



**Phosphomannose Isomerase (Entrez® Accession Number AAA24109):
Assessment of Amino Acid Sequence Similarity to Known or Putative
Toxins**

Data Requirement(s):	Not applicable
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Study Completion Date:	March 15, 2011
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Syngenta Study No.:	Not applicable
Report No.:	SSB-145-11
Task No.:	Not Applicable

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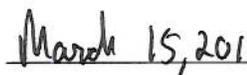
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Company: *Syngenta Seeds, Inc.*

Company Representative:

Scott Huber
Regulatory Affairs Manager



Date

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This is not a study as defined by 40 CFR Part 160.3 and is therefore not subject to Federal Insecticide, Fungicide, and Rodenticide Act Good Laboratory Practices Standards (GLPS). However, all components of this analysis were performed according to accepted scientific practices, and relevant records have been retained.

Study Director:

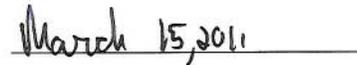
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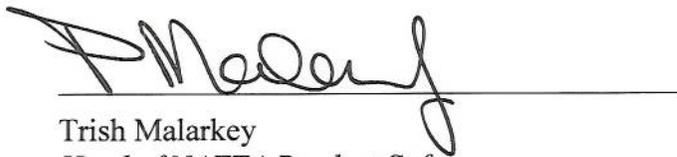
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TABLE OF CONTENTS

STATEMENTS OF DATA CONFIDENTIALITY CLAIMS	2
STATEMENT CONCERNING GOOD LABORATORY PRACTICES STANDARDS	3
LIST OF FIGURES.....	5
LIST OF ACRONYMS AND ABBREVIATIONS	6
SUMMARY.....	7
INTRODUCTION.....	8
MATERIALS AND METHODS	8
Sequence Similarity Search.....	8
Assessment of the Significance of Sequence Similarity	9
Analysis of Sequences Showing Significant Similarity to the PMI Amino Acid Sequence	9
RESULTS AND DISCUSSION.....	10
CONCLUSIONS.....	10
RECORDS RETENTION.....	10
CONTRIBUTING SCIENTISTS	10
REFERENCES.....	11
APPENDIX A	12
APPENDIX B	182
APPENDIX C	197

LIST OF FIGURES

Figure 1. Amino acid sequence of PMI 8

LIST OF ACRONYMS AND ABBREVIATIONS

BLASTP	Basic Local Alignment Search Tool for Proteins
BLOSUM62	Blocks Substitution Matrix62
<i>E</i> -value	Expectation value
FIFRA	Federal Insecticide, Fungicide, and Rodenticide Act
GLPS	Good Laboratory Practices Standards
<i>manA</i>	phosphomannose isomerase gene
PMI	phosphomannose isomerase protein
<i>pmi</i>	phosphomannose isomerase gene
NCBI	National Center for Biotechnology Information
US EPA	United States Environmental Protection Agency
®	Registered trademark

SUMMARY

The Basic Local Alignment Search Tool for Proteins program was used to search the National Center for Biotechnology Information Entrez® Protein Database to determine whether the phosphomannose isomerase protein (PMI) amino acid sequence showed significant similarity to known or putative toxins. The threshold value for determining significance of matches was based on searches conducted with randomly shuffled sequences of the amino acids comprising PMI. There were 1384 protein sequences identified as having significant sequence similarity to PMI amino acid sequence; however, none of these proteins were known or putative toxins.

INTRODUCTION

The purpose of this study is to determine whether the phosphomannose isomerase protein (PMI) amino acid sequence has significant similarity with proteins that are known or putative toxins.

The gene *pmi*, also known as *manA*, is from *Escherichia coli* and encodes the enzyme phosphomannose isomerase (PMI). Maize cells expressing *pmi* can utilize mannose as a primary carbon source whereas cells lacking *pmi* expression will fail to proliferate in a mannose-based culture medium; therefore, PMI has utility as a plant selectable marker.

The PMI amino acid sequence was systematically compared with the latest posting of the National Center for Biotechnology Information (NCBI) Entrez® Protein Database (NCBI 2011). This procedure identified (1) whether any proteins in the database showed significant similarity to the PMI amino acid sequence (*i.e.*, alignments with Basic Local Alignment Search Tool for Proteins [BLASTP] Expectation values [*E*-values] below an established threshold), indicating that the amino acid sequence might be closely related to the PMI amino acid sequence, and (2) whether any proteins showing sequence similarity to the PMI amino acid sequence were known or putative toxins.

MATERIALS AND METHODS

Sequence Similarity Search

The BLASTP program (Altschul *et al.* 1997) was used to search the NCBI Entrez® Protein Database with the PMI sequence of 391 amino acids as the query sequence (Entrez® Database Accession No. AAA24109, GenInfo Identifier 146722 [NCBI 2011] [Figure 1]).

Figure 1. Amino acid sequence of PMI

```

1  MQKLINSVQN YAWGSKTALT ELYGMENPSS QPMAELWMGA HPKSSSRVQN
51  AAGDIVSLRD VIESDKSTLL GEAVAKRFGE LPFLFKVLCA AQPLSIQVHP
101 NKHNSEIGFA KENAAGIPMD AAERNYKDPN HKPELVFALT PFLAMNAFRE
151 FSEIVSLLQP VAGAHPAIAH FLQQPDAERL SELFASLLNM QGEEKSRALA
201 ILKSALDSQQ GEPWQTIRLI SEFYPEDSGL FSPLLLNVVK LNPGEAMFLF
251 AETPHAYLQG VALEVMANSD NVLRAGLTPK YIDIPELVAN VKFEAKPANQ
301 LLTQPVKQGA ELDFPIPVD D FAFSLHDLS D KETTISQQSA AILFCVEGDA
351 TLWKGSQQQLQ LKPGESAFIA ANESPVTVKG HGRLARVYNK L
  
```

The NCBI Entrez® Protein Database was used to identify the potential similarity between the query protein amino acid sequence and known or putative toxins. For this analysis, the NCBI Entrez® Protein Database (containing 13,135,398 protein sequences) was accessed on March 1, 2011. The BLASTP is a program used to search protein sequences for sequence similarities. Most proteins are modular in nature and contain functional domains. Similarly, functional domains are conserved across different proteins from different species. The BLASTP algorithm is optimized to identify these domains or shorter sequence similarities present within the full length query sequence; as a result, this approach detects more similarities than would a search started by aligning two sequences over their entire length. The BLASTP program, version blastp 2.2.8 (Jan-

05-2004), was used to perform the similarity searches with the following default parameters:

Low complexity filter

E -value = 10

Word size = 3

Gap costs: existence = 11 and extension = 1

Similarity matrix: Blocks Substitution Matrix (BLOSUM62)

The E -value is a measure of the probability that matches between sequences occurred by chance. Search results involving comparisons between proteins with highly similar sequences yield E -values approaching zero; the probability that sequence similarities occurred by chance increases with higher E -values (Ponting 2001). The search identified all sequences in the database with search results yielding an E -value of 10 or lower.

Assessment of the Significance of Sequence Similarity

A threshold below which similarity to the query sequence is considered significant, and not the result of random similarity in amino acid composition, is required for meaningful analysis of database alignments. To assess the significance of sequence similarity to the PMI amino acid sequence, additional searches were conducted with shuffled versions of the PMI amino acid sequence. Five shuffled sequences were created through random shuffling of the PMI amino acid sequence using the modern version of the Fisher-Yates shuffle (Knuth 1998).

The resulting shuffled sequences all had the same amino acid composition as PMI (*i.e.*, the same number of residues of each specific amino acid), but were unlikely to have amino acid sequences similar to those of either PMI or other proteins found in the NCBI Entrez® Protein Database. Searches using these shuffled sequences provided an estimate of the background incidence of alignments that would be expected for any sequence with the same amino acid composition as PMI. Searches with the five shuffled versions of the PMI amino acid sequence identified sequences with search results yielding E -values that ranged from 1.3 - 8.4; therefore, the threshold E -value for significant amino acid sequence similarity to PMI was considered to be 1.3. Sequences with significant similarity to the PMI amino acid sequence (*i.e.*, E -values less than 1.3) were evaluated for source organism and biological function.

Analysis of Sequences Showing Significant Similarity to the PMI Amino Acid Sequence

The identity and biological function, if known, were determined for each protein identified in the BLASTP search as having significant similarity to the PMI amino acid sequence (*i.e.*, E -value less than 1.3). The NCBI Entrez® Protein Database records were accessed, if needed, using the Entrez® Accession Numbers. If an entry in the NCBI Entrez® Protein Database record was vague (*e.g.*, “hypothetical protein”), the individual record and supporting literature were examined in an attempt to clarify the identity and/or function of the protein associated with that record.

RESULTS AND DISCUSSION

The NCBI Entrez® Protein Database search identified 1384 sequences with significant similarity to the PMI amino acid sequence (*i.e.*, *E*-values less than 1.3) (Appendix A). These sequences were grouped into categories.

Of the 1384 sequences, 1208 alignments to proteins from 587 species were identified as known or putative phosphomannose isomerase enzymes or proteins involved in carbohydrate/sugar metabolism or transport. The *E*-values for alignments between these sequences and the PMI amino acid sequence ranged from 0 to 0.99. Appendix B shows the source organisms for these proteins.

An additional alignment was to ADP-L-glycero-D-manno-heptose-6-epimerase (AGME) from *Aspergillus terreus*. AGME is responsible for the synthesis of heptose, which is not present in mammalian cells (Deacon *et al.* 2000). AGME is not a known toxin and the product of AGME bioactivity, heptose, is not a known toxin. The *E*-value for this alignment was 4.8×10^{-11} .

An additional 175 alignments to proteins from 128 species were identified as hypothetical or unknown proteins of unspecified function. The *E*-values for alignments between these sequences and the PMI amino acid sequence ranged from 2.6×10^{-73} to 0.99. Appendix C shows the source organisms for these proteins. None of the proteins were identified as known or putative toxins.

CONCLUSIONS

The results of a comprehensive amino acid similarity search of the NCBI Entrez® Protein Database support the conclusion that the PMI amino acid sequence shows no significant similarity with any known or putative toxins.

RECORDS RETENTION

Raw data, the original copy of this report, and other relevant records are archived at Syngenta Crop Protection, LLC, 3054 East Cornwallis Road, Research Triangle Park, NC 27709-2257, USA.

CONTRIBUTING SCIENTISTS

The analytical work reported herein was conducted by Brian Harper, M.S. This work was conducted at Syngenta Biotechnology, Inc.

REFERENCES

- Altschul SF, Madden TL, Schäffer AA, Zhang J, Zhang Z, Miller W, Lipman DJ. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res* 25:3389–3402.
- Deacon A, Ni Y, Coleman Jr. WG, Ealick SE. 2000. The crystal structure of ADP-L-glycero-D-mannoheptose-6-epimerase: catalysis with a twist. *Structure* 8:453–462.
- Knuth DE. 1998. *The Art of Computer Programming, Vol. 2*, 3rd ed. Reading, MA: Harlow: Addison-Wesley. pp. 145–146.
- NCBI. 2011. Entrez® Protein database. Bethesda, MD: National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health. <http://www.ncbi.nlm.nih.gov/sites/entrez?db=Protein> (accessed March 1, 2011).
- Ponting C. 2001. Issues in predicting protein function from sequence. *Brief Bioinform* 2:19–29.
- US EPA. 1989. Good Laboratory Practice Standards. 40 CFR Part 160.3.

APPENDIX A. All sequences showing significant similarity to the PMI amino acid sequence in a BLASTP analysis of the NCBI Entrez® Protein Database

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1	NR gi 49176125 ref NP_416130.3 mannose-6-phosphate isomerase [Escherichia coli str. K-12 substr. MG1655] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase [Escherichia coli str. K-12 substr. W3110] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase [Escherichia coli str. K-12 substr. DH10B] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli 101-1] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase [Escherichia coli BW2952] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase [Escherichia sp. 4_1_40B] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli MS 182-1] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli MS 187-1] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli MS 116-1] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli MS 175-1] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli MS 196-1] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli MS 78-1] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli MS 146-1] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase [Escherichia coli H736] >gnl BL_ORD_ID 8723 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 8723 phosphomannose isomerase [Escherichia coli] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase [Escherichia coli str. K12 substr. W3110] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase [Escherichia coli str. K-12 substr. MG1655] >gnl BL_ORD_ID 8723 putative chitinase [Bacillus pumilus] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase [Escherichia coli str. K-12 substr. DH10B] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli 101-1] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase [Escherichia coli BW2952] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli DH1] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli MS 196-1] >gnl BL_ORD_ID 8723 mannose-6-phosphate	391	0	1 - 391 (25.58%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
	isomerase, class I [Escherichia coli MS 175-1] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli MS 182-1] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli MS 116-1] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli MS 187-1] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli MS 78-1] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli MS 146-1] >gnl BL_ORD_ID 8723 phosphomannose isomerase [Binary vector pBI121-ELEMENTS] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase [Escherichia coli ETEC H10407] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase [Escherichia coli DH1] >gnl BL_ORD_ID 8723 mannose-6-phosphate isomerase, class I [Escherichia coli 3431] >gnl BL_ORD_ID 8723 isomerase,phosphomannose			
2	NR gi 300918719 ref ZP_07135296.1 mannose-6-phosphate isomerase, class I [Escherichia coli MS 115-1] >gnl BL_ORD_ID 2601408 mannose-6-phosphate isomerase, class I [Escherichia coli MS 115-1]	391	0	1 - 391 (25.51%)
3	NR gi 253773431 ref YP_003036262.1 mannose-6-phosphate isomerase, class I [Escherichia coli BL21-Gold(DE3)pLysS AG] >gnl BL_ORD_ID 2904849 mannose-6-phosphate isomerase [Escherichia coli B str. REL606] >gnl BL_ORD_ID 2904849 mannose-6-phosphate isomerase [Escherichia coli BL21(DE3)] >gnl BL_ORD_ID 2904849 mannose-6-phosphate isomerase, class I [Escherichia coli 'BL21-Gold(DE3)pLysS AG'] >gnl BL_ORD_ID 2904849 mannose-6-phosphate isomerase [Escherichia coli B str. REL606] >gnl BL_ORD_ID 2904849 mannose-6-phosphate isomerase [Escherichia coli BL21(DE3)]	391	0	1 - 391 (25.51%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
4	<p>NR gi 15802027 ref NP_288048.1 mannose-6-phosphate isomerase [Escherichia coli O157:H7 EDL933] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase [Escherichia coli O157:H7 str. Sakai] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC4113] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC4401] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC4501] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC4486] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC4196] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC4076] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC869] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC508] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC4206] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC4045] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC4042] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC4115] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase [Escherichia coli O157:H7 str. TW14588] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase [Escherichia coli O157:H7 str. TW14359] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase [Escherichia coli O157:H7 str. FRIK2000] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase [Escherichia coli O157:H7 str. FRIK966] >gnl BL_ORD_ID 727493 Mannose-6-phosphate isomerase, class I [Escherichia coli O55:H7 str. CB9615] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase [Escherichia coli O157:H7 str. EDL933] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase [Escherichia coli O157:H7 str. Sakai] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC4196] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC4113] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC4076] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC4401] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC4486] >gnl BL_ORD_ID 727493 mannose-6-phosphate isomerase, class I [Escherichia coli O157:H7 str. EC4501] >gnl BL_ORD_ID 727493 mannose-6-phosphate</p>	391	0	1 - 391 (25.45%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
5	NR gi 209918925 ref YP_002293009.1 mannose-6-phosphate isomerase [Escherichia coli SE11] >gnl BL_ORD_ID 1036561 mannose-6-phosphate isomerase [Escherichia coli SE11]	391	0	1 - 391 (25.45%)
6	NR gi 30063128 ref NP_837299.1 mannose-6-phosphate isomerase [Shigella flexneri 2a str. 2457T] >gnl BL_ORD_ID 1131473 mannose-6-phosphate isomerase [Shigella flexneri 2a str. 301] >gnl BL_ORD_ID 1131473 mannose-6-phosphate isomerase [Shigella flexneri 5 str. 8401] >gnl BL_ORD_ID 1131473 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 1131473 mannose-6-phosphate isomerase [Shigella flexneri 2a str. 2457T] >gnl BL_ORD_ID 1131473 mannose-6-phosphate isomerase [Shigella flexneri 2a str. 301] >gnl BL_ORD_ID 1131473 mannose-6-phosphate isomerase [Shigella flexneri 5 str. 8401] >gnl BL_ORD_ID 1131473 Mannose-6-phosphate isomerase [Shigella flexneri 2002017] >gnl BL_ORD_ID 1131473 mannose-6-phosphate isomerase, class I [Shigella flexneri 2a str. 2457T]	391	0	1 - 391 (25.45%)
7	NR gi 157155328 ref YP_001462902.1 mannose-6-phosphate isomerase [Escherichia coli E24377A] >gnl BL_ORD_ID 396237 mannose-6-phosphate isomerase, class I [Escherichia coli E24377A]	391	0	1 - 391 (25.51%)
8	NR gi 320181369 gb EFW56288.1 Mannose-6-phosphate isomerase [Shigella boydii ATCC 9905]	391	0	1 - 391 (25.45%)
9	NR gi 300936068 ref ZP_07151013.1 mannose-6-phosphate isomerase, class I [Escherichia coli MS 21-1] >gnl BL_ORD_ID 2629388 mannose-6-phosphate isomerase, class I [Escherichia coli MS 21-1]	391	0	1 - 391 (25.45%)
10	NR gi 209769822 gb ACI83223.1 mannose-6-phosphate isomerase [Escherichia coli]	391	0	1 - 391 (25.38%)
11	NR gi 320184772 gb EFW59563.1 Mannose-6-phosphate isomerase [Shigella flexneri CDC 796-83]	391	0	1 - 391 (25.45%)
12	NR gi 209769818 gb ACI83221.1 mannose-6-phosphate isomerase [Escherichia coli] >gnl BL_ORD_ID 2435920 mannose-6-phosphate isomerase [Escherichia coli O157:H- str. 493-89] >gnl BL_ORD_ID 2435920 mannose-6-phosphate isomerase [Escherichia coli O157:H- str. H 2687]	391	0	1 - 391 (25.38%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
13	NR gi 74312062 ref YP_310481.1 mannose-6-phosphate isomerase [Shigella sonnei Ss046] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase [Shigella boydii Sb227] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase [Escherichia coli HS] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase, class I [Escherichia coli ATCC 8739] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase, class I [Shigella boydii CDC 3083-94] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase, class I [Escherichia coli 53638] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase, class I [Escherichia coli E110019] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase ManA [Escherichia coli O26:H11 str. 11368] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase ManA [Escherichia coli O111:H- str. 11128] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase, class I [Escherichia coli 1827-70] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase [Shigella sonnei Ss046] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase [Shigella boydii Sb227] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase, class I [Escherichia coli HS] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase, class I [Escherichia coli ATCC 8739] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase, class I [Shigella boydii CDC 3083-94] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase, class I [Escherichia coli 53638] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase, class I [Escherichia coli E110019] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase ManA [Escherichia coli O26:H11 str. 11368] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase ManA [Escherichia coli O111:H- str. 11128] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase, class I [Escherichia coli 1827-70] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase, class I [Escherichia coli EPECa14] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase, class I [Shigella sonnei 53G] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase, class I [Escherichia coli LT-68] >gnl BL_ORD_ID 384453 mannose-6-phosphate isomerase, class I [Escherichia coli 1180]	391	0	1 - 391 (25.45%)
14	NR gi 301026738 ref ZP_07190146.1 mannose-6-phosphate isomerase, class I [Escherichia coli MS 69-1] >gnl BL_ORD_ID 2595278 mannose-6-phosphate isomerase, class I [Escherichia coli MS 69-1]	391	0	1 - 391 (25.38%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
15	NR gi 218705113 ref YP_002412632.1 mannose-6-phosphate isomerase [Escherichia coli UMN026] >gnl BL_ORD_ID 1415529 mannose-6-phosphate isomerase [Escherichia coli FVEC1412] >gnl BL_ORD_ID 1415529 mannose-6-phosphate isomerase, class I [Escherichia coli MS 198-1] >gnl BL_ORD_ID 1415529 mannose-6-phosphate isomerase [Escherichia coli UMN026] >gnl BL_ORD_ID 1415529 mannose-6-phosphate isomerase [Escherichia coli FVEC1412] >gnl BL_ORD_ID 1415529 mannose-6-phosphate isomerase, class I [Escherichia coli MS 198-1]	391	0	1 - 391 (25.38%)
16	NR gi 194431835 ref ZP_03064125.1 mannose-6-phosphate isomerase, class I [Shigella dysenteriae 1012] >gnl BL_ORD_ID 496918 mannose-6-phosphate isomerase, class I [Shigella dysenteriae 1012]	391	0	1 - 391 (25.38%)
17	NR gi 293445987 ref ZP_06662409.1 phosphomannose isomerase type I [Escherichia coli B088] >gnl BL_ORD_ID 1704192 phosphomannose isomerase type I [Escherichia coli B088]	391	0	1 - 391 (25.38%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
18	NR gi 191165924 ref ZP_03027761.1 mannose-6-phosphate isomerase, class I [Escherichia coli B7A] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase, class I [Escherichia coli E22] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase, class I [Escherichia coli B171] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase [Escherichia coli IA11] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase [Escherichia coli 55989] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase [Shigella sp. D9] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase ManA [Escherichia coli O103:H2 str. 12009] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase, class I [Escherichia coli MS 107-1] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase, class I [Escherichia coli MS 119-7] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase [Escherichia coli TA271] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase [Escherichia coli H591] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase, class I [Escherichia coli MS 145-7] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase, class I [Escherichia coli B7A] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase, class I [Escherichia coli E22] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase, class I [Escherichia coli B171] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase [Escherichia coli 55989] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase [Escherichia coli IA11] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase ManA [Escherichia coli O103:H2 str. 12009] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase, class I [Escherichia coli MS 119-7] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase, class I [Escherichia coli MS 107-1] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase, class I [Escherichia coli MS 145-7] >gnl BL_ORD_ID 395617 Mannose-6-phosphate isomerase [Escherichia coli EC4100B] >gnl BL_ORD_ID 395617 mannose-6-phosphate isomerase, class I [Escherichia coli 1357]	391	0	1 - 391 (25.38%)
19	NR gi 284921536 emb CBG34608.1 mannose-6-phosphate isomerase [Escherichia coli 042]	391	0	1 - 391 (25.31%)
20	NR gi 323163540 gb EFZ49366.1 mannose-6-phosphate isomerase, class I [Escherichia coli E128010]	391	0	1 - 391 (25.31%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
21	NR gi 320174180 gb EFW49345.1 Mannose-6-phosphate isomerase [Shigella dysenteriae CDC 74-1112]	391	0	1 - 391 (25.38%)
22	NR gi 307221459 ref ZP_07507883.1 mannose-6-phosphate isomerase [Escherichia coli M718]	391	0	1 - 391 (25.38%)
23	NR gi 82777082 ref YP_403431.1 mannose-6-phosphate isomerase [Shigella dysenteriae Sd197] >gnl BL_ORD_ID 2085605 mannose-6-phosphate isomerase [Shigella dysenteriae Sd197]	391	0	1 - 391 (25.31%)
24	NR gi 293409922 ref ZP_06653498.1 phosphomannose isomerase type I [Escherichia coli B354] >gnl BL_ORD_ID 1750842 phosphomannose isomerase type I [Escherichia coli B354]	391	0	1 - 391 (25.31%)
25	NR gi 293414929 ref ZP_06657572.1 phosphomannose isomerase type I [Escherichia coli B185] >gnl BL_ORD_ID 1745665 phosphomannose isomerase type I [Escherichia coli B185]	391	0	1 - 391 (25.31%)
26	NR gi 300907242 ref ZP_07124901.1 mannose-6-phosphate isomerase, class I [Escherichia coli MS 84-1] >gnl BL_ORD_ID 2597899 mannose-6-phosphate isomerase, class I [Escherichia coli MS 124-1] >gnl BL_ORD_ID 2597899 mannose-6-phosphate isomerase, class I [Escherichia coli W] >gnl BL_ORD_ID 2597899 mannose-6-phosphate isomerase, class I [Escherichia coli MS 84-1] >gnl BL_ORD_ID 2597899 mannose-6-phosphate isomerase, class I [Escherichia coli MS 124-1] >gnl BL_ORD_ID 2597899 mannose-6-phosphate isomerase, class I [Escherichia coli W] >gnl BL_ORD_ID 2597899 mannose-6-phosphate isomerase [Escherichia coli W] >gnl BL_ORD_ID 2597899 mannose-6-phosphate isomerase, class I [Escherichia coli MS 85-1] >gnl BL_ORD_ID 2597899 mannose-6-phosphate isomerase, class I [Escherichia coli KO11]	391	0	1 - 391 (25.31%)
27	NR gi 170682319 ref YP_001743641.1 mannose-6-phosphate isomerase, class I [Escherichia coli SMS-3-5] >gnl BL_ORD_ID 2812931 mannose-6-phosphate isomerase, class I [Escherichia coli SMS-3-5]	391	0	1 - 391 (25.25%)
28	NR gi 218699821 ref YP_002407450.1 mannose-6-phosphate isomerase [Escherichia coli IAI39] >gnl BL_ORD_ID 1410603 mannose-6-phosphate isomerase [Escherichia coli IAI39]	391	0	1 - 391 (25.25%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
29	NR gi 215486789 ref YP_002329220.1 mannose-6-phosphate isomerase [Escherichia coli O127:H6 str. E2348/69] >gn BL_ORD_ID 1260247 mannose-6-phosphate isomerase, class I [Escherichia coli 2362-75] >gn BL_ORD_ID 1260247 mannose-6-phosphate isomerase [Escherichia coli O127:H6 str. E2348/69] >gn BL_ORD_ID 1260247 mannose-6-phosphate isomerase, class I [Escherichia coli 2362-75] >gn BL_ORD_ID 1260247 mannose-6-phosphate isomerase, class I [Escherichia coli RN587/1]	391	0	1 - 391 (25.31%)
30	NR gi 320195491 gb EFW70116.1 Mannose-6-phosphate isomerase [Escherichia coli WV_060327]	391	0	1 - 391 (25.25%)
31	NR gi 307560230 ref ZP_07623997.1 mannose-6-phosphate isomerase [Escherichia coli H299]	391	0	1 - 391 (25.25%)
32	NR gi 307349232 ref ZP_07618837.1 mannose-6-phosphate isomerase [Escherichia coli TA280]	391	0	1 - 391 (25.18%)
33	NR gi 307231082 ref ZP_07517493.1 mannose-6-phosphate isomerase [Escherichia coli TA143]	391	0	1 - 391 (25.25%)
34	NR gi 26247860 ref NP_753900.1 mannose-6-phosphate isomerase [Escherichia coli CFT073] >gn BL_ORD_ID 30014 mannose-6-phosphate isomerase [Escherichia coli 536] >gn BL_ORD_ID 30014 mannose-6-phosphate isomerase, class I [Escherichia coli F11] >gn BL_ORD_ID 30014 mannose-6-phosphate isomerase [Escherichia coli 83972] >gn BL_ORD_ID 30014 mannose-6-phosphate isomerase, class I [Escherichia coli MS 45-1] >gn BL_ORD_ID 30014 mannose-6-phosphate isomerase, class I [Escherichia coli MS 185-1] >gn BL_ORD_ID 30014 mannose-6-phosphate isomerase [Escherichia coli NC101] >gn BL_ORD_ID 30014 Mannose-6-phosphate isomerase [Escherichia coli CFT073] >gn BL_ORD_ID 30014 mannose-6-phosphate isomerase [Escherichia coli 536] >gn BL_ORD_ID 30014 mannose-6-phosphate isomerase, class I [Escherichia coli F11] >gn BL_ORD_ID 30014 mannose-6-phosphate isomerase [Escherichia coli 83972] >gn BL_ORD_ID 30014 mannose-6-phosphate isomerase, class I [Escherichia coli MS 185-1] >gn BL_ORD_ID 30014 mannose-6-phosphate isomerase, class I [Escherichia coli MS 45-1] >gn BL_ORD_ID 30014 mannose-6-phosphate isomerase [Escherichia coli NC101] >gn BL_ORD_ID 30014 mannose-6-phosphate isomerase [Escherichia coli ABU 83972] >gn BL_ORD_ID 30014 mannose-6-phosphate isomerase, class I [Escherichia coli MS 153-1]	391	0	1 - 391 (25.18%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
35	NR gi 300989857 ref ZP_07178993.1 mannose-6-phosphate isomerase, class I [Escherichia coli MS 200-1] >gnl BL_ORD_ID 2581026 mannose-6-phosphate isomerase, class I [Escherichia coli MS 200-1]	391	0	1 - 391 (25.12%)
36	NR gi 281178684 dbj BAI55014.1 mannose-6-phosphate isomerase [Escherichia coli SE15]	391	0	1 - 391 (25.12%)
37	NR gi 91210824 ref YP_540810.1 mannose-6-phosphate isomerase [Escherichia coli UTI89] >gnl BL_ORD_ID 209130 mannose-6-phosphate isomerase [Escherichia coli APEC O1] >gnl BL_ORD_ID 209130 mannose-6-phosphate isomerase [Escherichia coli S88] >gnl BL_ORD_ID 209130 mannose-6-phosphate isomerase [Escherichia coli UTI89] >gnl BL_ORD_ID 209130 mannose-6-phosphate isomerase [Escherichia coli APEC O1] >gnl BL_ORD_ID 209130 mannose-6-phosphate isomerase [Escherichia coli S88] >gnl BL_ORD_ID 209130 mannose-6-phosphate isomerase, class I [Escherichia coli IHE3034] >gnl BL_ORD_ID 209130 mannose-6-phosphate isomerase [Escherichia coli UM146]	391	0	1 - 391 (25.12%)
38	NR gi 307225821 ref ZP_07512232.1 mannose-6-phosphate isomerase [Escherichia coli TA206] >gnl BL_ORD_ID 2100341 Mannose-6-phosphate isomerase [Escherichia coli LF82] >gnl BL_ORD_ID 2100341 mannose-6-phosphate isomerase [Escherichia coli O83:H1 str. NRG 857C] >gnl BL_ORD_ID 2100341 mannose-6-phosphate isomerase, class I [Escherichia coli MS 16-3]	391	0	1 - 391 (25.12%)
39	NR gi 307143874 ref ZP_07502306.1 mannose-6-phosphate isomerase [Escherichia coli M605]	391	0	1 - 391 (25.05%)
40	NR gi 237705554 ref ZP_04536035.1 mannose-6-phosphate isomerase [Escherichia sp. 3_2_53FAA] >gnl BL_ORD_ID 2226319 mannose-6-phosphate isomerase [Escherichia sp. 3_2_53FAA] >gnl BL_ORD_ID 2226319 mannose-6-phosphate isomerase, class I [Escherichia coli MS 110-3]	391	0	1 - 391 (25.05%)
41	NR gi 218689559 ref YP_002397771.1 mannose-6-phosphate isomerase [Escherichia coli ED1a] >gnl BL_ORD_ID 1413096 mannose-6-phosphate isomerase [Escherichia coli ED1a]	391	0	1 - 391 (25.05%)
42	NR gi 298380759 ref ZP_06990358.1 mannose-6-phosphate isomerase [Escherichia coli FVEC1302] >gnl BL_ORD_ID 2338691 mannose-6-phosphate isomerase [Escherichia coli FVEC1302]	377	0	15 - 391 (26.24%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
43	NR gi 170768919 ref ZP_02903372.1 mannose-6-phosphate isomerase, class I [Escherichia albertii TW07627] >gnl BL_ORD_ID 105139 mannose-6-phosphate isomerase, class I [Escherichia albertii TW07627]	391	0	1 - 391 (24.20%)
44	NR gi 218548785 ref YP_002382576.1 mannose-6-phosphate isomerase [Escherichia fergusonii ATCC 35469] >gnl BL_ORD_ID 1405747 mannose-6-phosphate isomerase [Escherichia fergusonii ATCC 35469]	391	0	1 - 391 (22.83%)
45	NR gi 157145873 ref YP_001453192.1 hypothetical protein CKO_01624 [Citrobacter koseri ATCC BAA-895] >gnl BL_ORD_ID 2190813 hypothetical protein CKO_01624 [Citrobacter koseri ATCC BAA-895]	391	0	1 - 391 (22.57%)
46	NR gi 197248302 ref YP_002146578.1 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Agona str. SL483] >gnl BL_ORD_ID 2875284 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Javiana str. GA_MM04042433] >gnl BL_ORD_ID 2875284 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Paratyphi C strain RKS4594] >gnl BL_ORD_ID 2875284 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Agona str. SL483] >gnl BL_ORD_ID 2875284 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Javiana str. GA_MM04042433] >gnl BL_ORD_ID 2875284 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Paratyphi C strain RKS4594]	391	0	1 - 391 (22.11%)
47	NR gi 161503437 ref YP_001570549.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. arizonae serovar 62:z4,z23:-- str. RSK2980] >gnl BL_ORD_ID 2388424 hypothetical protein SARI_01511 [Salmonella enterica subsp. arizonae serovar 62:z4,z23:--]	391	0	1 - 391 (22.11%)
48	NR gi 168235542 ref ZP_02660600.1 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Schwarzengrund str. SL480] >gnl BL_ORD_ID 2833411 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633] >gnl BL_ORD_ID 2833411 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633] >gnl BL_ORD_ID 2833411 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Schwarzengrund str. SL480]	391	0	1 - 391 (22.04%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
49	NR gi 197264732 ref ZP_03164806.1 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA23] >gnl BL_ORD_ID 2672530 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853] >gnl BL_ORD_ID 2672530 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91] >gnl BL_ORD_ID 2672530 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Enteritidis str. P125109] >gnl BL_ORD_ID 2672530 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA23] >gnl BL_ORD_ID 2672530 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853] >gnl BL_ORD_ID 2672530 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91] >gnl BL_ORD_ID 2672530 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Enteritidis str. P125109]	391	0	1 - 391 (22.11%)
50	NR gi 323129735 gb ADX17165.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhimurium str. 4/74]	391	0	1 - 391 (22.11%)
51	NR gi 254220876 pdb 2WFP A Chain A, Crystal Structure Of Mannose 6-Phosphate Isomerase (Apo Form) From Salmonella Typhimurium	391	0	1 - 391 (22.11%)
52	NR gi 237824017 pdb 3H1M A Chain A, Crystal Structure Of Mannose 6-Phosphate Isomerase (Holo; Zinc Bound) >gnl BL_ORD_ID 2783023 Chain A, Crystal Structure Of Mannose 6-Phosphate Isomerase Bound With Zinc And Yttrium >gnl BL_ORD_ID 2783023 Chain A, Crystal Structure Of Mannose 6-Phosphate Isomerase From Salmonella Typhimurium Bound To Substrate (F6p)and Metal Atom (Zn)	391	0	1 - 391 (22.11%)
53	NR gi 168819219 ref ZP_02831219.1 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Weltevreden str. HI_N05-537] >gnl BL_ORD_ID 11291 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Weltevreden str. HI_N05-537] >gnl BL_ORD_ID 11291 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Weltevreden str. 2007-60-3289-1]	391	0	1 - 391 (22.11%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
54	NR gi 168240983 ref ZP_02665915.1 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Heidelberg str. SL486] >gnl BL_ORD_ID 2877942 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Hadar str. RI_05P066] >gnl BL_ORD_ID 2877942 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Newport str. SL317] >gnl BL_ORD_ID 2877942 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Virchow str. SL491] >gnl BL_ORD_ID 2877942 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Tennessee str. CDC07-0191] >gnl BL_ORD_ID 2877942 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Newport str. SL317] >gnl BL_ORD_ID 2877942 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Virchow str. SL491] >gnl BL_ORD_ID 2877942 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Heidelberg str. SL486] >gnl BL_ORD_ID 2877942 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Hadar str. RI_05P066]	391	0	1 - 391 (22.04%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
55	<p>NR gi 16764813 ref NP_460428.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2] >gnl BL_ORD_ID 1046164 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701] >gnl BL_ORD_ID 1046164 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 1046164 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2] >gnl BL_ORD_ID 1046164 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701] >gnl BL_ORD_ID 1046164 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhimurium str. D23580] >gnl BL_ORD_ID 1046164 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhimurium str. 14028S] >gnl BL_ORD_ID 1046164 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344] >gnl BL_ORD_ID 1046164 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhimurium str. T000240] >gnl BL_ORD_ID 1046164 Mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhimurium str. TN061786]</p>	391	0	1 - 391 (22.11%)
56	<p>NR gi 194444393 ref YP_002040714.1 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Newport str. SL254] >gnl BL_ORD_ID 2879356 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Newport str. SL254]</p>	391	0	1 - 391 (22.11%)
57	<p>NR gi 291085400 ref ZP_06352970.2 mannose-6-phosphate isomerase, class I [Citrobacter youngae ATCC 29220] >gnl BL_ORD_ID 1648490 mannose-6-phosphate isomerase, class I [Citrobacter youngae ATCC 29220]</p>	391	0	1 - 391 (22.17%)
58	<p>NR gi 283785169 ref YP_003365034.1 mannose-6-phosphate isomerase [Citrobacter rodentium ICC168] >gnl BL_ORD_ID 1340951 mannose-6-phosphate isomerase [Citrobacter rodentium ICC168]</p>	391	0	1 - 391 (22.17%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
59	NR gi 168229843 ref ZP_02654901.1 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Kentucky str. CDC 191] >gnl BL_ORD_ID 2831877 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Kentucky str. CVM29188] >gnl BL_ORD_ID 2831877 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Kentucky str. CVM29188] >gnl BL_ORD_ID 2831877 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Kentucky str. CDC 191]	391	0	1 - 391 (22.04%)
60	NR gi 167551560 ref ZP_02345314.1 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29] >gnl BL_ORD_ID 2674434 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29]	391	0	1 - 391 (22.04%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
61	<p>NR gi 322616085 gb EFY13001.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. 315996572] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. 495297-1] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. 495297-3] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. 495297-4] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. 515920-1] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. 515920-2] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. 531954] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. NC_MB110209-0054] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. OH_2009072675] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. CASC_09SCPH15965] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. 19N] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. 81038-01] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. MD_MDA09249507] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. 414877] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. 366867] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. 413180] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. 446600] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. 609458-1] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. 556150-1] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. 609460] >gnl BL_ORD_ID 1259180 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica</p>	391	0	1 - 391 (22.04%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
62	NR gi 161614113 ref YP_001588078.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7] >gnl BL_ORD_ID 2425487 hypothetical protein SPAB_01852 [Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7]	391	0	1 - 391 (22.04%)
63	NR gi 48820 emb CAA40399.1 phosphomannose isomerase [Salmonella enterica subsp. enterica serovar Typhimurium]	391	0	1 - 391 (22.04%)
64	NR gi 16760448 ref NP_456065.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. CT18] >gnl BL_ORD_ID 1039110 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. Ty2] >gnl BL_ORD_ID 1039110 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. E00-7866] >gnl BL_ORD_ID 1039110 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. E02-1180] >gnl BL_ORD_ID 1039110 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. E98-0664] >gnl BL_ORD_ID 1039110 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. M223] >gnl BL_ORD_ID 1039110 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. E98-3139] >gnl BL_ORD_ID 1039110 mannose-6-phosphate isomerase [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) >gnl BL_ORD_ID 1039110 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi] >gnl BL_ORD_ID 1039110 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. Ty2]	391	0	1 - 391 (22.04%)
65	NR gi 194447515 ref YP_002045503.1 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Heidelberg str. SL476] >gnl BL_ORD_ID 2878885 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Heidelberg str. SL476]	391	0	1 - 391 (21.98%)
66	NR gi 296102626 ref YP_003612772.1 mannose-6-phosphate isomerase [Enterobacter cloacae subsp. cloacae ATCC 13047] >gnl BL_ORD_ID 1982140 mannose-6-phosphate isomerase [Enterobacter cloacae subsp. cloacae ATCC 13047]	391	0	1 - 391 (21.91%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
67	NR gi 56413567 ref YP_150642.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] >gnl BL_ORD_ID 1839550 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601] >gnl BL_ORD_ID 1839550 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] >gnl BL_ORD_ID 1839550 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601]	391	0	1 - 391 (21.98%)
68	NR gi 309788436 ref ZP_07683040.1 mannose-6-phosphate isomerase, class I [Shigella dysenteriae 1617] >gnl BL_ORD_ID 306977 mannose-6-phosphate isomerase, class I [Shigella dysenteriae 1617]	344	0	48 - 391 (28.73%)
69	NR gi 102621435 gb ABF71065.1 mannose-6-phosphate isomerase [Enterobacter cloacae]	391	0	1 - 391 (21.85%)
70	NR gi 237731421 ref ZP_04561902.1 phosphohexomutase [Citrobacter sp. 30_2] >gnl BL_ORD_ID 2230085 phosphohexomutase [Citrobacter sp. 30_2]	391	0	1 - 391 (21.98%)
71	NR gi 146311486 ref YP_001176560.1 mannose-6-phosphate isomerase [Enterobacter sp. 638] >gnl BL_ORD_ID 916920 mannose-6-phosphate isomerase, type 1 [Enterobacter sp. 638]	390	0	1 - 390 (21.70%)
72	NR gi 261339623 ref ZP_05967481.1 mannose-6-phosphate isomerase, class I [Enterobacter cancerogenus ATCC 35316] >gnl BL_ORD_ID 2069180 mannose-6-phosphate isomerase, class I [Enterobacter cancerogenus ATCC 35316]	391	0	1 - 391 (21.59%)
73	NR gi 295096009 emb CBK85099.1 mannose-6-phosphate isomerase, type 1 [Enterobacter cloacae subsp. cloacae NCTC 9394]	391	0	1 - 391 (21.52%)
74	NR gi 323254823 gb EGA38620.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2010008283]	384	0	8 - 391 (22.31%)
75	NR gi 323221986 gb EGA06374.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Montevideo str. MB102109-0047]	376	0	16 - 391 (22.70%)
76	NR gi 311279519 ref YP_003941750.1 mannose-6-phosphate isomerase, class I [Enterobacter cloacae SCF1] >gnl BL_ORD_ID 288129 mannose-6-phosphate isomerase, class I [Enterobacter cloacae SCF1]	391	0	1 - 391 (20.87%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
77	NR gi 260597811 ref YP_003210382.1 mannose-6-phosphate isomerase [Cronobacter turicensis z3032] >gnl BL_ORD_ID 822737 Mannose-6-phosphate isomerase [Cronobacter turicensis z3032]	391	0	1 - 391 (20.80%)
78	NR gi 156934141 ref YP_001438057.1 hypothetical protein ESA_01968 [Cronobacter sakazakii ATCC BAA-894] >gnl BL_ORD_ID 2119014 hypothetical protein ESA_01968 [Cronobacter sakazakii ATCC BAA-894]	391	0	1 - 391 (20.67%)
79	NR gi 206576919 ref YP_002238770.1 mannose-6-phosphate isomerase, class I [Klebsiella pneumoniae 342] >gnl BL_ORD_ID 936886 mannose-6-phosphate isomerase, class I [Klebsiella variicola At-22] >gnl BL_ORD_ID 936886 phosphomannose isomerase type I [Klebsiella sp. 1_1_55] >gnl BL_ORD_ID 936886 mannose-6-phosphate isomerase, class I [Klebsiella pneumoniae 342] >gnl BL_ORD_ID 936886 mannose-6-phosphate isomerase, class I [Klebsiella variicola At-22] >gnl BL_ORD_ID 936886 phosphomannose isomerase type I [Klebsiella sp. 1_1_55]	391	0	1 - 391 (20.60%)
80	NR gi 262042852 ref ZP_06016001.1 mannose-6-phosphate isomerase [Klebsiella pneumoniae subsp. rhinoscleromatis ATCC 13884] >gnl BL_ORD_ID 764340 mannose-6-phosphate isomerase [Klebsiella pneumoniae subsp. rhinoscleromatis ATCC 13884]	391	0	1 - 391 (20.54%)
81	NR gi 238894530 ref YP_002919264.1 mannose-6-phosphate isomerase [Klebsiella pneumoniae NTUH-K2044] >gnl BL_ORD_ID 2823959 mannose-6-phosphate isomerase [Klebsiella pneumoniae NTUH-K2044]	391	0	1 - 391 (20.54%)
82	NR gi 152970067 ref YP_001335176.1 mannose-6-phosphate isomerase [Klebsiella pneumoniae subsp. pneumoniae MGH 78578] >gnl BL_ORD_ID 1941245 mannose-6-phosphate isomerase [Klebsiella pneumoniae subsp. pneumoniae MGH 78578]	391	0	1 - 391 (20.54%)
83	NR gi 62180054 ref YP_216471.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67] >gnl BL_ORD_ID 1886543 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67] >gnl BL_ORD_ID 1886543 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Choleraesuis str. A50]	359	0	33 - 391 (23.97%)
84	NR gi 297518688 ref ZP_06937074.1 mannose-6-phosphate isomerase [Escherichia coli OP50]	300	0	92 - 391 (33.22%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
85	NR gi 293396219 ref ZP_06640499.1 mannose-6-phosphate isomerase [Serratia odorifera DSM 4582] >gnl BL_ORD_ID 1740062 mannose-6-phosphate isomerase [Serratia odorifera DSM 4582]	391	0	1 - 391 (18.90%)
86	NR gi 270261697 ref ZP_06189970.1 mannose-6-phosphate isomerase [Serratia odorifera 4Rx13] >gnl BL_ORD_ID 1155321 mannose-6-phosphate isomerase [Serratia odorifera 4Rx13]	391	0	1 - 391 (18.97%)
87	NR gi 157370517 ref YP_001478506.1 mannose-6-phosphate isomerase, class I [Serratia proteamaculans 568] >gnl BL_ORD_ID 822806 mannose-6-phosphate isomerase, class I [Serratia proteamaculans 568]	391	0	1 - 391 (19.10%)
88	NR gi 227326436 ref ZP_03830460.1 mannose-6-phosphate isomerase [Pectobacterium carotovorum subsp. carotovorum WPP14]	390	0	1 - 390 (18.54%)
89	NR gi 253688426 ref YP_003017616.1 mannose-6-phosphate isomerase, class I [Pectobacterium carotovorum subsp. carotovorum PC1] >gnl BL_ORD_ID 276422 mannose-6-phosphate isomerase, class I [Pectobacterium carotovorum subsp. carotovorum PC1]	390	0	1 - 390 (18.41%)
90	NR gi 322832916 ref YP_004212943.1 mannose-6-phosphate isomerase, class I [Rahnella sp. Y9602] >gnl BL_ORD_ID 1178645 mannose-6-phosphate isomerase, class I [Rahnella sp. Y9602]	391	0	1 - 391 (18.38%)
91	NR gi 227111398 ref ZP_03825054.1 mannose-6-phosphate isomerase [Pectobacterium carotovorum subsp. brasiliensis PBR1692]	390	0	1 - 390 (18.41%)
92	NR gi 307131008 ref YP_003883024.1 mannose-6-phosphate isomerase [Dickeya dadantii 3937] >gnl BL_ORD_ID 4784 mannose-6-phosphate isomerase [Dickeya dadantii 3937]	390	0	1 - 390 (18.54%)
93	NR gi 283105184 gb ADB11058.1 mannose-6-isomerase [Serratia marcescens]	391	0	1 - 391 (18.45%)
94	NR gi 300716551 ref YP_003741354.1 Mannose-6-phosphate isomerase [Erwinia billingiae Eb661] >gnl BL_ORD_ID 2416255 Mannose-6-phosphate isomerase [Erwinia billingiae Eb661]	391	0	1 - 391 (18.58%)
95	NR gi 304397742 ref ZP_07379619.1 mannose-6-phosphate isomerase, class I [Pantoea sp. aB] >gnl BL_ORD_ID 2859672 mannose-6-phosphate isomerase, class I [Pantoea sp. aB]	391	0	1 - 391 (18.25%)
96	NR gi 251789739 ref YP_003004460.1 mannose-6-phosphate isomerase, class I [Dickeya zeae Ech1591] >gnl BL_ORD_ID 270131 mannose-6-phosphate isomerase, class I [Dickeya zeae Ech1591]	390	0	1 - 390 (18.28%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
97	NR gi 50121191 ref YP_050358.1 mannose-6-phosphate isomerase [Pectobacterium atrosepticum SCRI1043] >gnl BL_ORD_ID 1297522 mannose-6-phosphate isomerase [Pectobacterium atrosepticum SCRI1043]	390	0	1 - 390 (18.28%)
98	NR gi 308186766 ref YP_003930897.1 mannose-6-phosphate isomerase [Pantoea vagans C9-1] >gnl BL_ORD_ID 201029 mannose-6-phosphate isomerase [Pantoea vagans C9-1]	391	0	1 - 391 (18.12%)
99	NR gi 261821611 ref YP_003259717.1 mannose-6-phosphate isomerase, class I [Pectobacterium wasabiae WPP163] >gnl BL_ORD_ID 946825 mannose-6-phosphate isomerase, class I [Pectobacterium wasabiae WPP163]	390	0	1 - 390 (18.21%)
100	NR gi 271500620 ref YP_003333645.1 mannose-6-phosphate isomerase, class I [Dickeya dadantii Ech586] >gnl BL_ORD_ID 719714 mannose-6-phosphate isomerase, class I [Dickeya dadantii Ech586]	390	0	1 - 390 (18.28%)
101	NR gi 318605686 emb CBY27184.1 mannose-6-phosphate isomerase [Yersinia enterocolitica subsp. palearctica Y11]	389	0	1 - 389 (18.50%)
102	NR gi 123442286 ref YP_001006267.1 mannose-6-phosphate isomerase [Yersinia enterocolitica subsp. enterocolitica 8081] >gnl BL_ORD_ID 1172383 mannose-6-phosphate isomerase [Yersinia enterocolitica subsp. enterocolitica 8081]	389	0	1 - 389 (18.44%)
103	NR gi 238752201 ref ZP_04613682.1 Mannose-6-phosphate isomerase [Yersinia rohdei ATCC 43380] >gnl BL_ORD_ID 2854761 Mannose-6-phosphate isomerase [Yersinia rohdei ATCC 43380]	390	0	1 - 390 (18.21%)
104	NR gi 317047984 ref YP_004115632.1 mannose-6-phosphate isomerase, class I [Pantoea sp. At-9b] >gnl BL_ORD_ID 725001 mannose-6-phosphate isomerase, class I [Pantoea sp. At-9b]	391	0	1 - 391 (18.05%)
105	NR gi 238796498 ref ZP_04640006.1 Mannose-6-phosphate isomerase [Yersinia mollaretii ATCC 43969] >gnl BL_ORD_ID 2860505 Mannose-6-phosphate isomerase [Yersinia mollaretii ATCC 43969]	389	0	1 - 389 (18.44%)
106	NR gi 238790182 ref ZP_04633958.1 Mannose-6-phosphate isomerase [Yersinia frederiksenii ATCC 33641] >gnl BL_ORD_ID 445425 Mannose-6-phosphate isomerase [Yersinia frederiksenii ATCC 33641]	389	0	1 - 389 (18.37%)
107	NR gi 238786030 ref ZP_04629990.1 Mannose-6-phosphate isomerase [Yersinia bercovieri ATCC 43970] >gnl BL_ORD_ID 441511 Mannose-6-phosphate isomerase [Yersinia bercovieri ATCC 43970]	389	0	1 - 389 (18.44%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
108	NR gi 153947728 ref YP_001400849.1 mannose-6-phosphate isomerase, class I [Yersinia pseudotuberculosis IP 31758] >gnl BL_ORD_ID 2001684 mannose-6-phosphate isomerase, class I [Yersinia pseudotuberculosis IP 31758]	391	0	1 - 391 (18.12%)
109	NR gi 238756499 ref ZP_04617804.1 Mannose-6-phosphate isomerase [Yersinia ruckeri ATCC 29473] >gnl BL_ORD_ID 2850747 Mannose-6-phosphate isomerase [Yersinia ruckeri ATCC 29473]	391	0	1 - 391 (17.66%)
110	NR gi 51596511 ref YP_070702.1 mannose-6-phosphate isomerase [Yersinia pseudotuberculosis IP 32953] >gnl BL_ORD_ID 1319292 mannose-6-phosphate isomerase [Yersinia pseudotuberculosis IP 32953]	389	0	1 - 389 (18.31%)
111	NR gi 238758589 ref ZP_04619764.1 Mannose-6-phosphate isomerase [Yersinia aldovae ATCC 35236] >gnl BL_ORD_ID 2848742 Mannose-6-phosphate isomerase [Yersinia aldovae ATCC 35236]	389	0	1 - 389 (18.24%)
112	NR gi 238792160 ref ZP_04635795.1 Mannose-6-phosphate isomerase [Yersinia intermedia ATCC 29909] >gnl BL_ORD_ID 446957 Mannose-6-phosphate isomerase [Yersinia intermedia ATCC 29909]	389	0	1 - 389 (18.11%)
113	NR gi 22125994 ref NP_669417.1 mannose-6-phosphate isomerase [Yersinia pestis KIM 10] >gnl BL_ORD_ID 2727241 mannose-6-phosphate isomerase [Yersinia pestis Antiqua] >gnl BL_ORD_ID 2727241 mannose-6-phosphate isomerase [Yersinia pestis Nepal516] >gnl BL_ORD_ID 2727241 mannose-6-phosphate isomerase [Yersinia pestis Pestoides F] >gnl BL_ORD_ID 2727241 mannose-6-phosphate isomerase [Yersinia pestis KIM 10] >gnl BL_ORD_ID 2727241 mannose-6-phosphate isomerase [Yersinia pestis Nepal516] >gnl BL_ORD_ID 2727241 mannose-6-phosphate isomerase [Yersinia pestis Antiqua] >gnl BL_ORD_ID 2727241 mannose-6-phosphate isomerase [Yersinia pestis Pestoides F]	389	0	1 - 389 (18.24%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
114	<p>NR gi 45441857 ref NP_993396.1 mannose-6-phosphate isomerase [Yersinia pestis biovar Microtus str. 91001] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase [Yersinia pestis CA88-4125] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase [Yersinia pestis Angola] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase, class I [Yersinia pestis biovar Orientalis str. F1991016] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase, class I [Yersinia pestis biovar Orientalis str. IP275] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase, class I [Yersinia pestis biovar Antiqua str. E1979001] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase, class I [Yersinia pestis biovar Antiqua str. B42003004] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase, class I [Yersinia pestis biovar Antiqua str. UG05-0454] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase, class I [Yersinia pestis biovar Orientalis str. MG05-1020] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase, class I [Yersinia pestis biovar Mediaevalis str. K1973002] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase [Yersinia pestis FV-1] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase [Yersinia pestis CO92] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase [Yersinia pestis Pestoides A] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase [Yersinia pestis biovar Orientalis str. PEXU2] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase [Yersinia pestis biovar Orientalis str. India 195] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase [Yersinia pestis Nepal516] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase, class I [Yersinia pestis KIM D27] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase [Yersinia pestis Z176003] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase [Yersinia pestis biovar Microtus str. 91001] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase [Yersinia pestis CO92] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase [Yersinia pestis CA88-4125] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase, class I [Yersinia pestis Angola] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase, class I [Yersinia pestis biovar Orientalis str. IP275] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase, class I [Yersinia pestis biovar Orientalis str. F1991016] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase, class I [Yersinia pestis biovar Antiqua str. E1979001] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase, class I [Yersinia pestis biovar Antiqua str. B42003004] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase, class I [Yersinia pestis biovar Orientalis str. MG05-1020] >gnl BL_ORD_ID 995830 mannose-6-phosphate isomerase, class I [Yersinia pestis biovar Antiqua</p>	389	0	1 - 389 (18.24%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
115	NR gi 238762629 ref ZP_04623599.1 Mannose-6-phosphate isomerase [Yersinia kristensenii ATCC 33638] >gnl BL_ORD_ID 2845462 Mannose-6-phosphate isomerase [Yersinia kristensenii ATCC 33638]	390	0	1 - 390 (18.02%)
116	NR gi 317492063 ref ZP_07950494.1 phosphomannose isomerase type I [Enterobacteriaceae bacterium 9_2_54FAA] >gnl BL_ORD_ID 888289 phosphomannose isomerase type I [Enterobacteriaceae bacterium 9_2_54FAA]	391	0	1 - 391 (17.14%)
117	NR gi 291617385 ref YP_003520127.1 ManA [Pantoea ananatis LMG 20103] >gnl BL_ORD_ID 1656777 ManA [Pantoea ananatis LMG 20103]	391	0	1 - 391 (17.20%)
118	NR gi 242239333 ref YP_002987514.1 mannose-6-phosphate isomerase, class I [Dickeya dadantii Ech703] >gnl BL_ORD_ID 241262 mannose-6-phosphate isomerase, class I [Dickeya dadantii Ech703]	390	0	1 - 390 (17.55%)
119	NR gi 85059439 ref YP_455141.1 mannose-6-phosphate isomerase [Sodalis glossinidius str. 'morsitans'] >gnl BL_ORD_ID 1506822 mannose-6-phosphate isomerase [Sodalis glossinidius str. 'morsitans']	389	0	1 - 389 (17.51%)
120	NR gi 269139056 ref YP_003295757.1 mannose-6-phosphate isomerase, class I [Edwardsiella tarda EIB202] >gnl BL_ORD_ID 1070660 mannose-6-phosphate isomerase, class I [Edwardsiella tarda EIB202] >gnl BL_ORD_ID 1070660 mannose-6-phosphate isomerase, class I [Edwardsiella tarda FL6-60]	391	0	1 - 391 (16.48%)
121	NR gi 186895562 ref YP_001872674.1 mannose-6-phosphate isomerase, class I [Yersinia pseudotuberculosis PB1/+] >gnl BL_ORD_ID 288320 mannose-6-phosphate isomerase, class I [Yersinia pseudotuberculosis PB1/+]	357	0	33 - 389 (20.17%)
122	NR gi 238919975 ref YP_002933490.1 mannose-6-phosphate isomerase, class I, putative [Edwardsiella ictaluri 93-146] >gnl BL_ORD_ID 2890306 mannose-6-phosphate isomerase, class I, putative [Edwardsiella ictaluri 93-146]	391	0	1 - 391 (16.29%)
123	NR gi 170024223 ref YP_001720728.1 mannose-6-phosphate isomerase, class I [Yersinia pseudotuberculosis YPIII] >gnl BL_ORD_ID 83291 mannose-6-phosphate isomerase, class I [Yersinia pseudotuberculosis YPIII]	357	0	33 - 389 (20.17%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
124	NR gi 294636355 ref ZP_06714748.1 mannose-6-phosphate isomerase, class I [Edwardsiella tarda ATCC 23685] >gnl BL_ORD_ID 1652697 mannose-6-phosphate isomerase, class I [Edwardsiella tarda ATCC 23685]	391	0	1 - 391 (16.22%)
125	NR gi 253989637 ref YP_003040993.1 mannose-6-phosphate isomerase [Photorhabdus asymbiotica subsp. asymbiotica ATCC 43949] >gnl BL_ORD_ID 322081 mannose-6-phosphate isomerase [Photorhabdus asymbiotica]	390	0	1 - 389 (15.58%)
126	NR gi 37526262 ref NP_929606.1 mannose-6-phosphate isomerase (phosphomannose isomerase) (phosphohexomutase) (PMI) [Photorhabdus luminescens subsp. laumondii TTO1] >gnl BL_ORD_ID 1180691 mannose-6-phosphate isomerase (phosphomannose isomerase) (phosphohexomutase) (PMI) [Photorhabdus luminescens subsp. laumondii TTO1]	390	0	1 - 389 (15.38%)
127	NR gi 291326255 ref ZP_06123748.2 mannose-6-phosphate isomerase, class I [Providencia rettgeri DSM 1131] >gnl BL_ORD_ID 2095004 mannose-6-phosphate isomerase, class I [Providencia rettgeri DSM 1131]	391	0	1 - 390 (15.24%)
128	NR gi 300723249 ref YP_003712549.1 mannose-6-phosphate isomerase [Xenorhabdus nematophila ATCC 19061] >gnl BL_ORD_ID 2295341 mannose-6-phosphate isomerase [Xenorhabdus nematophila ATCC 19061]	390	0	1 - 389 (15.25%)
129	NR gi 290475326 ref YP_003468214.1 mannose-6-phosphate isomerase [Xenorhabdus bovienii SS-2004] >gnl BL_ORD_ID 1525388 mannose-6-phosphate isomerase [Xenorhabdus bovienii SS-2004]	392	5.61×10^{-129}	1 - 389 (14.71%)
130	NR gi 282599641 ref ZP_05971324.2 mannose-6-phosphate isomerase, class I [Providencia rustigianii DSM 4541] >gnl BL_ORD_ID 2077164 mannose-6-phosphate isomerase, class I [Providencia rustigianii DSM 4541]	390	5.61×10^{-129}	1 - 389 (14.86%)
131	NR gi 183599233 ref ZP_02960726.1 hypothetical protein PROSTU_02692 [Providencia stuartii ATCC 25827] >gnl BL_ORD_ID 253422 hypothetical protein PROSTU_02692 [Providencia stuartii ATCC 25827]	391	2.36×10^{-127}	1 - 389 (14.91%)
132	NR gi 212711773 ref ZP_03319901.1 hypothetical protein PROVALCAL_02848 [Providencia alcalifaciens DSM 30120] >gnl BL_ORD_ID 1196427 hypothetical protein PROVALCAL_02848 [Providencia alcalifaciens DSM 30120]	390	2.88×10^{-125}	1 - 389 (14.20%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
133	NR gi 213609628 ref ZP_03369454.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. E98-2068]	260	1.13 x 10 ⁻¹²¹	132 - 391 (33.13%)
134	NR gi 284007522 emb CBA73023.1 mannose-6-phosphate isomerase (phosphomannose isomerase) (phosphohexomutase) (PMI) [Arsenophonus nasoniae]	390	1.48 x 10 ⁻¹²¹	1 - 389 (14.53%)
135	NR gi 238897710 ref YP_002923389.1 mannose-6-phosphate isomerase [Candidatus Hamiltonella defensa 5AT (Acyrtosiphon pisum)] >gnl BL_ORD_ID 2701979 mannose-6-phosphate isomerase [Candidatus Hamiltonella defensa 5AT (Acyrtosiphon pisum)]	387	7.11 x 10 ⁻¹¹⁶	1 - 387 (14.22%)
136	NR gi 237809241 ref YP_002893681.1 mannose-6-phosphate isomerase, class I [Tolomonas auensis DSM 9187] >gnl BL_ORD_ID 1782961 mannose-6-phosphate isomerase, class I [Tolomonas auensis DSM 9187]	388	3.91 x 10 ⁻¹⁰⁶	3 - 387 (13.29%)
137	NR gi 269959908 ref ZP_06174285.1 conserved hypothetical protein [Vibrio harveyi 1DA3] >gnl BL_ORD_ID 1119012 conserved hypothetical protein [Vibrio harveyi 1DA3]	394	1.06 x 10 ⁻¹⁰³	3 - 389 (12.43%)
138	NR gi 84387455 ref ZP_00990474.1 phosphomannose isomerase [Vibrio splendidus 12B01] >gnl BL_ORD_ID 528953 phosphomannose isomerase [Vibrio splendidus 12B01]	396	3.10 x 10 ⁻¹⁰³	3 - 389 (12.56%)
139	NR gi 218676383 ref YP_002395202.1 putative mannose-6-phosphate isomerase [Vibrio splendidus LGP32] >gnl BL_ORD_ID 1401992 putative mannose-6-phosphate isomerase [Vibrio splendidus LGP32]	396	2.62 x 10 ⁻¹⁰²	3 - 389 (12.37%)
140	NR gi 86146687 ref ZP_01065008.1 phosphomannose isomerase [Vibrio sp. MED222] >gnl BL_ORD_ID 589308 phosphomannose isomerase [Vibrio sp. MED222]	396	7.63 x 10 ⁻¹⁰²	3 - 389 (12.37%)
141	NR gi 261251959 ref ZP_05944533.1 mannose-6-phosphate isomerase [Vibrio orientalis CIP 102891] >gnl BL_ORD_ID 908589 mannose-6-phosphate isomerase [Vibrio orientalis CIP 102891]	394	6.46 x 10 ⁻¹⁰¹	3 - 389 (12.24%)
142	NR gi 323496219 ref ZP_08101277.1 phosphomannose isomerase [Vibrio sinaloensis DSM 21326] >gnl BL_ORD_ID 1348115 phosphomannose isomerase [Vibrio sinaloensis DSM 21326]	394	1.03 x 10 ⁻⁹⁸	3 - 389 (12.18%)
143	NR gi 269960352 ref ZP_06174726.1 conserved hypothetical protein [Vibrio harveyi 1DA3] >gnl BL_ORD_ID 1118791 conserved hypothetical protein [Vibrio harveyi 1DA3]	394	6.68 x 10 ⁻⁹⁸	3 - 389 (12.05%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
144	NR gi 153832585 ref ZP_01985252.1 mannose-6-phosphate isomerase, class I [Vibrio harveyi HY01] >gnl BL_ORD_ID 1747074 mannose-6-phosphate isomerase, class I [Vibrio harveyi HY01]	394	5.66 x 10 ⁻⁹⁷	3 - 389 (12.05%)
145	NR gi 260779133 ref ZP_05888025.1 mannose-6-phosphate isomerase [Vibrio coralliilyticus ATCC BAA-450] >gnl BL_ORD_ID 859828 mannose-6-phosphate isomerase [Vibrio coralliilyticus ATCC BAA-450]	389	2.15 x 10 ⁻⁹⁶	4 - 388 (12.29%)
146	NR gi 37675847 ref NP_936243.1 phosphomannose isomerase [Vibrio vulnificus YJ016] >gnl BL_ORD_ID 1181903 phosphomannose isomerase [Vibrio vulnificus YJ016]	386	1.82 x 10 ⁻⁹⁵	4 - 386 (12.89%)
147	NR gi 315182488 gb ADT89401.1 phosphomannose isomerase [Vibrio furnissii NCTC 11218]	394	9.03 x 10 ⁻⁹⁵	3 - 389 (12.05%)
148	NR gi 315178402 gb ADT85316.1 mannose-6-phosphate isomerase, class I [Vibrio furnissii NCTC 11218]	388	2.01 x 10 ⁻⁹⁴	6 - 389 (12.22%)
149	NR gi 27367718 ref NP_763245.1 phosphomannose isomerase [Vibrio vulnificus CMCP6] >gnl BL_ORD_ID 1620337 mannose-6-phosphate isomerase, class I [Vibrio vulnificus CMCP6]	386	5.86 x 10 ⁻⁹⁴	4 - 386 (12.82%)
150	NR gi 153835970 ref ZP_01988637.1 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus AQ3810] >gnl BL_ORD_ID 1848816 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus AQ3810]	387	9.99 x 10 ⁻⁹⁴	6 - 389 (12.29%)
151	NR gi 260774386 ref ZP_05883300.1 mannose-6-phosphate isomerase [Vibrio metschnikovii CIP 69.14] >gnl BL_ORD_ID 863939 mannose-6-phosphate isomerase [Vibrio metschnikovii CIP 69.14]	388	2.22 x 10 ⁻⁹³	6 - 389 (12.62%)
152	NR gi 320157996 ref YP_004190374.1 mannose-6-phosphate isomerase [Vibrio vulnificus MO6-24/O] >gnl BL_ORD_ID 1069944 mannose-6-phosphate isomerase [Vibrio vulnificus MO6-24/O]	387	2.91 x 10 ⁻⁹³	4 - 386 (12.82%)
153	NR gi 153800446 ref ZP_01955032.1 mannose-6-phosphate isomerase [Vibrio cholerae MZO-3] >gnl BL_ORD_ID 1195992 mannose-6-phosphate isomerase [Vibrio cholerae V51] >gnl BL_ORD_ID 1195992 mannose-6-phosphate isomerase [Vibrio cholerae MZO-3] >gnl BL_ORD_ID 1195992 mannose-6-phosphate isomerase [Vibrio cholerae V51]	390	3.80 x 10 ⁻⁹³	4 - 389 (12.43%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
154	NR gi 229508074 ref ZP_04397579.1 mannose-6-phosphate isomerase [Vibrio cholerae BX 330286] >gnl BL_ORD_ID 2654857 mannose-6-phosphate isomerase [Vibrio cholerae B33] >gnl BL_ORD_ID 2654857 mannose-6-phosphate isomerase [Vibrio cholerae RC9] >gnl BL_ORD_ID 2654857 mannose-6-phosphate isomerase [Vibrio cholerae MJ-1236] >gnl BL_ORD_ID 2654857 mannose-6-phosphate isomerase [Vibrio cholerae RC9] >gnl BL_ORD_ID 2654857 mannose-6-phosphate isomerase [Vibrio cholerae B33] >gnl BL_ORD_ID 2654857 mannose-6-phosphate isomerase [Vibrio cholerae BX 330286] >gnl BL_ORD_ID 2654857 mannose-6-phosphate isomerase [Vibrio cholerae MJ-1236]	390	6.47 x 10 ⁻⁹³	4 - 389 (12.43%)
155	NR gi 254848915 ref ZP_05238265.1 mannose-6-phosphate isomerase [Vibrio cholerae MO10] >gnl BL_ORD_ID 2546550 mannose-6-phosphate isomerase [Vibrio cholera CIRS 101] >gnl BL_ORD_ID 2546550 mannose-6-phosphate isomerase [Vibrio cholerae INDRE 91/1] >gnl BL_ORD_ID 2546550 mannose-6-phosphate isomerase [Vibrio cholerae RC27] >gnl BL_ORD_ID 2546550 phosphomannose isomerase type I [Vibrio cholerae MAK 757] >gnl BL_ORD_ID 2546550 mannose-6-phosphate isomerase [Vibrio cholerae MO10] >gnl BL_ORD_ID 2546550 mannose-6-phosphate isomerase [Vibrio cholera CIRS 101] >gnl BL_ORD_ID 2546550 mannose-6-phosphate isomerase [Vibrio cholerae RC27] >gnl BL_ORD_ID 2546550 mannose-6-phosphate isomerase [Vibrio cholerae INDRE 91/1] >gnl BL_ORD_ID 2546550 phosphomannose isomerase type I [Vibrio cholerae MAK 757]	390	6.47 x 10 ⁻⁹³	4 - 389 (12.43%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
156	NR gi 15641829 ref NP_231461.1 mannose-6-phosphate isomerase [Vibrio cholerae O1 biovar El Tor str. N16961] >gnl BL_ORD_ID 1678772 mannose-6-phosphate isomerase [Vibrio cholerae 2740-80] >gnl BL_ORD_ID 1678772 mannose-6-phosphate isomerase [Vibrio cholerae O395] >gnl BL_ORD_ID 1678772 mannose-6-phosphate isomerase [Vibrio cholerae NCTC 8457] >gnl BL_ORD_ID 1678772 mannose-6-phosphate isomerase [Vibrio cholerae B33] >gnl BL_ORD_ID 1678772 mannose-6-phosphate isomerase [Vibrio cholerae M66-2] >gnl BL_ORD_ID 1678772 mannose-6-phosphate isomerase [Vibrio cholerae O1 biovar El Tor str. N16961] >gnl BL_ORD_ID 1678772 mannose-6-phosphate isomerase [Vibrio cholerae 2740-80] >gnl BL_ORD_ID 1678772 mannose-6-phosphate isomerase [Vibrio cholerae NCTC 8457] >gnl BL_ORD_ID 1678772 mannose-6-phosphate isomerase [Vibrio cholerae B33] >gnl BL_ORD_ID 1678772 mannose-6-phosphate isomerase [Vibrio cholerae O395] >gnl BL_ORD_ID 1678772 mannose-6-phosphate isomerase [Vibrio cholerae M66-2] >gnl BL_ORD_ID 1678772 mannose-6-phosphate isomerase [Vibrio cholerae O395]	390	6.47 x 10 ⁻⁹³	4 - 389 (12.43%)
157	NR gi 37677050 ref NP_937446.1 phosphomannose isomerase [Vibrio vulnificus YJ016] >gnl BL_ORD_ID 1184681 phosphomannose isomerase [Vibrio vulnificus YJ016]	397	6.47 x 10 ⁻⁹³	3 - 389 (11.68%)
158	NR gi 262404175 ref ZP_06080730.1 mannose-6-phosphate isomerase [Vibrio sp. RC586] >gnl BL_ORD_ID 1037798 mannose-6-phosphate isomerase [Vibrio sp. RC586]	390	1.10 x 10 ⁻⁹²	4 - 389 (12.43%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
159	NR gi 28901280 ref NP_800935.1 mannose-6-phosphate isomerase [Vibrio parahaemolyticus RIMD 2210633] >gnl BL_ORD_ID 1018139 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus AN-5034] >gnl BL_ORD_ID 1018139 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus Peru-466] >gnl BL_ORD_ID 1018139 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus K5030] >gnl BL_ORD_ID 1018139 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus AQ4037] >gnl BL_ORD_ID 1018139 mannose-6-phosphate isomerase [Vibrio parahaemolyticus RIMD 2210633] >gnl BL_ORD_ID 1018139 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus Peru-466] >gnl BL_ORD_ID 1018139 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus AN-5034] >gnl BL_ORD_ID 1018139 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus AQ4037] >gnl BL_ORD_ID 1018139 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus K5030]	387	1.44 x 10 ⁻⁹²	6 - 389 (12.22%)
160	NR gi 254229126 ref ZP_04922546.1 mannose-6-phosphate isomerase, class I [Vibrio sp. Ex25] >gnl BL_ORD_ID 404531 mannose-6-phosphate isomerase [Vibrio sp. Ex25] >gnl BL_ORD_ID 404531 mannose-6-phosphate isomerase, class I [Vibrio sp. Ex25] >gnl BL_ORD_ID 404531 mannose-6-phosphate isomerase [Vibrio sp. Ex25]	387	1.88 x 10 ⁻⁹²	6 - 389 (12.29%)
161	NR gi 229529148 ref ZP_04418538.1 mannose-6-phosphate isomerase [Vibrio cholerae 12129(1)] >gnl BL_ORD_ID 2649127 mannose-6-phosphate isomerase [Vibrio cholerae 12129(1)]	389	2.46 x 10 ⁻⁹²	4 - 389 (12.36%)
162	NR gi 117620647 ref YP_855973.1 mannose-6-phosphate isomerase, class I [Aeromonas hydrophila subsp. hydrophila ATCC 7966] >gnl BL_ORD_ID 779877 mannose-6-phosphate isomerase, class I [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	388	2.46 x 10 ⁻⁹²	6 - 390 (12.69%)
163	NR gi 153828574 ref ZP_01981241.1 mannose-6-phosphate isomerase [Vibrio cholerae 623-39] >gnl BL_ORD_ID 1749406 mannose-6-phosphate isomerase [Vibrio cholerae 623-39]	389	3.21 x 10 ⁻⁹²	4 - 389 (12.23%)
164	NR gi 145299855 ref YP_001142696.1 mannose-6-phosphate isomerase [Aeromonas salmonicida subsp. salmonicida A449] >gnl BL_ORD_ID 1479541 mannose-6-phosphate isomerase [Aeromonas salmonicida subsp. salmonicida A449]	388	3.21 x 10 ⁻⁹²	6 - 390 (12.75%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
165	NR gi 121727625 ref ZP_01680728.1 mannose-6-phosphate isomerase [Vibrio cholerae V52] >gnl BL_ORD_ID 400533 mannose-6-phosphate isomerase [Vibrio cholerae V52]	389	3.21 x 10 ⁻⁹²	4 - 389 (12.36%)
166	NR gi 269962875 ref ZP_06177215.1 conserved hypothetical protein [Vibrio harveyi 1DA3] >gnl BL_ORD_ID 1116462 conserved hypothetical protein [Vibrio harveyi 1DA3]	387	5.48 x 10 ⁻⁹²	6 - 389 (12.29%)
167	NR gi 262274375 ref ZP_06052186.1 mannose-6-phosphate isomerase [Grimontia hollisae CIP 101886] >gnl BL_ORD_ID 1004598 mannose-6-phosphate isomerase [Grimontia hollisae CIP 101886]	390	7.16 x 10 ⁻⁹²	4 - 389 (12.29%)
168	NR gi 153831539 ref ZP_01984206.1 mannose-6-phosphate isomerase, class I [Vibrio harveyi HY01] >gnl BL_ORD_ID 1746656 mannose-6-phosphate isomerase, class I [Vibrio harveyi HY01]	387	7.16 x 10 ⁻⁹²	6 - 389 (12.22%)
169	NR gi 163800232 ref ZP_02194133.1 mannose-6-phosphate isomerase [Vibrio sp. AND4] >gnl BL_ORD_ID 2344326 mannose-6-phosphate isomerase [Vibrio sp. AND4]	387	9.35 x 10 ⁻⁹²	6 - 389 (12.15%)
170	NR gi 156976410 ref YP_001447316.1 mannose-6-phosphate isomerase [Vibrio harveyi ATCC BAA-1116] >gnl BL_ORD_ID 2115417 hypothetical protein VIBHAR_05183 [Vibrio harveyi ATCC BAA-1116]	387	1.22 x 10 ⁻⁹¹	6 - 389 (12.22%)
171	NR gi 153832852 ref ZP_01985519.1 mannose-6-phosphate isomerase, class I [Vibrio harveyi HY01] >gnl BL_ORD_ID 1746862 mannose-6-phosphate isomerase, class I [Vibrio harveyi HY01]	394	1.22 x 10 ⁻⁹¹	3 - 389 (11.85%)
172	NR gi 54309876 ref YP_130896.1 putative mannose-6-phosphate isomerase [Photobacterium profundum SS9] >gnl BL_ORD_ID 1247307 putative mannose-6-phosphate isomerase [Photobacterium profundum SS9]	391	1.22 x 10 ⁻⁹¹	3 - 389 (12.10%)
173	NR gi 323491873 ref ZP_08097047.1 mannose-6-phosphate isomerase [Vibrio brasiliensis LMG 20546] >gnl BL_ORD_ID 1343709 mannose-6-phosphate isomerase [Vibrio brasiliensis LMG 20546]	399	2.08 x 10 ⁻⁹¹	4 - 389 (11.62%)
174	NR gi 197337261 ref YP_002158348.1 mannose-6-phosphate isomerase, class I [Vibrio fischeri MJ11] >gnl BL_ORD_ID 817697 mannose-6-phosphate isomerase, class I [Vibrio fischeri MJ11]	391	2.72 x 10 ⁻⁹¹	4 - 389 (11.91%)
175	NR gi 262191015 ref ZP_06049225.1 mannose-6-phosphate isomerase [Vibrio cholerae CT 5369-93] >gnl BL_ORD_ID 965682 mannose-6-phosphate isomerase [Vibrio cholerae CT 5369-93]	390	3.55 x 10 ⁻⁹¹	4 - 389 (12.43%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
176	NR gi 269959789 ref ZP_06174168.1 conserved hypothetical protein [Vibrio harveyi 1DA3] >gnl BL_ORD_ID 1119337 conserved hypothetical protein [Vibrio harveyi 1DA3]	395	1.03 x 10 ⁻⁹⁰	3 - 389 (11.67%)
177	NR gi 90410661 ref ZP_01218676.1 putative mannose-6-phosphate isomer [Photobacterium profundum 3TCK] >gnl BL_ORD_ID 172923 putative mannose-6-phosphate isomer [Photobacterium profundum 3TCK]	391	1.03 x 10 ⁻⁹⁰	3 - 389 (11.97%)
178	NR gi 258621422 ref ZP_05716456.1 phosphomannose isomerase [Vibrio mimicus VM573] >gnl BL_ORD_ID 735588 phosphomannose isomerase [Vibrio mimicus VM573]	390	1.35 x 10 ⁻⁹⁰	4 - 390 (12.36%)
179	NR gi 258626851 ref ZP_05721658.1 phosphomannose isomerase [Vibrio mimicus VM603] >gnl BL_ORD_ID 730660 phosphomannose isomerase [Vibrio mimicus VM603]	391	1.35 x 10 ⁻⁹⁰	4 - 390 (12.36%)
180	NR gi 59713893 ref YP_206668.1 mannose-6-phosphate isomerase [Vibrio fischeri ES114] >gnl BL_ORD_ID 2446422 mannose-6-phosphate isomerase [Vibrio fischeri ES114]	391	1.35 x 10 ⁻⁹⁰	4 - 389 (11.84%)
181	NR gi 261211893 ref ZP_05926180.1 mannose-6-phosphate isomerase [Vibrio sp. RC341] >gnl BL_ORD_ID 890195 mannose-6-phosphate isomerase [Vibrio sp. RC341]	389	1.76 x 10 ⁻⁹⁰	4 - 389 (12.42%)
182	NR gi 218677062 ref YP_002395881.1 Mannose-6-phosphate isomerase [Vibrio splendidus LGP32] >gnl BL_ORD_ID 1402578 Mannose-6-phosphate isomerase [Vibrio splendidus LGP32]	388	2.30 x 10 ⁻⁹⁰	4 - 389 (11.76%)
183	NR gi 297579348 ref ZP_06941276.1 mannose-6-phosphate isomerase [Vibrio cholerae RC385] >gnl BL_ORD_ID 1919412 mannose-6-phosphate isomerase [Vibrio cholerae RC385]	390	3.93 x 10 ⁻⁹⁰	4 - 389 (12.29%)
184	NR gi 262165942 ref ZP_06033679.1 mannose-6-phosphate isomerase [Vibrio mimicus VM223] >gnl BL_ORD_ID 962738 mannose-6-phosphate isomerase [Vibrio mimicus VM223]	391	5.13 x 10 ⁻⁹⁰	4 - 390 (12.30%)
185	NR gi 262171206 ref ZP_06038884.1 mannose-6-phosphate isomerase [Vibrio mimicus MB-451] >gnl BL_ORD_ID 960449 mannose-6-phosphate isomerase [Vibrio mimicus MB-451]	391	6.70 x 10 ⁻⁹⁰	4 - 390 (12.36%)
186	NR gi 269967731 ref ZP_06181779.1 putative mannose-6-phosphate isomerase [Vibrio alginolyticus 40B] >gnl BL_ORD_ID 1112780 putative mannose-6-phosphate isomerase [Vibrio alginolyticus 40B]	392	1.14 x 10 ⁻⁸⁹	6 - 389 (11.52%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
187	NR gi 86145001 ref ZP_01063333.1 mannose-6-phosphate isomerase [Vibrio sp. MED222] >gnl BL_ORD_ID 588974 mannose-6-phosphate isomerase [Vibrio sp. MED222]	388	1.49 x 10 ⁻⁸⁹	4 - 389 (11.69%)
188	NR gi 153836902 ref ZP_01989569.1 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus AQ3810] >gnl BL_ORD_ID 1848305 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus AQ3810]	392	1.95 x 10 ⁻⁸⁹	6 - 389 (11.45%)
189	NR gi 28900822 ref NP_800477.1 putative mannose-6-phosphate isomerase [Vibrio parahaemolyticus RIMD 2210633] >gnl BL_ORD_ID 936419 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus K5030] >gnl BL_ORD_ID 936419 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus Peru-466] >gnl BL_ORD_ID 936419 putative mannose-6-phosphate isomerase [Vibrio parahaemolyticus RIMD 2210633] >gnl BL_ORD_ID 936419 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus Peru-466] >gnl BL_ORD_ID 936419 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus K5030]	398	1.95 x 10 ⁻⁸⁹	6 - 389 (11.24%)
190	NR gi 156973026 ref YP_001443933.1 phosphomannose isomerase [Vibrio harveyi ATCC BAA-1116] >gnl BL_ORD_ID 2112588 hypothetical protein VIBHAR_00704 [Vibrio harveyi ATCC BAA-1116]	399	2.55 x 10 ⁻⁸⁹	3 - 389 (11.75%)
191	NR gi 262395388 ref YP_003287241.1 mannose-6-phosphate isomerase [Vibrio sp. Ex25] >gnl BL_ORD_ID 1037213 mannose-6-phosphate isomerase [Vibrio sp. Ex25]	398	3.32 x 10 ⁻⁸⁹	6 - 389 (11.11%)
192	NR gi 90579318 ref ZP_01235128.1 putative mannose-6-phosphate isomer [Vibrio angustum S14] >gnl BL_ORD_ID 187160 putative mannose-6-phosphate isomer [Vibrio angustum S14]	391	4.34 x 10 ⁻⁸⁹	3 - 389 (11.58%)
193	NR gi 148975197 ref ZP_01812121.1 mannose-6-phosphate isomerase [Vibrionales bacterium SWAT-3] >gnl BL_ORD_ID 1553512 mannose-6-phosphate isomerase [Vibrionales bacterium SWAT-3]	388	5.67 x 10 ⁻⁸⁹	4 - 389 (11.56%)
194	NR gi 84389383 ref ZP_00991189.1 mannose-6-phosphate isomerase [Vibrio splendidus 12B01] >gnl BL_ORD_ID 526246 mannose-6-phosphate isomerase [Vibrio splendidus 12B01]	388	5.67 x 10 ⁻⁸⁹	4 - 389 (11.56%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
195	NR gi 260901499 ref ZP_05909894.1 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus AQ4037] >gnl BL_ORD_ID 902573 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus AQ4037]	398	9.67 x 10 ⁻⁸⁹	6 - 389 (11.17%)
196	NR gi 84393738 ref ZP_00992487.1 putative mannose-6-phosphate isomerase [Vibrio splendidus 12B01] >gnl BL_ORD_ID 526181 putative mannose-6-phosphate isomerase [Vibrio splendidus 12B01]	388	1.26 x 10 ⁻⁸⁸	6 - 389 (11.96%)
197	NR gi 323496622 ref ZP_08101675.1 mannose-6-phosphate isomerase [Vibrio sinaloensis DSM 21326] >gnl BL_ORD_ID 1347994 mannose-6-phosphate isomerase [Vibrio sinaloensis DSM 21326]	390	2.16 x 10 ⁻⁸⁸	4 - 389 (11.57%)
198	NR gi 260877911 ref ZP_05890266.1 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus AN-5034] >gnl BL_ORD_ID 901346 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus AN-5034]	400	2.16 x 10 ⁻⁸⁸	3 - 389 (11.56%)
199	NR gi 193787986 dbj BAG50495.1 putative mannose-6-phosphate isomer [Vibrio parahaemolyticus]	400	2.16 x 10 ⁻⁸⁸	3 - 389 (11.56%)
200	NR gi 91224657 ref ZP_01259918.1 putative mannose-6-phosphate isomerase [Vibrio alginolyticus 12G01] >gnl BL_ORD_ID 218140 putative mannose-6-phosphate isomerase [Vibrio alginolyticus 12G01]	392	2.16 x 10 ⁻⁸⁸	6 - 389 (11.52%)
201	NR gi 90406771 ref ZP_01214964.1 putative mannose-6-phosphate isomer [Psychromonas sp. CNPT3] >gnl BL_ORD_ID 167620 putative mannose-6-phosphate isomer [Psychromonas sp. CNPT3]	389	3.68 x 10 ⁻⁸⁸	6 - 389 (11.96%)
202	NR gi 89072751 ref ZP_01159316.1 putative mannose-6-phosphate isomer [Photobacterium sp. SKA34] >gnl BL_ORD_ID 675538 putative mannose-6-phosphate isomer [Photobacterium sp. SKA34]	391	1.07 x 10 ⁻⁸⁷	3 - 389 (11.58%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
203	<p>NR gi 15640298 ref NP_229925.1 mannose-6-phosphate isomerase [Vibrio cholerae O1 biovar El Tor str. N16961] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae V52] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae O395] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae NCTC 8457] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae B33] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae M66-2] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae BX 330286] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae B33] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae RC9] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae TM 11079-80] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae 12129(1)] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae MJ-1236] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholera CIRS 101] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae INDRE 91/1] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae RC27] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase, class I [Vibrio cholerae MAK 757] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae O1 biovar El Tor str. N16961] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae V52] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae NCTC 8457] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae B33] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae O395] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae M66-2] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae O395] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae 12129(1)] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae TM 11079-80] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae RC9] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae B33] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae BX 330286] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae MJ-1236] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholera CIRS 101] >gnl BL_ORD_ID 1639557 mannose-6-phosphate isomerase [Vibrio cholerae RC27]</p>	388	2.38 x 10 ⁻⁸⁷	6 - 389 (12.02%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
204	NR gi 319999633 gb AAO07465.2 mannose-6-phosphate isomerase, class I [Vibrio vulnificus CMCP6]	391	4.06 x 10 ⁻⁸⁷	3 - 389 (11.71%)
205	NR gi 261252530 ref ZP_05945103.1 mannose-6-phosphate isomerase [Vibrio orientalis CIP 102891] >gnl BL_ORD_ID 905703 mannose-6-phosphate isomerase [Vibrio orientalis CIP 102891]	388	5.31 x 10 ⁻⁸⁷	4 - 389 (11.23%)
206	NR gi 209809655 ref YP_002265194.1 mannose-6-phosphate isomerase [Aliivibrio salmonicida LF11238] >gnl BL_ORD_ID 993191 mannose-6-phosphate isomerase [Aliivibrio salmonicida LF11238]	390	5.31 x 10 ⁻⁸⁷	6 - 389 (11.64%)
207	NR gi 320158827 ref YP_004191205.1 mannose-6-phosphate isomerase [Vibrio vulnificus MO6-24/O] >gnl BL_ORD_ID 1070558 mannose-6-phosphate isomerase [Vibrio vulnificus MO6-24/O]	390	6.93 x 10 ⁻⁸⁷	6 - 389 (11.83%)
208	NR gi 37676724 ref NP_937120.1 phosphomannose isomerase [Vibrio vulnificus YJ016] >gnl BL_ORD_ID 1184972 phosphomannose isomerase [Vibrio vulnificus YJ016]	391	9.05 x 10 ⁻⁸⁷	3 - 389 (11.64%)
209	NR gi 86144903 ref ZP_01063235.1 putative mannose-6-phosphate isomerase [Vibrio sp. MED222] >gnl BL_ORD_ID 589592 putative mannose-6-phosphate isomerase [Vibrio sp. MED222]	388	1.18 x 10 ⁻⁸⁶	6 - 389 (11.82%)
210	NR gi 149188525 ref ZP_01866818.1 putative mannose-6-phosphate isomerase [Vibrio shilonii AK1] >gnl BL_ORD_ID 1729333 putative mannose-6-phosphate isomerase [Vibrio shilonii AK1]	387	1.54 x 10 ⁻⁸⁶	6 - 388 (11.88%)
211	NR gi 254506205 ref ZP_05118349.1 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus 16] >gnl BL_ORD_ID 1493384 mannose-6-phosphate isomerase, class I [Vibrio parahaemolyticus 16]	391	2.02 x 10 ⁻⁸⁶	4 - 389 (11.18%)
212	NR gi 269102070 ref ZP_06154767.1 mannose-6-phosphate isomerase [Photobacterium damsela subsp. damsela CIP 102761] >gnl BL_ORD_ID 1074256 mannose-6-phosphate isomerase [Photobacterium damsela subsp. damsela CIP 102761]	377	5.87 x 10 ⁻⁸⁶	17 - 389 (12.45%)
213	NR gi 153834356 ref ZP_01987023.1 mannose-6-phosphate isomerase, class I [Vibrio harveyi HY01] >gnl BL_ORD_ID 1743886 mannose-6-phosphate isomerase, class I [Vibrio harveyi HY01]	396	1.11 x 10 ⁻⁸⁴	3 - 389 (11.48%)
214	NR gi 312881162 ref ZP_07740960.1 mannose-6-phosphate isomerase [Vibrio caribbenthicus ATCC BAA-2122] >gnl BL_ORD_ID 355726 mannose-6-phosphate isomerase [Vibrio caribbenthicus ATCC BAA-2122]	390	2.47 x 10 ⁻⁸⁴	4 - 388 (11.11%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
215	NR gi 153832381 ref ZP_01985048.1 mannose-6-phosphate isomerase, class I [Vibrio harveyi HY01] >gnl BL_ORD_ID 1746555 mannose-6-phosphate isomerase, class I [Vibrio harveyi HY01]	392	5.49 x 10 ⁻⁸⁴	3 - 390 (11.13%)
216	NR gi 302544899 ref ZP_07297241.1 mannose-6-phosphate isomerase, class I [Streptomyces hygrosopicus ATCC 53653] >gnl BL_ORD_ID 592896 mannose-6-phosphate isomerase, class I [Streptomyces hygrosopicus ATCC 53653]	397	3.23 x 10 ⁻⁷⁶	1 - 386 (10.79%)
217	NR gi 307719424 ref YP_003874956.1 mannose-6-phosphate isomerase [Spirochaeta thermophila DSM 6192] >gnl BL_ORD_ID 8688 mannose-6-phosphate isomerase [Spirochaeta thermophila DSM 6192]	393	3.57 x 10 ⁻⁷⁵	4 - 386 (10.75%)
218	NR gi 297157863 gb ADI07575.1 mannose-6-phosphate isomerase [Streptomyces bingchenggensis BCW-1]	401	4.66 x 10 ⁻⁷⁵	1 - 386 (10.63%)
219	NR gi 315186156 gb EFU19918.1 mannose-6-phosphate isomerase, class I [Spirochaeta thermophila DSM 6578]	392	2.31 x 10 ⁻⁷⁴	4 - 386 (10.80%)
220	NR gi 123444271 ref YP_001008239.1 mannose-6-phosphate isomerase [Yersinia enterocolitica subsp. enterocolitica 8081] >gnl BL_ORD_ID 1172336 mannose-6-phosphate isomerase [Yersinia enterocolitica subsp. enterocolitica 8081]	390	3.02 x 10 ⁻⁷⁴	3 - 388 (10.98%)
221	NR gi 289803379 ref ZP_06534008.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. AG3]	158	6.73 x 10 ⁻⁷⁴	1 - 158 (55.28%)
222	NR gi 238789505 ref ZP_04633290.1 Mannose-6-phosphate isomerase [Yersinia frederiksenii ATCC 33641] >gnl BL_ORD_ID 2861645 Mannose-6-phosphate isomerase [Yersinia frederiksenii ATCC 33641]	386	1.50 x 10 ⁻⁷³	8 - 388 (10.74%)
223	NR gi 307331843 ref ZP_07610942.1 mannose-6-phosphate isomerase, class I [Streptomyces violaceusniger Tu 4113] >gnl BL_ORD_ID 24249 mannose-6-phosphate isomerase, class I [Streptomyces violaceusniger Tu 4113]	397	2.56 x 10 ⁻⁷³	1 - 386 (10.47%)
224	NR gi 269963771 ref ZP_06178089.1 conserved hypothetical protein [Vibrio harveyi 1DA3] >gnl BL_ORD_ID 1115613 conserved hypothetical protein [Vibrio harveyi 1DA3]	308	2.56 x 10 ⁻⁷³	3 - 307 (15.92%)
225	NR gi 318607952 emb CBY29450.1 mannose-6-phosphate isomerase [Yersinia enterocolitica subsp. palearctica Y11]	390	3.34 x 10 ⁻⁷³	3 - 388 (10.85%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
226	NR gi 302521404 ref ZP_07273746.1 phosphomannose isomerase type I [Streptomyces sp. SPB78] >gnl BL_ORD_ID 549955 mannose-6-phosphate isomerase [Streptomyces sp. SA3_actG] >gnl BL_ORD_ID 549955 mannose-6-phosphate isomerase [Streptomyces sp. SA3_actF] >gnl BL_ORD_ID 549955 phosphomannose isomerase type I [Streptomyces sp. SPB78]	392	4.36 x 10 ⁻⁷³	1 - 386 (10.48%)
227	NR gi 289803378 ref ZP_06534007.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. AG3]	153	7.44 x 10 ⁻⁷³	172 - 324 (58.95%)
228	NR gi 213416650 ref ZP_03349794.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. E01-6750]	158	7.44 x 10 ⁻⁷³	15 - 172 (54.88%)
229	NR gi 295836951 ref ZP_06823884.1 mannose-6-phosphate isomerase, class I [Streptomyces sp. SPB74] >gnl BL_ORD_ID 821915 mannose-6-phosphate isomerase, class I [Streptomyces sp. SPB74]	392	4.82 x 10 ⁻⁷²	1 - 386 (10.28%)
230	NR gi 121586342 ref ZP_01676131.1 mannose-6-phosphate isomerase [Vibrio cholerae 2740-80] >gnl BL_ORD_ID 1102419 mannose-6-phosphate isomerase [Vibrio cholerae 2740-80]	328	8.23 x 10 ⁻⁷²	66 - 389 (14.59%)
231	NR gi 237808177 ref YP_002892617.1 mannose-6-phosphate isomerase, class I [Tolomonas auensis DSM 9187] >gnl BL_ORD_ID 1784055 mannose-6-phosphate isomerase, class I [Tolomonas auensis DSM 9187]	390	4.08 x 10 ⁻⁷¹	4 - 387 (10.72%)
232	NR gi 239941718 ref ZP_04693655.1 putative mannose-6-phosphate isomerase [Streptomyces roseosporus NRRL 15998] >gnl BL_ORD_ID 101899 putative mannose-6-phosphate isomerase [Streptomyces roseosporus NRRL 11379] >gnl BL_ORD_ID 101899 mannose-6-phosphate isomerase [Streptomyces roseosporus NRRL 15998] >gnl BL_ORD_ID 101899 mannose-6-phosphate isomerase [Streptomyces roseosporus NRRL 15998]	394	5.33 x 10 ⁻⁷¹	1 - 386 (10.56%)
233	NR gi 302534798 ref ZP_07287140.1 mannose-6-phosphate isomerase, class I [Streptomyces sp. C] >gnl BL_ORD_ID 587301 mannose-6-phosphate isomerase, class I [Streptomyces sp. C]	391	9.10 x 10 ⁻⁷¹	1 - 386 (10.60%)
234	NR gi 311897268 dbj BAJ29676.1 putative mannose-6-phosphate isomerase [Kitasatospora setae KM-6054]	389	1.55 x 10 ⁻⁷⁰	1 - 382 (10.64%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
235	NR gi 182438304 ref YP_001826023.1 putative mannose-6-phosphate isomerase [Streptomyces griseus subsp. griseus NBRC 13350] >gnl BL_ORD_ID 222784 mannose-6-phosphate isomerase, class I [Streptomyces sp. ACT-1] >gnl BL_ORD_ID 222784 putative mannose-6-phosphate isomerase [Streptomyces griseus subsp. griseus NBRC 13350] >gnl BL_ORD_ID 222784 mannose-6-phosphate isomerase, class I [Streptomyces sp. ACT-1]	394	2.03 x 10 ⁻⁷⁰	1 - 386 (10.44%)
236	NR gi 282866241 ref ZP_06275287.1 mannose-6-phosphate isomerase, class I [Streptomyces sp. ACTE] >gnl BL_ORD_ID 1310256 mannose-6-phosphate isomerase, class I [Streptomyces sp. ACTE]	393	7.70 x 10 ⁻⁷⁰	1 - 386 (10.68%)
237	NR gi 320010449 gb ADW05299.1 mannose-6-phosphate isomerase, class I [Streptomyces flavogriseus ATCC 33331]	406	3.82 x 10 ⁻⁶⁹	1 - 386 (10.13%)
238	NR gi 227832498 ref YP_002834205.1 mannose-6-phosphate isomerase [Corynebacterium aurimucosum ATCC 700975] >gnl BL_ORD_ID 2365716 mannose-6-phosphate isomerase [Corynebacterium aurimucosum ATCC 700975] >gnl BL_ORD_ID 2365716 mannose-6-phosphate isomerase [Corynebacterium aurimucosum ATCC 700975]	406	3.82 x 10 ⁻⁶⁹	1 - 382 (9.65%)
239	NR gi 158522026 ref YP_001529896.1 mannose-6-phosphate isomerase, class I [Desulfococcus oleovorans Hxd3] >gnl BL_ORD_ID 1100376 mannose-6-phosphate isomerase, class I [Desulfococcus oleovorans Hxd3]	397	1.11 x 10 ⁻⁶⁸	4 - 388 (10.34%)
240	NR gi 111023281 ref YP_706253.1 mannose-6-phosphate isomerase [Rhodococcus jostii RHA1] >gnl BL_ORD_ID 466530 mannose-6-phosphate isomerase [Rhodococcus jostii RHA1]	403	1.90 x 10 ⁻⁶⁸	1 - 389 (9.48%)
241	NR gi 294629700 ref ZP_06708260.1 phosphomannose isomerase type [Streptomyces sp. e14] >gnl BL_ORD_ID 1879862 phosphomannose isomerase type [Streptomyces sp. e14]	391	2.48 x 10 ⁻⁶⁸	1 - 386 (10.20%)
242	NR gi 320536881 ref ZP_08036874.1 mannose-6-phosphate isomerase, class I [Treponema phagedenis F0421] >gnl BL_ORD_ID 1108719 mannose-6-phosphate isomerase, class I [Treponema phagedenis F0421]	392	3.24 x 10 ⁻⁶⁸	3 - 382 (10.15%)
243	NR gi 302551847 ref ZP_07304189.1 phosphomannose isomerase type I [Streptomyces viridochromogenes DSM 40736] >gnl BL_ORD_ID 602911 phosphomannose isomerase type I [Streptomyces viridochromogenes DSM 40736]	391	3.24 x 10 ⁻⁶⁸	1 - 386 (10.34%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
244	NR gi 239981873 ref ZP_04704397.1 mannose-6-phosphate isomerase [Streptomyces albus J1074] >gnl BL_ORD_ID 110866 mannose-6-phosphate isomerase [Streptomyces albus J1074] >gnl BL_ORD_ID 110866 mannose-6-phosphate isomerase [Streptomyces albus J1074]	391	4.23 x 10 ⁻⁶⁸	1 - 386 (10.53%)
245	NR gi 226365789 ref YP_002783572.1 mannose-6-phosphate isomerase [Rhodococcus opacus B4] >gnl BL_ORD_ID 2145959 mannose-6-phosphate isomerase [Rhodococcus opacus B4]	403	9.41 x 10 ⁻⁶⁸	1 - 389 (9.42%)
246	NR gi 111022402 ref YP_705374.1 mannose-6-phosphate isomerase [Rhodococcus jostii RHA1] >gnl BL_ORD_ID 469228 mannose-6-phosphate isomerase [Rhodococcus jostii RHA1]	408	9.41 x 10 ⁻⁶⁸	1 - 388 (9.67%)
247	NR gi 21221468 ref NP_627247.1 mannose-6-phosphate isomerase [Streptomyces coelicolor A3(2)] >gnl BL_ORD_ID 779266 mannose-6-phosphate isomerase [Streptomyces lividans TK24] >gnl BL_ORD_ID 779266 phosphomannose isomerase type I [Streptomyces lividans TK24] >gnl BL_ORD_ID 779266 mannose-6-phosphate isomerase [Streptomyces coelicolor A3(2)] >gnl BL_ORD_ID 779266 phosphomannose isomerase type I [Streptomyces lividans TK24]	391	1.23 x 10 ⁻⁶⁷	1 - 386 (10.47%)
248	NR gi 254823002 ref ZP_05228003.1 mannose-6-phosphate isomerase, class I [Mycobacterium intracellulare ATCC 13950]	398	1.61 x 10 ⁻⁶⁷	1 - 381 (9.72%)
249	NR gi 169630681 ref YP_001704330.1 mannose-6-phosphate isomerase ManA [Mycobacterium abscessus ATCC 19977] >gnl BL_ORD_ID 63720 Probable mannose-6-phosphate isomerase ManA [Mycobacterium abscessus]	399	1.61 x 10 ⁻⁶⁷	1 - 388 (9.80%)
250	NR gi 297200118 ref ZP_06917515.1 phosphomannose isomerase type I [Streptomyces sviveus ATCC 29083] >gnl BL_ORD_ID 2099747 phosphomannose isomerase type I [Streptomyces sviveus ATCC 29083]	393	2.10 x 10 ⁻⁶⁷	1 - 386 (10.30%)
251	NR gi 72160422 ref YP_288079.1 mannose-6-phosphate isomerase [Thermobifida fusca YX] >gnl BL_ORD_ID 1691330 mannose-6-phosphate isomerase [Thermobifida fusca YX]	393	2.74 x 10 ⁻⁶⁷	1 - 384 (10.36%)
252	NR gi 212007857 gb ACJ22537.1 phosphomannose isomerase [Streptomyces nodosus]	391	3.58 x 10 ⁻⁶⁷	1 - 386 (10.73%)
253	NR gi 315445600 ref YP_004078479.1 mannose-6-phosphate isomerase, type 1 [Mycobacterium sp. Spyr1] >gnl BL_ORD_ID 797379 mannose-6-phosphate isomerase, type 1 [Mycobacterium sp. Spyr1]	394	4.67 x 10 ⁻⁶⁷	1 - 376 (9.92%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
254	NR gi 254392038 ref ZP_05007228.1 mannose-6-phosphate isomerase [Streptomyces clavuligerus ATCC 27064] >gnl BL_ORD_ID 836498 Mannose-6-phosphate isomerase [Streptomyces clavuligerus ATCC 27064] >gnl BL_ORD_ID 836498 mannose-6-phosphate isomerase [Streptomyces clavuligerus ATCC 27064] >gnl BL_ORD_ID 836498 Mannose-6-phosphate isomerase [Streptomyces clavuligerus ATCC 27064]	378	4.67 x 10 ⁻⁶⁷	1 - 373 (10.92%)
255	NR gi 145225302 ref YP_001135980.1 mannose-6-phosphate isomerase, class I [Mycobacterium gilvum PYR-GCK] >gnl BL_ORD_ID 704953 mannose-6-phosphate isomerase, type 1 [Mycobacterium gilvum PYR-GCK]	394	4.67 x 10 ⁻⁶⁷	1 - 376 (9.92%)
256	NR gi 300779620 ref ZP_07089476.1 mannose-6-phosphate isomerase [Corynebacterium genitalium ATCC 33030] >gnl BL_ORD_ID 2641240 mannose-6-phosphate isomerase [Corynebacterium genitalium ATCC 33030]	412	6.10 x 10 ⁻⁶⁷	1 - 382 (9.31%)
257	NR gi 254776654 ref ZP_05218170.1 mannose-6-phosphate isomerase, class I [Mycobacterium avium subsp. avium ATCC 25291]	398	6.10 x 10 ⁻⁶⁷	1 - 381 (9.72%)
258	NR gi 41409465 ref NP_962301.1 hypothetical protein MAP3367c [Mycobacterium avium subsp. paratuberculosis K-10] >gnl BL_ORD_ID 1743147 mannose-6-phosphate isomerase, class I [Mycobacterium avium 104] >gnl BL_ORD_ID 1743147 ManA [Mycobacterium avium subsp. paratuberculosis K-10] >gnl BL_ORD_ID 1743147 mannose-6-phosphate isomerase, class I [Mycobacterium avium 104]	398	6.10 x 10 ⁻⁶⁷	1 - 381 (9.72%)
259	NR gi 296168950 ref ZP_06850619.1 mannose-6-phosphate isomerase [Mycobacterium parascrofulaceum ATCC BAA-614] >gnl BL_ORD_ID 2068924 mannose-6-phosphate isomerase [Mycobacterium parascrofulaceum ATCC BAA-614]	392	1.78 x 10 ⁻⁶⁶	1 - 376 (9.83%)
260	NR gi 118618070 ref YP_906402.1 mannose-6-phosphate isomerase ManA [Mycobacterium ulcerans Agy99] >gnl BL_ORD_ID 880379 mannose-6-phosphate isomerase ManA [Mycobacterium ulcerans Agy99]	392	2.32 x 10 ⁻⁶⁶	1 - 376 (9.96%)
261	NR gi 239930885 ref ZP_04687838.1 mannose-6-phosphate isomerase [Streptomyces ghanaensis ATCC 14672] >gnl BL_ORD_ID 95059 mannose-6-phosphate isomerase [Streptomyces ghanaensis ATCC 14672] >gnl BL_ORD_ID 95059 mannose-6-phosphate isomerase [Streptomyces ghanaensis ATCC 14672]	391	3.03 x 10 ⁻⁶⁶	1 - 386 (10.27%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
262	NR gi 183981309 ref YP_001849600.1 mannose-6-phosphate isomerase ManA [Mycobacterium marinum M] >gnl BL_ORD_ID 237901 mannose-6-phosphate isomerase ManA [Mycobacterium marinum M]	392	3.03 x 10 ⁻⁶⁶	1 - 376 (9.96%)
263	NR gi 229489355 ref ZP_04383218.1 mannose-6-phosphate isomerase, class I [Rhodococcus erythropolis SK121] >gnl BL_ORD_ID 2645987 mannose-6-phosphate isomerase, class I [Rhodococcus erythropolis SK121]	406	3.95 x 10 ⁻⁶⁶	1 - 389 (9.34%)
264	NR gi 54026600 ref YP_120842.1 putative mannose-6-phosphate isomerase [Nocardia farcinica IFM 10152] >gnl BL_ORD_ID 1347634 putative mannose-6-phosphate isomerase [Nocardia farcinica IFM 10152]	402	5.17 x 10 ⁻⁶⁶	1 - 388 (9.47%)
265	NR gi 301064567 ref ZP_07204963.1 mannose-6-phosphate isomerase, class I [delta proteobacterium NaphS2] >gnl BL_ORD_ID 2617845 mannose-6-phosphate isomerase, class I [delta proteobacterium NaphS2]	386	6.75 x 10 ⁻⁶⁶	4 - 380 (10.47%)
266	NR gi 302560320 ref ZP_07312662.1 phosphomannose isomerase type I [Streptomyces griseoflavus Tu4000] >gnl BL_ORD_ID 608594 phosphomannose isomerase type I [Streptomyces griseoflavus Tu4000]	391	6.75 x 10 ⁻⁶⁶	1 - 386 (10.34%)
267	NR gi 296118800 ref ZP_06837376.1 mannose-6-phosphate isomerase, class I [Corynebacterium ammoniagenes DSM 20306] >gnl BL_ORD_ID 2076503 mannose-6-phosphate isomerase, class I [Corynebacterium ammoniagenes DSM 20306]	412	1.15 x 10 ⁻⁶⁵	1 - 387 (9.07%)
268	NR gi 226305646 ref YP_002765606.1 mannose-6-phosphate isomerase [Rhodococcus erythropolis PR4] >gnl BL_ORD_ID 2134627 mannose-6-phosphate isomerase [Rhodococcus erythropolis PR4]	406	1.15 x 10 ⁻⁶⁵	1 - 389 (9.40%)
269	NR gi 240172601 ref ZP_04751260.1 mannose-6-phosphate isomerase ManA [Mycobacterium kansasii ATCC 12478]	398	2.56 x 10 ⁻⁶⁵	1 - 381 (9.72%)
270	NR gi 29831594 ref NP_826228.1 mannose-6-phosphate isomerase [Streptomyces avermitilis MA-4680] >gnl BL_ORD_ID 2655886 putative mannose-6-phosphate isomerase [Streptomyces avermitilis MA-4680]	391	3.35 x 10 ⁻⁶⁵	1 - 386 (10.07%)
271	NR gi 218961850 ref YP_001741625.1 putative mannose-6-phosphate isomerase [Candidatus Cloacamonas acidaminovorans] >gnl BL_ORD_ID 2748604 putative mannose-6-phosphate isomerase [Candidatus Cloacamonas acidaminovorans]	383	9.74 x 10 ⁻⁶⁵	7 - 384 (10.16%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
272	NR gi 120402739 ref YP_952568.1 mannose-6-phosphate isomerase, class I [Mycobacterium vanbaalenii PYR-1] >gnl BL_ORD_ID 163164 mannose-6-phosphate isomerase, type 1 [Mycobacterium vanbaalenii PYR-1]	394	9.74 x 10 ⁻⁶⁵	1 - 376 (9.53%)
273	NR gi 15610391 ref NP_217772.1 mannose-6-phosphate isomerase [Mycobacterium tuberculosis H37Rv] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase [Mycobacterium tuberculosis CDC1551] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase [Mycobacterium bovis AF2122/97] >gnl BL_ORD_ID 27636 putative mannose-6-phosphate isomerase manA [Mycobacterium bovis BCG str. Pasteur 1173P2] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase [Mycobacterium tuberculosis H37Ra] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis F11] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis H37Ra] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis 02_1987] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis 94_M4241A] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis T92] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis EAS054] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis T85] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis GM 1503] >gnl BL_ORD_ID 27636 putative mannose-6-phosphate isomerase [Mycobacterium bovis BCG str. Tokyo 172] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis KZN 1435] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis C] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis '98-R604 INH-RIF-EM'] >gnl BL_ORD_ID 27636 putative mannose-6-phosphate isomerase [Mycobacterium tuberculosis KZN 4207] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis CPHL_A] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis T46] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase, class I [Mycobacterium tuberculosis T46] >gnl BL_ORD_ID 27636 mannose-6-phosphate	404	1.27 x 10 ⁻⁶⁴	1 - 388 (9.37%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
	<p>isomerase manA [Mycobacterium tuberculosis CPHL_A] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis KZN 605] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis 02_1987] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis T92] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis EAS054] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis T85] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis GM 1503] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase [Mycobacterium tuberculosis 210] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase [Mycobacterium tuberculosis KZN 4207] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase [Mycobacterium tuberculosis KZN R506] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis 94_M4241A] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu001] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu002] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu003] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu004] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu005] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu006] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu008] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu007] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu009] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu010] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu011] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu012] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase [Mycobacterium tuberculosis KZN V2475] >gnl BL_ORD_ID 27636 PROBABLE MANNOSE-6-PHOSPHATE ISOMERASE MANA</p>			

