLILARAAGTVL 184

Query: 69 SKDELLQAVWGGRIVS-ESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
S+D++L+ + G + T+ S I+ +R+ GD E I+T G+
Sbjct: 185 SRDDILKQLRGIEFDGLDRTVDSGISRLRRRFGDASPEPHKIKTGGDPGY 234

>gi|6714581|dbj|BAA89504.1| (AB029903) toxRS operon [Vibrio parahaemolyticus]
gi|6714584|dbj|BAA89506.1| (AB029904) toxRS operon [Vibrio parahaemolyticus]
gi|6714587|dbj|BAA89508.1| (AB029905) toxRS operon [Vibrio parahaemolyticus]
gi|6714590|dbj|BAA89510.1| (AB029906) toxRS operon [Vibrio parahaemolyticus]
gi|6714605|dbj|BAA89520.1| (AB029911) toxRS operon [Vibrio parahaemolyticus]
gi|6714608|dbj|BAA89522.1| (AB029912) toxRS operon [Vibrio parahaemolyticus]
gi|6714611|dbj|BAA89524.1| (AB029913) toxRS operon [Vibrio parahaemolyticus]
gi|17646083|dbj|BAB79249.1| (AB063111) toxR [Vibrio parahaemolyticus]
gi|17646086|dbj|BAB79251.1| (AB063112) toxR [Vibrio parahaemolyticus]
gi|17646089|dbj|BAB79253.1| (AB063113) toxR [Vibrio parahaemolyticus]
Length = 292

Score = 42.4 bits (98), Expect = 0.014
Identities = 22/78 (28%), Positives = 45/78 (57%), Gaps = 2/78 (2%)

Query: 45 QVSVGPQVFDLLLHLVGTRDRVVSKEDELLQAVW--GGRIVSESTITSHINAVRKAIGDT 102
+VV +G +LL L + V++++EL + VW G V +S++T I+ +RK + D+
Sbjct: 31 EVVRLGSNESRILLMLAERPNEVLTRNELHEFVWREQGFEVDDSSLTQAISTLRKMLKDS 90

Query: 103 GGEQRLIRTVARKGFRFV 120
++TV ++G++ +
Sbjct: 91 TKSPEFVKTVPKRGYQLI 108

>gi|6714593|dbj|BAA89512.1| (AB029907) toxRS operon [Vibrio parahaemolyticus]
gi|6714617|dbj|BAA89528.1| (AB029915) toxRS operon [Vibrio parahaemolyticus]
Length = 292

Score = 42.4 bits (98), Expect = 0.014
Identities = 22/78 (28%), Positives = 45/78 (57%), Gaps = 2/78 (2%)

Query: 45 QVSVGPQVFDLLLHLVGTRDRVVSKEDELLQAVW--GGRIVSESTITSHINAVRKAIGDT 102
+VV +G +LL L + V++++EL + VW G V +S++T I+ +RK + D+
Sbjct: 31 EVVRLGSNESRILLMLAERPNEVLTRNELHEFVWREQGFEVDDSSLTQAISTLRKMLKDS 90

Query: 103 GGEQRLIRTVARKGFRFV 120
++TV ++G++ +
Sbjct: 91 TKSPEFVKTVPKRGYQLI 108

>gi|730972|sp|Q05938|TOXR VIBPA CHOLERA TOXIN HOMOLOG TRANSCRIPTIONAL ACTIVATOR
gi|538823|pir||A47125 transcription activator of cholera toxin toxR - Vibrio
parahaemolyticus (strain AQ3815)
gi|295441|gb|AAA27576.1| (L11929) toxR [Vibrio parahaemolyticus]
Length = 292

Score = 42.4 bits (98), Expect = 0.014
Identities = 22/78 (28%), Positives = 45/78 (57%), Gaps = 2/78 (2%)

Query: 45 QVVSVPQVFDLLLHLVGTRDRVSKDELLQAVW--GGRIVSESTITSHINAVRKAIGDT 102
+VV +G +LL L + V+++EL + VW G V +S++T I+ +RK + D+
Sbjct: 31 EVVRLGSNESRILLMLAERPNEVLTRNELHEFVWREQGFEVDDSSLTQAISTLRKMLKDS 90

Query: 103 GGEQRLIRTVARKGFRFV 120
++TV ++G++ +
Sbjct: 91 TKSPEFVKTPKRGYQLI 108

>gi|6714602|dbj|BAA89518.1| (AB029910) toxRS operon [Vibrio parahaemolyticus]
gi|6714614|dbj|BAA89526.1| (AB029914) toxRS operon [Vibrio parahaemolyticus]
Length = 292

Score = 42.4 bits (98), Expect = 0.014
Identities = 22/78 (28%), Positives = 45/78 (57%), Gaps = 2/78 (2%)

Query: 45 QVVSVPQVFDLLLHLVGTRDRVSKDELLQAVW--GGRIVSESTITSHINAVRKAIGDT 102
+VV +G +LL L + V+++EL + VW G V +S++T I+ +RK + D+
Sbjct: 31 EVVRLGSNESRILLMLAERPNEVLTRNELHEFVWREQGFEVDDSSLTQAISTLRKMLKDS 90

Query: 103 GGEQRLIRTVARKGFRFV 120
++TV ++G++ +
Sbjct: 91 TKSPEFVKTPKRGYQLI 108

>gi|6714596|dbj|BAA89514.1| (AB029908) toxRS operon [Vibrio parahaemolyticus]
gi|6714599|dbj|BAA89516.1| (AB029909) toxRS operon [Vibrio parahaemolyticus]
Length = 292

Score = 42.4 bits (98), Expect = 0.014
Identities = 22/78 (28%), Positives = 45/78 (57%), Gaps = 2/78 (2%)

Query: 45 QVVSVPQVFDLLLHLVGTRDRVSKDELLQAVW--GGRIVSESTITSHINAVRKAIGDT 102
+VV +G +LL L + V+++EL + VW G V +S++T I+ +RK + D+
Sbjct: 31 EVVRLGSNESRILLMLAERPNEVLTRNELHEFVWREQGFEVDDSSLTQAISTLRKMLKDS 90

Query: 103 GGEQRLIRTVARKGFRFV 120
++TV ++G++ +
Sbjct: 91 TKSPEFVKTPKRGYQLI 108

>gi|5726300|gb|AAD48402.1|AF129010_1 (AF129010) response regulator SaeR [Staphylococcus aureus]
Length = 228

Score = 42.4 bits (98), Expect = 0.014
Identities = 28/96 (29%), Positives = 46/96 (47%), Gaps = 1/96 (1%)

Query: 25 QFMFGDYVLDQERRELTRRGQVVSVPQVFDLLLHLVGTRDRVSKDELLQAVWGGGRIVS 84
Q F + L +T G V + + F+LL +L + V+SK ELL+ VWG
Sbjct: 129 QLSFDELTILNSYVVTVNGHEVPMRFKQFELLWYLASRENEVISKSELLEKVGWGYDYDE 188

Query: 85 ES-TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
++ T+ HI+ +R+ + I TV G++F
Sbjct: 189 DANTVNVHIHRIREKLEKESFTTYTITTWGLGYKF 224

>gi|417621|sp|Q01473|RCAC_FREDI RcaC protein
gi|282227|pir||S27576 rcaC protein - Calothrix sp
gi|423999|pir||A47210 complementary chromatic adaptation protein RcaC - Fremyella
diplosiphon
Length = 632

Score = 42.4 bits (98), Expect = 0.015
Identities = 35/154 (22%), Positives = 69/154 (44%), Gaps = 12/154 (7%)

Query: 28 FGDYVLDQERRELTRRGQVVSVPQVFDLLHLVGTDRVVSVDKDELLQAVWGGR-IVSES 86
+GD +L+ E+T G +++ +DLL L+ V S +ELL +W SE+
Sbjct: 129 WGDLLLNPSTCEVTYNGCPLNLTMEYDLELLLRNCQHVSSEELDKLWSEDFPSEA 188

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDIRIGGIGEVQPVGPGAALQASGG 146
T+ SH+ +R + G I T+ +G+ ++ EV L +
Sbjct: 189 TVRSHVRLRLRHKLVAAGAPHDFIATMHGRGY----LKAPSTEEVNN-----LSVTPE 237

Query: 147 SGETASALVLPDKPSITVLPFQNLSGDPEQEYFA 180
+ ++A+++ + + + P + D +Q+Y A
Sbjct: 238 NNSHSAVIVKSRETESDRPQHLIPSDSQQYLA 271

>gi|17510937|ref|NP_491526.1| (NM_059125) Y110A7A.17.p [Caenorhabditis elegans]
gi|7331727|gb|AA60415.1| (AC006708) Hypothetical protein Y110A7A.17 [Caenorhabditis elegans]
Length = 788

Score = 42.4 bits (98), Expect = 0.015
Identities = 44/149 (29%), Positives = 70/149 (46%), Gaps = 8/149 (5%)

Query: 375 RAVELGRDDAVALTRSGHALGHLVGD-LDGGIALIDRARLLNPNFAPAWFLGGFLRVFRG 433
RA++L + A A T GH L +V D LD A LL+P AW+ G + + +
Sbjct: 586 RAIQLDKRFAYAYTLGHLE--IVQDELDKAAGSFRSALLSPRDYRAWYGLGLVHLKKE 643

Query: 434 EPESAIEHIEHAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALGNLPSLLVAV 493
+ +A+ +I+ A ++P ++ M + G+ D+ALV +RAL L L VA
Sbjct: 644 QNLTALTNIQKAVNINPTNRAMLCTLSQIEQQR---GQIDTALVLIDRAL-TLNPLDVAC 699

Query: 494 ALVAASHAL-AGRTEEARKTMQRLRALDP 521
+ A R EE + +L+A P
Sbjct: 700 RFNRSRLLEFANRNEECLVELDKLKASSP 728

>gi|19743660|gb|AAL92523.1| (AY081955) MAT-1 [Caenorhabditis elegans]
Length = 788

Score = 42.4 bits (98), Expect = 0.015
Identities = 44/149 (29%), Positives = 70/149 (46%), Gaps = 8/149 (5%)

Query: 375 RAVELGRDDAVALTRSGHALGHLVGD-LDGGIALIDRARLLNPNFAPAWFLGGFLRVFRG 433
RA++L + A A T GH L +V D LD A LL+P AW+ G + + +
Sbjct: 586 RAIQLDKRFAYAYTLGHLE--IVQDELDKAAGSFRSALLSPRDYRAWYGLGLVHLKKE 643

Query: 434 EPESAIEHIEHAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALGNLPSLLVAV 493
+ +A+ +I+ A ++P ++ M + G+ D+ALV +RAL L L VA
Sbjct: 644 QNLTALTNIQKAVNINPTNRAMLCTLSQIEQQR---GQIDTALVLIDRAL-TLNPLDVAC 699

Query: 494 ALVAASHAL-AGRTEEARKTMQRLRALDP 521
+ A R EE + +L+A P
Sbjct: 700 RFNRSRLLEFANRNEECLVELDKLKASSP 728

>gi|7242751|emb|CAB77324.1| (AL160331) putative response regulator [Streptomyces coelicolor
A3(2)]
Length = 223

Score = 42.0 bits (97), Expect = 0.016
Identities = 32/106 (30%), Positives = 52/106 (48%), Gaps = 2/106 (1%)

Query: 16 RGRPGD-AEVQFMFGDYVLDQERRELTRRGQVVSVPQVFDLLHLVGTDRVVSVDKDELL 74
RG P + A G +D +R +T G V + + FDLL L+ RV+++ +L+
Sbjct: 116 RGEPEEVAPAALEAGPVRMDVDRHVTVGGTKVDLPLKEFDLLEMLLRNAGRVLTRMQLI 175

Query: 75 QAVWGGRIVSES-TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
VWG V ++ T+ H+ +R I G R + TV G++F
Sbjct: 176 DRVWGADYVGDTKTLDVHVKRLRAKIEPDGPAPRYLVTVRGLGYKF 221

>gi|15601024|ref|NP_232654.1| (NC_002506) transcriptional regulator [Vibrio cholerae]
gi|11278057|pir||H82482 transcription regulator VCA0256 [imported] - Vibrio cholerae (group
O1 strain N16961)
gi|9657652|gb|AAF96167.1| (AE004365) transcriptional regulator [Vibrio cholerae]

Length = 223

Score = 42.0 bits (97), Expect = 0.016
Identities = 29/95 (30%), Positives = 46/95 (47%), Gaps = 6/95 (6%)

Query: 28 FG DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGRIV-SES 86
+ D V+D R + V + P+ F LLL L+ RV +DELL +WG + +
Sbjct: 131 YADIVVDVANRSVLHNQTPVELKPKFQLLLMLLQNPGRVYHRDELLNLIWGYQYFPTTR 190

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVG 121
T+ +HI +R+ + Q I T+ G+R G
Sbjct: 191 TVDNHILHLRQKL-----PQLDIETLRGVGYRLKG 220

>gi|387603|gb|AAA24892.1| (M95680) putative [Fremyella diplosiphon]
Length = 651

Score = 42.0 bits (97), Expect = 0.016
Identities = 35/154 (22%), Positives = 69/154 (44%), Gaps = 12/154 (7%)

Query: 28 FG DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGR-IVSES 86
+GD +L+ E+T G +++ +DLL L+ V S +ELL +W SE+
Sbjct: 129 WGDLLNLPSTCEVTYNGCPLNLTMEYDLELLLRNCQHVFSSEELLDKLWSSSEDFPSEA 188

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDIRIGGIGEVQPVGPGAALQASGG 146
T+ SH+ +R + G I T+ +G+ ++ EV L +
Sbjct: 189 TVRSHVRRRLRHKLVAAGAPHDFIATMHGRGY-----LKAPSTEEVNN-----LSVTPE 237

Query: 147 SGETASALVLPDKPSITVLPFQNLSGDPEQEYFA 180
+ ++A+++ + + + P + D +Q+Y A
Sbjct: 238 NNSHSAAVIVKSRETESDRPQHLIPSDSQQYLA 271

>gi|586203|sp|Q06239|VANR_ENTFC Regulatory protein vanR
gi|282285|pir||A41838 transcription activator VanR - Enterococcus faecium
gi|148327|gb|AAA24787.1| (M68910) vancomycin response regulator [Enterococcus faecium]
gi|148332|gb|AAA24790.1| (M84146) vanR [Enterococcus faecium]
gi|155039|gb|AAA65953.1| (M97297) vanR [Transposon Tn1546]
gi|383762|prf||1904198A vanR gene [Enterococcus faecalis]
Length = 231

Score = 42.0 bits (97), Expect = 0.016
Identities = 27/89 (30%), Positives = 44/89 (49%), Gaps = 2/89 (2%)

Query: 32 VLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGRIVSES--TIT 89
V++ E + +S+ P F+L L + VVS + L +WG S+S TIT
Sbjct: 140 VINVNTHECYLNEKQLSLTPTEFSILRILCENKGNVVSSELLFHEIWGDEYFSKSNNTIT 199

Query: 90 SHINAVRKAIGDTGGEQRLIRTVARKGFR 118
HI +R+ + DT + I+TV G++
Sbjct: 200 VHIRHLREKMNDTIDNPKYIKTVWGVGYK 228

>gi|13473757|ref|NP_105325.1| (NC_002678) two-component response regulator [Mesorhizobium loti]
gi|14024508|dbj|BAB51111.1| (AP003004) two-component response regulator [Mesorhizobium loti]
Length = 227

Score = 42.0 bits (97), Expect = 0.018
Identities = 28/89 (31%), Positives = 48/89 (53%), Gaps = 2/89 (2%)

Query: 30 DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGRIVSE-STI 88
D +D R +TR+GQ + + P+ F LL L+ RV+++ LL+ VW + S +
Sbjct: 132 DLEMDLIMRRVTRQGQPIDLQPREFSLLEVLMRGEGRVITRTMLLERVWDFHFDPKTSVV 191

Query: 89 TSHINAVRKAIGDTGGEQRLIRTVARKGF 117
+HI+ +R + D E +LI T+ G+
Sbjct: 192 ETHISRLRAKV-DKPFEAQLIHTIRNTGY 219

>gi|13892068|gb|AAK39631.1| (AY032724) ColR [Pseudomonas putida]
Length = 227

Score = 42.0 bits (97), Expect = 0.018

Identities = 28/103 (27%), Positives = 50/103 (48%), Gaps = 1/103 (0%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKEDELQ 75
R G D D + E+TR+G+++ + P LL L+ V+ ++ L +
Sbjct: 118 RRAQGGGRRTLQVADLSYDLDTLEVTRQGRLKLNPNVGLKLLAVLMQKSPHVLRRREVLEE 177

Query: 76 AVWGGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
A+WG ++ SH++ +R+ I D E+ L+ TV G+R
Sbjct: 178 ALWGDDCPDSDSLRSHVQLRQVI-DKPFKEKPLLHTVHGVGYR 219

>gi|13474926|ref|NP_106496.1| (NC_002678) phosphate regulatory protein [Mesorhizobium loti]
gi|14025682|dbj|BAB52282.1| (AP003007) phosphate regulatory protein [Mesorhizobium loti]
Length = 234

Score = 42.0 bits (97), Expect = 0.018
Identities = 28/105 (26%), Positives = 51/105 (47%), Gaps = 6/105 (5%)

Query: 18 RPDGADEVQ----FMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKEDEL 73
+PG ++ +G + + + G + +GP F++L HL+ +V S+DEL
Sbjct: 124 KPGSNAIENNSWLSYGSLEMKLDHRVCGNGHDIHLGPIEFNVLRHLLLEAPGKVFSRDEL 183

Query: 74 LQAVWGGRI-VSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
+ W I V T+ HI+ +R+A+ + +IRTV G+
Sbjct: 184 IGGAWPANIHVGVRTVDVHISRLRRAL-EAAGTGVIRTVRSAGY 227

>gi|15610382|ref|NP_217763.1| (NC_000962) mtrA [Mycobacterium tuberculosis H37Rv]
gi|7444062|pir||H70592 probable mtrA protein - Mycobacterium tuberculosis (strain H37Rv)
gi|2072713|emb|CAB08347.1| (Z95121) mtrA [Mycobacterium tuberculosis H37Rv]
Length = 228

Score = 41.6 bits (96), Expect = 0.020
Identities = 25/90 (27%), Positives = 48/90 (52%), Gaps = 1/90 (1%)

Query: 30 DYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKEDELLQAVWGGGRIVSESTIT 89
D +D ++TR G+ +S+ P FDLL+ L +V ++D LL+ VWG R +++ +
Sbjct: 135 DVEIDVPAHKVTRNGEQISLTPLEFDLLVALARKPRQVFTRDVLLEQVWGYRHPADTRLV 194

Query: 90 S-HINAVRKAIGDTGGEQRLIRTVARKGFR 118
+ H+ +R + ++ TV G++
Sbjct: 195 NVHVQRLRAKVEKDPENPTVVLTVRGVGYK 224

>gi|15842835|ref|NP_337872.1| (NC_002755) DNA-binding response regulator MtrA [Mycobacterium tuberculosis CDC1551]
gi|13883164|gb|AAK47686.1| (AE007145) DNA-binding response regulator MtrA [Mycobacterium tuberculosis CDC1551]
Length = 235

Score = 41.6 bits (96), Expect = 0.021
Identities = 25/90 (27%), Positives = 48/90 (52%), Gaps = 1/90 (1%)

Query: 30 DYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKEDELLQAVWGGGRIVSESTIT 89
D +D ++TR G+ +S+ P FDLL+ L +V ++D LL+ VWG R +++ +
Sbjct: 142 DVEIDVPAHKVTRNGEQISLTPLEFDLLVALARKPRQVFTRDVLLEQVWGYRHPADTRLV 201

Query: 90 S-HINAVRKAIGDTGGEQRLIRTVARKGFR 118
+ H+ +R + ++ TV G++
Sbjct: 202 NVHVQRLRAKVEKDPENPTVVLTVRGVGYK 231

>gi|3599371|gb|AAC64935.1| (AF082668) CsrR [Streptococcus pyogenes]
Length = 228

Score = 41.6 bits (96), Expect = 0.021
Identities = 28/94 (29%), Positives = 51/94 (53%), Gaps = 2/94 (2%)

Query: 25 QFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKEDELLQAVWG-GRIV 83
Q ++ D VL+ + R + R +S+ + +DLL L+ +RV++++ELL VW V
Sbjct: 131 QGIYRDLVLPQNRSVNRGDDDEISLTKREYDLLNIMTMNMRVMTREELLSNVWKYDEAV 190

Query: 84 SESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117

+ + +I +R I D G++ I+TV G+
Sbjct: 191 ETNVVDVYIRYLRGKI-DIPGKESYIQTVRGMGY 223

>gi|509815|gb|AAB07804.1| (U01971) MtrA [Mycobacterium tuberculosis]
Length = 225

Score = 41.6 bits (96), Expect = 0.021
Identities = 25/90 (27%), Positives = 48/90 (52%), Gaps = 1/90 (1%)

Query: 30 DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSESTIT 89
D +D ++TR G+ +S+ P FDLL+ L +V ++D LL+ VWG R +++ +
Sbjct: 132 DVEIDVPAHKVTRNGEQISLTPLEFDLLVALARKPRQVFTRDVLLQVWGYRHPADTRLV 191

Query: 90 S-HINAVRKAIGDTGGEQRLIRTVARKGFR 118
+ H+ +R + ++ TV G++
Sbjct: 192 NVHVQRLRAKVEKDPENPTVVLTVRGVGYK 221

>gi|7636029|emb|CAB88489.1| (AL353816) putative two-component system response regulator
[Streptomyces coelicolor A3(2)]
Length = 248

Score = 41.6 bits (96), Expect = 0.021
Identities = 27/91 (29%), Positives = 51/91 (55%), Gaps = 2/91 (2%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRI-VSES 86
F D +D RE++R G+ V + F LL + +V+++++L+AVWG S +
Sbjct: 151 FADLTMDLATREVSRAGRPVELTRTEFTLLEMFMAHPRQVLTREQILKAVWGFDFEPSSN 210

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
++ ++ +R+ + GGE RL+ TV G+
Sbjct: 211 SLDVYVMYLRRKT-EAGGEPRLVHTVRGVGY 240

>gi|15866137|gb|AAL10207.1|AF410884_3 (AF410884) MtrA [Mycobacterium avium subsp.
paratuberculosis]
Length = 225

Score = 41.6 bits (96), Expect = 0.021
Identities = 25/90 (27%), Positives = 48/90 (52%), Gaps = 1/90 (1%)

Query: 30 DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSESTIT 89
D +D ++TR G+ +S+ P FDLL+ L +V ++D LL+ VWG R +++ +
Sbjct: 132 DVEIDVPAHKVTRNGEQISLTPLEFDLLVALARKPRQVFTRDVLLQVWGYRHPADTRLV 191

Query: 90 S-HINAVRKAIGDTGGEQRLIRTVARKGFR 118
+ H+ +R + ++ TV G++
Sbjct: 192 NVHVQRLRAKVEKDPENPTVVLTVRGVGYK 221

>gi|15612935|ref|NP_241238.1| (NC_002570) two-component response regulator [Bacillus halodurans]
gi|10172985|dbj|BAB04091.1| (AP001508) two-component response regulator [Bacillus halodurans]
Length = 222

Score = 41.6 bits (96), Expect = 0.022
Identities = 22/97 (22%), Positives = 53/97 (53%), Gaps = 5/97 (5%)

Query: 23 EVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRI 82
E MF + +++ R++ R + + + P+ F+LL+ + + +V+S++++L VWG
Sbjct: 127 EDTLMFQELTINEKTRDVQRGNETIELTPKEFELLVFFIKNGQVLSREQILTNVWGFDY 186

Query: 83 VSESTIT-S-HINAVRKAIGDTGGEQRLIRTVARKGFR 118
++ + ++ +RK + T ++TV G+R
Sbjct: 187 YGDTNVIDVYRRLRKKLSLT----EALQTVRGVGYR 219

>gi|6002654|gb|AAF00081.1|AF095713_1 (AF095713) response regulator CsrR [Streptococcus pyogenes]
Length = 228

Score = 41.6 bits (96), Expect = 0.023
Identities = 28/94 (29%), Positives = 51/94 (53%), Gaps = 2/94 (2%)

Query: 25 QFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWG-GRIV 83

Q ++ D VL+ + R + R +S+ + +DLL L+ +RV+++ELL VW V
Sbjct: 131 QGIYRDLVLNPNQNSVNRGDDEISLTKREYDLLNLMNTNMNRVMTREELLSNVWKYDEAV 190

Query: 84 SESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117

+ + +I +R I D G++ I+TV G+

Sbjct: 191 ETNVVDVYIRYLRGKI-DIPGKESYIQTVRGMGY 223

>gi|15895992|ref|NP_349341.1| (NC_003030) Response regulator (CheY-like receiver domain and HTH-type DNA-binding) [Clostridium acetobutylicum]

gi|15025771|gb|AAK80681.1|AE007771_1 (AE007771) Response regulator (CheY-like receiver domain and

HTH-type DNA-binding) [Clostridium acetobutylicum]

Length = 225

Score = 41.6 bits (96), Expect = 0.024

Identities = 28/106 (26%), Positives = 52/106 (48%), Gaps = 8/106 (7%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSVSKDELLQ 75