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
	<p>(PHOSPHOMANNOSE ISOMERASE) (PHOSPHOMANNOISOMERASE) (PMI) (PHOSPHOHEXOISOMERASE) (PHOSPHOHEXOMUTASE) [Mycobacterium tuberculosis H37Rv] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase [Mycobacterium tuberculosis CDC1551] >gnl BL_ORD_ID 27636 PROBABLE MANNOSE-6-PHOSPHATE ISOMERASE MANA (PHOSPHOMANNOSE ISOMERASE) (PHOSPHOMANNOISOMERASE) (PMI) (PHOSPHOHEXOISOMERASE) (PHOSPHOHEXOMUTASE) [Mycobacterium bovis AF2122/97] >gnl BL_ORD_ID 27636 Probable mannose-6-phosphate isomerase manA [Mycobacterium bovis BCG str. Pasteur 1173P2] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis C] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase [Mycobacterium tuberculosis H37Ra] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis F11] >gnl BL_ORD_ID 27636 putative mannose-6-phosphate isomerase [Mycobacterium bovis BCG str. Tokyo 172] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis KZN 1435] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase, class I [Mycobacterium tuberculosis T46] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis CPHL_A] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis KZN 605] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis 02_1987] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis T92] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis EAS054] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis GM 1503] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis T85] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis 94_M4241A] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu001] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu002] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu003] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium</p>			

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
	tuberculosis SUMu004] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu005] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu006] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu007] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu008] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu009] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu010] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu011] >gnl BL_ORD_ID 27636 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis SUMu012]			
274	NR gi 256380312 ref YP_003103972.1 mannose-6-phosphate isomerase, class I [Actinosynnema mirum DSM 43827] >gnl BL_ORD_ID 2219930 mannose-6-phosphate isomerase, class I [Actinosynnema mirum DSM 43827]	398	2.17 x 10 ⁻⁶⁴	1 - 379 (9.91%)
275	NR gi 300932848 ref ZP_07148104.1 mannose-6-phosphate isomerase [Corynebacterium resistens DSM 45100]	403	3.70 x 10 ⁻⁶⁴	1 - 387 (10.28%)
276	NR gi 260206606 ref ZP_05774097.1 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis K85] >gnl BL_ORD_ID 820191 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis K85] >gnl BL_ORD_ID 820191 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis K85]	404	3.70 x 10 ⁻⁶⁴	1 - 388 (9.37%)
277	NR gi 302338756 ref YP_003803962.1 mannose-6-phosphate isomerase, class I [Spirochaeta smaragdinae DSM 11293] >gnl BL_ORD_ID 2709040 mannose-6-phosphate isomerase, class I [Spirochaeta smaragdinae DSM 11293]	392	4.83 x 10 ⁻⁶⁴	4 - 383 (9.96%)
278	NR gi 290959905 ref YP_003491087.1 mannose-6-phosphate isomerase [Streptomyces scabiei 87.22] >gnl BL_ORD_ID 884396 mannose-6-phosphate isomerase [Streptomyces scabiei 87.22]	391	4.83 x 10 ⁻⁶⁴	1 - 386 (10.01%)
279	NR gi 116669747 ref YP_830680.1 mannose-6-phosphate isomerase [Arthrobacter sp. FB24] >gnl BL_ORD_ID 257350 mannose-6-phosphate isomerase, type 1 [Arthrobacter sp. FB24]	398	6.31 x 10 ⁻⁶⁴	1 - 378 (10.23%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
280	NR gi 38233296 ref NP_939063.1 putative mannose-phosphate isomerase [Corynebacterium diphtheriae NCTC 13129] >gnl BL_ORD_ID 1190116 Putative mannose-phosphate isomerase [Corynebacterium diphtheriae]	399	8.25 x 10 ⁻⁶⁴	1 - 384 (9.48%)
281	NR gi 269957327 ref YP_003327116.1 mannose-6-phosphate isomerase, class I [Xylanimonas cellulositytica DSM 15894] >gnl BL_ORD_ID 2245642 mannose-6-phosphate isomerase, class I [Xylanimonas cellulositytica DSM 15894]	398	1.08 x 10 ⁻⁶³	4 - 385 (9.72%)
282	NR gi 227502884 ref ZP_03932933.1 possible mannose-6-phosphate isomerase [Corynebacterium accolens ATCC 49725] >gnl BL_ORD_ID 2250838 possible mannose-6-phosphate isomerase [Corynebacterium accolens ATCC 49725]	406	3.13 x 10 ⁻⁶³	1 - 381 (9.04%)
283	NR gi 15827331 ref NP_301594.1 putative mannose-6-phosphate isomerase [Mycobacterium leprae TN] >gnl BL_ORD_ID 1098023 putative mannose-6-phosphate isomerase [Mycobacterium leprae Br4923] >gnl BL_ORD_ID 1098023 putative mannose-6-phosphate isomerase [Mycobacterium leprae] >gnl BL_ORD_ID 1098023 putative mannose-6-phosphate isomerase [Mycobacterium leprae Br4923]	395	3.13 x 10 ⁻⁶³	1 - 376 (9.68%)
284	NR gi 306835483 ref ZP_07468500.1 mannose-6-phosphate isomerase [Corynebacterium accolens ATCC 49726] >gnl BL_ORD_ID 2889769 mannose-6-phosphate isomerase [Corynebacterium accolens ATCC 49726]	406	4.09 x 10 ⁻⁶³	1 - 381 (9.04%)
285	NR gi 323468709 gb ADX72394.1 mannose-6-phosphate isomerase, type 1 [Arthrobacter phenanthrenivorans Sphe3]	401	6.98 x 10 ⁻⁶³	1 - 378 (9.89%)
286	NR gi 300857929 ref YP_003782912.1 mannose-6-phosphate isomerase [Corynebacterium pseudotuberculosis FRC41] >gnl BL_ORD_ID 2646767 mannose-6-phosphate isomerase [Corynebacterium pseudotuberculosis FRC41] >gnl BL_ORD_ID 2646767 mannose-6-phosphate isomerase [Corynebacterium pseudotuberculosis C231] >gnl BL_ORD_ID 2646767 Phosphomannose isomerase [Corynebacterium pseudotuberculosis 1002] >gnl BL_ORD_ID 2646767 Phosphomannose isomerase [Corynebacterium pseudotuberculosis I19]	396	1.19 x 10 ⁻⁶²	1 - 384 (9.82%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
287	NR gi 296130226 ref YP_003637476.1 mannose-6-phosphate isomerase, class I [Cellulomonas flavigena DSM 20109] >gnl BL_ORD_ID 2626251 mannose-6-phosphate isomerase, class I [Cellulomonas flavigena DSM 20109]	399	1.56 x 10 ⁻⁶²	1 - 386 (9.48%)
288	NR gi 220912028 ref YP_002487337.1 mannose-6-phosphate isomerase, class I [Arthrobacter chlorophenicus A6] >gnl BL_ORD_ID 1514101 mannose-6-phosphate isomerase, class I [Arthrobacter chlorophenicus A6]	409	1.56 x 10 ⁻⁶²	1 - 378 (9.74%)
289	NR gi 19551976 ref NP_599978.1 phosphomannose isomerase [Corynebacterium glutamicum ATCC 13032] >gnl BL_ORD_ID 774854 mannose-6-phosphate isomerase [Corynebacterium glutamicum ATCC 13032] >gnl BL_ORD_ID 774854 Phosphomannose isomerase [Corynebacterium glutamicum ATCC 13032] >gnl BL_ORD_ID 774854 MANNOSE-6-PHOSPHATE ISOMERASE [Corynebacterium glutamicum ATCC 13032]	403	1.56 x 10 ⁻⁶²	1 - 387 (9.11%)
290	NR gi 145294910 ref YP_001137731.1 hypothetical protein cgR_0857 [Corynebacterium glutamicum R] >gnl BL_ORD_ID 1476882 hypothetical protein [Corynebacterium glutamicum R]	403	2.03 x 10 ⁻⁶²	1 - 387 (9.11%)
291	NR gi 108798301 ref YP_638498.1 mannose-6-phosphate isomerase [Mycobacterium sp. MCS] >gnl BL_ORD_ID 231665 mannose-6-phosphate isomerase [Mycobacterium sp. KMS] >gnl BL_ORD_ID 231665 mannose-6-phosphate isomerase, type 1 [Mycobacterium sp. MCS] >gnl BL_ORD_ID 231665 mannose-6-phosphate isomerase, type 1 [Mycobacterium sp. KMS]	393	2.03 x 10 ⁻⁶²	1 - 376 (9.52%)
292	NR gi 22023937 gb AAM89255.1 AF527174_1 phosphomannose isomerase [Mycobacterium smegmatis str. MC2 155]	392	2.65 x 10 ⁻⁶²	1 - 376 (9.83%)
293	NR gi 320539007 ref ZP_08038682.1 putative mannose-6-phosphate isomerase [Serratia symbiotica str. Tucson] >gnl BL_ORD_ID 1084271 putative mannose-6-phosphate isomerase [Serratia symbiotica str. Tucson]	173	3.46 x 10 ⁻⁶²	1 - 173 (39.76%)
294	NR gi 319949853 ref ZP_08023865.1 mannose-6-phosphate isomerase [Dietzia cinnamea P4] >gnl BL_ORD_ID 1032023 mannose-6-phosphate isomerase [Dietzia cinnamea P4]	388	4.52 x 10 ⁻⁶²	8 - 380 (10.30%)
295	NR gi 307700969 ref ZP_07637994.1 mannose-6-phosphate isomerase, class I [Mobiluncus mulieris FB024-16] >gnl BL_ORD_ID 136625 mannose-6-phosphate isomerase, class I [Mobiluncus mulieris FB024-16]	394	1.01 x 10 ⁻⁶¹	1 - 382 (9.28%)
296	NR gi 291008025 ref ZP_06565998.1 mannose-6-phosphate isomerase [Saccharopolyspora erythraea NRRL 2338]	396	1.01 x 10 ⁻⁶¹	1 - 379 (9.82%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
297	NR gi 269217408 ref ZP_06161262.1 mannose-6-phosphate isomerase, class I [Actinomyces sp. oral taxon 848 str. F0332] >gnl BL_ORD_ID 1105264 mannose-6-phosphate isomerase, class I [Actinomyces sp. oral taxon 848 str. F0332]	420	1.01 x 10 ⁻⁶¹	1 - 386 (8.90%)
298	NR gi 255323827 ref ZP_05364953.1 mannose-6-phosphate isomerase, class I [Corynebacterium tuberculostearicum SK141] >gnl BL_ORD_ID 457808 mannose-6-phosphate isomerase, class I [Corynebacterium tuberculostearicum SK141]	413	1.01 x 10 ⁻⁶¹	1 - 388 (8.68%)
299	NR gi 227875202 ref ZP_03993344.1 possible mannose-6-phosphate isomerase [Mobiluncus mulieris ATCC 35243] >gnl BL_ORD_ID 2382363 mannose-6-phosphate isomerase, class I [Mobiluncus mulieris 28-1] >gnl BL_ORD_ID 2382363 mannose-6-phosphate isomerase [Mobiluncus mulieris ATCC 35239] >gnl BL_ORD_ID 2382363 possible mannose-6-phosphate isomerase [Mobiluncus mulieris ATCC 35243] >gnl BL_ORD_ID 2382363 mannose-6-phosphate isomerase, class I [Mobiluncus mulieris 28-1] >gnl BL_ORD_ID 2382363 mannose-6-phosphate isomerase [Mobiluncus mulieris ATCC 35239]	394	1.01 x 10 ⁻⁶¹	1 - 382 (9.28%)
300	NR gi 258654287 ref YP_003203443.1 mannose-6-phosphate isomerase, class I [Nakamurella multipartita DSM 44233] >gnl BL_ORD_ID 729507 mannose-6-phosphate isomerase, class I [Nakamurella multipartita DSM 44233]	395	1.32 x 10 ⁻⁶¹	6 - 380 (10%)
301	NR gi 258652463 ref YP_003201619.1 mannose-6-phosphate isomerase, class I [Nakamurella multipartita DSM 44233] >gnl BL_ORD_ID 728910 mannose-6-phosphate isomerase, class I [Nakamurella multipartita DSM 44233]	396	1.72 x 10 ⁻⁶¹	6 - 391 (9.95%)
302	NR gi 296138916 ref YP_003646159.1 mannose-6-phosphate isomerase, class I [Tsukamurella paurometabola DSM 20162] >gnl BL_ORD_ID 2413555 mannose-6-phosphate isomerase, class I [Tsukamurella paurometabola DSM 20162]	410	1.72 x 10 ⁻⁶¹	1 - 391 (8.86%)
303	NR gi 227505507 ref ZP_03935556.1 possible mannose-6-phosphate isomerase [Corynebacterium striatum ATCC 6940] >gnl BL_ORD_ID 2302602 possible mannose-6-phosphate isomerase [Corynebacterium striatum ATCC 6940]	406	1.72 x 10 ⁻⁶¹	1 - 379 (9.52%)
304	NR gi 119718421 ref YP_925386.1 mannose-6-phosphate isomerase [Nocardioides sp. JS614] >gnl BL_ORD_ID 359362 mannose-6-phosphate isomerase [Nocardioides sp. JS614]	413	1.72 x 10 ⁻⁶¹	1 - 385 (9.20%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
305	NR gi 269796358 ref YP_003315813.1 mannose-6-phosphate isomerase, class I [Sanguibacter keddieii DSM 10542] >gnl BL_ORD_ID 1093423 mannose-6-phosphate isomerase, class I [Sanguibacter keddieii DSM 10542]	411	2.25 x 10 ⁻⁶¹	3 - 388 (8.94%)
306	NR gi 311739827 ref ZP_07713661.1 mannose-6-phosphate isomerase [Corynebacterium pseudogenitalium ATCC 33035] >gnl BL_ORD_ID 2361193 mannose-6-phosphate isomerase [Corynebacterium pseudogenitalium ATCC 33035]	402	2.25 x 10 ⁻⁶¹	1 - 377 (9.10%)
307	NR gi 256833207 ref YP_003161934.1 mannose-6-phosphate isomerase, class I [Jonesia denitrificans DSM 20603] >gnl BL_ORD_ID 552817 mannose-6-phosphate isomerase, class I [Jonesia denitrificans DSM 20603]	424	2.93 x 10 ⁻⁶¹	1 - 388 (9.12%)
308	NR gi 119961167 ref YP_947086.1 mannose-6-phosphate isomerase, class I [Arthrobacter aurescens TC1] >gnl BL_ORD_ID 1059013 mannose-6-phosphate isomerase, class I [Arthrobacter aurescens TC1]	398	3.83 x 10 ⁻⁶¹	1 - 378 (9.85%)
309	NR gi 305679618 ref ZP_07402428.1 mannose-6-phosphate isomerase, class I [Corynebacterium matruchotii ATCC 14266] >gnl BL_ORD_ID 301963 mannose-6-phosphate isomerase, class I [Corynebacterium matruchotii ATCC 14266]	400	8.53 x 10 ⁻⁶¹	1 - 383 (9.25%)
310	NR gi 225020664 ref ZP_03709856.1 hypothetical protein CORMATOL_00671 [Corynebacterium matruchotii ATCC 33806] >gnl BL_ORD_ID 1897257 hypothetical protein CORMATOL_00671 [Corynebacterium matruchotii ATCC 33806]	400	8.53 x 10 ⁻⁶¹	1 - 383 (9.25%)
311	NR gi 296393061 ref YP_003657945.1 mannose-6-phosphate isomerase, class I [Segniliparus rotundus DSM 44985] >gnl BL_ORD_ID 2108469 mannose-6-phosphate isomerase, class I [Segniliparus rotundus DSM 44985]	388	1.11 x 10 ⁻⁶⁰	1 - 378 (10.03%)
312	NR gi 162452975 ref YP_001615342.1 mannose-6-phosphate isomerase [Sorangium cellulosum 'So ce 56'] >gnl BL_ORD_ID 2400567 Mannose-6-phosphate isomerase [Sorangium cellulosum 'So ce 56']	400	1.11 x 10 ⁻⁶⁰	1 - 386 (9.56%)
313	NR gi 300789827 ref YP_003770118.1 mannose-6-phosphate isomerase [Amycolatopsis mediterranei U32] >gnl BL_ORD_ID 2483285 mannose-6-phosphate isomerase [Amycolatopsis mediterranei U32]	401	1.46 x 10 ⁻⁶⁰	1 - 382 (9.45%)
314	NR gi 126433968 ref YP_001069659.1 mannose-6-phosphate isomerase [Mycobacterium sp. JLS] >gnl BL_ORD_ID 245250 mannose-6-phosphate isomerase, type 1 [Mycobacterium sp. JLS]	393	2.48 x 10 ⁻⁶⁰	1 - 376 (9.32%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
315	NR gi 229819357 ref YP_002880883.1 mannose-6-phosphate isomerase, class I [Beutenbergia cavernae DSM 12333] >gnl BL_ORD_ID 2222786 mannose-6-phosphate isomerase, class I [Beutenbergia cavernae DSM 12333]	398	5.53 x 10 ⁻⁶⁰	1 - 386 (9.34%)
316	NR gi 134102890 ref YP_001108551.1 mannose-6-phosphate isomerase [Saccharopolyspora erythraea NRRL 2338] >gnl BL_ORD_ID 1417214 mannose-6-phosphate isomerase [Saccharopolyspora erythraea NRRL 2338]	386	7.22 x 10 ⁻⁶⁰	11 - 379 (10.07%)
317	NR gi 262203186 ref YP_003274394.1 mannose-6-phosphate isomerase, class I [Gordonia bronchialis DSM 43247] >gnl BL_ORD_ID 977077 mannose-6-phosphate isomerase, class I [Gordonia bronchialis DSM 43247]	412	9.43 x 10 ⁻⁶⁰	1 - 391 (8.95%)
318	NR gi 257057069 ref YP_003134901.1 mannose-6-phosphate isomerase [Saccharomonospora viridis DSM 43017] >gnl BL_ORD_ID 535726 mannose-6-phosphate isomerase [Saccharomonospora viridis DSM 43017]	398	9.43 x 10 ⁻⁶⁰	1 - 382 (9.28%)
319	NR gi 308176552 ref YP_003915958.1 class I mannose-6-phosphate isomerase [Arthrobacter arilaitensis Re117] >gnl BL_ORD_ID 168482 class I mannose-6-phosphate isomerase [Arthrobacter arilaitensis Re117]	401	1.23 x 10 ⁻⁵⁹	1 - 382 (9.27%)
320	NR gi 163841756 ref YP_001626161.1 mannose-6-phosphate isomerase [Renibacterium salmoninarum ATCC 33209] >gnl BL_ORD_ID 2531299 mannose-6-phosphate isomerase [Renibacterium salmoninarum ATCC 33209]	387	2.10 x 10 ⁻⁵⁹	1 - 375 (10.48%)
321	NR gi 302530040 ref ZP_07282382.1 mannose-6-phosphate isomerase, class I [Streptomyces sp. AA4] >gnl BL_ORD_ID 2776803 mannose-6-phosphate isomerase, class I [Streptomyces sp. AA4]	400	2.75 x 10 ⁻⁵⁹	6 - 382 (9.63%)
322	NR gi 170781080 ref YP_001709412.1 mannose-6-phosphate isomerase [Clavibacter michiganensis subsp. sepedonicus] >gnl BL_ORD_ID 54381 mannose-6-phosphate isomerase [Clavibacter michiganensis subsp. sepedonicus]	411	2.75 x 10 ⁻⁵⁹	4 - 382 (9.24%)
323	NR gi 51246310 ref YP_066194.1 mannose-6-phosphate isomerase [Desulfotalea psychrophila LSv54] >gnl BL_ORD_ID 1311275 related to mannose-6-phosphate isomerase [Desulfotalea psychrophila LSv54]	380	7.99 x 10 ⁻⁵⁹	8 - 369 (9.77%)
324	NR gi 319442838 ref ZP_07991994.1 putative mannose-6-phosphate isomerase [Corynebacterium variabile DSM 44702]	388	1.36 x 10 ⁻⁵⁸	7 - 371 (10.23%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
325	NR gi 284029565 ref YP_003379496.1 mannose-6-phosphate isomerase, class I [Kribbella flavida DSM 17836] >gnl BL_ORD_ID 2334395 mannose-6-phosphate isomerase, class I [Kribbella flavida DSM 17836]	387	1.78 x 10 ⁻⁵⁸	3 - 382 (9.81%)
326	NR gi 25027320 ref NP_737374.1 putative mannose-6-phosphate isomerase [Corynebacterium efficiens YS-314] >gnl BL_ORD_ID 911300 mannose-6-phosphate isomerase [Corynebacterium efficiens YS-314] >gnl BL_ORD_ID 911300 putative mannose-6-phosphate isomerase [Corynebacterium efficiens YS-314] >gnl BL_ORD_ID 911300 mannose-6-phosphate isomerase [Corynebacterium efficiens YS-314]	389	1.78 x 10 ⁻⁵⁸	1 - 373 (9.32%)
327	NR gi 227497981 ref ZP_03928161.1 possible mannose-6-phosphate isomerase [Actinomyces urogenitalis DSM 15434] >gnl BL_ORD_ID 2209162 possible mannose-6-phosphate isomerase [Actinomyces urogenitalis DSM 15434]	394	2.32 x 10 ⁻⁵⁸	1 - 382 (9.15%)
328	NR gi 317506117 ref ZP_07963941.1 mannose-6-phosphate isomerase [Segniliparus rugosus ATCC BAA-974] >gnl BL_ORD_ID 869990 mannose-6-phosphate isomerase [Segniliparus rugosus ATCC BAA-974]	387	3.96 x 10 ⁻⁵⁸	1 - 381 (9.28%)
329	NR gi 297560089 ref YP_003679063.1 mannose-6-phosphate isomerase, class I [Nocardiopsis dassonvillei subsp. dassonvillei DSM 43111] >gnl BL_ORD_ID 2443378 mannose-6-phosphate isomerase, class I [Nocardiopsis dassonvillei subsp. dassonvillei DSM 43111]	392	3.96 x 10 ⁻⁵⁸	1 - 384 (10.15%)
330	NR gi 271966341 ref YP_003340537.1 Mannose-6-phosphate isomerase [Streptosporangium roseum DSM 43021] >gnl BL_ORD_ID 2733685 Mannose-6-phosphate isomerase [Streptosporangium roseum DSM 43021]	389	5.18 x 10 ⁻⁵⁸	3 - 384 (9.45%)
331	NR gi 213610043 ref ZP_03369869.1 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Typhi str. E98-2068]	129	5.18 x 10 ⁻⁵⁸	1 - 129 (66.71%)
332	NR gi 148272207 ref YP_001221768.1 putative mannose-6-phosphate isomerase [Clavibacter michiganensis subsp. michiganensis NCPPB 382] >gnl BL_ORD_ID 1630356 putative mannose-6-phosphate isomerase [Clavibacter michiganensis subsp. michiganensis NCPPB 382]	411	5.18 x 10 ⁻⁵⁸	4 - 382 (9.29%)
333	NR gi 296037180 ref ZP_06829765.1 mannose-6-phosphate isomerase [Rhodococcus equi ATCC 33707] >gnl BL_ORD_ID 2046835 mannose-6-phosphate isomerase [Rhodococcus equi ATCC 33707]	361	6.76 x 10 ⁻⁵⁸	38 - 379 (11.05%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
334	NR gi 289704927 ref ZP_06501344.1 mannose-6-phosphate isomerase, class I [Micrococcus luteus SK58] >gnl BL_ORD_ID 1561531 mannose-6-phosphate isomerase, class I [Micrococcus luteus SK58]	387	8.83 x 10 ⁻⁵⁸	8 - 374 (10.02%)
335	NR gi 297572152 ref YP_003697926.1 mannose-6-phosphate isomerase, class I [Arcanobacterium haemolyticum DSM 20595] >gnl BL_ORD_ID 2190087 mannose-6-phosphate isomerase, class I [Arcanobacterium haemolyticum DSM 20595]	413	1.15 x 10 ⁻⁵⁷	1 - 387 (8.21%)
336	NR gi 284992674 ref YP_003411228.1 mannose-6-phosphate isomerase, class I [Geodermatophilus obscurus DSM 43160] >gnl BL_ORD_ID 2266495 mannose-6-phosphate isomerase, class I [Geodermatophilus obscurus DSM 43160]	394	1.15 x 10 ⁻⁵⁷	1 - 386 (9.34%)
337	NR gi 239917057 ref YP_002956615.1 mannose-6-phosphate isomerase, class I [Micrococcus luteus NCTC 2665] >gnl BL_ORD_ID 201761 mannose-6-phosphate isomerase, class I [Micrococcus luteus NCTC 2665] >gnl BL_ORD_ID 201761 mannose-6-phosphate isomerase, class I [Micrococcus luteus NCTC 2665]	387	3.36 x 10 ⁻⁵⁷	8 - 374 (9.88%)
338	NR gi 145593522 ref YP_001157819.1 mannose-6-phosphate isomerase, class I [Salinispora tropica CNB-440] >gnl BL_ORD_ID 1531640 mannose-6-phosphate isomerase [Salinispora tropica CNB-440]	389	3.36 x 10 ⁻⁵⁷	1 - 382 (9.45%)
339	NR gi 301156614 emb CBW16085.1 mannose-6-phosphate isomerase [Haemophilus parainfluenzae T3T1]	387	4.38 x 10 ⁻⁵⁷	3 - 374 (9.35%)
340	NR gi 297626999 ref YP_003688762.1 Phosphomannose isomerase [Propionibacterium freudenreichii subsp. shermanii CIRM-BIA1] >gnl BL_ORD_ID 2187085 Phosphomannose isomerase [Propionibacterium freudenreichii subsp. shermanii CIRM-BIA1]	393	5.72 x 10 ⁻⁵⁷	1 - 380 (9.65%)
341	NR gi 291303447 ref YP_003514725.1 mannose-6-phosphate isomerase class I [Stackebrandtia nassauensis DSM 44728] >gnl BL_ORD_ID 1618984 mannose-6-phosphate isomerase, class I [Stackebrandtia nassauensis DSM 44728]	399	5.72 x 10 ⁻⁵⁷	1 - 382 (8.98%)
342	NR gi 227486956 ref ZP_03917272.1 mannose-6-phosphate isomerase [Corynebacterium glucuronolyticum ATCC 51867] >gnl BL_ORD_ID 2263404 mannose-6-phosphate isomerase [Corynebacterium glucuronolyticum ATCC 51867]	396	5.72 x 10 ⁻⁵⁷	1 - 380 (9.31%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
343	NR gi 315654786 ref ZP_07907691.1 mannose-6-phosphate isomerase [Mobiluncus curtisii ATCC 51333] >gnl BL_ORD_ID 833577 mannose-6-phosphate isomerase [Mobiluncus curtisii ATCC 51333]	397	1.28 x 10 ⁻⁵⁶	1 - 382 (8.88%)
344	NR gi 238063005 ref ZP_04607714.1 mannose-6-phosphate isomerase, class I [Micromonospora sp. ATCC 39149] >gnl BL_ORD_ID 2798012 mannose-6-phosphate isomerase, class I [Micromonospora sp. ATCC 39149]	399	1.28 x 10 ⁻⁵⁶	1 - 382 (9.17%)
345	NR gi 298346203 ref YP_003718890.1 putative mannose-6-phosphate isomerase [Mobiluncus curtisii ATCC 43063] >gnl BL_ORD_ID 2312752 possible mannose-6-phosphate isomerase [Mobiluncus curtisii ATCC 43063]	397	1.28 x 10 ⁻⁵⁶	1 - 382 (8.82%)
346	NR gi 227549509 ref ZP_03979558.1 possible mannose-6-phosphate isomerase [Corynebacterium lipophiloflavum DSM 44291] >gnl BL_ORD_ID 2252635 possible mannose-6-phosphate isomerase [Corynebacterium lipophiloflavum DSM 44291]	387	1.28 x 10 ⁻⁵⁶	3 - 382 (10.02%)
347	NR gi 260906695 ref ZP_05915017.1 phosphomannose isomerase [Brevibacterium linens BL2]	432	1.67 x 10 ⁻⁵⁶	1 - 384 (8.79%)
348	NR gi 315657293 ref ZP_07910175.1 mannose-6-phosphate isomerase [Mobiluncus curtisii subsp. holmesii ATCC 35242] >gnl BL_ORD_ID 834391 mannose-6-phosphate isomerase [Mobiluncus curtisii subsp. holmesii ATCC 35242]	397	2.18 x 10 ⁻⁵⁶	1 - 382 (8.88%)
349	NR gi 304390037 ref ZP_07371991.1 mannose-6-phosphate isomerase [Mobiluncus curtisii subsp. curtisii ATCC 35241] >gnl BL_ORD_ID 2840472 mannose-6-phosphate isomerase [Mobiluncus curtisii subsp. curtisii ATCC 35241]	397	2.18 x 10 ⁻⁵⁶	1 - 382 (8.82%)
350	NR gi 227541883 ref ZP_03971932.1 possible mannose-6-phosphate isomerase [Corynebacterium glucuronolyticum ATCC 51866] >gnl BL_ORD_ID 2292399 possible mannose-6-phosphate isomerase [Corynebacterium glucuronolyticum ATCC 51866]	396	2.18 x 10 ⁻⁵⁶	1 - 380 (9.25%)
351	NR gi 256423044 ref YP_003123697.1 mannose-6-phosphate isomerase, class I [Chitinophaga pinensis DSM 2588] >gnl BL_ORD_ID 2603970 mannose-6-phosphate isomerase, class I [Chitinophaga pinensis DSM 2588]	382	2.84 x 10 ⁻⁵⁶	3 - 366 (9.73%)
352	NR gi 152967813 ref YP_001363597.1 mannose-6-phosphate isomerase, class I [Kineococcus radiotolerans SRS30216] >gnl BL_ORD_ID 1952699 mannose-6-phosphate isomerase, class I [Kineococcus radiotolerans SRS30216]	397	2.84 x 10 ⁻⁵⁶	1 - 384 (9.45%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
353	NR gi 213964847 ref ZP_03393046.1 mannose-6-phosphate isomerase, class I [Corynebacterium amycolatum SK46] >gnl BL_ORD_ID 1250326 mannose-6-phosphate isomerase, class I [Corynebacterium amycolatum SK46]	382	3.71 x 10 ⁻⁵⁶	1 - 371 (9.46%)
354	NR gi 88855625 ref ZP_01130288.1 mannose-6-phosphate isomerase [marine actinobacterium PHSC20C1] >gnl BL_ORD_ID 651030 mannose-6-phosphate isomerase [marine actinobacterium PHSC20C1]	393	3.71 x 10 ⁻⁵⁶	4 - 384 (9.39%)
355	NR gi 312140684 ref YP_004008020.1 mannose-6-phosphate isomerase mana [Rhodococcus equi 103S] >gnl BL_ORD_ID 527149 mannose-6-phosphate isomerase ManA [Rhodococcus equi 103S]	346	4.85 x 10 ⁻⁵⁶	53 - 379 (11.53%)
356	NR gi 320531369 ref ZP_08032339.1 mannose-6-phosphate isomerase, class I [Actinomyces sp. oral taxon 171 str. F0337] >gnl BL_ORD_ID 1104563 mannose-6-phosphate isomerase, class I [Actinomyces sp. oral taxon 171 str. F0337]	405	6.33 x 10 ⁻⁵⁶	1 - 386 (8.84%)
357	NR gi 260577918 ref ZP_05845848.1 mannose-6-phosphate isomerase [Corynebacterium jeikeium ATCC 43734] >gnl BL_ORD_ID 738865 mannose-6-phosphate isomerase [Corynebacterium jeikeium ATCC 43734]	395	6.33 x 10 ⁻⁵⁶	1 - 386 (9.74%)
358	NR gi 159036557 ref YP_001535810.1 mannose-6-phosphate isomerase, class I [Salinispora arenicola CNS-205] >gnl BL_ORD_ID 1030664 mannose-6-phosphate isomerase, class I [Salinispora arenicola CNS-205]	389	1.08 x 10 ⁻⁵⁵	1 - 382 (9.52%)
359	NR gi 68536728 ref YP_251433.1 mannose-6-phosphate isomerase [Corynebacterium jeikeium K411] >gnl BL_ORD_ID 1431762 mannose-6-phosphate isomerase [Corynebacterium jeikeium K411]	395	2.40 x 10 ⁻⁵⁵	1 - 386 (9.74%)
360	NR gi 300781647 ref ZP_07091501.1 mannose-6-phosphate isomerase [Corynebacterium genitalium ATCC 33030] >gnl BL_ORD_ID 713621 mannose-6-phosphate isomerase [Corynebacterium genitalium ATCC 33030]	408	3.14 x 10 ⁻⁵⁵	1 - 379 (9.07%)
361	NR gi 50954314 ref YP_061602.1 mannose-6-phosphate isomerase [Leifsonia xyli subsp. xyli str. CTCB07] >gnl BL_ORD_ID 2411489 mannose-6-phosphate isomerase [Leifsonia xyli subsp. xyli str. CTCB07]	387	3.14 x 10 ⁻⁵⁵	6 - 384 (9.68%)
362	NR gi 256391443 ref YP_003113007.1 mannose-6-phosphate isomerase, class I [Catenulispora acidiphila DSM 44928] >gnl BL_ORD_ID 2619682 mannose-6-phosphate isomerase, class I [Catenulispora acidiphila DSM 44928]	401	9.14 x 10 ⁻⁵⁵	1 - 380 (9.14%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
363	NR gi 118468938 ref YP_886206.1 mannose-6-phosphate isomerase, class I [Mycobacterium smegmatis str. MC2 155] >gnl BL_ORD_ID 853586 mannose-6-phosphate isomerase, class I [Mycobacterium smegmatis str. MC2 155]	361	1.19 x 10 ⁻⁵⁴	32 - 376 (10.66%)
364	NR gi 229819668 ref YP_002881194.1 mannose-6-phosphate isomerase, class I [Beutenbergia cavernae DSM 12333] >gnl BL_ORD_ID 2224301 mannose-6-phosphate isomerase, class I [Beutenbergia cavernae DSM 12333]	388	2.66 x 10 ⁻⁵⁴	7 - 384 (9.37%)
365	NR gi 88797690 ref ZP_01113278.1 mannose-6-phosphate isomerase [Reinekea sp. MED297] >gnl BL_ORD_ID 633613 mannose-6-phosphate isomerase [Reinekea sp. MED297]	389	2.66 x 10 ⁻⁵⁴	4 - 388 (9.12%)
366	NR gi 304362272 ref ZP_07359517.1 mannose-6-phosphate isomerase, class I [Actinomyces viscosus C505]	405	3.47 x 10 ⁻⁵⁴	1 - 386 (8.72%)
367	NR gi 258544726 ref ZP_05704960.1 mannose-6-phosphate isomerase (phosphomannose isomerase) (phosphohexomutase) [Cardiobacterium hominis ATCC 15826] >gnl BL_ORD_ID 711590 mannose-6-phosphate isomerase (phosphomannose isomerase) (phosphohexomutase) [Cardiobacterium hominis ATCC 15826]	394	3.47 x 10 ⁻⁵⁴	3 - 383 (9.47%)
368	NR gi 237786079 ref YP_002906784.1 mannose-6-phosphate isomerase [Corynebacterium kroppenstedtii DSM 44385] >gnl BL_ORD_ID 2773472 mannose-6-phosphate isomerase [Corynebacterium kroppenstedtii DSM 44385]	455	4.54 x 10 ⁻⁵⁴	1 - 388 (7.25%)
369	NR gi 257067466 ref YP_003153721.1 mannose-6-phosphate isomerase, class I [Brachybacterium faecium DSM 4810] >gnl BL_ORD_ID 533200 mannose-6-phosphate isomerase, class I [Brachybacterium faecium DSM 4810]	395	5.92 x 10 ⁻⁵⁴	9 - 386 (8.97%)
370	NR gi 311744327 ref ZP_07718131.1 mannose-6-phosphate isomerase [Aeromicrobium marinum DSM 15272] >gnl BL_ORD_ID 1862591 mannose-6-phosphate isomerase [Aeromicrobium marinum DSM 15272]	397	7.74 x 10 ⁻⁵⁴	1 - 388 (9.14%)
371	NR gi 315502046 ref YP_004080933.1 mannose-6-phosphate isomerase, class i [Micromonospora sp. L5] >gnl BL_ORD_ID 1465922 mannose-6-phosphate isomerase, class I [Micromonospora sp. L5]	388	7.74 x 10 ⁻⁵⁴	1 - 382 (9.43%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
372	NR gi 302865498 ref YP_003834135.1 mannose-6-phosphate isomerase, class I [Micromonospora aurantiaca ATCC 27029] >gnl BL_ORD_ID 1194678 mannose-6-phosphate isomerase, class I [Micromonospora aurantiaca ATCC 27029]	388	1.01 x 10 ⁻⁵³	1 - 382 (9.43%)
373	NR gi 223041625 ref ZP_03611823.1 mannose-6-phosphate isomerase [Actinobacillus minor 202] >gnl BL_ORD_ID 1747666 mannose-6-phosphate isomerase [Actinobacillus minor 202]	389	5.01 x 10 ⁻⁵³	3 - 374 (9.45%)
374	NR gi 295395831 ref ZP_06806019.1 mannose-6-phosphate isomerase [Brevibacterium mcbrellneri ATCC 49030] >gnl BL_ORD_ID 1966251 mannose-6-phosphate isomerase [Brevibacterium mcbrellneri ATCC 49030]	400	1.91 x 10 ⁻⁵²	1 - 384 (9.31%)
375	NR gi 261867845 ref YP_003255767.1 mannose-6-phosphate isomerase, class I [Aggregatibacter actinomycetemcomitans D11S-1] >gnl BL_ORD_ID 942226 mannose-6-phosphate isomerase, class I [Aggregatibacter actinomycetemcomitans D11S-1]	383	2.49 x 10 ⁻⁵²	4 - 372 (9.27%)
376	NR gi 170719141 ref YP_001784288.1 mannose-6-phosphate isomerase, class I [Haemophilus somnus 2336] >gnl BL_ORD_ID 202780 mannose-6-phosphate isomerase, class I [Haemophilus somnus 2336]	383	7.24 x 10 ⁻⁵²	3 - 371 (9.34%)
377	NR gi 260914383 ref ZP_05920852.1 mannose-6-phosphate isomerase [Pasteurella dagmatis ATCC 43325] >gnl BL_ORD_ID 873820 mannose-6-phosphate isomerase [Pasteurella dagmatis ATCC 43325]	389	9.46 x 10 ⁻⁵²	3 - 372 (9.19%)
378	NR gi 15602694 ref NP_245766.1 Pmi [Pasteurella multocida subsp. multocida str. Pm70] >gnl BL_ORD_ID 1538388 Pmi [Pasteurella multocida subsp. multocida str. Pm70]	386	1.61 x 10 ⁻⁵¹	3 - 374 (9.19%)
379	NR gi 172040156 ref YP_001799870.1 mannose-6-phosphate isomerase [Corynebacterium urealyticum DSM 7109] >gnl BL_ORD_ID 185530 mannose-6-phosphate isomerase [Corynebacterium urealyticum DSM 7109]	412	2.11 x 10 ⁻⁵¹	1 - 386 (8.48%)
380	NR gi 323356995 ref YP_004223391.1 phosphomannose isomerase [Microbacterium testaceum StLB037] >gnl BL_ORD_ID 1330487 phosphomannose isomerase [Microbacterium testaceum StLB037]	384	4.69 x 10 ⁻⁵¹	4 - 380 (9.63%)
381	NR gi 240948093 ref ZP_04752503.1 mannose-6-phosphate isomerase [Actinobacillus minor NM305] >gnl BL_ORD_ID 157456 mannose-6-phosphate isomerase [Actinobacillus minor NM305]	389	4.69 x 10 ⁻⁵¹	3 - 374 (9.19%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
382	NR gi 113460750 ref YP_718817.1 mannose-6-phosphate isomerase [Haemophilus somnus 129PT] >gnl BL_ORD_ID 47677 mannose-6-phosphate isomerase, type 1 [Haemophilus somnus 129PT]	384	8.01 x 10 ⁻⁵¹	3 - 372 (9.16%)
383	NR gi 293390321 ref ZP_06634655.1 mannose-6-phosphate isomerase, class I [Aggregatibacter actinomycetemcomitans D7S-1] >gnl BL_ORD_ID 1637519 mannose-6-phosphate isomerase, class I [Aggregatibacter actinomycetemcomitans D7S-1]	383	1.05 x 10 ⁻⁵⁰	4 - 372 (9.14%)
384	NR gi 209695114 ref YP_002263043.1 mannose-6-phosphate isomerase (phosphomannose isomerase) [Aliivibrio salmonicida LFI1238] >gnl BL_ORD_ID 991283 mannose-6-phosphate isomerase (phosphomannose isomerase) [Aliivibrio salmonicida LFI1238]	382	1.05 x 10 ⁻⁵⁰	9 - 388 (9.53%)
385	NR gi 315634010 ref ZP_07889299.1 mannose-6-phosphate isomerase [Aggregatibacter segnis ATCC 33393] >gnl BL_ORD_ID 822541 mannose-6-phosphate isomerase [Aggregatibacter segnis ATCC 33393]	380	1.37 x 10 ⁻⁵⁰	8 - 372 (9.14%)
386	NR gi 296271460 ref YP_003654092.1 mannose-6-phosphate isomerase [Thermobispora bispora DSM 43833] >gnl BL_ORD_ID 2096787 mannose-6-phosphate isomerase, class I [Thermobispora bispora DSM 43833]	386	1.37 x 10 ⁻⁵⁰	1 - 382 (9.26%)
387	NR gi 117929305 ref YP_873856.1 mannose-6-phosphate isomerase [Acidothermus cellulolyticus 11B] >gnl BL_ORD_ID 665285 mannose-6-phosphate isomerase, type 1 [Acidothermus cellulolyticus 11B]	396	3.97 x 10 ⁻⁵⁰	3 - 387 (8.74%)
388	NR gi 251792195 ref YP_003006915.1 mannose-6-phosphate isomerase, class I [Aggregatibacter aphrophilus NJ8700] >gnl BL_ORD_ID 266284 mannose-6-phosphate isomerase, class I [Aggregatibacter aphrophilus NJ8700]	385	6.78 x 10 ⁻⁵⁰	3 - 372 (8.77%)
389	NR gi 52424669 ref YP_087806.1 ManA protein [Mannheimia succiniciproducens MBEL55E] >gnl BL_ORD_ID 1816172 ManA protein [Mannheimia succiniciproducens MBEL55E]	384	1.51 x 10 ⁻⁴⁹	3 - 372 (8.95%)
390	NR gi 312199857 ref YP_004019918.1 mannose-6-phosphate isomerase [Frankia sp. Eul1c] >gnl BL_ORD_ID 1220576 Mannose-6-phosphate isomerase [Frankia sp. Eul1c]	372	7.49 x 10 ⁻⁴⁹	4 - 348 (9.61%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
391	<p>NR gi 46143297 ref ZP_00204432.1 COG1482: Phosphomannose isomerase [Actinobacillus pleuropneumoniae serovar 1 str. 4074] >gnl BL_ORD_ID 136960 mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae L20] >gnl BL_ORD_ID 136960 mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 3 str. JL03] >gnl BL_ORD_ID 136960 mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 7 str. AP76] >gnl BL_ORD_ID 136960 mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 2 str. 4226] >gnl BL_ORD_ID 136960 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 2 str. S1536] >gnl BL_ORD_ID 136960 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 4 str. M62] >gnl BL_ORD_ID 136960 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 10 str. D13039] >gnl BL_ORD_ID 136960 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 12 str. 1096] >gnl BL_ORD_ID 136960 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 13 str. N273] >gnl BL_ORD_ID 136960 mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 5b str. L20] >gnl BL_ORD_ID 136960 mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 3 str. JL03] >gnl BL_ORD_ID 136960 mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 7 str. AP76] >gnl BL_ORD_ID 136960 mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 2 str. 4226] >gnl BL_ORD_ID 136960 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 2 str. S1536] >gnl BL_ORD_ID 136960 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 4 str. M62] >gnl BL_ORD_ID 136960 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 10 str. D13039] >gnl BL_ORD_ID 136960 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 12 str. 1096] >gnl BL_ORD_ID 136960 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 13 str. N273]</p>	393	9.79 x 10 ⁻⁴⁹	3 - 378 (8.74%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
392	NR gi 307246318 ref ZP_07528397.1 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 1 str. 4074] >gnl BL_ORD_ID 12577 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 9 str. CVJ13261] >gnl BL_ORD_ID 12577 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 11 str. 56153] >gnl BL_ORD_ID 12577 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 1 str. 4074] >gnl BL_ORD_ID 12577 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 9 str. CVJ13261] >gnl BL_ORD_ID 12577 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 11 str. 56153]	393	1.28 x 10 ⁻⁴⁸	3 - 378 (8.74%)
393	NR gi 303250765 ref ZP_07336960.1 mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 6 str. Femo] >gnl BL_ORD_ID 2819111 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 6 str. Femo] >gnl BL_ORD_ID 2819111 mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 6 str. Femo] >gnl BL_ORD_ID 2819111 Mannose-6-phosphate isomerase [Actinobacillus pleuropneumoniae serovar 6 str. Femo]	393	1.67 x 10 ⁻⁴⁸	3 - 378 (8.35%)
394	NR gi 297519912 ref ZP_06938298.1 mannose-6-phosphate isomerase [Escherichia coli OP50]	98	8.28 x 10 ⁻⁴⁸	1 - 98 (102.04%)
395	NR gi 158317605 ref YP_001510113.1 mannose-6-phosphate isomerase, class I [Frankia sp. EAN1pec] >gnl BL_ORD_ID 314483 mannose-6-phosphate isomerase, class I [Frankia sp. EAN1pec]	401	8.28 x 10 ⁻⁴⁸	3 - 384 (8.83%)
396	NR gi 152978608 ref YP_001344237.1 mannose-6-phosphate isomerase, class I [Actinobacillus succinogenes 130Z] >gnl BL_ORD_ID 385868 mannose-6-phosphate isomerase, class I [Actinobacillus succinogenes 130Z]	383	1.41 x 10 ⁻⁴⁷	4 - 371 (9%)
397	NR gi 311112922 ref YP_003984144.1 mannose-6-phosphate isomerase [Rothia dentocariosa ATCC 17931] >gnl BL_ORD_ID 2177549 mannose-6-phosphate isomerase [Rothia dentocariosa ATCC 17931]	392	1.85 x 10 ⁻⁴⁷	4 - 384 (8.53%)
398	NR gi 300744307 ref ZP_07073326.1 mannose-6-phosphate isomerase, class I [Rothia dentocariosa M567] >gnl BL_ORD_ID 2593309 mannose-6-phosphate isomerase, class I [Rothia dentocariosa M567]	392	2.41 x 10 ⁻⁴⁷	4 - 384 (8.72%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
399	NR gi 262197419 ref YP_003268628.1 mannose-6-phosphate isomerase, class I [Haliangium ochraceum DSM 14365] >gnl BL_ORD_ID 2320945 mannose-6-phosphate isomerase, class I [Haliangium ochraceum DSM 14365]	335	4.11 x 10 ⁻⁴⁷	3 - 321 (11.50%)
400	NR gi 227495268 ref ZP_03925584.1 mannose-6-phosphate isomerase [Actinomyces coleocanis DSM 15436] >gnl BL_ORD_ID 2207662 mannose-6-phosphate isomerase [Actinomyces coleocanis DSM 15436]	393	9.16 x 10 ⁻⁴⁷	11 - 387 (8.81%)
401	NR gi 167855950 ref ZP_02478698.1 mannose-6-phosphate isomerase [Haemophilus parasuis 29755] >gnl BL_ORD_ID 2778641 mannose-6-phosphate isomerase [Haemophilus parasuis SH0165] >gnl BL_ORD_ID 2778641 mannose-6-phosphate isomerase [Haemophilus parasuis 29755] >gnl BL_ORD_ID 2778641 mannose-6-phosphate isomerase [Haemophilus parasuis SH0165]	391	1.20 x 10 ⁻⁴⁶	3 - 372 (8.70%)
402	NR gi 288916511 ref ZP_06410888.1 mannose-6-phosphate isomerase, class I [Frankia sp. EUN1f] >gnl BL_ORD_ID 1489250 mannose-6-phosphate isomerase, class I [Frankia sp. EUN1f]	362	1.56 x 10 ⁻⁴⁶	3 - 349 (10.15%)
403	NR gi 322513533 ref ZP_08066634.1 mannose-6-phosphate isomerase [Actinobacillus ureae ATCC 25976] >gnl BL_ORD_ID 1224288 mannose-6-phosphate isomerase [Actinobacillus ureae ATCC 25976]	391	2.04 x 10 ⁻⁴⁶	3 - 378 (8.57%)
404	NR gi 308094734 ref ZP_07663026.1 phosphomannose isomerase type I [Vibrio parahaemolyticus AN-5034] >gnl BL_ORD_ID 212280 phosphomannose isomerase type I [Vibrio parahaemolyticus AN-5034]	269	2.04 x 10 ⁻⁴⁶	135 - 389 (15.34%)
405	NR gi 184199976 ref YP_001854183.1 mannose-6-phosphate isomerase [Kocuria rhizophila DC2201] >gnl BL_ORD_ID 249484 mannose-6-phosphate isomerase [Kocuria rhizophila DC2201]	320	2.67 x 10 ⁻⁴⁶	3 - 310 (11.72%)
406	NR gi 34497767 ref NP_901982.1 mannose-6-phosphate isomerase [Chromobacterium violaceum ATCC 12472] >gnl BL_ORD_ID 1728793 mannose-6-phosphate isomerase [Chromobacterium violaceum ATCC 12472]	372	3.48 x 10 ⁻⁴⁶	9 - 369 (9.97%)
407	NR gi 254787306 ref YP_003074735.1 mannose-6-phosphate isomerase, class I [Teredinibacter turnerae T7901] >gnl BL_ORD_ID 88047 mannose-6-phosphate isomerase, class I [Teredinibacter turnerae T7901]	372	5.94 x 10 ⁻⁴⁶	1 - 352 (9.32%)
408	NR gi 320162611 gb EFW39510.1 mannose-6-phosphate isomerase [Capsaspora owczarzewski ATCC 30864]	398	1.32 x 10 ⁻⁴⁵	4 - 369 (8.65%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
409	NR gi 33151928 ref NP_873281.1 mannose-6-phosphate isomerase [Haemophilus ducreyi 35000HP] >gnl BL_ORD_ID 1720786 mannose-6-phosphate isomerase [Haemophilus ducreyi 35000HP]	389	1.73 x 10 ⁻⁴⁵	3 - 372 (8.06%)
410	NR gi 225710674 gb ACO11183.1 Mannose-6-phosphate isomerase [Caligus rogercresseyi]	355	5.03 x 10 ⁻⁴⁵	8 - 323 (11.11%)
411	NR gi 169868160 ref XP_001840654.1 mannose-6-phosphate isomerase [Coprinopsis cinerea okayama7#130] >gnl BL_ORD_ID 757355 mannose-6-phosphate isomerase [Coprinopsis cinerea okayama7#130]	423	6.56 x 10 ⁻⁴⁵	3 - 382 (8.05%)
412	NR gi 294786603 ref ZP_06751857.1 mannose-6-phosphate isomerase, class I [Parascardovia denticolens F0305] >gnl BL_ORD_ID 1944094 mannose-6-phosphate isomerase [Parascardovia denticolens DSM 10105] >gnl BL_ORD_ID 1944094 mannose-6-phosphate isomerase, class I [Parascardovia denticolens F0305] >gnl BL_ORD_ID 1944094 mannose-6-phosphate isomerase [Parascardovia denticolens DSM 10105]	422	1.46 x 10 ⁻⁴⁴	9 - 380 (7.36%)
413	NR gi 314922684 gb EFS86515.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL001PA1]	397	1.91 x 10 ⁻⁴⁴	1 - 385 (8.38%)
414	NR gi 313835163 gb EFS72877.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL037PA2] >gnl BL_ORD_ID 741766 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL044PA1] >gnl BL_ORD_ID 741766 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL037PA3]	402	1.91 x 10 ⁻⁴⁴	1 - 387 (8.66%)
415	NR gi 282853045 ref ZP_06262382.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes J139] >gnl BL_ORD_ID 1324332 mannose-6-phosphate isomerase, class I [Propionibacterium acnes J139] >gnl BL_ORD_ID 1324332 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL082PA2] >gnl BL_ORD_ID 1324332 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL110PA3] >gnl BL_ORD_ID 1324332 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL110PA4] >gnl BL_ORD_ID 1324332 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL060PA1] >gnl BL_ORD_ID 1324332 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL050PA2]	397	1.91 x 10 ⁻⁴⁴	1 - 385 (8.38%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
416	<p>NR gi 50841502 ref YP_054729.1 mannose-6-phosphate isomerase [Propionibacterium acnes KPA171202] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes SK187] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes J165] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes SK137] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase [Propionibacterium acnes KPA171202] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes SK187] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes J165] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes SK137] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL013PA1] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL074PA1] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL110PA1] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL087PA2] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL083PA1] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL025PA1] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL059PA1] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL046PA2] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL036PA1] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL036PA2] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL063PA1] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL063PA2] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL007PA1] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL056PA1] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL086PA1] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL005PA4] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL050PA1] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL050PA3] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL036PA3] >gnl BL_ORD_ID 2408726 mannose-6-phosphate isomerase, class I</p>	397	1.91 x 10 ⁻⁴⁴	1 - 385 748 of 1200