+G D +F F D VLD E +T + + + + +L L+ +V +K + +

Sbjct: 121 KGTSIDKTNRFTEFKDLVLDSENHIVTINNEPIELTVKEYKILELLISNPKKVFTKQNIKE 180

Query: 76 AVWGGR-IVSESTITSHINAVRKAI--GDTGGEQRLIRTVARKGFR 118

+VW I+ E +T H++ +R + GDT I+TV G++

Sbjct: 181 SVWSEYILDERVVTVHVSNLRNKLKHGDT-----YIKTVWGIGYK 221

>gi|12744844|gb|AAK06808.1|AF324838_27 (AF324838) putative regulator SimReg1 [Streptomyces antibioticus]

Length = 251

Score = 41.6 bits (96), Expect = 0.025

Identities = 28/92 (30%), Positives = 47/92 (50%), Gaps = 5/92 (5%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSVSKDELLQAVWGGRIVSES- 86

FG +D +RR +TR G V + + FD+L L RV ++++++ VWG ++

Sbjct: 151 FGPVRIDLQRRSVTRDGEHVPLTRKEFDMALLATDPGRVFTREQIMFEVWGHGAGDTR 210

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118

T+ H+ +RK + L+ TV GFR

Sbjct: 211 TLGVHVTGIRKKL----RMPELVETVRGVGFR 238

>gi|12644198|sp|P30260|CC27_HUMAN Protein CDC27Hs (Cell division cycle protein 27 homolog) (H-NUC)

gi|2135326|pir||I52835 H-NUC - human

gi|998472|gb|AAB34378.1| (S78234) H-NUC [Homo sapiens]

Length = 824

Score = 41.6 bits (96), Expect = 0.025

Identities = 54/210 (25%), Positives = 94/210 (44%), Gaps = 27/210 (12%)

Query: 286 ERAEMERAKRKPTESLDAHDYLLRGMALHSGT--HEAIEAALPLFYRAI-ELDQEFASA 342

E +E +A+R +E +Y + GM +++S T H + AL + + + ++D+ A

Sbjct: 511 ELSEYMQAERIFSEVRRIENYRVEGM-EIYSTTLWHLQKDVALSVLSKDLTDMDKNSPEA 569

Query: 343 YAGAAWCYFWRKLNQWMDRAEEIAEGARLARRAVELGRDDAVALTRSGHALGHLVGDL 402

+ A C+ + R +IA + +RA+++ + A A T GH L +LD

Sbjct: 570 WCAAGNCF-----SLQREHDIA--IKFFQRAIQVDPNYAYATLLGHEF-VLTEELD 618

Query: 403 GGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIE-HIEHAARLSPLDQEMFRMQAG 461

+A A +NP AW+ G + ++ E S E H + A ++P Q+

Sbjct: 619 KALACFRNAINRPNRHYNAYGLGMI-YYQKEKFSLAEMHFQKALDINP-----QSS 669

Query: 462 TALAHFFAGRFDSALVWAERALGNLPSLLV 491

L H G AL +E+AL L +V

Sbjct: 670 VLLCHI--GVVQHALLKKSEKALDTLNKAIV 697

>gi|15079681|gb|AAH11656.1|AAH11656 (BC011656) Unknown (protein for MGC:12709) [Homo sapiens],
Length = 830

Score = 41.6 bits (96), Expect = 0.025

Identities = 54/210 (25%), Positives = 94/210 (44%), Gaps = 27/210 (12%)

Query: 286 ERAEMERAKRKPTESLDAHDYYLRGMAKLHSGT--HEAIEAALPLFYRAI-ELDQEFASA 342
E +E +A+R +E +Y + GM +++S T H + AL + + + ++D+ A
Sbjct: 517 ELSEYMQAERIFSEVRRIENYRVEGM-EIYSTTLWHLQKDVALSVLSKDLTMDKNSPEA 575

Query: 343 YAGAAWCYFWRKLNQWMDRAEEIAEGARLARRAVELGRDDAVALTRSGHALGHLVGDLD 402
+ A C+ + R +IA + +RA+++ + A A T GH L +LD
Sbjct: 576 WCAAGNCF-----SLQREHDIA--IKFFQRAIQVDPNYAYAYTLGHEF-VLTEELD 624

Query: 403 GGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIE-HIEHAARLSPLDQEMFRMQAG 461
+A A +NP AW+ G + ++ E S E H + A ++P Q+
Sbjct: 625 KALACFRNAIRVNPVRHYNAYWGLGMI-YYKQEKFSLAEMHFQKALDINP-----QSS 675

Query: 462 TALAHFFAGRFDSALVWAERALGNLPSLLV 491
L H G AL +E+AL L +V
Sbjct: 676 VLLCHI--GVVQHALLKKSEKALDTLNKAIV 703

>gi|16554577|ref|NP_001247.2| (NM_001256) cell division cycle protein 27; anaphase-promoting complex, protein 3; cell division cycle protein 27 homolog; nuc2 homolog [Homo sapiens]
Length = 824

Score = 41.6 bits (96), Expect = 0.025
Identities = 54/210 (25%), Positives = 94/210 (44%), Gaps = 27/210 (12%)

Query: 286 ERAEMERAKRKPTESLDAHDYYLRGMAKLHSGT--HEAIEAALPLFYRAI-ELDQEFASA 342
E +E +A+R +E +Y + GM +++S T H + AL + + + ++D+ A
Sbjct: 511 ELSEYMQAERIFSEVRRIENYRVEGM-EIYSTTLWHLQKDVALSVLSKDLTMDKNSPEA 569

Query: 343 YAGAAWCYFWRKLNQWMDRAEEIAEGARLARRAVELGRDDAVALTRSGHALGHLVGDLD 402
+ A C+ + R +IA + +RA+++ + A A T GH L +LD
Sbjct: 570 WCAAGNCF-----SLQREHDIA--IKFFQRAIQVDPNYAYAYTLGHEF-VLTEELD 618

Query: 403 GGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIE-HIEHAARLSPLDQEMFRMQAG 461
+A A +NP AW+ G + ++ E S E H + A ++P Q+
Sbjct: 619 KALACFRNAIRVNPVRHYNAYWGLGMI-YYKQEKFSLAEMHFQKALDINP-----QSS 669

Query: 462 TALAHFFAGRFDSALVWAERALGNLPSLLV 491
L H G AL +E+AL L +V
Sbjct: 670 VLLCHI--GVVQHALLKKSEKALDTLNKAIV 697

>gi|18587728|ref|XP_067035.2| (XM_067035) cell division cycle protein 27 [Homo sapiens]
Length = 830

Score = 41.6 bits (96), Expect = 0.025
Identities = 54/210 (25%), Positives = 94/210 (44%), Gaps = 27/210 (12%)

Query: 286 ERAEMERAKRKPTESLDAHDYYLRGMAKLHSGT--HEAIEAALPLFYRAI-ELDQEFASA 342
E +E +A+R +E +Y + GM +++S T H + AL + + + ++D+ A
Sbjct: 517 ELSEYMQAERIFSEVRRIENYRVEGM-EIYSTTLWHLQKDVALSVLSKDLTMDKNSPEA 575

Query: 343 YAGAAWCYFWRKLNQWMDRAEEIAEGARLARRAVELGRDDAVALTRSGHALGHLVGDLD 402
+ A C+ + R +IA + +RA+++ + A A T GH L +LD
Sbjct: 576 WCAAGNCF-----SLQREHDIA--IKFFQRAIQVDPNYAYAYTLGHEF-VLTEELD 624

Query: 403 GGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIE-HIEHAARLSPLDQEMFRMQAG 461
+A A +NP AW+ G + ++ E S E H + A ++P Q+
Sbjct: 625 KALACFRNAIRVNPVRHYNAYWGLGMI-YYKQEKFSLAEMHFQKALDINP-----QSS 675

Query: 462 TALAHFFAGRFDSALVWAERALGNLPSLLV 491
L H G AL +E+AL L +V
Sbjct: 676 VLLCHI--GVVQHALLKKSEKALDTLNKAIV 703

>gi|2134884|pir||A48792 CDC27 - human
gi|7459513|pir||S53647 CDC27 protein - human
gi|405833|gb|AAA60471.1| (U00001) Human homologue of S. pombe nuc2+ and A. nidulans bimA
[Homo sapiens]
Length = 823

Score = 41.6 bits (96), Expect = 0.025
Identities = 54/210 (25%), Positives = 94/210 (44%), Gaps = 27/210 (12%)

Query: 286 ERAEMERAKRKPTESLDAHDYYLRGMAKLHSGT--HEAIEAALPLFYRAI-ELDQEFASA 342
E +E +A+R +E +Y + GM +++S T H + AL + + + ++D+ A
Sbjct: 510 ELSEYMQAERIFSEVRRIENYRVEGM-EIYSTTLWHLQKDVALSVLKDLTMDKNSPEA 568

Query: 343 YAGAAWCYFWRKLNQWMDRAEEIEGARLARRAVELGRDDAVALTRSGHALGHLVGDLD 402
+ A C+ + R +IA + +RA+++ + A A T GH L +LD
Sbjct: 569 WCAAGNCF-----SLQREHDIA--IKFFQRAIQVDPNYAYAYTLGHEF-VLTEELD 617

Query: 403 GGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIE-HIEHAARLSPLDQEMFRMQAG 461
+A A +NP AW+ G + ++ E S E H + A ++P Q+
Sbjct: 618 KALACFRNAIRVNPRHYNAWYGLGMI-YYKQEKFSLAEMHFQKALDINP-----QSS 668

Query: 462 TALAHFFAGRFDSALVWAERALGNLPSLLV 491
L H G AL +E+AL L +V
Sbjct: 669 VLLCHI--GVVQHALLKKSEKALDTLNKAIV 696

>gi|15673576|ref|NP_267750.1| (NC_002662) two-component system regulator [Lactococcus lactis subsp. lactis]
gi|12724600|gb|AAK05692.1|AE006390_2 (AE006390) two-component system regulator [Lactococcus lactis subsp. lactis]
Length = 230

Score = 41.2 bits (95), Expect = 0.028
Identities = 30/104 (28%), Positives = 52/104 (49%), Gaps = 2/104 (1%)

Query: 15 ERGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTDRDRVVSKEDELL 74
E G + F D V+D+ R + R +V+ + + +DLLL L+ VV+++ L+
Sbjct: 122 EHGHAVERAENTSFRDLVIDKTNRTVHRGKKVIDLTRREYDLLLLTLMQNVGDVVTREHLV 181

Query: 75 QAVWGGRIVSESTIT-HINAVRKAIGDTGGEQRLIRTVARKGF 117
VWG +E+ + +I +R I D G+ I+TV G+
Sbjct: 182 SQVWGYEEGTETNVVDVYIRYLRNKI-DVEGQDSYIQTVRGLGY 224

>gi|8177554|gb|AAF73970.1| (U81166) putative response regulator Rra [Lactococcus lactis subsp. cremoris]
Length = 230

Score = 41.2 bits (95), Expect = 0.028
Identities = 30/104 (28%), Positives = 52/104 (49%), Gaps = 2/104 (1%)

Query: 15 ERGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTDRDRVVSKEDELL 74
E G + F D V+D+ R + R +V+ + + +DLLL L+ VV+++ L+
Sbjct: 122 EHGHAVERAENTSFRDLVIDKTNRTVHRGKKVIDLTRREYDLLLLTLMQNVGDVVTREHLV 181

Query: 75 QAVWGGRIVSESTIT-HINAVRKAIGDTGGEQRLIRTVARKGF 117
VWG +E+ + +I +R I D G+ I+TV G+
Sbjct: 182 SQVWGYEEGTETNVVDVYIRYLRNKI-DVEGQDSYIQTVRGLGY 224

>gi|15608121|ref|NP_215496.1| (NC_000962) hypothetical protein Rv0981 [Mycobacterium tuberculosis H37Rv]
gi|15840406|ref|NP_335443.1| (NC_002755) DNA-binding response regulator [Mycobacterium tuberculosis CDC1551]
gi|7444060|pir||A70821 hypothetical protein Rv0981 - Mycobacterium tuberculosis (strain H37RV)
gi|2916942|emb|CAA17580.1| (AL021999) hypothetical protein Rv0981 [Mycobacterium tuberculosis H37Rv]
gi|13880575|gb|AAK45257.1| (AE006985) DNA-binding response regulator [Mycobacterium tuberculosis CDC1551]
Length = 230

Score = 41.2 bits (95), Expect = 0.029
Identities = 32/105 (30%), Positives = 52/105 (49%), Gaps = 4/105 (3%)

Query: 16 RGRPGDA--EVQFMFGDYVLDQERRELTRRGQVSVGPGQVFDLLHLVGTRDRVVSKDEL 73
R +P DA + F D LD RE+ R + +S+ F LL L+ RV+++ +
Sbjct: 120 RTKPEDAAESMAMRFSDLTLDPVTRVNRGQRRISLTRTEFALLEMLIANPRRVLTSSRI 179

Query: 74 LQAVWGGRI-VSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
L+ VWG S + + ++ +R+ + GE RLI TV G+
Sbjct: 180 LEEVWGFDFPTSGNALEVYVGYLRKKT-EADGEPRLIHTVRGVGY 223

>gi|17547806|ref|NP_521208.1| (NC_003295) PROBABLE RESPONSE REGULATOR TRANSCRIPTION REGULATOR
PROTEIN [Ralstonia solanacearum]
gi|17430111|emb|CAD16796.1| (AL646073) PROBABLE RESPONSE REGULATOR TRANSCRIPTION REGULATOR
PROTEIN [Ralstonia solanacearum]
Length = 234

Score = 41.2 bits (95), Expect = 0.029
Identities = 25/66 (37%), Positives = 39/66 (58%), Gaps = 2/66 (3%)

Query: 14 SERGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPGQVFDLLHLVGTRDRVVSKDEL 73
++RG G + + FGD +D RR ++R G+ V + P + LL L+G R V++ EL
Sbjct: 128 AKRGEDGGSIIA--FGDVQVDLARRLVSRNGEPVHLTPIEYRLAVLLGRRGTVMTHREL 185

Query: 74 LQAVWG 79
L+ VWG
Sbjct: 186 LREVWG 191

>gi|11321503|gb|AAG34188.1|AF321122_7 (AF321122) Sim1 [Streptomyces antibioticus]
gi|16224023|gb|AAL15604.1|AF322256_25 (AF322256) Sim1 [Streptomyces antibioticus]
Length = 251

Score = 41.2 bits (95), Expect = 0.029
Identities = 28/92 (30%), Positives = 47/92 (50%), Gaps = 5/92 (5%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPGQVFDLLHLVGTRDRVVSKDELLQAVWGGRIVSES- 86
FG +D +RR +TR G V + + FD+L L RV ++++++ VWG ++
Sbjct: 151 FGPVRIDLQRRSVTRDGEHVPLTRKEFDMLALLATDPGRVFTREQIMFEVWGHGAGDTR 210

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
T+ H+ +RK + L+ TV GFR
Sbjct: 211 TLGVHVTGIRKKL----RMPELVETVRGVGFR 238

>gi|777765|gb|AAB38544.1| (L41661) srrB [Synechococcus sp.]
Length = 237

Score = 41.2 bits (95), Expect = 0.030
Identities = 29/88 (32%), Positives = 44/88 (49%), Gaps = 1/88 (1%)

Query: 33 LDQERRELTRRGQVSVGPGQVFDLLHLVGTRDRVVSKDELLQAVWGGRIVSESTIT-H 91
+D RRE++ GQ + + FDLL L DRV ++ L+QAVW V + + H
Sbjct: 139 IDPARREVSFAGQPILLTALEFDLLHFLATHPDRVWRRNALIQAVWEYDYVDQRVVDVH 198

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRF 119
I +RK + I+TV G++F
Sbjct: 199 IGQIRKKLEVNPELACPIQTVRGVGYKF 226

>gi|19704766|ref|NP_604328.1| (NC_003454) Tetratricopeptide repeat family protein [Fusobacterium
nucleatum subsp. nucleatum ATCC 25586]
gi|19715094|gb|AAL95627.1| (AE010648) Tetratricopeptide repeat family protein [Fusobacterium
nucleatum subsp. nucleatum ATCC 25586]
Length = 657

Score = 41.2 bits (95), Expect = 0.030
Identities = 34/138 (24%), Positives = 65/138 (46%), Gaps = 13/138 (9%)

Query: 357 GWMVDRAEEIAEGARLARRAVELGRDDAVALTRSGHALGHL-----VGDLGGIALIDR 410
GW+ + E+ +G + +++ ELGR+D+ G LG L + L G+ ++D
Sbjct: 380 GWIYNELEKYEDGLQFLQKSQELGREDSWIYAEIGQCLGRLGKYEIEKLEKKGLEILDE 439

Query: 411 ARLLNPNFAPAWFLG---GFL--RVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALA 465
+ N N F+ G+L ++ +P A+ H +AAR D + + G L

Sbjct: 440 DK-TNENIQERIFINSEIGWLYGKIENSDPNEAL-HYLYAARDLGRDDQWLNAEIGWELG 497

Query: 466 HFFAGRFDSALVWAERAL 483
+ G+ + A+ + ER++

Sbjct: 498 YNDKGKDEEAIKYFERSI 515

>gi|15614143|ref|NP_242446.1| (NC_002570) two-component response regulator [Bacillus halodurans]
gi|10174197|dbj|BAB05299.1| (AP001512) two-component response regulator [Bacillus halodurans]
Length = 238

Score = 41.2 bits (95), Expect = 0.031
Identities = 24/95 (25%), Positives = 51/95 (53%), Gaps = 2/95 (2%)

Query: 27 MFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVRVSKDELLQAVWGGRIVSE- 85
+F +D + +T Q +++ P+ ++LL +L + D+V S+++LL+ VW +
Sbjct: 139 VFPHLSIDNDAHRVTVADEINLTPKEYELLYLAQSPDKVFSREQLLKDVWNYDFFGDL 198

Query: 86 STITSHINAVRKAIGDTGGE-QRLIRTVARKGFRF 119
T+ +HI +R+ + + +I TV G++F
Sbjct: 199 RTVDTHIKRLREKLNVRVSPQAASMISTVWGVGYKF 233

>gi|15827334|ref|NP_301597.1| (NC_002677) putative two-component response regulator
[Mycobacterium leprae]
gi|13092883|emb|CAC30282.1| (AL583919) putative two-component response regulator [Mycobacterium
leprae]
Length = 228

Score = 41.2 bits (95), Expect = 0.031
Identities = 25/90 (27%), Positives = 48/90 (52%), Gaps = 1/90 (1%)

Query: 30 DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVRVSKDELLQAVWGGRIVSESTIT 89
D +D ++TR G+ +S+ P FDL+ L +V ++D LL+ VWG R +++ +
Sbjct: 135 DVDIDVPAHKVTRNGEHISLTPLEFDLLVALARKPRQVFTRDVLLEQVWGYRHPADTRLV 194

Query: 90 S-HINAVRKAIGDTGGEQRLIRTVARKGFR 118
+ H+ +R + ++ TV G++
Sbjct: 195 NVHVQRLRAKVEKDPENPTVVLTVRGVGYK 224

>gi|15807647|ref|NP_295328.1| (NC_001263) response regulator [Deinococcus radiodurans]
Length = 243

Score = 41.2 bits (95), Expect = 0.031
Identities = 27/88 (30%), Positives = 48/88 (53%), Gaps = 6/88 (6%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVRVSKDELLQAVWGGRIVSESTIT-SH 91
LD R + R G+ V++ + F LL L RV ++DEL+ VW GR +ES + ++
Sbjct: 157 LDWTSRAVFRSGERVALTAKESFLLLEVLASHPGRVYTRDELIDRVWDGRFDAESNVVDY 216

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRF 119
+ +R+ +GD +++T+ G+ F
Sbjct: 217 VRNLRRKLGD-----EVVQTMRGVGYSF 239

>gi|15805769|ref|NP_294466.1| (NC_001263) response regulator [Deinococcus radiodurans]
gi|7473777|pir|H75480 response regulator - Deinococcus radiodurans (strain R1)
gi|6458452|gb|AAF10321.1|AE001930_2 (AE001930) response regulator [Deinococcus radiodurans]
Length = 225

Score = 41.2 bits (95), Expect = 0.034
Identities = 27/88 (30%), Positives = 48/88 (53%), Gaps = 1/88 (1%)

Query: 30 DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVRVSKDELLQAVWGGRIVSESTIT 89
D V++ + RE+ R G+ V + + F+LL L +V S+ E+ + VW + +
Sbjct: 134 DLVMLDGREIFRGGRRVELSAKEFELLELLARNPGKVFSRFEIEEKVWPEYTGGSNVVD 193

Query: 90 SHINAVRKAIGDTGGEQRLIRTVARKGF 117
+I +R+ + + GGE+RLI TV G+
Sbjct: 194 VYIGYLRRKL-EEGGERRLIHTVRGVGY 220

>gi|18309930|ref|NP_561864.1| (NC_003366) two-component response regulator [Clostridium

perfringens]
gi|18144608|dbj|BAB80654.1| (AP003188) two-component response regulator [Clostridium
perfringens]
Length = 229

Score = 41.2 bits (95), Expect = 0.034
Identities = 24/92 (26%), Positives = 46/92 (49%), Gaps = 1/92 (1%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSVSKDELLQAVWGGRIV-SES 86
+ + +L+ RE+ +G+ + + + F +L LV +V +K L + VW + ++
Sbjct: 136 YKNLILEPRSREVVKVGEEIQLTSKEFKILELLVCNPKKVFTRKANLFETVWEEFLGDDN 195

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
TI HI+ +R I E I+T+ GF+
Sbjct: 196 TINVHISNLRNKNLLDNENDYIKTIWGVGFK 227

>gi|15895700|ref|NP_349049.1| (NC_003030) Response regulator (CheY-like domain and HTH-type
DNA-binding domain) [Clostridium acetobutylicum]
gi|15025451|gb|AAK80389.1|AE007743_11 (AE007743) Response regulator (CheY-like domain and HTH-
type
DNA-binding domain) [Clostridium acetobutylicum]
Length = 224

Score = 40.8 bits (94), Expect = 0.038
Identities = 24/106 (22%), Positives = 53/106 (49%), Gaps = 4/106 (3%)

Query: 15 ERGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSVSKDELL 74
+R +P + F +D E+T + + + P+ +DLL++ + +++D++L
Sbjct: 118 KRIQPNESKQVQNFQDGLKIDAISHEVTIEDKEIYLSPEYDILLIYFSNNKGITLTRDKIL 177

Query: 75 QAVWGGRIVSE-STITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
VWG + T+ +H+ +R+ + D + L+ TV G++F
Sbjct: 178 DNVWGEDYYGDLRTVDTHVKRLREKLQD---KAYLVATVRGSGYKF 220

>gi|15613318|ref|NP_241621.1| (NC_002570) two-component response regulator [Bacillus halodurans]
gi|10173369|dbj|BAB04474.1| (AP001509) two-component response regulator [Bacillus halodurans]
Length = 232

Score = 40.8 bits (94), Expect = 0.039
Identities = 26/84 (30%), Positives = 46/84 (53%), Gaps = 2/84 (2%)

Query: 35 QERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSVSKDELLQAVWGG-RIVSESTITSHIN 93
++R + GQ V P+ F LL+ L + +VS+D+LL+A+W V ++T+ +I
Sbjct: 141 RDRNTIELNGQKVECSPEFRLLICAEHVENIVSRDKLLEAIWDEIDFVDDNTLNVNIR 200

Query: 94 AVRKAIGDTGGEQRLIRTVARKGF 117
R+ + D G I+TV +G+
Sbjct: 201 RGRRLLEDIGITDA-IQTVRGQGY 223

>gi|4104608|gb|AAD10267.1| (AF036968) putative response regulator [Lactobacillus sakei]
Length = 246

Score = 40.8 bits (94), Expect = 0.039
Identities = 24/75 (32%), Positives = 44/75 (58%), Gaps = 3/75 (4%)

Query: 46 VVSVGPQVFDLLLHLVGTRDRVSVSKDELLQAVWGGRIV-SESTITSHINAVRKAIGDTGG 104
++ + P+ FDLL L +V S+++LL+ VW + E T+ +HI +R+ I + G
Sbjct: 166 ILDLTPKEFDLLKTLAKNPRQVFSREQLLELVWDYQYFGDERTVDAHIKKLRQKIEEVG- 224

Query: 105 EQRLIRTVARKGFRF 119
++I+TV G++F
Sbjct: 225 -PQVIQTVWGVGYKF 238

>gi|17887423|gb|AAL40886.1| (AY065624) transcriptional regulator ToxR [Listonella anguillarum]
Length = 288

Score = 40.8 bits (94), Expect = 0.041
Identities = 24/94 (25%), Positives = 49/94 (51%), Gaps = 7/94 (7%)

Query: 32 VLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVKDELLQAVW--GGRIVSESTIT 89
+L+QE + + V +G +LL L + V+++ EL + VW G V +S++T
Sbjct: 23 LLEQENEQ-----EAVRLGSNESRILLLCERPNEVITRHELHEFVWREQGFEVDDSSLT 77

Query: 90 SHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDI 123
I+ +RK + D ++TV ++G++ + +
Sbjct: 78 QAISTLRKMLKDQTKSPEFVKTVPKRGYQMIASV 111