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
417	NR gi 62510811 sp Q8HXX2.3 MPI_MACFA RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 869547 mannose-6-phosphate isomerase [Macaca fascicularis]	403	3.26 x 10 ⁻⁴⁴	7 - 374 (8.50%)
418	NR gi 320095919 ref ZP_08027541.1 mannose-6- phosphate isomerase [Actinomyces sp. oral taxon 178 str. F0338] >gnl BL_ORD_ID 1071363 mannose-6-phosphate isomerase [Actinomyces sp. oral taxon 178 str. F0338]	414	5.56 x 10 ⁻⁴⁴	1 - 387 (7.88%)
419	NR gi 313803562 gb EFS44744.1 mannose-6- phosphate isomerase, class I [Propionibacterium acnes HL110PA2]	397	5.56 x 10 ⁻⁴⁴	1 - 385 (8.38%)
420	NR gi 149639141 ref XP_001511999.1 PREDICTED: hypothetical protein [Ornithorhynchus anatinus]	402	5.56 x 10 ⁻⁴⁴	8 - 374 (8.91%)
421	NR gi 148727240 ref NP_001092020.1 mannose-6- phosphate isomerase [Pan troglodytes] >gnl BL_ORD_ID 1603872 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 1603872 mannose phosphate isomerase [Pan troglodytes verus]	403	5.56 x 10 ⁻⁴⁴	7 - 374 (8.50%)
422	NR gi 78369406 ref NP_001030361.1 mannose-6- phosphate isomerase [Bos taurus] >gnl BL_ORD_ID 2013580 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 2013580 Mannose phosphate isomerase [Bos taurus]	402	5.56 x 10 ⁻⁴⁴	8 - 374 (8.54%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
423	NR gi 4505235 ref NP_002426.1 mannose-6-phosphate isomerase [Homo sapiens] >gnl BL_ORD_ID 981944 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexamutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 981944 phosphomannose isomerase [Homo sapiens] >gnl BL_ORD_ID 981944 mannose phosphate isomerase [Homo sapiens] >gnl BL_ORD_ID 981944 Mannose phosphate isomerase [Homo sapiens] >gnl BL_ORD_ID 981944 mannose phosphate isomerase, isoform CRA_b [Homo sapiens] >gnl BL_ORD_ID 981944 unnamed protein product [Homo sapiens] >gnl BL_ORD_ID 981944 mannose phosphate isomerase [synthetic construct] >gnl BL_ORD_ID 981944 mannose phosphate isomerase [synthetic construct] >gnl BL_ORD_ID 981944 phosphomannose isomerase	403	5.56 x 10 ⁻⁴⁴	7 - 374 (8.50%)
424	NR gi 161016085 gb ABX56008.1 mannose-6-phosphate isomerase [Mytilus edulis]	407	7.26 x 10 ⁻⁴⁴	7 - 374 (8.45%)
425	NR gi 91080999 ref XP_975088.1 PREDICTED: similar to mannose-6-phosphate isomerase [Tribolium castaneum] >gnl BL_ORD_ID 250868 hypothetical protein TcasGA2_TC007395 [Tribolium castaneum]	391	9.48 x 10 ⁻⁴⁴	8 - 373 (9.16%)
426	NR gi 161016093 gb ABX56012.1 mannose-6-phosphate isomerase [Mytilus edulis]	407	1.62 x 10 ⁻⁴³	7 - 374 (8.45%)
427	NR gi 161016089 gb ABX56010.1 mannose-6-phosphate isomerase [Mytilus edulis]	407	1.62 x 10 ⁻⁴³	7 - 374 (8.45%)
428	NR gi 87122475 ref ZP_01078355.1 ManA protein [Marinomonas sp. MED121] >gnl BL_ORD_ID 593309 ManA protein [Marinomonas sp. MED121]	391	1.62 x 10 ⁻⁴³	14 - 384 (8.24%)
429	NR gi 294790617 ref ZP_06755775.1 mannose-6-phosphate isomerase, class I [Scardovia inopinata F0304] >gnl BL_ORD_ID 1929512 mannose-6-phosphate isomerase, class I [Scardovia inopinata F0304]	423	2.11 x 10 ⁻⁴³	9 - 380 (7.32%)
430	NR gi 213027124 ref ZP_03341571.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. 404ty]	99	2.11 x 10 ⁻⁴³	123 - 221 (90.81%)
431	NR gi 156555620 ref XP_001603028.1 PREDICTED: hypothetical protein [Nasonia vitripennis]	395	2.11 x 10 ⁻⁴³	7 - 374 (9.10%)
432	NR gi 161016091 gb ABX56011.1 mannose-6-phosphate isomerase [Mytilus edulis]	407	2.76 x 10 ⁻⁴³	7 - 374 (8.45%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
433	NR gi 161016087 gb ABX56009.1 mannose-6-phosphate isomerase [Mytilus edulis]	407	2.76 x 10 ⁻⁴³	7 - 374 (8.33%)
434	NR gi 156254294 gb ABU62655.1 mannose-6-phosphate isomerase [Mytilus trossulus]	407	2.76 x 10 ⁻⁴³	7 - 374 (8.45%)
435	NR gi 125563598 gb EAZ08978.1 hypothetical protein Osl_31243 [Oryza sativa Indica Group]	397	2.76 x 10 ⁻⁴³	2 - 371 (8.57%)
436	NR gi 224061763 ref XP_002195681.1 PREDICTED: similar to mannose-6-phosphate isomerase [Taeniopygia guttata]	409	3.60 x 10 ⁻⁴³	8 - 374 (8.73%)
437	NR gi 51854221 ref NP_001004081.1 mannose-6-phosphate isomerase [Rattus norvegicus] >gnl BL_ORD_ID 1316515 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 1316515 Mannose phosphate isomerase (mapped) [Rattus norvegicus] >gnl BL_ORD_ID 1316515 mannose phosphate isomerase (mapped) [Rattus norvegicus]	402	3.60 x 10 ⁻⁴³	8 - 374 (8.66%)
438	NR gi 301616158 ref XP_002937526.1 PREDICTED: mannose-6-phosphate isomerase [Xenopus (Silurana) tropicalis]	404	4.70 x 10 ⁻⁴³	7 - 374 (8.82%)
439	NR gi 213419676 ref ZP_03352742.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. E01-6750]	95	4.70 x 10 ⁻⁴³	229 - 323 (98.61%)
440	NR gi 156254290 gb ABU62653.1 mannose-6-phosphate isomerase [Mytilus edulis]	406	4.70 x 10 ⁻⁴³	7 - 374 (8.31%)
441	NR gi 283458755 ref YP_003363394.1 phosphomannose isomerase [Rothia mucilaginosa DY-18] >gnl BL_ORD_ID 1348728 phosphomannose isomerase [Rothia mucilaginosa DY-18]	396	6.14 x 10 ⁻⁴³	4 - 384 (8.23%)
442	NR gi 255327684 ref ZP_05368750.1 mannose-6-phosphate isomerase, class I [Rothia mucilaginosa ATCC 25296] >gnl BL_ORD_ID 454518 mannose-6-phosphate isomerase, class I [Rothia mucilaginosa ATCC 25296]	392	6.14 x 10 ⁻⁴³	4 - 384 (8.40%)
443	NR gi 242004715 ref XP_002423224.1 Mannose-6-phosphate isomerase, putative [Pediculus humanus corporis] >gnl BL_ORD_ID 1162166 Mannose-6-phosphate isomerase, putative [Pediculus humanus corporis]	359	6.14 x 10 ⁻⁴³	3 - 343 (9.70%)
444	NR gi 161016083 gb ABX56007.1 mannose-6-phosphate isomerase [Mytilus edulis]	407	1.05 x 10 ⁻⁴²	7 - 374 (8.39%)
445	NR gi 314928634 gb EFS92465.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL044PA1]	384	1.37 x 10 ⁻⁴²	1 - 373 (8.21%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
446	NR gi 313835491 gb EFS73205.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL037PA2] >gnl BL_ORD_ID 742092 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL037PA3]	384	1.37 x 10 ⁻⁴²	1 - 373 (8.21%)
447	NR gi 291411634 ref XP_002722093.1 PREDICTED: mannose phosphate isomerase [Oryctolagus cuniculus]	401	1.37 x 10 ⁻⁴²	8 - 374 (8.52%)
448	NR gi 229522882 ref ZP_04412296.1 mannose-6-phosphate isomerase [Vibrio cholerae TM 11079-80] >gnl BL_ORD_ID 2653187 mannose-6-phosphate isomerase [Vibrio furnissii CIP 102972] >gnl BL_ORD_ID 2653187 mannose-6-phosphate isomerase [Vibrio cholerae TM 11079-80] >gnl BL_ORD_ID 2653187 mannose-6-phosphate isomerase [Vibrio furnissii CIP 102972] >gnl BL_ORD_ID 2653187 ManA protein [Vibrio furnissii NCTC 11218]	359	1.79 x 10 ⁻⁴²	8 - 352 (9.54%)
449	NR gi 115698972 ref XP_780304.2 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus] >gnl BL_ORD_ID 699286 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus]	420	1.79 x 10 ⁻⁴²	7 - 374 (8.05%)
450	NR gi 297697125 ref XP_002825722.1 PREDICTED: LOW QUALITY PROTEIN: mannose-6-phosphate isomerase-like [Pongo abelii]	404	3.98 x 10 ⁻⁴²	7 - 374 (8.33%)
451	NR gi 14290579 gb AAH09068.1 Mannose phosphate isomerase [Mus musculus]	402	3.98 x 10 ⁻⁴²	8 - 374 (8.66%)
452	NR gi 91206392 ref NP_080113.1 mannose-6-phosphate isomerase [Mus musculus] >gnl BL_ORD_ID 744267 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 744267 phosphomannose isomerase [Mus musculus] >gnl BL_ORD_ID 744267 Mannose phosphate isomerase [Mus musculus] >gnl BL_ORD_ID 744267 unnamed protein product [Mus musculus] >gnl BL_ORD_ID 744267 mCG4013 [Mus musculus]	402	3.98 x 10 ⁻⁴²	8 - 374 (8.66%)
453	NR gi 16878311 gb AAH17351.1 MPI protein [Homo sapiens]	385	5.20 x 10 ⁻⁴²	7 - 374 (8.77%)
454	NR gi 260796729 ref XP_002593357.1 hypothetical protein BRAFLDRAFT_261743 [Branchiostoma floridae] >gnl BL_ORD_ID 1098051 hypothetical protein BRAFLDRAFT_261743 [Branchiostoma floridae]	409	6.79 x 10 ⁻⁴²	7 - 374 (8.43%)
455	NR gi 119619701 gb EAW99295.1 mannose phosphate isomerase, isoform CRA_a [Homo sapiens]	393	6.79 x 10 ⁻⁴²	14 - 374 (8.61%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
456	NR gi 256273748 gb EEU08673.1 Pmi40p [Saccharomyces cerevisiae JAY291]	415	8.87 x 10 ⁻⁴²	7 - 370 (7.78%)
457	NR gi 67971098 dbj BAE01891.1 unnamed protein product [Macaca fascicularis]	393	8.87 x 10 ⁻⁴²	14 - 374 (8.61%)
458	NR gi 291239915 ref XP_002739863.1 PREDICTED: mannose phosphate isomerase-like [Saccoglossus kowalevskii]	408	1.16 x 10 ⁻⁴¹	7 - 373 (8.11%)
459	NR gi 198412278 ref XP_002126287.1 PREDICTED: similar to Mannose phosphate isomerase (mapped) [Ciona intestinalis]	398	1.16 x 10 ⁻⁴¹	3 - 372 (8.33%)
460	NR gi 149692238 ref XP_001493832.1 PREDICTED: mannose phosphate isomerase [Equus caballus]	402	1.16 x 10 ⁻⁴¹	8 - 374 (8.35%)
461	NR gi 121701325 ref XP_001268927.1 mannose-6-phosphate isomerase, class I [Aspergillus clavatus NRRL 1] >gnl BL_ORD_ID 947091 mannose-6-phosphate isomerase, class I [Aspergillus clavatus NRRL 1]	430	1.16 x 10 ⁻⁴¹	8 - 372 (7.57%)
462	NR gi 74315945 ref NP_001028282.1 mannose-6-phosphate isomerase [Danio rerio] >gnl BL_ORD_ID 1979881 Zgc:110773 [Danio rerio]	402	1.51 x 10 ⁻⁴¹	8 - 374 (8.79%)
463	NR gi 297832896 ref XP_002884330.1 hypothetical protein ARALYDRAFT_477494 [Arabidopsis lyrata subsp. lyrata] >gnl BL_ORD_ID 2256400 hypothetical protein ARALYDRAFT_477494 [Arabidopsis lyrata subsp. lyrata]	401	1.98 x 10 ⁻⁴¹	1 - 372 (8.46%)
464	NR gi 293189588 ref ZP_06608307.1 mannose-6-phosphate isomerase, class I [Actinomyces odontolyticus F0309] >gnl BL_ORD_ID 1830477 mannose-6-phosphate isomerase, class I [Actinomyces odontolyticus F0309]	409	1.98 x 10 ⁻⁴¹	1 - 387 (7.77%)
465	NR gi 260940925 ref XP_002615302.1 hypothetical protein CLUG_04184 [Clavisporea lusitaniae ATCC 42720] >gnl BL_ORD_ID 2886302 hypothetical protein CLUG_04184 [Clavisporea lusitaniae ATCC 42720]	414	1.98 x 10 ⁻⁴¹	9 - 370 (8.34%)
466	NR gi 151944710 gb EDN62969.1 mannose-6-phosphate isomerase [Saccharomyces cerevisiae YJM789]	413	1.98 x 10 ⁻⁴¹	9 - 370 (7.80%)
467	NR gi 315604735 ref ZP_07879798.1 mannose-6-phosphate isomerase [Actinomyces sp. oral taxon 180 str. F0310] >gnl BL_ORD_ID 808651 mannose-6-phosphate isomerase [Actinomyces sp. oral taxon 180 str. F0310]	409	2.58 x 10 ⁻⁴¹	1 - 387 (7.65%)
468	NR gi 313814362 gb EFS52076.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL025PA1]	387	2.58 x 10 ⁻⁴¹	1 - 373 (8.21%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
469	NR gi 295130008 ref YP_003580671.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes SK137] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes SK137] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL013PA1] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL074PA1] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL083PA1] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL059PA1] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL063PA2] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL007PA1] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL056PA1] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL050PA1] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL050PA3] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL067PA1] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL002PA1] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL037PA1] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL053PA1] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL045PA1] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL005PA1] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL078PA1] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL038PA1] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL046PA1] >gnl BL_ORD_ID 1254394 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL030PA2]	387	2.58 x 10 ⁻⁴¹	1 - 373 (8.21%)
470	NR gi 76780352 gb AAI06454.1 LOC733350 protein [Xenopus laevis]	404	2.58 x 10 ⁻⁴¹	7 - 374 (8.70%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
471	NR gi 313802578 gb EFS43800.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL110PA2]	387	3.37 x 10 ⁻⁴¹	1 - 373 (8.21%)
472	NR gi 313792973 gb EFS41040.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL110PA1] >gnl BL_ORD_ID 737496 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL082PA1] >gnl BL_ORD_ID 737496 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL030PA1]	387	3.37 x 10 ⁻⁴¹	1 - 373 (8.21%)
473	NR gi 296213713 ref XP_002753391.1 PREDICTED: mannose-6-phosphate isomerase [Callithrix jacchus]	403	3.37 x 10 ⁻⁴¹	7 - 374 (8.07%)
474	NR gi 289641036 ref ZP_06473205.1 Mannose-6-phosphate isomerase [Frankia symbiont of Datisca glomerata] >gnl BL_ORD_ID 1547800 Mannose-6-phosphate isomerase [Frankia symbiont of Datisca glomerata]	360	3.37 x 10 ⁻⁴¹	3 - 324 (9.41%)
475	NR gi 254581726 ref XP_002496848.1 ZYRO0D09526p [Zygosaccharomyces rouxii] >gnl BL_ORD_ID 8739 ZYRO0D09526p [Zygosaccharomyces rouxii]	410	3.37 x 10 ⁻⁴¹	9 - 374 (7.79%)
476	NR gi 224531982 ref ZP_03672614.1 mannose-6-phosphate isomerase, class I [Borrelia valaisiana VS116] >gnl BL_ORD_ID 2689445 mannose-6-phosphate isomerase, class I [Borrelia valaisiana VS116]	381	3.37 x 10 ⁻⁴¹	6 - 383 (8.89%)
477	NR gi 119953196 ref YP_945405.1 mannose-6-phosphate isomerase [Borrelia turicatae 91E135] >gnl BL_ORD_ID 2172392 mannose-6-phosphate isomerase [Borrelia turicatae 91E135]	383	3.37 x 10 ⁻⁴¹	6 - 384 (8.66%)
478	NR gi 126272492 ref XP_001379636.1 PREDICTED: hypothetical protein [Monodelphis domestica]	403	3.37 x 10 ⁻⁴¹	8 - 372 (8.13%)
479	NR gi 50841934 ref YP_055161.1 phosphomannose isomerase [Propionibacterium acnes KPA171202] >gnl BL_ORD_ID 2409332 mannose-6-phosphate isomerase, class I [Propionibacterium acnes SK187] >gnl BL_ORD_ID 2409332 phosphomannose isomerase [Propionibacterium acnes KPA171202] >gnl BL_ORD_ID 2409332 mannose-6-phosphate isomerase, class I [Propionibacterium acnes SK187]	387	3.37 x 10 ⁻⁴¹	1 - 373 (8.21%)
480	NR gi 314954961 gb EFS99367.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL027PA1]	384	4.40 x 10 ⁻⁴¹	1 - 373 (8.21%)
481	NR gi 314915909 gb EFS79740.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL005PA4]	384	4.40 x 10 ⁻⁴¹	1 - 373 (8.21%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
482	NR gi 313840218 gb EFS77932.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL086PA1]	387	4.40 x 10 ⁻⁴¹	1 - 373 (8.21%)
483	NR gi 224534623 ref ZP_03675197.1 mannose-6-phosphate isomerase, class I [Borrelia spielmanii A14S] >gnl BL_ORD_ID 738290 mannose-6-phosphate isomerase, class I [Borrelia spielmanii A14S]	378	5.75 x 10 ⁻⁴¹	6 - 383 (8.47%)
484	NR gi 194038650 ref XP_001926526.1 PREDICTED: mannose-6-phosphate isomerase [Sus scrofa] >gnl BL_ORD_ID 567403 PREDICTED: mannose-6-phosphate isomerase [Sus scrofa]	403	5.75 x 10 ⁻⁴¹	8 - 374 (8.25%)
485	NR gi 6320839 ref NP_010918.1 Pmi40p [Saccharomyces cerevisiae S288c] >gnl BL_ORD_ID 933139 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 933139 Pmi40p: mannose-6-phosphate isomerase [Saccharomyces cerevisiae] >gnl BL_ORD_ID 933139 mannose-6-phosphate isomerase [Saccharomyces cerevisiae RM11-1a] >gnl BL_ORD_ID 933139 Pmi40p [Saccharomyces cerevisiae EC1118] >gnl BL_ORD_ID 933139 TPA: Mannose-6-phosphate isomerase, catalyzes the interconversion of fructose-6-P and mannose-6-P; required for early steps in protein mannosylation [Saccharomyces cerevisiae S288c]	413	5.75 x 10 ⁻⁴¹	9 - 370 (7.74%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
486	NR gi 289428390 ref ZP_06430076.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes J165] >gnl BL_ORD_ID 1522919 mannose-6-phosphate isomerase, class I [Propionibacterium acnes J165] >gnl BL_ORD_ID 1522919 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL087PA2] >gnl BL_ORD_ID 1522919 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL046PA2] >gnl BL_ORD_ID 1522919 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL036PA1] >gnl BL_ORD_ID 1522919 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL036PA2] >gnl BL_ORD_ID 1522919 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL063PA1] >gnl BL_ORD_ID 1522919 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL036PA3] >gnl BL_ORD_ID 1522919 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL002PA2] >gnl BL_ORD_ID 1522919 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL072PA2] >gnl BL_ORD_ID 1522919 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL005PA2] >gnl BL_ORD_ID 1522919 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL005PA3] >gnl BL_ORD_ID 1522919 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL002PA3] >gnl BL_ORD_ID 1522919 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL072PA1]	387	7.51 x 10 ⁻⁴¹	1 - 373 (8.14%)
487	NR gi 156066103 ref XP_001598973.1 hypothetical protein SS1G_01063 [Sclerotinia sclerotiorum 1980] >gnl BL_ORD_ID 2037912 hypothetical protein SS1G_01063 [Sclerotinia sclerotiorum 1980]	431	7.51 x 10 ⁻⁴¹	8 - 376 (7.43%)
488	NR gi 90083042 dbj BAE90603.1 unnamed protein product [Macaca fascicularis]	393	7.51 x 10 ⁻⁴¹	14 - 374 (8.55%)
489	NR gi 315099839 gb EFT71815.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL059PA2]	387	9.81 x 10 ⁻⁴¹	1 - 373 (8.14%)
490	NR gi 313231452 emb CBY08566.1 unnamed protein product [Oikopleura dioica]	372	9.81 x 10 ⁻⁴¹	7 - 352 (9.25%)
491	NR gi 301775200 ref XP_002923019.1 PREDICTED: mannose-6-phosphate isomerase-like [Ailuropoda melanoleuca]	403	9.81 x 10 ⁻⁴¹	7 - 374 (8.19%)
492	NR gi 302687722 ref XP_003033541.1 hypothetical protein SCHCODRAFT_54767 [Schizophyllum commune H4-8] >gnl BL_ORD_ID 2513065 hypothetical protein SCHCODRAFT_54767 [Schizophyllum commune H4-8]	413	9.81 x 10 ⁻⁴¹	3 - 371 (7.86%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
493	NR gi 296475407 gb DAA17522.1 mannose-6-phosphate isomerase [Bos taurus]	374	9.81 x 10 ⁻⁴¹	8 - 348 (9.08%)
494	NR gi 281344652 gb EFB20236.1 hypothetical protein PANDA_012087 [Ailuroпода melanoleuca]	403	9.81 x 10 ⁻⁴¹	7 - 374 (8.19%)
495	NR gi 170117333 ref XP_001889854.1 mannos-6-phosphate isomerase [Laccaria bicolor S238N-H82] >gnl BL_ORD_ID 2578128 mannos-6-phosphate isomerase [Laccaria bicolor S238N-H82]	359	9.81 x 10 ⁻⁴¹	3 - 317 (10.16%)
496	NR gi 157128248 ref XP_001661364.1 mannose-6-phosphate isomerase [Aedes aegypti] >gnl BL_ORD_ID 375487 mannose-6-phosphate isomerase [Aedes aegypti]	400	9.81 x 10 ⁻⁴¹	3 - 375 (8.56%)
497	NR gi 168072 gb AAA33319.1 phosphomannose isomerase [Emericella nidulans]	429	9.81 x 10 ⁻⁴¹	8 - 372 (7.39%)
498	NR gi 296415716 ref XP_002837532.1 hypothetical protein [Tuber melanosporum Mel28] >gnl BL_ORD_ID 2035789 unnamed protein product [Tuber melanosporum]	378	1.28 x 10 ⁻⁴⁰	18 - 371 (8.68%)
499	NR gi 196012668 ref XP_002116196.1 hypothetical protein TRIADDRAFT_30639 [Trichoplax adhaerens] >gnl BL_ORD_ID 417405 hypothetical protein TRIADDRAFT_30639 [Trichoplax adhaerens]	426	1.28 x 10 ⁻⁴⁰	3 - 374 (7.71%)
500	NR gi 154509381 ref ZP_02045023.1 hypothetical protein ACTODO_01912 [Actinomyces odontolyticus ATCC 17982] >gnl BL_ORD_ID 2011423 hypothetical protein ACTODO_01912 [Actinomyces odontolyticus ATCC 17982]	409	1.28 x 10 ⁻⁴⁰	1 - 387 (7.77%)
501	NR gi 19113237 ref NP_596445.1 mannose-6-phosphate isomerase (predicted) [Schizosaccharomyces pombe 972h-] >gnl BL_ORD_ID 2735874 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 2735874 mannose-6-phosphate isomerase (predicted) [Schizosaccharomyces pombe]	424	1.28 x 10 ⁻⁴⁰	1 - 388 (7.96%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
502	NR gi 67516771 ref XP_658271.1 MANA_EMENI Mannose-6-phosphate isomerase (Phosphomannose isomerase) (PMI) (Phosphohexomutase) [Aspergillus nidulans FGSC A4] >gnl BL_ORD_ID 101933 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 101933 MANA_EMENI Mannose-6-phosphate isomerase (Phosphomannose isomerase) (PMI) (Phosphohexomutase) [Aspergillus nidulans FGSC A4] >gnl BL_ORD_ID 101933 TPA: Mannose-6-phosphate isomerase (EC 5.3.1.8)(Phosphomannose isomerase)(PMI)(Phosphohexomutase) [Source:UniProtKB/Swiss-Prot;Acc:P29951] [Aspergillus nidulans FGSC A4]	429	1.28 x 10 ⁻⁴⁰	8 - 372 (7.39%)
503	NR gi 315078597 gb EFT50628.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL053PA2]	387	1.67 x 10 ⁻⁴⁰	1 - 373 (8.14%)
504	NR gi 312067839 ref XP_003136932.1 mannose-6-phosphate isomerase [Loa loa] >gnl BL_ORD_ID 187685 mannose-6-phosphate isomerase [Loa loa]	407	1.67 x 10 ⁻⁴⁰	1 - 382 (7.79%)
505	NR gi 302420243 ref XP_003007952.1 mannose-6-phosphate isomerase [Verticillium albo-atrum VaMs.102] >gnl BL_ORD_ID 930546 mannose-6-phosphate isomerase [Verticillium albo-atrum VaMs.102]	431	1.67 x 10 ⁻⁴⁰	8 - 371 (7.32%)
506	NR gi 296809479 ref XP_002845078.1 mannose-6-phosphate isomerase [Arthroderma otae CBS 113480] >gnl BL_ORD_ID 2880477 mannose-6-phosphate isomerase [Arthroderma otae CBS 113480]	426	1.67 x 10 ⁻⁴⁰	8 - 371 (7.16%)
507	NR gi 303282631 ref XP_003060607.1 predicted protein [Micromonas pusilla CCMP1545] >gnl BL_ORD_ID 2180601 predicted protein [Micromonas pusilla CCMP1545]	397	1.67 x 10 ⁻⁴⁰	7 - 374 (8.50%)
508	NR gi 315090573 gb EFT62549.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL110PA4] >gnl BL_ORD_ID 767842 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL050PA2]	387	2.19 x 10 ⁻⁴⁰	1 - 373 (8.14%)
509	NR gi 315082563 gb EFT54539.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL027PA2]	387	2.19 x 10 ⁻⁴⁰	1 - 373 (8.08%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
510	NR gi 314965155 gb EFT09254.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL082PA2] >gnl BL_ORD_ID 755853 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL110PA3] >gnl BL_ORD_ID 755853 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL060PA1]	387	2.19 x 10 ⁻⁴⁰	1 - 373 (8.14%)
511	NR gi 315047987 ref XP_003173368.1 mannose-6-phosphate isomerase [Arthroderma gypseum CBS 118893] >gnl BL_ORD_ID 500582 mannose-6-phosphate isomerase [Arthroderma gypseum CBS 118893]	427	2.19 x 10 ⁻⁴⁰	8 - 371 (7.07%)
512	NR gi 282853520 ref ZP_06262857.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes J139] >gnl BL_ORD_ID 1324777 mannose-6-phosphate isomerase, class I [Propionibacterium acnes J139]	387	2.19 x 10 ⁻⁴⁰	1 - 373 (8.14%)
513	NR gi 187918272 ref YP_001883835.1 mannose-6-phosphate isomerase [Borrelia hermsii DAH] >gnl BL_ORD_ID 2171477 mannose-6-phosphate isomerase [Borrelia hermsii DAH]	377	2.19 x 10 ⁻⁴⁰	6 - 382 (8.80%)
514	NR gi 157141652 ref XP_001647737.1 mannose-6-phosphate isomerase [Aedes aegypti] >gnl BL_ORD_ID 296533 mannose-6-phosphate isomerase [Aedes aegypti] >gnl BL_ORD_ID 296533 mannose-6-phosphate isomerase [Aedes aegypti]	407	2.19 x 10 ⁻⁴⁰	3 - 375 (8.45%)
515	NR gi 172166 gb AAA34872.1 phosphomannose isomerase [Saccharomyces cerevisiae]	413	2.19 x 10 ⁻⁴⁰	9 - 370 (7.68%)
516	NR gi 15232927 ref NP_186906.1 MEE31 (MATERNAL EFFECT EMBRYO ARREST 31); mannose-6-phosphate isomerase [Arabidopsis thaliana] >gnl BL_ORD_ID 2686708 putative mannose-6-phosphate isomerase [Arabidopsis thaliana] >gnl BL_ORD_ID 2686708 putative mannose-6-phosphate isomerase [Arabidopsis thaliana] >gnl BL_ORD_ID 2686708 putative mannose-6-phosphate isomerase [Arabidopsis thaliana]	401	3.73 x 10 ⁻⁴⁰	1 - 372 (8.40%)
517	NR gi 321470932 gb EFX81906.1 hypothetical protein DAPPUDRAFT_128126 [Daphnia pulex]	406	4.87 x 10 ⁻⁴⁰	8 - 380 (8.19%)
518	NR gi 115491975 ref XP_001210615.1 mannose-6-phosphate isomerase [Aspergillus terreus NIH2624] >gnl BL_ORD_ID 581958 mannose-6-phosphate isomerase [Aspergillus terreus NIH2624]	429	4.87 x 10 ⁻⁴⁰	8 - 372 (7.12%)
519	NR gi 307172441 gb EFN63894.1 Mannose-6-phosphate isomerase [Camponotus floridanus]	397	6.36 x 10 ⁻⁴⁰	7 - 374 (8.57%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
520	NR gi 119619704 gb EAW99298.1 mannose phosphate isomerase, isoform CRA_d [Homo sapiens]	375	6.36 x 10 ⁻⁴⁰	14 - 374 (8.89%)
521	NR gi 321262142 ref XP_003195790.1 mannose-6-phosphate isomerase [Cryptococcus gattii WM276] >gnl BL_ORD_ID 982850 mannose-6-phosphate isomerase [Cryptococcus gattii WM276]	425	1.08 x 10 ⁻³⁹	3 - 373 (7.47%)
522	NR gi 314922264 gb EFS86095.1 mannose-6-phosphate isomerase, class I [Propionibacterium acnes HL001PA1]	387	1.08 x 10 ⁻³⁹	1 - 373 (8.08%)
523	NR gi 149240133 ref XP_001525942.1 mannose-6-phosphate isomerase [Lodderomyces elongisporus NRRL YB-4239] >gnl BL_ORD_ID 1599966 mannose-6-phosphate isomerase [Lodderomyces elongisporus NRRL YB-4239]	415	1.08 x 10 ⁻³⁹	9 - 372 (7.78%)
524	NR gi 148906560 gb ABR16432.1 unknown [Picea sitchensis]	316	1.42 x 10 ⁻³⁹	9 - 294 (11.62%)
525	NR gi 226508860 ref NP_001140476.1 hypothetical protein LOC100272536 [Zea mays] >gnl BL_ORD_ID 718565 unknown [Zea mays] >gnl BL_ORD_ID 718565 mannose-6-phosphate isomerase [Zea mays]	310	1.42 x 10 ⁻³⁹	7 - 294 (11.65%)
526	NR gi 154294274 ref XP_001547579.1 hypothetical protein BC1G_13823 [Botryotinia fuckeliana B05.10] >gnl BL_ORD_ID 1928863 hypothetical protein BC1G_13823 [Botryotinia fuckeliana B05.10]	431	1.42 x 10 ⁻³⁹	8 - 376 (7.27%)
527	NR gi 111220726 ref YP_711520.1 mannose-6-phosphate isomerase [Frankia alni ACN14a] >gnl BL_ORD_ID 497858 mannose-6-phosphate isomerase [Frankia alni ACN14a]	429	1.42 x 10 ⁻³⁹	9 - 384 (7.50%)
528	NR gi 71024169 ref XP_762314.1 hypothetical protein UM06167.1 [Ustilago maydis 521] >gnl BL_ORD_ID 128485 hypothetical protein UM06167.1 [Ustilago maydis 521]	439	1.42 x 10 ⁻³⁹	3 - 388 (7.26%)
529	NR gi 312382538 gb EFR27962.1 hypothetical protein AND_04741 [Anopheles darlingi]	404	1.85 x 10 ⁻³⁹	3 - 376 (8.21%)
530	NR gi 226504684 ref NP_001147755.1 LOC100281365 [Zea mays] >gnl BL_ORD_ID 1062255 mannose-6-phosphate isomerase [Zea mays]	395	1.85 x 10 ⁻³⁹	7 - 372 (8.52%)
531	NR gi 219684637 ref ZP_03539580.1 mannose-6-phosphate isomerase, class I [Borrelia garinii PBr] >gnl BL_ORD_ID 735147 mannose-6-phosphate isomerase, class I [Borrelia garinii PBr]	381	1.85 x 10 ⁻³⁹	6 - 383 (8.54%)
532	NR gi 159473797 ref XP_001695020.1 mannose-6-phosphate isomerase [Chlamydomonas reinhardtii] >gnl BL_ORD_ID 2264331 mannose-6-phosphate isomerase [Chlamydomonas reinhardtii]	379	1.85 x 10 ⁻³⁹	1 - 350 (8.98%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
533	NR gi 145240207 ref XP_001392750.1 mannose-6-phosphate isomerase [Aspergillus niger CBS 513.88] >gnl BL_ORD_ID 1447489 unnamed protein product [Aspergillus niger]	429	1.85 x 10 ⁻³⁹	8 - 372 (7.12%)
534	NR gi 111115236 ref YP_709854.1 mannose-6-phosphate isomerase [Borrelia afzelii PKo] >gnl BL_ORD_ID 484542 mannose-6-phosphate isomerase, class I [Borrelia afzelii ACA-1] >gnl BL_ORD_ID 484542 mannose-6-phosphate isomerase [Borrelia afzelii PKo] >gnl BL_ORD_ID 484542 mannose-6-phosphate isomerase, class I [Borrelia afzelii ACA-1]	378	1.85 x 10 ⁻³⁹	6 - 383 (8.33%)
535	NR gi 302901272 ref XP_003048401.1 predicted protein [Nectria haematococca mpVI 77-13-4] >gnl BL_ORD_ID 567982 predicted protein [Nectria haematococca mpVI 77-13-4]	419	2.42 x 10 ⁻³⁹	8 - 371 (7.52%)
536	NR gi 240272995 gb EER36519.1 phosphomannose isomerase [Ajellomyces capsulatus H143]	430	2.42 x 10 ⁻³⁹	8 - 372 (7.14%)
537	NR gi 119495286 ref XP_001264431.1 mannose-6-phosphate isomerase, class I [Neosartorya fischeri NRRL 181] >gnl BL_ORD_ID 965156 mannose-6-phosphate isomerase, class I [Neosartorya fischeri NRRL 181]	430	2.42 x 10 ⁻³⁹	8 - 372 (7.36%)
538	NR gi 50547167 ref XP_501053.1 YALI0B18348p [Yarrowia lipolytica] >gnl BL_ORD_ID 1300215 YALI0B18348p [Yarrowia lipolytica]	413	2.42 x 10 ⁻³⁹	9 - 383 (8.09%)
539	NR gi 255572106 ref XP_002526993.1 mannose-6-phosphate isomerase, putative [Ricinus communis] >gnl BL_ORD_ID 1763481 mannose-6-phosphate isomerase, putative [Ricinus communis]	411	3.16 x 10 ⁻³⁹	2 - 379 (7.82%)
540	NR gi 168046489 ref XP_001775706.1 predicted protein [Physcomitrella patens subsp. patens] >gnl BL_ORD_ID 2501762 predicted protein [Physcomitrella patens subsp. patens]	396	3.16 x 10 ⁻³⁹	1 - 374 (8.10%)
541	NR gi 9965934 gb AAG10203.1 AF291701_1 mannose-6-phosphate isomerase [Cryptococcus neoformans var. neoformans]	425	3.16 x 10 ⁻³⁹	3 - 373 (7.47%)
542	NR gi 15219821 ref NP_176878.1 DIN9 (DARK INDUCIBLE 9); mannose-6-phosphate isomerase [Arabidopsis thaliana] >gnl BL_ORD_ID 1086561 Putative mannose-6-phosphate isomerase [Arabidopsis thaliana] >gnl BL_ORD_ID 1086561 phosphomannose isomerase (din9) [Arabidopsis thaliana] >gnl BL_ORD_ID 1086561 At1g67070 [Arabidopsis thaliana]	420	3.16 x 10 ⁻³⁹	1 - 388 (7.26%)
543	NR gi 281201812 gb EFA76020.1 mannose-6-phosphate isomerase [Polysphondylium pallidum PN500]	401	4.12 x 10 ⁻³⁹	3 - 379 (7.90%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
544	NR gi 134114948 ref XP_773772.1 hypothetical protein CNBH2250 [Cryptococcus neoformans var. neoformans B-3501A] >gnl BL_ORD_ID 183871 hypothetical protein CNBH2250 [Cryptococcus neoformans var. neoformans B-3501A]	424	4.12 x 10 ⁻³⁹	3 - 373 (7.34%)
545	NR gi 239609970 gb EEQ86957.1 mannose-6-phosphate isomerase [Ajellomyces dermatitidis ER-3]	428	5.38 x 10 ⁻³⁹	8 - 372 (7.04%)
546	NR gi 261198709 ref XP_002625756.1 mannose-6-phosphate isomerase [Ajellomyces dermatitidis SLH14081] >gnl BL_ORD_ID 28656 mannose-6-phosphate isomerase [Ajellomyces dermatitidis SLH14081]	428	5.38 x 10 ⁻³⁹	8 - 372 (7.04%)
547	NR gi 195942249 ref ZP_03087631.1 mannose-6-phosphate isomerase (manA) [Borrelia burgdorferi 80a] >gnl BL_ORD_ID 733025 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi N40]	377	5.38 x 10 ⁻³⁹	6 - 382 (8.51%)
548	NR gi 125534942 gb EAY81490.1 hypothetical protein Osl_36663 [Oryza sativa Indica Group]	418	5.38 x 10 ⁻³⁹	3 - 384 (7.78%)
549	NR gi 118384042 ref XP_001025174.1 mannose-6-phosphate isomerase, class I family protein [Tetrahymena thermophila] >gnl BL_ORD_ID 2536853 mannose-6-phosphate isomerase, class I family protein [Tetrahymena thermophila SB210]	397	5.38 x 10 ⁻³⁹	3 - 372 (7.99%)
550	NR gi 77551788 gb ABA94585.1 mannose-6-phosphate isomerase, class I family protein, expressed [Oryza sativa Japonica Group]	418	5.38 x 10 ⁻³⁹	3 - 384 (7.78%)
551	NR gi 74000763 ref XP_535543.2 PREDICTED: similar to mannose-6- phosphate isomerase isoform 1 [Canis familiaris]	404	5.38 x 10 ⁻³⁹	7 - 373 (8.09%)
552	NR gi 58271098 ref XP_572705.1 mannose-6-phosphate isomerase [Cryptococcus neoformans var. neoformans JEC21] >gnl BL_ORD_ID 1404999 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 1404999 mannose-6-phosphate isomerase [Cryptococcus neoformans var. neoformans JEC21]	424	5.38 x 10 ⁻³⁹	3 - 373 (7.34%)
553	NR gi 225557976 gb EEH06261.1 phosphomannose isomerase [Ajellomyces capsulatus G186AR]	430	7.03 x 10 ⁻³⁹	8 - 372 (7.09%)
554	NR gi 238489193 ref XP_002375834.1 mannose-6-phosphate isomerase, class I [Aspergillus flavus NRRL3357] >gnl BL_ORD_ID 1541514 mannose-6-phosphate isomerase [Aspergillus oryzae RIB40] >gnl BL_ORD_ID 1541514 mannose-6-phosphate isomerase, class I [Aspergillus flavus NRRL3357]	429	7.03 x 10 ⁻³⁹	8 - 372 (7.12%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
555	NR gi 212532091 ref XP_002146202.1 mannose-6-phosphate isomerase, class I [Penicillium marneffeii ATCC 18224] >gnl BL_ORD_ID 1055703 mannose-6-phosphate isomerase, class I [Penicillium marneffeii ATCC 18224]	430	7.03 x 10 ⁻³⁹	8 - 372 (7.19%)
556	NR gi 224533725 ref ZP_03674313.1 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi CA-11.2a] >gnl BL_ORD_ID 736226 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi CA-11.2a]	377	7.03 x 10 ⁻³⁹	6 - 382 (8.51%)
557	NR gi 225549117 ref ZP_03770092.1 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi 94a] >gnl BL_ORD_ID 2890811 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi 94a]	377	7.03 x 10 ⁻³⁹	6 - 382 (8.51%)
558	NR gi 86739461 ref YP_479861.1 mannose-6-phosphate isomerase [Frankia sp. Ccl3] >gnl BL_ORD_ID 125728 mannose-6-phosphate isomerase, type 1 [Frankia sp. Ccl3]	429	7.03 x 10 ⁻³⁹	4 - 384 (6.96%)
559	NR gi 51970910 dbj BAD44147.1 phosphomannose isomerase (din9) [Arabidopsis thaliana]	420	7.03 x 10 ⁻³⁹	1 - 388 (7.26%)
560	NR gi 47214706 emb CAG01059.1 unnamed protein product [Tetraodon nigroviridis]	402	7.03 x 10 ⁻³⁹	8 - 374 (8.54%)
561	NR gi 312218745 emb CBX98690.1 similar to mannose-6-phosphate isomerase [Leptosphaeria maculans]	430	9.18 x 10 ⁻³⁹	8 - 376 (7.30%)
562	NR gi 309802586 ref ZP_07696690.1 phosphomannose isomerase type I [Bifidobacterium dentium JCVIHMP022] >gnl BL_ORD_ID 227794 phosphomannose isomerase type I [Bifidobacterium dentium JCVIHMP022]	432	9.18 x 10 ⁻³⁹	9 - 378 (6.75%)
563	NR gi 306823477 ref ZP_07456852.1 mannose-6-phosphate isomerase [Bifidobacterium dentium ATCC 27679] >gnl BL_ORD_ID 2886638 mannose-6-phosphate isomerase [Bifidobacterium dentium ATCC 27679]	432	9.18 x 10 ⁻³⁹	9 - 378 (6.75%)
564	NR gi 242774684 ref XP_002478490.1 mannose-6-phosphate isomerase, class I [Talaromyces stipitatus ATCC 10500] >gnl BL_ORD_ID 1464678 mannose-6-phosphate isomerase, class I [Talaromyces stipitatus ATCC 10500]	434	9.18 x 10 ⁻³⁹	8 - 372 (7.22%)
565	NR gi 195651523 gb ACG45229.1 mannose-6-phosphate isomerase [Zea mays]	309	9.18 x 10 ⁻³⁹	7 - 294 (11.62%)
566	NR gi 225551938 ref ZP_03772878.1 mannose-6-phosphate isomerase, class I [Borrelia sp. SV1] >gnl BL_ORD_ID 736686 mannose-6-phosphate isomerase, class I [Borrelia sp. SV1]	377	9.18 x 10 ⁻³⁹	6 - 382 (8.51%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
567	NR gi 226496033 ref NP_001140535.1 hypothetical protein LOC100272600 [Zea mays] >gnl BL_ORD_ID 718675 unknown [Zea mays]	309	9.18 x 10 ⁻³⁹	7 - 294 (11.62%)
568	NR gi 225549612 ref ZP_03770578.1 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi 118a] >gnl BL_ORD_ID 2889626 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi 118a]	377	9.18 x 10 ⁻³⁹	6 - 382 (8.51%)
569	NR gi 216264499 ref ZP_03436491.1 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi 156a] >gnl BL_ORD_ID 2814669 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi 156a]	377	9.18 x 10 ⁻³⁹	6 - 382 (8.51%)
570	NR gi 15594752 ref NP_212541.1 mannose-6-phosphate isomerase (manA) [Borrelia burgdorferi B31] >gnl BL_ORD_ID 1554683 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi ZS7] >gnl BL_ORD_ID 1554683 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi 72a] >gnl BL_ORD_ID 1554683 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi 64b] >gnl BL_ORD_ID 1554683 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi WI91-23] >gnl BL_ORD_ID 1554683 mannose-6-phosphate isomerase (manA) [Borrelia burgdorferi B31] >gnl BL_ORD_ID 1554683 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi ZS7] >gnl BL_ORD_ID 1554683 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi 72a] >gnl BL_ORD_ID 1554683 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi 64b] >gnl BL_ORD_ID 1554683 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi WI91-23] >gnl BL_ORD_ID 1554683 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi JD1]	377	9.18 x 10 ⁻³⁹	6 - 382 (8.51%)
571	NR gi 66809505 ref XP_638475.1 mannose-6-phosphate isomerase [Dictyostelium discoideum AX4] >gnl BL_ORD_ID 232816 RecName: Full=Probable mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 232816 mannose-6-phosphate isomerase [Dictyostelium discoideum AX4]	435	9.18 x 10 ⁻³⁹	9 - 390 (7.40%)
572	NR gi 219685450 ref ZP_03540268.1 mannose-6-phosphate isomerase, class I [Borrelia garinii Far04] >gnl BL_ORD_ID 1199765 mannose-6-phosphate isomerase, class I [Borrelia garinii Far04]	381	1.20 x 10 ⁻³⁸	6 - 383 (8.40%)
573	NR gi 225452055 ref XP_002283926.1 PREDICTED: hypothetical protein [Vitis vinifera]	402	1.20 x 10 ⁻³⁸	1 - 372 (7.86%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
574	NR gi 154271602 ref XP_001536654.1 mannose-6-phosphate isomerase [Ajellomyces capsulatus NAm1] >gnl BL_ORD_ID 1911976 mannose-6-phosphate isomerase [Ajellomyces capsulatus NAm1]	427	1.20 x 10 ⁻³⁸	8 - 372 (7.13%)
575	NR gi 147841344 emb CAN60179.1 hypothetical protein VITISV_011365 [Vitis vinifera]	402	1.20 x 10 ⁻³⁸	1 - 372 (7.86%)
576	NR gi 319919482 gb ADV78259.1 mannose-6-phosphate isomerase [Metarhizium anisopliae] >gnl BL_ORD_ID 1135051 mannose-6-phosphate isomerase [Metarhizium acridum CQMa 102]	418	1.57 x 10 ⁻³⁸	8 - 371 (7.44%)
577	NR gi 283455452 ref YP_003360016.1 mannose-6-phosphate isomerase [Bifidobacterium dentium Bd1] >gnl BL_ORD_ID 1344516 Mannose-6-phosphate isomerase [Bifidobacterium dentium Bd1]	432	1.57 x 10 ⁻³⁸	9 - 378 (6.64%)
578	NR gi 241723778 ref XP_002404302.1 mannose-6-phosphate isomerase, putative [Ixodes scapularis] >gnl BL_ORD_ID 1300715 mannose-6-phosphate isomerase, putative [Ixodes scapularis]	391	1.57 x 10 ⁻³⁸	8 - 374 (8.76%)
579	NR gi 226321721 ref ZP_03797247.1 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi Bol26] >gnl BL_ORD_ID 2820424 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi Bol26]	377	1.57 x 10 ⁻³⁸	6 - 382 (8.51%)
580	NR gi 83770581 dbj BAE60714.1 unnamed protein product [Aspergillus oryzae]	399	1.57 x 10 ⁻³⁸	29 - 372 (7.85%)
581	NR gi 322704955 gb EFY96545.1 mannose-6-phosphate isomerase [Metarhizium anisopliae ARSEF 23]	418	2.05 x 10 ⁻³⁸	8 - 371 (7.44%)
582	NR gi 258572354 ref XP_002544939.1 phosphomannose isomerase type I [Uncinocarpus reesii 1704] >gnl BL_ORD_ID 2803965 phosphomannose isomerase type I [Uncinocarpus reesii 1704]	393	2.05 x 10 ⁻³⁸	29 - 371 (7.77%)
583	NR gi 195145520 ref XP_002013740.1 GL24302 [Drosophila persimilis] >gnl BL_ORD_ID 569838 GL24302 [Drosophila persimilis]	398	2.05 x 10 ⁻³⁸	3 - 375 (8.27%)
584	NR gi 289178225 gb ADC85471.1 Mannose-6-phosphate isomerase [Bifidobacterium animalis subsp. lactis BB-12]	315	2.67 x 10 ⁻³⁸	9 - 288 (10.98%)
585	NR gi 255725522 ref XP_002547690.1 mannose-6-phosphate isomerase [Candida tropicalis MYA-3404] >gnl BL_ORD_ID 134792 mannose-6-phosphate isomerase [Candida tropicalis MYA-3404]	416	2.67 x 10 ⁻³⁸	9 - 370 (7.86%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
586	NR gi 198452021 ref XP_001358591.2 GA21062 [Drosophila pseudoobscura pseudoobscura] >gnl BL_ORD_ID 856581 GA21062 [Drosophila pseudoobscura pseudoobscura]	398	2.67 x 10 ⁻³⁸	3 - 375 (8.27%)
587	NR gi 195445298 ref XP_002070264.1 GK11962 [Drosophila willistonii] >gnl BL_ORD_ID 623720 GK11962 [Drosophila willistonii]	396	2.67 x 10 ⁻³⁸	3 - 375 (8.10%)
588	NR gi 190346040 gb EDK38036.2 hypothetical protein PGUG_02134 [Pichia guilliermondii ATCC 6260]	315	2.67 x 10 ⁻³⁸	9 - 288 (11.79%)
589	NR gi 183602009 ref ZP_02963378.1 phosphomannose isomerase [Bifidobacterium animalis subsp. lactis HN019] >gnl BL_ORD_ID 245466 phosphomannose isomerase [Bifidobacterium animalis subsp. lactis AD011] >gnl BL_ORD_ID 245466 mannose-6-phosphate isomerase ManA [Bifidobacterium animalis subsp. lactis BI-04] >gnl BL_ORD_ID 245466 mannose-6-phosphate isomerase ManA [Bifidobacterium animalis subsp. lactis DSM 10140] >gnl BL_ORD_ID 245466 phosphomannose isomerase [Bifidobacterium animalis subsp. lactis HN019] >gnl BL_ORD_ID 245466 phosphomannose isomerase [Bifidobacterium animalis subsp. lactis AD011] >gnl BL_ORD_ID 245466 mannose-6-phosphate isomerase ManA [Bifidobacterium animalis subsp. lactis BI-04] >gnl BL_ORD_ID 245466 mannose-6-phosphate isomerase ManA [Bifidobacterium animalis subsp. lactis DSM 10140] >gnl BL_ORD_ID 245466 mannose-6-phosphate isomerase ManA [Bifidobacterium animalis subsp. lactis V9]	315	2.67 x 10 ⁻³⁸	9 - 288 (10.98%)
590	NR gi 171676543 ref XP_001903224.1 hypothetical protein [Podospora anserina S mat+] >gnl BL_ORD_ID 144466 unnamed protein product [Podospora anserina S mat+]	414	2.67 x 10 ⁻³⁸	10 - 371 (7.06%)
591	NR gi 70995886 ref XP_752698.1 mannose-6-phosphate isomerase, class I [Aspergillus fumigatus Af293] >gnl BL_ORD_ID 117781 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 117781 mannose 6 phosphate isomerase, putative [Aspergillus fumigatus] >gnl BL_ORD_ID 117781 mannose-6-phosphate isomerase, class I [Aspergillus fumigatus Af293] >gnl BL_ORD_ID 117781 mannose-6-phosphate isomerase, class I [Aspergillus fumigatus A1163]	430	2.67 x 10 ⁻³⁸	8 - 372 (7.30%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
592	NR gi 261599625 gb ACX85786.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 969093 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 969093 mannose-6-phosphate isomerase [Anopheles sudaicus]	372	3.49 x 10 ⁻³⁸	25 - 376 (8.67%)
593	NR gi 261599587 gb ACX85767.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	3.49 x 10 ⁻³⁸	25 - 376 (8.56%)
594	NR gi 51558025 gb AAU06585.1 mannosephosphate isomerase [Aspergillus fumigatus]	430	3.49 x 10 ⁻³⁸	8 - 372 (7.30%)
595	NR gi 261599579 gb ACX85763.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	4.56 x 10 ⁻³⁸	25 - 376 (8.56%)
596	NR gi 256087654 ref XP_002579980.1 mannose-6-phosphate isomerase [Schistosoma mansoni] >gnl BL_ORD_ID 2840065 mannose-6-phosphate isomerase, putative [Schistosoma mansoni]	419	4.56 x 10 ⁻³⁸	1 - 352 (7.69%)
597	NR gi 146421023 ref XP_001486463.1 hypothetical protein PGUG_02134 [Meyerozyma guilliermondii ATCC 6260]	315	4.56 x 10 ⁻³⁸	9 - 288 (11.79%)
598	NR gi 71997620 ref NP_499174.3 hypothetical protein ZK632.4 [Caenorhabditis elegans] >gnl BL_ORD_ID 1228977 RecName: Full=Probable mannose-6-phosphate isomerase; AltName: Full=Phosphohexamutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 1228977 C. elegans protein ZK632.4, confirmed by transcript evidence [Caenorhabditis elegans]	393	4.56 x 10 ⁻³⁸	3 - 371 (7.96%)
599	NR gi 308502053 ref XP_003113211.1 hypothetical protein CRE_25254 [Caenorhabditis remanei] >gnl BL_ORD_ID 262641 hypothetical protein CRE_25254 [Caenorhabditis remanei]	421	5.95 x 10 ⁻³⁸	3 - 374 (7.33%)
600	NR gi 261599607 gb ACX85777.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 969086 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	5.95 x 10 ⁻³⁸	25 - 376 (8.56%)
601	NR gi 261599597 gb ACX85772.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	5.95 x 10 ⁻³⁸	25 - 376 (8.56%)
602	NR gi 261599545 gb ACX85746.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	386	5.95 x 10 ⁻³⁸	15 - 376 (8.26%)
603	NR gi 294950259 ref XP_002786540.1 Mannose-6-phosphate isomerase, putative [Perkinsus marinus ATCC 50983] >gnl BL_ORD_ID 75970 Mannose-6-phosphate isomerase, putative [Perkinsus marinus ATCC 50983]	366	5.95 x 10 ⁻³⁸	7 - 352 (9.03%)
604	NR gi 74000761 ref XP_867149.1 PREDICTED: similar to mannose-6- phosphate isomerase isoform 2 [Canis familiaris]	386	5.95 x 10 ⁻³⁸	7 - 373 (8.32%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
605	NR gi 261599647 gb ACX85797.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	372	7.77 x 10 ⁻³⁸	25 - 376 (8.67%)
606	NR gi 261599635 gb ACX85791.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	372	7.77 x 10 ⁻³⁸	25 - 376 (8.67%)
607	NR gi 261599627 gb ACX85787.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 969094 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 969094 mannose-6-phosphate isomerase [Anopheles sundaicus]	386	7.77 x 10 ⁻³⁸	15 - 376 (8.26%)
608	NR gi 261599617 gb ACX85782.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 969090 mannose-6-phosphate isomerase [Anopheles sundaicus]	376	7.77 x 10 ⁻³⁸	25 - 376 (8.56%)
609	NR gi 261599581 gb ACX85764.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 969076 mannose-6-phosphate isomerase [Anopheles sundaicus]	376	7.77 x 10 ⁻³⁸	25 - 376 (8.56%)
610	NR gi 261599555 gb ACX85751.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	376	7.77 x 10 ⁻³⁸	25 - 376 (8.56%)
611	NR gi 261599535 gb ACX85741.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	376	7.77 x 10 ⁻³⁸	25 - 376 (8.56%)
612	NR gi 119181575 ref XP_001241992.1 hypothetical protein CIMG_05888 [Coccidioides immitis RS]	394	7.77 x 10 ⁻³⁸	29 - 371 (7.86%)
613	NR gi 50307393 ref XP_453675.1 hypothetical protein [Kluyveromyces lactis NRRL Y-1140] >gnl BL_ORD_ID 2985201 KLLA0D13728p [Kluyveromyces lactis]	406	7.77 x 10 ⁻³⁸	9 - 370 (7.89%)
614	NR gi 51598663 ref YP_072851.1 mannose-6-phosphate isomerase [Borrelia garinii PBi] >gnl BL_ORD_ID 2415798 mannose-6-phosphate isomerase [Borrelia garinii PBi]	378	7.77 x 10 ⁻³⁸	6 - 383 (8.19%)
615	NR gi 66564896 ref XP_623842.1 PREDICTED: similar to Mannose-6-phosphate isomerase (Phosphomannose isomerase) (PMI) (Phosphohexomutase) [Apis mellifera]	394	7.77 x 10 ⁻³⁸	8 - 373 (8.82%)
616	NR gi 268573370 ref XP_002641662.1 Hypothetical protein CBG09990 [Caenorhabditis briggsae]	396	7.77 x 10 ⁻³⁸	3 - 374 (7.53%)
617	NR gi 310796007 gb EFQ31468.1 phosphomannose isomerase type I [Glomerella graminicola M1.001]	429	1.02 x 10 ⁻³⁷	3 - 371 (7.17%)
618	NR gi 261599649 gb ACX85798.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	376	1.02 x 10 ⁻³⁷	25 - 376 (8.56%)
619	NR gi 261599637 gb ACX85792.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 969097 mannose-6-phosphate isomerase [Anopheles sundaicus]	376	1.02 x 10 ⁻³⁷	25 - 376 (8.56%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
620	NR gi 261599567 gb ACX85757.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 969071 mannose-6-phosphate isomerase [Anopheles sundaicus]	376	1.02 x 10 ⁻³⁷	25 - 376 (8.56%)
621	NR gi 261599543 gb ACX85745.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	376	1.02 x 10 ⁻³⁷	25 - 376 (8.56%)
622	NR gi 261599527 gb ACX85737.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	376	1.02 x 10 ⁻³⁷	25 - 376 (8.56%)
623	NR gi 195111004 ref XP_002000069.1 GI22736 [Drosophila mojavensis] >gnl BL_ORD_ID 556641 GI22736 [Drosophila mojavensis]	396	1.02 x 10 ⁻³⁷	3 - 375 (8.04%)
624	NR gi 226481343 emb CAX73569.1 mannose phosphate isomerase [Schistosoma japonicum]	419	1.33 x 10 ⁻³⁷	1 - 352 (7.69%)
625	NR gi 150865360 ref XP_001384544.2 mannose-6-phosphate isomerase [Scheffersomyces stipitis CBS 6054] >gnl BL_ORD_ID 1811962 mannose-6-phosphate isomerase [Scheffersomyces stipitis CBS 6054]	428	1.33 x 10 ⁻³⁷	9 - 380 (7.53%)
626	NR gi 115434298 ref NP_001041907.1 Os01g0127900 [Oryza sativa Japonica Group] >gnl BL_ORD_ID 1004689 putative mannose-6-phosphate isomerase [Oryza sativa Japonica Group] >gnl BL_ORD_ID 1004689 Os01g0127900 [Oryza sativa Japonica Group] >gnl BL_ORD_ID 1004689 unnamed protein product [Oryza sativa Japonica Group]	399	1.33 x 10 ⁻³⁷	7 - 371 (7.98%)
627	NR gi 302846415 ref XP_002954744.1 hypothetical protein VOLCADRAFT_65163 [Volvox carteri f. nagariensis] >gnl BL_ORD_ID 2570383 hypothetical protein VOLCADRAFT_65163 [Volvox carteri f. nagariensis]	353	1.73 x 10 ⁻³⁷	1 - 321 (9.39%)
628	NR gi 261599595 gb ACX85771.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	376	1.73 x 10 ⁻³⁷	25 - 376 (8.56%)
629	NR gi 261599591 gb ACX85769.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	376	1.73 x 10 ⁻³⁷	25 - 376 (8.56%)
630	NR gi 261599575 gb ACX85761.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 969074 mannose-6-phosphate isomerase [Anopheles sundaicus]	376	1.73 x 10 ⁻³⁷	25 - 376 (8.56%)
631	NR gi 261599557 gb ACX85752.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 969069 mannose-6-phosphate isomerase [Anopheles sundaicus]	376	1.73 x 10 ⁻³⁷	25 - 376 (8.56%)
632	NR gi 261599537 gb ACX85742.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	372	1.73 x 10 ⁻³⁷	25 - 376 (8.67%)
633	NR gi 261599521 gb ACX85734.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 969055 mannose-6-phosphate isomerase [Anopheles sundaicus]	376	1.73 x 10 ⁻³⁷	25 - 376 (8.56%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
634	NR gi 255085142 ref XP_002505002.1 predicted protein [Micromonas sp. RCC299] >gnl BL_ORD_ID 2193112 predicted protein [Micromonas sp. RCC299]	405	1.73 x 10 ⁻³⁷	7 - 388 (8.35%)
635	NR gi 255937185 ref XP_002559619.1 Pc13g12020 [Penicillium chrysogenum Wisconsin 54-1255] >gnl BL_ORD_ID 1123593 Pc13g12020 [Penicillium chrysogenum Wisconsin 54-1255]	428	1.73 x 10 ⁻³⁷	8 - 371 (7.10%)
636	NR gi 261599645 gb ACX85796.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	2.26 x 10 ⁻³⁷	25 - 376 (8.56%)
637	NR gi 261599573 gb ACX85760.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	2.26 x 10 ⁻³⁷	25 - 376 (8.49%)
638	NR gi 261599571 gb ACX85759.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	2.26 x 10 ⁻³⁷	25 - 376 (8.49%)
639	NR gi 261599561 gb ACX85754.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	2.26 x 10 ⁻³⁷	25 - 376 (8.56%)
640	NR gi 261599539 gb ACX85743.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 969063 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	2.26 x 10 ⁻³⁷	25 - 376 (8.56%)
641	NR gi 261599529 gb ACX85738.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 969058 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	2.26 x 10 ⁻³⁷	25 - 376 (8.56%)
642	NR gi 261599525 gb ACX85736.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	2.26 x 10 ⁻³⁷	25 - 376 (8.56%)
643	NR gi 261599517 gb ACX85732.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	2.26 x 10 ⁻³⁷	25 - 376 (8.56%)
644	NR gi 303318615 ref XP_003069307.1 mannose-6-phosphate isomerase, putative [Coccidioides posadasii C735 delta SOWgp] >gnl BL_ORD_ID 186424 mannose-6-phosphate isomerase, putative [Coccidioides posadasii C735 delta SOWgp] >gnl BL_ORD_ID 186424 mannose-6-phosphate isomerase [Coccidioides posadasii str. Silveira]	396	2.26 x 10 ⁻³⁷	29 - 371 (7.72%)
645	NR gi 194376306 dbj BAG62912.1 unnamed protein product [Homo sapiens]	363	2.26 x 10 ⁻³⁷	38 - 374 (9.11%)
646	NR gi 84498028 ref ZP_00996825.1 putative mannose-6-phosphate isomerase [Janibacter sp. HTCC2649] >gnl BL_ORD_ID 530780 putative mannose-6-phosphate isomerase [Janibacter sp. HTCC2649]	382	2.26 x 10 ⁻³⁷	12 - 384 (8.22%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
647	NR gi 74025940 ref XP_829536.1 phosphomannose isomerase [Trypanosoma brucei TREU927] >gnl BL_ORD_ID 337541 phosphomannose isomerase, putative [Trypanosoma brucei] >gnl BL_ORD_ID 337541 phosphomannose isomerase, putative [Trypanosoma brucei gambiense DAL972]	382	2.26 x 10 ⁻³⁷	1 - 348 (8.70%)
648	NR gi 261599651 gb ACX85799.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	2.95 x 10 ⁻³⁷	25 - 376 (8.56%)
649	NR gi 261599549 gb ACX85748.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 969066 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	2.95 x 10 ⁻³⁷	25 - 376 (8.56%)
650	NR gi 261599533 gb ACX85740.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	2.95 x 10 ⁻³⁷	25 - 376 (8.49%)
651	NR gi 261599531 gb ACX85739.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	2.95 x 10 ⁻³⁷	25 - 376 (8.49%)
652	NR gi 224009798 ref XP_002293857.1 hypothetical protein THAPSDRAFT_9679 [Thalassiosira pseudonana CCMP1335] >gnl BL_ORD_ID 1569145 hypothetical protein THAPSDRAFT_9679 [Thalassiosira pseudonana CCMP1335]	410	2.95 x 10 ⁻³⁷	9 - 378 (7.97%)
653	NR gi 189207993 ref XP_001940330.1 mannose-6-phosphate isomerase [Pyrenophora tritici-repentis Pt-1C-BFP] >gnl BL_ORD_ID 324859 mannose-6-phosphate isomerase [Pyrenophora tritici-repentis Pt-1C-BFP]	428	2.95 x 10 ⁻³⁷	8 - 376 (7.04%)
654	NR gi 311318239 gb EFQ86984.1 hypothetical protein PTT_17636 [Pyrenophora teres f. teres 0-1]	433	3.86 x 10 ⁻³⁷	8 - 376 (6.99%)
655	NR gi 297838435 ref XP_002887099.1 predicted protein [Arabidopsis lyrata subsp. lyrata] >gnl BL_ORD_ID 2259070 predicted protein [Arabidopsis lyrata subsp. lyrata]	422	3.86 x 10 ⁻³⁷	1 - 388 (7.19%)
656	NR gi 302496330 ref XP_003010167.1 mannose-6-phosphate isomerase, class I [Arthroderma benhamiae CBS 112371] >gnl BL_ORD_ID 1661686 mannose-6-phosphate isomerase, class I [Arthroderma benhamiae CBS 112371]	402	3.86 x 10 ⁻³⁷	35 - 371 (7.55%)
657	NR gi 261599585 gb ACX85766.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	376	3.86 x 10 ⁻³⁷	25 - 376 (8.56%)
658	NR gi 155675714 gb ABU25177.1 mannose phosphate isomerase [Leishmania braziliensis]	392	3.86 x 10 ⁻³⁷	3 - 350 (8.40%)
659	NR gi 224079321 ref XP_002305820.1 predicted protein [Populus trichocarpa] >gnl BL_ORD_ID 1717348 predicted protein [Populus trichocarpa]	415	5.04 x 10 ⁻³⁷	1 - 372 (7.55%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
666	NR gi 39971313 ref XP_367047.1 hypothetical protein MGG_10677 [Magnaporthe oryzae 70-15] >gnl BL_ORD_ID 2910085 hypothetical protein MGG_10677 [Magnaporthe grisea 70-15]	416	6.58 x 10 ⁻³⁷	8 - 371 (7.05%)
667	NR gi 154343169 ref XP_001567530.1 phosphomannose isomerase [Leishmania braziliensis MHOM/BR/75/M2904] >gnl BL_ORD_ID 2093920 mannose phosphate isomerase [Leishmania braziliensis] >gnl BL_ORD_ID 2093920 phosphomannose isomerase [Leishmania braziliensis MHOM/BR/75/M2904] >gnl BL_ORD_ID 2093920 mannose phosphate isomerase [Leishmania braziliensis] >gnl BL_ORD_ID 2093920 mannose phosphate isomerase [Leishmania braziliensis] >gnl BL_ORD_ID 2093920 mannose phosphate isomerase [Leishmania sp.] >gnl BL_ORD_ID 2093920 mannose phosphate isomerase [Leishmania sp.] >gnl BL_ORD_ID 2093920 mannose phosphate isomerase [Leishmania braziliensis]	392	6.58 x 10 ⁻³⁷	3 - 350 (8.33%)
668	NR gi 46117278 ref XP_384657.1 hypothetical protein FG04481.1 [Gibberella zeae PH-1]	418	6.58 x 10 ⁻³⁷	8 - 371 (6.87%)
669	NR gi 155675720 gb ABU25180.1 mannose phosphate isomerase [Leishmania braziliensis]	392	8.59 x 10 ⁻³⁷	3 - 350 (8.33%)
670	NR gi 94469769 gb ABF20338.1 mannose phosphate isomerase [Leishmania infantum]	381	8.59 x 10 ⁻³⁷	9 - 350 (8.61%)
671	NR gi 60617303 gb AAX31279.1 phosphomannose isomerase [Cyamopsis tetragonoloba]	401	8.59 x 10 ⁻³⁷	1 - 371 (7.90%)
672	NR gi 58381243 ref XP_311105.2 AGAP000053-PA [Anopheles gambiae str. PEST] >gnl BL_ORD_ID 214530 AGAP000053-PA [Anopheles gambiae str. PEST]	396	8.59 x 10 ⁻³⁷	3 - 372 (7.84%)
673	NR gi 224127678 ref XP_002329337.1 predicted protein [Populus trichocarpa] >gnl BL_ORD_ID 1737736 predicted protein [Populus trichocarpa]	327	1.12 x 10 ⁻³⁶	7 - 294 (10.66%)
674	NR gi 213406153 ref XP_002173848.1 mannose-6-phosphate isomerase [Schizosaccharomyces japonicus yFS275] >gnl BL_ORD_ID 1152904 mannose-6-phosphate isomerase [Schizosaccharomyces japonicus yFS275]	376	1.12 x 10 ⁻³⁶	29 - 372 (8.06%)
675	NR gi 163963077 gb ABY50490.1 mannose phosphate isomerase [Leishmania sp.]	392	1.12 x 10 ⁻³⁶	3 - 350 (8.33%)
676	NR gi 94469753 gb ABF20330.1 mannose phosphate isomerase [Leishmania infantum]	381	1.12 x 10 ⁻³⁶	9 - 350 (8.61%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
678	NR gi 261599519 gb ACX85733.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	369	1.47 x 10 ⁻³⁶	25 - 369 (8.74%)
679	NR gi 225683043 gb EEH21327.1 mannose-6-phosphate isomerase [Paracoccidioides brasiliensis Pb03]	426	1.47 x 10 ⁻³⁶	8 - 371 (7%)
680	NR gi 193662263 ref XP_001950664.1 PREDICTED: similar to Mannose-6-phosphate isomerase (Phosphomannose isomerase) (PMI) (Phosphohexomutase) [Acyrtosiphon pisum]	389	1.91 x 10 ⁻³⁶	8 - 372 (8.86%)
681	NR gi 156837190 ref XP_001642627.1 hypothetical protein Kpol_312p8 [Vanderwaltozyma polyspora DSM 70294] >gnl BL_ORD_ID 2072373 hypothetical protein Kpol_312p8 [Vanderwaltozyma polyspora DSM 70294]	416	1.91 x 10 ⁻³⁶	3 - 374 (6.99%)
682	NR gi 51701678 sp Q8J093.1 MPI_PICAN RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 977962 phosphomannose isomerase [Pichia angusta] >gnl BL_ORD_ID 977962 phosphomannose isomerase [Pichia angusta] >gnl BL_ORD_ID 977962 Mannose-6-phosphate isomerase [Pichia angusta DL-1]	407	1.91 x 10 ⁻³⁶	3 - 371 (8.09%)
683	NR gi 294655250 ref XP_457357.2 DEHA2B09350p [Debaryomyces hansenii CBS767] >gnl BL_ORD_ID 910505 DEHA2B09350p [Debaryomyces hansenii]	421	2.50 x 10 ⁻³⁶	9 - 370 (7.67%)
684	NR gi 155675722 gb ABU25181.1 mannose phosphate isomerase [Leishmania guyanensis] >gnl BL_ORD_ID 2077655 mannose phosphate isomerase [Leishmania panamensis]	392	2.50 x 10 ⁻³⁶	3 - 350 (8.27%)
685	NR gi 94469741 gb ABF20324.1 mannose phosphate isomerase [Leishmania donovani]	381	2.50 x 10 ⁻³⁶	9 - 350 (8.61%)
686	NR gi 309361631 emb CAP29510.2 hypothetical protein CBG_09990 [Caenorhabditis briggsae AF16]	396	3.27 x 10 ⁻³⁶	3 - 374 (7.46%)
687	NR gi 261599599 gb ACX85773.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	324	3.27 x 10 ⁻³⁶	15 - 322 (10.48%)
688	NR gi 219114725 ref XP_002178158.1 mannose-6-phosphate isomerase, type [Phaeodactylum tricornutum CCAP 1055/1] >gnl BL_ORD_ID 1333576 mannose-6-phosphate isomerase, type [Phaeodactylum tricornutum CCAP 1055/1]	409	3.27 x 10 ⁻³⁶	4 - 377 (7.53%)
689	NR gi 195391837 ref XP_002054566.1 GJ22739 [Drosophila virilis] >gnl BL_ORD_ID 610753 GJ22739 [Drosophila virilis]	398	4.26 x 10 ⁻³⁶	3 - 375 (8.21%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
690	NR gi 170040692 ref XP_001848124.1 mannose-6-phosphate isomerase [Culex quinquefasciatus] >gnl BL_ORD_ID 2782069 mannose-6-phosphate isomerase [Culex quinquefasciatus]	389	4.26 x 10 ⁻³⁶	3 - 369 (8.26%)
691	NR gi 94469775 gb ABF20341.1 mannose phosphate isomerase [Leishmania tropica]	386	4.26 x 10 ⁻³⁶	3 - 350 (8.32%)
692	NR gi 300176619 emb CBK24284.2 unnamed protein product [Blastocystis hominis]	317	5.57 x 10 ⁻³⁶	1 - 294 (11.05%)
693	NR gi 224486443 gb ACN51988.1 mannose-phosphate isomerase [Daphnia pulex]	310	5.57 x 10 ⁻³⁶	34 - 324 (11.65%)
694	NR gi 224486441 gb ACN51987.1 mannose-phosphate isomerase [Daphnia pulex] >gnl BL_ORD_ID 1886478 mannose-phosphate isomerase [Daphnia pulex] >gnl BL_ORD_ID 1886478 mannose-phosphate isomerase [Daphnia pulex]	310	5.57 x 10 ⁻³⁶	34 - 324 (11.65%)
695	NR gi 155675726 gb ABU25183.1 mannose phosphate isomerase [Leishmania lainsoni]	386	5.57 x 10 ⁻³⁶	3 - 350 (8.19%)
696	NR gi 94469755 gb ABF20331.1 mannose phosphate isomerase [Leishmania infantum] >gnl BL_ORD_ID 1173870 mannose phosphate isomerase [Leishmania donovani archibaldi] >gnl BL_ORD_ID 1173870 mannose phosphate isomerase [Leishmania donovani archibaldi]	381	5.57 x 10 ⁻³⁶	9 - 350 (8.54%)
697	NR gi 261599611 gb ACX85779.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	324	7.27 x 10 ⁻³⁶	15 - 322 (10.48%)
698	NR gi 261599551 gb ACX85749.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 969067 mannose-6-phosphate isomerase [Anopheles sudaicus]	314	7.27 x 10 ⁻³⁶	25 - 322 (10.95%)
699	NR gi 226290498 gb EEH45982.1 mannose-6-phosphate isomerase [Paracoccidioides brasiliensis Pb18]	396	7.27 x 10 ⁻³⁶	29 - 371 (7.65%)
700	NR gi 224486375 gb ACN51954.1 mannose-phosphate isomerase [Daphnia parvula]	309	7.27 x 10 ⁻³⁶	34 - 324 (11.73%)
701	NR gi 161016081 gb ABX56006.1 mannose-6-phosphate isomerase [Mytilus edulis]	405	7.27 x 10 ⁻³⁶	3 - 371 (7.86%)
702	NR gi 157873955 ref XP_001685475.1 phosphomannose isomerase [Leishmania major strain Friedlin] >gnl BL_ORD_ID 125775 phosphomannose isomerase [Leishmania major strain Friedlin]	387	7.27 x 10 ⁻³⁶	3 - 350 (8.35%)
703	NR gi 157833529 pdb 1PMI A Chain A, Human Rantes	318	7.27 x 10 ⁻³⁶	9 - 288 (11.08%)
704	NR gi 68482860 ref XP_714656.1 hypothetical protein CaO19.8968 [Candida albicans SC5314] >gnl BL_ORD_ID 156195 hypothetical protein CaO19.8968 [Candida albicans SC5314]	318	7.27 x 10 ⁻³⁶	9 - 288 (11.08%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
705	NR gi 68483056 ref XP_714562.1 hypothetical protein CaO19.1390 [Candida albicans SC5314] >gnl BL_ORD_ID 18537 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 18537 mannose-6-phosphate isomerase [Candida albicans] >gnl BL_ORD_ID 18537 hypothetical protein CaO19.1390 [Candida albicans SC5314] >gnl BL_ORD_ID 18537 mannose-6-phosphate isomerase [Candida albicans WO-1]	318	7.27 x 10 ⁻³⁶	9 - 288 (11.08%)
706	NR gi 261599613 gb ACX85780.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	314	9.50 x 10 ⁻³⁶	25 - 322 (10.95%)
707	NR gi 224486449 gb ACN51991.1 mannose-phosphate isomerase [Daphnia pulex] >gnl BL_ORD_ID 1886481 mannose-phosphate isomerase [Daphnia pulex]	310	9.50 x 10 ⁻³⁶	34 - 324 (11.97%)
708	NR gi 94469773 gb ABF20340.1 mannose phosphate isomerase [Leishmania gerbilli]	387	9.50 x 10 ⁻³⁶	3 - 350 (8.35%)
709	NR gi 241952248 ref XP_002418846.1 mannose-6-phosphate isomerase, putative; phosphohexomutase, putative; phosphomannose isomerase, putative [Candida dubliniensis CD36] >gnl BL_ORD_ID 1790270 mannose-6-phosphate isomerase, putative [Candida dubliniensis CD36]	322	1.24 x 10 ⁻³⁵	9 - 288 (11.19%)
710	NR gi 161016079 gb ABX56005.1 mannose-6-phosphate isomerase [Mytilus edulis]	405	1.62 x 10 ⁻³⁵	3 - 371 (7.86%)
711	NR gi 161016077 gb ABX56004.1 mannose-6-phosphate isomerase [Mytilus edulis]	405	1.62 x 10 ⁻³⁵	3 - 371 (7.86%)
712	NR gi 116197385 ref XP_001224504.1 hypothetical protein CHGG_06848 [Chaetomium globosum CBS 148.51] >gnl BL_ORD_ID 618628 hypothetical protein CHGG_06848 [Chaetomium globosum CBS 148.51]	433	1.62 x 10 ⁻³⁵	10 - 378 (6.51%)
713	NR gi 322821903 gb EFZ28104.1 phosphomannose isomerase, putative [Trypanosoma cruzi]	373	2.12 x 10 ⁻³⁵	3 - 352 (8.70%)
714	NR gi 195055696 ref XP_001994749.1 GH17406 [Drosophila grimshawi] >gnl BL_ORD_ID 532931 GH17406 [Drosophila grimshawi]	389	2.12 x 10 ⁻³⁵	3 - 375 (8.20%)
715	NR gi 322494249 emb CBZ29548.1 putative phosphomannose isomerase [Leishmania mexicana MHOM/GT/2001/U1103]	380	2.76 x 10 ⁻³⁵	9 - 350 (8.17%)
716	NR gi 194764695 ref XP_001964464.1 GF23036 [Drosophila ananassae] >gnl BL_ORD_ID 427355 GF23036 [Drosophila ananassae]	397	2.76 x 10 ⁻³⁵	3 - 375 (8.06%)
717	NR gi 161016075 gb ABX56003.1 mannose-6-phosphate isomerase [Mytilus edulis]	405	2.76 x 10 ⁻³⁵	3 - 371 (7.80%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
718	NR gi 161016071 gb ABX56001.1 mannose-6-phosphate isomerase [Mytilus edulis]	405	2.76 x 10 ⁻³⁵	3 - 371 (7.80%)
719	NR gi 155675730 gb ABU25185.1 mannose phosphate isomerase [Leishmania mexicana]	380	2.76 x 10 ⁻³⁵	9 - 350 (8.17%)
720	NR gi 302653869 ref XP_003018751.1 mannose-6-phosphate isomerase, class I [Trichophyton verrucosum HKI 0517] >gnl BL_ORD_ID 1670193 mannose-6-phosphate isomerase, class I [Trichophyton verrucosum HKI 0517]	399	3.61 x 10 ⁻³⁵	38 - 371 (7.54%)
721	NR gi 254572503 ref XP_002493361.1 Mannose-6-phosphate isomerase, catalyzes the interconversion of fructose-6-P and mannose-6-P [Pichia pastoris GS115] >gnl BL_ORD_ID 2818507 Mannose-6-phosphate isomerase, catalyzes the interconversion of fructose-6-P and mannose-6-P [Pichia pastoris GS115]	410	3.61 x 10 ⁻³⁵	8 - 369 (7.38%)
722	NR gi 207346047 gb EDZ72664.1 YER003Cp-like protein [Saccharomyces cerevisiae AWRI1631] >gnl BL_ORD_ID 987390 Pmi40p [Saccharomyces cerevisiae Vin13]	376	3.61 x 10 ⁻³⁵	38 - 370 (8.35%)
723	NR gi 11342604 emb CAC17142.1 phosphomannose isomerase [Leishmania mexicana]	380	3.61 x 10 ⁻³⁵	9 - 350 (8.17%)
724	NR gi 29336946 sp Q9GP38.1 MPI_ECHMU RecName: Full=Probable mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 1039916 putative mannose-6-phosphate-isomerase [Echinococcus multilocularis]	426	3.61 x 10 ⁻³⁵	1 - 372 (7.38%)
725	NR gi 194902767 ref XP_001980758.1 GG17103 [Drosophila erecta] >gnl BL_ORD_ID 446346 GG17103 [Drosophila erecta]	398	4.72 x 10 ⁻³⁵	3 - 375 (8.08%)
726	NR gi 156254288 gb ABU62652.1 mannose-6-phosphate isomerase [Mytilus edulis]	408	6.16 x 10 ⁻³⁵	3 - 371 (7.75%)
727	NR gi 255716958 ref XP_002554760.1 KLTH0F13134p [Lachancea thermotolerans] >gnl BL_ORD_ID 5237 KLTH0F13134p [Lachancea thermotolerans]	414	8.04 x 10 ⁻³⁵	9 - 370 (7.64%)
728	NR gi 295674945 ref XP_002798018.1 mannose-6-phosphate isomerase [Paracoccidioides brasiliensis Pb01] >gnl BL_ORD_ID 2150962 mannose-6-phosphate isomerase [Paracoccidioides brasiliensis Pb01]	396	8.04 x 10 ⁻³⁵	29 - 371 (7.53%)
729	NR gi 195499574 ref XP_002097007.1 GE25982 [Drosophila yakuba] >gnl BL_ORD_ID 638603 GE25982 [Drosophila yakuba]	400	8.04 x 10 ⁻³⁵	3 - 375 (8.06%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
730	NR gi 50290739 ref XP_447802.1 hypothetical protein [Candida glabrata CBS 138] >gnl BL_ORD_ID 1194382 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 1194382 phosphomannose isomerase 40 [Candida glabrata] >gnl BL_ORD_ID 1194382 unnamed protein product [Candida glabrata]	409	8.04 x 10 ⁻³⁵	9 - 372 (7.77%)
731	NR gi 323333902 gb EGA75291.1 Pmi40p [Saccharomyces cerevisiae AWRI796] >gnl BL_ORD_ID 1350506 Pmi40p [Saccharomyces cerevisiae Lalvin QA23] >gnl BL_ORD_ID 1350506 Pmi40p [Saccharomyces cerevisiae VL3]	357	1.05 x 10 ⁻³⁴	57 - 370 (8.87%)
732	NR gi 309304873 gb EFP81464.1 mannose-6-phosphate isomerase [Puccinia graminis f. sp. tritici CRL 75-36-700-3]	407	1.05 x 10 ⁻³⁴	3 - 371 (8.21%)
733	NR gi 156254292 gb ABU62654.1 mannose-6-phosphate isomerase [Mytilus trossulus]	405	1.05 x 10 ⁻³⁴	3 - 371 (7.74%)
734	NR gi 195330284 ref XP_002031834.1 GM23834 [Drosophila sechellia] >gnl BL_ORD_ID 586693 GM23834 [Drosophila sechellia]	400	1.79 x 10 ⁻³⁴	3 - 375 (8%)
735	NR gi 161016073 gb ABX56002.1 mannose-6-phosphate isomerase [Mytilus edulis]	405	1.79 x 10 ⁻³⁴	3 - 371 (7.74%)
736	NR gi 155675728 gb ABU25184.1 mannose phosphate isomerase [Leishmania amazonensis]	378	1.79 x 10 ⁻³⁴	11 - 350 (8.19%)
737	NR gi 71651967 ref XP_814649.1 phosphomannose isomerase [Trypanosoma cruzi strain CL Brener] >gnl BL_ORD_ID 348238 phosphomannose isomerase, putative [Trypanosoma cruzi]	373	1.79 x 10 ⁻³⁴	3 - 352 (8.62%)
738	NR gi 261599623 gb ACX85785.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	372	3.06 x 10 ⁻³⁴	25 - 376 (8.45%)
739	NR gi 123490992 ref XP_001325733.1 mannose-6-phosphate isomerase, class I family protein [Trichomonas vaginalis G3] >gnl BL_ORD_ID 1152189 mannose-6-phosphate isomerase, class I family protein [Trichomonas vaginalis G3]	370	3.06 x 10 ⁻³⁴	1 - 352 (8.33%)
740	NR gi 21356061 ref NP_649940.1 CG8417 [Drosophila melanogaster] >gnl BL_ORD_ID 1626472 CG8417 [Drosophila melanogaster] >gnl BL_ORD_ID 1626472 GH10745p [Drosophila melanogaster] >gnl BL_ORD_ID 1626472 RH55676p [Drosophila melanogaster] >gnl BL_ORD_ID 1626472 CG8417-PA [synthetic construct] >gnl BL_ORD_ID 1626472 CG8417-PA [synthetic construct]	400	3.06 x 10 ⁻³⁴	3 - 375 (8%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
741	NR gi 71404644 ref XP_805011.1 phosphomannose isomerase [Trypanosoma cruzi strain CL Brener] >gnl BL_ORD_ID 344571 phosphomannose isomerase, putative [Trypanosoma cruzi]	373	3.99 x 10 ⁻³⁴	3 - 352 (8.48%)
742	NR gi 171741181 ref ZP_02916988.1 hypothetical protein BIFDEN_00253 [Bifidobacterium dentium ATCC 27678] >gnl BL_ORD_ID 173142 hypothetical protein BIFDEN_00253 [Bifidobacterium dentium ATCC 27678]	412	1.16 x 10 ⁻³³	29 - 378 (6.77%)
743	NR gi 322802340 gb EFZ22736.1 hypothetical protein SINV_15264 [Solenopsis invicta]	400	2.59 x 10 ⁻³³	7 - 373 (8%)
744	NR gi 260825319 ref XP_002607614.1 hypothetical protein BRAFLDRAFT_57753 [Branchiostoma floridae] >gnl BL_ORD_ID 1097804 hypothetical protein BRAFLDRAFT_57753 [Branchiostoma floridae]	410	2.59 x 10 ⁻³³	9 - 373 (7.26%)
745	NR gi 307103781 gb EFN52038.1 hypothetical protein CHLNCDRAFT_139231 [Chlorella variabilis]	412	3.38 x 10 ⁻³³	1 - 371 (7.54%)
746	NR gi 170586338 ref XP_001897936.1 mannose-6-phosphate isomerase, class I family protein [Brugia malayi] >gnl BL_ORD_ID 2312518 mannose-6-phosphate isomerase, class I family protein [Brugia malayi]	404	5.76 x 10 ⁻³³	1 - 379 (7.17%)
747	NR gi 289614101 emb CBI59116.1 unnamed protein product [Sordaria macrospora]	436	7.53 x 10 ⁻³³	8 - 371 (6.47%)
748	NR gi 203287853 ref YP_002222868.1 mannose-6-phosphate isomerase [Borrelia recurrentis A1] >gnl BL_ORD_ID 920832 mannose-6-phosphate isomerase [Borrelia recurrentis A1]	371	7.53 x 10 ⁻³³	6 - 369 (8.57%)
749	NR gi 203284317 ref YP_002222057.1 mannose-6-phosphate isomerase [Borrelia duttonii Ly] >gnl BL_ORD_ID 919646 mannose-6-phosphate isomerase [Borrelia duttonii Ly]	371	7.53 x 10 ⁻³³	6 - 369 (8.57%)
750	NR gi 222616236 gb EEE52368.1 hypothetical protein OsJ_34433 [Oryza sativa Japonica Group]	379	9.83 x 10 ⁻³³	38 - 384 (8.56%)
751	NR gi 85084868 ref XP_957390.1 mannose-6-phosphate isomerase [Neurospora crassa OR74A] >gnl BL_ORD_ID 23728 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 23728 mannose-6-phosphate isomerase [Neurospora crassa OR74A] >gnl BL_ORD_ID 23728 probable phosphomannose isomerase (manA) [Neurospora crassa]	439	9.83 x 10 ⁻³³	8 - 371 (6.44%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
752	NR gi 167535493 ref XP_001749420.1 hypothetical protein [Monosiga brevicollis MX1] >gnl BL_ORD_ID 2543252 predicted protein [Monosiga brevicollis MX1]	283	1.28 x 10 ⁻³²	8 - 274 (12.73%)
753	NR gi 301091669 ref XP_002896014.1 mannose-6-phosphate isomerase, putative [Phytophthora infestans T30-4] >gnl BL_ORD_ID 978374 mannose-6-phosphate isomerase, putative [Phytophthora infestans T30-4]	307	3.74 x 10 ⁻³²	38 - 332 (11.67%)
754	NR gi 302811331 ref XP_002987355.1 hypothetical protein SELMODRAFT_125724 [Selaginella moellendorffii] >gnl BL_ORD_ID 2533607 hypothetical protein SELMODRAFT_129293 [Selaginella moellendorffii] >gnl BL_ORD_ID 2533607 hypothetical protein SELMODRAFT_129293 [Selaginella moellendorffii] >gnl BL_ORD_ID 2533607 hypothetical protein SELMODRAFT_125724 [Selaginella moellendorffii]	318	6.37 x 10 ⁻³²	1 - 293 (10.78%)
755	NR gi 156375265 ref XP_001630002.1 predicted protein [Nematostella vectensis] >gnl BL_ORD_ID 2095942 predicted protein [Nematostella vectensis]	377	6.37 x 10 ⁻³²	38 - 384 (8.66%)
756	NR gi 168004289 ref XP_001754844.1 predicted protein [Physcomitrella patens subsp. patens] >gnl BL_ORD_ID 2522243 predicted protein [Physcomitrella patens subsp. patens]	313	8.32 x 10 ⁻³²	7 - 294 (10.92%)
757	NR gi 227549546 ref ZP_03979595.1 possible mannose-6-phosphate isomerase [Corynebacterium lipophiloflavum DSM 44291] >gnl BL_ORD_ID 2252600 possible mannose-6-phosphate isomerase [Corynebacterium lipophiloflavum DSM 44291]	156	1.42 x 10 ⁻³¹	3 - 158 (30.82%)
758	NR gi 145341936 ref XP_001416055.1 predicted protein [Ostreococcus lucimarinus CCE9901] >gnl BL_ORD_ID 1485719 predicted protein [Ostreococcus lucimarinus CCE9901]	415	1.42 x 10 ⁻³¹	1 - 373 (6.68%)
759	NR gi 323452066 gb EGB07941.1 hypothetical protein AURANDRAFT_2565 [Aureococcus anophagefferens]	305	1.85 x 10 ⁻³¹	11 - 288 (11.93%)
760	NR gi 309812572 ref ZP_07706317.1 phosphomannose isomerase type I [Dermacoccus sp. Ellin185] >gnl BL_ORD_ID 278211 phosphomannose isomerase type I [Dermacoccus sp. Ellin185]	398	1.85 x 10 ⁻³¹	1 - 388 (7.45%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
761	NR gi 45187876 ref NP_984099.1 ADR003Cp [Ashbya gossypii ATCC 10895] >gnl BL_ORD_ID 1230643 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 1230643 ADR003Cp [Ashbya gossypii ATCC 10895]	406	1.85 x 10 ⁻³¹	9 - 370 (7.22%)
762	NR gi 296087268 emb CBI33642.3 unnamed protein product [Vitis vinifera]	333	3.16 x 10 ⁻³¹	64 - 372 (9.47%)
763	NR gi 28493089 ref NP_787250.1 mannose-6-phosphate isomerase [Tropheryma whipplei str. Twist] >gnl BL_ORD_ID 1636369 mannose-6-phosphate isomerase [Tropheryma whipplei str. Twist]	315	5.39 x 10 ⁻³¹	4 - 317 (9.77%)
764	NR gi 323305202 gb EGA58949.1 Pmi40p [Saccharomyces cerevisiae FostersB]	290	7.05 x 10 ⁻³¹	38 - 300 (11.65%)
765	NR gi 46121905 ref XP_385506.1 hypothetical protein FG05330.1 [Gibberella zeae PH-1]	372	1.20 x 10 ⁻³⁰	34 - 384 (8.38%)
766	NR gi 317156893 ref XP_001826088.2 mannose-6-phosphate isomerase [Aspergillus oryzae RIB40]	379	1.57 x 10 ⁻³⁰	30 - 371 (8.15%)
767	NR gi 308801034 ref XP_003075298.1 putative mannose-6-phosphate isomerase (ISS) [Ostreococcus tauri] >gnl BL_ORD_ID 719312 putative mannose-6-phosphate isomerase (ISS) [Ostreococcus tauri]	351	1.57 x 10 ⁻³⁰	1 - 325 (8.77%)
768	NR gi 28572296 ref NP_789076.1 mannose-6-phosphate isomerase [Tropheryma whipplei TW08/27] >gnl BL_ORD_ID 2732717 mannose-6-phosphate isomerase [Tropheryma whipplei TW08/27]	336	1.57 x 10 ⁻³⁰	4 - 335 (8.95%)
769	NR gi 209876980 ref XP_002139932.1 phosphomannose isomerase type I family protein [Cryptosporidium muris RN66] >gnl BL_ORD_ID 1020359 phosphomannose isomerase type I family protein [Cryptosporidium muris RN66]	335	2.68 x 10 ⁻³⁰	7 - 294 (8.73%)
770	NR gi 309356890 emb CAP36419.2 hypothetical protein CBG_19118 [Caenorhabditis briggsae AF16]	400	7.79 x 10 ⁻³⁰	1 - 361 (7.63%)
771	NR gi 262386217 gb ACY64978.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	261	7.79 x 10 ⁻³⁰	25 - 278 (13.36%)
772	NR gi 83774832 dbj BAE64955.1 unnamed protein product [Aspergillus oryzae]	382	7.79 x 10 ⁻³⁰	30 - 371 (8.02%)
773	NR gi 268558840 ref XP_002637411.1 Hypothetical protein CBG19118 [Caenorhabditis briggsae]	400	7.79 x 10 ⁻³⁰	1 - 361 (7.63%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
774	NR gi 262386229 gb ACY64984.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055171 mannose-6-phosphate isomerase [Anopheles sundaicus]	261	1.02 x 10 ⁻²⁹	25 - 278 (13.36%)
775	NR gi 262386221 gb ACY64980.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	261	1.02 x 10 ⁻²⁹	25 - 278 (13.36%)
776	NR gi 262386215 gb ACY64977.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	261	1.02 x 10 ⁻²⁹	25 - 278 (13.36%)
777	NR gi 224486445 gb ACN51989.1 mannose-phosphate isomerase [Daphnia pulex]	264	1.02 x 10 ⁻²⁹	41 - 287 (14.20%)
778	NR gi 262386573 gb ACY65156.1 mannose-6-phosphate isomerase [Anopheles subpictus]	261	1.33 x 10 ⁻²⁹	25 - 278 (13.36%)
779	NR gi 262386565 gb ACY65152.1 mannose-6-phosphate isomerase [Anopheles subpictus]	261	1.33 x 10 ⁻²⁹	25 - 278 (13.36%)
780	NR gi 262386333 gb ACY65036.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055198 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	1.33 x 10 ⁻²⁹	25 - 278 (13.10%)
781	NR gi 262386227 gb ACY64983.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	261	1.33 x 10 ⁻²⁹	25 - 278 (13.36%)
782	NR gi 262386219 gb ACY64979.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055167 mannose-6-phosphate isomerase [Anopheles sundaicus]	261	1.33 x 10 ⁻²⁹	25 - 278 (13.36%)
783	NR gi 262386213 gb ACY64976.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	261	1.33 x 10 ⁻²⁹	25 - 278 (13.36%)
784	NR gi 262386159 gb ACY64949.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	275	1.33 x 10 ⁻²⁹	15 - 278 (12.56%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
785	NR gi 27366947 ref NP_762474.1 phosphomannose isomerase [Vibrio vulnificus CMCP6]	125	1.33 x 10 ⁻²⁹	6 - 130 (39.68%)
786	NR gi 262386387 gb ACY65063.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	271	1.74 x 10 ⁻²⁹	15 - 278 (12.66%)
787	NR gi 262386379 gb ACY65059.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 1055209 mannose-6-phosphate isomerase [Anopheles sudaicus]	261	1.74 x 10 ⁻²⁹	25 - 278 (13.36%)
788	NR gi 262386307 gb ACY65023.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	1.74 x 10 ⁻²⁹	25 - 278 (13.10%)
789	NR gi 262386161 gb ACY64950.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	1.74 x 10 ⁻²⁹	25 - 278 (13.24%)
790	NR gi 262386145 gb ACY64942.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 1055151 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	1.74 x 10 ⁻²⁹	25 - 278 (13.24%)
791	NR gi 262386141 gb ACY64940.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 1055149 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	1.74 x 10 ⁻²⁹	25 - 278 (13.24%)
792	NR gi 262386577 gb ACY65158.1 mannose-6-phosphate isomerase [Anopheles subpictus]	261	2.27 x 10 ⁻²⁹	25 - 278 (13.36%)
793	NR gi 262386571 gb ACY65155.1 mannose-6-phosphate isomerase [Anopheles subpictus]	261	2.27 x 10 ⁻²⁹	25 - 278 (13.36%)
794	NR gi 262386569 gb ACY65154.1 mannose-6-phosphate isomerase [Anopheles subpictus] >gnl BL_ORD_ID 1055231 mannose-6-phosphate isomerase [Anopheles subpictus]	261	2.27 x 10 ⁻²⁹	25 - 278 (13.36%)
795	NR gi 262386375 gb ACY65057.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	261	2.27 x 10 ⁻²⁹	25 - 278 (13.36%)
796	NR gi 262386371 gb ACY65055.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	261	2.27 x 10 ⁻²⁹	25 - 278 (13.36%)
797	NR gi 262386337 gb ACY65038.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 1055199 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	2.27 x 10 ⁻²⁹	25 - 278 (13.10%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
798	NR gi 262386313 gb ACY65026.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055194 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	2.27 x 10 ⁻²⁹	25 - 278 (13.10%)
799	NR gi 262386311 gb ACY65025.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	2.27 x 10 ⁻²⁹	25 - 278 (13.10%)
800	NR gi 262386303 gb ACY65021.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	275	2.27 x 10 ⁻²⁹	15 - 278 (12.43%)
801	NR gi 262386225 gb ACY64982.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	261	2.27 x 10 ⁻²⁹	25 - 278 (13.36%)
802	NR gi 262386519 gb ACY65129.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	2.96 x 10 ⁻²⁹	25 - 278 (13.24%)
803	NR gi 262386403 gb ACY65071.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055217 mannose-6-phosphate isomerase [Anopheles sundaicus]	275	2.96 x 10 ⁻²⁹	15 - 278 (12.43%)
804	NR gi 262386373 gb ACY65056.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	2.96 x 10 ⁻²⁹	25 - 278 (13.10%)
805	NR gi 262386321 gb ACY65030.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055196 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	2.96 x 10 ⁻²⁹	25 - 278 (13.10%)
806	NR gi 262386305 gb ACY65022.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	2.96 x 10 ⁻²⁹	25 - 278 (13.10%)
807	NR gi 262386289 gb ACY65014.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055186 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	2.96 x 10 ⁻²⁹	25 - 278 (13.10%)
808	NR gi 262386281 gb ACY65010.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055183 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	2.96 x 10 ⁻²⁹	25 - 278 (13.10%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
809	NR gi 262386157 gb ACY64948.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	2.96 x 10 ⁻²⁹	25 - 278 (13.24%)
810	NR gi 194376082 dbj BAG57385.1 unnamed protein product [Homo sapiens]	281	2.96 x 10 ⁻²⁹	7 - 260 (12.54%)
811	NR gi 119619703 gb EAW99297.1 mannose phosphate isomerase, isoform CRA_c [Homo sapiens]	281	2.96 x 10 ⁻²⁹	7 - 260 (12.41%)
812	NR gi 262386579 gb ACY65159.1 mannose-6-phosphate isomerase [Anopheles subpictus]	262	3.87 x 10 ⁻²⁹	25 - 278 (13.55%)
813	NR gi 262386437 gb ACY65088.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	3.87 x 10 ⁻²⁹	25 - 278 (13.10%)
814	NR gi 262386397 gb ACY65068.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 1055215 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	3.87 x 10 ⁻²⁹	25 - 278 (13.10%)
815	NR gi 262386383 gb ACY65061.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	3.87 x 10 ⁻²⁹	25 - 278 (13.10%)
816	NR gi 262386301 gb ACY65020.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	3.87 x 10 ⁻²⁹	25 - 278 (13.10%)
817	NR gi 262386269 gb ACY65004.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 1055180 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	3.87 x 10 ⁻²⁹	25 - 278 (13.10%)
818	NR gi 262386173 gb ACY64956.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 1055157 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	3.87 x 10 ⁻²⁹	25 - 278 (13.10%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
821	NR gi 262386393 gb ACY65066.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055214 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055214 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055214 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	5.05 x 10 ⁻²⁹	25 - 278 (13.10%)
822	NR gi 262386389 gb ACY65064.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055213 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	5.05 x 10 ⁻²⁹	25 - 278 (13.10%)
823	NR gi 262386385 gb ACY65062.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	5.05 x 10 ⁻²⁹	25 - 278 (13.10%)
824	NR gi 262386209 gb ACY64974.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055163 mannose-6-phosphate isomerase [Anopheles sundaicus]	261	5.05 x 10 ⁻²⁹	25 - 278 (13.36%)
825	NR gi 262386183 gb ACY64961.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055161 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055161 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	5.05 x 10 ⁻²⁹	25 - 278 (13.10%)
826	NR gi 262386171 gb ACY64955.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055156 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	5.05 x 10 ⁻²⁹	25 - 278 (13.10%)
827	NR gi 262386143 gb ACY64941.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	5.05 x 10 ⁻²⁹	25 - 278 (13.24%)
828	NR gi 261599615 gb ACX85781.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	376	5.05 x 10 ⁻²⁹	25 - 376 (7.78%)
829	NR gi 262386521 gb ACY65130.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055228 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	6.59 x 10 ⁻²⁹	25 - 278 (13.10%)
830	NR gi 262386505 gb ACY65122.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055225 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	6.59 x 10 ⁻²⁹	25 - 278 (13.10%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
831	NR gi 262386317 gb ACY65028.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 1055195 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	6.59 x 10 ⁻²⁹	25 - 278 (13.10%)
832	NR gi 262386309 gb ACY65024.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	6.59 x 10 ⁻²⁹	25 - 278 (13.10%)
833	NR gi 262386261 gb ACY65000.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 1055178 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	6.59 x 10 ⁻²⁹	25 - 278 (13.10%)