>gi|15777925|dbj|BAB68524.1| (AB042547) ToxR [Listonella anguillarum]
Length = 288

Score = 40.8 bits (94), Expect = 0.041
Identities = 24/94 (25%), Positives = 49/94 (51%), Gaps = 7/94 (7%)

Query: 32 VLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVKDELLQAVW--GGRIVSESTIT 89
+L+QE + + V +G +LL L + V+++ EL + VW G V +S++T
Sbjct: 23 LLEQENEQ-----EAVRLGSNESRILLLCERPNEVITRHELHEFVWREQGFEVDDSSLT 77

Query: 90 SHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDI 123
I+ +RK + D ++TV ++G++ + +
Sbjct: 78 QAISTLRKMLKDQTKSPEFVKTVPKRGYQMIASV 111

>gi|13540875|ref|NP_110563.1| (NC_002689) TPR-repeat-containing protein [Thermoplasma volcanium]
Length = 242

Score = 40.8 bits (94), Expect = 0.042
Identities = 55/222 (24%), Positives = 97/222 (42%), Gaps = 23/222 (10%)

Query: 303 AHDYYLRGMAKLHSGTHEAIEAALPLFYRAIELDQEFASAYAGAAWCYFWRKLNQWVDR 362
A DY RG++ + G + + A+ F +AI + + A Y Y+ K D+
Sbjct: 22 ADDYNERGISYFNIGKY---DKAVEEFTKAISIINDDADLYHNRGMAYYSMK---AYDQ 74

Query: 363 AEEIAEGARLARRAVELGRDDAVALTRSGHALGHL---VGDLGGIALIDRARLLNPNFA 419
A E E R++ L + + +ALG + +G+ + + + A L +
Sbjct: 75 AIEDFE-----RSISLDPNS----SDYHNALGSVYEDMGNYEKALEEFNSAIRLEDDL 124

Query: 420 PAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHHFFAGRFDSALVWA 479
++ G + GE E AI+ AA L DQ ++ + AL GR+D AL
Sbjct: 125 DYYNVRGNGVYKWLGEIEKAIQDYSKAADLDYTDQ-IYVYKYEALTSL--GRYDEALET 181

Query: 480 ERALGNLPSLLVAVALVAASHALAGRTEEARKTMQRLRALDP 521
++A+ +P+ +A+ A R EEAR ++ + L+P
Sbjct: 182 DKAIKVVPANYNILAMKAELLIKMKRYEERPVIEVEEKLNP 223

>gi|14324257|dbj|BAB59185.1| (AP000991) hypothetical protein [Thermoplasma volcanium]
Length = 240

Score = 40.8 bits (94), Expect = 0.042
Identities = 55/222 (24%), Positives = 97/222 (42%), Gaps = 23/222 (10%)

Query: 303 AHDYYLRGMAKLHSGTHEAIEAALPLFYRAIELDQEFASAYAGAAWCYFWRKLNQWVDR 362
A DY RG++ + G + + A+ F +AI + + A Y Y+ K D+
Sbjct: 20 ADDYNERGISYFNIGKY---DKAVEEFTKAISIINDDADLYHNRGMAYYSMK---AYDQ 72

Query: 363 AEEIAEGARLARRAVELGRDDAVALTRSGHALGHL---VGDLGGIALIDRARLLNPNFA 419
A E E R++ L + + +ALG + +G+ + + + A L +
Sbjct: 73 AIEDFE-----RSISLDPNS----SDYHNALGSVYEDMGNYEKALEEFNSAIRLEDDL 122

Query: 420 PAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHHFFAGRFDSALVWA 479
++ G + GE E AI+ AA L DQ ++ + AL GR+D AL
Sbjct: 123 DYYNVRGNGVYKWLGEIEKAIQDYSKAADLDYTDQ-IYVYKYEALTSL--GRYDEALET 179

Query: 480 ERALGNLPSLLVAVALVAASHALAGRTEEARKTMQRLRALDP 521
++A+ +P+ +A+ A R EEAR ++ + L+P
Sbjct: 180 DKAIKVVPANYNILAMKAELLIKMKRYEERPVIEVEEKLNP 221

>gi|6174678|dbj|BAA85986.1| (AB024522) gcrR [Streptococcus mutans]
Length = 230

Score = 40.4 bits (93), Expect = 0.046
Identities = 28/91 (30%), Positives = 48/91 (51%), Gaps = 2/91 (2%)

Query: 28 FG DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSEST 87
+ D LD R R G + + + FDLL LV ++V+++ELL VW +E+
Sbjct: 135 YRDLKLDVHNRAAIRNGETIPLTKREFDLLNALVENINQVMTREELLARVWKYDQEAETN 194

Query: 88 ITS-HINAVRKAIGDTGGEQRLIRTVARKGF 117
+ +I +R I D G++ I+TV G+
Sbjct: 195 VVDVYIRYLRGKI-DVPGKESYIQTVRGMGY 224

>gi|15229253|ref|NP_187074.1| (NM_111295) putative O-linked GlcNAc transferase [Arabidopsis thaliana]
gi|6721161|gb|AAF26789.1|AC016829_13 (AC016829) putative O-linked GlcNAc transferase [Arabidopsis thaliana]
gi|18139887|gb|AAL60196.1|AF441079_1 (AF441079) O-linked N-acetyl glucosamine transferase [Arabidopsis thaliana]
gi|20259324|gb|AAM13988.1| (AY090938) putative O-linked GlcNAc transferase [Arabidopsis thaliana]
Length = 977

Score = 40.4 bits (93), Expect = 0.048
Identities = 63/272 (23%), Positives = 103/272 (37%), Gaps = 32/272 (11%)

Query: 277 VVGAIAPQVERAEMERAKRKPTESLDAHDYYLRGMAKLHSGTHERA--IEAALPLFYRAIE 334
++GAI Q++ +M A+ + E+L + + + E + A+ + AIE
Sbjct: 92 LIGAIYYQLQEYDMCIARNE--EALRIQPQFAECYGNMANAWKEKGDTRAIRYYLIAIE 149

Query: 335 LDQEFASAYAGAACYFWR-----KLNGWMVDRAEE-----IAEGA 370
L FA A++ A Y + LN +VD I E
Sbjct: 150 LRPNFADAWSNLASAYMRKGRLEATQCCQALSLNPLLDVDAHSNLGNLMAQGLIHEAY 209

Query: 371 RLARRAVELGRDDAVALTRSGHALGHLVGDLGGIALIDRARLLNPNFAPAWFLGGFLRV 430
AV + A+A + L GDL+ + A L P F A+ G +
Sbjct: 210 SCYLEAVRIQPTFAIAWSNLA-GLFMESGDLNRLQYKEAVKLPAPFPDAYLNLGNVYK 268

Query: 431 FRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALHFFAGRFDSALVWAERALGNLPSLL 490
G P AI +HA ++ P F A ++ G+ D A+ ++AL P L
Sbjct: 269 ALGRPTEAIMCYQHALQMRPNSAMAF---GNIASIYYEQQLDLAIRHYQALS RDPFL 325

Query: 491 VAVALVAASHALAGRTEEARCTMQRLRALDPS 522
A + + GR +EA + + AL P+
Sbjct: 326 EAYNNLGNALKDIGRVDEAVRCYNQCLALQPN 357

>gi|17549661|ref|NP_523001.1| (NC_003296) PROBABLE TWO-COMPONENT RESPONSE REGULATOR TRANSCRIPTION
REGULATOR PROTEIN [Ralstonia solanacearum]
gi|17431915|emb|CAD18593.1| (AL646084) PROBABLE TWO-COMPONENT RESPONSE REGULATOR TRANSCRIPTION
REGULATOR PROTEIN [Ralstonia solanacearum]
Length = 226

Score = 40.4 bits (93), Expect = 0.048
Identities = 31/105 (29%), Positives = 53/105 (49%), Gaps = 3/105 (2%)

Query: 16 RGRPGDAEVQFM-FGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELL 74
RGR +V + D VLD+ER ++TR G+ +++ + L L+ R+ S++ +L
Sbjct: 118 RGREQRPKNVNLQVADLVDRERMVTRAGKPIALTAKELAFLELLMSAPGRIYSRERIL 177

Query: 75 QAVWGGRIVSESTITS-HINAVRKAIGDTGGEQRLIRTVARKGFR 118
VWG + I ++ +R I D G L++TV G+R
Sbjct: 178 SNVWGANEDPLTNIVDVYVRRRLRSKI-DEGQPVPLKTVRGLGYR 221

>gi|16079802|ref|NP_390626.1| (NC_000964) similar to hypothetical proteins [Bacillus subtilis]
gi|7459506|pir||H69978 conserved hypothetical protein yrrB - Bacillus subtilis
gi|2635194|emb|CAB14690.1| (Z99117) similar to hypothetical proteins [Bacillus subtilis]
gi|2635212|emb|CAB14707.1| (Z99118) similar to hypothetical proteins [Bacillus subtilis]
Length = 206

Score = 40.0 bits (92), Expect = 0.058
Identities = 50/195 (25%), Positives = 84/195 (42%), Gaps = 33/195 (16%)

Query: 285 VERAEMERAKRKPTESL-----DAHDYYLRGMAKLHSGTHEAIEAALPLFYRAIELDQEF 339
++ + E+A T+++ DA Y A L S +E +E AL + +A+ELD
Sbjct: 1 MQEGDYEKAAEAFTKAIEENKEDAIPYI--NFANLLSSVNE-LERALAFYDKALELDSSA 57

Query: 340 ASAYAGAAWCYFWRKL-----NG---WMVDRAEEIEAGARLA----RR 375
A+AY GA Y +++ NG +M+ E +LA +R
Sbjct: 58 ATAYYGAGNVYVVKEMYKEAKDMFEKALRAGMENGDLFYMLGTVLVKLEQPKLALPYLQR 117

Query: 376 AVELGRDDAVALTRSGHALGHLVGDLGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEP 435
AVEL +D A + G L + G LD ++ +P A A++ G ++
Sbjct: 118 AVELNENDTEARFQFGMCLAN-EGMLDEALSQFAAVTEQDPGHADAFYNAGVTYAYKENR 176

Query: 436 ESAIEHIEHAARLSP 450
E A+E ++ A + P
Sbjct: 177 EKALEMLDKAIDIQP 191

>gi|18311081|ref|NP_563015.1| (NC_003366) two-component response regulator [Clostridium
perfringens]
gi|5103040|dbj|BAA78773.1| (AB028738) Response regulator protein VirI [Clostridium
perfringens]
gi|18145764|dbj|BAB81805.1| (AP003193) two-component response regulator [Clostridium
perfringens]
Length = 232

Score = 40.0 bits (92), Expect = 0.061
Identities = 21/99 (21%), Positives = 52/99 (52%), Gaps = 5/99 (5%)

Query: 25 QFMFGDYVLDQERRELTRRGQVVSQVQVFDLLLHLVGTRDRVVSQKDELLQAVWGGRIVS 84
+F+ G + ++ R++ + + + P+ +LLL+ + + +S+D++L VWG
Sbjct: 134 EFIIGPIKIKRQSRKVYLNNEEIRLKPKEIELLLYFLDNPNISLSRDQILDGVWGEEYFG 193

Query: 85 E-STITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
+ T+ H+ +R+ + + + +I T+ G+ F G+
Sbjct: 194 DFRTVDVHVRLRQKLNN---EEIETIFGLGYMFKGE 228

>gi|15599577|ref|NP_253071.1| (NC_002516) probable two-component response regulator [Pseudomonas
aeruginosa]
gi|11352344|pir||F83097 probable two-component response regulator PA4381 [imported] -
Pseudomonas aeruginosa (strain PA01)
gi|9950611|gb|AAG07769.1|AE004854_5 (AE004854) probable two-component response regulator
[Pseudomonas
aeruginosa]
Length = 227

Score = 40.0 bits (92), Expect = 0.068
Identities = 29/103 (28%), Positives = 46/103 (44%), Gaps = 1/103 (0%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVVSQVQVFDLLLHLVGTRDRVVSQKDELLQ 75
R G + D D + E+ R G+ + + P LL L+ VV +D L +
Sbjct: 118 RRAQGGRRRELSVADLSYDLDTLEVVRAGKSLKLNPIGLKLLAVLMQKSPHVVRDALEE 177

Query: 76 AVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
AVWG ++ SH++ +R+ I D L+ TV G+R
Sbjct: 178 AVWGDDCPDSLSRSHVQLRQVI-DKPFVSALLHTVHGVGYR 219

>gi|15613383|ref|NP_241686.1| (NC_002570) two-component response regulator [Bacillus halodurans]
gi|10173434|dbj|BAB04539.1| (AP001509) two-component response regulator [Bacillus halodurans]
Length = 234

Score = 40.0 bits (92), Expect = 0.071
Identities = 23/90 (25%), Positives = 48/90 (52%), Gaps = 1/90 (1%)

Query: 30 DYVLDQERRELTRRGQVVSQVQVFDLLLHLVGTRDRVVSQKDELLQAVWGGRIVS-ESTI 88
+ V++ + ++G+ + + + F +L V +V +K++L ++VW S E+ I
Sbjct: 140 ELVVELSSFTVKKKGEEIKLTAKEFQILKLFVTHPKKVFTKEQLYRSVWNDDYSDENVI 199

Query: 89 TSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
HI +R+ I DT + + I+T+ G+R
Sbjct: 200 NVHIRRLREKIEDTPSKPQYIKTIWGIGYR 229

>gi|16080525|ref|NP_391352.1| (NC_000964) similar to two-component response regulator [YvcQ]
[Bacillus subtilis]
gi|7444040|pir||D70032 two-component response regulator [YvcQ] homolog yvcP - Bacillus
subtilis
gi|1945655|emb|CAB08062.1| (Z94043) hypothetical protein [Bacillus subtilis]
gi|2635985|emb|CAB15477.1| (Z99121) similar to two-component response regulator [YvcQ]
[Bacillus subtilis]
Length = 237

Score = 40.0 bits (92), Expect = 0.072
Identities = 22/67 (32%), Positives = 40/67 (58%), Gaps = 2/67 (2%)

Query: 54 FDLLHLVGTRDRVSKDELLQAVWGG-RIVSESTITSHINAVRKAIGDTGGEQRLIRTV 112
F LL V ++VS+DELL+A+W V ++T+T ++N +R+ + + G I T+
Sbjct: 162 FQLLSIFVREHKIVSRDELLEALWDDVDFVDDNTLTNVNRLRRKL-ENAGLTDICISTI 220

Query: 113 ARKGFRF 119
+G++F
Sbjct: 221 RGQGYQF 227

>gi|15805807|ref|NP_294505.1| (NC_001263) response regulator, OmpR/PhoB family [Deinococcus
radiodurans]
gi|7473779|pir||A75476 response regulator, OmpR/PhoB family - Deinococcus radiodurans
(strain R1)
gi|6458493|gb|AAF10359.1|AE001933_3 (AE001933) response regulator, OmpR/PhoB family
[Deinococcus
radiodurans]
Length = 222

Score = 40.0 bits (92), Expect = 0.074
Identities = 28/90 (31%), Positives = 44/90 (48%), Gaps = 2/90 (2%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSESTI 88
G + ++R + G V + P+ FDLL L RV S+ E+ + VW G + S S +
Sbjct: 129 GALEIHPQKRLCSYNGHEVRLSPKEFDLLTFLARQPGRVYSRQEIEREVWNGELPSNSNV 188

Query: 89 TS-HINAVRKAIGDTGGEQRLIRTVARKGF 117
H+ +R + D G +IRTV G+
Sbjct: 189 VDVHMANMRAKLRDLDG-YGVIRTVRGIGY 217

>gi|9294730|gb|AAF86641.1|AF162694_5 (AF162694) response regulator VanRc [Enterococcus
gallinarum]
Length = 231

Score = 40.0 bits (92), Expect = 0.075
Identities = 23/75 (30%), Positives = 44/75 (58%), Gaps = 1/75 (1%)

Query: 44 GQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIV-SESTITSHINAVRKAIGDT 102
G+ V + P F +LL+L + VVS + L +AVW + + + +T+ +HI +R+ + +
Sbjct: 153 GKEVFLTPIEFKILLYLFEHQGSVVSSETLFEAVWKEKYLDNNNTVMAHIAIRLREKLHEE 212

Query: 103 GGEQRLIRTVARKGF 117
+ +LI+TV G+
Sbjct: 213 PRKPKLIKTVWGVGY 227

>gi|19745448|ref|NP_606584.1| (NC_003485) CovR [Streptococcus pyogenes MGAS8232]
gi|19747562|gb|AAL97083.1| (AE009978) CovR [Streptococcus pyogenes MGAS8232]
Length = 228

Score = 39.7 bits (91), Expect = 0.078
Identities = 27/94 (28%), Positives = 50/94 (52%), Gaps = 2/94 (2%)

Query: 25 QFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWG-GRIV 83
Q ++ D VL+ + R + R + + + +DLL L+ +RV++++ELL VW V

Sbjct: 131 QGIYRDLVLNPQNRSVNRGDDEIPLTKREYDLLNILMTNMNRVMTREELLSNVWKYDEAV 190

Query: 84 SESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117

+ + +I +R I D G++ I+TV G+

Sbjct: 191 ETNVVDVYIRYLRGKI-DIPGKESYIQTVRGMGY 223

>gi|17227839|ref|NP_484387.1| (NC_003272) hypothetical protein [Nostoc sp. PCC 7120]
gi|17129688|dbj|BAB72301.1| (AP003582) ORF_ID:all0343~hypothetical protein [Nostoc sp. PCC 7120]
Length = 154

Score = 39.7 bits (91), Expect = 0.081
Identities = 22/63 (34%), Positives = 36/63 (56%)

Query: 397 LVGDLGGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMF 456

L GD+ G I ++A L+NPN+A A+ G +V G+ + AIE ++ AA + +E

Sbjct: 80 LSGDMKGAIEDFNQAILINPNYAEAYKGRGVAKVQLGDEKEAIEDLQKAADIFQEQEETA 139

Query: 457 RMQ 459

+ Q

Sbjct: 140 KYQ 142

>gi|4104595|gb|AAD10258.1| (AF036964) putative response regulator [Lactobacillus sakei]
Length = 224

Score = 39.7 bits (91), Expect = 0.081
Identities = 25/73 (34%), Positives = 43/73 (58%), Gaps = 2/73 (2%)

Query: 46 VVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGG-RIVSESTITSHINAVRKAIGDTGG 104

VV + + LL L+ ++VS+++LL+A+W R V ++T+T +IN +RK I G

Sbjct: 150 VVDLSKNEYKLLQFLMRQHGQIVSREKLLRALWDDERFVDDNTLTVNINRLRKKIEQAGL 209

Query: 105 EQRLIRTVARKGF 117

E I+T +G+

Sbjct: 210 ED-YIQTIGQGY 221

>gi|5825487|gb|AAD53266.1| (AF166120) transmembrane transcription activator [Vibrio vulnificus]
Length = 290

Score = 39.7 bits (91), Expect = 0.082
Identities = 21/78 (26%), Positives = 44/78 (55%), Gaps = 2/78 (2%)

Query: 45 QVSVGPQVFDLLHLVGTRDRVSKDELLQAVW--GGRIVSESTITSHINAVRKAIGDT 102

+V +G +LL L + V++++EL + VW G V +S++T I+ +RK + D+

Sbjct: 31 EVTRLGSNESRILLLLSEKPNVLTRELHEFVWREQGFEVDDSSLTQAISTLRKMLKDS 90

Query: 103 GGEQRLIRTVARKGFRFV 120

++TV ++G++ +

Sbjct: 91 TKSPEFVKTVPKRGYQLI 108

>gi|18202894|sp|Q9F868|RGX3_MYCSM Sensory transduction protein regX3
gi|9964001|gb|AAG09797.1|AF258346_2 (AF258346) response regulator RegX3 [Mycobacterium smegmatis]
Length = 228

Score = 39.7 bits (91), Expect = 0.085
Identities = 25/94 (26%), Positives = 49/94 (51%), Gaps = 1/94 (1%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGGRIVSES-T 87

G +D ER ++ G+ +++ + FDLL +L+ RV+++ +L+ VWG V ++ T

Sbjct: 135 GPVRMDVERHVSVNGEPITLPLKEFDLLEYLMRNSGRVLTRGQLIDRVWGADYVGDTKT 194

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVG 121

+ H+ +R I + + TV G++ G

Sbjct: 195 LDVHVKRLRSKIEEDPANPVHLVTVRGLGYKLEG 228

>gi|6318168|emb|CAB60254.1| (AJ250862) MrsR2 protein [Bacillus sp. HIL-Y85/54728]
Length = 240

Score = 39.7 bits (91), Expect = 0.087
Identities = 21/89 (23%), Positives = 43/89 (47%)

Query: 31 YVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSESTIT 90
+ +D L G + Q LL++ +++SK ++ + VWG +ST+
Sbjct: 142 FKIDPNTGRVLVNGTRIDCPAQEMKLLIYFCEHPNQILSKHQIKYKDVWGEFYGGDSTVMV 201

Query: 91 HINAVRKAIGDTGGEQRLIRTVARKGFRF 119
H+ +R+ + + R I+TV +G+ F
Sbjct: 202 HVRRLREKLEEDPSRPRWIKTVRGQGYIF 230

>gi|16612082|gb|AAL27445.1|AF430807_10 (AF430807) VanRE [Enterococcus faecalis]
Length = 229

Score = 39.7 bits (91), Expect = 0.096
Identities = 20/72 (27%), Positives = 40/72 (54%), Gaps = 1/72 (1%)

Query: 47 VSVGQVFDLLHLVGTRDRVSKDELLQAVWG-GRIVSESTITSHINAVRKAIGDTGGE 105
+ + P FD+L +L RV+S +EL + VW + + +T+ +HI +R+ + + +
Sbjct: 154 IKLTPIEFDILWYLCRNEGRVISSEELFEKVWKEDYLENNNTVMAHIAKIREKMHEKPRQ 213

Query: 106 QRLIRTVARKGF 117
+I+TV G+
Sbjct: 214 PNIKTVWGVGY 225

>gi|15606362|ref|NP_213741.1| (NC_000918) hypothetical protein [Aquifex aeolicus]
gi|12230801|sp|O67178|YA88_AQUAE Hypothetical protein AQ_1088
gi|7459514|pir||G70393 conserved hypothetical protein aq_1088 - Aquifex aeolicus
gi|2983568|gb|AAC07141.1| (AE000722) hypothetical protein [Aquifex aeolicus]
Length = 761

Score = 39.7 bits (91), Expect = 0.098
Identities = 42/149 (28%), Positives = 63/149 (42%), Gaps = 5/149 (3%)

Query: 366 IAEGARLARRAVELGRDDAVALTRSGHALGHLVGDLGGIALIDRARLLNPNFAPAWFLG 425
+ + R+ ++A++ D R G AL + G L+ +RA LNP +
Sbjct: 85 VEDAERVLLKALKKFSVDVDDALYARLG-ALYYSQGLKEEAQHYWERALS LNPKNVEILYNL 143

Query: 426 GFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALGN 485
G L + +GE E A++ E A RL P +E + L R D + R L
Sbjct: 144 GVLHLNKGLEKALDLFERALRLKPDFRE---AEEKTLILLSLNRIDELVEEYYRELEK 200

Query: 486 LPSSLVAVALVAASHALAGRTEEARKTMQ 514
P+ V + L + AGR EAR Q
Sbjct: 201 NPNEEVYIKLGNTLYT-AGRLAEARAVFQ 228

>gi|18460982|gb|AAK53981.1| (AY033089) VanRc-2 [Enterococcus casseliflavus]
gi|18476141|gb|AAK58492.1| (AY033764) response regulator VanRc3 [Enterococcus flavescens]
Length = 231

Score = 39.3 bits (90), Expect = 0.10
Identities = 22/75 (29%), Positives = 44/75 (58%), Gaps = 1/75 (1%)

Query: 44 GQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIV-SESTITSHINAVRKAIGDT 102
G+ V + P F +LL+L + VV+ + L +AVW + + + +T+ +HI +R+ + +
Sbjct: 153 GKEVFLTPIEFKILLYLFEHQGSVASETLFEAVWKEKYLDNNNTVMAHIA RLREKLNEQ 212

Query: 103 GGEQRLIRTVARKGF 117
+ +LI+TV G+
Sbjct: 213 PRKPKLIKTVWGVGY 227

>gi|15616473|ref|NP_244779.1| (NC_002570) two-component response regulator [Bacillus halodurans]
gi|10176536|dbj|BAB07630.1| (AP001520) two-component response regulator [Bacillus halodurans]
Length = 231

Score = 39.3 bits (90), Expect = 0.10
Identities = 17/72 (23%), Positives = 44/72 (60%), Gaps = 1/72 (1%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVW-GGRIVSESTITSH 91
+D E ++ + F +L L+ +++V++D+L+++W R +S++T+T +
Sbjct: 137 IDYESNTVSNHVGSIELSKNEFFILKRLIERKNKIVTRDDLRSLWEDERFISDNTLTVN 196

Query: 92 INAVRKAIGDTG 103
+N +RK + + G
Sbjct: 197 VNRLRKRLDELG 208

>gi|15893581|ref|NP_346930.1| (NC_003030) Response regulator (CheY domain, HTH domain)
[Clostridium acetobutylicum]
gi|15023129|gb|AAK78270.1|AE007542_7 (AE007542) Response regulator (CheY domain, HTH domain)
[Clostridium acetobutylicum]
Length = 235