834	NR gi 262386249 gb ACY64994.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 1055176 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	6.59 x 10 ⁻²⁹	25 - 278 (13.10%)
835	NR gi 262386241 gb ACY64990.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 1055173 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	6.59 x 10 ⁻²⁹	25 - 278 (13.10%)
836	NR gi 145501371 ref XP_001436667.1 hypothetical protein [Paramecium tetraurelia strain d4-2] >gnl BL_ORD_ID 1222898 unnamed protein product [Paramecium tetraurelia]	395	6.59 x 10 ⁻²⁹	1 - 369 (7.82%)
837	NR gi 262386499 gb ACY65119.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	8.61 x 10 ⁻²⁹	25 - 278 (13.10%)
838	NR gi 262386431 gb ACY65085.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 1055218 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	8.61 x 10 ⁻²⁹	25 - 278 (13.10%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
840	NR gi 262386351 gb ACY65045.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	8.61 x 10 ⁻²⁹	25 - 278 (13.10%)
841	NR gi 262386347 gb ACY65043.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055202 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	8.61 x 10 ⁻²⁹	25 - 278 (13.10%)
842	NR gi 262386293 gb ACY65016.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	8.61 x 10 ⁻²⁹	25 - 278 (13.10%)
843	NR gi 262386285 gb ACY65012.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055184 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	8.61 x 10 ⁻²⁹	25 - 278 (13.10%)
844	NR gi 262386275 gb ACY65007.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	8.61 x 10 ⁻²⁹	25 - 278 (12.96%)
845	NR gi 262386273 gb ACY65006.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	8.61 x 10 ⁻²⁹	25 - 278 (12.96%)
846	NR gi 262386265 gb ACY65002.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055179 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	8.61 x 10 ⁻²⁹	25 - 278 (13.10%)
847	NR gi 262386195 gb ACY64967.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	8.61 x 10 ⁻²⁹	25 - 278 (13.10%)
848	NR gi 262386377 gb ACY65058.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	1.12 x 10 ⁻²⁸	25 - 278 (13.10%)
849	NR gi 262386345 gb ACY65042.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	1.12 x 10 ⁻²⁸	25 - 278 (13.10%)
850	NR gi 262386253 gb ACY64996.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055177 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055177 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	1.12 x 10 ⁻²⁸	25 - 278 (13.10%)
851	NR gi 262386247 gb ACY64993.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	1.12 x 10 ⁻²⁸	25 - 278 (12.96%)
852	NR gi 262386245 gb ACY64992.1 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	1.12 x 10 ⁻²⁸	25 - 278 (12.96%)
853	NR gi 262386177 gb ACY64958.1 mannose-6-phosphate isomerase [Anopheles sundaicus] >gnl BL_ORD_ID 1055158 mannose-6-phosphate isomerase [Anopheles sundaicus]	265	1.12 x 10 ⁻²⁸	25 - 278 (13.10%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
854	NR gi 170594573 ref XP_001902038.1 mannose-6-phosphate isomerase, class I family protein [Brugia malayi] >gnl BL_ORD_ID 2309230 mannose-6-phosphate isomerase, class I family protein [Brugia malayi]	418	1.12 x 10 ⁻²⁸	1 - 369 (6.75%)
855	NR gi 262386513 gb ACY65126.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	1.47 x 10 ⁻²⁸	25 - 278 (13.10%)
856	NR gi 262386481 gb ACY65110.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 1055223 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	1.47 x 10 ⁻²⁸	25 - 278 (13.10%)
857	NR gi 262386469 gb ACY65104.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 1055220 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	1.47 x 10 ⁻²⁸	25 - 278 (13.10%)
858	NR gi 262386331 gb ACY65035.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	1.47 x 10 ⁻²⁸	25 - 278 (13.10%)
859	NR gi 262386287 gb ACY65013.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	1.47 x 10 ⁻²⁸	25 - 278 (13.10%)
860	NR gi 262386239 gb ACY64989.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	1.47 x 10 ⁻²⁸	25 - 278 (12.96%)
861	NR gi 262386179 gb ACY64959.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 1055159 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	1.92 x 10 ⁻²⁸	25 - 278 (13.10%)
862	NR gi 262386181 gb ACY64960.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	258	2.51 x 10 ⁻²⁸	32 - 278 (13.52%)
863	NR gi 312067769 ref XP_003136899.1 mannose-6-phosphate isomerase [Loa loa] >gnl BL_ORD_ID 187712 mannose-6-phosphate isomerase [Loa loa]	401	3.27 x 10 ⁻²⁸	1 - 352 (7.28%)
864	NR gi 262386581 gb ACY65160.1 mannose-6-phosphate isomerase [Anopheles subpictus]	262	3.27 x 10 ⁻²⁸	25 - 278 (13.26%)
865	NR gi 262386567 gb ACY65153.1 mannose-6-phosphate isomerase [Anopheles subpictus]	261	3.27 x 10 ⁻²⁸	25 - 278 (13.21%)
866	NR gi 308470719 ref XP_003097592.1 hypothetical protein CRE_14866 [Caenorhabditis remanei] >gnl BL_ORD_ID 237294 hypothetical protein CRE_14866 [Caenorhabditis remanei]	434	4.27 x 10 ⁻²⁸	1 - 384 (6.48%)
867	NR gi 85093719 ref XP_959748.1 hypothetical protein NCU02322 [Neurospora crassa OR74A] >gnl BL_ORD_ID 73661 predicted protein [Neurospora crassa OR74A]	400	4.27 x 10 ⁻²⁸	3 - 376 (7.13%)
868	NR gi 308094733 ref ZP_07663025.1 mannose-6-phosphate isomerase [Vibrio parahaemolyticus AN-5034] >gnl BL_ORD_ID 212279 mannose-6-phosphate isomerase [Vibrio parahaemolyticus AN-5034]	122	5.58 x 10 ⁻²⁸	6 - 127 (39.64%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
869	NR gi 262386359 gb ACY65049.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	5.58 x 10 ⁻²⁸	25 - 278 (12.96%)
870	NR gi 302890315 ref XP_003044042.1 predicted protein [Nectria haematococca mpVI 77-13-4] >gnl BL_ORD_ID 563645 predicted protein [Nectria haematococca mpVI 77-13-4]	357	5.58 x 10 ⁻²⁸	34 - 370 (8.32%)
871	NR gi 262386343 gb ACY65041.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	1.24 x 10 ⁻²⁷	25 - 278 (12.82%)
872	NR gi 156044560 ref XP_001588836.1 hypothetical protein SS1G_10384 [Sclerotinia sclerotiorum 1980] >gnl BL_ORD_ID 2043214 hypothetical protein SS1G_10384 [Sclerotinia sclerotiorum 1980]	389	1.24 x 10 ⁻²⁷	10 - 369 (7.53%)
873	NR gi 262386475 gb ACY65107.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	265	1.62 x 10 ⁻²⁷	25 - 278 (12.96%)
874	NR gi 171678493 ref XP_001904196.1 hypothetical protein [Podospora anserina S mat+] >gnl BL_ORD_ID 145434 unnamed protein product [Podospora anserina S mat+]	404	1.62 x 10 ⁻²⁷	3 - 381 (6.68%)
875	NR gi 238493017 ref XP_002377745.1 mannose-6-phosphate isomerase, putative [Aspergillus flavus NRRL3357] >gnl BL_ORD_ID 1539848 mannose-6-phosphate isomerase, putative [Aspergillus flavus NRRL3357]	371	2.77 x 10 ⁻²⁷	38 - 371 (8.21%)
876	NR gi 213027123 ref ZP_03341570.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. 404ty]	65	2.77 x 10 ⁻²⁷	234 - 298 (149.11%)
877	NR gi 20563689 gb AAM28199.1 AF504648_1 mannose phosphate isomerase isoform [Homo sapiens]	271	3.62 x 10 ⁻²⁷	14 - 260 (12.66%)
878	NR gi 17557650 ref NP_504843.1 hypothetical protein C05C8.7 [Caenorhabditis elegans] >gnl BL_ORD_ID 2679018 Hypothetical protein C05C8.7 [Caenorhabditis elegans]	405	6.17 x 10 ⁻²⁷	1 - 361 (7.13%)
879	NR gi 289571482 ref ZP_06451709.1 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis T17] >gnl BL_ORD_ID 1559313 mannose-6-phosphate isomerase manA [Mycobacterium tuberculosis T17]	226	1.05 x 10 ⁻²⁶	176 - 388 (15.66%)
880	NR gi 321262891 ref XP_003196164.1 mannose-6-phosphate isomerase [Cryptococcus gattii WM276] >gnl BL_ORD_ID 983198 mannose-6-phosphate isomerase, putative [Cryptococcus gattii WM276]	367	1.80 x 10 ⁻²⁶	31 - 352 (8.32%)
881	NR gi 290985219 ref XP_002675323.1 mannose phosphate isomerase [Naegleria gruberi] >gnl BL_ORD_ID 1436261 mannose phosphate isomerase [Naegleria gruberi]	338	5.23 x 10 ⁻²⁶	38 - 348 (9.01%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
882	NR gi 66359836 ref XP_627096.1 mannose-6-phosphate isomerase [Cryptosporidium parvum lowa II] >gn BL_ORD_ID 147276 mannose-6-phosphate isomerase [Cryptosporidium parvum lowa II]	327	5.23 x 10 ⁻²⁶	32 - 295 (9.45%)
883	NR gi 221120372 ref XP_002165961.1 PREDICTED: similar to Mannose phosphate isomerase (mapped), partial [Hydra magnipapillata]	284	6.82 x 10 ⁻²⁶	8 - 260 (12.40%)
884	NR gi 297609411 ref NP_001063081.2 Os09g0389000 [Oryza sativa Japonica Group] >gn BL_ORD_ID 1286357 putative mannose-6-phosphate isomerase (Phosphomannose isomerase) (PMI) (Phosphohexomutase) [Oryza sativa Japonica Group] >gn BL_ORD_ID 1286357 hypothetical protein OsJ_29229 [Oryza sativa Japonica Group] >gn BL_ORD_ID 1286357 Os09g0389000 [Oryza sativa Japonica Group]	308	6.82 x 10 ⁻²⁶	86 - 371 (10.22%)
885	NR gi 312213486 emb CBX93568.1 similar to mannose-6-phosphate isomerase [Leptosphaeria maculans]	376	1.52 x 10 ⁻²⁵	16 - 370 (7.85%)
886	NR gi 121707114 ref XP_001271736.1 mannose-6-phosphate isomerase, class I [Aspergillus clavatus NRRL 1] >gn BL_ORD_ID 950555 mannose-6-phosphate isomerase, class I [Aspergillus clavatus NRRL 1]	282	1.99 x 10 ⁻²⁵	13 - 280 (11.32%)
887	NR gi 58259875 ref XP_567350.1 mannose-6-phosphate isomerase [Cryptococcus neoformans var. neoformans JEC21] >gn BL_ORD_ID 189389 hypothetical protein CNBJ1720 [Cryptococcus neoformans var. neoformans B-3501A] >gn BL_ORD_ID 189389 hypothetical protein CNBJ1720 [Cryptococcus neoformans var. neoformans B-3501A] >gn BL_ORD_ID 189389 mannose-6-phosphate isomerase, putative [Cryptococcus neoformans var. neoformans JEC21]	404	2.59 x 10 ⁻²⁵	31 - 380 (7.48%)
888	NR gi 213027984 ref ZP_03342431.1 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Typhi str. 404ty]	80	3.39 x 10 ⁻²⁵	312 - 391 (93.75%)
889	NR gi 169773527 ref XP_001821232.1 mannose-6-phosphate isomerase, class I [Aspergillus oryzae RIB40] >gn BL_ORD_ID 1516199 mannose-6-phosphate isomerase, class I [Aspergillus flavus NRRL3357] >gn BL_ORD_ID 1516199 unnamed protein product [Aspergillus oryzae] >gn BL_ORD_ID 1516199 mannose-6-phosphate isomerase, class I [Aspergillus flavus NRRL3357]	384	3.39 x 10 ⁻²⁵	8 - 366 (7.66%)
890	NR gi 154290333 ref XP_001545763.1 hypothetical protein BC1G_15797 [Botryotinia fuckeliana B05.10] >gn BL_ORD_ID 1934069 hypothetical protein BC1G_15797 [Botryotinia fuckeliana B05.10]	389	4.42 x 10 ⁻²⁵	10 - 369 (7.01%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
891	NR gi 189200164 ref XP_001936419.1 mannose-6-phosphate isomerase [Pyrenophora tritici-repentis Pt-1C-BFP] >gnl BL_ORD_ID 330728 mannose-6-phosphate isomerase [Pyrenophora tritici-repentis Pt-1C-BFP]	376	7.55 x 10 ⁻²⁵	16 - 370 (7.50%)
892	NR gi 119500846 ref XP_001267180.1 mannose-6-phosphate isomerase, class I [Neosartorya fischeri NRRL 181] >gnl BL_ORD_ID 962721 mannose-6-phosphate isomerase, class I [Neosartorya fischeri NRRL 181]	285	2.20 x 10 ⁻²⁴	13 - 280 (11.45%)
893	NR gi 298705507 emb CBJ28774.1 Mannose-6-phosphate isomerase [Ectocarpus siliculosus]	338	2.87 x 10 ⁻²⁴	1 - 264 (9.01%)
894	NR gi 311320417 gb EFQ88370.1 hypothetical protein PTT_15766 [Pyrenophora teres f. teres 0-1]	376	3.74 x 10 ⁻²⁴	16 - 370 (7.50%)
895	NR gi 116204357 ref XP_001227989.1 hypothetical protein CHGG_10062 [Chaetomium globosum CBS 148.51] >gnl BL_ORD_ID 612758 hypothetical protein CHGG_10062 [Chaetomium globosum CBS 148.51]	296	4.89 x 10 ⁻²⁴	3 - 280 (10.39%)
896	NR gi 159125103 gb EDP50220.1 mannose-6-phosphate isomerase, class I [Aspergillus fumigatus A1163]	285	6.39 x 10 ⁻²⁴	13 - 280 (11.57%)
897	NR gi 70994328 ref XP_751984.1 mannose-6-phosphate isomerase, class I [Aspergillus fumigatus Af293] >gnl BL_ORD_ID 253638 mannose-6-phosphate isomerase, class I [Aspergillus fumigatus Af293]	285	8.34 x 10 ⁻²⁴	13 - 280 (11.57%)
898	NR gi 310795095 gb EFQ30556.1 phosphomannose isomerase type I [Glomerella graminicola M1.001]	406	1.86 x 10 ⁻²³	3 - 370 (6.67%)
899	NR gi 242221716 ref XP_002476600.1 predicted protein [Postia placenta Mad-698-R] >gnl BL_ORD_ID 1555411 predicted protein [Postia placenta Mad-698-R]	338	1.86 x 10 ⁻²³	3 - 299 (8.40%)
900	NR gi 115397885 ref XP_001214534.1 conserved hypothetical protein [Aspergillus terreus NIH2624] >gnl BL_ORD_ID 577863 conserved hypothetical protein [Aspergillus terreus NIH2624]	254	2.43 x 10 ⁻²³	35 - 280 (13.64%)
901	NR gi 322694436 gb EFY86266.1 mannose-6-phosphate isomerase [Metarhizium acridum CQMa 102]	425	3.17 x 10 ⁻²³	3 - 384 (6.53%)
902	NR gi 164658826 ref XP_001730538.1 hypothetical protein MGL_2334 [Malassezia globosa CBS 7966] >gnl BL_ORD_ID 2334958 hypothetical protein MGL_2334 [Malassezia globosa CBS 7966]	292	3.17 x 10 ⁻²³	126 - 384 (10.79%)
903	NR gi 195572162 ref XP_002104065.1 GD18644 [Drosophila simulans] >gnl BL_ORD_ID 653983 GD18644 [Drosophila simulans]	379	9.22 x 10 ⁻²³	3 - 358 (7.80%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
904	NR gi 302407051 ref XP_003001361.1 mannose-6-phosphate isomerase [Verticillium albo-atrum VaMs.102] >gnl BL_ORD_ID 936809 mannose-6-phosphate isomerase [Verticillium albo-atrum VaMs.102]	398	2.05 x 10 ⁻²²	3 - 370 (7.20%)
905	NR gi 145257327 ref XP_001401688.1 mannose-6-phosphate isomerase, class I [Aspergillus niger CBS 513.88] >gnl BL_ORD_ID 1431530 unnamed protein product [Aspergillus niger]	290	2.27 x 10 ⁻²¹	8 - 280 (10.94%)
906	NR gi 259487056 tpe CBF85422.1 TPA: mannose-6-phosphate isomerase, class I (AFU_orthologue; AFUA_4G08410) [Aspergillus nidulans FGSC A4]	283	2.97 x 10 ⁻²¹	7 - 280 (11.11%)
907	NR gi 307203228 gb EFN82383.1 Mannose-6-phosphate isomerase [Harpegnathos saltator]	381	5.06 x 10 ⁻²¹	7 - 373 (7.44%)
908	NR gi 84997563 ref XP_953503.1 mannose-6 phosphate isomerase [Theileria annulata strain Ankara] >gnl BL_ORD_ID 1419506 mannose-6 phosphate isomerase, putative [Theileria annulata]	324	5.06 x 10 ⁻²¹	3 - 283 (8.95%)
909	NR gi 194379428 dbj BAG63680.1 unnamed protein product [Homo sapiens]	224	1.13 x 10 ⁻²⁰	38 - 260 (14.95%)
910	NR gi 322698891 gb EFY90657.1 mannose-6-phosphate isomerase [Metarhizium acridum CQMa 102]	405	1.47 x 10 ⁻²⁰	3 - 371 (6.34%)
911	NR gi 289616999 emb CBI56282.1 unnamed protein product [Sordaria macrospora]	405	1.92 x 10 ⁻²⁰	3 - 376 (6.52%)
912	NR gi 255581330 ref XP_002531475.1 mannose-6-phosphate isomerase, putative [Ricinus communis] >gnl BL_ORD_ID 1759031 mannose-6-phosphate isomerase, putative [Ricinus communis]	406	1.92 x 10 ⁻²⁰	1 - 386 (6.67%)
913	NR gi 67522517 ref XP_659319.1 hypothetical protein AN1715.2 [Aspergillus nidulans FGSC A4] >gnl BL_ORD_ID 98023 hypothetical protein AN1715.2 [Aspergillus nidulans FGSC A4]	255	2.51 x 10 ⁻²⁰	35 - 280 (12.30%)
914	NR gi 297737798 emb CBI26999.3 unnamed protein product [Vitis vinifera]	265	7.31 x 10 ⁻²⁰	53 - 294 (11.82%)
915	NR gi 169608866 ref XP_001797852.1 hypothetical protein SNOG_07518 [Phaeosphaeria nodorum SN15] >gnl BL_ORD_ID 2379999 hypothetical protein SNOG_07518 [Phaeosphaeria nodorum SN15]	255	9.54 x 10 ⁻²⁰	38 - 280 (12.45%)
916	NR gi 323453384 gb EGB09256.1 hypothetical protein AURANDRAFT_25430 [Aureococcus anophagefferens]	314	1.63 x 10 ⁻¹⁹	12 - 293 (8.52%)
917	NR gi 297296911 ref XP_002804915.1 PREDICTED: mannose-6-phosphate isomerase-like isoform 5 [Macaca mulatta]	230	2.78 x 10 ⁻¹⁹	7 - 216 (14.37%)
918	NR gi 109081956 ref XP_001098369.1 PREDICTED: mannose-6-phosphate isomerase-like isoform 1 [Macaca mulatta]	230	2.78 x 10 ⁻¹⁹	7 - 216 (14.37%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
919	NR gi 224486303 gb ACN51917.1 mannose-phosphate isomerase [Daphnia magna]	207	4.74 x 10 ⁻¹⁹	70 - 260 (17.73%)
920	NR gi 224486297 gb ACN51914.1 mannose-phosphate isomerase [Daphnia magna]	207	4.74 x 10 ⁻¹⁹	70 - 260 (17.73%)
921	NR gi 224486289 gb ACN51910.1 mannose-phosphate isomerase [Daphnia magna] >gnl BL_ORD_ID 1886438 mannose-phosphate isomerase [Daphnia magna] >gnl BL_ORD_ID 1886438 mannose-phosphate isomerase [Daphnia magna] >gnl BL_ORD_ID 1886438 mannose-phosphate isomerase [Daphnia magna]	207	4.74 x 10 ⁻¹⁹	70 - 260 (17.73%)
922	NR gi 224486287 gb ACN51909.1 mannose-phosphate isomerase [Daphnia magna] >gnl BL_ORD_ID 1886437 mannose-phosphate isomerase [Daphnia magna]	207	4.74 x 10 ⁻¹⁹	70 - 260 (17.73%)
923	NR gi 224486291 gb ACN51911.1 mannose-phosphate isomerase [Daphnia magna]	207	8.08 x 10 ⁻¹⁹	70 - 260 (16.80%)
924	NR gi 224486285 gb ACN51908.1 mannose-phosphate isomerase [Daphnia magna]	207	1.06 x 10 ⁻¹⁸	70 - 260 (17.73%)
925	NR gi 242069051 ref XP_002449802.1 hypothetical protein SORBIDRAFT_05g023560 [Sorghum bicolor] >gnl BL_ORD_ID 226951 hypothetical protein SORBIDRAFT_05g023560 [Sorghum bicolor]	263	1.80 x 10 ⁻¹⁸	135 - 372 (10.99%)
926	NR gi 164499319 gb ABY59229.1 At1g67070-like protein [Arabidopsis lyrata subsp. petraea]	197	1.80 x 10 ⁻¹⁸	183 - 372 (16.49%)
927	NR gi 164499317 gb ABY59228.1 At1g67070-like protein [Arabidopsis lyrata subsp. petraea]	197	2.35 x 10 ⁻¹⁸	183 - 372 (16.49%)
928	NR gi 261338200 ref ZP_05966084.1 phosphomannose isomerase type I [Bifidobacterium gallicum DSM 20093] >gnl BL_ORD_ID 2053857 phosphomannose isomerase type I [Bifidobacterium gallicum DSM 20093]	146	3.07 x 10 ⁻¹⁸	9 - 148 (25.80%)
928	NR gi 261338200 ref ZP_05966084.1 phosphomannose isomerase type I [Bifidobacterium gallicum DSM 20093] >gnl BL_ORD_ID 2053857 phosphomannose isomerase type I [Bifidobacterium gallicum DSM 20093]	146	3.07 x 10 ⁻¹⁸	9 - 148 (25.80%)
929	NR gi 242800758 ref XP_002483653.1 mannose-6-phosphate isomerase, class I [Talaromyces stipitatus ATCC 10500] >gnl BL_ORD_ID 1459692 mannose-6-phosphate isomerase, class I [Talaromyces stipitatus ATCC 10500]	256	6.84 x 10 ⁻¹⁸	29 - 280 (10.83%)
930	NR gi 302680280 ref XP_003029822.1 hypothetical protein SCHCODRAFT_236671 [Schizophyllum commune H4-8] >gnl BL_ORD_ID 2509379 hypothetical protein SCHCODRAFT_236671 [Schizophyllum commune H4-8]	312	1.17 x 10 ⁻¹⁷	1 - 276 (9.35%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
931	NR gi 316971911 gb EFV55633.1 mannose-6-phosphate isomerase [Trichinella spiralis]	269	1.99 x 10 ⁻¹⁷	1 - 246 (11.06%)
932	NR gi 255936431 ref XP_002559242.1 Pc13g08170 [Penicillium chrysogenum Wisconsin 54-1255] >gnl BL_ORD_ID 1123217 Pc13g08170 [Penicillium chrysogenum Wisconsin 54-1255]	297	1.99 x 10 ⁻¹⁷	8 - 279 (9.41%)
933	NR gi 71029746 ref XP_764516.1 mannose-6-phosphate isomerase [Theileria parva strain Muguga] >gnl BL_ORD_ID 316246 mannose-6-phosphate isomerase, putative [Theileria parva]	419	1.99 x 10 ⁻¹⁷	3 - 373 (6.44%)
934	NR gi 213025872 ref ZP_03340319.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. 404ty]	50	3.39 x 10 ⁻¹⁷	2 - 51 (172%)
935	NR gi 297296913 ref XP_002804916.1 PREDICTED: mannose-6-phosphate isomerase-like isoform 6 [Macaca mulatta] >gnl BL_ORD_ID 2231615 PREDICTED: mannose-6-phosphate isomerase-like isoform 7 [Macaca mulatta]	220	5.79 x 10 ⁻¹⁷	14 - 216 (14.67%)
936	NR gi 212540758 ref XP_002150534.1 mannose-6-phosphate isomerase, class I [Penicillium marneffei ATCC 18224] >gnl BL_ORD_ID 1052061 mannose-6-phosphate isomerase, class I [Penicillium marneffei ATCC 18224]	396	5.79 x 10 ⁻¹⁷	13 - 376 (5.93%)
937	NR gi 164499289 gb ABY59214.1 At1g67070 [Arabidopsis thaliana] >gnl BL_ORD_ID 2594891 At1g67070 [Arabidopsis thaliana]	197	7.56 x 10 ⁻¹⁷	183 - 372 (15.72%)
938	NR gi 297296905 ref XP_002804912.1 PREDICTED: mannose-6-phosphate isomerase-like isoform 2 [Macaca mulatta]	198	9.88 x 10 ⁻¹⁷	31 - 216 (17.09%)
939	NR gi 164499299 gb ABY59219.1 At1g67070 [Arabidopsis thaliana]	197	9.88 x 10 ⁻¹⁷	183 - 372 (15.72%)
940	NR gi 164499301 gb ABY59220.1 At1g67070 [Arabidopsis thaliana]	197	1.29 x 10 ⁻¹⁶	183 - 372 (15.72%)
941	NR gi 76157332 gb AAX28286.2 SJCHGC09301 protein [Schistosoma japonicum]	177	1.29 x 10 ⁻¹⁶	1 - 168 (21.71%)
942	NR gi 213023431 ref ZP_03337878.1 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Typhi str. 404ty]	57	1.68 x 10 ⁻¹⁶	46 - 102 (135.42%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
943	NR gi 164499297 gb ABY59218.1 At1g67070 [Arabidopsis thaliana] >gnl BL_ORD_ID 2594892 At1g67070 [Arabidopsis thaliana] >gnl BL_ORD_ID 2594892 At1g67070 [Arabidopsis thaliana]	197	1.68 x 10 ⁻¹⁶	183 - 372 (15.46%)
944	NR gi 255636465 gb ACU18571.1 unknown [Glycine max]	269	2.87 x 10 ⁻¹⁶	135 - 384 (10.78%)
945	NR gi 261599661 gb ACX85804.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	173	4.90 x 10 ⁻¹⁶	217 - 376 (20.72%)
945	NR gi 261599661 gb ACX85804.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	173	4.90 x 10 ⁻¹⁶	217 - 376 (20.72%)
946	NR gi 261599659 gb ACX85803.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	173	4.90 x 10 ⁻¹⁶	217 - 376 (20.72%)
946	NR gi 261599659 gb ACX85803.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	173	4.90 x 10 ⁻¹⁶	217 - 376 (20.72%)
947	NR gi 261599655 gb ACX85801.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 969102 mannose-6-phosphate isomerase [Anopheles sudaicus]	173	6.40 x 10 ⁻¹⁶	217 - 376 (20.72%)
947	NR gi 261599655 gb ACX85801.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 969102 mannose-6-phosphate isomerase [Anopheles sudaicus]	173	6.40 x 10 ⁻¹⁶	217 - 376 (20.72%)
948	NR gi 261599631 gb ACX85789.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 969095 mannose-6-phosphate isomerase [Anopheles sudaicus]	173	6.40 x 10 ⁻¹⁶	217 - 376 (20.72%)
948	NR gi 261599631 gb ACX85789.1 mannose-6-phosphate isomerase [Anopheles sudaicus] >gnl BL_ORD_ID 969095 mannose-6-phosphate isomerase [Anopheles sudaicus]	173	6.40 x 10 ⁻¹⁶	217 - 376 (20.72%)
949	NR gi 164499313 gb ABY59226.1 At1g67070 [Arabidopsis thaliana]	197	6.40 x 10 ⁻¹⁶	183 - 372 (15.20%)
950	NR gi 125524263 gb EAY72377.1 hypothetical protein Osl_00230 [Oryza sativa Indica Group]	201	6.40 x 10 ⁻¹⁶	180 - 371 (15.59%)
951	NR gi 226320534 ref ZP_03796098.1 mannose-6-phosphate isomerase [Borrelia burgdorferi 29805] >gnl BL_ORD_ID 736076 mannose-6-phosphate isomerase [Borrelia burgdorferi 29805]	134	1.09 x 10 ⁻¹⁵	6 - 139 (30.07%)
952	NR gi 115486163 ref NP_001068225.1 Os11g0600900 [Oryza sativa Japonica Group] >gnl BL_ORD_ID 543198 Os11g0600900 [Oryza sativa Japonica Group]	206	1.09 x 10 ⁻¹⁵	193 - 384 (16.26%)
953	NR gi 156089363 ref XP_001612088.1 phosphomannose isomerase type I family protein [Babesia bovis] >gnl BL_ORD_ID 2056927 phosphomannose isomerase type I family protein [Babesia bovis]	349	1.43 x 10 ⁻¹⁵	1 - 300 (7.64%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
954	NR gi 298708160 emb CBJ30500.1 Mannose-6-phosphate isomerase [Ectocarpus siliculosus]	163	1.86 x 10 ⁻¹⁵	1 - 155 (22.21%)
954	NR gi 298708160 emb CBJ30500.1 Mannose-6-phosphate isomerase [Ectocarpus siliculosus]	163	1.86 x 10 ⁻¹⁵	1 - 155 (22.21%)
955	NR gi 67474993 ref XP_653227.1 phosphomannose isomerase [Entamoeba histolytica HM-1:IMSS] >gnl BL_ORD_ID 220166 phosphomannose isomerase, putative [Entamoeba histolytica HM-1:IMSS]	297	4.15 x 10 ⁻¹⁵	1 - 287 (8.84%)
956	NR gi 320587024 gb EFW99671.1 mannose-6-phosphate isomerase class 1 [Grosmania clavigera kw1407]	290	5.42 x 10 ⁻¹⁵	135 - 376 (9.04%)
957	NR gi 227937356 gb ACP43318.1 mannose-6-phosphate isomerase [Citrus maxima]	202	1.21 x 10 ⁻¹⁴	193 - 386 (14.95%)
958	NR gi 167385334 ref XP_001737303.1 mannose-6-phosphate isomerase [Entamoeba dispar SAW760] >gnl BL_ORD_ID 2605172 mannose-6-phosphate isomerase, putative [Entamoeba dispar SAW760]	299	1.21 x 10 ⁻¹⁴	1 - 287 (8.95%)
959	NR gi 226320977 ref ZP_03796523.1 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi 29805] >gnl BL_ORD_ID 736140 mannose-6-phosphate isomerase, class I [Borrelia burgdorferi 29805]	163	2.69 x 10 ⁻¹⁴	220 - 382 (21.08%)
960	NR gi 299469685 emb CBN76539.1 Mannose-6-phosphate isomerase [Ectocarpus siliculosus]	162	3.51 x 10 ⁻¹⁴	2 - 155 (20.57%)
961	NR gi 10834550 gb AAG23720.1 AF159377_1 phosphomannose isomerase [Arabidopsis thaliana]	173	7.83 x 10 ⁻¹⁴	1 - 156 (19.71%)
962	NR gi 297296907 ref XP_002804913.1 PREDICTED: mannose-6-phosphate isomerase-like isoform 3 [Macaca mulatta]	222	1.02 x 10 ⁻¹³	7 - 216 (14.41%)
963	NR gi 268325456 emb CBH39044.1 hypothetical protein, putative phosphomannomutase/mannose-6-phosphate isomerase fusion protein [uncultured archaeon] >gnl BL_ORD_ID 1082790 hypothetical protein, putative phosphomannomutase/mannose-6-phosphate isomerase fusion protein [uncultured archaeon]	334	1.33 x 10 ⁻¹³	8 - 305 (7.62%)
964	NR gi 28631110 gb AAO49672.1 putative phosphomannose isomerase [Haemophilus influenzae] >gnl BL_ORD_ID 2365812 unnamed protein product [Haemophilus influenzae 10810]	194	1.74 x 10 ⁻¹³	135 - 315 (17.27%)
965	NR gi 298705510 emb CBJ28777.1 Mannose-6-phosphate isomerase, N-terminal fragment [Ectocarpus siliculosus]	177	2.28 x 10 ⁻¹³	1 - 154 (19.15%)
966	NR gi 289607868 emb CBI60706.1 unnamed protein product [Sordaria macrospora]	217	2.97 x 10 ⁻¹³	3 - 204 (13.80%)
967	NR gi 239788515 dbj BAH70933.1 ACYPI000187 [Acyrtosiphon pisum]	163	2.97 x 10 ⁻¹³	8 - 161 (24.09%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
968	NR gi 118095540 ref XP_001233064.1 PREDICTED: hypothetical protein [Gallus gallus]	192	6.63 x 10 ⁻¹³	36 - 211 (17.09%)
969	NR gi 261599605 gb ACX85776.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	78	1.48 x 10 ⁻¹²	227 - 304 (64.10%)
970	NR gi 221506650 gb EEE32267.1 mannose-6-phosphate isomerase, putative [Toxoplasma gondii VEG]	139	1.48 x 10 ⁻¹²	173 - 294 (26.40%)
971	NR gi 237831779 ref XP_002365187.1 mannose-6-phosphate isomerase, putative [Toxoplasma gondii ME49] >gnl BL_ORD_ID 1143204 mannose-6-phosphate isomerase, putative [Toxoplasma gondii ME49]	139	1.48 x 10 ⁻¹²	173 - 294 (26.40%)
972	NR gi 308452055 ref XP_003088900.1 hypothetical protein CRE_16544 [Caenorhabditis remanei] >gnl BL_ORD_ID 241817 hypothetical protein CRE_16544 [Caenorhabditis remanei]	181	2.52 x 10 ⁻¹²	217 - 384 (17.70%)
973	NR gi 221486965 gb EEE25211.1 mannose-6-phosphate isomerase, putative [Toxoplasma gondii GT1]	139	7.33 x 10 ⁻¹²	173 - 294 (25.88%)
974	NR gi 38048667 gb AAR10236.1 similar to Drosophila melanogaster CG8417 [Drosophila yakuba]	160	1.63 x 10 ⁻¹¹	3 - 154 (23.05%)
975	NR gi 115396184 ref XP_001213731.1 ADP-L-glycero-D-manno-heptose-6-epimerase [Aspergillus terreus NIH2624] >gnl BL_ORD_ID 579529 ADP-L-glycero-D-manno-heptose-6-epimerase [Aspergillus terreus NIH2624]	159	4.75 x 10 ⁻¹¹	217 - 364 (17.80%)
976	NR gi 261599663 gb ACX85805.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	122	1.38 x 10 ⁻¹⁰	25 - 142 (32.25%)
977	NR gi 261599593 gb ACX85770.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	122	3.08 x 10 ⁻¹⁰	25 - 142 (32.25%)
978	NR gi 261599621 gb ACX85784.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	120	5.25 x 10 ⁻¹⁰	25 - 140 (32.64%)
979	NR gi 298705511 emb CBJ28778.1 Mannose-6-phosphate isomerase, C-terminal fragment [Ectocarpus siliculosus]	96	6.86 x 10 ⁻¹⁰	233 - 317 (44.49%)
980	NR gi 261599589 gb ACX85768.1 mannose-6-phosphate isomerase [Anopheles sudaicus]	120	1.17 x 10 ⁻⁹	25 - 140 (32.64%)
981	NR gi 213423046 ref ZP_03356064.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. E01-6750]	34	3.40 x 10 ⁻⁹	206 - 239 (259.53%)
982	NR gi 169614804 ref XP_001800818.1 hypothetical protein SNOG_10550 [Phaeosphaeria nodorum SN15] >gnl BL_ORD_ID 2381082 hypothetical protein SNOG_10550 [Phaeosphaeria nodorum SN15]	131	3.76 x 10 ⁻⁸	8 - 130 (26.80%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
983	NR gi 242048130 ref XP_002461811.1 hypothetical protein SORBIDRAFT_02g008440 [Sorghum bicolor] >gn BL_ORD_ID 216666 hypothetical protein SORBIDRAFT_02g008440 [Sorghum bicolor]	152	6.42 x 10 ⁻⁸	135 - 272 (20.34%)
984	NR gi 297296909 ref XP_002804914.1 PREDICTED: mannose-6-phosphate isomerase-like isoform 4 [Macaca mulatta]	229	2.44 x 10 ⁻⁷	7 - 216 (10.87%)
985	NR gi 70948191 ref XP_743638.1 hypothetical protein [Plasmodium chabaudi chabaudi] >gn BL_ORD_ID 1374501 conserved hypothetical protein [Plasmodium chabaudi chabaudi]	81	2.44 x 10 ⁻⁷	214 - 294 (41.15%)
986	NR gi 68071641 ref XP_677734.1 hypothetical protein [Plasmodium berghei strain ANKA] >gn BL_ORD_ID 1385626 hypothetical protein PB000597.02.0 [Plasmodium berghei]	75	1.21 x 10 ⁻⁶	220 - 294 (46.23%)
987	NR gi 913619 gb AAB32921.1 type I phosphomannose isomerase, type I PMI [Pneumocystis carinii, rat lung isolate, Peptide Partial, 134 aa]	133	1.58 x 10 ⁻⁶	130 - 249 (24.31%)
988	NR gi 83318149 ref XP_731469.1 phosphomannose isomerase type I [Plasmodium yoelii yoelii str. 17XNL] >gn BL_ORD_ID 36142 Phosphomannose isomerase type I, putative [Plasmodium yoelii yoelii]	75	1.58 x 10 ⁻⁶	220 - 294 (48%)
989	NR gi 164658824 ref XP_001730537.1 hypothetical protein MGL_2333 [Malassezia globosa CBS 7966] >gn BL_ORD_ID 2334957 hypothetical protein MGL_2333 [Malassezia globosa CBS 7966]	90	2.06 x 10 ⁻⁶	1 - 79 (44.44%)
990	NR gi 213419677 ref ZP_03352743.1 mannose-6-phosphate isomerase, class I [Salmonella enterica subsp. enterica serovar Typhi str. E01-6750] >gn BL_ORD_ID 1221076 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. AG3]	40	3.52 x 10 ⁻⁶	352 - 391 (181.25%)
991	NR gi 156082223 ref XP_001608600.1 mannose-6-phosphate isomerase [Plasmodium vivax Sal-1] >gn BL_ORD_ID 1719090 mannose-6-phosphate isomerase, putative [Plasmodium vivax]	85	6.01 x 10 ⁻⁶	211 - 295 (37.36%)
992	NR gi 227549547 ref ZP_03979596.1 conserved hypothetical protein [Corynebacterium lipophiloflavum DSM 44291] >gn BL_ORD_ID 2252601 conserved hypothetical protein [Corynebacterium lipophiloflavum DSM 44291]	115	7.84 x 10 ⁻⁶	266 - 380 (31.76%)
993	NR gi 109085398 ref XP_001118322.1 PREDICTED: mannose-6-phosphate isomerase-like isoform 1 [Macaca mulatta]	120	7.84 x 10 ⁻⁶	263 - 374 (28.48%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
994	NR gi 317131822 ref YP_004091136.1 glucokinase, ROK family [Ethanolgenens harbinense YUAN-3] >gnl BL_ORD_ID 1555809 glucokinase, ROK family [Ethanolgenens harbinense YUAN-3]	100	1.02 x 10 ⁻⁵	3 - 101 (34%)
995	NR gi 221052170 ref XP_002257661.1 mannose-6-phosphate isomerase [Plasmodium knowlesi strain H] >gnl BL_ORD_ID 524863 mannose-6-phosphate isomerase, putative [Plasmodium knowlesi strain H]	75	1.02 x 10 ⁻⁵	220 - 294 (48%)
996	NR gi 228472729 ref ZP_04057487.1 mannose-6-phosphate isomerase, class I [Capnocytophaga gingivalis ATCC 33624] >gnl BL_ORD_ID 2428736 mannose-6-phosphate isomerase, class I [Capnocytophaga gingivalis ATCC 33624]	102	1.34 x 10 ⁻⁵	13 - 105 (40.37%)
997	NR gi 124512730 ref XP_001349498.1 mannose-6-phosphate isomerase, putative [Plasmodium falciparum 3D7] >gnl BL_ORD_ID 2587016 mannose-6-phosphate isomerase, putative [Plasmodium falciparum 3D7]	81	1.34 x 10 ⁻⁵	214 - 294 (39.63%)
998	NR gi 76155603 gb AAAX26894.2 SJCHGC01797 protein [Schistosoma japonicum]	129	1.75 x 10 ⁻⁵	256 - 352 (25.24%)
999	NR gi 297298833 ref XP_002805289.1 PREDICTED: mannose-6-phosphate isomerase-like isoform 2 [Macaca mulatta]	117	2.98 x 10 ⁻⁵	266 - 374 (29.22%)
1000	NR gi 269120418 ref YP_003308595.1 mannose-6-phosphate isomerase, class I [Sebaldella termitidis ATCC 33386] >gnl BL_ORD_ID 2749627 mannose-6-phosphate isomerase, class I [Sebaldella termitidis ATCC 33386]	103	6.64 x 10 ⁻⁵	13 - 108 (33.93%)
1001	NR gi 46451849 gb AAS98025.1 mannose-6-phosphate isomerase [Plutella xylostella]	120	8.67 x 10 ⁻⁵	126 - 231 (25%)
1002	NR gi 294616329 ref ZP_06696122.1 mannose-6-phosphate isomerase [Enterococcus faecium E1636] >gnl BL_ORD_ID 1811358 mannose-6-phosphate isomerase [Enterococcus faecium E1636]	100	0.0001	9 - 107 (37%)
1003	NR gi 218282799 ref ZP_03488963.1 hypothetical protein EUBIFOR_01549 [Eubacterium bifforme DSM 3989] >gnl BL_ORD_ID 1387157 hypothetical protein EUBIFOR_01549 [Eubacterium bifforme DSM 3989]	100	0.0001	3 - 101 (36%)
1004	NR gi 305667782 ref YP_003864069.1 mannose-6-phosphate isomerase [Maribacter sp. HTCC2170] >gnl BL_ORD_ID 628064 mannose-6-phosphate isomerase [Maribacter sp. HTCC2170]	101	0.0001	13 - 105 (37.25%)
1005	NR gi 310778550 ref YP_003966883.1 mannose-6-phosphate isomerase, type 1 [Ilyobacter polytropus DSM 2926] >gnl BL_ORD_ID 366651 mannose-6-phosphate isomerase, type 1 [Ilyobacter polytropus DSM 2926]	93	0.0002	13 - 101 (39.31%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1006	NR gi 291459410 ref ZP_06598800.1 mannose-6-phosphate isomerase, class I [Oribacterium sp. oral taxon 078 str. F0262] >gnl BL_ORD_ID 1716557 mannose-6-phosphate isomerase, class I [Oribacterium sp. oral taxon 078 str. F0262]	100	0.0002	3 - 101 (36%)
1007	NR gi 291458174 ref ZP_06597564.1 mannose-6-phosphate isomerase, class I [Oribacterium sp. oral taxon 078 str. F0262] >gnl BL_ORD_ID 1715188 mannose-6-phosphate isomerase, class I [Oribacterium sp. oral taxon 078 str. F0262]	112	0.0003	3 - 108 (29.50%)
1008	NR gi 237736533 ref ZP_04567014.1 mannose-6-phosphate isomerase [Fusobacterium mortiferum ATCC 9817] >gnl BL_ORD_ID 2679284 mannose-6-phosphate isomerase [Fusobacterium mortiferum ATCC 9817]	91	0.0003	13 - 101 (39.85%)
1009	NR gi 227871830 ref ZP_03990232.1 possible mannose-6-phosphate isomerase [Oribacterium sinus F0268] >gnl BL_ORD_ID 2380649 possible mannose-6-phosphate isomerase [Oribacterium sinus F0268]	110	0.0003	3 - 101 (28.93%)
1010	NR gi 183233488 ref XP_001913867.1 mannose-6-phosphate isomerase [Entamoeba histolytica HM-1:IMSS] >gnl BL_ORD_ID 86982 mannose-6-phosphate isomerase, putative [Entamoeba histolytica HM-1:IMSS]	70	0.0003	218 - 287 (55.10%)
1011	NR gi 257126867 ref YP_003164981.1 mannose-6-phosphate isomerase, class I [Leptotrichia buccalis DSM 1135] >gnl BL_ORD_ID 2442619 mannose-6-phosphate isomerase, class I [Leptotrichia buccalis C-1013-b]	106	0.0003	13 - 116 (32.04%)
1012	NR gi 163789464 ref ZP_02183903.1 mannose-6-phosphate isomerase [Carnobacterium sp. AT7] >gnl BL_ORD_ID 2355255 mannose-6-phosphate isomerase [Carnobacterium sp. AT7]	107	0.0003	8 - 108 (32.32%)
1013	NR gi 295105410 emb CBL02954.1 mannose-6-phosphate isomerase, class I [Faecalibacterium prausnitzii SL3/3]	102	0.0004	1 - 101 (36.52%)
1014	NR gi 292669464 ref ZP_06602890.1 mannose-6-phosphate isomerase [Selenomonas noxia ATCC 43541] >gnl BL_ORD_ID 1851743 mannose-6-phosphate isomerase [Selenomonas noxia ATCC 43541]	100	0.0004	3 - 101 (34%)
1015	NR gi 260891046 ref ZP_05902309.1 mannose-6-phosphate isomerase, class I [Leptotrichia hofstadii F0254] >gnl BL_ORD_ID 893491 mannose-6-phosphate isomerase, class I [Leptotrichia hofstadii F0254]	106	0.0006	13 - 116 (31.15%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1016	NR gi 225027712 ref ZP_03716904.1 hypothetical protein EUBHAL_01971 [Eubacterium hallii DSM 3353] >gnl BL_ORD_ID 1905617 hypothetical protein EUBHAL_01971 [Eubacterium hallii DSM 3353]	100	0.0006	3 - 101 (37%)
1017	NR gi 323532813 gb EGB22686.1 mannose-6-phosphate isomerase, class I [Desulfotomaculum nigrificans DSM 574]	95	0.0007	9 - 101 (35.45%)
1018	NR gi 302876011 ref YP_003844644.1 mannose-6-phosphate isomerase, class I [Clostridium cellulovorans 743B] >gnl BL_ORD_ID 246577 mannose-6-phosphate isomerase, class I [Clostridium cellulovorans 743B] >gnl BL_ORD_ID 246577 mannose-6-phosphate isomerase, class I [Clostridium cellulovorans 743B]	160	0.0007	235 - 388 (16.01%)
1019	NR gi 115698976 ref XP_001178670.1 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus] >gnl BL_ORD_ID 699287 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus]	137	0.0007	258 - 374 (21.31%)
1020	NR gi 297296917 ref XP_002804918.1 PREDICTED: mannose-6-phosphate isomerase-like isoform 8 [Macaca mulatta]	142	0.0010	86 - 216 (20.33%)
1021	NR gi 323343069 ref ZP_08083300.1 mannose-6-phosphate isomerase [Erysipelothrix rhusiopathiae ATCC 19414] >gnl BL_ORD_ID 776326 mannose-6-phosphate isomerase [Erysipelothrix rhusiopathiae ATCC 19414]	112	0.0010	3 - 108 (30.29%)
1022	NR gi 304317428 ref YP_003852573.1 mannose-6-phosphate isomerase, class I [Thermoanaerobacterium thermosaccharolyticum DSM 571] >gnl BL_ORD_ID 441656 mannose-6-phosphate isomerase, class I [Thermoanaerobacterium thermosaccharolyticum DSM 571]	103	0.0013	13 - 108 (31.11%)
1023	NR gi 60115681 ref YP_209472.1 putative mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67] >gnl BL_ORD_ID 1772916 putative mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]	96	0.0013	293 - 387 (36.90%)
1024	NR gi 322804692 emb CBZ02244.1 mannose-6-phosphate isomerase [Clostridium botulinum H04402 065]	113	0.0016	3 - 114 (27.41%)
1025	NR gi 299142914 ref ZP_07036041.1 mannose-6-phosphate isomerase, class I [Prevotella oris C735] >gnl BL_ORD_ID 2369848 mannose-6-phosphate isomerase, class I [Prevotella oris C735]	91	0.0016	13 - 101 (39.85%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1026	NR gi 281424045 ref ZP_06254958.1 mannose-6-phosphate isomerase, class I [Prevotella oris F0302] >gnl BL_ORD_ID 1288976 mannose-6-phosphate isomerase, class I [Prevotella oris F0302]	91	0.0016	13 - 101 (39.85%)
1027	NR gi 261878968 ref ZP_06005395.1 mannose-6-phosphate isomerase [Prevotella bergensis DSM 17361] >gnl BL_ORD_ID 954606 mannose-6-phosphate isomerase [Prevotella bergensis DSM 17361]	93	0.0016	13 - 101 (40.46%)
1028	NR gi 262038733 ref ZP_06012093.1 mannose-6-phosphate isomerase, class I [Leptotrichia goodfellowii F0264] >gnl BL_ORD_ID 948848 mannose-6-phosphate isomerase, class I [Leptotrichia goodfellowii F0264]	103	0.0016	13 - 108 (32.05%)
1029	NR gi 253583630 ref ZP_04860828.1 mannose-6-phosphate isomerase [Fusobacterium varium ATCC 27725] >gnl BL_ORD_ID 287779 mannose-6-phosphate isomerase [Fusobacterium varium ATCC 27725]	91	0.0016	13 - 101 (38.64%)
1030	NR gi 168239748 ref ZP_02664806.1 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. SL480] >gnl BL_ORD_ID 2835051 mannose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. SL480]	84	0.0016	305 - 387 (45.36%)
1031	NR gi 257468226 ref ZP_05632322.1 mannose-6-phosphate isomerase, class I [Fusobacterium ulcerans ATCC 49185] >gnl BL_ORD_ID 671750 phosphohexomutase [Fusobacterium ulcerans ATCC 49185] >gnl BL_ORD_ID 671750 phosphohexomutase [Fusobacterium ulcerans ATCC 49185]	91	0.0021	13 - 101 (37.44%)
1032	NR gi 170760632 ref YP_001785752.1 mannose-6-phosphate isomerase, class I [Clostridium botulinum A3 str. Loch Maree] >gnl BL_ORD_ID 75001 mannose-6-phosphate isomerase, class I [Clostridium botulinum A3 str. Loch Maree]	101	0.0021	3 - 102 (31.37%)
1033	NR gi 168181280 ref ZP_02615944.1 mannose-6-phosphate isomerase, class I [Clostridium botulinum Bf] >gnl BL_ORD_ID 2854080 mannose-6-phosphate isomerase, class I [Clostridium botulinum Ba4 str. 657] >gnl BL_ORD_ID 2854080 mannose-6-phosphate isomerase, class I [Clostridium botulinum Bf] >gnl BL_ORD_ID 2854080 mannose-6-phosphate isomerase, class I [Clostridium botulinum Ba4 str. 657]	101	0.0021	3 - 102 (30.39%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1034	NR gi 319953915 ref YP_004165182.1 mannose-6-phosphate isomerase, type 1 [Cellulophaga algicola DSM 14237] >gnl BL_ORD_ID 1028184 mannose-6-phosphate isomerase, type 1 [Cellulophaga algicola DSM 14237]	56	0.0028	57 - 105 (82.91%)
1035	NR gi 283782398 ref YP_003373153.1 mannose-6-phosphate isomerase, class I [Pirellula staleyi DSM 6068] >gnl BL_ORD_ID 1353944 mannose-6-phosphate isomerase, class I [Pirellula staleyi DSM 6068]	95	0.0028	8 - 101 (34.35%)
1036	NR gi 228911375 ref ZP_04075177.1 ManA (Mannose-6-phosphate isomerase) [Bacillus thuringiensis IBL 200] >gnl BL_ORD_ID 2596576 ManA (Mannose-6-phosphate isomerase) [Bacillus thuringiensis IBL 200]	96	0.0028	13 - 107 (41.23%)
1037	NR gi 187776978 ref ZP_02993451.1 hypothetical protein CLOSP0_00523 [Clostridium sporogenes ATCC 15579] >gnl BL_ORD_ID 315169 hypothetical protein CLOSP0_00523 [Clostridium sporogenes ATCC 15579]	101	0.0028	3 - 102 (30.39%)
1038	NR gi 157363545 ref YP_001470312.1 mannose-6-phosphate isomerase type I [Thermotoga lettingae TMO] >gnl BL_ORD_ID 2199638 mannose-6-phosphate isomerase type I [Thermotoga lettingae TMO]	100	0.0028	3 - 101 (32%)
1039	NR gi 149372353 ref ZP_01891541.1 mannose-6-phosphate isomerase [unidentified eubacterium SCB49] >gnl BL_ORD_ID 1804988 mannose-6-phosphate isomerase [unidentified eubacterium SCB49]	71	0.0028	33 - 101 (61.49%)
1040	NR gi 152974973 ref YP_001374490.1 mannose-6-phosphate isomerase, class I [Bacillus cereus subsp. cytotoxis NVH 391-98] >gnl BL_ORD_ID 693941 mannose-6-phosphate isomerase, class I [Bacillus cytotoxicus NVH 391-98]	96	0.0036	13 - 107 (41.23%)
1041	NR gi 170757517 ref YP_001780066.1 mannose-6-phosphate isomerase, class I [Clostridium botulinum B1 str. Okra] >gnl BL_ORD_ID 41128 mannose-6-phosphate isomerase, class I [Clostridium botulinum B1 str. Okra]	112	0.0048	3 - 113 (27.11%)
1042	NR gi 153939247 ref YP_001389783.1 mannose-6-phosphate isomerase, class I [Clostridium botulinum F str. Langeland] >gnl BL_ORD_ID 1999046 mannose-6-phosphate isomerase, class I [Clostridium botulinum F str. Langeland] >gnl BL_ORD_ID 1999046 mannose-6-phosphate isomerase, class I [Clostridium botulinum F str. 230613]	112	0.0048	3 - 113 (27.11%)
1043	NR gi 58651775 emb CAI50955.1 mannose-6-phosphate isomerase [uncultured bacterium]	91	0.0048	13 - 101 (36.23%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1044	NR gi 67585381 ref XP_665100.1 hypothetical protein [Cryptosporidium hominis TU502] >gnl BL_ORD_ID 210938 hypothetical protein Chro.80224 [Cryptosporidium hominis]	104	0.0048	266 - 352 (26.81%)
1045	NR gi 323536132 gb EGB25905.1 mannose-6-phosphate isomerase, class I [Thermoanaerobacterium xylanolyticum LX-11]	90	0.01	13 - 101 (37.03%)
1046	NR gi 322516497 ref ZP_08069415.1 mannose-6-phosphate isomerase [Streptococcus vestibularis ATCC 49124] >gnl BL_ORD_ID 1227432 mannose-6-phosphate isomerase [Streptococcus vestibularis ATCC 49124]	113	0.01	4 - 108 (28.97%)
1047	NR gi 315224746 ref ZP_07866569.1 mannose-6-phosphate isomerase [Capnocytophaga ochracea F0287] >gnl BL_ORD_ID 753870 mannose-6-phosphate isomerase [Capnocytophaga ochracea F0287]	101	0.01	13 - 105 (37.25%)
1048	NR gi 313681053 ref YP_004058792.1 mannose-6-phosphate isomerase, type 1 [Oceanithermus profundus DSM 14977] >gnl BL_ORD_ID 637718 mannose-6-phosphate isomerase, type 1 [Oceanithermus profundus DSM 14977]	115	0.01	13 - 121 (27.22%)
1049	NR gi 256819303 ref YP_003140582.1 mannose-6-phosphate isomerase, class I [Capnocytophaga ochracea DSM 7271] >gnl BL_ORD_ID 2618157 mannose-6-phosphate isomerase, class I [Capnocytophaga ochracea DSM 7271]	101	0.01	13 - 105 (37.25%)
1050	NR gi 258512113 ref YP_003185547.1 mannose-6-phosphate isomerase, class I [Alicyclobacillus acidocaldarius subsp. acidocaldarius DSM 446] >gnl BL_ORD_ID 2417272 mannose-6-phosphate isomerase, class I [Alicyclobacillus acidocaldarius subsp. acidocaldarius DSM 446]	115	0.01	13 - 123 (27.97%)
1051	NR gi 260588874 ref ZP_05854787.1 mannose-6-phosphate isomerase, class I [Blautia hansenii DSM 20583] >gnl BL_ORD_ID 2051564 mannose-6-phosphate isomerase, class I [Blautia hansenii DSM 20583]	100	0.01	3 - 101 (35%)
1052	NR gi 213961855 ref ZP_03390121.1 mannose-6-phosphate isomerase, class I [Capnocytophaga sputigena Capno] >gnl BL_ORD_ID 1253519 mannose-6-phosphate isomerase, class I [Capnocytophaga sputigena Capno]	101	0.01	13 - 105 (37.25%)
1053	NR gi 194015294 ref ZP_03053910.1 mannose-6-phosphate isomerase, class I [Bacillus pumilus ATCC 7061] >gnl BL_ORD_ID 564975 mannose-6-phosphate isomerase, class I [Bacillus pumilus ATCC 7061]	104	0.01	4 - 106 (33.29%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1054	NR gi 157693986 ref YP_001488448.1 mannose-6-phosphate isomerase [Bacillus pumilus SAFR-032] >gnl BL_ORD_ID 2231160 mannose-6-phosphate isomerase [Bacillus pumilus SAFR-032]	104	0.01	4 - 106 (33.29%)
1055	NR gi 148378415 ref YP_001252956.1 mannose-6-phosphate isomerase, class I [Clostridium botulinum A str. ATCC 3502] >gnl BL_ORD_ID 1659559 mannose-6-phosphate isomerase, class I [Clostridium botulinum A str. ATCC 19397] >gnl BL_ORD_ID 1659559 mannose-6-phosphate isomerase, class I [Clostridium botulinum A str. Hall] >gnl BL_ORD_ID 1659559 mannose-6-phosphate isomerase [Clostridium botulinum A str. ATCC 3502] >gnl BL_ORD_ID 1659559 mannose-6-phosphate isomerase, class I [Clostridium botulinum A str. ATCC 19397] >gnl BL_ORD_ID 1659559 mannose-6-phosphate isomerase, class I [Clostridium botulinum A str. Hall]	101	0.01	3 - 102 (29.41%)
1056	NR gi 86134627 ref ZP_01053209.1 phosphomannose isomerase type I [Polaribacter sp. MED152] >gnl BL_ORD_ID 576444 phosphomannose isomerase type I [Polaribacter sp. MED152]	107	0.01	13 - 116 (32.32%)
1057	NR gi 309792794 ref ZP_07687237.1 mannose-6-phosphate isomerase [Oscillochloris trichoides DG6] >gnl BL_ORD_ID 228472 mannose-6-phosphate isomerase [Oscillochloris trichoides DG6]	116	0.01	13 - 122 (27.50%)
1058	NR gi 317131872 ref YP_004091186.1 mannose-6-phosphate isomerase, class I [Ethanoligenens harbinense YUAN-3] >gnl BL_ORD_ID 1554546 mannose-6-phosphate isomerase, class I [Ethanoligenens harbinense YUAN-3]	100	0.01	3 - 101 (33%)
1059	NR gi 253578768 ref ZP_04856039.1 mannose-6-phosphate isomerase [Ruminococcus sp. 5_1_39B_FAA] >gnl BL_ORD_ID 300560 mannose-6-phosphate isomerase [Ruminococcus sp. 5_1_39BFAA]	96	0.01	9 - 101 (39.06%)
1060	NR gi 254479757 ref ZP_05093037.1 mannose-6-phosphate isomerase, class I [Carboxydibrachium pacificum DSM 12653] >gnl BL_ORD_ID 1344012 mannose-6-phosphate isomerase, class I [Carboxydibrachium pacificum DSM 12653]	102	0.01	13 - 113 (29.79%)
1061	NR gi 167772424 ref ZP_02444477.1 hypothetical protein ANACOL_03801 [Anaerotruncus colihominis DSM 17241] >gnl BL_ORD_ID 2727949 hypothetical protein ANACOL_03801 [Anaerotruncus colihominis DSM 17241]	95	0.01	9 - 101 (34.35%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1062	NR gi 89890642 ref ZP_01202152.1 mannose-6-phosphate isomerase [Flavobacteria bacterium BBFL7] >gnl BL_ORD_ID 154334 mannose-6-phosphate isomerase [Flavobacteria bacterium BBFL7]	151	0.01	13 - 150 (20.17%)
1063	NR gi 20808170 ref NP_623341.1 phosphomannose isomerase [Thermoanaerobacter tengcongensis MB4] >gnl BL_ORD_ID 1685364 Phosphomannose isomerase [Thermoanaerobacter tengcongensis MB4]	102	0.01	13 - 113 (29.79%)
1064	NR gi 53712946 ref YP_098938.1 mannose-6-phosphate isomerase [Bacteroides fragilis YCH46] >gnl BL_ORD_ID 1330507 putative mannose-6-phosphate isomerase [Bacteroides fragilis NCTC 9343] >gnl BL_ORD_ID 1330507 mannose-6-phosphate isomerase [Bacteroides sp. 3_2_5] >gnl BL_ORD_ID 1330507 mannose-6-phosphate isomerase, class I [Bacteroides sp. 2_1_16] >gnl BL_ORD_ID 1330507 mannose-6-phosphate isomerase [Bacteroides fragilis YCH46] >gnl BL_ORD_ID 1330507 putative mannose-6-phosphate isomerase [Bacteroides fragilis NCTC 9343] >gnl BL_ORD_ID 1330507 mannose-6-phosphate isomerase [Bacteroides sp. 3_2_5] >gnl BL_ORD_ID 1330507 mannose-6-phosphate isomerase, class I [Bacteroides sp. 2_1_16] >gnl BL_ORD_ID 1330507 putative mannose-6-phosphate isomerase [Bacteroides fragilis 638R]	134	0.01	27 - 142 (22.28%)
1065	NR gi 319745641 gb EFV97941.1 mannose-6-phosphate isomerase [Streptococcus agalactiae ATCC 13813]	108	0.01	7 - 108 (32.58%)
1066	NR gi 317502612 ref ZP_07960733.1 mannose-6-phosphate isomerase [Prevotella salivae DSM 15606] >gnl BL_ORD_ID 858935 mannose-6-phosphate isomerase [Prevotella salivae DSM 15606]	72	0.01	32 - 101 (54.01%)
1067	NR gi 297622433 ref YP_003703867.1 mannose-6-phosphate isomerase, class I [Truepera radiovictrix DSM 17093] >gnl BL_ORD_ID 2208186 mannose-6-phosphate isomerase, class I [Truepera radiovictrix DSM 17093]	116	0.01	13 - 122 (25.27%)
1068	NR gi 269124075 ref YP_003306652.1 Mannose-6-phosphate isomerase [Streptobacillus moniliformis DSM 12112] >gnl BL_ORD_ID 2729784 Mannose-6-phosphate isomerase [Streptobacillus moniliformis DSM 12112]	106	0.01	13 - 116 (31.15%)
1069	NR gi 224025909 ref ZP_03644275.1 hypothetical protein BACCOPRO_02655 [Bacteroides coprophilus DSM 18228] >gnl BL_ORD_ID 1816479 hypothetical protein BACCOPRO_02655 [Bacteroides coprophilus DSM 18228]	106	0.01	13 - 116 (28.48%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1070	NR gi 315641841 ref ZP_07896845.1 mannose-6-phosphate isomerase [Enterococcus italicus DSM 15952] >gnl BL_ORD_ID 827087 mannose-6-phosphate isomerase [Enterococcus italicus DSM 15952]	105	0.01	9 - 108 (30.84%)
1071	NR gi 293401845 ref ZP_06645986.1 mannose-6-phosphate isomerase, class I [Erysipelotrichaceae bacterium 5_2_54FAA] >gnl BL_ORD_ID 1696067 mannose-6-phosphate isomerase, class I [Erysipelotrichaceae bacterium 5_2_54FAA]	170	0.01	235 - 387 (14.19%)
1072	NR gi 256961171 ref ZP_05565342.1 mannose-6-phosphate isomerase [Enterococcus faecalis Merz96] >gnl BL_ORD_ID 614724 mannose-6-phosphate isomerase, class I [Enterococcus faecalis R712] >gnl BL_ORD_ID 614724 mannose-6-phosphate isomerase, class I [Enterococcus faecalis S613] >gnl BL_ORD_ID 614724 mannose-6-phosphate isomerase, class I [Enterococcus faecalis DAPTO 512] >gnl BL_ORD_ID 614724 mannose-6-phosphate isomerase, class I [Enterococcus faecalis DAPTO 516] >gnl BL_ORD_ID 614724 mannose-6-phosphate isomerase [Enterococcus faecalis Merz96] >gnl BL_ORD_ID 614724 mannose-6-phosphate isomerase, class I [Enterococcus faecalis R712] >gnl BL_ORD_ID 614724 mannose-6-phosphate isomerase, class I [Enterococcus faecalis S613] >gnl BL_ORD_ID 614724 mannose-6-phosphate isomerase, class I [Enterococcus faecalis DAPTO 512] >gnl BL_ORD_ID 614724 mannose-6-phosphate isomerase, class I [Enterococcus faecalis DAPTO 516]	105	0.01	9 - 108 (33.56%)
1073	NR gi 255281858 ref ZP_05346413.1 mannose-6-phosphate isomerase, class I [Bryantella formatexigens DSM 14469] >gnl BL_ORD_ID 2034496 mannose-6-phosphate isomerase, class I [Bryantella formatexigens DSM 14469]	100	0.01	3 - 101 (35%)
1074	NR gi 146298030 ref YP_001192621.1 mannose-6-phosphate isomerase, class I [Flavobacterium johnsoniae UW101] >gnl BL_ORD_ID 181737 mannose-6-phosphate isomerase, class I [Flavobacterium johnsoniae UW101]	56	0.01	57 - 105 (86.09%)
1075	NR gi 86144085 ref ZP_01062423.1 mannose-6-phosphate isomerase [Leeuwenhoekiella blandensis MED217] >gnl BL_ORD_ID 584686 mannose-6-phosphate isomerase [Leeuwenhoekiella blandensis MED217]	101	0.01	13 - 111 (34.31%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1076	NR gi 319902656 ref YP_004162384.1 mannose-6-phosphate isomerase, type 1 [Bacteroides helcogenes P 36-108] >gnl BL_ORD_ID 1023333 mannose-6-phosphate isomerase, type 1 [Bacteroides helcogenes P 36-108]	87	0.02	27 - 105 (43.60%)
1077	NR gi 312868334 ref ZP_07728534.1 mannose-6-phosphate isomerase, class I [Streptococcus parasanguinis F0405] >gnl BL_ORD_ID 440970 mannose-6-phosphate isomerase, class I [Streptococcus parasanguinis F0405]	107	0.02	8 - 108 (32.32%)
1078	NR gi 304383475 ref ZP_07365937.1 mannose-6-phosphate isomerase [Prevotella marshii DSM 16973] >gnl BL_ORD_ID 2847004 mannose-6-phosphate isomerase [Prevotella marshii DSM 16973]	92	0.02	13 - 102 (40.17%)
1079	NR gi 296875892 ref ZP_06899953.1 mannose-6-phosphate isomerase [Streptococcus parasanguinis ATCC 15912] >gnl BL_ORD_ID 2166610 mannose-6-phosphate isomerase [Streptococcus parasanguinis ATCC 15912]	107	0.02	8 - 108 (32.32%)
1080	NR gi 295099871 emb CBK88960.1 mannose-6-phosphate isomerase, type 1 [Eubacterium cylindroides T2-87]	100	0.02	3 - 101 (34%)
1081	NR gi 268611411 ref ZP_06145138.1 mannose-1-phosphate guanylyltransferase [Ruminococcus flavofaciens FD-1]	116	0.02	3 - 116 (28.24%)
1082	NR gi 228900930 ref ZP_04065144.1 ManA (Mannose-6-phosphate isomerase) [Bacillus thuringiensis IBL 4222] >gnl BL_ORD_ID 2602101 ManA (Mannose-6-phosphate isomerase) [Bacillus thuringiensis IBL 4222]	96	0.02	13 - 107 (39.06%)
1083	NR gi 225869177 ref YP_002745125.1 mannose-6-phosphate isomerase [Streptococcus equi subsp. zooepidemicus] >gnl BL_ORD_ID 2008701 mannose-6-phosphate isomerase [Streptococcus equi subsp. zooepidemicus]	111	0.02	4 - 108 (30.03%)
1084	NR gi 218288900 ref ZP_03493151.1 mannose-6-phosphate isomerase, class I [Alicyclobacillus acidocaldarius LAA1] >gnl BL_ORD_ID 1398355 mannose-6-phosphate isomerase, class I [Alicyclobacillus acidocaldarius LAA1]	115	0.02	13 - 123 (26.46%)
1085	NR gi 196249850 ref ZP_03148546.1 mannose-6-phosphate isomerase, class I [Geobacillus sp. G11MC16] >gnl BL_ORD_ID 778620 mannose-6-phosphate isomerase, class I [Geobacillus sp. G11MC16]	109	0.02	9 - 116 (31.98%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1086	NR gi 138897027 ref YP_001127480.1 mannose-6 phosphate isomelase [Geobacillus thermodenitrificans NG80-2] >gnl BL_ORD_ID 1466494 Mannnose-6 phosphate isomelase [Geobacillus thermodenitrificans NG80-2]	109	0.02	9 - 116 (31.98%)
1087	NR gi 159897414 ref YP_001543661.1 mannose-6-phosphate isomerase [Herpetosiphon aurantiacus ATCC 23779] >gnl BL_ORD_ID 562978 Mannose-6-phosphate isomerase [Herpetosiphon aurantiacus ATCC 23779]	105	0.02	13 - 116 (29.93%)
1088	NR gi 77409007 ref ZP_00785727.1 mannose-6-phosphate isomerase, class I [Streptococcus agalactiae COH1] >gnl BL_ORD_ID 416649 mannose-6-phosphate isomerase, class I [Streptococcus agalactiae COH1]	108	0.02	7 - 108 (32.58%)
1089	NR gi 22537828 ref NP_688679.1 mannose-6-phosphate isomerase, class I [Streptococcus agalactiae 2603V/R] >gnl BL_ORD_ID 6219 mannose-6-phosphate isomerase, class I [Streptococcus agalactiae NEM316] >gnl BL_ORD_ID 6219 mannose-6-phosphate isomerase, class I [Streptococcus agalactiae A909] >gnl BL_ORD_ID 6219 mannose-6-phosphate isomerase, class I [Streptococcus agalactiae 18RS21] >gnl BL_ORD_ID 6219 mannose-6-phosphate isomerase, class I [Streptococcus agalactiae H36B] >gnl BL_ORD_ID 6219 mannose-6-phosphate isomerase, class I [Streptococcus agalactiae CJB111] >gnl BL_ORD_ID 6219 mannose-6-phosphate isomerase, class I [Streptococcus agalactiae 515] >gnl BL_ORD_ID 6219 mannose-6-phosphate isomerase, class I [Streptococcus agalactiae 2603V/R] >gnl BL_ORD_ID 6219 Unknown [Streptococcus agalactiae NEM316] >gnl BL_ORD_ID 6219 mannose-6-phosphate isomerase, class I [Streptococcus agalactiae A909] >gnl BL_ORD_ID 6219 mannose-6-phosphate isomerase, class I [Streptococcus agalactiae 18RS21] >gnl BL_ORD_ID 6219 mannose-6-phosphate isomerase, class I [Streptococcus agalactiae 515] >gnl BL_ORD_ID 6219 mannose-6-phosphate isomerase, class I [Streptococcus agalactiae CJB111] >gnl BL_ORD_ID 6219 mannose-6-phosphate isomerase, class I [Streptococcus agalactiae H36B]	108	0.02	7 - 108 (32.58%)
1090	NR gi 323463844 gb ADX75997.1 mannose-6-phosphate isomerase, class I [Staphylococcus pseudintermedius ED99]	94	0.02	9 - 101 (38.48%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1091	NR gi 319893101 ref YP_004149976.1 Mannose-6-phosphate isomerase [Staphylococcus pseudintermedius HKU10-03] >gnl BL_ORD_ID 936241 Mannose-6-phosphate isomerase [Staphylococcus pseudintermedius HKU10-03]	94	0.02	9 - 101 (38.48%)
1092	NR gi 317479225 ref ZP_07938360.1 mannose-6-phosphate isomerase [Bacteroides sp. 4_1_36] >gnl BL_ORD_ID 877598 mannose-6-phosphate isomerase [Bacteroides sp. 4_1_36]	87	0.02	27 - 105 (43.60%)
1093	NR gi 296442597 ref ZP_06884659.1 mannose-6-phosphate isomerase, class I [Clostridium lentocellum DSM 5427] >gnl BL_ORD_ID 2135037 mannose-6-phosphate isomerase, class I [Clostridium lentocellum DSM 5427]	102	0.02	1 - 101 (31.72%)
1094	NR gi 295104422 emb CBL01966.1 mannose-6-phosphate isomerase, type 1 [Faecalibacterium prausnitzii SL3/3]	100	0.02	3 - 101 (31%)
1095	NR gi 195977511 ref YP_002122755.1 mannose-6-phosphate isomerase Pmi [Streptococcus equi subsp. zooepidemicus MGCS10565] >gnl BL_ORD_ID 743258 mannose-6-phosphate isomerase Pmi [Streptococcus equi subsp. zooepidemicus MGCS10565]	102	0.02	13 - 108 (34.60%)
1096	NR gi 160943654 ref ZP_02090886.1 hypothetical protein FAEPRAM212_01146 [Faecalibacterium prausnitzii M21/2] >gnl BL_ORD_ID 2298665 hypothetical protein FAEPRAM212_01146 [Faecalibacterium prausnitzii M21/2]	100	0.02	3 - 101 (31%)
1097	NR gi 154493679 ref ZP_02032999.1 hypothetical protein PARMER_03020 [Parabacteroides merdae ATCC 43184] >gnl BL_ORD_ID 2021529 hypothetical protein PARMER_03020 [Parabacteroides merdae ATCC 43184]	86	0.02	28 - 105 (41.92%)
1098	NR gi 298209139 ref YP_003717318.1 putative mannose-6-phosphate isomerase [Croceibacter atlanticus HTCC2559] >gnl BL_ORD_ID 509781 putative mannose-6-phosphate isomerase [Croceibacter atlanticus HTCC2559]	96	0.02	13 - 106 (34.72%)
1099	NR gi 322373211 ref ZP_08047747.1 mannose-6-phosphate isomerase, class I [Streptococcus sp. C150] >gnl BL_ORD_ID 1186229 mannose-6-phosphate isomerase, class I [Streptococcus sp. C150]	109	0.03	8 - 108 (30.30%)
1100	NR gi 320104792 ref YP_004180383.1 mannose-6-phosphate isomerase, type 1 [Isosphaera pallida ATCC 43644] >gnl BL_ORD_ID 1051620 mannose-6-phosphate isomerase, type 1 [Isosphaera pallida ATCC 43644]	90	0.03	13 - 101 (41.98%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1101	NR gi 315173343 gb EFU17360.1 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX1346]	105	0.03	9 - 108 (32.66%)
1102	NR gi 315150026 gb EFT94042.1 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0012]	105	0.03	9 - 108 (32.66%)
1103	NR gi 313203555 ref YP_004042212.1 mannose-6-phosphate isomerase, type 1 [Paludibacter propionigenes WB4] >gnl BL_ORD_ID 593373 mannose-6-phosphate isomerase, type 1 [Paludibacter propionigenes WB4]	106	0.03	13 - 116 (30.26%)
1104	NR gi 312863373 ref ZP_07723611.1 mannose-6-phosphate isomerase, class I [Streptococcus vestibularis F0396] >gnl BL_ORD_ID 445554 mannose-6-phosphate isomerase, class I [Streptococcus vestibularis F0396]	109	0.03	8 - 108 (30.30%)
1105	NR gi 307287585 ref ZP_07567628.1 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0109] >gnl BL_ORD_ID 2922127 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0109]	105	0.03	9 - 108 (32.66%)
1106	NR gi 301309135 ref ZP_07215079.1 mannose-6-phosphate isomerase, class I [Bacteroides sp. 20_3] >gnl BL_ORD_ID 2655334 mannose-6-phosphate isomerase, class I [Bacteroides sp. 20_3]	86	0.03	28 - 105 (44.62%)
1107	NR gi 298375071 ref ZP_06985028.1 mannose-6-phosphate isomerase, class I [Bacteroides sp. 3_1_19] >gnl BL_ORD_ID 2332962 mannose-6-phosphate isomerase, class I [Bacteroides sp. 3_1_19]	86	0.03	28 - 105 (44.62%)
1108	NR gi 270293940 ref ZP_06200142.1 mannose-6-phosphate isomerase, class I [Bacteroides sp. D20] >gnl BL_ORD_ID 1179970 mannose-6-phosphate isomerase, class I [Bacteroides sp. D20]	87	0.03	27 - 105 (43.60%)
1109	NR gi 262384513 ref ZP_06077647.1 mannose-6-phosphate isomerase [Bacteroides sp. 2_1_33B] >gnl BL_ORD_ID 1020566 mannose-6-phosphate isomerase [Bacteroides sp. 2_1_33B]	86	0.03	28 - 105 (44.62%)
1110	NR gi 260888641 ref ZP_05899904.1 mannose-6-phosphate isomerase, class I [Selenomonas sputigena ATCC 35185] >gnl BL_ORD_ID 896663 mannose-6-phosphate isomerase, class I [Selenomonas sputigena ATCC 35185]	112	0.03	3 - 108 (26.30%)
1111	NR gi 257888271 ref ZP_05667924.1 mannose-6-phosphate isomerase [Enterococcus faecium 1,141,733] >gnl BL_ORD_ID 702680 mannose-6-phosphate isomerase [Enterococcus faecium 1,141,733]	106	0.03	9 - 108 (30.26%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1112	NR gi 257090732 ref ZP_05585093.1 mannose-6-phosphate isomerase [Enterococcus faecalis CH188] >gnl BL_ORD_ID 628981 mannose-6-phosphate isomerase [Enterococcus faecalis CH188]	105	0.03	9 - 108 (32.66%)
1113	NR gi 257084428 ref ZP_05578789.1 mannose-6-phosphate isomerase [Enterococcus faecalis Fly1] >gnl BL_ORD_ID 626762 mannose-6-phosphate isomerase [Enterococcus faecalis Fly1]	105	0.03	9 - 108 (32.66%)
1114	NR gi 256853902 ref ZP_05559267.1 mannose-6-phosphate isomerase [Enterococcus faecalis T8] >gnl BL_ORD_ID 554359 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0411] >gnl BL_ORD_ID 554359 mannose-6-phosphate isomerase [Enterococcus faecalis T8] >gnl BL_ORD_ID 554359 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0411] >gnl BL_ORD_ID 554359 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX4000]	105	0.03	9 - 108 (32.66%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1115	NR gi 255975054 ref ZP_05425640.1 mannose-6-phosphate isomerase [Enterococcus faecalis T2] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase [Enterococcus faecalis HIP11704] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase [Enterococcus faecalis JH1] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase [Enterococcus faecalis D6] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase [Enterococcus faecalis X98] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase, class I [Enterococcus faecalis PC1.1] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX4248] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0855] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0860] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase [Enterococcus faecalis T2] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase [Enterococcus faecalis HIP11704] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase [Enterococcus faecalis JH1] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase [Enterococcus faecalis D6] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase [Enterococcus faecalis X98] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase, class I [Enterococcus faecalis PC1.1] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0860] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0855] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX4248] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX2137] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0043] >gnl BL_ORD_ID 505106 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX1341]	105	0.03	9 - 108 (32.66%)
1116	NR gi 255008448 ref ZP_05280574.1 putative mannose-6-phosphate isomerase [Bacteroides fragilis 3_1_12] >gnl BL_ORD_ID 412211 mannose-6-phosphate isomerase [Bacteroides fragilis 3_1_12] >gnl BL_ORD_ID 412211 mannose-6-phosphate isomerase [Bacteroides fragilis 3_1_12]	70	0.03	44 - 106 (57.14%)
1117	NR gi 229545043 ref ZP_04433768.1 class I mannose-6-phosphate isomerase [Enterococcus faecalis TX1322] >gnl BL_ORD_ID 2633984 class I mannose-6-phosphate isomerase [Enterococcus faecalis TX1322]	105	0.03	9 - 108 (32.66%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1118	NR gi 228475525 ref ZP_04060243.1 mannose-6-phosphate isomerase, class I [Staphylococcus hominis SK119] >gnl BL_ORD_ID 2425962 mannose-6-phosphate isomerase, class I [Staphylococcus hominis SK119]	120	0.03	9 - 114 (27.78%)
1119	NR gi 228477633 ref ZP_04062262.1 mannose-6-phosphate isomerase, class I [Streptococcus salivarius SK126] >gnl BL_ORD_ID 2423995 mannose-6-phosphate isomerase, class I [Streptococcus salivarius SK126]	109	0.03	8 - 108 (30.30%)
1120	NR gi 257784119 ref YP_003179336.1 mannose-6-phosphate isomerase, class I [Atopobium parvulum DSM 20469] >gnl BL_ORD_ID 2337313 mannose-6-phosphate isomerase, class I [Atopobium parvulum DSM 20469]	93	0.03	10 - 101 (38.15%)
1121	NR gi 227519727 ref ZP_03949776.1 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0104] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis ATCC 29200] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase [Enterococcus faecalis T1] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase [Enterococcus faecalis ATCC 4200] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase [Enterococcus faecalis T3] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase [Enterococcus faecalis DS5] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase [Enterococcus faecalis E1 Sol] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase [Enterococcus faecalis AR01/DG] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TUSoD Ef11] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX2134] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0470] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0635] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0102] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0104] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis ATCC 29200] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase [Enterococcus faecalis T1] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase [Enterococcus faecalis ATCC 4200] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase [Enterococcus faecalis T3]	105	0.03	9 - 108 (32.66%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
	>gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase [Enterococcus faecalis DS5] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase [Enterococcus faecalis E1Sol] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase [Enterococcus faecalis ARO1/DG] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, type 1 [Enterococcus sp. 7L76] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TUSoD Ef11] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX2134] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0102] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0635] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0470] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0017] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0027] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX2141] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX4244] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0031] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0312] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0645] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX1302] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0630] >gnl BL_ORD_ID 2247988 mannose-6-phosphate isomerase, class I [Enterococcus faecalis 62]			
1122	NR gi 260881542 ref ZP_05404687.2 mannose-6-phosphate isomerase, class I [Mitsuokella multacida DSM 20544] >gnl BL_ORD_ID 2053062 mannose-6-phosphate isomerase, class I [Mitsuokella multacida DSM 20544]	100	0.03	3 - 101 (30%)
1123	NR gi 218262494 ref ZP_03476940.1 hypothetical protein PRABACTJOHN_02618 [Parabacteroides johnsonii DSM 18315] >gnl BL_ORD_ID 1390555 hypothetical protein PRABACTJOHN_02618 [Parabacteroides johnsonii DSM 18315]	86	0.03	28 - 105 (41.92%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1124	NR gi 168177758 ref ZP_02612422.1 mannose-6-phosphate isomerase, class I [Clostridium botulinum NCTC 2916] >gnl BL_ORD_ID 2851629 mannose-6-phosphate isomerase, class I [Clostridium botulinum A2 str. Kyoto] >gnl BL_ORD_ID 2851629 mannose-6-phosphate isomerase, class I [Clostridium botulinum NCTC 2916] >gnl BL_ORD_ID 2851629 mannose-6-phosphate isomerase, class I [Clostridium botulinum A2 str. Kyoto]	112	0.03	3 - 113 (26.30%)
1125	NR gi 160888932 ref ZP_02069935.1 hypothetical protein BACUNI_01352 [Bacteroides uniformis ATCC 8492] >gnl BL_ORD_ID 2145833 hypothetical protein BACUNI_01352 [Bacteroides uniformis ATCC 8492]	87	0.03	27 - 105 (43.60%)
1126	NR gi 150008351 ref YP_001303094.1 mannose-6-phosphate isomerase [Parabacteroides distasonis ATCC 8503] >gnl BL_ORD_ID 1884675 mannose-6-phosphate isomerase [Bacteroides sp. 2_1_7] >gnl BL_ORD_ID 1884675 mannose-6-phosphate isomerase, class I [Parabacteroides sp. D13] >gnl BL_ORD_ID 1884675 mannose-6-phosphate isomerase [Parabacteroides distasonis ATCC 8503] >gnl BL_ORD_ID 1884675 mannose-6-phosphate isomerase, class I [Parabacteroides sp. D13]	86	0.03	28 - 105 (44.62%)
1127	NR gi 125717629 ref YP_001034762.1 mannose-6-phosphate isomerase, putative [Streptococcus sanguinis SK36] >gnl BL_ORD_ID 1271917 mannose-6-phosphate isomerase [Streptococcus sanguinis VMC66] >gnl BL_ORD_ID 1271917 Mannose-6-phosphate isomerase, putative [Streptococcus sanguinis SK36] >gnl BL_ORD_ID 1271917 mannose-6-phosphate isomerase [Streptococcus sanguinis VMC66]	109	0.03	8 - 108 (31.98%)
1128	NR gi 118444692 ref YP_877669.1 mannose-6-phosphate isomerase, class I [Clostridium novyi NT] >gnl BL_ORD_ID 840896 mannose-6-phosphate isomerase, class I [Clostridium novyi NT]	100	0.03	3 - 101 (31%)
1128	NR gi 118444692 ref YP_877669.1 mannose-6-phosphate isomerase, class I [Clostridium novyi NT] >gnl BL_ORD_ID 840896 mannose-6-phosphate isomerase, class I [Clostridium novyi NT]	100	0.03	3 - 101 (31%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1129	NR gi 29377076 ref NP_816230.1 mannose-6-phosphate isomerase, class I [Enterococcus faecalis V583] >gnl BL_ORD_ID 1565246 mannose-6-phosphate isomerase, class I [Enterococcus faecalis HH22] >gnl BL_ORD_ID 1565246 mannose-6-phosphate isomerase [Enterococcus faecalis T11] >gnl BL_ORD_ID 1565246 mannose-6-phosphate isomerase, class I [Enterococcus faecalis V583] >gnl BL_ORD_ID 1565246 mannose-6-phosphate isomerase, class I [Enterococcus faecalis HH22] >gnl BL_ORD_ID 1565246 mannose-6-phosphate isomerase [Enterococcus faecalis T11] >gnl BL_ORD_ID 1565246 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0309B] >gnl BL_ORD_ID 1565246 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX0309A]	105	0.03	9 - 108 (32.66%)
1130	NR gi 220932985 ref YP_002509893.1 mannose-6-phosphate isomerase, class I [Halothermothrix orenii H 168] >gnl BL_ORD_ID 702433 mannose-6-phosphate isomerase, class I [Halothermothrix orenii H 168]	91	0.03	13 - 101 (37.44%)
1131	NR gi 322391641 ref ZP_08065109.1 mannose-6-phosphate isomerase [Streptococcus peroris ATCC 700780] >gnl BL_ORD_ID 1171147 mannose-6-phosphate isomerase [Streptococcus peroris ATCC 700780]	111	0.04	5 - 108 (30.03%)
1132	NR gi 317057498 ref YP_004105965.1 mannose-6-phosphate isomerase, class I [Ruminococcus albus 7] >gnl BL_ORD_ID 2843028 mannose-6-phosphate isomerase, class I [Ruminococcus albus 7]	93	0.04	9 - 101 (34.69%)
1133	NR gi 282878429 ref ZP_06287215.1 mannose-6-phosphate isomerase, class I [Prevotella buccalis ATCC 35310] >gnl BL_ORD_ID 1255121 mannose-6-phosphate isomerase, class I [Prevotella buccalis ATCC 35310]	45	0.04	57 - 100 (118.51%)
1134	NR gi 262283346 ref ZP_06061112.1 mannose-6-phosphate isomerase [Streptococcus sp. 2_1_36FAA] >gnl BL_ORD_ID 1012205 mannose-6-phosphate isomerase [Streptococcus sp. 2_1_36FAA]	104	0.04	13 - 108 (34.21%)
1135	NR gi 189463666 ref ZP_03012451.1 hypothetical protein BACCOP_04392 [Bacteroides coprocola DSM 17136] >gnl BL_ORD_ID 380717 hypothetical protein BACCOP_04392 [Bacteroides coprocola DSM 17136]	76	0.04	42 - 116 (48.47%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1136	NR gi 169351689 ref ZP_02868627.1 hypothetical protein CLOSPI_02470 [Clostridium spiroforme DSM 1552] >gnl BL_ORD_ID 69808 hypothetical protein CLOSPI_02470 [Clostridium spiroforme DSM 1552]	112	0.04	3 - 108 (26.30%)
1137	NR gi 157149838 ref YP_001451019.1 mannose-6-phosphate isomerase, class I [Streptococcus gordonii str. Challis substr. CH1] >gnl BL_ORD_ID 2186381 mannose-6-phosphate isomerase, class I [Streptococcus gordonii str. Challis substr. CH1]	104	0.04	13 - 108 (34.21%)
1138	NR gi 126662138 ref ZP_01733137.1 mannose-6-phosphate isomerase [Flavobacteria bacterium BAL38] >gnl BL_ORD_ID 1375607 mannose-6-phosphate isomerase [Flavobacteria bacterium BAL38]	191	0.04	30 - 201 (14.80%)
1139	NR gi 22901277 gb AAN09933.1 AF469471_1 mannose-6-phosphate isomerase [Nicotiana tabacum]	50	0.04	53 - 102 (96%)
1140	NR gi 321314940 ref YP_004207227.1 mannose-6-phosphate isomerase manA [Bacillus subtilis BSn5] >gnl BL_ORD_ID 1082066 mannose-6-phosphate isomerase manA [Bacillus subtilis BSn5]	96	0.05	13 - 107 (40.15%)
1141	NR gi 315170159 gb EFU14176.1 mannose-6-phosphate isomerase, class I [Enterococcus faecalis TX1342]	105	0.05	9 - 108 (32.66%)
1142	NR gi 314934753 ref ZP_07842112.1 mannose-6-phosphate isomerase, class I [Staphylococcus caprae C87] >gnl BL_ORD_ID 725711 mannose-6-phosphate isomerase, class I [Staphylococcus caprae C87]	106	0.05	9 - 108 (31.15%)
1143	NR gi 309778207 ref ZP_07673140.1 mannose-6-phosphate isomerase, class I [Erysipelotrichaceae bacterium 3_1_53] >gnl BL_ORD_ID 299658 mannose-6-phosphate isomerase, class I [Erysipelotrichaceae bacterium 3_1_53]	161	0.05	235 - 383 (15.04%)
1144	NR gi 294776892 ref ZP_06742355.1 phosphomannose isomerase type I [Bacteroides vulgatus PC510] >gnl BL_ORD_ID 1924664 phosphomannose isomerase type I [Bacteroides vulgatus PC510]	86	0.05	42 - 116 (40.56%)
1145	NR gi 291543450 emb CBL16559.1 mannose-6-phosphate isomerase, type 1 [Ruminococcus sp. 18P13]	100	0.05	3 - 101 (32%)
1146	NR gi 291483708 dbj BAI84783.1 mannose-6-phosphate isomerase [Bacillus subtilis subsp. natto BEST195]	96	0.05	13 - 107 (40.15%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1147	NR gi 257899705 ref ZP_05679358.1 mannose-6-phosphate isomerase [Enterococcus faecium Com15] >gnl BL_ORD_ID 706459 mannose-6-phosphate isomerase, class I [Enterococcus faecium E980] >gnl BL_ORD_ID 706459 mannose-6-phosphate isomerase [Enterococcus faecium Com15] >gnl BL_ORD_ID 706459 mannose-6-phosphate isomerase, class I [Enterococcus faecium E980]	106	0.05	9 - 108 (30.26%)
1148	NR gi 257882272 ref ZP_05661925.1 mannose-6-phosphate isomerase [Enterococcus faecium 1,231,502] >gnl BL_ORD_ID 698572 mannose-6-phosphate isomerase, class I [Enterococcus faecium E1071] >gnl BL_ORD_ID 698572 mannose-6-phosphate isomerase, class I [Enterococcus faecium U0317] >gnl BL_ORD_ID 698572 mannose-6-phosphate isomerase [Enterococcus faecium 1,231,502] >gnl BL_ORD_ID 698572 mannose-6-phosphate isomerase, class I [Enterococcus faecium E1071] >gnl BL_ORD_ID 698572 mannose-6-phosphate isomerase, class I [Enterococcus faecium U0317]	106	0.05	9 - 108 (30.26%)
1149	NR gi 297544968 ref YP_003677270.1 mannose-6-phosphate isomerase, class I [Thermoanaerobacter mathranii subsp. mathranii str. A3] >gnl BL_ORD_ID 445979 mannose-6-phosphate isomerase, class I [Thermoanaerobacter mathranii subsp. mathranii str. A3]	102	0.05	13 - 113 (28.83%)
1150	NR gi 228946119 ref ZP_04108454.1 ManA (Mannose-6-phosphate isomerase) [Bacillus thuringiensis serovar monterrey BGSC 4AJ1] >gnl BL_ORD_ID 2583015 ManA (Mannose-6-phosphate isomerase) [Bacillus thuringiensis serovar monterrey BGSC 4AJ1]	96	0.05	13 - 107 (39.06%)
1151	NR gi 291296630 ref YP_003508028.1 Mannose-6-phosphate isomerase [Meiothermus ruber DSM 1279] >gnl BL_ORD_ID 2405945 Mannose-6-phosphate isomerase [Meiothermus ruber DSM 1279]	90	0.05	13 - 101 (39.51%)
1152	NR gi 227552494 ref ZP_03982543.1 mannose-6-phosphate isomerase [Enterococcus faecium TX1330] >gnl BL_ORD_ID 2289109 mannose-6-phosphate isomerase [Enterococcus faecium Com12] >gnl BL_ORD_ID 2289109 mannose-6-phosphate isomerase, class I [Enterococcus faecium PC4.1] >gnl BL_ORD_ID 2289109 mannose-6-phosphate isomerase [Enterococcus faecium TX1330] >gnl BL_ORD_ID 2289109 mannose-6-phosphate isomerase [Enterococcus faecium Com12] >gnl BL_ORD_ID 2289109 mannose-6-phosphate isomerase, class I [Enterococcus faecium PC4.1]	106	0.05	9 - 108 (30.26%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1153	NR gi 225869870 ref YP_002745817.1 mannose-6-phosphate isomerase [Streptococcus equi subsp. equi 4047] >gnl BL_ORD_ID 2006195 mannose-6-phosphate isomerase [Streptococcus equi subsp. equi 4047]	111	0.05	4 - 108 (29.22%)
1154	NR gi 212693835 ref ZP_03301963.1 hypothetical protein BACDOR_03357 [Bacteroides dorei DSM 17855] >gnl BL_ORD_ID 1184754 mannose-6-phosphate isomerase [Bacteroides sp. 9_1_42FAA] >gnl BL_ORD_ID 1184754 mannose-6-phosphate isomerase [Bacteroides sp. D4] >gnl BL_ORD_ID 1184754 mannose-6-phosphate isomerase [Bacteroides sp. 3_1_33FAA] >gnl BL_ORD_ID 1184754 hypothetical protein BACDOR_03357 [Bacteroides dorei DSM 17855] >gnl BL_ORD_ID 1184754 mannose-6-phosphate isomerase [Bacteroides dorei 5_1_36/D4] >gnl BL_ORD_ID 1184754 mannose-6-phosphate isomerase [Bacteroides sp. 9_1_42FAA] >gnl BL_ORD_ID 1184754 mannose-6-phosphate isomerase [Bacteroides sp. 3_1_33FAA]	86	0.05	42 - 116 (40.56%)
1155	NR gi 160941716 ref ZP_02089043.1 hypothetical protein CLOBOL_06612 [Clostridium bolteae ATCC BAA-613] >gnl BL_ORD_ID 2289571 hypothetical protein CLOBOL_06612 [Clostridium bolteae ATCC BAA-613]	129	0.05	9 - 126 (22.23%)
1156	NR gi 150004257 ref YP_001299001.1 mannose-6-phosphate isomerase [Bacteroides vulgatus ATCC 8482] >gnl BL_ORD_ID 1886907 mannose-6-phosphate isomerase [Bacteroides sp. 4_3_47FAA] >gnl BL_ORD_ID 1886907 mannose-6-phosphate isomerase [Bacteroides sp. 3_1_40A] >gnl BL_ORD_ID 1886907 mannose-6-phosphate isomerase [Bacteroides vulgatus ATCC 8482] >gnl BL_ORD_ID 1886907 mannose-6-phosphate isomerase [Bacteroides sp. 4_3_47FAA] >gnl BL_ORD_ID 1886907 mannose-6-phosphate isomerase [Bacteroides sp. 3_1_40A]	86	0.05	42 - 116 (40.56%)
1157	NR gi 149196514 ref ZP_01873568.1 sugar kinase [Lentisphaera araneosa HTCC2155] >gnl BL_ORD_ID 1789667 sugar kinase [Lentisphaera araneosa HTCC2155]	91	0.05	13 - 102 (37.44%)
1158	NR gi 116873545 ref YP_850326.1 mannose-6-phosphate isomerase, class I [Listeria welshimeri serovar 6b str. SLCC5334] >gnl BL_ORD_ID 766359 mannose-6-phosphate isomerase, class I [Listeria welshimeri serovar 6b str. SLCC5334]	99	0.05	9 - 107 (31.63%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1159	NR gi 116513270 ref YP_812176.1 phosphomannose isomerase [Lactobacillus delbrueckii subsp. bulgaricus ATCC BAA-365] >gnl BL_ORD_ID 733183 mannose-6-phosphate isomerase, type 1 [Lactobacillus delbrueckii subsp. bulgaricus ATCC BAA-365]	102	0.05	13 - 108 (31.72%)
1160	NR gi 55821704 ref YP_140146.1 mannose-6-phosphate isomerase [Streptococcus thermophilus LMG 18311] >gnl BL_ORD_ID 1836097 mannose-6-phosphate isomerase [Streptococcus thermophilus CNRZ1066] >gnl BL_ORD_ID 1836097 mannose-6-phosphate isomerase [Streptococcus thermophilus LMD-9] >gnl BL_ORD_ID 1836097 mannose-6-phosphate isomerase [Streptococcus thermophilus LMG 18311] >gnl BL_ORD_ID 1836097 mannose-6-phosphate isomerase [Streptococcus thermophilus CNRZ1066] >gnl BL_ORD_ID 1836097 Phosphomannose isomerase [Streptococcus thermophilus LMD-9] >gnl BL_ORD_ID 1836097 Mannose-6-phosphate isomerase, class I [Streptococcus thermophilus ND03]	102	0.05	13 - 108 (34.60%)
1161	NR gi 16078267 ref NP_389084.1 mannose-6 phosphate isomerase [Bacillus subtilis subsp. subtilis str. 168] >gnl BL_ORD_ID 795952 mannose-6-phosphate isomerase [Bacillus subtilis subsp. subtilis str. 168] >gnl BL_ORD_ID 795952 mannose-6-phosphate isomerase [Bacillus subtilis subsp. subtilis str. NCIB 3610] >gnl BL_ORD_ID 795952 mannose-6-phosphate isomerase [Bacillus subtilis subsp. subtilis str. JH642] >gnl BL_ORD_ID 795952 mannose-6-phosphate isomerase [Bacillus subtilis subsp. subtilis str. SMY] >gnl BL_ORD_ID 795952 RecName: Full=Mannose-6-phosphate isomerase manA; AltName: Full=Phosphohexomutase; Short=PMI >gnl BL_ORD_ID 795952 mannose-6 phosphate isomerase ; cupin family [Bacillus subtilis subsp. subtilis str. 168]	96	0.05	13 - 107 (40.15%)
1162	NR gi 69245316 ref ZP_00603360.1 Mannose-6-phosphate isomerase, type I [Enterococcus faecium DO] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase [Enterococcus faecium 1,230,933] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase [Enterococcus faecium 1,231,501] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase [Enterococcus faecium 1,231,410] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase [Enterococcus faecium 1,231,408] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium DO] >gnl BL_ORD_ID 44837 mannose-6-phosphate	106	0.05	9 - 108 (30.26%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
	<p>isomerase [Enterococcus faecium C68] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase [Enterococcus faecium TC 6] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium D344SRF] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium E1039] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium E1162] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium E1636] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium E1679] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium TX0133a04] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium TX0133C] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium TX0082] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium TX0133A] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium TX0133B] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium TX0133a01] >gnl BL_ORD_ID 44837 Mannose-6-phosphate isomerase, type I [Enterococcus faecium DO] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase [Enterococcus faecium 1,230,933] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase [Enterococcus faecium 1,231,501] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase [Enterococcus faecium 1,231,410] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase [Enterococcus faecium 1,231,408] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase [Enterococcus faecium C68] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase [Enterococcus faecium TC 6] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium D344SRF] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium E1636] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium E1679] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium E1039] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium E1162] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium TX0133a01] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium TX0133B]</p>			