Score = 39.3 bits (90), Expect = 0.11
Identities = 23/89 (25%), Positives = 48/89 (53%), Gaps = 1/89 (1%)

Query: 31 YVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVS-ESTIT 89
+ +D E+ E+ + + + LL +LV ++ ++SK+++ AVW V ++TI
Sbjct: 144 FTIDFEKGEIINKDKSTILRAKELLLKYLVENKNIILSKEKIVNAVWEDDYVGYNNTIM 203

Query: 90 SHINAVRKAIGDTGGEQRLIRTVARKGFR 118
HI +R+ + D + I TV G++
Sbjct: 204 VHIRKLRQKLEDDPSNPKYILTVMKGLGYK 232

>gi|141358|sp|P19737|YREC_SYNP2 Hypothetical 28.7 kDa protein in recA 3' region
gi|76352|pir|Q3YCRQ hypothetical protein (recA 3' region) - Synechococcus sp. (strain
PCC 7002) (fragment)
gi|1196960|gb|AAA88637.1| (M29495) unknown protein [Synechococcus sp.]
Length = 256

Score = 39.3 bits (90), Expect = 0.11
Identities = 47/185 (25%), Positives = 74/185 (39%), Gaps = 7/185 (3%)

Query: 367 AEGARLARRAVELGRDDAVALTRSGHALGHLVGDLGGIALIDRARLLNPNFAPAWFLGG 426
A+ + R+A+ L ++A G+AL L G+ + RA L + A + G
Sbjct: 60 AQAVQHYRQALTLEANNARIHGALGYALSQ-L-GNYSEAVTAYRRATELEDDNAEFFNALG 118

Query: 427 FLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQAGTALAHEFFAGRFDSALVWAERALGNL 486
F G+ SAI + A +L P + G A F AG +D ALV + L
Sbjct: 119 FNLAQSGDNRSAINAYQRATQLQPNN---LAYSGLATVQFRAGDYDQALVAYRKVLAKD 175

Query: 487 PSLIVAVALVAASHALAGRTEEAR---KTMQRLRALDPSLRVSTLRDWLPIHRPEDLARF 543
+ +A+ S GR +EA + R R D LR+ W ++ + F
Sbjct: 176 SNNTMALQNSLTSLQLGRNQEAALFPDLLRQRPNDALRIKAAVTWFGLNDRDQAI AF 235

Query: 544 ADGLR 548
+ R
Sbjct: 236 LEEAR 240

>gi|16803547|ref|NP_465032.1| (NC_003210) similar to two-component response regulators [Listeria
monocytogenes EGD-e]
gi|16410936|emb|CAC99585.1| (AL591979) similar to two-component response regulators [Listeria
monocytogenes]
Length = 228

Score = 39.3 bits (90), Expect = 0.12
Identities = 25/91 (27%), Positives = 50/91 (54%), Gaps = 4/91 (4%)

Query: 31 YVLDQERRELTRRGQV-SVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIV-SESTI 88
+ + + RE+ + +++ ++ P+ FDLL L+ +V S+++LL+ VWG + E T+
Sbjct: 136 FKISKRTREIFYQDELLDALTPKEFDLLYFLMQHPRQVFSREQLLEQVWGYQFYGDERTV 195

Query: 89 TSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
HI +R+ I + + TV G++F
Sbjct: 196 DVHIKRLRQKIATE--TKPFLHTVWGVGYKF 224

>gi|18310175|ref|NP_562109.1| (NC_003366) two-component response regulator [Clostridium
perfringens]

gi|18144854|dbj|BAB80899.1| (AP003189) two-component response regulator [Clostridium perfringens]
Length = 225

Score = 39.3 bits (90), Expect = 0.12
Identities = 24/92 (26%), Positives = 48/92 (52%), Gaps = 1/92 (1%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSVKDELLQAVWGGRIV-SEST 87
G+ L +E + + G++V++ + F +L L+ RV +K ++ + VW + ++T
Sbjct: 131 GNLELSKEGCTVKKDGEIVTLNAKEFKILEMLMSNIGRVFTKKQIYENVWQEEYLGDDNT 190

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
I HI+ +R I + I+T+ G+RF
Sbjct: 191 IMVHISHLRDKIEEDPKNPCKIKTIRGIGYRF 222

>gi|15640999|ref|NP_230630.1| (NC_002505) cholera toxin transcriptional activator [Vibrio cholerae]
gi|12644128|sp|P15795|TOXR_VIBCH Cholera toxin transcriptional activator
gi|11283111|pir||E82257 cholera toxin transcription activator VC0984 [imported] - Vibrio cholerae (group O1 strain N16961)
gi|9655444|gb|AAF94145.1| (AE004179) cholera toxin transcriptional activator [Vibrio cholerae]
Length = 294

Score = 39.3 bits (90), Expect = 0.12
Identities = 22/94 (23%), Positives = 51/94 (53%), Gaps = 7/94 (7%)

Query: 32 VLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSVKDELLQAVW--GGRIVSESTIT 89
++D+E E +++ +G +L L + V+S+++L VW G V +S++T
Sbjct: 35 LIDKEDSE-----EIIRLGSNESRIILWLLAQRPNVISRNDLHDFVWREQGFVDDSSLT 89

Query: 90 SHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDI 123
I+ +RK + D+ + ++TV ++G++ + +
Sbjct: 90 QAISTLRKMLKDSTKSPQYVKTVPKRGYQLIARV 123

>gi|79261|pir||A25970 transcription activator of cholera toxin - Vibrio cholerae
gi|155249|gb|AAA27549.1| (M21249) toxR DNA binding protein [Vibrio cholerae]
Length = 294

Score = 39.3 bits (90), Expect = 0.12
Identities = 22/94 (23%), Positives = 51/94 (53%), Gaps = 7/94 (7%)

Query: 32 VLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSVKDELLQAVW--GGRIVSESTIT 89
++D+E E +++ +G +L L + V+S+++L VW G V +S++T
Sbjct: 35 LIDKEDSE-----EIIRLGSNESRIILWLLAQRPNVISRNDLHDFVWREQGFVDDSSLT 89

Query: 90 SHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDI 123
I+ +RK + D+ + ++TV ++G++ + +
Sbjct: 90 QAISTLRKMLKDSTKSPQYVKTVPKRGYQLIARV 123

>gi|15825402|gb|AAL09685.1| (AF414370) ToxR [Serratia marcescens]
Length = 279

Score = 39.3 bits (90), Expect = 0.12
Identities = 22/94 (23%), Positives = 51/94 (53%), Gaps = 7/94 (7%)

Query: 32 VLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSVKDELLQAVW--GGRIVSESTIT 89
++D+E E +++ +G +L L + V+S+++L VW G V +S++T
Sbjct: 27 LIDKEDSE-----EIIRLGSNESRIILWLLAQRPNVISRNDLHDFVWREQGFVDDSSLT 81

Query: 90 SHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDI 123
I+ +RK + D+ + ++TV ++G++ + +
Sbjct: 82 QAISTLRKMLKDSTKSPQYVKTVPKRGYQLIARV 115

>gi|16122893|ref|NP_406206.1| (NC_003143) two-component regulatory protein response regulator KdpE [Yersinia pestis]
gi|15980667|emb|CAC92927.1| (AJ414153) two-component regulatory protein response regulator KdpE [Yersinia pestis]

Length = 209

Score = 39.3 bits (90), Expect = 0.12
Identities = 25/94 (26%), Positives = 47/94 (49%), Gaps = 1/94 (1%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRIVSES- 86
F D +D R++TR G+ + + P F LL L+ +V+++ +LL VWG V S
Sbjct: 115 FADISVDLINRQVTRAGENLHLPTEFRLLTALLANAGKVITQRQLLNQVWGPVNYVEHSH 174

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRFV 120
+ ++ +R+ + + + T G+RF+
Sbjct: 175 YLRIYMGHLRQKLEADPTRPKHLLTETGVGYRFI 208

>gi|143328|gb|AAA22661.1| (M16775) phoP protein (put.); putative [Bacillus subtilis]
Length = 241

Score = 39.3 bits (90), Expect = 0.13
Identities = 30/109 (27%), Positives = 55/109 (49%), Gaps = 3/109 (2%)

Query: 12 PDSEGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKD 71
P SE + + E Q + GD + + E + + + P+ F+LLL+L + RV+++D
Sbjct: 126 PSSEM-KNDEMEGQIVIGDLKILPDHYEAFKESQLELTPKEFELLYLGRHKGRVLTRD 184

Query: 72 ELLQAVWGGRIVSESTITS-HINAVRKA-IGDTGGEQRLIRTVARKGFR 118
LL AVW ++ I HI+ +R I + + I+T+ G++
Sbjct: 185 LLLSAVWNYDFAGDTRIVDVHISHLRPTKIENNTKKPIYIKTIRGLGYK 233

>gi|15792585|ref|NP_282408.1| (NC_002163) two-component regulator [Campylobacter jejuni]
gi|11278076|pir||G81333 two-component regulator Cj1261 [imported] - Campylobacter jejuni
(strain NCTC 11168)
gi|2984736|gb|AAC08021.1| (AF053960) response regulator protein [Campylobacter jejuni]
gi|6968694|emb|CAB73515.1| (AL139077) two-component regulator [Campylobacter jejuni]
Length = 223

Score = 39.3 bits (90), Expect = 0.13
Identities = 21/91 (23%), Positives = 47/91 (51%)

Query: 31 YVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRIVSESTITS 90
+ +D+ R E+T +V+++ P F++L +L+ VS+++L+ + ++
Sbjct: 133 FKIDERRHEITYEDKVLTLTPAEFETLEYLIQHQHGYSVSREQLVSRCKNLKDKDSKSLDV 192

Query: 91 HINAVRKAIGDTGGEQRLIRTVARKGFRFVG 121
I +R IGD+ + I +V G++ +G
Sbjct: 193 IIGRLRVKIGDSSKSPKHIFSVRGIGYKLIG 223

>gi|17229920|ref|NP_486468.1| (NC_003272) two-component hybrid sensor and regulator [Nostoc sp.
PCC 7120]
gi|17131520|dbj|BAB74127.1| (AP003589) two-component hybrid sensor and regulator [Nostoc sp.
PCC 7120]
Length = 1627

Score = 38.9 bits (89), Expect = 0.13
Identities = 30/117 (25%), Positives = 52/117 (43%), Gaps = 2/117 (1%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGR-IVSES 86
+G+ LD E+ ++S+ P+ + LL + RV S +L+ +W E
Sbjct: 129 WGNLQLDPSSEVRYNQNLSSLTPKEYALLEFLRHSRRVFCSCSMILEHIWSYEDTPGEE 188

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF-VGDIRIGGIGEVQPVGPAALQ 142
+ +HI +R + + G L+ TV G+R + G EV+QP G + Q
Sbjct: 189 AVRTHIKGLRMLRNAGAPGDLVETVYGIGYRLKAQEEQSGKEEVKQPTSKGKSQQ 245

>gi|16080375|ref|NP_391202.1| (NC_000964) similar to two-component response regulator [YvrG]
[Bacillus subtilis]
gi|7475948|pir||C70047 two-component response regulator [YvrG] homolog yvrH - Bacillus
subtilis
gi|2635819|emb|CAB15312.1| (Z99120) similar to two-component response regulator [YvrG]
[Bacillus subtilis]
gi|2635835|emb|CAB15327.1| (Z99121) similar to two-component response regulator [YvrG]

[Bacillus subtilis]
gi|2832806|emb|CAA11730.1| (AJ223978) putative DNA binding response regulator, YvrH [Bacillus subtilis]
Length = 369

Score = 38.9 bits (89), Expect = 0.14
Identities = 24/96 (25%), Positives = 44/96 (45%), Gaps = 1/96 (1%)

Query: 26 FMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSVSKDELLQAVWGGRIVSE 85
+ + + + EL G+ V+ Q+ LL + + V+SKD++ + VWG +
Sbjct: 266 YTYDYFTFSPQNAELIVGGEAVACSAQLQLLQYFCEHPNVVLSKDQIYEKVGWGPSYGD 325

Query: 86 -STITSHINAVRKAIGDTGGEQRLIRTVARKGFRFV 120
+T+ HI +R+ I TV G+RF+
Sbjct: 326 NNTVMVHIRKLREKTERDPSNPEYIVTVRGLGYRFI 361

>gi|9081852|gb|AAF82619.1|AF157829_2 (AF157829) PhoP3 response regulator [Myxococcus xanthus]
Length = 233

Score = 38.9 bits (89), Expect = 0.15
Identities = 36/104 (34%), Positives = 60/104 (57%), Gaps = 3/104 (2%)

Query: 18 RPGDAEVQ-FMFGDYVLDQERREL-TRRGQVSVGPQVFDLLHLVGTRDRVSVSKDELLQ 75
R G A V+ F Y +D +RR++ + G V + FDLL LV R+RV+ +DE+L
Sbjct: 124 RSGAAPVKGLRFAGYRMDLDRRKVESPAGAPVELTRTEFDLLAFLVRERERVLRDEILD 183

Query: 76 AVWGGRIVSES-TITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
AVWG +V + T+ + +++++K +G + I+TV G+R
Sbjct: 184 AVWGRDVVDPHPTVDNFVSSLKKKLGNSTSRFAIQTVRGVGYR 227

>gi|13476389|ref|NP_107959.1| (NC_002678) two-component response regulator [Mesorhizobium loti]
gi|14027150|dbj|BAB54104.1| (AP003012) two-component response regulator [Mesorhizobium loti]
Length = 239

Score = 38.9 bits (89), Expect = 0.15
Identities = 27/109 (24%), Positives = 55/109 (49%), Gaps = 2/109 (1%)

Query: 14 SERGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSVSKDEL 73
+ R +AE + GD LD+ + R + +++ P+ F LL +L+ +VV++ L
Sbjct: 131 NRRASAKEAETVYRVGDLELDRLSHSVRRAAREITLQPREFRLLLEYLMRHAGQVVTRTML 190

Query: 74 LQAVWGGRIVSESTIT-HINAVRKAIGDTGGEQRLIRTVARKGFRFVG 121
L+ VW ++ + H++ +R I + G ++ ++ TV G+ G
Sbjct: 191 LENVDYHFDPTQTNVIDVHVSRLRGKI-EKGFDPKILHTVRGAGYMLKG 238

>gi|15888321|ref|NP_354002.1| (NC_003062) AGR_C_1793p [Agrobacterium tumefaciens] [Agrobacterium tumefaciens str. C58 (Cereon)]
gi|17934886|ref|NP_531676.1| (NC_003304) two component response regulator [Agrobacterium tumefaciens str. C58 (U. Washington)]
gi|15155989|gb|AAK86787.1| (AE008028) AGR_C_1793p [Agrobacterium tumefaciens str. C58 (Cereon)]
gi|17739364|gb|AAL41992.1| (AE009062) two component response regulator [Agrobacterium tumefaciens str. C58 (U. Washington)]
Length = 252

Score = 38.9 bits (89), Expect = 0.16
Identities = 26/103 (25%), Positives = 57/103 (55%), Gaps = 3/103 (2%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSVSKDELLQ 75
+G+P + ++ + GD LD+ ++ R G+ + + P+ F LL +L+ +VV++ LL+
Sbjct: 146 KGKP-EQDMIYRVGDLELDRLSHDVRGGKEILLQPREFRLLLEYLMKNAGQVVTRTMLLE 204

Query: 76 AVWGGRIVSESTIT-HINAVRKAIGDTGGEQRLIRTVARKGF 117
VW ++ + H++ +R I + E+ L++T+ G+
Sbjct: 205 NVWDYHFDPTQTNVIDVHVSRLRSKI-EKDFEKPPLLKTIRGAGY 246

>gi|15896467|ref|NP_349816.1| (NC_003030) Response regulator (CheY-like receiver domain and HTH-type DNA-binding domain) [Clostridium acetobutylicum]

gi|15026293|gb|AAK81156.1|AE007818_2 (AE007818) Response regulator (CheY-like receiver domain and

HTH-type DNA-binding domain) [Clostridium acetobutylicum]
Length = 228

Score = 38.9 bits (89), Expect = 0.16
Identities = 21/74 (28%), Positives = 43/74 (57%), Gaps = 3/74 (4%)

Query: 47 VSVGPOVFDLLLHLVGTRDRVSVSKDELLQAVWGGRIVSES-TITSHINAVRKAIGDTGGE 105
+ + P+ F+LL +L +++V ++++LL VWG +S T+ H+ +R+ + + G
Sbjct: 154 IKMPKPEFELLYLANNKNKVFTRQQLCEVWGYDYPGDSRTVDVHVKRLREKLHEGNGW 213

Query: 106 QRLIRTVARKGFRF 119
I+TV G++F
Sbjct: 214 D--IQTVWGVGYKF 225

>gi|17549382|ref|NP_522722.1| (NC_003296) PROBABLE TWO-COMPONENT RESPONSE REGULATOR TRANSCRIPTION

REGULATOR PROTEIN [Ralstonia solanacearum]
gi|17431635|emb|CAD18312.1| (AL646083) PROBABLE TWO-COMPONENT RESPONSE REGULATOR TRANSCRIPTION
REGULATOR PROTEIN [Ralstonia solanacearum]
Length = 219

Score = 38.9 bits (89), Expect = 0.16
Identities = 24/87 (27%), Positives = 44/87 (49%), Gaps = 1/87 (1%)

Query: 33 LDQERRELTRRGQVSVSGPOVFDLLLHLVGTRDRVSVSKDELLQAVWGG-RIVSESTITSH 91
+D T RGQ + + P F LL L R++S+ LL+ ++ R+V++ T+ +H
Sbjct: 130 IDNTAYSATLRGQRLDLTPVEFRLLSALANAPGRILSRANLLEQIYDDHRVVTDRDVTDT 189

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFR 118
+ +R+ + LI +V G+R
Sbjct: 190 VKNLRRKMELVSPGTELIHSVYGVGYR 216

>gi|15894784|ref|NP_348133.1| (NC_003030) Response regulator (CheY-like receiver domain and a HTH) [Clostridium acetobutylicum]
gi|3025460|gb|AAC12853.1| (U58131) PhoP [Clostridium acetobutylicum]
gi|15024453|gb|AAK79473.1|AE007661_3 (AE007661) Response regulator (CheY-like receiver domain and a HTH)
[Clostridium acetobutylicum]
Length = 217

Score = 38.9 bits (89), Expect = 0.17
Identities = 21/97 (21%), Positives = 51/97 (51%), Gaps = 5/97 (5%)

Query: 23 EVQFMFGDYVLDQERRELTRRGQVSVSGPOVFDLLLHLVGTRDRVSVSKDELLQAVWGGRI 82
E F D + E L + GQ++ + + F+L +L+ ++ V++++ + + +WG
Sbjct: 122 EKSLKFEDIEVQLEEMRLKNGQIIDLTVKEFELAAYLKKNKIVLTRERIAEELWGYDY 181

Query: 83 VSE-STITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
+ + TI ++I +RK + + ++T+ + G+R
Sbjct: 182 LGDCRTIDNYIQKIRKKL----DWKDKVKTIKMGYR 214

>gi|16127555|ref|NP_422119.1| (NC_002696) DNA-binding response regulator [Caulobacter crescentus CB15]
gi|13425023|gb|AAK25287.1| (AE005994) DNA-binding response regulator [Caulobacter crescentus CB15]
Length = 236

Score = 38.5 bits (88), Expect = 0.17
Identities = 24/83 (28%), Positives = 42/83 (49%), Gaps = 1/83 (1%)

Query: 18 RPDGAEVQFMFGDYVLDQERRELTRRGQVSVSGPOVFDLLLHLVGTRDRVSVSKDELLQAV 77
RP +G Y LD + + GQV ++ P+ F L L R +S++ LL+ +
Sbjct: 122 RPASQPQTEYGHYRLDPGAQTASWNGQVEALTPKEFQLASLLFSNLSRPLSREYLLRRI 181

Query: 78 WGGRIVSES-TITSHINAVRKAI 99
WG R E+ T+ +H++ +R +

Sbjct: 182 WGQRPDLETRTLDAHVSRLRSKL 204

>gi|16125434|ref|NP_419998.1| (NC_002696) DNA-binding response regulator [Caulobacter crescentus CB15]
gi|13422504|gb|AAK23166.1| (AE005795) DNA-binding response regulator [Caulobacter crescentus CB15]
Length = 254

Score = 38.5 bits (88), Expect = 0.17
Identities = 31/98 (31%), Positives = 50/98 (50%), Gaps = 3/98 (3%)

Query: 28 FGDYVLDQERREL-TRRGQVSVGPQVFDLLHLVGTDRDVSVDKDELLQAVWG-GRIVSE 85
F + LD RREL + + VV++ F LL V RV+++D+LL G +
Sbjct: 154 FAGWRLDLVRRELSPQSIVVNLSSGEFSLRAFVERPQVRLTRDQLDLARGRDSDAYD 213

Query: 86 STITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGGDI 123
I I+ +R+ + D GG + LIRT+ +G+ F +
Sbjct: 214 RAIDVQISRLRRKLDDGGGSE-LIRTIRSEGYMFTAKV 250

>gi|8134654|sp|O07130|RGX3_MYCBO Sensory transduction protein regX3
gi|2190436|emb|CAA73956.1| (Y13627) RegX3 [Mycobacterium bovis BCG]
Length = 227

Score = 38.5 bits (88), Expect = 0.18
Identities = 29/110 (26%), Positives = 53/110 (47%), Gaps = 4/110 (3%)

Query: 16 RGRPGDAEVQ---FMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVSVDKDE 72
RG D+E+ G +D ER ++ G +++ + FDLL +L+ RV+++ +
Sbjct: 118 RGGDDSEMSDGVLES GPVRMDVERHVSVNGDTITLPLKEFDLLEYLMRNSGRVLTRGQ 177

Query: 73 LLQAVWGGRIVSES-TITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVG 121
L+ VWG V ++ T+ H+ +R I + TV G++ G
Sbjct: 178 LIDRVWGADYVGDTKTLDVHVKRLRSKIEADPANPVHLVTVRGLGYKLEG 227

>gi|15902380|ref|NP_357930.1| (NC_003098) Response regulator [Streptococcus pneumoniae R6]
gi|15457893|gb|AAK99140.1| (AE008414) Response regulator [Streptococcus pneumoniae R6]
Length = 229

Score = 38.5 bits (88), Expect = 0.18
Identities = 23/86 (26%), Positives = 52/86 (59%), Gaps = 3/86 (3%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVSVDKDELLQAVWGGRIVSESTITS-H 91
+D E + R +++++ + +DLL L+G++ +V+++++LL++VW +E+ I +
Sbjct: 142 IDVEHHTVYRGEEMIALTRREYDLATLMGSK-KVLTREQLLESVWKYESATETNIVDVY 200

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGF 117
I +R + D G++ I+TV G+
Sbjct: 201 IRYLRSKL-DVKGQKSYIKTVRGGVY 225

>gi|15839882|ref|NP_334919.1| (NC_002755) DNA-binding response regulator RegX3 [Mycobacterium tuberculosis CDC1551]
gi|13880018|gb|AAK44733.1| (AE006952) DNA-binding response regulator RegX3 [Mycobacterium tuberculosis CDC1551]
Length = 230

Score = 38.5 bits (88), Expect = 0.18
Identities = 29/110 (26%), Positives = 53/110 (47%), Gaps = 4/110 (3%)

Query: 16 RGRPGDAEVQ---FMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVSVDKDE 72
RG D+E+ G +D ER ++ G +++ + FDLL +L+ RV+++ +
Sbjct: 121 RGGDDSEMSDGVLES GPVRMDVERHVSVNGDTITLPLKEFDLLEYLMRNSGRVLTRGQ 180

Query: 73 LLQAVWGGRIVSES-TITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVG 121
L+ VWG V ++ T+ H+ +R I + TV G++ G
Sbjct: 181 LIDRVWGADYVGDTKTLDVHVKRLRSKIEADPANPVHLVTVRGLGYKLEG 230 •

>gi|4104605|gb|AAD10265.1| (AF036967) putative response regulator [Lactobacillus sakei]
Length = 228

Score = 38.5 bits (88), Expect = 0.18
Identities = 25/92 (27%), Positives = 47/92 (50%), Gaps = 2/92 (2%)

Query: 29 GDYVLDQERRELTR-RGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGR-IVSES 86
G V+ ++ E+T G+ + + F +L L +RV S D++ + VW IVS
Sbjct: 134 GPLVIKRDSHEVTTIAGKQQLTALFEGILYLLASHPNRVFSADDIFERVWKQESIVSAK 193

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
T+ H++ +R I + +++I TV G++
Sbjct: 194 TVMVHVSHLRDKIEEATDGEKVIETVWGVGYK 225

>gi|15607632|ref|NP_215005.1| (NC_000962) regX3 [Mycobacterium tuberculosis H37Rv]
gi|1731207|sp|Q11156|RGX3_MYCTU Sensory transduction protein regX3
gi|7444027|pir||F70744 probable regX3 protein - Mycobacterium tuberculosis (strain H37RV)
gi|1449289|emb|CAB00952.1| (Z77162) regX3 [Mycobacterium tuberculosis H37Rv]
gi|2190480|emb|CAA73958.1| (Y13628) RegX3 [Mycobacterium tuberculosis]
Length = 227

Score = 38.5 bits (88), Expect = 0.18
Identities = 29/110 (26%), Positives = 53/110 (47%), Gaps = 4/110 (3%)

Query: 16 RGRPGDAEVQ---FMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDE 72
RG D+E+ G +D ER ++ G +++ + FDLL +L+ RV+++ +
Sbjct: 118 RGGDDSEMSDGVLESGPVRMDVERHVSVNGDTITLPLKEFDLLEYLMRNSGRVLTGRQ 177

Query: 73 LLQAVWGGRIVSES-TITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVG 121
L+ VWG V ++ T+ H+ +R I + TV G++ G
Sbjct: 178 LIDRVWGADYVGDTKTLDVHVKRLRSKIEADPANPVHLVTVRGLGYKLEG 227

>gi|15900299|ref|NP_344903.1| (NC_003028) DNA-binding response regulator [Streptococcus pneumoniae TIGR4]
gi|14971845|gb|AAK74543.1| (AE007349) DNA-binding response regulator [Streptococcus pneumoniae TIGR4]
Length = 229

Score = 38.5 bits (88), Expect = 0.18
Identities = 23/86 (26%), Positives = 52/86 (59%), Gaps = 3/86 (3%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSESTITS-H 91
+D E + R +++++ + +DLL L+G++ +V+++++LL++VW +E+ I +
Sbjct: 142 IDVEHHTVYRGEEMIALTRREYDLLATLMGSK-KVLTREQLLESVWKYESATETNIVDVY 200

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGF 117
I +R + D G++ I+TV G+
Sbjct: 201 IRYLRSKL-DVKGQKSYIKTVRGVGY 225

>gi|6448492|emb|CAB61229.1| (Y15706) vanr protein [Bacillus circulans]
Length = 231

Score = 38.5 bits (88), Expect = 0.18
Identities = 22/74 (29%), Positives = 39/74 (51%), Gaps = 2/74 (2%)

Query: 47 VSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSES--TITSHINAVRKAIGDTGG 104
+S+ P F +L L + VVS +++ +WG ++S TIT HI +R+ + T
Sbjct: 155 LSLTPTEFSILRILCENKGNVVSSEQIFHEIWGEEYFNKSNNTITVHIRHLREKMNTID 214

Query: 105 EQRLIRTVARKGFR 118
+ I+TV G++
Sbjct: 215 NPKYIKTVWGVGYK 228

>gi|15893941|ref|NP_347290.1| (NC_003030) Response regulator (CheY-like receiver domain and HTH DNA binding domain) [Clostridium acetobutylicum]
gi|15023528|gb|AAK78630.1|AE007581_1 (AE007581) Response regulator (CheY-like receiver domain and HTH DNA binding domain) [Clostridium acetobutylicum]
Length = 221

Score = 38.5 bits (88), Expect = 0.18
Identities = 26/90 (28%), Positives = 48/90 (52%), Gaps = 2/90 (2%)

Query: 30 DYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKEDELLQAVWGGRIVSES-TI 88
D +D + + + +++++ + +D+L L +VS +E+++ VWG S I
Sbjct: 131 DLNIDTKAKSVKVGKELITLTAREYDILELLCYNYPNIVSAEEIIEHVWGDNDNQFSNVI 190

Query: 89 TSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
HI +R+ I +GGE LI T+ KG+R
Sbjct: 191 RVHIANLRRRIKCSGGET-LIETLKGGKYR 219

>gi|15896754|ref|NP_350103.1| (NC_003030) Response regulator (CheY-like receiver domain and
HTH-type DNA-binding domain) [Clostridium
acetobutylicum]
gi|15026610|gb|AAK81443.1|AE007848_7 (AE007848) Response regulator (CheY-like receiver domain
and
HTH-type DNA-binding domain) [Clostridium
acetobutylicum]
Length = 230

Score = 38.5 bits (88), Expect = 0.19
Identities = 21/88 (23%), Positives = 47/88 (52%), Gaps = 3/88 (3%)

Query: 32 VLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKEDELLQAVWGGRIVSESTITSH 91
+L+ + E + +++ + F +L LV + V+++++ + VWG +T+T H
Sbjct: 142 ILNDKTFEAFNNRKLNLSTKEFQILSMLVHNPNNVLTREQIYEHVWGDEYGEINVTVH 201

Query: 92 INAVRKAIGDTGGEQRLIRTVARKGFRF 119
I +RK +G E I+T+ G+++
Sbjct: 202 IKNIRKKLGP---EYDFIKTIWIGIKY 226

>gi|17987612|ref|NP_540246.1| (NC_003317) TWO COMPONENT RESPONSE REGULATOR [Brucella melitensis]
gi|17983321|gb|AAL52510.1| (AE009571) TWO COMPONENT RESPONSE REGULATOR [Brucella melitensis]
Length = 235

Score = 38.5 bits (88), Expect = 0.19
Identities = 28/103 (27%), Positives = 53/103 (51%), Gaps = 2/103 (1%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKEDELLQ 75
R P +A+ + GD LD+ R+ +++ P+ F LL +L+ +VV++ LL+
Sbjct: 118 RSSPREADTIYRVGDLELDRLTHTARRQSVDTITLQPREFRLELYLMRHAGQVVTTRTMLLE 177

Query: 76 AVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
VW ++ + HI+ +R I + G ++ L+ TV G+
Sbjct: 178 NVWDYHFDPQTNVIDVHISRLRSKI-EKGFDEPLLHTVRGAGY 219

>gi|493217|gb|AAA20502.1| (L29053) toxR [Vibrio fischeri]
Length = 316

Score = 38.5 bits (88), Expect = 0.20
Identities = 22/78 (28%), Positives = 44/78 (56%), Gaps = 2/78 (2%)

Query: 45 QVSVSGPQVFDLLLHLVGTRDRVVSKEDELLQAVW--GGRIVSESTITSHINAVRKAIGDT 102
+++ +G +L L+ +VVS+ EL + VW G V +S++T I+ +RK + D
Sbjct: 31 EIIRLGGNESRVLSLLIQEPGVSRHELHEYVWRDQGFVDDSSLTQAISTLRKMLQDP 90

Query: 103 GGEQRLIRTVARKGFRFV 120
++TV ++G++F+
Sbjct: 91 TKLPVYVKTVPKRGYQFI 108

>gi|15641723|ref|NP_231355.1| (NC_002505) DNA-binding response regulator TorR [Vibrio cholerae]
gi|11278067|pir||G82164 DNA-binding response regulator TorR VC1719 [imported] - Vibrio
cholerae (group O1 strain N16961)
gi|9656239|gb|AAF94869.1| (AE004250) DNA-binding response regulator TorR [Vibrio cholerae]
Length = 234

Score = 38.5 bits (88), Expect = 0.20
Identities = 26/97 (26%), Positives = 51/97 (51%), Gaps = 3/97 (3%)

Query: 28 FGQVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKEDELLQAVWGGR--VSE 85
FG++ D +RR L+R G+ V + ++LL+ L ++V+S++ +L + R+ ++

Sbjct: 139 FGEWTFDVQRRALSRNGEPVKLTAEYELLVALSSYPNQVLSRERILNMI-SHRVDAPND 197

Query: 86 STITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122

TI I +R + ++ TV +G+ F GD

Sbjct: 198 RTIDVLIRRMRAKMEMDPKNPQIFVTVHGEYMFAGD 234

>gi|15792551|ref|NP_282374.1| (NC_002163) putative two-component regulator [Campylobacter jejuni]

gi|11278075|pir||E81329 probable two-component regulator Cj1227c [imported] - Campylobacter jejuni (strain NCTC 11168)

gi|6968660|emb|CAB73481.1| (AL139077) putative two-component regulator [Campylobacter jejuni]
Length = 224

Score = 38.5 bits (88), Expect = 0.21

Identities = 25/93 (26%), Positives = 48/93 (50%), Gaps = 7/93 (7%)

Query: 30 DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVRVSKDELLQAVWGGGRIVSESTIT 89

D V DQ + +T +GQ +++ FD+L +L+ VVS++EL V+ +SE +

Sbjct: 132 DLVYDQYKHIITMKGQELTLTNAEFDILSYLIKKEGGVVSREEL---VYNCSISSEDSSN 188

Query: 90 SHINA---VRKAIGDTGGEQRLIRTVARKGFR 118

I+ +R+ +GD + I ++ G++

Sbjct: 189 KSIDVIISRIRQKMGDDPKTPKYIHSIRGIGYK 221

>gi|17546367|ref|NP_519769.1| (NC_003295) PROBABLE OXIDATIVE STRESS RESISTANCE TWO-COMPONENT RESPONSE REGULATOR TRANSCRIPTION REGULATOR PROTEIN [Ralstonia solanacearum]

gi|17428664|emb|CAD15350.1| (AL646065) PROBABLE OXIDATIVE STRESS RESISTANCE TWO-COMPONENT RESPONSE REGULATOR TRANSCRIPTION REGULATOR PROTEIN [Ralstonia solanacearum]
Length = 240

Score = 38.5 bits (88), Expect = 0.21

Identities = 27/107 (25%), Positives = 51/107 (47%), Gaps = 1/107 (0%)

Query: 17 GRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVRVSKDELLQA 76

G P + F FGD+VL+ R L + + +++ F +L + +S+++L++

Sbjct: 131 GAPSETPETFAFGDFVLNLATRTLKKNDEEITLTTGEFSVLKVFARHPRQPLSREKLMEM 190

Query: 77 VWGGRI-VSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122

G V + ++ I+ +RK I R I+TV G+ F+ D

Sbjct: 191 ARGREYEVFDRSLDVQISRLRKLIEPDASNPRFIQTVMWGLGYVFIPD 237

>gi|15607128|ref|NP_214510.1| (NC_000918) hypothetical protein [Aquifex aeolicus]

gi|7459516|pir||A70489 conserved hypothetical protein aq_2197 - Aquifex aeolicus

gi|2984391|gb|AAC07909.1| (AE000777) hypothetical protein [Aquifex aeolicus]
Length = 162

Score = 38.5 bits (88), Expect = 0.21

Identities = 28/87 (32%), Positives = 41/87 (46%), Gaps = 4/87 (4%)

Query: 396 HLVGDLGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEM 455

H++GDLD I L ++ + P A AW G+ RG E AIE + A + P

Sbjct: 22 HMLGDLDAKIELYRKSIDVYPT-AEAWTFLGWAYSMRGNYEGAIEACKRAIEIDPDFGNP 60

Query: 456 FRMQAGTALAHFFAGRFDSALVWAERA 482

+ G+ L G+ D A+ W E+A

Sbjct: 81 YN-DIGSYLIEL--GKLDEAIEWLEKA 104

>gi|15896896|ref|NP_350245.1| (NC_003030) Response regulator (CheY-like receiver domain and HTH-type DNA-binding domain) [Clostridium acetobutylicum]

gi|15026765|gb|AAK81585.1|AE007861_7 (AE007861) Response regulator (CheY-like receiver domain and

HTH-type DNA-binding domain) [Clostridium acetobutylicum]
Length = 225

Score = 38.1 bits (87), Expect = 0.22

Identities = 24/93 (25%), Positives = 49/93 (51%), Gaps = 6/93 (6%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIV-SEST 87
G+Y + +++R + R + + + + F+LL +L ++ V+S++++L VWG S+
Sbjct: 135 GEYTISKQQLVFFRNEELQLTNKEFELLSYLSDNKNNVISREQILNVNWGDDYFGSDRV 194

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGFRFV 120
+ I +RK I + I TV G++ V
Sbjct: 195 VDDTIRRLRKKI-----NKLTITETVYGYGYKLV 222

>gi|17547886|ref|NP_521288.1| (NC_003295) HYPOTHETICAL PROTEIN [Ralstonia solanacearum]
gi|17430192|emb|CAD16955.1| (AL646074) HYPOTHETICAL PROTEIN [Ralstonia solanacearum]
Length = 296

Score = 38.1 bits (87), Expect = 0.23
Identities = 43/160 (26%), Positives = 68/160 (41%), Gaps = 7/160 (4%)

Query: 325 ALPLFYRAIELDQEFASAYAGAAWCYFWRKLNWMDRAEEIAEGARL-ARRAVELGRDD 383
++ F AI FA+AY G A Y G V A E A++ AR+A+++ D
Sbjct: 4 SIEYFQLAIGYQPNFAAAYDGVADAYTMLACRG--VSPARETFHQAKMAARKALQIEPDL 61

Query: 384 AVALTRSGHALGHVLGDLDGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIE 443
A H H +D + RA LNP A A++ + G E AI +
Sbjct: 62 GEAYASLAHVRLHDWDVLERDFL-RAIELNPGHAIAYYWYAEYLMAGRAEDIAIARVR 120

Query: 444 HAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERAL 483
+ ++ PL+ + + A+ + A R+D A +AL
Sbjct: 121 QSQQMDPLNSV---LNSSVAIILYLARRYDQAREELNKAL 157

>gi|18310907|ref|NP_562841.1| (NC_003366) two-component response regulator [Clostridium
perfringens]
gi|18145589|dbj|BAB81631.1| (AP003192) two-component response regulator [Clostridium
perfringens]
Length = 265

Score = 38.1 bits (87), Expect = 0.27
Identities = 23/93 (24%), Positives = 47/93 (49%), Gaps = 4/93 (4%)

Query: 28 FG DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSE-S 86
F +++ E+ G+ + + P+ +DLL++L +S+D +L VWG +
Sbjct: 173 FNGLTINKLSHEVKLNGEELLSPEKYDLLIYLSSNEGIALSRDRILDNVWGYDYFGDIR 232

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
T+ ++I +R+ + D + I TV G++F
Sbjct: 233 TVDTNIKRLREKLLD---KANYIATVRGSGYKF 262

>gi|17231280|ref|NP_487828.1| (NC_003272) two-component response regulator [Nostoc sp. PCC 7120]
gi|17132922|dbj|BAB75487.1| (AP003594) two-component response regulator [Nostoc sp. PCC 7120]
Length = 238

Score = 38.1 bits (87), Expect = 0.27
Identities = 23/96 (23%), Positives = 46/96 (46%), Gaps = 1/96 (1%)

Query: 25 QFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVS 84
+ +F ++ E RE+T + +++ F++L L + S+ +L+Q +WG V
Sbjct: 135 RLIFKQLAINPEGREVTLNKPLNLTALEFNILHFLASHPGQAWSRPQLIQKIWGCYVVG 194

Query: 85 ESTITS-HINAVRKAIGDTGGEQRLIRTVARKGFRF 119
+ + HI +RK + I+TV G++F
Sbjct: 195 DGRVVDVHIGQLRKKLESSTSIPEFIKTVRGYGYKF 230

>gi|16080092|ref|NP_390918.1| (NC_000964) similar to two-component response regulator [YtsB]
[Bacillus subtilis]
gi|7444045|pir||G70000 two-component response regulator [YtsB] homolog ytsA - Bacillus
subtilis
gi|2293175|gb|AAC00253.1| (AF008220) signal transduction regulator [Bacillus subtilis]
gi|2635524|emb|CAB15018.1| (Z99119) similar to two-component response regulator [YtsB]
[Bacillus subtilis]
Length = 231

Score = 38.1 bits (87), Expect = 0.28
Identities = 18/58 (31%), Positives = 40/58 (68%), Gaps = 2/58 (3%)

Query: 43 RGQVSVSGPQVFDLLHLVGTDRDVSVDKDELLQAVWGG-RIVSESTITSHINAVRKAI 99
+G V ++F +L L+ +++VS++EL+++W R VS++T+T ++N +RK +
Sbjct: 148 KGSVELTKNEMF-ILKQLIEQKNKIVSREELIRSLWNDERFVSDNTLTNVNRLRKKL 204

>gi|15599296|ref|NP_252790.1| (NC_002516) probable two-component response regulator [Pseudomonas aeruginosa]
gi|11352341|pir|F83133 probable two-component response regulator PA4101 [imported] -
Pseudomonas aeruginosa (strain PA01)
gi|9950302|gb|AAG07488.1|AE004826_6 (AE004826) probable two-component response regulator [Pseudomonas aeruginosa]
Length = 246

Score = 37.7 bits (86), Expect = 0.30
Identities = 29/100 (29%), Positives = 50/100 (50%), Gaps = 2/100 (2%)

Query: 28 FGDYVLDQERRE-LTRRGQVSVSGPQVFDLLHLVGTDRDVSVDKDELLQAVWGGRI-VSE 85
FG + LD R L G VV++ + LL + RV+S+D+LL G + +
Sbjct: 142 FGQWQLDTSARHLDDAGTVVALSGAEYRLLRVFLDHPQVRVLSRDQLNLTLQGREADIFD 201

Query: 86 STITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDRI 125
+I ++ +R+ +GD E I+TV +G+ F +R+
Sbjct: 202 RSIDLLVSRRLRQLGDDAREPEYIKTVRSEGYVFSPLVRL 241

>gi|15964775|ref|NP_385128.1| (NC_003047) PUTATIVE TRANSCRIPTION REGULATOR PROTEIN [Sinorhizobium meliloti]
gi|15073953|emb|CAC45594.1 (AL591785) PUTATIVE TRANSCRIPTION REGULATOR PROTEIN [Sinorhizobium meliloti]
Length = 233

Score = 37.7 bits (86), Expect = 0.30
Identities = 27/108 (25%), Positives = 56/108 (51%), Gaps = 3/108 (2%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVSGPQVFDLLHLVGTDRDVSVDKDELLQ 75
+G P + ++ + GD LD+ + R+G+ + + P+ F LL +L+ +VV++ LL+
Sbjct: 123 KGAP-EQDMVYRVGDLELDRLSHSVRRQGKEIPLQPREFRLLLEYLMKNAGQVVTRTMLLE 181

Query: 76 AVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
VW ++ + H++ +R I + + L+RT+ G+ D
Sbjct: 182 NVWDYHFDPQTNVIDVHVSRLRSKI-EKDFDPPLRLTIRGAGYMIKDD 228

>gi|14140153|emb|CAC39070.1| (AJ307662) anaphase-promoting complex subunit 8-like protein [Oryza sativa]
Length = 616

Score = 37.7 bits (86), Expect = 0.31
Identities = 38/151 (25%), Positives = 67/151 (44%), Gaps = 14/151 (9%)

Query: 374 RRAVELGRDDAVALTRSGHALGHLVGDLGGIALIDRARLLNPNFAPAWFLGGFLRVFRG 433
+RA++L R A T GH L + I RA +NP AW+ G + G
Sbjct: 381 QRALKLNRKYLSAWTLMGHEFVEL-KNTPAAIDAYRRAVDINPRDYRAWYGLGQIYEMMG 439

Query: 434 EPESAIEHIEHAARLSPLDQEMFRMQAGTALAHFFAG----RFDSALVWAERALGNLPSL 489
P A+ + ++ L P D ++ A+A + + A+ ER+ N +
Sbjct: 440 MPFYAVVYFRKSSYLQPNDRALW-----NAMAQCYESDQLQMIEEAICYERSANNNDTE 494

Query: 490 LVAVALVAASHALAGRTEEA----RKTMRQL 516
+A+ +A H + G++EEA +K ++R+
Sbjct: 495 GIALHQLAKLHGMGLQSEEAFFYKKNLERM 525

>gi|17231314|ref|NP_487862.1| (NC_003272) two-component response regulator [Nostoc sp. PCC 7120]
gi|17132956|dbj|BAB75521.1| (AP003594) two-component response regulator [Nostoc sp. PCC 7120]
Length = 242

Score = 37.7 bits (86), Expect = 0.31
Identities = 26/94 (27%), Positives = 42/94 (44%), Gaps = 3/94 (3%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWG---GRIVSE 85
G+ +D +R++ + + + + F LL LV S+ E+LQ VWG R V
Sbjct: 140 GNIKIDTNKRQVYKGDRIIRLTGMEFSLLELLVSRSGEAFSRSEILQEVWGYTPERHVDT 199

Query: 86 STITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
+ HI+ +R + D LI T G+ F
Sbjct: 200 RVVDVHISRLRAKLEDDPSNPELILTARGTGYLE 233

>gi|19705092|ref|NP_602587.1| (NC_003454) Tetratricopeptide repeat family protein [Fusobacterium
nucleatum subsp. nucleatum ATCC 25586]
gi|19713016|gb|AAL93886.1| (AE010481) Tetratricopeptide repeat family protein [Fusobacterium
nucleatum subsp. nucleatum ATCC 25586]
Length = 628

Score = 37.7 bits (86), Expect = 0.32
Identities = 38/134 (28%), Positives = 57/134 (42%), Gaps = 11/134 (8%)

Query: 323 EAALPLFYRAIELDQEFASAYAGAACYFWRKLNQWMDRAEEIAEGARLARRAVELGRD 382
E A+ + RAIEL+ AS Y A Y+ D+A E + +A++L +
Sbjct: 44 EEAINDYNRAIELNLNNASYYNRCASYCSN----KYDKAIEDYD-----KAIKLNPN 93

Query: 383 DAVALTRSGHALGHLVGDLGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHI 442
DA GH+ L I D+A L+PN A ++ GF + + AIE
Sbjct: 94 DACYFNNRGRHSYFAL-NKYSEAIEDYDKAIKLDPNNASYYYKRGFSYYALNKYDKAIEDY 152

Query: 443 EHAARLSPLDQEMF 456
A +L P + F
Sbjct: 153 NKAIKLDPNNAAYF 166

>gi|1149660|emb|CAA60222.1| (X86502) hypC [Clostridium perfringens]
Length = 110

Score = 37.7 bits (86), Expect = 0.32
Identities = 23/93 (24%), Positives = 47/93 (49%), Gaps = 4/93 (4%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGGRIVSE-S 86
F +++ E+ G+ + + P+ +DLL++L +S+D +L VWG +
Sbjct: 18 FNGLTINKLSHEVKLNGEELLSPEYDLLIYLSSNEGIALSRDRILDNVWGYDYFGDIR 77

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
T+ ++I +R+ + D + I TV G++F
Sbjct: 78 TVDTNIKRLREKLLD---KANYIATVRGSGYKF 107

>gi|2613086|gb|AAB84277.1| (AF030315) OmpR [Enterobacter cloacae]
Length = 192

Score = 37.7 bits (86), Expect = 0.33
Identities = 29/107 (27%), Positives = 50/107 (46%), Gaps = 1/107 (0%)

Query: 17 GRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQA 76
G P E FG + L+ RE+ R + + + F +L LV +S+D+L+
Sbjct: 82 GAPSQEEAVIAFGKFKLNLGTREMFREDEPMPLTNGEFAVLKALVSHPREPLSRDKLMNL 141

Query: 77 VWGGRIVS-ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
G + E++I I+ +R+ + + R I+TV G+ FV D
Sbjct: 142 ARGREYSAMEASIDVQISRLRRMVEEDPAHPRIQTVWGLGYVFPD 188

>gi|7481652|pir||T34824 probable turgor pressure regulator kdpE - Streptomyces coelicolor
gi|2815358|emb|CAA16481.1| (AL021530) putative turgor pressure regulator [Streptomyces
coelicolor A3(2)]
Length = 227

Score = 37.7 bits (86), Expect = 0.33
Identities = 28/101 (27%), Positives = 50/101 (48%), Gaps = 1/101 (0%)

Query: 20 GDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWG 79

G+ EV ++ +D +++ R G+ V + P + LL LV R+VS+ +LLQ VWG
Sbjct: 125 GEDEVVVDTPFTVDLAAKVNRRGRDVRTPTEWHLLLEVLRNTGRLVVSQKQLLQEVWG 184

Query: 80 GRIVSEST-ITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
+E+ + ++ +R+ + R T G+RF

Sbjct: 185 PSYGTETNYLRVYMAQLRRKLEADPAHPRHFITEPGMGYRF 225

>gi|12483701|gb|AAG53726.1|AF176556_2 (AF176556) LrrrB [Lactococcus lactis]
Length = 236

Score = 37.7 bits (86), Expect = 0.34
Identities = 21/71 (29%), Positives = 42/71 (58%), Gaps = 1/71 (1%)

Query: 32 VLDQERRELTRRGQVVSQVQVFDLLHLVGTRDRVVSQKDELLQAVWGGRIVSES-TITS 90

V+D ++E+T +V+ + + F++L L + ++S++ELLQ WG +E+ TI
Sbjct: 148 VIDFTKKEVTFDAKVLDTLTKREFEILELLAKRQGEIISREELLQHFWSISDAETRTIDV 207

Query: 91 HINAVRKAIGD 101
I+ +RK + +

Sbjct: 208 LISKIRKKLNN 218

>gi|3288064|emb|CAB09801.1| (Z97065) RisA protein [Bordetella bronchiseptica]
gi|3288070|emb|CAA12131.1| (AJ224800) RisA protein [Bordetella avium]
gi|3288083|emb|CAA12132.1| (AJ224801) RisA protein [Bordetella parapertussis]
gi|3288101|emb|CAA12129.1| (AJ224798) RisA protein [Bordetella pertussis]
Length = 244

Score = 37.7 bits (86), Expect = 0.34
Identities = 30/107 (28%), Positives = 48/107 (44%), Gaps = 1/107 (0%)