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
	>gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium TX0133A] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium TX0133C] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium TX0133a04] >gnl BL_ORD_ID 44837 mannose-6-phosphate isomerase, class I [Enterococcus faecium TX0082]			
1163	NR gi 322385121 ref ZP_08058768.1 mannose-6-phosphate isomerase [Streptococcus cristatus ATCC 51100] >gnl BL_ORD_ID 1184487 mannose-6-phosphate isomerase [Streptococcus cristatus ATCC 51100]	109	0.07	8 - 108 (30.30%)
1164	NR gi 295134061 ref YP_003584737.1 phosphomannose isomerase type I [Zunongwangia profunda SM-A87] >gnl BL_ORD_ID 1974772 phosphomannose isomerase type I [Zunongwangia profunda SM-A87]	101	0.07	13 - 105 (32.35%)
1165	NR gi 294639536 ref ZP_06717561.1 mannose-6-phosphate isomerase, class I [Ruminococcus albus 8] >gnl BL_ORD_ID 1758659 mannose-6-phosphate isomerase, class I [Ruminococcus albus 8]	100	0.07	3 - 101 (32%)
1166	NR gi 257870643 ref ZP_05650296.1 mannose-6-phosphate isomerase [Enterococcus gallinarum EG2] >gnl BL_ORD_ID 693714 mannose-6-phosphate isomerase [Enterococcus gallinarum EG2]	105	0.07	9 - 108 (29.03%)
1167	NR gi 229032888 ref ZP_04188843.1 ManA (Mannose-6-phosphate isomerase) [Bacillus cereus AH1271] >gnl BL_ORD_ID 2534859 ManA (Mannose-6-phosphate isomerase) [Bacillus cereus AH1271]	108	0.07	8 - 108 (30.01%)
1168	NR gi 229136771 ref ZP_04265420.1 Mannose-6-phosphate isomerase [Bacillus cereus BDRD-ST196] >gnl BL_ORD_ID 2490047 Mannose-6-phosphate isomerase [Bacillus cereus BDRD-ST196]	108	0.07	8 - 108 (28.30%)
1169	NR gi 167462257 ref ZP_02327346.1 mannose-6 phosphate isomerase [Paenibacillus larvae subsp. larvae BRL-230010] >gnl BL_ORD_ID 2665782 mannose-6 phosphate isomerase-like protein [Paenibacillus larvae subsp. larvae B-3650] >gnl BL_ORD_ID 2665782 mannose-6 phosphate isomerase-like protein [Paenibacillus larvae subsp. larvae B-3650]	91	0.07	13 - 101 (38.64%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1170	NR gi 220928607 ref YP_002505516.1 mannose-6-phosphate isomerase, class I [Clostridium cellulolyticum H10] >gnl BL_ORD_ID 899320 mannose-6-phosphate isomerase, class I [Clostridium cellulolyticum H10]	117	0.07	9 - 121 (27.76%)
1171	NR gi 52082112 ref YP_080903.1 mannose-6-phosphate isomerase [Bacillus licheniformis ATCC 14580] >gnl BL_ORD_ID 1813275 Pmi [Bacillus licheniformis ATCC 14580] >gnl BL_ORD_ID 1813275 pmi protein [Bacillus sp. BT1B_CT2] >gnl BL_ORD_ID 1813275 mannose-6-phosphate isomerase [Bacillus licheniformis ATCC 14580] >gnl BL_ORD_ID 1813275 Pmi [Bacillus licheniformis ATCC 14580] >gnl BL_ORD_ID 1813275 pmi protein [Bacillus sp. BT1B_CT2]	103	0.07	13 - 108 (33.93%)
1172	NR gi 88803627 ref ZP_01119152.1 mannose-6-phosphate isomerase [Polaribacter irgensii 23-P] >gnl BL_ORD_ID 637664 mannose-6-phosphate isomerase [Polaribacter irgensii 23-P]	61	0.07	57 - 116 (67.18%)
1173	NR gi 319946369 ref ZP_08020607.1 mannose-6-phosphate isomerase [Streptococcus australis ATCC 700641] >gnl BL_ORD_ID 1047678 mannose-6-phosphate isomerase [Streptococcus australis ATCC 700641]	107	0.09	8 - 108 (31.44%)
1174	NR gi 308175595 ref YP_003922300.1 mannose-6-phosphate isomerase [Bacillus amyloliquefaciens DSM 7] >gnl BL_ORD_ID 133578 mannose-6-phosphate isomerase [Bacillus amyloliquefaciens DSM 7]	103	0.09	13 - 108 (33.93%)
1175	NR gi 297531658 ref YP_003672933.1 mannose-6-phosphate isomerase, class I [Geobacillus sp. C56-T3] >gnl BL_ORD_ID 2218244 mannose-6-phosphate isomerase, class I [Geobacillus sp. C56-T3]	94	0.09	9 - 101 (38.48%)
1176	NR gi 293370098 ref ZP_06616663.1 mannose-6-phosphate isomerase, class I [Bacteroides ovatus SD CMC 3f] >gnl BL_ORD_ID 1839890 mannose-6-phosphate isomerase, class I [Bacteroides sp. D22] >gnl BL_ORD_ID 1839890 mannose-6-phosphate isomerase, class I [Bacteroides ovatus SD CMC 3f] >gnl BL_ORD_ID 1839890 mannose-6-phosphate isomerase, class I [Bacteroides sp. D22]	87	0.09	27 - 105 (39.63%)
1177	NR gi 312112720 ref YP_003991036.1 mannose-6-phosphate isomerase, class I [Geobacillus sp. Y4.1MC1] >gnl BL_ORD_ID 452100 mannose-6-phosphate isomerase, class I [Geobacillus sp. Y4.1MC1]	94	0.09	9 - 101 (37.35%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1178	NR gi 241888992 ref ZP_04776296.1 mannose-6-phosphate isomerase, class I [Gemella haemolysans ATCC 10379] >gnl BL_ORD_ID 190170 mannose-6-phosphate isomerase, class I [Gemella haemolysans ATCC 10379]	105	0.09	13 - 116 (30.84%)
1179	NR gi 254445941 ref ZP_05059417.1 phosphomannose isomerase type I [Verrucomicrobiae bacterium DG1235] >gnl BL_ORD_ID 879128 phosphomannose isomerase type I [Verrucomicrobiae bacterium DG1235]	93	0.09	9 - 100 (32.38%)
1180	NR gi 168333837 ref ZP_02692080.1 mannose-6-phosphate isomerase, class I [Epulopiscium sp. 'N.t. morphotype B']	115	0.09	3 - 116 (28.73%)
1181	NR gi 160883749 ref ZP_02064752.1 hypothetical protein BACOVA_01721 [Bacteroides ovatus ATCC 8483] >gnl BL_ORD_ID 2070242 mannose-6-phosphate isomerase, class I [Bacteroides sp. 3_1_23] >gnl BL_ORD_ID 2070242 hypothetical protein BACOVA_01721 [Bacteroides ovatus ATCC 8483] >gnl BL_ORD_ID 2070242 mannose-6-phosphate isomerase, class I [Bacteroides sp. 3_1_23]	87	0.09	27 - 105 (39.63%)
1182	NR gi 91216572 ref ZP_01253538.1 putative mannose-6-phosphate isomerase [Psychroflexus torquis ATCC 700755] >gnl BL_ORD_ID 211648 putative mannose-6-phosphate isomerase [Psychroflexus torquis ATCC 700755]	101	0.09	13 - 105 (32.35%)
1183	NR gi 56421999 ref YP_149317.1 mannose-6-phosphate isomerase [Geobacillus kaustophilus HTA426] >gnl BL_ORD_ID 1369508 mannose-6-phosphate isomerase [Geobacillus kaustophilus HTA426]	94	0.09	9 - 101 (38.48%)
1184	NR gi 322387401 ref ZP_08061011.1 mannose-6-phosphate isomerase [Streptococcus infantis ATCC 700779] >gnl BL_ORD_ID 1168015 mannose-6-phosphate isomerase [Streptococcus infantis ATCC 700779]	111	0.12	5 - 108 (30.03%)
1185	NR gi 317476816 ref ZP_07936059.1 mannose-6-phosphate isomerase [Bacteroides eggerthii 1_2_48FAA] >gnl BL_ORD_ID 878911 mannose-6-phosphate isomerase [Bacteroides eggerthii 1_2_48FAA]	87	0.12	27 - 105 (42.28%)
1186	NR gi 315659752 ref ZP_07912611.1 mannose-6-phosphate isomerase [Staphylococcus lugdunensis M23590] >gnl BL_ORD_ID 835662 mannose-6-phosphate isomerase [Staphylococcus lugdunensis M23590]	106	0.12	9 - 108 (30.26%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1187	NR gi 315612816 ref ZP_07887727.1 mannose-6-phosphate isomerase [Streptococcus sanguinis ATCC 49296] >gnl BL_ORD_ID 809725 mannose-6-phosphate isomerase [Streptococcus sanguinis ATCC 49296]	107	0.12	8 - 108 (29.70%)
1188	NR gi 313617868 gb EFR90063.1 mannose-6-phosphate isomerase, class I [Listeria innocua FSL S4-378]	99	0.12	9 - 107 (30.61%)
1189	NR gi 313122813 ref YP_004033072.1 phosphomannose isomerase [Lactobacillus delbrueckii subsp. bulgaricus ND02] >gnl BL_ORD_ID 569909 Phosphomannose isomerase [Lactobacillus delbrueckii subsp. bulgaricus ND02]	101	0.12	13 - 108 (30.39%)
1190	NR gi 312892279 ref ZP_07751775.1 mannose-6-phosphate isomerase, type 1 [Mucilaginibacter paludis DSM 18603] >gnl BL_ORD_ID 470592 mannose-6-phosphate isomerase, type 1 [Mucilaginibacter paludis DSM 18603]	101	0.12	13 - 105 (35.29%)
1191	NR gi 300812455 ref ZP_07092882.1 mannose-6-phosphate isomerase, class I [Lactobacillus delbrueckii subsp. bulgaricus PB2003/044-T3-4] >gnl BL_ORD_ID 2632013 mannose-6-phosphate isomerase, class I [Lactobacillus delbrueckii subsp. bulgaricus PB2003/044-T3-4]	102	0.12	13 - 108 (31.72%)
1192	NR gi 295396818 ref ZP_06806950.1 mannose-6-phosphate isomerase [Aerococcus viridans ATCC 11563] >gnl BL_ORD_ID 1969627 mannose-6-phosphate isomerase [Aerococcus viridans ATCC 11563]	108	0.12	13 - 116 (32.58%)
1193	NR gi 294497895 ref YP_003561595.1 mannose-6-phosphate isomerase [Bacillus megaterium QM B1551] >gnl BL_ORD_ID 1918039 mannose-6-phosphate isomerase [Bacillus megaterium QM B1551]	94	0.12	9 - 101 (36.21%)
1194	NR gi 317131560 ref YP_004090874.1 mannose-6-phosphate isomerase, class I [Ethanoligenens harbinense YUAN-3] >gnl BL_ORD_ID 1554233 mannose-6-phosphate isomerase, class I [Ethanoligenens harbinense YUAN-3]	116	0.12	3 - 111 (27.50%)
1195	NR gi 289549610 ref YP_003470514.1 Mannose-6-phosphate isomerase [Staphylococcus lugdunensis HKU09-01] >gnl BL_ORD_ID 1532045 Mannose-6-phosphate isomerase [Staphylococcus lugdunensis HKU09-01]	106	0.12	9 - 108 (30.26%)
1196	NR gi 251783260 ref YP_002997565.1 mannose-6-phosphate isomerase [Streptococcus dysgalactiae subsp. equisimilis GGS_124] >gnl BL_ORD_ID 260042 mannose-6-phosphate isomerase [Streptococcus dysgalactiae subsp. equisimilis GGS_124]	111	0.12	4 - 108 (28.41%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1197	NR gi 269121713 ref YP_003309890.1 mannose-6-phosphate isomerase, class I [Sebaldella termitidis ATCC 33386] >gnl BL_ORD_ID 2747826 mannose-6-phosphate isomerase, class I [Sebaldella termitidis ATCC 33386]	91	0.12	13 - 101 (32.60%)
1198	NR gi 229824584 ref ZP_04450653.1 hypothetical protein GCWU000282_01928 [Catonella morbi ATCC 51271] >gnl BL_ORD_ID 2735977 hypothetical protein GCWU000282_01928 [Catonella morbi ATCC 51271]	107	0.12	8 - 108 (29.70%)
1199	NR gi 237716025 ref ZP_04546506.1 mannose-6-phosphate isomerase [Bacteroides sp. D1] >gnl BL_ORD_ID 2690270 mannose-6-phosphate isomerase [Bacteroides sp. 2_2_4] >gnl BL_ORD_ID 2690270 mannose-6-phosphate isomerase, class I [Bacteroides sp. 2_1_22] >gnl BL_ORD_ID 2690270 mannose-6-phosphate isomerase, class I [Bacteroides ovatus SD CC 2a] >gnl BL_ORD_ID 2690270 mannose-6-phosphate isomerase, class I [Bacteroides xylanisolvens SD CC 1b] >gnl BL_ORD_ID 2690270 mannose-6-phosphate isomerase [Bacteroides sp. D1] >gnl BL_ORD_ID 2690270 mannose-6-phosphate isomerase [Bacteroides sp. 2_2_4] >gnl BL_ORD_ID 2690270 mannose-6-phosphate isomerase, class I [Bacteroides sp. 2_1_22] >gnl BL_ORD_ID 2690270 mannose-6-phosphate isomerase, class I [Bacteroides ovatus SD CC 2a] >gnl BL_ORD_ID 2690270 mannose-6-phosphate isomerase, class I [Bacteroides xylanisolvens SD CC 1b] >gnl BL_ORD_ID 2690270 mannose-6-phosphate isomerase, type 1 [Bacteroides xylanisolvens XB1A]	87	0.12	27 - 105 (39.63%)
1200	NR gi 223044269 ref ZP_03614305.1 mannose-6-phosphate isomerase, class I [Staphylococcus capitis SK14] >gnl BL_ORD_ID 1681266 mannose-6-phosphate isomerase, class I [Staphylococcus capitis SK14]	105	0.12	9 - 108 (29.93%)
1201	NR gi 261420873 ref YP_003254555.1 mannose-6-phosphate isomerase, class I [Geobacillus sp. Y412MC61] >gnl BL_ORD_ID 1546909 mannose-6-phosphate isomerase, class I [Geobacillus sp. Y412MC52] >gnl BL_ORD_ID 1546909 mannose-6-phosphate isomerase, class I [Geobacillus sp. Y412MC61] >gnl BL_ORD_ID 1546909 mannose-6-phosphate isomerase, class I [Geobacillus sp. Y412MC52]	94	0.12	9 - 101 (38.48%)
1202	NR gi 218129966 ref ZP_03458770.1 hypothetical protein BACEGG_01549 [Bacteroides eggerthii DSM 20697] >gnl BL_ORD_ID 1356189 hypothetical protein BACEGG_01549 [Bacteroides eggerthii DSM 20697]	87	0.12	27 - 105 (42.28%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1203	NR gi 229816374 ref ZP_04446679.1 hypothetical protein COLINT_03422 [Collinsella intestinalis DSM 13280] >gnl BL_ORD_ID 1115791 hypothetical protein COLINT_03422 [Collinsella intestinalis DSM 13280]	90	0.12	13 - 100 (38.27%)
1204	NR gi 160932051 ref ZP_02079442.1 hypothetical protein CLOLEP_00885 [Clostridium leptum DSM 753] >gnl BL_ORD_ID 2152898 hypothetical protein CLOLEP_00885 [Clostridium leptum DSM 753]	167	0.12	235 - 384 (15.78%)
1205	NR gi 154687691 ref YP_001422852.1 Pmi [Bacillus amyloliquefaciens FZB42] >gnl BL_ORD_ID 2034893 Pmi [Bacillus amyloliquefaciens FZB42]	95	0.12	13 - 106 (34.35%)
1206	NR gi 229541573 ref ZP_04430633.1 mannose-6-phosphate isomerase, class I [Bacillus coagulans 36D1] >gnl BL_ORD_ID 1251749 mannose-6-phosphate isomerase, class I [Bacillus coagulans 36D1]	103	0.12	13 - 108 (34.87%)
1207	NR gi 156741070 ref YP_001431199.1 mannose-6-phosphate isomerase [Roseiflexus castenholzii DSM 13941] >gnl BL_ORD_ID 817718 Mannose-6-phosphate isomerase [Roseiflexus castenholzii DSM 13941]	105	0.12	13 - 109 (30.84%)
1208	NR gi 104773293 ref YP_618273.1 mannose-6-phosphate isomerase [Lactobacillus delbrueckii subsp. bulgaricus ATCC 11842] >gnl BL_ORD_ID 318114 Mannose-6-phosphate isomerase [Lactobacillus delbrueckii subsp. bulgaricus ATCC 11842]	102	0.12	13 - 108 (31.72%)
1209	NR gi 29345783 ref NP_809286.1 mannose-6-phosphate isomerase [Bacteroides thetaiotaomicron VPI-5482] >gnl BL_ORD_ID 1577138 mannose-6-phosphate isomerase [Bacteroides sp. 1_1_6] >gnl BL_ORD_ID 1577138 mannose-6-phosphate isomerase, class I [Bacteroides sp. 1_1_14] >gnl BL_ORD_ID 1577138 mannose-6-phosphate isomerase [Bacteroides thetaiotaomicron VPI-5482] >gnl BL_ORD_ID 1577138 mannose-6-phosphate isomerase [Bacteroides sp. 1_1_6] >gnl BL_ORD_ID 1577138 mannose-6-phosphate isomerase, class I [Bacteroides sp. 1_1_14]	87	0.12	27 - 105 (39.63%)
1210	NR gi 16801280 ref NP_471548.1 hypothetical protein lin2215 [Listeria innocua Clip11262] >gnl BL_ORD_ID 967851 lin2215 [Listeria innocua Clip11262]	99	0.12	9 - 107 (30.61%)
1211	NR gi 323127982 gb ADX25279.1 Mannose-6-phosphate isomerase [Streptococcus dysgalactiae subsp. equisimilis ATCC 12394]	111	0.15	4 - 108 (28.41%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1212	NR gi 322390154 ref ZP_08063687.1 mannose-6-phosphate isomerase [Streptococcus parasanguinis ATCC 903] >gnl BL_ORD_ID 1169044 mannose-6-phosphate isomerase [Streptococcus parasanguinis ATCC 903]	107	0.15	8 - 108 (31.44%)
1213	NR gi 319939819 ref ZP_08014175.1 mannose-6-phosphate isomerase [Streptococcus anginosus 1_2_62CV] >gnl BL_ORD_ID 1065525 mannose-6-phosphate isomerase [Streptococcus anginosus 1_2_62CV]	97	0.15	8 - 103 (35.07%)
1214	NR gi 319400375 gb EFV88610.1 mannose-6-phosphate isomerase, class I [Staphylococcus epidermidis FRI909]	106	0.15	9 - 108 (32.93%)
1215	NR gi 319645560 ref ZP_07999792.1 ManA protein [Bacillus sp. BT1B_CT2] >gnl BL_ORD_ID 956220 ManA protein [Bacillus sp. BT1B_CT2]	96	0.15	13 - 107 (36.90%)
1216	NR gi 313622896 gb EFR93203.1 mannose-6-phosphate isomerase, class I [Listeria innocua FSL J1-023]	99	0.15	9 - 107 (30.61%)
1217	NR gi 307266223 ref ZP_07547765.1 mannose-6-phosphate isomerase, class I [Thermoanaerobacter wieselii Rt8.B1] >gnl BL_ORD_ID 44136 mannose-6-phosphate isomerase, class I [Thermoanaerobacter wieselii Rt8.B1]	102	0.15	13 - 113 (27.87%)
1218	NR gi 295402427 ref ZP_06812380.1 mannose-6-phosphate isomerase, class I [Geobacillus thermoglucosidasius C56-YS93] >gnl BL_ORD_ID 1970003 mannose-6-phosphate isomerase, class I [Geobacillus thermoglucosidasius C56-YS93]	107	0.15	9 - 108 (31.44%)
1219	NR gi 257876270 ref ZP_05655923.1 mannose-6-phosphate isomerase [Enterococcus casseliflavus EC20] >gnl BL_ORD_ID 695805 mannose-6-phosphate isomerase [Enterococcus casseliflavus EC20]	105	0.15	9 - 108 (29.03%)
1220	NR gi 257866670 ref ZP_05646323.1 mannose-6-phosphate isomerase [Enterococcus casseliflavus EC30] >gnl BL_ORD_ID 689813 mannose-6-phosphate isomerase [Enterococcus casseliflavus EC10] >gnl BL_ORD_ID 689813 mannose-6-phosphate isomerase [Enterococcus casseliflavus EC30] >gnl BL_ORD_ID 689813 mannose-6-phosphate isomerase [Enterococcus casseliflavus EC10]	105	0.15	9 - 108 (29.03%)
1221	NR gi 255671704 gb ACU26462.1 phosphomannose isomerase [uncultured bacterium HF186_25m_13D19]	57	0.15	52 - 107 (76.95%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1222	NR gi 255671693 gb ACU26452.1 phosphomannose isomerase [uncultured bacterium HF186_25m_18N5] >gnl BL_ORD_ID 494834 phosphomannose isomerase [uncultured bacterium HF186_25m_27D22]	57	0.15	52 - 107 (76.95%)
1223	NR gi 289578731 ref YP_003477358.1 mannose-6-phosphate isomerase, class I [Thermoanaerobacter italicus Ab9] >gnl BL_ORD_ID 443794 mannose-6-phosphate isomerase, class I [Thermoanaerobacter italicus Ab9]	102	0.15	13 - 113 (27.87%)
1224	NR gi 253576187 ref ZP_04853519.1 mannose-6-phosphate isomerase, class I [Paenibacillus sp. oral taxon 786 str. D14] >gnl BL_ORD_ID 295450 mannose-6-phosphate isomerase, class I [Paenibacillus sp. oral taxon 786 str. D14]	107	0.15	9 - 108 (32.32%)
1225	NR gi 239637437 ref ZP_04678419.1 mannose-6-phosphate isomerase, class I [Staphylococcus warneri L37603] >gnl BL_ORD_ID 30712 mannose-6-phosphate isomerase, class I [Staphylococcus warneri L37603]	107	0.15	13 - 116 (30.57%)
1226	NR gi 228975341 ref ZP_04135897.1 ManA (Mannose-6-phosphate isomerase) [Bacillus thuringiensis serovar thuringiensis str. T01001] >gnl BL_ORD_ID 2570057 ManA (Mannose-6-phosphate isomerase) [Bacillus thuringiensis serovar thuringiensis str. T01001]	101	0.15	8 - 107 (31.37%)
1227	NR gi 228942408 ref ZP_04104946.1 Mannose-6-phosphate isomerase [Bacillus thuringiensis serovar berliner ATCC 10792] >gnl BL_ORD_ID 2565711 Mannose-6-phosphate isomerase [Bacillus thuringiensis Bt407] >gnl BL_ORD_ID 2565711 Mannose-6-phosphate isomerase [Bacillus thuringiensis Bt407] >gnl BL_ORD_ID 2565711 Mannose-6-phosphate isomerase [Bacillus thuringiensis serovar berliner ATCC 10792]	101	0.15	8 - 107 (31.37%)
1228	NR gi 255691991 ref ZP_05415666.1 mannose-6-phosphate isomerase, class I [Bacteroides finegoldii DSM 17565] >gnl BL_ORD_ID 2042585 mannose-6-phosphate isomerase, class I [Bacteroides finegoldii DSM 17565]	87	0.15	27 - 105 (39.63%)
1229	NR gi 239627454 ref ZP_04670485.1 mannose-6-phosphate isomerase [Clostridiales bacterium 1_7_47_FAA] >gnl BL_ORD_ID 1839426 mannose-6-phosphate isomerase [Clostridiales bacterium 1_7_47FAA]	90	0.15	13 - 101 (39.51%)
1230	NR gi 254445420 ref ZP_05058896.1 hypothetical protein VDG1235_3663 [Verrucomicrobiae bacterium DG1235] >gnl BL_ORD_ID 878611 hypothetical protein VDG1235_3663 [Verrucomicrobiae bacterium DG1235]	125	0.15	19 - 129 (22.40%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1231	NR gi 223935171 ref ZP_03627089.1 Mannose-6-phosphate isomerase [bacterium Ellin514] >gnl BL_ORD_ID 275468 Mannose-6-phosphate isomerase [bacterium Ellin514]	89	0.15	13 - 100 (37.88%)
1232	NR gi 239828677 ref YP_002951301.1 mannose-6-phosphate isomerase, class I [Geobacillus sp. WCH70] >gnl BL_ORD_ID 158111 mannose-6-phosphate isomerase, class I [Geobacillus sp. WCH70]	107	0.15	9 - 108 (31.44%)
1233	NR gi 167763477 ref ZP_02435604.1 hypothetical protein BACSTE_01851 [Bacteroides stercoris ATCC 43183] >gnl BL_ORD_ID 2733501 hypothetical protein BACSTE_01851 [Bacteroides stercoris ATCC 43183]	87	0.15	27 - 105 (42.28%)
1234	NR gi 153808024 ref ZP_01960692.1 hypothetical protein BACCAC_02310 [Bacteroides caccae ATCC 43185] >gnl BL_ORD_ID 1784898 hypothetical protein BACCAC_02310 [Bacteroides caccae ATCC 43185]	87	0.15	27 - 105 (39.63%)
1235	NR gi 52080478 ref YP_079269.1 mannose-6-phosphate isomerase [Bacillus licheniformis ATCC 14580] >gnl BL_ORD_ID 1740840 hypothetical protein BLi02107 [Bacillus licheniformis ATCC 14580] >gnl BL_ORD_ID 1740840 mannose-6-phosphate isomerase [Bacillus licheniformis ATCC 14580] >gnl BL_ORD_ID 1740840 ManA [Bacillus licheniformis ATCC 14580]	96	0.15	13 - 107 (36.90%)
1236	NR gi 315221239 ref ZP_07863162.1 mannose-6-phosphate isomerase, class I [Streptococcus anginosus F0211] >gnl BL_ORD_ID 788472 mannose-6-phosphate isomerase, class I [Streptococcus anginosus F0211]	92	0.20	13 - 103 (37.80%)
1237	NR gi 313885527 ref ZP_07819277.1 mannose-6-phosphate isomerase, class I [Eremococcus coleocola ACS-139-V-Col8] >gnl BL_ORD_ID 599813 mannose-6-phosphate isomerase, class I [Eremococcus coleocola ACS-139-V-Col8]	110	0.20	8 - 108 (29.75%)
1238	NR gi 312863587 ref ZP_07723825.1 mannose-6-phosphate isomerase, class I [Streptococcus vestibularis F0396] >gnl BL_ORD_ID 445763 mannose-6-phosphate isomerase [Streptococcus vestibularis ATCC 49124] >gnl BL_ORD_ID 445763 mannose-6-phosphate isomerase, class I [Streptococcus vestibularis F0396] >gnl BL_ORD_ID 445763 mannose-6-phosphate isomerase [Streptococcus vestibularis ATCC 49124]	102	0.20	13 - 108 (34.60%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1239	NR gi 307708469 ref ZP_07644935.1 mannose-6-phosphate isomerase, class I [Streptococcus mitis NCTC 12261] >gnl BL_ORD_ID 137612 mannose-6-phosphate isomerase, class I [Streptococcus mitis NCTC 12261]	107	0.20	8 - 108 (29.70%)
1240	NR gi 306829168 ref ZP_07462358.1 mannose-6-phosphate isomerase [Streptococcus mitis ATCC 6249] >gnl BL_ORD_ID 2878664 mannose-6-phosphate isomerase [Streptococcus mitis ATCC 6249]	107	0.20	8 - 108 (30.57%)
1241	NR gi 304406254 ref ZP_07387911.1 mannose-6-phosphate isomerase, class I [Paenibacillus curdlanolyticus YK9] >gnl BL_ORD_ID 2852618 mannose-6-phosphate isomerase, class I [Paenibacillus curdlanolyticus YK9]	107	0.20	9 - 108 (29.70%)
1242	NR gi 300727807 ref ZP_07061189.1 phosphomannose isomerase type I [Prevotella bryantii B14] >gnl BL_ORD_ID 2469693 phosphomannose isomerase type I [Prevotella bryantii B14]	47	0.20	56 - 101 (108.64%)
1243	NR gi 296330206 ref ZP_06872687.1 putative phosphohexomutase ; cupin family protein [Bacillus subtilis subsp. spizizenii ATCC 6633] >gnl BL_ORD_ID 2104307 putative phosphohexomutase; cupin family protein [Bacillus subtilis subsp. spizizenii str. W23] >gnl BL_ORD_ID 2104307 putative phosphohexomutase ; cupin family protein [Bacillus subtilis subsp. spizizenii ATCC 6633] >gnl BL_ORD_ID 2104307 putative phosphohexomutase; cupin family protein [Bacillus subtilis subsp. spizizenii str. W23]	105	0.20	13 - 116 (29.93%)
1244	NR gi 291545798 emb CBL18906.1 mannose-6-phosphate isomerase, class I [Ruminococcus sp. SR1/5]	93	0.20	9 - 100 (35.84%)
1245	NR gi 288801357 ref ZP_06406811.1 mannose-6-phosphate isomerase, class I [Prevotella sp. oral taxon 299 str. F0039] >gnl BL_ORD_ID 1473527 mannose-6-phosphate isomerase, class I [Prevotella sp. oral taxon 299 str. F0039]	44	0.20	58 - 100 (113.64%)
1246	NR gi 284802557 ref YP_003414422.1 hypothetical protein LM5578_2313 [Listeria monocytogenes 08-5578] >gnl BL_ORD_ID 1427469 hypothetical protein LM5923_2264 [Listeria monocytogenes 08-5923] >gnl BL_ORD_ID 1427469 hypothetical protein LM5578_2313 [Listeria monocytogenes 08-5578] >gnl BL_ORD_ID 1427469 hypothetical protein LM5923_2264 [Listeria monocytogenes 08-5923]	99	0.20	9 - 107 (29.59%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1247	NR gi 282880375 ref ZP_06289086.1 mannose-6-phosphate isomerase, class I [Prevotella timonensis CRIS 5C-B1] >gnl BL_ORD_ID 1258310 mannose-6-phosphate isomerase, class I [Prevotella timonensis CRIS 5C-B1]	45	0.20	57 - 100 (108.64%)
1248	NR gi 242371636 ref ZP_04817210.1 mannose-6-phosphate isomerase [Staphylococcus epidermidis M23864:W1] >gnl BL_ORD_ID 257819 mannose-6-phosphate isomerase [Staphylococcus epidermidis M23864:W1]	107	0.20	13 - 116 (30.57%)
1249	NR gi 299822311 ref ZP_07054197.1 mannose-6-phosphate isomerase [Listeria grayi DSM 20601] >gnl BL_ORD_ID 2635443 mannose-6-phosphate isomerase [Listeria grayi DSM 20601]	106	0.20	9 - 108 (29.37%)
1250	NR gi 229099694 ref ZP_04230621.1 ManA (Mannose-6-phosphate isomerase) [Bacillus cereus Rock3-29] >gnl BL_ORD_ID 2510023 ManA (Mannose-6-phosphate isomerase) [Bacillus cereus Rock3-29]	101	0.20	8 - 107 (31.37%)
1251	NR gi 221635889 ref YP_002523765.1 mannose-6-phosphate isomerase, class I [Thermomicrobium roseum DSM 5159] >gnl BL_ORD_ID 1603107 mannose-6-phosphate isomerase, class I [Thermomicrobium roseum DSM 5159]	92	0.20	13 - 101 (33.08%)
1252	NR gi 183222429 ref YP_001840425.1 mannose-6-phosphate isomerase [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)'] >gnl BL_ORD_ID 2758394 mannose-6-phosphate isomerase [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)'] >gnl BL_ORD_ID 2758394 Mannose-6-phosphate isomerase [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)'] >gnl BL_ORD_ID 2758394 Mannose-6-phosphate isomerase (Phosphomannose isomerase) [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)']	90	0.20	13 - 101 (37.03%)
1253	NR gi 167750398 ref ZP_02422525.1 hypothetical protein EUBSIR_01372 [Eubacterium siraeum DSM 15702] >gnl BL_ORD_ID 2719127 hypothetical protein EUBSIR_01372 [Eubacterium siraeum DSM 15702] >gnl BL_ORD_ID 2719127 mannose-6-phosphate isomerase, type 1 [Eubacterium siraeum V10Sc8a]	100	0.20	3 - 101 (32%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1254	NR gi 167039962 ref YP_001662947.1 mannose-6-phosphate isomerase, class I [Thermoanaerobacter sp. X514] >gnl BL_ORD_ID 647961 mannose-6-phosphate isomerase, class I [Thermoanaerobacter ethanolicus CCSD1] >gnl BL_ORD_ID 647961 mannose-6-phosphate isomerase, class I [Thermoanaerobacter sp. X561] >gnl BL_ORD_ID 647961 mannose-6-phosphate isomerase, class I [Thermoanaerobacter sp. X513] >gnl BL_ORD_ID 647961 mannose-6-phosphate isomerase, class I [Thermoanaerobacter sp. X514] >gnl BL_ORD_ID 647961 mannose-6-phosphate isomerase, class I [Thermoanaerobacter ethanolicus CCSD1] >gnl BL_ORD_ID 647961 mannose-6-phosphate isomerase, class I [Thermoanaerobacter sp. X561] >gnl BL_ORD_ID 647961 mannose-6-phosphate isomerase, class I [Thermoanaerobacter sp. X513]	102	0.20	13 - 113 (27.87%)
1255	NR gi 27469147 ref NP_765784.1 mannose-6-phosphate isomerase [Staphylococcus epidermidis ATCC 12228] >gnl BL_ORD_ID 1686823 mannose-6-phosphate isomerase, class I [Staphylococcus epidermidis RP62A] >gnl BL_ORD_ID 1686823 mannose-6-phosphate isomerase [Staphylococcus epidermidis BCM-HMP0060] >gnl BL_ORD_ID 1686823 mannose-6-phosphate isomerase, class I [Staphylococcus epidermidis SK135] >gnl BL_ORD_ID 1686823 mannose-6-phosphate isomerase [Staphylococcus epidermidis M23864:W2(grey)] >gnl BL_ORD_ID 1686823 mannose-6-phosphate isomerase [Staphylococcus epidermidis ATCC 12228] >gnl BL_ORD_ID 1686823 mannose-6-phosphate isomerase, class I [Staphylococcus epidermidis RP62A] >gnl BL_ORD_ID 1686823 mannose-6-phosphate isomerase [Staphylococcus epidermidis BCM-HMP0060] >gnl BL_ORD_ID 1686823 mannose-6-phosphate isomerase, class I [Staphylococcus epidermidis SK135] >gnl BL_ORD_ID 1686823 mannose-6-phosphate isomerase [Staphylococcus epidermidis M23864:W2(grey)]	106	0.20	9 - 108 (32.93%)
1256	NR gi 167037161 ref YP_001664739.1 mannose-6-phosphate isomerase, class I [Thermoanaerobacter pseudethanolicus ATCC 33223] >gnl BL_ORD_ID 409211 mannose-6-phosphate isomerase, class I [Thermoanaerobacter brockii subsp. finnij Ako-1] >gnl BL_ORD_ID 409211 mannose-6-phosphate isomerase, class I [Thermoanaerobacter pseudethanolicus ATCC 33223] >gnl BL_ORD_ID 409211 mannose-6-phosphate isomerase, class I [Thermoanaerobacter brockii subsp. finnij Ako-1]	102	0.20	13 - 113 (27.87%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1257	NR gi 315283177 ref ZP_07871428.1 mannose-6-phosphate isomerase, class I [Listeria marthii FSL S4-120] >gnl BL_ORD_ID 704715 mannose-6-phosphate isomerase, class I [Listeria marthii FSL S4-120]	99	0.26	9 - 107 (29.59%)
1258	NR gi 311067027 ref YP_003971950.1 mannose-6-phosphate isomerase manA [Bacillus atrophaeus 1942] >gnl BL_ORD_ID 421370 mannose-6-phosphate isomerase manA [Bacillus atrophaeus 1942]	89	0.26	13 - 100 (44.19%)
1259	NR gi 307704554 ref ZP_07641460.1 mannose-6-phosphate isomerase, class I [Streptococcus mitis SK597] >gnl BL_ORD_ID 143012 mannose-6-phosphate isomerase, class I [Streptococcus mitis SK597]	107	0.26	8 - 108 (29.70%)
1260	NR gi 307706971 ref ZP_07643770.1 mannose-6-phosphate isomerase, class I [Streptococcus mitis SK321] >gnl BL_ORD_ID 139421 mannose-6-phosphate isomerase, class I [Streptococcus mitis SK321]	107	0.26	8 - 108 (29.70%)
1261	NR gi 306825622 ref ZP_07458961.1 mannose-6-phosphate isomerase [Streptococcus sp. oral taxon 071 str. 73H25AP] >gnl BL_ORD_ID 2881198 mannose-6-phosphate isomerase [Streptococcus sp. oral taxon 071 str. 73H25AP]	107	0.26	8 - 108 (29.70%)
1262	NR gi 302669368 ref YP_003832518.1 mannose-6-phosphate isomerase ManA [Butyrivibrio proteoclasticus B316] >gnl BL_ORD_ID 2770811 mannose-6-phosphate isomerase ManA [Butyrivibrio proteoclasticus B316]	112	0.26	3 - 108 (24.71%)
1263	NR gi 301301109 ref ZP_07207266.1 mannose-6-phosphate isomerase, class I [Lactobacillus salivarius ACS-116-V-Col5a] >gnl BL_ORD_ID 2658144 mannose-6-phosphate isomerase, class I [Lactobacillus salivarius ACS-116-V-Col5a]	106	0.26	9 - 108 (31.15%)
1264	NR gi 300215193 gb ADJ79609.1 Mannose-6-phosphate isomerase [Lactobacillus salivarius CECT 5713]	106	0.26	9 - 108 (31.15%)
1265	NR gi 291514171 emb CBK63381.1 mannose-6-phosphate isomerase, type 1 [Alistipes shahii WAL 8301]	61	0.26	57 - 116 (69.87%)
1266	NR gi 293365047 ref ZP_06611764.1 mannose-6-phosphate isomerase [Streptococcus oralis ATCC 35037] >gnl BL_ORD_ID 1702332 mannose-6-phosphate isomerase, class I [Streptococcus oralis ATCC 35037] >gnl BL_ORD_ID 1702332 mannose-6-phosphate isomerase [Streptococcus oralis ATCC 35037] >gnl BL_ORD_ID 1702332 mannose-6-phosphate isomerase, class I [Streptococcus oralis ATCC 35037]	107	0.26	8 - 108 (29.70%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1267	NR gi 289168260 ref YP_003446529.1 mannose-6-phosphate isomerase [Streptococcus mitis B6] >gnl BL_ORD_ID 1511934 mannose-6-phosphate isomerase [Streptococcus mitis B6]	107	0.26	8 - 108 (29.70%)
1268	NR gi 270292267 ref ZP_06198481.1 mannose-6-phosphate isomerase [Streptococcus sp. M143] >gnl BL_ORD_ID 1181955 mannose-6-phosphate isomerase [Streptococcus sp. M143]	107	0.26	8 - 108 (29.70%)
1269	NR gi 260170848 ref ZP_05757260.1 mannose-6-phosphate isomerase [Bacteroides sp. D2] >gnl BL_ORD_ID 812773 conserved hypothetical protein [Bacteroides sp. D2] >gnl BL_ORD_ID 812773 conserved hypothetical protein [Bacteroides sp. D2]	87	0.26	27 - 105 (38.31%)
1270	NR gi 238927179 ref ZP_04658939.1 possible mannose-6-phosphate isomerase [Selenomonas flueggei ATCC 43531] >gnl BL_ORD_ID 2903682 possible mannose-6-phosphate isomerase [Selenomonas flueggei ATCC 43531]	100	0.26	3 - 101 (30%)
1271	NR gi 228942402 ref ZP_04104940.1 ManA (Mannose-6-phosphate isomerase) [Bacillus thuringiensis serovar berliner ATCC 10792] >gnl BL_ORD_ID 2565705 ManA (Mannose-6-phosphate isomerase) [Bacillus thuringiensis serovar thuringiensis str. T01001] >gnl BL_ORD_ID 2565705 ManA (Mannose-6-phosphate isomerase) [Bacillus thuringiensis Bt407] >gnl BL_ORD_ID 2565705 ManA (Mannose-6-phosphate isomerase) [Bacillus thuringiensis Bt407] >gnl BL_ORD_ID 2565705 ManA (Mannose-6-phosphate isomerase) [Bacillus thuringiensis serovar thuringiensis str. T01001] >gnl BL_ORD_ID 2565705 ManA (Mannose-6-phosphate isomerase) [Bacillus thuringiensis serovar berliner ATCC 10792]	96	0.26	13 - 107 (37.98%)
1272	NR gi 227891356 ref ZP_04009161.1 mannose-6-phosphate isomerase [Lactobacillus salivarius ATCC 11741] >gnl BL_ORD_ID 2395443 mannose-6-phosphate isomerase [Lactobacillus salivarius ATCC 11741]	106	0.26	9 - 108 (31.15%)
1273	NR gi 225390492 ref ZP_03760216.1 hypothetical protein CLOSTASPAR_04247 [Clostridium asparagiforme DSM 15981] >gnl BL_ORD_ID 1926733 hypothetical protein CLOSTASPAR_04247 [Clostridium asparagiforme DSM 15981]	90	0.26	13 - 101 (37.03%)
1274	NR gi 198274206 ref ZP_03206738.1 hypothetical protein BACPLE_00346 [Bacteroides plebeius DSM 17135] >gnl BL_ORD_ID 890787 hypothetical protein BACPLE_00346 [Bacteroides plebeius DSM 17135]	61	0.26	42 - 101 (69.87%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1275	NR gi 74052658 gb AAZ95238.1 phosphomannose isomerase [Bacillus subtilis]	103	0.26	13 - 108 (32.99%)
1276	NR gi 15896171 ref NP_349520.1 mannose-6 phosphate isomelase [Clostridium acetobutylicum ATCC 824] >gnl BL_ORD_ID 1660868 Mannose-6 phosphate isomelase [Clostridium acetobutylicum ATCC 824]	158	0.26	236 - 388 (14.82%)
1277	NR gi 163847400 ref YP_001635444.1 mannose-6-phosphate isomerase [Chloroflexus aurantiacus J-10-fl] >gnl BL_ORD_ID 406965 Mannose-6-phosphate isomerase [Chloroflexus sp. Y-400-fl] >gnl BL_ORD_ID 406965 Mannose-6-phosphate isomerase [Chloroflexus aurantiacus J-10-fl] >gnl BL_ORD_ID 406965 Mannose-6-phosphate isomerase [Chloroflexus sp. Y-400-fl]	90	0.26	13 - 101 (33.33%)
1278	NR gi 322376954 ref ZP_08051447.1 mannose-6-phosphate isomerase, class I [Streptococcus sp. M334] >gnl BL_ORD_ID 1190070 mannose-6-phosphate isomerase, class I [Streptococcus sp. M334]	107	0.34	8 - 108 (29.70%)
1279	NR gi 315660302 ref ZP_07913157.1 mannose-6-phosphate isomerase [Staphylococcus lugdunensis M23590] >gnl BL_ORD_ID 835456 mannose-6-phosphate isomerase [Staphylococcus lugdunensis M23590]	91	0.34	13 - 100 (37.44%)
1280	NR gi 323344801 ref ZP_08085025.1 mannose-6-phosphate isomerase [Prevotella oralis ATCC 33269] >gnl BL_ORD_ID 811935 mannose-6-phosphate isomerase [Prevotella oralis ATCC 33269]	51	0.34	53 - 100 (92.27%)
1281	NR gi 313636908 gb EFS02512.1 mannose-6-phosphate isomerase, class I [Listeria seeligeri FSL S4-171]	106	0.34	9 - 108 (28.48%)
1282	NR gi 312143102 ref YP_003994548.1 mannose-6-phosphate isomerase, class I [Halanaerobium sp. 'sapolanicus'] >gnl BL_ORD_ID 536681 mannose-6-phosphate isomerase, class I [Halanaerobium sp. 'sapolanicus']	117	0.34	13 - 126 (27.03%)
1283	NR gi 309775165 ref ZP_07670177.1 mannose-6-phosphate isomerase, class I [Erysipelotrichaceae bacterium 3_1_53] >gnl BL_ORD_ID 302625 mannose-6-phosphate isomerase, class I [Erysipelotrichaceae bacterium 3_1_53]	84	0.34	19 - 101 (35.43%)
1284	NR gi 309799988 ref ZP_07694188.1 mannose-6-phosphate isomerase, class I [Streptococcus infantis SK1302] >gnl BL_ORD_ID 213516 mannose-6-phosphate isomerase, class I [Streptococcus infantis SK1302]	107	0.34	8 - 108 (29.70%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1285	NR gi 308068127 ref YP_003869732.1 Mannose-6-phosphate isomerase (Phosphomannose isomerase) [Paenibacillus polymyxa E681] >gnl BL_ORD_ID 2901902 Mannose-6-phosphate isomerase (Phosphomannose isomerase) [Paenibacillus polymyxa E681]	160	0.34	13 - 161 (17.19%)
1286	NR gi 298373597 ref ZP_06983586.1 mannose-6-phosphate isomerase, class I [Bacteroidetes oral taxon 274 str. F0058] >gnl BL_ORD_ID 2337052 mannose-6-phosphate isomerase, class I [Bacteroidetes oral taxon 274 str. F0058]	61	0.34	57 - 116 (64.49%)
1287	NR gi 291530931 emb CBK96516.1 mannose-6-phosphate isomerase, type 1 [Eubacterium siraeum 70/3]	100	0.34	3 - 101 (30%)
1288	NR gi 269963772 ref ZP_06178090.1 conserved hypothetical protein [Vibrio harveyi 1DA3] >gnl BL_ORD_ID 1115614 conserved hypothetical protein [Vibrio harveyi 1DA3]	61	0.34	331 - 390 (53.75%)
1289	NR gi 255029115 ref ZP_05301066.1 hypothetical protein LmonL_08251 [Listeria monocytogenes LO28]	99	0.34	9 - 107 (29.59%)
1290	NR gi 224477133 ref YP_002634739.1 putative mannose-6-phosphate isomerase [Staphylococcus carnosus subsp. carnosus TM300] >gnl BL_ORD_ID 1672873 putative mannose-6-phosphate isomerase [Staphylococcus carnosus subsp. carnosus TM300]	90	0.34	13 - 101 (38.27%)
1291	NR gi 210632331 ref ZP_03297298.1 hypothetical protein COLSTE_01192 [Collinsella stercoris DSM 13279] >gnl BL_ORD_ID 1117559 hypothetical protein COLSTE_01192 [Collinsella stercoris DSM 13279]	102	0.34	3 - 101 (30.75%)
1292	NR gi 169345742 ref ZP_02865701.1 mannose-6-phosphate isomerase, class I [Clostridium perfringens C str. JGS1495] >gnl BL_ORD_ID 2867298 mannose-6-phosphate isomerase, class I [Clostridium perfringens C str. JGS1495]	159	0.34	236 - 388 (14.24%)
1293	NR gi 139439549 ref ZP_01772981.1 Hypothetical protein COLAER_02008 [Collinsella aerofaciens ATCC 25986] >gnl BL_ORD_ID 1410799 Hypothetical protein COLAER_02008 [Collinsella aerofaciens ATCC 25986]	92	0.34	13 - 101 (35.45%)
1294	NR gi 110803662 ref YP_698527.1 mannose-6-phosphate isomerase, class I [Clostridium perfringens SM101] >gnl BL_ORD_ID 455446 mannose-6-phosphate isomerase, class I [Clostridium perfringens SM101]	159	0.34	236 - 388 (14.24%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1295	NR gi 90962582 ref YP_536498.1 mannose-6-phosphate isomerase [Lactobacillus salivarius UCC118] >gnl BL_ORD_ID 2490237 Mannose-6-phosphate isomerase [Lactobacillus salivarius UCC118]	106	0.34	9 - 108 (31.15%)
1296	NR gi 18310169 ref NP_562103.1 mannose-6-phosphate isomerase, class I [Clostridium perfringens str. 13] >gnl BL_ORD_ID 1102293 mannose-6-phosphate isomerase, class I [Clostridium perfringens ATCC 13124] >gnl BL_ORD_ID 1102293 mannose-6-phosphate isomerase, class I [Clostridium perfringens E str. JGS1987] >gnl BL_ORD_ID 1102293 mannose-6-phosphate isomerase, class I [Clostridium perfringens CPE str. F4969] >gnl BL_ORD_ID 1102293 mannose-6-phosphate isomerase, class I [Clostridium perfringens NCTC 8239] >gnl BL_ORD_ID 1102293 mannose-6-phosphate isomerase, class I [Clostridium perfringens D str. JGS1721] >gnl BL_ORD_ID 1102293 mannose-6-phosphate isomerase [Clostridium perfringens str. 13] >gnl BL_ORD_ID 1102293 mannose-6-phosphate isomerase, class I [Clostridium perfringens ATCC 13124] >gnl BL_ORD_ID 1102293 mannose-6-phosphate isomerase, class I [Clostridium perfringens E str. JGS1987] >gnl BL_ORD_ID 1102293 mannose-6-phosphate isomerase, class I [Clostridium perfringens CPE str. F4969] >gnl BL_ORD_ID 1102293 mannose-6-phosphate isomerase, class I [Clostridium perfringens D str. JGS1721] >gnl BL_ORD_ID 1102293 mannose-6-phosphate isomerase, class I [Clostridium perfringens NCTC 8239]	159	0.34	236 - 388 (14.24%)
1297	NR gi 16804149 ref NP_465634.1 hypothetical protein lmo2110 [Listeria monocytogenes EGD-e] >gnl BL_ORD_ID 863354 hypothetical protein LmonFR_00980 [Listeria monocytogenes FSL R2-561] >gnl BL_ORD_ID 863354 lmo2110 [Listeria monocytogenes EGD-e]	99	0.34	9 - 107 (29.59%)
1298	NR gi 89095821 ref ZP_01168715.1 mannose-6-phosphate isomerase [Bacillus sp. NRRL B-14911] >gnl BL_ORD_ID 689000 mannose-6-phosphate isomerase [Bacillus sp. NRRL B-14911]	109	0.34	9 - 116 (29.46%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1299	NR gi 47095822 ref ZP_00233427.1 mannose-6-phosphate isomerase, class I [Listeria monocytogenes str. 1/2a F6854] >gnl BL_ORD_ID 166071 mannose-6-phosphate isomerase [Listeria monocytogenes FSL N3-165] >gnl BL_ORD_ID 166071 hypothetical protein LmonJ_05234 [Listeria monocytogenes J0161] >gnl BL_ORD_ID 166071 mannose-6-phosphate isomerase [Listeria monocytogenes J2818] >gnl BL_ORD_ID 166071 mannose-6-phosphate isomerase [Listeria monocytogenes F6900] >gnl BL_ORD_ID 166071 hypothetical protein LmonocytFSL_06285 [Listeria monocytogenes FSL J2-003] >gnl BL_ORD_ID 166071 mannose-6-phosphate isomerase, class I [Listeria monocytogenes str. 1/2a F6854] >gnl BL_ORD_ID 166071 mannose-6-phosphate isomerase [Listeria monocytogenes FSL N3-165] >gnl BL_ORD_ID 166071 mannose-6-phosphate isomerase [Listeria monocytogenes F6900] >gnl BL_ORD_ID 166071 mannose-6-phosphate isomerase [Listeria monocytogenes J2818]	99	0.34	9 - 107 (29.59%)
1300	NR gi 321313123 ref YP_004205410.1 putative phosphohexomutase ; cupin family protein [Bacillus subtilis BSn5] >gnl BL_ORD_ID 1080969 putative phosphohexomutase ; cupin family protein [Bacillus subtilis BSn5]	105	0.45	13 - 116 (31.74%)
1301	NR gi 315128499 gb EFT84505.1 mannose-6-phosphate isomerase [Staphylococcus aureus subsp. aureus CGS03]	90	0.45	13 - 101 (37.03%)
1302	NR gi 313607603 gb EFR83883.1 mannose-6-phosphate isomerase, class I [Listeria monocytogenes FSL F2-208]	99	0.45	9 - 107 (29.59%)
1303	NR gi 313900446 ref ZP_07833939.1 mannose-6-phosphate isomerase, class I [Clostridium sp. HGF2] >gnl BL_ORD_ID 618460 mannose-6-phosphate isomerase, class I [Clostridium sp. HGF2]	161	0.45	235 - 383 (14.27%)
1304	NR gi 295111788 emb CBL28538.1 mannose-6-phosphate isomerase, class I [Synergistetes bacterium SGP1]	94	0.45	9 - 101 (32.82%)
1305	NR gi 289435460 ref YP_003465332.1 mannose-6-phosphate isomerase [Listeria seeligeri serovar 1/2b str. SLCC3954] >gnl BL_ORD_ID 1528885 mannose-6-phosphate isomerase [Listeria seeligeri serovar 1/2b str. SLCC3954]	106	0.45	9 - 108 (28.48%)
1306	NR gi 255017331 ref ZP_05289457.1 mannose-6-phosphate isomerase, class I [Listeria monocytogenes FSL F2-515]	99	0.45	9 - 107 (29.59%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1307	NR gi 227485594 ref ZP_03915910.1 mannose-6-phosphate isomerase [Anaerococcus lactolyticus ATCC 51172] >gnl BL_ORD_ID 2310843 mannose-6-phosphate isomerase [Anaerococcus lactolyticus ATCC 51172]	105	0.45	13 - 116 (33.56%)
1308	NR gi 290894123 ref ZP_06557095.1 mannose-6-phosphate isomerase [Listeria monocytogenes FSL J2-071] >gnl BL_ORD_ID 2024887 mannose-6-phosphate isomerase [Listeria monocytogenes FSL J2-071]	99	0.45	9 - 107 (29.59%)
1309	NR gi 217963729 ref YP_002349407.1 mannose-6-phosphate isomerase, class I [Listeria monocytogenes HCC23] >gnl BL_ORD_ID 1322277 mannose-6-phosphate isomerase, class I [Listeria monocytogenes HCC23] >gnl BL_ORD_ID 1322277 mannose-6-phosphate isomerase, class I [Listeria monocytogenes L99]	99	0.45	9 - 107 (29.59%)
1310	NR gi 251795224 ref YP_003009955.1 mannose-6-phosphate isomerase, class I [Paenibacillus sp. JDR-2] >gnl BL_ORD_ID 24647 mannose-6-phosphate isomerase, class I [Paenibacillus sp. JDR-2]	107	0.45	9 - 108 (28.82%)
1311	NR gi 163789311 ref ZP_02183752.1 mannose-6-phosphate isomerase [Flavobacteriales bacterium ALC-1] >gnl BL_ORD_ID 2355314 mannose-6-phosphate isomerase [Flavobacteriales bacterium ALC-1]	101	0.45	13 - 105 (31.37%)
1312	NR gi 160938229 ref ZP_02085584.1 hypothetical protein CLOBOL_03125 [Clostridium bolteae ATCC BAA-613] >gnl BL_ORD_ID 2292944 hypothetical protein CLOBOL_03125 [Clostridium bolteae ATCC BAA-613]	90	0.45	13 - 101 (38.27%)
1313	NR gi 224498444 ref ZP_03666793.1 hypothetical protein LmonF1_01619 [Listeria monocytogenes Finland 1988] >gnl BL_ORD_ID 2175052 hypothetical protein Lmon1_09843 [Listeria monocytogenes 10403S]	99	0.45	9 - 107 (29.59%)
1314	NR gi 154687991 ref YP_001423152.1 YdhS [Bacillus amyloliquefaciens FZB42] >gnl BL_ORD_ID 2033296 YdhS [Bacillus amyloliquefaciens FZB42]	103	0.45	13 - 108 (32.99%)
1315	NR gi 150025834 ref YP_001296660.1 mannose-6-phosphate isomerase [Flavobacterium psychrophilum JIP02/86] >gnl BL_ORD_ID 1853770 Mannose-6-phosphate isomerase [Flavobacterium psychrophilum JIP02/86]	110	0.45	13 - 105 (28.10%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1316	NR gi 46908346 ref YP_014735.1 mannose-6-phosphate isomerase, class I [Listeria monocytogenes str. 4b F2365] >gnl BL_ORD_ID 1790391 mannose-6-phosphate isomerase [Listeria monocytogenes FSL J1-194] >gnl BL_ORD_ID 1790391 mannose-6-phosphate isomerase, class I [Listeria monocytogenes FSL J1-175] >gnl BL_ORD_ID 1790391 mannose-6-phosphate isomerase, class I [Listeria monocytogenes serotype 4b str. F2365] >gnl BL_ORD_ID 1790391 mannose-6-phosphate isomerase [Listeria monocytogenes FSL J1-194]	99	0.45	9 - 107 (29.59%)
1317	NR gi 51893121 ref YP_075812.1 mannose-6 phosphate isomerase [Symbiobacterium thermophilum IAM 14863] >gnl BL_ORD_ID 1321219 mannose-6 phosphate isomerase [Symbiobacterium thermophilum IAM 14863]	94	0.45	13 - 100 (38.48%)
1318	NR gi 46015375 pdb 1QWR A Chain A, Crystal Structure Analysis Of The Mannose 6-Phosphate Isomerase From Bacillus Subtilis >gnl BL_ORD_ID 1236618 Chain B, Crystal Structure Analysis Of The Mannose 6-Phosphate Isomerase From Bacillus Subtilis	105	0.45	13 - 116 (31.74%)
1319	NR gi 16080632 ref NP_391460.1 phosphohexomutase ; cupin family [Bacillus subtilis subsp. subtilis str. 168] >gnl BL_ORD_ID 967610 mannose-6-phosphate isomerase [Bacillus subtilis subsp. subtilis str. 168] >gnl BL_ORD_ID 967610 mannose-6-phosphate isomerase [Bacillus subtilis subsp. subtilis str. NCIB 3610] >gnl BL_ORD_ID 967610 mannose-6-phosphate isomerase [Bacillus subtilis subsp. subtilis str. JH642] >gnl BL_ORD_ID 967610 mannose-6-phosphate isomerase [Bacillus subtilis subsp. subtilis str. SMY] >gnl BL_ORD_ID 967610 RecName: Full=Putative mannose-6-phosphate isomerase yvyl; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 967610 unknown [Bacillus subtilis subsp. subtilis str. 168] >gnl BL_ORD_ID 967610 hypothetical protein [Bacillus subtilis] >gnl BL_ORD_ID 967610 putative phosphohexomutase ; cupin family [Bacillus subtilis subsp. subtilis str. 168]	105	0.45	13 - 116 (31.74%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1320	NR gi 47091780 ref ZP_00229575.1 mannose-6-phosphate isomerase, class I [Listeria monocytogenes str. 4b H7858] >gnl BL_ORD_ID 167566 mannose-6 phosphate isomerase [Listeria monocytogenes Clip81459] >gnl BL_ORD_ID 167566 mannose-6-phosphate isomerase [Listeria monocytogenes FSL R2-503] >gnl BL_ORD_ID 167566 mannose-6-phosphate isomerase [Listeria monocytogenes HPB2262] >gnl BL_ORD_ID 167566 mannose-6-phosphate isomerase, class I [Listeria monocytogenes FSL N1-017] >gnl BL_ORD_ID 167566 mannose-6-phosphate isomerase, class I [Listeria monocytogenes str. 4b H7858] >gnl BL_ORD_ID 167566 Putative mannose-6 phosphate isomerase [Listeria monocytogenes serotype 4b str. CLIP 80459] >gnl BL_ORD_ID 167566 mannose-6-phosphate isomerase [Listeria monocytogenes FSL R2-503] >gnl BL_ORD_ID 167566 mannose-6-phosphate isomerase [Listeria monocytogenes HPB2262] >gnl BL_ORD_ID 167566 mannose-6-phosphate isomerase, class I [Listeria monocytogenes FSL N1-017]	99	0.45	9 - 107 (29.59%)
1321	NR gi 314934213 ref ZP_07841574.1 mannose-6-phosphate isomerase, class I [Staphylococcus caprae C87] >gnl BL_ORD_ID 726088 mannose-6-phosphate isomerase, class I [Staphylococcus caprae C87]	107	0.58	13 - 116 (29.70%)
1322	NR gi 315304215 ref ZP_07874581.1 mannose-6-phosphate isomerase, class I [Listeria ivanovii FSL F6-596] >gnl BL_ORD_ID 712302 mannose-6-phosphate isomerase, class I [Listeria ivanovii FSL F6-596]	106	0.58	9 - 108 (29.37%)
1323	NR gi 311070083 ref YP_003975006.1 putative phosphohexomutase ; cupin family protein [Bacillus atrophaeus 1942] >gnl BL_ORD_ID 424393 putative phosphohexomutase ; cupin family protein [Bacillus atrophaeus 1942]	103	0.58	13 - 108 (32.99%)
1324	NR gi 309388749 gb ADO76629.1 mannose-6-phosphate isomerase, class I [Halanaerobium praevalens DSM 2228]	117	0.58	13 - 126 (27.03%)
1325	NR gi 302392875 ref YP_003828695.1 mannose-6-phosphate isomerase, type 1 [Acetohalobium arabaticum DSM 5501] >gnl BL_ORD_ID 2757923 mannose-6-phosphate isomerase, type 1 [Acetohalobium arabaticum DSM 5501]	122	0.58	33 - 148 (22.17%)
1326	NR gi 294675498 ref YP_003576114.1 mannose-6-phosphate isomerase, class I [Prevotella ruminicola 23] >gnl BL_ORD_ID 1933871 mannose-6-phosphate isomerase, class I [Prevotella ruminicola 23]	91	0.58	57 - 136 (33.81%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1327	NR gi 290579824 ref YP_003484216.1 mannose-6-phosphate isomerase [Streptococcus mutans NN2025] >gnl BL_ORD_ID 409386 mannose-6-phosphate isomerase [Streptococcus mutans NN2025]	102	0.58	13 - 108 (32.68%)
1328	NR gi 254992985 ref ZP_05275175.1 mannose-6-phosphate isomerase, class I [Listeria monocytogenes FSL J2-064]	99	0.58	9 - 107 (29.59%)
1329	NR gi 241895242 ref ZP_04782538.1 mannose-6-phosphate isomerase [Weissella paramesenteroides ATCC 33313] >gnl BL_ORD_ID 196211 mannose-6-phosphate isomerase [Weissella paramesenteroides ATCC 33313]	104	0.58	13 - 108 (32.36%)
1330	NR gi 297565367 ref YP_003684339.1 Mannose-6-phosphate isomerase [Meiothermus silvanus DSM 9946] >gnl BL_ORD_ID 2408454 Mannose-6-phosphate isomerase [Meiothermus silvanus DSM 9946]	90	0.58	13 - 101 (38.27%)
1331	NR gi 254557159 ref YP_003063576.1 mannose-6-phosphate isomerase [Lactobacillus plantarum JDM1] >gnl BL_ORD_ID 2389070 mannose-6-phosphate isomerase [Lactobacillus plantarum subsp. plantarum ATCC 14917] >gnl BL_ORD_ID 2389070 mannose-6-phosphate isomerase [Lactobacillus plantarum subsp. plantarum ST-III] >gnl BL_ORD_ID 2389070 mannose-6-phosphate isomerase [Lactobacillus plantarum JDM1] >gnl BL_ORD_ID 2389070 mannose-6-phosphate isomerase [Lactobacillus plantarum subsp. plantarum ATCC 14917] >gnl BL_ORD_ID 2389070 mannose-6-phosphate isomerase [Lactobacillus plantarum subsp. plantarum ST-III]	102	0.58	13 - 108 (30.75%)
1332	NR gi 223043932 ref ZP_03613973.1 mannose-6-phosphate isomerase, class I [Staphylococcus capitis SK14] >gnl BL_ORD_ID 1681570 mannose-6-phosphate isomerase, class I [Staphylococcus capitis SK14]	107	0.58	13 - 116 (29.70%)
1333	NR gi 24380201 ref NP_722156.1 mannose-6-phosphate isomerase [Streptococcus mutans UA159] >gnl BL_ORD_ID 846572 RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI >gnl BL_ORD_ID 846572 mannose-6-phosphate isomerase [Streptococcus mutans UA159]	102	0.58	13 - 108 (32.68%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1334	NR gi 28378954 ref NP_785846.1 mannose-6-phosphate isomerase [Lactobacillus plantarum WCFS1] >gnl BL_ORD_ID 826879 mannose-6-phosphate isomerase [Lactobacillus plantarum WCFS1]	102	0.58	13 - 108 (30.75%)
1335	NR gi 451216 dbj BAA04021.1 Mannosephosphate Isomerase [Streptococcus mutans]	102	0.58	13 - 108 (32.68%)
1336	NR gi 116493082 ref YP_804817.1 phosphomannose isomerase [Pediococcus pentosaceus ATCC 25745] >gnl BL_ORD_ID 181457 Phosphomannose isomerase [Pediococcus pentosaceus ATCC 25745]	102	0.58	13 - 108 (31.72%)
1337	NR gi 110636889 ref YP_677096.1 mannose-6-phosphate isomerase [Cytophaga hutchinsonii ATCC 33406] >gnl BL_ORD_ID 75924 mannose-6-phosphate isomerase, type 1 [Cytophaga hutchinsonii ATCC 33406]	91	0.58	13 - 101 (36.23%)
1338	NR gi 322374658 ref ZP_08049172.1 mannose-6-phosphate isomerase, class I [Streptococcus sp. C300] >gnl BL_ORD_ID 1187860 mannose-6-phosphate isomerase, class I [Streptococcus sp. C300]	107	0.76	8 - 108 (29.70%)
1339	NR gi 320335370 ref YP_004172081.1 Mannose-6-phosphate isomerase [Deinococcus maricopensis DSM 21211] >gnl BL_ORD_ID 1056198 Mannose-6-phosphate isomerase [Deinococcus maricopensis DSM 21211]	75	0.76	28 - 101 (48%)
1340	NR gi 310640915 ref YP_003945673.1 mannose-6-phosphate isomerase, class i [Paenibacillus polymyxa SC2] >gnl BL_ORD_ID 310959 Mannose-6-phosphate isomerase, class I [Paenibacillus polymyxa SC2]	158	0.76	13 - 161 (16.82%)
1341	NR gi 302391013 ref YP_003826833.1 mannose-6-phosphate isomerase, type 1 [Acetohalobium arabaticum DSM 5501] >gnl BL_ORD_ID 2756064 mannose-6-phosphate isomerase, type 1 [Acetohalobium arabaticum DSM 5501]	120	0.76	27 - 141 (22.23%)
1342	NR gi 302344115 ref YP_003808644.1 Mannose-6-phosphate isomerase [Desulfarculus baarsii DSM 2075] >gnl BL_ORD_ID 2713742 Mannose-6-phosphate isomerase [Desulfarculus baarsii DSM 2075]	92	0.76	13 - 101 (33.08%)
1343	NR gi 291486145 dbj BAI87220.1 mannose-6-phosphate isomerase [Bacillus subtilis subsp. natto BEST195]	105	0.76	13 - 116 (31.74%)
1344	NR gi 288927418 ref ZP_06421265.1 mannose-6-phosphate isomerase, class I [Prevotella sp. oral taxon 317 str. F0108] >gnl BL_ORD_ID 1472150 mannose-6-phosphate isomerase, class I [Prevotella sp. oral taxon 317 str. F0108]	72	0.76	31 - 100 (52.08%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1345	NR gi 260911298 ref ZP_05917897.1 mannose-6-phosphate isomerase [Prevotella sp. oral taxon 472 str. F0295] >gn BL_ORD_ID 876789 mannose-6-phosphate isomerase [Prevotella sp. oral taxon 472 str. F0295]	72	0.76	31 - 100 (52.08%)
1346	NR gi 242372378 ref ZP_04817952.1 mannose-6-phosphate isomerase [Staphylococcus epidermidis M23864:W1] >gn BL_ORD_ID 257095 mannose-6-phosphate isomerase [Staphylococcus epidermidis M23864:W1]	106	0.76	9 - 108 (31.15%)
1347	NR gi 228936549 ref ZP_04099345.1 ManA (Mannose-6-phosphate isomerase) [Bacillus thuringiensis serovar andalusiensis BGSC 4AW1] >gn BL_ORD_ID 2584454 ManA (Mannose-6-phosphate isomerase) [Bacillus thuringiensis serovar andalusiensis BGSC 4AW1]	96	0.76	13 - 107 (37.98%)
1348	NR gi 229147793 ref ZP_04276136.1 ManA (Mannose-6-phosphate isomerase) [Bacillus cereus BDRD-ST24] >gn BL_ORD_ID 2485685 ManA (Mannose-6-phosphate isomerase) [Bacillus cereus BDRD-ST24]	96	0.76	13 - 107 (37.98%)
1349	NR gi 225867241 ref YP_002752619.1 mannose-6-phosphate isomerase, class I [Bacillus cereus 03BB102] >gn BL_ORD_ID 2111910 mannose-6-phosphate isomerase, class I [Bacillus cereus 03BB102]	101	0.76	8 - 107 (31.37%)
1350	NR gi 222098722 ref YP_002532780.1 mana [Bacillus cereus Q1] >gn BL_ORD_ID 1623009 ManA [Bacillus cereus Q1]	96	0.76	13 - 107 (37.98%)
1351	NR gi 195189477 ref XP_002029447.1 GL26959 [Drosophila persimilis] >gn BL_ORD_ID 584133 GL26959 [Drosophila persimilis]	37	0.76	224 - 260 (131.49%)
1352	NR gi 187935609 ref YP_001887310.1 mannose-6-phosphate isomerase, class I [Clostridium botulinum B str. Eklund 17B] >gn BL_ORD_ID 310936 mannose-6-phosphate isomerase, class I [Clostridium botulinum B str. Eklund 17B]	71	0.76	33 - 101 (45.62%)
1353	NR gi 182413486 ref YP_001818552.1 mannose-6-phosphate isomerase type I [Opitutus terrae PB90-1] >gn BL_ORD_ID 213424 mannose-6-phosphate isomerase type I [Opitutus terrae PB90-1]	95	0.76	9 - 100 (32.14%)
1354	NR gi 163787317 ref ZP_02181764.1 mannose-6-phosphate isomerase [Flavobacteriales bacterium ALC-1] >gn BL_ORD_ID 2357132 mannose-6-phosphate isomerase [Flavobacteriales bacterium ALC-1]	106	0.76	13 - 116 (30.26%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1355	NR gi 219848627 ref YP_002463060.1 Mannose-6-phosphate isomerase [Chloroflexus aggregans DSM 9485] >gnl BL_ORD_ID 803734 Mannose-6-phosphate isomerase [Chloroflexus aggregans DSM 9485]	90	0.76	13 - 101 (32.10%)
1356	NR gi 15616478 ref NP_244784.1 mannose-6-phosphate isomerase [Bacillus halodurans C-125] >gnl BL_ORD_ID 1023908 mannose-6 phosphate isomelase [Bacillus halodurans] >gnl BL_ORD_ID 1023908 mannose-6-phosphate isomerase [Bacillus halodurans C-125]	103	0.76	13 - 108 (34.87%)
1357	NR gi 86131967 ref ZP_01050563.1 mannose-6-phosphate isomerase [Dokdonia donghaensis MED134] >gnl BL_ORD_ID 573168 mannose-6-phosphate isomerase [Dokdonia donghaensis MED134]	45	0.76	57 - 100 (103.71%)
1358	NR gi 323187166 gb EFZ72480.1 hypothetical protein ECRN5871_4549 [Escherichia coli RN587/1]	40	0.99	25 - 64 (112.50%)
1359	NR gi 320529318 ref ZP_08030407.1 mannose-6-phosphate isomerase, class I [Selenomonas artemidis F0399] >gnl BL_ORD_ID 1106308 mannose-6-phosphate isomerase, class I [Selenomonas artemidis F0399]	102	0.99	1 - 101 (30.75%)
1360	NR gi 319399624 gb EFV87879.1 mannose-6-phosphate isomerase, class I [Staphylococcus epidermidis FRI909]	92	0.99	13 - 101 (34.26%)
1361	NR gi 313896060 ref ZP_07829614.1 mannose-6-phosphate isomerase, class I [Selenomonas sp. oral taxon 137 str. F0430] >gnl BL_ORD_ID 623171 mannose-6-phosphate isomerase, class I [Selenomonas sp. oral taxon 137 str. F0430]	102	0.99	1 - 101 (30.75%)
1362	NR gi 309379360 emb CBX22133.1 unnamed protein product [Neisseria lactamica Y92-1009]	86	0.99	177 - 259 (40.56%)
1363	NR gi 307126923 ref YP_003878954.1 mannose-6-phosphate isomerase, class I [Streptococcus pneumoniae 670-6B] >gnl BL_ORD_ID 2918797 mannose-6-phosphate isomerase, class I [Streptococcus pneumoniae 670-6B]	107	0.99	8 - 108 (28.82%)
1364	NR gi 303237019 ref ZP_07323591.1 phosphomannose isomerase type I [Prevotella disiens FB035-09AN] >gnl BL_ORD_ID 2793013 phosphomannose isomerase type I [Prevotella disiens FB035-09AN]	62	0.99	46 - 106 (59.84%)
1365	NR gi 293366108 ref ZP_06612796.1 mannose-6-phosphate isomerase [Staphylococcus epidermidis M23864:W2(grey)] >gnl BL_ORD_ID 1703761 mannose-6-phosphate isomerase [Staphylococcus epidermidis M23864:W2(grey)]	92	0.99	13 - 101 (34.26%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1366	NR gi 289550233 ref YP_003471137.1 mannose-6-phosphate isomerase, class I [Staphylococcus lugdunensis HKU09-01] >gnl BL_ORD_ID 1532659 mannose-6-phosphate isomerase, class I [Staphylococcus lugdunensis HKU09-01]	91	0.99	13 - 100 (36.23%)
1367	NR gi 253682270 ref ZP_04863067.1 mannose-6-phosphate isomerase, class I [Clostridium botulinum D str. 1873] >gnl BL_ORD_ID 310671 mannose-6-phosphate isomerase, class I [Clostridium botulinum D str. 1873]	115	0.99	3 - 116 (26.46%)
1368	NR gi 242241551 ref ZP_04795996.1 mannose-6-phosphate isomerase [Staphylococcus epidermidis W23144] >gnl BL_ORD_ID 249665 mannose-6-phosphate isomerase [Staphylococcus epidermidis W23144]	92	0.99	13 - 101 (34.26%)
1369	NR gi 228477315 ref ZP_04061953.1 mannose-6-phosphate isomerase, class I [Streptococcus salivarius SK126] >gnl BL_ORD_ID 2424747 mannose-6-phosphate isomerase, class I [Streptococcus salivarius SK126]	102	0.99	13 - 108 (32.68%)
1370	NR gi 227533104 ref ZP_03963153.1 mannose-6-phosphate isomerase [Lactobacillus paracasei subsp. paracasei ATCC 25302] >gnl BL_ORD_ID 2296622 mannose-6-phosphate isomerase [Lactobacillus paracasei subsp. paracasei ATCC 25302]	90	0.99	13 - 101 (34.57%)
1371	NR gi 191637105 ref YP_001986271.1 Mannose-6-phosphate isomerase [Lactobacillus casei BL23] >gnl BL_ORD_ID 466298 Mannose-6-phosphate isomerase [Lactobacillus casei BL23]	90	0.99	13 - 101 (34.57%)
1372	NR gi 168490824 ref ZP_02714967.1 mannose-6-phosphate isomerase, class I [Streptococcus pneumoniae CDC0288-04] >gnl BL_ORD_ID 2888510 mannose-6-phosphate isomerase, class I [Streptococcus pneumoniae CDC0288-04]	107	0.99	8 - 108 (28.82%)
1373	NR gi 168484859 ref ZP_02709804.1 mannose-6-phosphate isomerase, class I [Streptococcus pneumoniae CDC1873-00] >gnl BL_ORD_ID 2887436 mannose-6-phosphate isomerase, class I [Streptococcus pneumoniae CDC1873-00]	107	0.99	8 - 108 (28.82%)
1374	NR gi 168186727 ref ZP_02621362.1 mannose-6-phosphate isomerase, class I [Clostridium botulinum C str. Eklund] >gnl BL_ORD_ID 2858271 mannose-6-phosphate isomerase, class I [Clostridium botulinum C str. Eklund]	100	0.99	3 - 101 (29%)
1375	NR gi 163755851 ref ZP_02162969.1 mannose-6-phosphate isomerase [Kordia algicida OT-1] >gnl BL_ORD_ID 2411142 mannose-6-phosphate isomerase [Kordia algicida OT-1]	102	0.99	13 - 105 (30.75%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1376	NR gi 148989813 ref ZP_01821107.1 mannose-6-phosphate isomerase [Streptococcus pneumoniae SP6-BS73] >gnl BL_ORD_ID 1651037 mannose-6-phosphate isomerase [Streptococcus pneumoniae SP6-BS73]	107	0.99	8 - 108 (28.82%)
1377	NR gi 149003345 ref ZP_01828234.1 mannose-6-phosphate isomerase [Streptococcus pneumoniae SP14-BS69] >gnl BL_ORD_ID 1610562 mannose-6-phosphate isomerase [Streptococcus pneumoniae G54] >gnl BL_ORD_ID 1610562 mannose-6-phosphate isomerase [Streptococcus pneumoniae ATCC 700669] >gnl BL_ORD_ID 1610562 mannose-6-phosphate isomerase [Streptococcus pneumoniae SP14-BS69] >gnl BL_ORD_ID 1610562 mannose-6-phosphate isomerase [Streptococcus pneumoniae G54] >gnl BL_ORD_ID 1610562 mannose-6-phosphate isomerase [Streptococcus pneumoniae ATCC 700669]	107	0.99	8 - 108 (28.82%)
1378	NR gi 148997189 ref ZP_01824843.1 mannose-6-phosphate isomerase [Streptococcus pneumoniae SP11-BS70] >gnl BL_ORD_ID 1610313 mannose-6-phosphate isomerase, class I [Streptococcus pneumoniae MLV-016] >gnl BL_ORD_ID 1610313 phosphomannose isomerase [Streptococcus pneumoniae AP200] >gnl BL_ORD_ID 1610313 mannose-6-phosphate isomerase [Streptococcus pneumoniae SP11-BS70] >gnl BL_ORD_ID 1610313 mannose-6-phosphate isomerase, class I [Streptococcus pneumoniae MLV-016] >gnl BL_ORD_ID 1610313 Phosphomannose isomerase [Streptococcus pneumoniae AP200]	107	0.99	8 - 108 (28.82%)
1379	NR gi 118480308 ref YP_897459.1 mannose-6-phosphate isomerase [Bacillus thuringiensis str. Al Hakam] >gnl BL_ORD_ID 861089 mannose-6-phosphate isomerase, type 1 [Bacillus thuringiensis str. Al Hakam]	101	0.99	8 - 107 (31.37%)
1380	NR gi 160878814 ref YP_001557782.1 phosphomannose isomerase-like protein [Clostridium phytofermentans ISDg] >gnl BL_ORD_ID 328910 phosphomannose isomerase-like protein [Clostridium phytofermentans ISDg]	95	0.99	19 - 102 (27.71%)