Query: 17 GRPGDAEVQFMFGDYVLDQERRELTRRGQVVSQVQVFDLLHLVGTRDRVVSQKDELLQA 76
G P FG YVL+ R LTR G+ V + F +L +S+D+L++

Sbjct: 135 GAPSQENESIAFGPYVLNLSTRTLTRNGEQVPITTGFEFSVLKVFARHPKIPLSRDKLMEL 194

Query: 77 VWGGRIVS-ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
G + + ++ I+ +RK I + I+TV G+ FV D

Sbjct: 195 ARGREYEAFFDRSLDVQISRLRLKIEPNPSKPVFIQTVWGLGYVFPD 241

>gi|16272824|ref|NP_439045.1| (NC_000907) aerobic respiration control protein ARCA (arca)
[Haemophilus influenzae Rd]
gi|1168484|sp|P44918|ARCA_HAEIN Aerobic respiration control protein arca homolog
gi|1073828|pir||I64099 aerobic respiration control protein arca homolog - Haemophilus
influenzae (strain Rd KW20)
gi|1573901|gb|AAC22542.1| (U32770) aerobic respiration control protein ARCA (arca)
[Haemophilus influenzae Rd]
Length = 236

Score = 37.7 bits (86), Expect = 0.35
Identities = 31/120 (25%), Positives = 53/120 (43%), Gaps = 3/120 (2%)

Query: 6 ILFASCPDSEGRPGDAEVQFMFGDYVLDQERREL-TRRGQVVSQVQVFDLLHLVGTR 64
+L + P E+ E + F + LD L T GQ + F +LH

Sbjct: 117 LLHRAMPHQEKENTFGREF-YRFNGWKLDLNSHSLITPEGQEFKLPRSEFRAMLHFCENP 175

Query: 65 DRVVSQKDELLQAVWGGRIVSES-TITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 123

++ +++ELL+ + G + + T+ I +RK D +I T+ +G+RF GDI
Sbjct: 176 GKLQTRELLKKMTGRELKPDRTVDVTIRIRKHFEDHPNTPNIIMTIHGEGRFCGDI 235

>gi|17545795|ref|NP_519197.1| (NC_003295) PROBABLE TWO-COMPONENT SYSTEM RESPONSE REGULATOR
TRANSCRIPTION REGULATOR PROTEIN [Ralstonia solanacearum]
gi|17428089|emb|CAD14778.1| (AL646062) PROBABLE TWO-COMPONENT SYSTEM RESPONSE REGULATOR
TRANSCRIPTION REGULATOR PROTEIN [Ralstonia solanacearum]
Length = 251

Score = 37.7 bits (86), Expect = 0.35
Identities = 24/94 (25%), Positives = 48/94 (50%), Gaps = 1/94 (1%)

Query: 25 QFMFGDYVLDQERRELTRRGQVVSQVQVFDLLHLVGTRDRVVSQKDELLQAVWGGRIVS 84
+ G Y +D++ R + R +SV + F+L L L R++++ ++ A+WG +

Sbjct: 140 EIKLGHYTVDRQNRSIHLRETPLSVHAREFELALLLFANVGRILTRTDIELALWGRELSP 199

Query: 85 ES-TITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
S T+ +H++ +RK + T +R + GF

Sbjct: 200 YSRITDTHVSRLRKKLLLPENGLRLRAIYGHGF 233

>gi|15601292|ref|NP_232923.1| (NC_002506) DNA-binding response regulator [Vibrio cholerae]
gi|11278056|pir||H82447 DNA-binding response regulator VCA0532 [imported] - Vibrio cholerae
(group O1 strain N16961)
gi|9657939|gb|AAF96435.1| (AE004384) DNA-binding response regulator [Vibrio cholerae]
Length = 230

Score = 37.7 bits (86), Expect = 0.35
Identities = 27/99 (27%), Positives = 50/99 (50%), Gaps = 1/99 (1%)

Query: 23 EVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVVSKDELLQAVWGGRI 82
+ +F GD VLD +++T+ G+ V + +++L L +V++ ++L+ VWGG

Sbjct: 130 QTRFELGDLVLDLVLKQVTKAGEPVKLTKEYNILKLLAKNMGKVLTHKQILKEVWGGNY 189

Query: 83 VS-ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFV 120
V + H+ +R + D + R I T G+R V

Sbjct: 190 VEHHHYVRIHVAQLRHKVEDNPAQPRFILTENGVGYRLV 228

>gi|13122184|emb|CAC32360.1| (AL583945) putative two component system response regulator
[Streptomyces coelicolor]
Length = 271

Score = 37.7 bits (86), Expect = 0.36
Identities = 26/90 (28%), Positives = 46/90 (50%), Gaps = 3/90 (3%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDVVSKDELLQAVWGGRIVSESTI 88
GD LD++ E+TR G + + F+LL L+ RV+SK ++L VW ++ +

Sbjct: 177 GDLTLDEDSHEVTRSGDGIHLTATEFELLRFLMRNPRRVLSKAQILDRVWSYDFGGQANV 236

Query: 89 TS-HINAVRKAIGDTGGEQRLIRTVARKGF 117
+I+ +R+ I G + +I T G+

Sbjct: 237 VELYISYLRKI--DAGREPMIHTRRGAGY 264

>gi|16262974|ref|NP_435767.1| (NC_003037) putative response regulator of two-component system
[Sinorhizobium meliloti]
gi|14523624|gb|AAK65179.1| (AE007243) putative response regulator of two-component system
[Sinorhizobium meliloti]
Length = 240

Score = 37.7 bits (86), Expect = 0.36
Identities = 42/139 (30%), Positives = 61/139 (43%), Gaps = 18/139 (12%)

Query: 8 FASCPDSEGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRDV 67
+ S PD R E F D ++ R + R G VS+ F LLL L+ D V

Sbjct: 119 YGSRPDVSR-----EQIFRHADIEMNVTRIRVMRNGHAVSLALQFRLLLQLLSMPD V 172

Query: 68 VSKDELLQAVWGGRI-VSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDIRIG 126
S+D+L+ A W V T+ HI +R+A+ G + +IRTV G+ G

Sbjct: 173 HSRDDLIAAGWPPEAEVEPRTVDIHIGHIRRALNQFGPD--VIRTVRSIGYSLDG----- 225

Query: 127 GIGEVQPVGPGAALQASG 145
+ P G AL ++G

Sbjct: 226 ----LAAPGGKSGALHSAG 240

>gi|5713266|gb|AAD47875.1|AF170884_1 (AF170884) transmembrane regulatory protein ToxR [Vibrio
hollisae]
Length = 193

Score = 37.7 bits (86), Expect = 0.36
Identities = 21/83 (25%), Positives = 40/83 (47%), Gaps = 7/83 (8%)

Query: 83 VSESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGDIRIGGIGEVQPVGPGAALQ 142
V +S++T I+ +RK++ D+ ++TV ++G++ V + + EV P + +

Sbjct: 6 VDDSSLTQSISTLRKSLKDKSTKSPMFVKTPKRGYQVVCSEVYNEQEVELPEPAASVID 65

Query: 143 ASGGSGE-----TASALVLPD 158
+ E TA L LPD
Sbjct: 66 ETAAKKEPELLSDNTAQTLPD 88

>gi|15600078|ref|NP_253572.1| (NC_002516) two-component response regulator [Pseudomonas aeruginosa]
gi|11352748|pir||G83036 two-component response regulator PA4885 [imported] - Pseudomonas aeruginosa (strain PAO1)
gi|9951159|gb|AAG08270.1|AE004901_12 (AE004901) two-component response regulator [Pseudomonas aeruginosa]
Length = 229

Score = 37.7 bits (86), Expect = 0.37
Identities = 30/102 (29%), Positives = 49/102 (47%), Gaps = 1/102 (0%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVVSKEDELLQ 75
RG +AE Q D LD RR+++R+GQV+++ + F LL L+ V+S+ +
Sbjct: 117 RGVVREAE-QVQLADLQLDVLRRKVSRRGQVIALTNKEFALLHLLMRREGEVLSRTLIAS 175

Query: 76 AVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
VW S++ + +A D +LI TV G+
Sbjct: 176 EVWDMNFDSDTNVVDVAIKRLRAKVDNPFPPNKLIHTVRGIGY 217

>gi|15839123|ref|NP_299811.1| (NC_002488) two-component system, regulatory protein [Xylella fastidiosa 9a5c]
gi|11278060|pir||B82546 two-component system, regulatory protein XF2534 [imported] - Xylella fastidiosa (strain 9a5c)
gi|9107741|gb|AAF85331.1|AE004060_6 (AE004060) two-component system, regulatory protein [Xylella fastidiosa 9a5c]
Length = 225

Score = 37.7 bits (86), Expect = 0.37
Identities = 25/90 (27%), Positives = 46/90 (50%), Gaps = 1/90 (1%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVVSKEDELLQAVWGGRIVSESTI 88
GD + + E+ RRG+++ + P +L L+ VV++ +L VWG + ++
Sbjct: 131 GDLEYNLDTEVRRRGKLLQLNPTGLKILQALMEATPAVVTRQDLETRVWGEELPDSDSL 190

Query: 89 TSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
HI+ +R A+ D + LI+T G+R
Sbjct: 191 RVHIHGLR-AVVDKPFDPVLIQTRHGIGYR 219

>gi|15902120|ref|NP_357670.1| (NC_003098) Response regulator [Streptococcus pneumoniae R6]
gi|15457611|gb|AAK98880.1| (AE008392) Response regulator [Streptococcus pneumoniae R6]
Length = 232

Score = 37.4 bits (85), Expect = 0.38
Identities = 26/103 (25%), Positives = 53/103 (51%), Gaps = 3/103 (2%)

Query: 18 RPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVVSKEDELLQAV 77
R G+ E+ G+ ++ E+ +++ + + F+LL L +RV SK +L + +
Sbjct: 123 RGGETEL-ISLGNLKMNHSSHEVQIGEMLDLTVKSEFELLWILASNPVFSKTDLYEKI 181

Query: 78 WGGRIVSES-TITSHINAVRKAIGDTGGEQR-LIRTVARKGFR 118
W V ++ T+ HI+A+R+ + +Q I+TV G++
Sbjct: 182 WKEDYVDDTNTLNVIHALRQELAKYSSDQTPTIKTVWGLGYK 224

>gi|15610261|ref|NP_217640.1| (NC_000962) hypothetical protein Rv3124 [Mycobacterium tuberculosis H37Rv]
gi|7478883|pir||C70922 probable regulatoryprotein - Mycobacterium tuberculosis (strain H37RV)
gi|2076697|emb|CAB08381.1| (Z95150) hypothetical protein Rv3124 [Mycobacterium tuberculosis H37Rv]
Length = 289

Score = 37.4 bits (85), Expect = 0.38

Identities = 27/88 (30%), Positives = 49/88 (55%), Gaps = 4/88 (4%)

Query: 39 ELTRRGQVSVG-PQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSES--TITSHINAV 95
EL RG + +G P+ +L L+ +R++VV+ D L+QA+W + + T+ ++I +
Sbjct: 10 ELNLRGTKLPLGTPKQRAVLAMLLSRNQVVAADALVQAIWEKSPPARARRTVHTYICNL 69

Query: 96 RKAIGDTGGEQRLIRTVARKGFR-FVGD 122
R+ + D G + R I G+R +GD
Sbjct: 70 RRTLSDAGVDSRNILVSEPPGYRLLIGD 97

>gi|15614507|ref|NP_242810.1| (NC_002570) two-component response regulator [Bacillus halodurans]
gi|10174562|dbj|BAB05663.1| (AP001513) two-component response regulator [Bacillus halodurans]
Length = 229

Score = 37.4 bits (85), Expect = 0.38
Identities = 26/99 (26%), Positives = 49/99 (49%), Gaps = 5/99 (5%)

Query: 26 FMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSE 85
+ F + + R++ GQ +S+ + +DLL+ L+ R RV +++ L +WG
Sbjct: 133 YRFNELRIQPSGRKVFVNGQEISLTKEYDLLVFLLEHRGRVFTREHLHDRLWGMTQQG 192

Query: 86 S--TITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
+ T+ +HI +R + R I+TV G++F D
Sbjct: 193 TLRTVDTHIKTLRLKLKPA---DRFIKTVWGVGYKFEVD 228

>gi|15842697|ref|NP_337734.1| (NC_002755) transcriptional regulator, AfsR/DnrI/RedD family
[Mycobacterium tuberculosis CDC1551]
gi|13883017|gb|AAK47548.1| (AE007136) transcriptional regulator, AfsR/DnrI/RedD family
[Mycobacterium tuberculosis CDC1551]
Length = 311

Score = 37.4 bits (85), Expect = 0.39
Identities = 27/88 (30%), Positives = 49/88 (55%), Gaps = 4/88 (4%)

Query: 39 ELTRRGQVSVG-PQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSES--TITSHINAV 95
EL RG + +G P+ +L L+ +R++VV+ D L+QA+W + + T+ ++I +
Sbjct: 32 ELNLRGTKLPLGTPKQRAVLAMLLSRNQVVAADALVQAIWEKSPPARARRTVHTYICNL 91

Query: 96 RKAIGDTGGEQRLIRTVARKGFR-FVGD 122
R+ + D G + R I G+R +GD
Sbjct: 92 RRTLSDAGVDSRNILVSEPPGYRLLIGD 119

>gi|20090223|ref|NP_616298.1| (NC_003552) O-linked GlcNAc transferase [Methanosarcina
acetivorans
str. C2A]
gi|19915215|gb|AAM04778.1| (AE010806) O-linked GlcNAc transferase [Methanosarcina acetivorans
str. C2A]
Length = 400

Score = 37.4 bits (85), Expect = 0.40
Identities = 35/128 (27%), Positives = 54/128 (41%), Gaps = 11/128 (8%)

Query: 323 EAALPLFYRAIELDQEFASAYAGAACYFWRKLNQWMDRAEEIEGARLARRAVELGRD 382
E A+ + +A+EL ++ +A+ G A LN + +A E + +E D
Sbjct: 138 ERAVEAYGKALELRDPYNAWYGKA-----LN---LSQAGSYEEAVEAYEKVLEESPD 187

Query: 383 DAVALTRSGHALGHLVGDLDGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHI 442
A G ALG + G D I D+A ++P F AW+ G G A++
Sbjct: 188 YKEAWAGKGIALGQM-GRYDEAIIAYDKAIEIDPGFLEAWYYKGVLDLSLGSQRQALKAY 246

Query: 443 EHAARLSP 450
E A L P
Sbjct: 247 EKAVELDP 254

Score = 33.1 bits (74), Expect = 8.8
Identities = 50/199 (25%), Positives = 77/199 (38%), Gaps = 14/199 (7%)

Query: 323 EAALPLFYRAIELDQEFASAYAGAACYFWRKLNQWMDRAEEIEGARLARRAVELGRD 382

+ A+ + +AIE+D F AW Y G +D + + +AVEL +
Sbjct: 206 DEAIAYDKAIEIDPGFLE-----AWYY-----KGVLDLSLGSRRQALKAYEKAVELDPE 255
Query: 383 DAVALTRSGHALGHLVGDLDGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHI 442
+ A G L +L + I D+A +N + W+ GF E A+E
Sbjct: 256 NDDAWNNGIDLENL-EKYEEAINAFDKAIAINSSENSDVWYNKGFTLSQMHRFEEAVEAY 314
Query: 443 EHAARLSPLDQEMFRMQAGTALAHEFFAGRFDSALVWAERALGNLPSLLVAVALVAASHAL 502
A +L P E + G LA F+ AL E+AL + A +
Sbjct: 315 RKATQLDPEYLEAY-TSLGFVLAQL--KNFEEALETYEKALELDQGAADSWFGKAVCLSF 371
Query: 503 AGRTEEARKTMQRLRALDP 521
GR EEA ++ +DP
Sbjct: 372 LGREEEAEDAYRKAVIDP 390

>gi|79118|pir||S01366 regulatory protein ompR - Salmonella typhimurium
gi|47664|emb|CAA30934.1| (X12374) ompR regulatory protein (AA 1 - 239) [Salmonella
typhimurium]
gi|587570|emb|CAA55076.1| (X78270) ompR [Salmonella typhi]
Length = 239

Score = 37.4 bits (85), Expect = 0.41
Identities = 29/107 (27%), Positives = 49/107 (45%), Gaps = 1/107 (0%)

Query: 17 GRPGDAEVQFMFGDYVLDQERRELTRRGQVVSQVQVFDLLHLVGTDRVVSKEDELLQA 76
G P E FG + L+ RE+ R + + + F +L LV +S+D+L+
Sbjct: 129 GAPSQEEAVIAFGKFKLNLGTREMFREDEPMPLTSGEFAVLKALVSHPREPLSRDKLMNL 188
Query: 77 VWGGRIVS-ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
G + E +I I+ +R+ + + R I+TV G+ FV D
Sbjct: 189 ARGREYSAMERSIDVQISRLRRMVEEDPAHPRYIQTWVWGLGYVFPD 235

>gi|2108342|emb|CAA70146.1| (Y08950) OmpR protein [Yersinia enterocolitica]
Length = 239

Score = 37.4 bits (85), Expect = 0.42
Identities = 29/107 (27%), Positives = 49/107 (45%), Gaps = 1/107 (0%)

Query: 17 GRPGDAEVQFMFGDYVLDQERRELTRRGQVVSQVQVFDLLHLVGTDRVVSKEDELLQA 76
G P E FG + L+ RE+ R + + + F +L LV +S+D+L+
Sbjct: 129 GAPSQEETVIAFGKFKLNLGTREMFREDEPMPLTSGEFAVLKALVSHPREPLSRDKLMNL 188
Query: 77 VWGGRIVS-ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
G + E +I I+ +R+ + + R I+TV G+ FV D
Sbjct: 189 ARGREYSAMERSIDVQISRLRRMVEEDPAHPRYIQTWVWGLGYVFPD 235

>gi|15892516|ref|NP_360230.1| (NC_003103) petR protein [Rickettsia conorii]
gi|15619676|gb|AAL03131.1| (AE008620) petR protein [Rickettsia conorii]
Length = 226

Score = 37.4 bits (85), Expect = 0.43
Identities = 24/90 (26%), Positives = 44/90 (48%), Gaps = 3/90 (3%)

Query: 28 FGDYVLDQERRELTRRGQVVSQVQVFDLLHLVGTDRVVSKEDELLQAVWGGRIVSEST 87
FG+ + + +E T+ Q+VS+ LL L+ + S+ EL + + G +S +
Sbjct: 136 FGNNFYNSDTKEFTKNNQIVSLSTEQKLEILIKNSGKSTSRFELS KIMGG---LSMRS 192
Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
I I +R I D E + ++TV +G+
Sbjct: 193 IDVQITRIRSKIEDNPKEPKYLKTVRNEGY 222

>gi|17942992|pdb|1KGS|A Chain A, Crystal Structure At 1.50 A Of An OmpRPHOB HOMOLOG FROM
Thermotoga Maritima
Length = 225

Score = 37.4 bits (85), Expect = 0.43
Identities = 21/82 (25%), Positives = 42/82 (50%), Gaps = 1/82 (1%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVVSQVQVFDLLHLVGTDRVVSKEDELLQ 75

R + + + GD +LD ++ R + + + + +L +LV ++RVV+K+EL +
Sbjct: 119 RRKSESSTKLVCGLDITATKKAYRGSKEIDLTKKEYQILEYLVXNKNRVVTKEELQE 178

Query: 76 AVWG-GRIVSESTITSHINAVR 96
+W V + SHI +R
Sbjct: 179 HLWSFDDEVFSDVLRSHIKNLR 200

>gi|16264749|ref|NP_437541.1| (NC_003078) putative two component response regulator protein
[Sinorhizobium meliloti]
gi|15140887|emb|CAC49401.1| (AL603645) putative two component response regulator protein
[Sinorhizobium meliloti]
Length = 232

Score = 37.4 bits (85), Expect = 0.43
Identities = 32/107 (29%), Positives = 51/107 (46%), Gaps = 3/107 (2%)

Query: 16 RGRPGDAEV--QFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDEL 73
R R G A V FG +D R + G+ ++ FD+L+ L R +S+++L
Sbjct: 118 RRRNGSAAVARTLRFGRLEIDPGSRVSRIDGRECTLSYQFDVLVALAENPGRTLSREQL 177

Query: 74 LQAVWGGRIVS-ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
+ AV G + + + +I HI+ +R AI R I TV G+ F
Sbjct: 178 MDAVKGEEELDAFDRSIDVHISRIRAAIESDPKHPRIITVRGAGYVF 224

>gi|15803909|ref|NP_289945.1| (NC_002655) response regulator (sensor, EnvZ) affecting
transcription of ompC and ompF: outer membrane protein
synthesis [Escherichia coli O157:H7 EDL933]
gi|15833501|ref|NP_312274.1| (NC_002695) response regulator OmpR [Escherichia coli O157:H7]
gi|16131282|ref|NP_417864.1| (NC_000913) response regulator (sensor, EnvZ) affecting
transcription of ompC and ompF: outer membrane protein
synthesis [Escherichia coli K12]
gi|16762785|ref|NP_458402.1| (NC_003198) two-component response regulator OmpR [Salmonella
enterica subsp. enterica serovar Typhi]
gi|16766790|ref|NP_462405.1| (NC_003197) response regulator in two-component regulatory system
with EnvZ, affecting transcription of ompC and ompF
(OmpR family) [Salmonella typhimurium LT2]
gi|129158|sp|P03025|OMPR_ECOLI Transcriptional regulatory protein ompR
gi|7429063|pir||RGECOR osmosensor response regulator ompR - Escherichia coli
gi|453287|gb|AAA16241.1| (J01656) OmpR protein [Escherichia coli]
gi|602089|emb|CAA54510.1| (X77305) ompR [Salmonella typhi]
gi|606339|gb|AAA58202.1| (U18997) CG Site No. 434; alternate name ompB [Escherichia coli]
gi|1789809|gb|AAC76430.1| (AE000416) response regulator (sensor, EnvZ) affecting
transcription of ompC and ompF: outer membrane protein
synthesis [Escherichia coli K12]
gi|12518032|gb|AAG58506.1|AE005562.9 (AE005562) response regulator (sensor, EnvZ) affecting
transcription of ompC and ompF: outer membrane protein
synthesis [Escherichia coli O157:H7 EDL933]
gi|13276842|emb|CAC34268.1| (AJ288905) OmpR protein [Shigella flexneri]
gi|13363721|dbj|BAB37670.1| (AP002565) response regulator OmpR [Escherichia coli O157:H7]
gi|16422061|gb|AAL22364.1| (AE008861) response regulator in two-component regulatory system
with EnvZ, affecting transcription of ompC and ompF
(OmpR family) [Salmonella typhimurium LT2]
gi|16505091|emb|CAD08112.1| (AL627281) two-component response regulator OmpR [Salmonella
enterica subsp. enterica serovar Typhi]
Length = 239

Score = 37.4 bits (85), Expect = 0.44
Identities = 29/107 (27%), Positives = 49/107 (45%), Gaps = 1/107 (0%)

Query: 17 GRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQA 76
G P E FG + L+ RE+ R + + + F +L LV +S+D+L+
Sbjct: 129 GAPSQEEAVIAFGKFKLNLGTREMFREDEPMLTSGEFAVLKALVSHPREPLSRDKLMNL 188

Query: 77 VWGGRIVS-ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
G + E +I I+ +R+ + + R I+TV G+ FV D
Sbjct: 189 ARGREYSAMERSIDVQISRLRMVEEDPAHPRIYQTVWGLGYVFPD 235

>gi|2613088|gb|AAB84278.1| (AF030316) OmpR [Yersinia enterocolitica]
Length = 192

Score = 37.4 bits (85), Expect = 0.44
Identities = 29/107 (27%), Positives = 49/107 (45%), Gaps = 1/107 (0%)

Query: 17 GRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQA 76
G P E FG + L+ RE+ R + + + F +L LV +S+D+L+
Sbjct: 82 GAPSQEEAVIAFGKFKLNLGTREMFREDEPMPLTSGEFAVLKALVSHPREPLSRDKLMNL 141

Query: 77 VWGGRIVS-ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
G + E +I I+ +R+ + + R I+TV G+ FV D
Sbjct: 142 ARGREYSAMERSIDVQISRLRRMVEEDPAHPRIQTVWGLGYVFVDP 188

>gi|16804460|ref|NP_465945.1| (NC_003210) similar to two-component response regulator [Listeria monocytogenes EGD-e]
gi|16411910|emb|CAD00500.1| (AL591983) similar to two-component response regulator [Listeria monocytogenes]
Length = 231

Score = 37.4 bits (85), Expect = 0.44
Identities = 22/93 (23%), Positives = 47/93 (49%), Gaps = 1/93 (1%)

Query: 27 MFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSES 86
+ G V+D+ +T G+ + + FD+L L RV S + + + +W + + S
Sbjct: 136 IIGPIVVDRGLHVTVGGKELHLLTSEFDILFLLASEPGRVFSSEYIFEKIWQEKALGAS 195

Query: 87 -TITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
T+ HI+ +R + + G + +I+T+ G++
Sbjct: 196 KTMVHISNLRDKLREAMGGENVIKTIWGVGYK 228

>gi|15602084|ref|NP_245156.1| (NC_002663) ArcA [Pasteurella multocida]
gi|12720444|gb|AAK02303.1| (AE006056) ArcA [Pasteurella multocida]
Length = 236