Alignment rank	Protein name	Amino acid length	E-value	Query range and identity
1381	NR gi 57867644 ref YP_189316.1 mannose-6-phosphate isomerase, class I [Staphylococcus epidermidis RP62A] >gnl BL_ORD_ID 1791666 mannose-6-phosphate isomerase, class I [Staphylococcus epidermidis BCM-HMP0060] >gnl BL_ORD_ID 1791666 mannose-6-phosphate isomerase, class I [Staphylococcus epidermidis SK135] >gnl BL_ORD_ID 1791666 mannose-6-phosphate isomerase, class I [Staphylococcus epidermidis RP62A] >gnl BL_ORD_ID 1791666 mannose-6-phosphate isomerase, class I [Staphylococcus epidermidis BCM-HMP0060] >gnl BL_ORD_ID 1791666 mannose-6-phosphate isomerase, class I [Staphylococcus epidermidis SK135]	92	0.99	13 - 101 (34.26%)
1382	NR gi 27468661 ref NP_765298.1 mannose-6 phosphate isomerase pmi [Staphylococcus epidermidis ATCC 12228] >gnl BL_ORD_ID 1653503 mannose-6 phosphate isomerase pmi [Staphylococcus epidermidis ATCC 12228]	92	0.99	13 - 101 (34.26%)
1383	NR gi 116493860 ref YP_805594.1 phosphomannose isomerase [Lactobacillus casei ATCC 334] >gnl BL_ORD_ID 241879 mannose-6-phosphate isomerase, type 1 [Lactobacillus casei ATCC 334]	90	0.99	13 - 101 (34.57%)
1384	NR gi 15900631 ref NP_345235.1 mannose-6-phosphate isomerase [Streptococcus pneumoniae TIGR4] >gnl BL_ORD_ID 15637 hypothetical protein SpneT_02001300 [Streptococcus pneumoniae TIGR4] >gnl BL_ORD_ID 15637 mannose-6-phosphate isomerase [Streptococcus pneumoniae SP3-BS71] >gnl BL_ORD_ID 15637 mannose-6-phosphate isomerase, class I [Streptococcus pneumoniae 70585] >gnl BL_ORD_ID 15637 mannose-6-phosphate isomerase [Streptococcus pneumoniae TIGR4] >gnl BL_ORD_ID 15637 mannose-6-phosphate isomerase [Streptococcus pneumoniae SP3-BS71] >gnl BL_ORD_ID 15637 mannose-6-phosphate isomerase, class I [Streptococcus pneumoniae 70585] >gnl BL_ORD_ID 15637 mannose-6-phosphate isomerase [Streptococcus pneumoniae OXC141]	107	0.99	8 - 108 (28.82%)