Score = 37.4 bits (85), Expect = 0.45
Identities = 25/101 (24%), Positives = 47/101 (45%), Gaps = 2/101 (1%)

Query: 25 QFMFGDYVLDQERRELTR-RGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIV 83
Q+ F + LD R L G+ + F +LH ++ +++ELL+ + G +
Sbjct: 135 QYRFNGWTLNLNSRTLINPEGEEYKLPSEFRAMLHFCENPGKIQTRELLKKMTGRELK 194

Query: 84 SES-TITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 123
+ T+ I +RK D +I T+ +G+RF G++
Sbjct: 195 PQDRTVDVTIRIRKHFEDHPETPEIIATIHGEGYRFCGEL 235

>gi|16764820|ref|NP_460435.1| (NC_003197) response regulator in two-component regulatory system with RstB (OmpR family) [Salmonella typhimurium LT2]
gi|16419994|gb|AAL20394.1| (AE008764) response regulator in two-component regulatory system with RstB (OmpR family) [Salmonella typhimurium LT2]
Length = 243

Score = 37.4 bits (85), Expect = 0.46
Identities = 24/93 (25%), Positives = 45/93 (47%), Gaps = 1/93 (1%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVS-ES 86
FG +D R + G +S+ F+LL L +++ +D LL+ + G +
Sbjct: 141 FGALTIDPLNRAVQLNGDFISLSTADFELLWELATHAGQIMDRDALLKTLRGVNYDGLDR 200

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
++ I+ +RK + D+ E I+T+ KG+ F
Sbjct: 201 SVDVAISRLRKKLLDSAAEPYRIKTI RNKG YLF 233

>gi|15900027|ref|NP_344631.1| (NC_003028) DNA-binding response regulator [Streptococcus pneumoniae TIGR4]
gi|5830538|emb|CAB54578.1| (AJ006397) response regulator [Streptococcus pneumoniae]
gi|14971549|gb|AAK74271.1| (AE007325) DNA-binding response regulator [Streptococcus pneumoniae TIGR4]
Length = 232

Score = 37.4 bits (85), Expect = 0.46

Identities = 26/103 (25%), Positives = 53/103 (51%), Gaps = 3/103 (2%)

Query: 18 RPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSKDELLQAV 77
R G+ E+ G+ ++ E+ +++ + + F+LL L +RV SK +L + +
Sbjct: 123 RGGETEL-ISLGNLKMNHSSHEVQIGEEMDLTVKSFELLWILASNPVFSKTDLYEKI 181

Query: 78 WGGRIVSES-TITSHINAVRKAIGDTGGEQR-LIRTVARKGFR 118
W V ++ T+ HI+A+R+ + +Q I+TV G++
Sbjct: 182 WKEDYVDDTNTLVNHIHALRQELAKYSSDQTPTIKTVWGLGYK 224

>gi|16760440|ref|NP_456057.1| (NC_003198) putative two-component response regulator [Salmonella enterica subsp. enterica serovar Typhi]
gi|16502736|emb|CAD01892.1| (AL627271) putative two-component response regulator [Salmonella enterica subsp. enterica serovar Typhi]
Length = 243

Score = 37.4 bits (85), Expect = 0.46
Identities = 24/93 (25%), Positives = 45/93 (47%), Gaps = 1/93 (1%)

Query: 28 FG DYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSKDELLQAVWGGRIVS-ES 86
FG +D R + G +S+ F+LL L +++ +D LL+ + G +
Sbjct: 141 FGALTIDPLNRAVQLNGDFISLSTADFELLWELATHAGQIMDRDALLKTLRGVNYDGLDR 200

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFRF 119
++ I+ +RK + D+ E I+T+ KG+ F
Sbjct: 201 SVDVAISRLRKKLLDSAAEPYRIKTIRNKGYLEF 233

>gi|16120479|ref|NP_403792.1| (NC_003143) transcriptional regulatory protein [Yersinia pestis]
gi|15978241|emb|CAC88999.1| (AJ414141) transcriptional regulatory protein [Yersinia pestis]
Length = 239

Score = 37.4 bits (85), Expect = 0.48
Identities = 29/107 (27%), Positives = 49/107 (45%), Gaps = 1/107 (0%)

Query: 17 GRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSKDELLQA 76
G P E FG + L+ RE+ R + + + F +L LV +S+D+L+
Sbjct: 129 GAPSQEEAIIAFGKFKLNLGTREMFREDEPMPLTSGEFAVLKALVSHPREPLSRDKLMNL 188

Query: 77 VWGGRIVS-ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
G + E +I I+ +R+ + + R I+TV G+ FV D
Sbjct: 189 ARGREYSAMERSIDVQISRLRMVEEDPAHPRYIQTWGLGYVFPD 235

>gi|15828317|ref|NP_302580.1| (NC_002677) probable two-component system response regulator [Mycobacterium leprae]
gi|1731206|sp|P54884|RGX3_MYCLE Sensory transduction protein regX3
gi|2145927|pir||S72906 phosphate sensor phoP - Mycobacterium leprae
gi|467058|gb|AAA17242.1| (U00018) phoP; B2168_C3_248 [Mycobacterium leprae]
gi|13094010|emb|CAC31956.1| (AL583925) probable two-component system response regulator [Mycobacterium leprae]
Length = 198

Score = 37.4 bits (85), Expect = 0.48
Identities = 25/88 (28%), Positives = 46/88 (51%), Gaps = 4/88 (4%)

Query: 16 RGRPGDAEVQ---FMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVSKDE 72
RG D+E+ G +D ER ++ G +++ + FDLL +L+ RV+++ +
Sbjct: 89 RGGDDDDSEISDGVLESGPLRMDVERHVSVNGYAITLPLKEFDLLEYLMRNSGRVLRGQ 148

Query: 73 LLQAVWGGRIVSES-TITSHINAVRKAI 99
L+ VWG V ++ T+ H+ +R I
Sbjct: 149 LIDRVWGVYVGDTKTLDVHVKRLRSKI 176

>gi|16262977|ref|NP_435770.1| (NC_003037) putative response regulator of two-component system [Sinorhizobium meliloti]
gi|14523627|gb|AAK65182.1| (AE007243) putative response regulator of two-component system [Sinorhizobium meliloti]
Length = 249

Score = 37.0 bits (84), Expect = 0.49

Identities = 30/106 (28%), Positives = 49/106 (45%), Gaps = 2/106 (1%)

Query: 13 DSEGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDE 72
D + P E +FG ++ RR + + G F+LL L+ RV S+ E
Sbjct: 136 DKQPTDPAREETAATFAGALRIEGRRLVRYGDEGAQFGRIEFNLLRCLLEAPGRVRSRLE 195

Query: 73 LLQAVW-GGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
L++A W R V T+ H+ +R+ + G + LIRT+ G+
Sbjct: 196 LIEAAWPSNRYVQPRTVDVHVARLRRELERLTG-RPLIRTIRATGY 240

>gi|16081218|ref|NP_393517.1| (NC_002578) 72K mitochondrial outer membrane protein related
protein [Thermoplasma acidophilum]
gi|10639185|emb|CAC11187.1| (AL445063) 72K mitochondrial outer membrane protein related protein
[Thermoplasma acidophilum]
Length = 201

Score = 37.0 bits (84), Expect = 0.51
Identities = 27/90 (30%), Positives = 45/90 (50%), Gaps = 3/90 (3%)

Query: 432 RGEPEAIEHIEHAARLSPLDQEMFRMQAGTALAHEFFAGRFDSALVWAERALGNLPSLLV 491
+G+ + A+E AA L DQ +F + AL + GR + AL E+A+ +P+
Sbjct: 96 KGDVDKALEDYSKAADLDSTDQ-IFVYKKEALMNL--GRLEALATIEKAIKIVPANYN 152

Query: 492 AVALVAASHALAGRTEEARKTMQRLRALDP 521
+ + A GR EEA + ++ + LDP
Sbjct: 153 YLLMKADVLIRMGRKEEASEVIEVEKLDLP 182

Score = 34.3 bits (77), Expect = 3.8
Identities = 35/138 (25%), Positives = 63/138 (45%), Gaps = 11/138 (7%)

Query: 322 IEAALPLFYRAIELDQEFASAYAGAACYFWRKLNWMDRAEEIAEGARLARRAVELGR 381
++ A+ F AI+++ + Y Y W+K + VD+A E +A +L
Sbjct: 65 VDKAIQEFETAARKIENDIPDYNNRGDAY-WKKGD---VDKALEDYS-----KAADLDS 114

Query: 382 DDAVALTRSGHALGHLVGDLGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEH 441
D + + + AL +L G L+ +A I++A + P + + + G E A E
Sbjct: 115 TDQIFVYKKEALMNL-GRLEALATIEKAIKIVPANYNLLMKADVLIRMGRKEEASEV 173

Query: 442 IEHAARLSPLDQEMFRMQ 459
IE +L P +QE R++
Sbjct: 174 IEEVEKLDPGNQEAERLR 191

>gi|496695|emb|CAA56022.1| (X79489) CDC27 D-618 protein [Saccharomyces cerevisiae]
Length = 618

Score = 37.0 bits (84), Expect = 0.52
Identities = 49/200 (24%), Positives = 80/200 (39%), Gaps = 16/200 (8%)

Query: 323 EAALPLFYRAIELDQEFASAYAGAACYFWRKLNWMDRAEEIAEGARLARRAVELGRD 382
+AA+ F +A +LD FA AY L G + R+A+
Sbjct: 417 DAAIKAFKATQLDPNFAYAYT-----LQGHEHSSNDSSDSAKTCYRKALACDPQ 466

Query: 383 DAVALTRSGHALGHLVGDLGGIALIDRARLLNP-NFAPAWFLGGFLRVFRGEPESAIEH 441
A G + L G + + ++AR +NP N GG L G E A+++
Sbjct: 467 HYNAYYGLGTSAMKL-GQYEEALLYFEKARSINPVNVVLICCCGGSLEKL-GYKEKALQY 524

Query: 442 IEHAARLSPLDQEMFRMQAGTALAHEFFAGRFDSALVWAERALGNLPSLLVAVALVAASHA 501
E A L P + + + G L + R++ AL E + +P A L+ ++
Sbjct: 525 YELACHLQP-TSSLSKYKMGQLL--YSMTRYNVALQTFEELVKLVLPDDATAHYLLGQTYR 581

Query: 502 LAGRTEEARKTMQRLRALDP 521
+ GR ++A K + LDP
Sbjct: 582 IVGRKKDAIKELTVAMNLDLP 601

Score = 34.7 bits (78), Expect = 3.0
Identities = 31/127 (24%), Positives = 52/127 (40%), Gaps = 3/127 (2%)

Query: 400 DLDGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQ 459
D D I ++A L+PNFA A+ L G +SA A P + +
Sbjct: 415 DHDAAIKAFKATQLDPNFAYAYTLQGHEHSSNDSSDSAKTCYRKALACDP---QHYNAY 471

Query: 460 AGTALAHFFAGRFDSALVWAERALGNLPSLLVAVALVAASHALAGRTEEARKTMQRLRAL 519
G + G+++ AL++ E+A P +V + S G E+A + + L
Sbjct: 472 YGLGTSAMKLGQYEEALLYFEKARSINPVNVVLICCCGGSLEKLGKEKALQYYELACHL 531

Query: 520 DPSLRVS 526
P+ +S
Sbjct: 532 QPTSSLS 538

>gi|6319387|ref|NP_009469.1| (NC_001134) Protein required for cell cycle; Cdc27p [Saccharomyces cerevisiae]
gi|584897|sp|P38042|CC27_YEAST Cell division control protein 27
gi|626118|pir||S45825 cell division control protein CDC27 - yeast (Saccharomyces cerevisiae)
gi|536136|emb|CAA84905.1| (Z35845) ORF YBL084c [Saccharomyces cerevisiae]
Length = 758

Score = 37.0 bits (84), Expect = 0.52
Identities = 49/200 (24%), Positives = 80/200 (39%), Gaps = 16/200 (8%)

Query: 323 EAALPLFYRAIELDQEFASAYAGAAWCYFWRKLNQWVDRAEEIAEGARLARRAVELGRD 382
+AA+ F +A +LD FA AY L G + R+A+
Sbjct: 557 DAAIKAFKATQLDPNFAYAYT-----LQGHEHSSNDSSDSAKTCYRKALACDPQ 606

Query: 383 DAVALTRSGHALGHLVGDLGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEH 441
A G + L G + + ++AR +NP N GG L G E A+++
Sbjct: 607 HYNAYYGLGTSAMKL-GQYEEALLYFEKARSINPVNVVLICCCGGSLEKL-GYKEKALQY 664

Query: 442 IEHAARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALGNLPSLLVAVALVAASHA 501
E A L P + + + G L + R++ AL E + +P A L+ ++
Sbjct: 665 YELACHLQP-TSSLSKYKMGQLL--YSMTRYNVALQTFEELVKLVDPDDATAHYLLGQTYR 721

Query: 502 LAGRTEEARKTMQRLRALDP 521
+ GR ++A K + LDP
Sbjct: 722 IVGRKKDAIKELTVAMNLDLP 741

Score = 34.7 bits (78), Expect = 3.0
Identities = 31/127 (24%), Positives = 52/127 (40%), Gaps = 3/127 (2%)

Query: 400 DLDGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMFRMQ 459
D D I ++A L+PNFA A+ L G +SA A P + +
Sbjct: 555 DHDAAIKAFKATQLDPNFAYAYTLQGHEHSSNDSSDSAKTCYRKALACDP---QHYNAY 611

Query: 460 AGTALAHFFAGRFDSALVWAERALGNLPSLLVAVALVAASHALAGRTEEARKTMQRLRAL 519
G + G+++ AL++ E+A P +V + S G E+A + + L
Sbjct: 612 YGLGTSAMKLGQYEEALLYFEKARSINPVNVVLICCCGGSLEKLGKEKALQYYELACHL 671

Query: 520 DPSLRVS 526
P+ +S
Sbjct: 672 QPTSSLS 678

>gi|7669466|gb|AAF66142.1| (U81488) putative response regulator [Lactococcus lactis subsp. cremoris]
Length = 228

Score = 37.0 bits (84), Expect = 0.53
Identities = 30/98 (30%), Positives = 50/98 (50%), Gaps = 7/98 (7%)

Query: 31 YVLDQERRELTRR-----GQVVSVGPOVFDLLHLVGTRDRVVSKEDELLQAVWGGRI-VS 84
Y LD + +LT G+ V++ + F LL + + R VVS+ ++L VWG
Sbjct: 131 YELDYLKVDLTAHTTEVAGKTVNLTQREFALLSYFLEHRGIVVSRADILDDVWGMDFDQ 190

Query: 85 ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
E+T+ +++ +R I D + LI TV G+R G+
Sbjct: 191 ENTVDAYVRYLRATI-DLPNHKS LIETVRGVGYRLNGE 227

>gi|2194039|pdb|1ODD| Ompr C-Terminal Domain (Ompr-C) From Escherichia Coli
Length = 118

Score = 37.0 bits (84), Expect = 0.54
Identities = 29/107 (27%), Positives = 49/107 (45%), Gaps = 1/107 (0%)

Query: 17 GRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQA 76
G P E FG + L+ RE+ R + + + F +L LV +S+D+L+
Sbjct: 8 GAPSQEEAVIAFGKFKLNLGTREMFREDEPMPLTSGEFAVLKALVSHPREPLSRDKLMNL 67

Query: 77 VWGGRIVS-ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
G + E +I I+ +R+ + + R I+TV G+ FV D
Sbjct: 68 ARGREYSAMERSIDVQISRLRRMVEEDPAHPRYIQTWGLGYVFPD 114

>gi|18311346|ref|NP_563280.1| (NC_003366) two-component response regulator [Clostridium
perfringens]
gi|18146030|dbj|BAB82070.1| (AP003194) two-component response regulator [Clostridium
perfringens]
Length = 232

Score = 37.0 bits (84), Expect = 0.55
Identities = 23/90 (25%), Positives = 43/90 (47%), Gaps = 1/90 (1%)

Query: 30 DYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGGGRIV-SESTI 88
D +D +++++ RG+ + + + +L L R+ S E+ + VW SE+T+
Sbjct: 140 DLTIDTVNKQVSLRGENIKLTATEYKILTLASHPGRIFSIKEIYERVWEEPFYKSENTV 199

Query: 89 TSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
T HI +R+ I E I+ V G++
Sbjct: 200 TVHIRRMREKIEINSKEPEYIKVVWGLGYK 229

>gi|6117972|gb|AAF03932.1|AF139908_2 (AF139908) LisR [Listeria monocytogenes]
Length = 226

Score = 37.0 bits (84), Expect = 0.55
Identities = 23/104 (22%), Positives = 52/104 (49%), Gaps = 2/104 (1%)

Query: 15 ERGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELL 74
E + + + ++++E R + R +++ + + +LLL L+ + V++++ LL
Sbjct: 120 ENAEQSAKQTTQLQYRNLIKEKNRIVKRDEEIIDLTREYELLTLMENVNIVLTREVLL 179

Query: 75 QAVWGGGRIVSESTITS-HINAVRKAIGDTGGEQRLIRTVARKGF 117
VWG E+ + ++ +R I D E+ I+TV G+
Sbjct: 180 NKVWGYETEVEETNVVDVYVRYLRNKI-DHPDEESYIQTVRGTGY 222

>gi|2076608|emb|CAB08413.1| (Z95151) unknown [Mycobacterium leprae]
Length = 120

Score = 37.0 bits (84), Expect = 0.56
Identities = 30/100 (30%), Positives = 50/100 (50%), Gaps = 9/100 (9%)

Query: 17 GRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQA 76
GR + F D LD+E E + ++VS+ P F LL +V V++ +L
Sbjct: 15 GRAAPCTARLSFADVELDEETHEAWKADELVSLSPTFTLLRCVVINAGTVLNTPNILDH 74

Query: 77 VW----GGRIVSESTITSHINAVRKAIGDTGGEQRLIRTV 112
VW GG + + + S++ +R+ I DT E+RL+ T+
Sbjct: 75 VWCYRFGGPV---NMVESYVLYLRRQI-DT-REKRLHL 109

>gi|17351934|gb|AAL38203.1|AF319447_1 (AF319447) putative response regulator RR96 [Listeria
monocytogenes]
Length = 232

Score = 37.0 bits (84), Expect = 0.56
Identities = 22/91 (24%), Positives = 46/91 (50%), Gaps = 1/91 (1%)

Query: 29 GDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGGGRIVSES-T 87
G V+D+ +T G+ + + FD+L L RV S + + + +W + + S T

Sbjct: 139 GPIVVDRLHVVTVGGKELHLLTTFEFDILFLLASEPGRVFSSEYIFEKIWQEKALGASKT 198

Query: 88 ITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
+ HI+ +R + + G + +I+T+ G++

Sbjct: 199 VMVHISNLRDKLREAMGGENVIKTIWGVGYK 229

>gi|18309822|ref|NP_561756.1| (NC_003366) two-component response regulator [Clostridium perfringens]
gi|18144500|dbj|BAB80546.1| (AP003188) two-component response regulator [Clostridium perfringens]
Length = 222

Score = 37.0 bits (84), Expect = 0.56
Identities = 19/77 (24%), Positives = 42/77 (53%), Gaps = 1/77 (1%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGGR-VSES 86
+GD L+ ++ RG+ + +L HL+ + VVS+++L+ +W I V ++

Sbjct: 130 YGDLKLNLSNGTISCRGKEELTKNELKILSHLLKNKGNVVSREDLMDYMWNSDIFVDDN 189

Query: 87 TITSHINAVRKAIGDTG 103
T++ ++ +RK + + G

Sbjct: 190 TLSVNVTRLRKKLEEVG 206

>gi|541208|pir||S41887 ompR protein - Salmonella typhi
Length = 239

Score = 37.0 bits (84), Expect = 0.57
Identities = 29/107 (27%), Positives = 48/107 (44%), Gaps = 1/107 (0%)

Query: 17 GRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQA 76
G P E FG + L+ RE+ R + + + F +L LV +S+D L+

Sbjct: 129 GAPSQEEAVIAFGKFKLNLGTREMFREDEPMPLTSGEFAVLKALVSHPREPLSRDNLMLN 188

Query: 77 VWGGRIVS-ESTITSHINAVRKAIGDTGGEQRLIRTVARKGFRFVGD 122
G + E +I I+ +R+ + + R I+TV G+ FV D

Sbjct: 189 ARGREYSAMERSIDVQISRLRMVEEDPAHPRIQTVWGLGYVFVDP 235

>gi|7481739|pir||T36369 response regulator - Streptomyces coelicolor
gi|3980223|emb|CAA10325.1| (AJ131213) response regulator [Streptomyces coelicolor A3(2)]
gi|4585590|emb|CAB40858.1| (AL049628) response regulator [Streptomyces coelicolor A3(2)]
Length = 234

Score = 37.0 bits (84), Expect = 0.59
Identities = 29/92 (31%), Positives = 43/92 (46%), Gaps = 6/92 (6%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWG-GRIVSES 86
FGD +D + E+ R G+ V + P LLL V+S+D+LL+ VW G

Sbjct: 145 FGDLEVDTDGMEVRRAGRPVGLTPTEMLLLEFSSAPGTVLSRDKLLERVWDYGWGGDTR 204

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
+ H+ +R IG Q I TV G++

Sbjct: 205 VVDVHVQRLRTKIG-----QDRIETVRGFGYK 231

>gi|15893516|ref|NP_346865.1| (NC_003030) Response regulator (CheY-like receiver domain and HTH DNA-binding domain) [Clostridium acetobutylicum]
gi|15023057|gb|AAK78205.1|AE007535_7 (AE007535) Response regulator (CheY-like receiver domain and HTH DNA-binding domain) [Clostridium acetobutylicum]
Length = 223

Score = 37.0 bits (84), Expect = 0.61
Identities = 19/91 (20%), Positives = 48/91 (51%), Gaps = 3/91 (3%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGGR-IVSES 86
F D ++ + + + + F ++ L+ D +VS+++++Q +W + ++

Sbjct: 132 FKDVIIISLKNNTVYYNENSIELTKNEFKIIYVLMKNHDSIVSREKIMQELWQDESFDIDN 191

Query: 87 TITSHINAVRKAIGDTGGEQRLIRTVARKGF 117
T+T +IN +RK + + G + I+T+ +G+

Sbjct: 192 TLTVNINRLRKKLKEIGVD--FIKTIKGQGY 220

>gi|13472041|ref|NP_103608.1| (NC_002678) hypothetical protein [Mesorhizobium loti]
gi|14022786|dbj|BAB49394.1| (AP002999) hypothetical protein [Mesorhizobium loti]
Length = 551

Score = 37.0 bits (84), Expect = 0.62
Identities = 27/98 (27%), Positives = 47/98 (47%), Gaps = 3/98 (3%)

Query: 360 VDRAEEIAEGARLARRAVELGRDDAVA-LTRSGHALGHLVGDLDGGIALIDRARLLNPNF 418
V+ A +IA + E + A A R+G + GD D A D+A +NP

Sbjct: 37 VEAHKIAACTAIIEDKAEASDNRAAYFNAGALIRR--GDNDADAFADYDKAIGINPEL 94

Query: 419 APAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMF 456
+ A++ G + V +G+ + AI +++ A L P + E +

Sbjct: 95 SAAYYNGIILVLKGDYDRAITYLDQAIFLDPDNAEFY 132

Score = 33.1 bits (74), Expect = 7.5
Identities = 50/181 (27%), Positives = 76/181 (41%), Gaps = 24/181 (13%)

Query: 300 SLD AHD---YYLRGMAKLHSGTHEAIEAALPLFYRAIELDQEFASAY--AGAAWCYFWRK 354
SLD D Y +G+A L G + A+ F AI LD + A+AY G W RK

Sbjct: 259 SLDPDTPSIRYKGLAWLRKGDG---DRAIDFDEAIRLDPKMAAAYYDRGTEWL---RK 312

Query: 355 LNGWMVDRAEEIAEGARLARRAVELGRDDAVALTRSGHALGHLVGDLDGGIALIDRARLL 414
DR I + + + + L +A+AL G L L G+ + +A ++RA L

Sbjct: 313 -----GDRDRAITDYSEV----ITLEPTNAMALNDRGFVLNEL-GEYERALADLNRAIGL 362

Query: 415 NPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQEMFERMQAGTALAHFFAGRFDS 474
+P A + R +G+ A+ A L P + AG +F++G

Sbjct: 363 DPKQAKIYSNRAIARAAGKDFAPALADYNQAIALDPNFPNAY---AGRGFVNIFYSGMLAK 419

Query: 475 A 475

A

Sbjct: 420 A 420

>gi|15643165|ref|NP_228209.1| (NC_000853) response regulator [Thermotoga maritima]
gi|7444051|pir|H72382 response regulator - Thermotoga maritima (strain MSB8)
gi|4980903|gb|AAD35484.1|AE001719_10 (AE001719) response regulator [Thermotoga maritima]
Length = 225

Score = 37.0 bits (84), Expect = 0.63
Identities = 21/82 (25%), Positives = 42/82 (50%), Gaps = 1/82 (1%)