APPENDIX B. Sources of the sequences identified as known or putative phosphomannose isomerase enzymes or proteins appearing to be involved in carbohydrate/sugar metabolism or transport showing significant sequence similarity to the PMI amino acid sequence in BLASTP analysis

Organism	No. of proteins	E-value
<i>Acetohalobium arabaticum</i>	2	0.581766 - 0.75981
<i>Acidothermus cellulolyticus</i>	1	3.97E-50
<i>Actinobacillus minor</i>	2	5.01E-53 - 4.69E-51
<i>Actinobacillus pleuropneumoniae</i>	3	9.79E-49 - 1.67E-48
<i>Actinobacillus succinogenes</i>	1	1.41E-47
<i>Actinobacillus ureae</i>	1	2.04E-46
<i>Actinomyces coleocanis</i>	1	9.16E-47
<i>Actinomyces odontolyticus</i>	1	1.98E-41
<i>Actinomyces</i> sp.	4	1.01E-61 - 2.58E-41
<i>Actinomyces urogenitalis</i>	1	2.32E-58
<i>Actinomyces viscosus</i>	1	3.47E-54
<i>Actinosynnema mirum</i>	1	2.17E-64
<i>Acyrtosiphon pisum</i>	1	1.91E-36
<i>Aedes aegypti</i>	2	9.81E-41 - 2.19E-40
<i>Aerococcus viridans</i>	1	0.1172
<i>Aeromicrobium marinum</i>	1	7.74E-54
<i>Aeromonas hydrophila</i>	1	2.46E-92
<i>Aeromonas salmonicida</i>	1	3.21E-92
<i>Aggregatibacter actinomycetemcomitans</i>	2	2.49E-52 - 1.05E-50
<i>Aggregatibacter aphrophilus</i>	1	6.78E-50
<i>Aggregatibacter segnis</i>	1	1.37E-50
<i>Ailuropoda melanoleuca</i>	1	9.81E-41
<i>Ajellomyces capsulatus</i>	3	2.42E-39 - 1.2E-38
<i>Ajellomyces dermatitidis</i>	2	5.38E-39
<i>Alicyclobacillus acidocaldarius</i>	2	0.0062 - 0.0181
<i>Aliivibrio salmonicida</i>	2	5.31E-87 - 1.05E-50
<i>Alistipes shahii</i>	1	0.2611
<i>Amycolatopsis mediterranei</i>	1	1.46E-60
<i>Anaerococcus lactolyticus</i>	1	0.4454
<i>Anopheles subpictus</i>	8	1.33E-29 - 3.27E-28
<i>Anopheles sudaicus</i>	133	3.49E-38 - 1.17E-09
<i>Apis mellifera</i>	1	7.77E-38
<i>Arabidopsis lyrata</i>	1	1.98E-41
<i>Arabidopsis thaliana</i>	4	3.73E-40 - 7.83E-14
<i>Arcanobacterium haemolyticum</i>	1	1.15E-57
<i>Arsenophonus nasoniae</i>	1	1.48E-121

Organism	No. of proteins	E-value
<i>Arthrobacter arilaitensis</i>	1	1.23E-59
<i>Arthrobacter aurescens</i>	1	3.83E-61
<i>Arthrobacter chlorophenolicus</i>	1	1.56E-62
<i>Arthrobacter phenanthrenivorans</i>	1	6.98E-63
<i>Arthrobacter sp.</i>	1	6.31E-64
<i>Arthroderma benhamiae</i>	1	3.86E-37
<i>Arthroderma gypseum</i>	1	2.19E-40
<i>Arthroderma otae</i>	1	1.67E-40
<i>Ashbya gossypii</i>	1	1.85E-31
<i>Aspergillus clavatus</i>	2	1.16E-41 - 1.99E-25
<i>Aspergillus flavus</i>	2	7.03E-39 - 2.77E-27
<i>Aspergillus fumigatus</i>	4	2.67E-38 - 8.34E-24
<i>Aspergillus nidulans</i>	2	1.28E-40 - 2.97E-21
<i>Aspergillus oryzae</i>	2	1.57E-30 - 3.39E-25
<i>Aspergillus terreus</i>	1	4.87E-40
<i>Atopobium parvulum</i>	1	0.031
<i>Babesia bovis</i>	1	1.43E-15
<i>Bacillus amyloliquefaciens</i>	2	0.0898 - 0.1172
<i>Bacillus atrophaeus</i>	2	0.261143 - 0.581766
<i>Bacillus cereus</i>	7	0.00364395 - 0.75981
<i>Bacillus coagulans</i>	1	0.11722
<i>Bacillus halodurans</i>	1	0.75981
<i>Bacillus licheniformis</i>	2	0.0687219 - 0.153097
<i>Bacillus megaterium</i>	1	0.1172
<i>Bacillus pumilus</i>	2	0.0062
<i>Bacillus sp.</i>	2	0.1531 - 0.3411
<i>Bacillus subtilis</i>	9	0.0526 - 0.7598
<i>Bacillus thuringiensis</i>	8	0.0028 - 0.9923
bacterium <i>Ellin514</i>	1	0.1531
<i>Bacteroides dorei</i>	1	0.0526
<i>Bacteroides eggerthii</i>	1	0.1172
<i>Bacteroides finegoldii</i>	1	0.1531
<i>Bacteroides fragilis</i>	2	0.0081 - 0.0308
<i>Bacteroides helcogenes</i>	1	0.0181
<i>Bacteroides ovatus</i>	1	0.0898
<i>Bacteroides sp.</i>	7	0.0236 - 0.2611
<i>Bacteroides thetaiotaomicron</i>	1	0.1172
<i>Bacteroides vulgatus</i>	2	0.0526
<i>Bacteroidetes oral</i>	1	0.3411
<i>Beutenbergia cavernae</i>	2	5.53E-60 - 2.66E-54

Organism	No. of proteins	E-value
<i>Bifidobacterium animalis</i>	2	2.67E-38
<i>Bifidobacterium dentium</i>	3	9.18E-39 - 1.57E-38
<i>Bifidobacterium gallicum</i>	1	3.07E-18
<i>Blautia hansenii</i>	1	0.0062
<i>Borrelia afzelii</i>	1	1.85E-39
<i>Borrelia burgdorferi</i>	9	5.38E-39 - 2.69E-14
<i>Borrelia duttonii</i>	1	7.53E-33
<i>Borrelia garinii</i>	3	1.85E-39 - 7.77E-38
<i>Borrelia hermsii</i>	1	2.19E-40
<i>Borrelia recurrentis</i>	1	7.53E-33
<i>Borrelia sp.</i>	1	9.18E-39
<i>Borrelia spielmanii</i>	1	5.75E-41
<i>Borrelia turicatae</i>	1	3.37E-41
<i>Borrelia valaisiana</i>	1	3.37E-41
<i>Bos taurus</i>	2	5.56E-44 - 9.81E-41
<i>Brachybacterium faecium</i>	1	5.92E-54
<i>Brevibacterium linens</i>	1	1.67E-56
<i>Brevibacterium mcbrellneri</i>	1	1.91E-52
<i>Brugia malayi</i>	2	5.76E-33 - 1.12E-28
<i>Bryantella formatexigens</i>	1	0.0138
<i>Butyrivibrio proteoclasticus</i>	1	0.2611
<i>Caenorhabditis elegans</i>	1	4.56E-38
<i>Caligus rogercresseyi</i>	1	5.03E-45
<i>Callithrix jacchus</i>	1	3.37E-41
<i>Camponotus floridanus</i>	1	6.36E-40
<i>Candida albicans</i>	1	7.27E-36
<i>Candida dubliniensis</i>	1	1.24E-35
<i>Candida tropicalis</i>	1	2.67E-38
<i>Candidatus Cloacamonas</i>	1	9.74E-65
<i>Candidatus Hamiltonella</i>	1	7.11E-116
<i>Canis familiaris</i>	2	5.38E-39 - 5.95E-38
<i>Capnocytophaga gingivalis</i>	1	0.00001
<i>Capnocytophaga ochracea</i>	2	0.0062
<i>Capnocytophaga sputigena</i>	1	0.0062
<i>Capsaspora owczarzaki</i>	1	1.32E-45
<i>Carboxydibrachium pacificum</i>	1	0.0081
<i>Cardiobacterium hominis</i>	1	3.47E-54
<i>Carnobacterium sp.</i>	1	0.0003
<i>Catenulispora acidiphila</i>	1	9.14E-55
<i>Cellulomonas flavigena</i>	1	1.56E-62

Organism	No. of proteins	E-value
<i>Cellulophaga algicola</i>	1	0.0028
<i>Chitinophaga pinensis</i>	1	2.84E-56
<i>Chlamydomonas reinhardtii</i>	1	1.85E-39
<i>Chloroflexus aggregans</i>	1	0.75981
<i>Chloroflexus aurantiacus</i>	1	0.2611
<i>Chromobacterium violaceum</i>	1	3.48E-46
<i>Ciona intestinalis</i>	1	1.16E-41
<i>Citrobacter koseri</i>	1	0
<i>Citrobacter rodentium</i>	1	0
<i>Citrobacter</i> sp.	1	0
<i>Citrobacter youngae</i>	1	0
<i>Citrus maxima</i>	1	1.21E-14
<i>Clavibacter michiganensis</i>	2	2.75E-59 - 5.18E-58
<i>Clostridiales bacterium</i>	1	0.1531
<i>Clostridium acetobutylicum</i>	1	0.2611
<i>Clostridium botulinum</i>	10	0.0016 - 0.9923
<i>Clostridium cellulolyticum</i>	1	0.0687
<i>Clostridium cellulovorans</i>	1	0.0007
<i>Clostridium lentocellum</i>	1	0.0236
<i>Clostridium novyi</i>	1	0.0308
<i>Clostridium perfringens</i>	3	0.3410
<i>Clostridium phytofermentans</i>	1	0.9923
<i>Clostridium</i> sp.	1	0.4454
<i>Coccidioides posadasii</i>	1	2.26E-37
<i>Corynebacterium accolens</i>	2	3.13E-63 - 4.09E-63
<i>Corynebacterium ammoniagenes</i>	1	1.15E-65
<i>Corynebacterium amycolatum</i>	1	3.71E-56
<i>Corynebacterium aurimucosum</i>	1	3.82E-69
<i>Corynebacterium diphtheriae</i>	1	8.25E-64
<i>Corynebacterium efficiens</i>	1	1.78E-58
<i>Corynebacterium genitalium</i>	2	6.1E-67 - 3.14E-55
<i>Corynebacterium glucuronolyticum</i>	2	5.72E-57 - 2.18E-56
<i>Corynebacterium glutamicum</i>	1	1.56E-62
<i>Corynebacterium jeikeium</i>	2	6.33E-56 - 2.4E-55
<i>Corynebacterium kroppenstedtii</i>	1	4.54E-54
<i>Corynebacterium lipophiloflavum</i>	2	1.28E-56 - 1.42E-31
<i>Corynebacterium matruchotii</i>	1	8.53E-61
<i>Corynebacterium pseudogenitalium</i>	1	2.25E-61
<i>Corynebacterium pseudotuberculosis</i>	1	1.19E-62
<i>Corynebacterium resistens</i>	1	3.7E-64

Organism	No. of proteins	E-value
<i>Corynebacterium striatum</i>	1	1.72E-61
<i>Corynebacterium tuberculostearicum</i>	1	1.01E-61
<i>Corynebacterium urealyticum</i>	1	2.11E-51
<i>Corynebacterium variabile</i>	1	1.36E-58
<i>Croceibacter atlanticus</i>	1	0.0236194
<i>Cronobacter sakazakii</i>	1	0
<i>Cronobacter turicensis</i>	1	0
<i>Cryptococcus gattii</i>	2	1.08E-39 - 1.8E-26
<i>Cryptococcus neoformans</i>	3	3.16E-39 - 2.59E-25
<i>Cryptosporidium muris</i>	1	2.68E-30
<i>Cryptosporidium parvum</i>	1	5.23E-26
<i>Culex quinquefasciatus</i>	1	4.26E-36
<i>Cyamopsis tetragonoloba</i>	1	8.59E-37
<i>Cytophaga hutchinsonii</i>	1	0.581766
<i>Danio rerio</i>	1	1.51E-41
<i>Daphnia magna</i>	6	4.74E-19 - 1.06E-18
<i>Daphnia parvula</i>	1	7.27E-36
<i>Daphnia pulex</i>	4	5.57E-36 - 1.02E-29
<i>Deinococcus maricopensis</i>	1	0.7598
<i>delta proteobacterium</i>	1	6.75E-66
<i>Dermacoccus</i> sp.	1	1.85E-31
<i>Desulfarculus baarsii</i>	1	0.75981
<i>Desulfococcus oleovorans</i>	1	1.11E-68
<i>Desulfotalea psychrophila</i>	1	7.99E-59
<i>Desulfotomaculum nigrificans</i>	1	0.0007
<i>Dickeya dadantii</i>	3	0
<i>Dickeya zeae</i>	1	0
<i>Dictyostelium discoideum</i>	1	9.18E-39
<i>Dietzia cinnamea</i>	1	4.52E-62
<i>Dokdonia donghaensis</i>	1	0.75981
<i>Echinococcus multilocularis</i>	1	3.61E-35
<i>Ectocarpus siliculosus</i>	5	2.87E-24 -6.86E-10
<i>Edwardsiella ictaluri</i>	1	0
<i>Edwardsiella tarda</i>	2	0
<i>Emericella nidulans</i>	1	9.81E-41
<i>Entamoeba dispar</i>	1	1.21E-41
<i>Entamoeba histolytica</i>	2	4.15E-15 - .0003
<i>Enterobacter cancerogenus</i>	1	0
<i>Enterobacter cloacae</i>	4	0
<i>Enterobacter</i> sp.	1	0

Organism	No. of proteins	E-value
<i>Enterobacteriaceae bacterium</i>	1	0
<i>Enterococcus casseliflavus</i>	2	0.1531
<i>Enterococcus faecalis</i>	12	0.0138 - 0.0526
<i>Enterococcus faecium</i>	6	0.0001 - 0.0526
<i>Enterococcus gallinarum</i>	1	0.0687
<i>Enterococcus italicus</i>	1	0.0138
<i>Epulopiscium sp.</i>	1	0.0898
<i>Equus caballus</i>	1	1.16E-41
<i>Eremococcus coleocola</i>	1	0.2
<i>Erwinia billingiae</i>	1	0
<i>Erysipelothrix rhusiopathiae</i>	1	0.001
<i>Erysipelotrichaceae bacterium</i>	3	0.0138 - 0.3411
<i>Escherichia albertii</i>	1	0
<i>Escherichia coli</i>	36	0 - 8.28E-48
<i>Escherichia fergusonii</i>	1	0
<i>Escherichia sp.</i>	1	0
<i>Ethanoligenens harbinense</i>	3	0.00001 - 0.1172
<i>Eubacterium cylindroides</i>	1	0.018
<i>Eubacterium siraeum</i>	2	0.1999 - 0.3411
<i>Faecalibacterium prausnitzii</i>	2	0.0004 - 0.0236
<i>Flavobacteria bacterium</i>	2	0.0081 - 0.0403
<i>Flavobacteriales bacterium</i>	2	0.4454 - 0.7598
<i>Flavobacterium johnsoniae</i>	1	0.0138
<i>Flavobacterium psychrophilum</i>	1	0.4454
<i>Frankia alni</i>	1	1.42E-39
<i>Frankia sp.</i>	4	7.49E-49 - 7.03E-39
<i>Frankia symbiont</i>	1	3.37E-41
<i>Fusobacterium mortiferum</i>	1	0.0003
<i>Fusobacterium ulcerans</i>	1	0.0021
<i>Fusobacterium varium</i>	1	0.0016
<i>Gemella haemolysans</i>	1	0.0898
<i>Geobacillus kaustophilus</i>	1	0.0898
<i>Geobacillus sp.</i>	5	0.0181 - 0.1531
<i>Geobacillus thermodenitrificans</i>	1	0.0181
<i>Geobacillus thermoglucosidasius</i>	1	0.1531
<i>Geodermatophilus obscurus</i>	1	1.15E-57
<i>Glomerella graminicola</i>	2	1.02E-37 - 1.86E-23
<i>Gordonia bronchialis</i>	1	9.43E-60
<i>Grimontia hollisae</i>	1	7.16E-92
<i>Grosmannia clavigera</i>	1	5.40E-15

Organism	No. of proteins	E-value
<i>Haemophilus ducreyi</i>	1	1.73E-45
<i>Haemophilus influenzae</i>	1	1.74E-13
<i>Haemophilus parainfluenzae</i>	1	4.38E-57
<i>Haemophilus parasuis</i>	1	1.2E-46
<i>Haemophilus somnus</i>	2	7.24E-52 - 8.01E-51
<i>Halanaerobium praevalens</i>	1	0.5818
<i>Halanaerobium</i> sp.	1	0.3411
<i>Haliangium ochraceum</i>	1	4.11E-47
<i>Halothermothrix orenii</i>	1	0.0308
<i>Harpegnathos saltator</i>	1	5.06E-21
<i>Herpetosiphon aurantiacus</i>	1	0.0181
<i>Homo sapiens</i>	6	5.56E-44 - 3.62E-27
<i>Hydra magnipapillata</i>	1	6.82E-26
<i>Ilyobacter polytropus</i>	1	0.0002
<i>Isosphaera pallida</i>	1	0.0308
<i>Ixodes scapularis</i>	1	1.57E-38
<i>Janibacter</i> sp.	1	2.26E-37
<i>Jonesia denitrificans</i>	1	2.93E-61
<i>Kineococcus radiotolerans</i>	1	2.84E-56
<i>Kitasatospora setae</i>	1	1.55E-70
<i>Klebsiella pneumoniae</i>	4	0
<i>Kocuria rhizophila</i>	1	2.67E-46
<i>Kordia algicida</i>	1	0.992343
<i>Kribbella flavida</i>	1	1.78E-58
<i>Laccaria bicolor</i>	1	9.81E-41
<i>Lactobacillus casei</i>	2	0.9923
<i>Lactobacillus delbrueckii</i>	4	0.0526 - 0.1172
<i>Lactobacillus paracasei</i>	1	0.9923
<i>Lactobacillus plantarum</i>	2	0.5817
<i>Lactobacillus salivarius</i>	4	0.2611 - 0.3411
<i>Leeuwenhoekiella blandensis</i>	1	0.0138
<i>Leifsonia xyli</i>	1	3.14E-55
<i>Leishmania amazonensis</i>	1	1.79E-34
<i>Leishmania braziliensis</i>	4	3.86E-37 - 8.59E-37
<i>Leishmania donovani</i>	1	2.5E-36
<i>Leishmania gerbilli</i>	1	9.5E-36
<i>Leishmania guyanensis</i>	1	2.5E-36
<i>Leishmania infantum</i>	4	8.59E-37 - 5.57E-36
<i>Leishmania lainsoni</i>	1	5.57E-36
<i>Leishmania major</i>	1	7.27E-36

Organism	No. of proteins	E-value
<i>Leishmania mexicana</i>	3	2.76E-35 - 3.61E-35
<i>Leishmania peruviana</i>	1	5.04E-37
<i>Leishmania sp.</i>	4	5.04E-37 - 1.12E-36
<i>Leishmania tropica</i>	1	4.26E-36
<i>Lentisphaera araneosa</i>	1	0.0526
<i>Leptosphaeria maculans</i>	2	9.18E-39 - 1.52E-25
<i>Leptospira biflexa</i>	1	0.2
<i>Leptotrichia buccalis</i>	1	0.0003
<i>Leptotrichia goodfellowii</i>	1	0.0016
<i>Leptotrichia hofstadii</i>	1	0.0006
<i>Listeria grayi</i>	1	0.2
<i>Listeria innocua</i>	2	0.1172 - 0.1531
<i>Listeria ivanovii</i>	1	0.5818
<i>Listeria marthii</i>	1	0.2611
<i>Listeria monocytogenes</i>	9	0.3411 - 0.5818
<i>Listeria seeligeri</i>	2	0.3411 - 0.4454
<i>Listeria welshimeri</i>	1	0.0526
<i>Loa loa</i>	2	1.67E-40 - 3.27E-28
<i>Lodderomyces elongisporus</i>	1	1.08E-39
<i>Macaca fascicularis</i>	1	3.26E-44
<i>Macaca mulatta</i>	9	2.78E-19 - 0.001
<i>Mannheimia succiniciproducens</i>	1	1.51E-49
<i>Maribacter sp.</i>	1	0.0001
<i>marine actinobacterium</i>	1	3.71E-56
<i>Marinomonas sp.</i>	1	1.62E-43
<i>Meiothermus ruber</i>	1	0.0526
<i>Meiothermus silvanus</i>	1	0.5818
<i>Metarhizium acridum</i>	2	3.17E-23 - 1.47E-20
<i>Metarhizium anisopliae</i>	2	1.57E-38 - 2.05E-38
<i>Microbacterium testaceum</i>	1	4.69E-51
<i>Micrococcus luteus</i>	2	8.83E-58 - 3.36E-57
<i>Micromonas pusilla</i>	1	1.67E-40
<i>Micromonospora aurantiaca</i>	1	1.01E-53
<i>Micromonospora sp.</i>	2	1.28E-56 - 7.74E-54
<i>Mitsuokella multacida</i>	1	0.031
<i>Mobiluncus curtisii</i>	4	1.28E-56 - 2.18E-56
<i>Mobiluncus mulieris</i>	2	1.01E-61
<i>Mucilaginibacter paludis</i>	1	0.1172
<i>Mus musculus</i>	2	3.98E-42
<i>Mycobacterium abscessus</i>	1	1.61E-67

Organism	No. of proteins	E-value
<i>Mycobacterium avium</i>	2	6.1E-67
<i>Mycobacterium gilvum</i>	1	4.67E-67
<i>Mycobacterium intracellulare</i>	1	1.61E-67
<i>Mycobacterium kansasii</i>	1	2.56E-65
<i>Mycobacterium leprae</i>	1	3.13E-63
<i>Mycobacterium marinum</i>	1	3.03E-66
<i>Mycobacterium parascrofulaceum</i>	1	1.78E-66
<i>Mycobacterium smegmatis</i>	2	2.65E-62 - 1.19E-54
<i>Mycobacterium sp.</i>	3	4.67E-67 - 2.48E-60
<i>Mycobacterium tuberculosis</i>	3	1.27E-64 - 1.05E-26
<i>Mycobacterium ulcerans</i>	1	2.32E-66
<i>Mycobacterium vanbaalenii</i>	1	9.74E-65
<i>Mytilus edulis</i>	14	7.26E-44 - 1.79E-34
<i>Mytilus trossulus</i>	2	2.76E-43 - 1.05E-34
<i>Naegleria gruberi</i>	1	5.23E-26
<i>Nakamurella multipartita</i>	2	1.32E-61 - 1.72E-61
<i>Nectria haematococca</i>	1	2.42E-39
<i>Neosartorya fischeri</i>	2	2.42E-39 - 2.2E-24
<i>Neurospora crassa</i>	1	9.83E-33
<i>Nicotiana tabacum</i>	1	0.0403
<i>Nocardia farcinica</i>	1	5.17E-66
<i>Nocardioides sp.</i>	1	1.72E-61
<i>Nocardiopsis dassonvillei</i>	1	3.96E-58
<i>Oceanithermus profundus</i>	1	0.0062
<i>Opiritatus terrae</i>	1	0.7598
<i>Oribacterium sinus</i>	1	0.0003
<i>Oribacterium sp.</i>	2	0.0002 - 0.0003
<i>Oryctolagus cuniculus</i>	1	1.37E-42
<i>Oryza sativa</i>	4	5.38E-39 - 1.09E-15
<i>Oscillochloris trichoides</i>	1	0.0081
<i>Ostreococcus tauri</i>	1	1.57E-30
<i>Paenibacillus curdlanolyticus</i>	1	0.2
<i>Paenibacillus larvae</i>	1	0.0687
<i>Paenibacillus polymyxa</i>	2	0.3411 - 0.7598
<i>Paenibacillus sp.</i>	2	0.1531 - 0.4454
<i>Paludibacter propionicigenes</i>	1	0.0308
<i>Pan troglodytes</i>	1	5.56E-44
<i>Pantoea ananatis</i>	1	0
<i>Pantoea sp.</i>	2	0
<i>Pantoea vagans</i>	1	0

Organism	No. of proteins	E-value
<i>Parabacteroides distasonis</i>	1	0.0308
<i>Paracoccidioides brasiliensis</i>	3	1.47E-36 - 8.04E-35
<i>Parascardovia denticolens</i>	1	1.46E-44
<i>Pasteurella dagmatis</i>	1	9.46E-52
<i>Pasteurella multocida</i>	1	1.61E-51
<i>Pectobacterium atrosepticum</i>	1	0
<i>Pectobacterium carotovorum</i>	3	0
<i>Pectobacterium wasabiae</i>	1	0
<i>Pediculus humanus</i>	1	6.14E-43
<i>Pediococcus pentosaceus</i>	1	0.581766
<i>Penicillium marneffeii</i>	2	7.03E-39 - 5.79E-17
<i>Perkinsus marinus</i>	1	5.95E-38
<i>Phaeodactylum tricorutum</i>	1	3.27E-36
<i>Photobacterium damsela</i>	1	5.87E-86
<i>Photobacterium profundum</i>	2	1.22E-91 - 1.03E-90
<i>Photobacterium sp.</i>	1	1.07E-87
<i>Photorhabdus asymbiotica</i>	1	0
<i>Photorhabdus luminescens</i>	1	0
<i>Phytophthora infestans</i>	1	3.74E-32
<i>Pichia angusta</i>	1	1.91E-36
<i>Pichia pastoris</i>	1	3.61E-35
<i>Pirellula staleyii</i>	1	0.0028
<i>Plasmodium falciparum</i>	1	0.00001
<i>Plasmodium knowlesi</i>	1	0.00001
<i>Plasmodium vivax</i>	1	0.000006
<i>Plasmodium yoelii</i>	1	0.000002
<i>Plutella xylostella</i>	1	0.00009
<i>Pneumocystis carinii</i>	1	0.000002
<i>Polaribacter irgensii</i>	1	0.0687
<i>Polaribacter sp.</i>	1	0.0062
<i>Polysphondylium pallidum</i>	1	4.12E-39
<i>Pongo abelii</i>	1	3.98E-42
<i>Populus trichocarpa</i>	1	5.04E-37
<i>Prevotella bergensis</i>	1	0.0016357
<i>Prevotella bryantii</i>	1	0.2
<i>Prevotella buccalis</i>	1	0.0403
<i>Prevotella disiens</i>	1	0.9923
<i>Prevotella marshii</i>	1	0.0181
<i>Prevotella oralis</i>	1	0.341063
<i>Prevotella oris</i>	2	0.0016

Organism	No. of proteins	E-value
<i>Prevotella ruminicola</i>	1	0.5818
<i>Prevotella salivae</i>	1	0.0106
<i>Prevotella</i> sp.	3	0.2 - 0.7598
<i>Prevotella timonensis</i>	1	0.2
<i>Propionibacterium acnes</i>	23	1.91E-44 - 1.08E-39
<i>Propionibacterium freudenreichii</i>	1	5.72E-57
<i>Providencia alcalifaciens</i>	1	2.88E-125
<i>Providencia rettgeri</i>	1	0
<i>Providencia rustigianii</i>	1	5.61E-129
<i>Providencia stuartii</i>	1	2.36E-127
<i>Psychroflexus torquis</i>	1	0.0898
<i>Psychromonas</i> sp.	1	3.68E-88
<i>Puccinia graminis</i>	1	1.05E-34
<i>Pyrenophora tritici-repentis</i>	2	2.95E-37 - 7.55E-25
<i>Rahnella</i> sp.	1	0
<i>Rattus norvegicus</i>	1	3.6E-43
<i>Reinekea</i> sp.	1	2.66E-54
<i>Renibacterium salmoninarum</i>	1	2.1E-59
<i>Rhodococcus equi</i>	2	6.76E-58 - 4.85E-56
<i>Rhodococcus erythropolis</i>	2	3.95E-66 - 1.15E-65
<i>Rhodococcus jostii</i>	2	1.9E-68 - 9.41E-68
<i>Rhodococcus opacus</i>	1	9.41E-68
<i>Ricinus communis</i>	2	3.16E-39 - 1.92E-20
<i>Roseiflexus castenholzii</i>	1	0.117222
<i>Rothia dentocariosa</i>	2	1.85E-47 - 2.41E-47
<i>Rothia mucilaginosa</i>	2	6.14E-43
<i>Ruminococcus albus</i>	2	0.0403 - 0.0687
<i>Ruminococcus flavefaciens</i>	1	0.0181
<i>Ruminococcus</i> sp.	3	0.0081 - 0.2
<i>Saccharomonospora viridis</i>	1	9.43E-60
<i>Saccharomyces cerevisiae</i>	6	8.87E-42 - 7.05E-31
<i>Saccharopolyspora erythraea</i>	2	1.01E-61 - 7.22E-60
<i>Saccoglossus kowalevskii</i>	1	1.16E-41
<i>Salinispora arenicola</i>	1	1.08E-55
<i>Salinispora tropica</i>	1	3.36E-57
<i>Salmonella enterica</i>	35	0 - 0.0017
<i>Salmonella typhimurium</i>	2	0
<i>Sanguibacter keddieii</i>	1	2.25E-61
<i>Scardovia inopinata</i>	1	2.11E-43
<i>Scheffersomyces stipitis</i>	1	1.33E-37

Organism	No. of proteins	E-value
<i>Schistosoma japonicum</i>	1	1.33E-37
<i>Schistosoma mansoni</i>	1	4.56E-38
<i>Schizophyllum commune</i>	1	9.81E-41
<i>Schizosaccharomyces japonicus</i>	1	1.12E-36
<i>Schizosaccharomyces pombe</i>	1	1.28E-40
<i>Sebaldella termitidis</i>	2	0.00007 - 0.1172
<i>Segniliparus rotundus</i>	1	1.11E-60
<i>Segniliparus rugosus</i>	1	3.96E-58
<i>Selenomonas artemidis</i>	1	0.9923
<i>Selenomonas flueggei</i>	1	0.2611
<i>Selenomonas noxia</i>	1	0.0004
<i>Selenomonas sp.</i>	1	0.9923
<i>Selenomonas sputigena</i>	1	0.0308
<i>Serratia marcescens</i>	1	0
<i>Serratia odorifera</i>	2	0
<i>Serratia proteamaculans</i>	1	0
<i>Serratia symbiotica</i>	1	3.46E-62
<i>Shigella boydii</i>	1	0
<i>Shigella dysenteriae</i>	4	0
<i>Shigella flexneri</i>	2	0
<i>Shigella sonnei</i>	1	0
<i>Sodalis glossinidius</i>	1	0
<i>Sorangium cellulosum</i>	1	1.11E-60
<i>Sorghum bicolor</i>	1	1.8E-18
<i>Spirochaeta smaragdinae</i>	1	4.83E-64
<i>Spirochaeta thermophila</i>	2	3.57E-75 - 2.31E-74
<i>Stackebrandtia nassauensis</i>	1	5.72E-57
<i>Staphylococcus aureus</i>	1	0.4454
<i>Staphylococcus capitis</i>	2	0.1172 - 0.5818
<i>Staphylococcus caprae</i>	2	0.0526 - 0.5818
<i>Staphylococcus carnosus</i>	1	0.3411
<i>Staphylococcus epidermidis</i>	9	0.1531 - 0.9923
<i>Staphylococcus hominis</i>	1	0.0308
<i>Staphylococcus lugdunensis</i>	4	0.1172 - 0.9923
<i>Staphylococcus pseudintermedius</i>	2	0.0236
<i>Staphylococcus warneri</i>	1	0.1531
<i>Streptobacillus moniliformis</i>	1	0.0106
<i>Streptococcus agalactiae</i>	3	0.0106 - 0.0181
<i>Streptococcus anginosus</i>	2	0.1531 - 0.2
<i>Streptococcus australis</i>	1	0.0898

Organism	No. of proteins	E-value
<i>Streptococcus cristatus</i>	1	0.0687
<i>Streptococcus dysgalactiae</i>	2	0.1172 - 0.1531
<i>Streptococcus equi</i>	3	0.0181 - 0.0526
<i>Streptococcus gordonii</i>	1	0.0403
<i>Streptococcus infantis</i>	2	0.1172 - 0.3411
<i>Streptococcus mitis</i>	5	0.2 - 0.2611
<i>Streptococcus mutans</i>	3	0.5818
<i>Streptococcus oralis</i>	1	0.2611
<i>Streptococcus parasanguinis</i>	3	0.0181 - 0.1531
<i>Streptococcus peroris</i>	1	0.0403
<i>Streptococcus pneumoniae</i>	7	0.9923
<i>Streptococcus salivarius</i>	2	0.0308 - 0.9923
<i>Streptococcus sanguinis</i>	2	0.0308 - 0.1172
<i>Streptococcus sp.</i>	6	0.0308 - 0.7598
<i>Streptococcus thermophilus</i>	1	0.0526
<i>Streptococcus vestibularis</i>	3	0.0062 - 0.2
<i>Streptomyces albus</i>	1	4.23E-68
<i>Streptomyces avermitilis</i>	1	3.35E-65
<i>Streptomyces bingchenggensis</i>	1	4.66E-75
<i>Streptomyces clavuligerus</i>	1	4.67E-67
<i>Streptomyces coelicolor</i>	1	1.23E-67
<i>Streptomyces flavogriseus</i>	1	3.82E-69
<i>Streptomyces ghanaensis</i>	1	3.03E-66
<i>Streptomyces griseoflavus</i>	1	6.75E-66
<i>Streptomyces griseus</i>	1	2.03E-70
<i>Streptomyces hygrosopicus</i>	1	3.23E-76
<i>Streptomyces nodosus</i>	1	3.58E-67
<i>Streptomyces roseosporus</i>	1	5.33E-71
<i>Streptomyces scabiei</i>	1	4.83E-64
<i>Streptomyces sp.</i>	6	4.36E-73 - 2.75E-59
<i>Streptomyces sviveus</i>	1	2.1E-67
<i>Streptomyces violaceusniger</i>	1	2.56E-73
<i>Streptomyces viridochromogenes</i>	1	3.24E-68
<i>Streptosporangium roseum</i>	1	5.18E-58
<i>Sus scrofa</i>	1	5.75E-41
<i>Symbiobacterium thermophilum</i>	1	0.4454
<i>Synergistetes bacterium</i>	1	0.4454
<i>Taeniopygia guttata</i>	1	3.6E-43
<i>Talaromyces stipitatus</i>	2	9.18E-39 - 6.84E-18
<i>Teredinibacter turnerae</i>	1	5.94E-46

Organism	No. of proteins	E-value
<i>Tetrahymena thermophila</i>	1	5.38E-39
<i>Theileria annulata</i>	1	5.06E-21
<i>Theileria parva</i>	1	1.99E-17
<i>Thermoanaerobacter italicus</i>	1	0.1531
<i>Thermoanaerobacter mathranii</i>	1	0.0526
<i>Thermoanaerobacter pseudethanolicus</i>	1	0.2
<i>Thermoanaerobacter</i> sp.	1	0.2
<i>Thermoanaerobacter tengcongensis</i>	1	0.0081
<i>Thermoanaerobacter wiegelii</i>	1	0.1531
<i>Thermoanaerobacterium thermosaccharolyticum</i>	1	0.0012
<i>Thermoanaerobacterium xylanolyticum</i>	1	0.0062
<i>Thermobifida fusca</i>	1	2.74E-67
<i>Thermobispora bispora</i>	1	1.37E-50
<i>Thermomicrobium roseum</i>	1	0.2
<i>Thermotoga lettingae</i>	1	0.0028
<i>Tolomonas auensis</i>	2	3.91E-106 - 4.08E-71
<i>Toxoplasma gondii</i>	3	1.48E-12 - 7.33E-12
<i>Treponema phagedenis</i>	1	3.24E-68
<i>Tribolium castaneum</i>	1	9.48E-44
<i>Trichinella spiralis</i>	1	1.99E-17
<i>Trichomonas vaginalis</i>	1	3.06E-34
<i>Trichophyton verrucosum</i>	1	3.61E-35
<i>Tropheryma whipplei</i>	2	5.39E-31 - 1.57E-30
<i>Truepera radiovictrix</i>	1	0.0106023
<i>Trypanosoma brucei</i>	1	2.26E-37
<i>Trypanosoma cruzi</i>	3	2.12E-35 - 3.99E-34
<i>Tsukamurella paurometabola</i>	1	1.72E-61
<i>Tuber melanosporum</i>	1	1.28E-40
<i>Uncinocarpus reesii</i>	1	2.05E-38
uncultured archaeon	1	1.33E-13
uncultured bacterium	3	0.0048 - 0.1531
unidentified eubacterium	1	0.0028
Verrucomicrobiae bacterium	1	0.0898
<i>Verticillium albo-atrum</i>	2	1.67E-40 - 2.05E-22
<i>Vibrio alginolyticus</i>	2	1.14E-89 - 2.16E-88
<i>Vibrio angustum</i>	1	4.34E-89
<i>Vibrio brasiliensis</i>	1	2.08E-91
<i>Vibrio caribbenthicus</i>	1	2.47E-84
<i>Vibrio cholerae</i>	12	3.8E-93 - 1.79E-42
<i>Vibrio coralliilyticus</i>	1	2.15E-96

Organism	No. of proteins	E-value
<i>Vibrio fischeri</i>	2	2.72E-91 - 1.35E-90
<i>Vibrio furnissii</i>	2	9.03E-95 - 2.01E-94
<i>Vibrio harveyi</i>	11	1.06E-103 - 5.49E-84
<i>Vibrio metschnikovii</i>	1	2.22E-93
<i>Vibrio mimicus</i>	4	1.35E-90 - 6.7E-90
<i>Vibrio orientalis</i>	2	6.46E-101 - 5.31E-87
<i>Vibrio parahaemolyticus</i>	10	9.99E-94 - 5.58E-28
<i>Vibrio shilonii</i>	1	1.54E-86
<i>Vibrio sinaloensis</i>	2	1.03E-98 - 2.16E-88
<i>Vibrio sp.</i>	8	7.63E-102 - 1.18E-86
<i>Vibrio splendidus</i>	5	3.1E-103 - 1.26E-88
<i>Vibrio vulnificus</i>	9	1.82E-95 - 1.33E-29
<i>Vibrionales bacterium</i>	1	5.67E-89
<i>Weissella paramesenteroides</i>	1	0.581766
<i>Xenopus (Silurana)</i>	1	4.7E-43
<i>Xenorhabdus bovienii</i>	1	5.61E-129
<i>Xenorhabdus nematophila</i>	1	0
<i>Xylanimonas cellulositytica</i>	1	1.08E-63
<i>Yersinia aldovae</i>	1	0
<i>Yersinia bercovieri</i>	1	0
<i>Yersinia enterocolitica</i>	4	0 - 3.34E-73
<i>Yersinia frederiksenii</i>	2	0 - 1.5E-73
<i>Yersinia intermedia</i>	1	0
<i>Yersinia kristensenii</i>	1	0
<i>Yersinia mollaretii</i>	1	0
<i>Yersinia pestis</i>	2	0
<i>Yersinia pseudotuberculosis</i>	4	0
<i>Yersinia rohdei</i>	1	0
<i>Yersinia ruckeri</i>	1	0
<i>Zea mays</i>	1	1.85E-39
<i>Zunongwangia profunda</i>	1	0.0687

APPENDIX C. Sources of the hypothetical / unknown proteins showing significant sequence similarity to the PMI amino acid sequence in BLASTP analysis

Organism	No. of proteins	E-value
<i>Actinomyces odontolyticus</i>	1	1.28E-40
<i>Acyrtosiphon pisum</i>	1	2.97E-13
<i>Ailuropoda melanoleuca</i>	1	9.81E-41
<i>Anaerotruncus colihominis</i>	1	0.0081
<i>Anopheles darlingi</i>	1	1.85E-39
<i>Anopheles gambiae</i>	1	8.59E-37
<i>Arabidopsis lyrata</i>	3	3.86E-37 - 2.35E-18
<i>Arabidopsis thaliana</i>	5	7.56E-17 - 6.4E-16
<i>Aspergillus nidulans</i>	1	2.51E-20
<i>Aspergillus niger</i>	2	1.85E-39 - 2.27E-21
<i>Aspergillus oryzae</i>	2	1.57E-38 - 7.79E-30
<i>Aspergillus terreus</i>	1	2.43E-23
<i>Aureococcus anophagefferens</i>	2	1.85E-31 - 1.63E-19
<i>Bacillus amyloliquefaciens</i>	1	0.4454
<i>Bacteroides caccae</i>	1	0.1531
<i>Bacteroides coprocola</i>	1	0.0403
<i>Bacteroides coprophilus</i>	1	0.011
<i>Bacteroides eggerthii</i>	1	0.1172
<i>Bacteroides ovatus</i>	1	0.0898
<i>Bacteroides plebeius</i>	1	0.2611
<i>Bacteroides stercoris</i>	1	0.1531
<i>Bacteroides uniformis</i>	1	0.0308
<i>Bifidobacterium dentium</i>	1	1.16E-33
<i>Blastocystis hominis</i>	1	5.57E-36
<i>Botryotinia fuckeliana</i>	2	1.42E-39 - 4.42E-25
<i>Branchiostoma floridae</i>	2	6.79E-42 - 2.59E-33
<i>Caenorhabditis briggsae</i>	4	7.77E-38 - 7.79E-30
<i>Caenorhabditis elegans</i>	1	6.17E-27
<i>Caenorhabditis remanei</i>	3	5.95E-38 - 2.52E-12
<i>Candida albicans</i>	2	7.27E-36
<i>Candida glabrata</i>	1	8.04E-35
<i>Catonella morbi</i>	1	0.1172
<i>Chaetomium globosum</i>	2	1.62E-35 - 4.89E-24
<i>Chlorella variabilis</i>	1	3.38E-33
<i>Clavispora lusitaniae</i>	1	1.98E-41
<i>Clostridium asparagiforme</i>	1	0.2611
<i>Clostridium boltea</i>	2	0.0526 - 0.4454

Organism	No. of proteins	E-value
<i>Clostridium leptum</i>	1	0.1172
<i>Clostridium spiroforme</i>	1	0.0403
<i>Clostridium sporogenes</i>	1	0.0028
<i>Coccidioides immitis</i>	1	7.77E-38
<i>Collinsella aerofaciens</i>	1	0.3411
<i>Collinsella intestinalis</i>	1	0.1172
<i>Collinsella stercoris</i>	1	0.3411
<i>Coprinopsis cinerea</i>	1	6.56E-45
<i>Corynebacterium glutamicum</i>	1	2.03E-62
<i>Corynebacterium lipophiloflavum</i>	1	7.84E-06
<i>Corynebacterium matruchotii</i>	1	8.53E-61
<i>Cryptococcus neoformans</i>	1	4.12E-39
<i>Cryptosporidium hominis</i>	1	0.00475915
<i>Daphnia pulex</i>	1	4.87E-40
<i>Debaryomyces hansenii</i>	1	2.5E-36
<i>Drosophila ananassae</i>	1	2.76E-35
<i>Drosophila erecta</i>	1	4.72E-35
<i>Drosophila grimshawi</i>	1	2.12E-35
<i>Drosophila melanogaster</i>	1	3.06E-34
<i>Drosophila mojavensis</i>	1	1.02E-37
<i>Drosophila persimilis</i>	2	2.05E-38 - 0.7598
<i>Drosophila pseudoobscura</i>	1	2.67E-38
<i>Drosophila sechellia</i>	1	1.79E-34
<i>Drosophila simulans</i>	1	9.22E-23
<i>Drosophila virilis</i>	1	4.26E-36
<i>Drosophila willistoni</i>	1	2.67E-38
<i>Drosophila yakuba</i>	2	8.04E-35 - 1.63E-11
<i>Escherichia coli</i>	1	0.9923
<i>Eubacterium bifforme</i>	1	0.0001
<i>Eubacterium hallii</i>	1	0.0006
<i>Faecalibacterium prausnitzii</i>	1	0.0236
<i>Gallus gallus</i>	1	6.63E-13
<i>Gibberella zeae</i>	2	6.58E-37 - 1.2E-30
<i>Glycine max</i>	1	2.87E-16
<i>Homo sapiens</i>	3	2.26E-37 - 1.13E-20
<i>Kluyveromyces lactis</i>	1	7.77E-38
<i>Lachancea thermotolerans</i>	1	8.04E-35
<i>Listeria innocua</i>	1	0.117222
<i>Listeria monocytogenes</i>	3	0.2 - 0.4454
<i>Macaca fascicularis</i>	2	8.87E-42 - 7.51E-41

Organism	No. of proteins	E-value
<i>Magnaporthe oryzae</i>	1	6.58E-37
<i>Malassezia globosa</i>	2	3.17E-23 - 2.06E-06
<i>Meyerozyma guilliermondii</i>	1	4.56E-38
<i>Micromonas</i> sp.	1	1.73E-37
<i>Monodelphis domestica</i>	1	3.37E-41
<i>Monosiga brevicollis</i>	1	1.28E-32
<i>Nasonia vitripennis</i>	1	2.11E-43
<i>Nectria haematococca</i>	1	5.58E-28
<i>Neisseria lactamica</i>	1	0.9923
<i>Nematostella vectensis</i>	1	6.37E-32
<i>Neurospora crassa</i>	1	4.27E-28
<i>Oikopleura dioica</i>	1	9.81E-41
<i>Ornithorhynchus anatinus</i>	1	5.56E-44
<i>Oryza sativa</i>	4	2.76E-43 - 6.4E-16
<i>Ostreococcus lucimarinus</i>	1	1.42E-31
<i>Parabacteroides johnsonii</i>	1	0.0308
<i>Parabacteroides merdae</i>	1	0.0236
<i>Paramecium tetraurelia</i>	1	6.59E-29
<i>Penicillium chrysogenum</i>	2	1.73E-37 - 1.99E-17
<i>Phaeosphaeria nodorum</i>	2	9.54E-20 - 3.76E-08
<i>Physcomitrella patens</i>	2	3.16E-39 - 8.32E-32
<i>Picea sitchensis</i>	1	1.42E-39
<i>Pichia guilliermondii</i>	1	2.67E-38
<i>Plasmodium berghei</i>	1	1.21E-06
<i>Plasmodium chabaudi</i>	1	2.44E-07
<i>Podospora anserina</i>	2	2.67E-38 - 1.62E-27
<i>Populus trichocarpa</i>	1	1.12E-36
<i>Postia placenta</i>	1	1.86E-23
<i>Pyrenophora teres</i>	2	3.86E-37 - 3.74E-24
<i>Saccharomyces cerevisiae</i>	1	3.61E-35
<i>Schistosoma japonicum</i>	2	1.29E-16 - 1.75E-05
<i>Schizophyllum commune</i>	1	1.17E-17
<i>Sclerotinia sclerotiorum</i>	2	7.51E-41 - 1.24E-27
<i>Selaginella moellendorffii</i>	1	6.37E-32
<i>Solenopsis invicta</i>	1	2.59E-33
<i>Sordaria macrospora</i>	3	7.53E-33 - 2.97E-13
<i>Sorghum bicolor</i>	1	6.42E-08
<i>Strongylocentrotus purpuratus</i>	2	1.79E-42 - 0.000734231
<i>Tetraodon nigroviridis</i>	1	7.03E-39
<i>Thalassiosira pseudonana</i>	1	2.95E-37

Organism	No. of proteins	E-value
<i>Trichoplax adhaerens</i>	1	1.28E-40
<i>Ustilago maydis</i>	1	1.42E-39
<i>Vanderwaltozyma polyspora</i>	1	1.91E-36
<i>Verrucomicrobiae bacterium</i>	1	0.1531
<i>Vibrio harveyi</i>	2	2.56E-73 - 0.3411
<i>Vitis vinifera</i>	4	1.2E-38 - 7.31E-20
<i>Volvox carteri</i>	1	1.73E-37
<i>Xenopus laevis</i>	1	2.58E-41
<i>Yarrowia lipolytica</i>	1	2.42E-39
<i>Zea mays</i>	3	1.42E-39 - 9.18E-39
<i>Zygosaccharomyces rouxii</i>	1	3.37E-41