Query: 16 RGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVVSKEDELQ 75

R + + + GD +LD ++ R + + + + +L +LV ++RVV+K+EL +

Sbjct: 119 RRKSESSTKLVCGLDILDTATKAYRGSKEIDLTKKEYQILEYLVNMKNRVVTKEELQE 178

Query: 76 AVWG-GRIVSESTITSHINAVR 96

+W V + SHI +R

Sbjct: 179 HLWSFDDEVFSDVLRSHIKNLR 200

>gi|16800482|ref|NP_470750.1| (NC_003212) two-component response regulator [Listeria innocua]
gi|16803417|ref|NP_464902.1| (NC_003210) two-component response regulator [Listeria
monocytogenes EGD-e]
gi|16410793|emb|CAC99455.1| (AL591978) two-component response regulator [Listeria
monocytogenes]
gi|16413887|emb|CAC96645.1| (AL596168) two-component response regulator [Listeria innocua]
Length = 226

Score = 37.0 bits (84), Expect = 0.64
Identities = 23/104 (22%), Positives = 52/104 (49%), Gaps = 2/104 (1%)

Query: 15 ERGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVVSKEDELQ 74

E + + + +++E R + R +++ + + ++LLL L+ + V++++ LL

Sbjct: 120 ENAEQSAKQTTLQYRNLIKEKRNIVKRDEEIIDLTKELEYELLLTMENVNIVLTREVLL 179

Query: 75 QAVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRTVARKGF 117

VWG E+ + ++ +R I D E+ I+TV G+

Sbjct: 180 NKVWGYETEVEETNVVDVYVRYLRNKI-DHPDEESYIQTVRGTGY 222

>gi|15673417|ref|NP_267591.1| (NC_002662) two-component system regulator [Lactococcus lactis subsp. lactis]
gi|12724424|gb|AAK05533.1|AE006373_12 (AE006373) two-component system regulator [Lactococcus lactis subsp. lactis]
Length = 236

Score = 36.6 bits (83), Expect = 0.65
Identities = 22/71 (30%), Positives = 42/71 (58%), Gaps = 1/71 (1%)

Query: 32 VLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRIVSESTITS 90
V+D ++E+T +V+ + + F++L L ++VS++ELLQ WG +E+ TI

Sbjct: 148 VIDFIKKEVTFDEKVLDTKREFEILELLAKREGKIVSREELLQHFWSISDTAETRTIDV 207

Query: 91 HINAVRKAIGD 101
I+ +RK + +

Sbjct: 208 LISKIRKKLNN 218

>gi|7339508|emb|CAB82844.1| (AJ277080) putative response regulator [Amycolatopsis mediterranei]
gi|14530100|emb|CAC42209.1| (AJ319869) rA protein [Amycolatopsis mediterranei]
Length = 224

Score = 36.6 bits (83), Expect = 0.65
Identities = 26/91 (28%), Positives = 44/91 (47%), Gaps = 1/91 (1%)

Query: 30 DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRIVSESTIT 89
D +D ++ RG+ VS+ P LLL L RV+S+ +LL+ VW + +S +

Sbjct: 131 DLRIDTTSLTSSRGEPVSLTPTELRLLLTLSRAPGRVLSRQQLLEEVWEHDYLGDSRLV 190

Query: 90 SH-INAVRKAIGDTGGEQRLIRTVARKGFRF 119
+ + +R I ++TV G+RF

Sbjct: 191 DNCVQRLRAKIEADPAPEYVQTVRGFGYRF 221

>gi|15613825|ref|NP_242128.1| (NC_002570) BH1262~unknown conserved protein [Bacillus halodurans]
gi|10173878|dbj|BAB04981.1| (AP001511) BH1262~unknown conserved protein [Bacillus halodurans]
Length = 214

Score = 36.6 bits (83), Expect = 0.67
Identities = 21/65 (32%), Positives = 32/65 (48%), Gaps = 1/65 (1%)

Query: 362 RAEIEAGARLARRAVELGRDDAVALTRSGHALGHLVGDLGGIALIDRARLLNPNFAPA 421
R E E A+ A+E D + G+ LG +VG+LD + D+A L + APA

Sbjct: 2 REENYEAAKAFNAIEANPSDPIGFVNFNLLG-MVGELDKALIFFDKAIGLQEDCAPA 60

Query: 422 WFLGG 426
++ G

Sbjct: 61 YYGAG 65

>gi|17232815|ref|NP_489363.1| (NC_003272) two-component transcription regulator, complementary chromatic adaptation protein RcaC homolog [Nostoc sp. PCC 7120]
gi|17134462|dbj|BAB77022.1| (AP003599) ORF_ID:all15323~two-component transcription regulator, complementary chromatic adaptation protein RcaC homolog [Nostoc sp. PCC 7120]
Length = 610

Score = 36.6 bits (83), Expect = 0.68
Identities = 23/93 (24%), Positives = 43/93 (45%), Gaps = 2/93 (2%)

Query: 28 FG DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVVSKDELLQAVWGGRI--VSE 85
+G LD E+T + +++ + F +L + R S+ +++ +W E

Sbjct: 129 WGSRLDPSSCEVTYADKPLNLTAKEFSILELFLRNNQRTFSRGAIVEKLWSAEKDPPEE 188

Query: 86 STITSHINAVRKAIGDTGGEQRLIRTVARKGFR 118
+TI SHI ++R+ + G I TV G+R

Sbjct: 189 NTKSHIKSLRQKLQAAGANYAFIETVYGMGYR 221

>gi|16126989|ref|NP_421553.1| (NC_002696) DNA-binding response regulator [Caulobacter crescentus CB15]
gi|13424351|gb|AAK24721.1| (AE005941) DNA-binding response regulator [Caulobacter crescentus CB15]
Length = 223

Score = 36.6 bits (83), Expect = 0.71
Identities = 26/106 (24%), Positives = 52/106 (48%), Gaps = 2/106 (1%)

Query: 14 SERGRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDEL 73
S R G G+ ++ R + R+G+ + + P+ F LL ++ + V++ L
Sbjct: 116 SRRRETGAVATTCLKVGELENNLNRTVHRQGEIDLQPREFQLLEFMMRHAGQSVTRTML 175

Query: 74 LQAVWGGRIVSESTITSHINAVRKAIGDTGGEQRLIRT VARKGFR 118
L+ VW ++ + HI+ +R I D G ++ +++TV G+R
Sbjct: 176 LEKVWEYHFDPTQNVIDVHISRLRSKI-DKGFDRAMLQTVRGAGYR 220

>gi|699378|gb|AA63138.1| (U15187) mtrX [Mycobacterium leprae]
Length = 113

Score = 36.6 bits (83), Expect = 0.74
Identities = 30/100 (30%), Positives = 50/100 (50%), Gaps = 9/100 (9%)

Query: 17 GRPGDAEVQFMFGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQA 76
GR + F D LD+E E + ++VS+ P F LL +V V++ +L
Sbjct: 8 GRAAPCTARLSFADVELDEETHEAWKADELVSLSPTFTLLRCVVINAGTVLNTPNILDH 67

Query: 77 VW---GGRIVSESTITSHINAVRKAIGDTGGEQRLIRT V 112
VW GG + + + S++ +R+ I DT E+RL+ T+
Sbjct: 68 WVCYRFGGPV---NMVESYVLYLRQI-DT-REKRLHLTL 102

>gi|10956625|ref|NP_066761.1| (NC_002576) two-component response regulator-like protein [Rhodococcus equi]
gi|10657873|gb|AAG21712.1| (AF116907) two-component response regulator-like protein [Rhodococcus equi]
gi|10801063|dbj|BAB16617.1| (AP001204) two-component response regulator [Rhodococcus equi]
Length = 252

Score = 36.6 bits (83), Expect = 0.75
Identities = 22/77 (28%), Positives = 42/77 (53%), Gaps = 4/77 (5%)

Query: 44 GQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWGGRIVSESTITSHINAVRKAIGDTG 103
G +++ + FDLL + + + S+ +LL+ VW ST+T H+ +RK +G+
Sbjct: 159 GDMITLTSREFDLLAYFMKNPFVIHSRQDLLEVRVWWSYGLSTVTVHVRRLRKRLGNYS 218

Query: 104 GEQRLIRT VARKGFRFV 120
I TV +G+R++
Sbjct: 219 ----RIETVWGRGYRWI 231

>gi|15596996|ref|NP_250490.1| (NC_002516) probable two-component response regulator [Pseudomonas aeruginosa]
gi|11352322|pir||C83420 probable two-component response regulator PA1799 [imported] - Pseudomonas aeruginosa (strain PA01)
gi|9947782|gb|AAG05188.1|AE004606_2 (AE004606) probable two-component response regulator [Pseudomonas aeruginosa]
Length = 235

Score = 36.6 bits (83), Expect = 0.75
Identities = 27/93 (29%), Positives = 44/93 (47%), Gaps = 1/93 (1%)

Query: 28 FG DYVLDQERRELTRRGQVSVGPQVFDLLHLVGTRDRVSKDELLQAVWG-GRIVSES 86
FG +D+ RRE G + + F+LL L ++S+DE+L + G G
Sbjct: 136 FGKLNIDRRRREAELEGLIELTMEFELLWLLASQAGEILSRDEILNQIRGIGFDGLNR 195

Query: 87 TITSHINAVRKAIGDTGGEQRLIRT VARKGFRF 119
++ I+ +R + D E I+TV KG+ F
Sbjct: 196 SVDVCISKLRNKLKDNPREPVRIKTVWGKGYLF 228

>gi|3687663|gb|AAC62213.1| (AF049873) LcoR [Lactococcus lactis]
Length = 222

Score = 36.6 bits (83), Expect = 0.78
Identities = 19/71 (26%), Positives = 41/71 (56%), Gaps = 1/71 (1%)

Query: 28 FGDYVLDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWGGRI-VSES 86
F + LD+E+ ++ +++ V P F+LL + ++ V S+++++ +WG V
Sbjct: 127 FKNLSLDKEKFQIWINQKLEVTPIEFNLLDMFLTHQNHVFSREQIIEHIWGLTADVDNR 186

Query: 87 TITSHINAVRK 97
T+ SHI +R+
Sbjct: 187 TVDSHIRNLR 197

>gi|6862579|gb|AAD30119.2| (AF135388) DNA binding response regulator RpaB [Tolypothrix sp. PCC 7601]
Length = 233

Score = 36.6 bits (83), Expect = 0.82
Identities = 25/90 (27%), Positives = 40/90 (43%), Gaps = 3/90 (3%)

Query: 33 LDQERRELTRRGQVSVGPQVFDLLHLVGTDRVSVSKDELLQAVWG---GRIVSESTIT 89
+D +R++ + + + + F LL LV S+ E+LQ VWG R V +
Sbjct: 135 IDTNKRQVYKGDERTIRLTGMEFSLLELLVSRSGEAFSRSEILQEVWGYTPERHVDTRVVD 194

Query: 90 SHINAVRKAIGDTGGEQRLIRTAVARKGFRF 119
HI+ +R + D LI T G+ F
Sbjct: 195 VHISRLRAKLEDDPSNPILITARGTGYLE 224

>gi|15790410|ref|NP_280234.1| (NC_002607) Vng1389c [Halobacterium sp. NRC-1]
gi|10580896|gb|AAG19714.1| (AE005057) Vng1389c [Halobacterium sp. NRC-1]
Length = 270

Score = 36.6 bits (83), Expect = 0.83
Identities = 41/153 (26%), Positives = 68/153 (43%), Gaps = 23/153 (15%)

Query: 93 NAVRKAIGDTGGEQRLIRTAVARKGFRFVGDIRIGGIGEVQPVGPAALQASGGSGGETAS 152
++V + T E +IR V F I +G G+ +PVG AL G +G+
Sbjct: 111 SSVYELFASTRAEPGVIRDV-----FDVAIELGRKGQKGPVG---ALFVVGDAK--- 158

Query: 153 ALVLPDKPSITVLPFQNLSGDPEQEYFADGIVEDIITALSRIWLFVIARN----SSFRY 208
V+ ++ PF+ + D IV ++ SR+ FVI+ + SS+RY
Sbjct: 159 --VMTKSRLSYNPFKEK-----SHVHVGDPIVNVMLKEFSRLDGAFVISDSGKIVSSYRY 211

Query: 209 KGRAVEVKDVGRELGVRYVLEGSVRKSGNRVRI 241
E D+ + LG R++ G++ + N V I
Sbjct: 212 LEPGAEGTDIPKGLGARHMAAGAITRDTNAVAI 244

>gi|15679902|ref|NP_275211.1| (NC_000916) TPR-repeat-containing protein [Methanothermobacter thermotrophicus]
gi|7459509|pir||E69190 conserved hypothetical protein MTH68 - Methanobacterium thermoautotrophicum (strain Delta H)
Length = 228

Score = 36.2 bits (82), Expect = 0.91
Identities = 46/197 (23%), Positives = 74/197 (37%), Gaps = 14/197 (7%)

Query: 325 ALPLFYRAIELDQEFASAYAGAAWCYFWRKLNQWMDRAEEIAEGARLARRAVELGRDDA 384
AL F +AIEL+ + A+ G + + E + + ++L D
Sbjct: 20 ALKCFEKAIELNPKNYRAWG-----TKGITLHNLKIYEEALKCYDKVLQNLQDD 69

Query: 385 VALTRSGHALGHLVGDLGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEH 444
A G L G D + ++A +NP A AW G + G E A+E E
Sbjct: 70 KAWNNKGLVFNEL-GRYDESLECYEKALQINPKLAEAWNNKGVVLSLGRYEEALECYEK 128

Query: 445 AARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALGNLPSLLVAVALVAASHALAG 504
A + P D + + G L G++ AL ++AL P A
Sbjct: 129 ALEIDPEDDKTWN-NKGLVLEEL--GKYKDALECFQKALEINPEFADAWKWKGIILEDLK 185

Query: 505 RTEEARKTMQRLRALDP 521
+ EE+ K ++ L+P
Sbjct: 186 KPEESLKCYKKALKLNP 202

Score = 33.1 bits (74), Expect = 8.6
Identities = 27/131 (20%), Positives = 54/131 (40%), Gaps = 11/131 (8%)

Query: 323 EAALPLFYRAIELDQEFASAYAGAAWCYFWRKLNQWMDRAEEIAEGARLARRAVELGRD 382
+ +L + +A++++ + A A+ G ++ E +A+E+ +
Sbjct: 86 DESLECYEKALQINPKLAEAWN-----KGVVLSSELGRYEEALECYEKALEIDPE 135

Query: 383 DAVALTRSGHALGHLVGDLGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHI 442
D G L L G + +A +NP FA AW G + +PE +++
Sbjct: 136 DDKTWNKGLVLEEL-GKYKDALECFQKALEINPEFADAWKWKGIILEDLKKPEESLKCY 194

Query: 443 EHAARLSPLDQ 453
+ A +L+P Q
Sbjct: 195 KKALKLNPPKQ 205

>gi|15678111|ref|NP_275226.1| (NC_000916) O-linked GlcNAc transferase [Methanothermobacter
thermautotrophicus]
gi|7459511|pir||F69210 conserved hypothetical protein MTH83 - Methanobacterium
thermoautotrophicum (strain Delta H)
gi|2621120|gb|AAB84589.1| (AE000799) O-linked GlcNAc transferase [Methanothermobacter
thermautotrophicus]
Length = 379

Score = 36.2 bits (82), Expect = 0.91
Identities = 46/197 (23%), Positives = 74/197 (37%), Gaps = 14/197 (7%)

Query: 325 ALPLFYRAIELDQEFASAYAGAAWCYFWRKLNQWMDRAEEIAEGARLARRAVELGRDDA 384
AL F +AIEL+ + A+ G + + E + + +L D
Sbjct: 171 ALKCFEKAIELNPKNYRAWG-----TKGITLHNLKIYEEALKCYDKVLQNPQDD 220

Query: 385 VALTRSGHALGHLVGDLGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEH 444
A G L G D + ++A +NP A AW G + G E A+E E
Sbjct: 221 KAWNNGKLVFNEL-GRYDESLECYEKALQINPKLAEAWNNGKVVLSSELGRYEEALECYEK 279

Query: 445 AARLSPLDQEMFRMQAGTALAHFFAGRFDSALVWAERALGNLPSLLVAVALVAASHALAG 504
A + P D + + G L G++ AL ++AL P A
Sbjct: 280 ALEIDPEDDKTWN-NKGLVLEEL--GKYKDALECFQKALEINPEFADAWKWKGIILEDLK 336

Query: 505 RTEEARKTMQRLRALDP 521
+ EE+ K ++ L+P
Sbjct: 337 KPEESLKCYKKALKLNP 353

Score = 33.1 bits (74), Expect = 8.6
Identities = 27/131 (20%), Positives = 54/131 (40%), Gaps = 11/131 (8%)

Query: 323 EAALPLFYRAIELDQEFASAYAGAAWCYFWRKLNQWMDRAEEIAEGARLARRAVELGRD 382
+ +L + +A++++ + A A+ G ++ E +A+E+ +
Sbjct: 237 DESLECYEKALQINPKLAEAWN-----KGVVLSSELGRYEEALECYEKALEIDPE 286

Query: 383 DAVALTRSGHALGHLVGDLGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHI 442
D G L L G + +A +NP FA AW G + +PE +++
Sbjct: 287 DDKTWNKGLVLEEL-GKYKDALECFQKALEINPEFADAWKWKGIILEDLKKPEESLKCY 345

Query: 443 EHAARLSPLDQ 453
+ A +L+P Q
Sbjct: 346 KKALKLNPPKQ 356

>gi|18311222|ref|NP_563156.1| (NC_003366) two-component response regulator [Clostridium
perfringens]
gi|18145905|dbj|BAB81946.1| (AP003193) two-component response regulator [Clostridium
perfringens]
Length = 155

Score = 36.2 bits (82), Expect = 0.93
Identities = 23/91 (25%), Positives = 42/91 (45%), Gaps = 1/91 (1%)

Query: 30 DYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGGGRIVSESTIT 89
++ LD + L + + V P+ F L+ + + ++DELL VWG + I
Sbjct: 63 NFKLDLYSQSLYKENVEIDVTPKEFLLMKIFMQNPGKAFTREDELLNLVWGIDFFGDPKIV 122

Query: 90 S-HINAVRKAIGDTGGEQRLIRTVARKGFRF 119
+I +R I + + + I TV G+R+
Sbjct: 123 DVNIRRLRSKIEENSSKPKYIETVWGTGYRW 153

>gi|15669130|ref|NP_247935.1| (NC_000909) transformation sensitive protein [Methanococcus jannaschii]
gi|2842583|sp|Q58350|Y940_METJA Hypothetical protein MJ0940
gi|2129316|pir||D64417 transformation sensitive protein homolog - Methanococcus jannaschii
gi|1591608|gb|AAB98944.1| (U67537) transformation sensitive protein [Methanococcus jannaschii]
Length = 318

Score = 36.2 bits (82), Expect = 0.95
Identities = 34/126 (26%), Positives = 53/126 (41%), Gaps = 8/126 (6%)

Query: 399 GDLDGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARLS--PLDQEMF 456
G+L + +D+A LNP+F A FL G+ +IE +E S P+ +
Sbjct: 31 GNLESLEYLDKALELNPDKFAKFLKAISLAILGDINKSIECLEDTITSNSNDPVAYALL 90

Query: 457 RMQAGTALAHFFAGRFDSALVWAERALGNLPSLLVAVALVAASHALAGRTEEARKTMQRL 516
+ G FD+AL E++LG A L L+G+ +E K RL
Sbjct: 91 -----GQLYELLGNFDNALECYEKSGLGIEEFATAFFLKVLCGLSGKYDELKCCDRL 144

Query: 517 RALDPS 522
+ P+
Sbjct: 145 ISFAPN 150

>gi|17227939|ref|NP_484487.1| (NC_003272) hypothetical protein [Nostoc sp. PCC 7120]
gi|17129788|dbj|BAB72401.1| (AP003582) ORF_ID:all0443~hypothetical protein [Nostoc sp. PCC 7120]
Length = 290

Score = 36.2 bits (82), Expect = 0.96
Identities = 44/180 (24%), Positives = 77/180 (42%), Gaps = 23/180 (12%)

Query: 360 VDRAEEIAEGARLARRAVELGR----DDAVALTRSGHALG-----HLVGDG----- 401
+D A+ +G LA+ A +LG+ + A+A R L L+G L
Sbjct: 35 LDKPAKLEKQGLSLAQEAQQLGQFQQYELALARARLASQLAPGNDKVVWFLGLQLQTKNF 94

Query: 402 DGGIALIDRARLLNPNFAPAWFLGGFLRVFRGEPESAIEHIEHAARLSPLDQE-MFRMQA 460
DG IA ++R++ +NP A F G + + ++AIEH + L P + + +F +
Sbjct: 95 DGAIASLNRSKTINPKNADVLFGALGSANFQKKYQAAIEHYQAGLALKPNEADGLFDL-- 152

Query: 461 GTALAHFFAGRFDSALVWAERALGNLPSLLVAVALVAASHALAGRTEEARKTMQRLRALD 520
A++ GR A+ +A+ A+ + + G EA K Q ++D
Sbjct: 153 --GNAYYMIGRLPDAIAQYNKAVAQDRKFWPAINNIGLINYEQGNVSEAIKRWQTAVSID 210

>gi|15896015|ref|NP_349364.1| (NC_003030) Response regulator (CheY receiver domain and HTH-type DNA-binding domain) [Clostridium acetobutylicum]
gi|15025797|gb|AAK80704.1|AE007774_1 (AE007774) Response regulator (CheY receiver domain and HTH-type DNA-binding domain) [Clostridium acetobutylicum]
Length = 228

Score = 36.2 bits (82), Expect = 0.99
Identities = 26/95 (27%), Positives = 48/95 (50%), Gaps = 3/95 (3%)

Query: 27 MFGDYVLDQERRELTRRGQVSVGPQVFDLLLHLVGTRDRVVSKDELLQAVWGGGRIVSES 86
+ G +++ E+ + ++S+ P ++LL +L+ +SKD++L+ VWG E
Sbjct: 135 VIGPFLIKDSAHEIYKDDILSLSPTEYNLLKYLLNNGIALSKDQILEKVVWGYDFTGEK 194

Query: 87 TITS-HINAVRKAIGDTGGEQRLIRTVARKGFRFV 120
I +I +R I D +IRTV G++ V
Sbjct: 195 NIVEVYIRYLRLDKISDK--NHTIIRTVRGVGYKVV 227

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: Apr 29, 2002 3:56 AM
Number of letters in database: 290,391,215
Number of sequences in database: 925,521

Lambda	K	H
0.322	0.139	0.410

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 308,048,510
Number of Sequences: 925521
Number of extensions: 12958400
Number of successful extensions: 41604
Number of sequences better than 10.0: 603
Number of HSP's better than 10.0 without gapping: 265
Number of HSP's successfully gapped in prelim test: 342
Number of HSP's that attempted gapping in prelim test: 40924
Number of HSP's gapped (non-prelim): 801
length of query: 554
length of database: 290,391,215
effective HSP length: 125
effective length of query: 429
effective length of database: 174,701,090
effective search space: 74946767610
effective search space used: 74946767610
T: 11
A: 40
X1: 16 (7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.9 bits)
S2: 74 (33.1 bits)

LITERATURE CITED

- Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410.
- Astwood, J., and Fuchs, R. 1996. Allergenicity of foods derived from transgenic plants. Monogr. Allergy **32**:105-120
- Codex *Ad Hoc* Intergovernmental Task Force on Foods Derived from Biotechnology, 2001. Report of the Working Group on Allergenicity. Codex Alimentaris. Vancouver, Canada, 10-12 September 2001.
- Crickmore, N., Zeigler, D.R., Schnepf, E., Van Rie, J., Lereclus, D., Baum, J., Bravo, A. and Dean, D.H. 2002. *Bacillus thuringiensis* toxin nomenclature. http://www.biols.susx.ac.uk/Home/Neil_Crickmore/Bt/index.html
- Grochulski, P., Masson, L., Borisova, S., Pusztai-Carey, M., Schwartz, J.L., Brousseau, R., Cygler, M. 1995. *Bacillus thuringiensis* CryIA(a) Insecticidal Toxin: Crystal Structure and Channel Formation. J. Mol. Biol. **254**(3):447-64.
- Hofte, H., and Whiteley, H.R. 1989. Insecticidal crystal proteins of *Bacillus thuringiensis*. Microbiol. Rev. **53**(2):242-55.
- Metcalf, D., Astwood, J., Townsend, R., Sampson, H., Taylor, S., and Fuchs, R. 1996. Assessment of allergenic potential of foods derived from genetically engineered crop plants. Crit. Rev. Food Sci. Nutr. **36**(S):S165-S186.
- Mizuki, E., Park, Y.S., Saitoh, H., Yamashita, S., Akao, T., Higuchi, K., Ohba, M. 2000. Parasporin, a human leukemic cell-recognizing parasporal protein of *Bacillus thuringiensis*. Clin. Diagn. Lab. Immunol. **7**(4):625-34.
- Pearson, W.R. 2000. Flexible sequence similarity searching with the FASTA3 program package. Methods Mol Biol **132**:185-219.
- Schnepf, E., Crickmore, N., Van Rie, J., Lereclus, D., Baum, J., Feitelson, J., Zeigler, D.R., Dean, D.H. 1998 *Bacillus thuringiensis* and its pesticidal crystal proteins. Microbiol. Mol. Biol. Rev. **62**(3):775-806.