



HPPD W336 PROTEIN
AMINO ACID SEQUENCE HOMOLOGY
SEARCH WITH KNOWN TOXINS

DATA REQUIREMENT
No applicable guidelines

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PAGE 1 OF 116



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APPROVALS PAGE

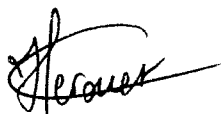
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TABLE OF CONTENTS

APPROVALS PAGE.....	2
TABLE OF CONTENTS.....	3
SUMMARY	4
1. MATERIAL AND METHODS	5
1.1. Amino acid query sequence.....	5
1.2. Search design.....	5
1.3. Protein databases.....	6
2. RESULTS	7
3. CONCLUSION.....	9
4. REFERENCES	10
5. ACRONYMS AND ABBREVIATIONS.....	11
6. TABLES.....	12
6.1. Table 1 - BLASTP sequence similarities of the HPPD W336 protein with proteins from the Uniprot_Swissprot database.....	12
6.2. Table 2 - BLASTP sequence similarities of the HPPD W336 protein with proteins from the Uniprot_TREMBL database.....	15
6.3. Table 3 - BLASTP sequence similarities of the HPPD W336 protein with proteins from the PDB database.....	41
6.4. Table 4 - BLASTP sequence similarities of the HPPD W336 protein with proteins from the DAD database.....	42
6.5. Table 5 - BLASTP sequence similarities of the HPPD W336 protein with proteins from the GenPept database	83
7. FIGURES.....	107
7.1. Figure 1 – Alignment of the HPPD W336 sequence with the VLLY sequence	107
7.2. Figure 2 – Alignment of the HPPD W336 and VLLY sequences with a dataset of HPPD extracted from Uniprot_Swissprot	108
7.3. Figure 3 – Alignment of the HPPD W336 sequence with the Legiolysin sequence	114
8. ANNEX 1 – DESCRIPTION OF THE SEQUENCES INCLUDED IN THE HPPD DATASET	115

SUMMARY

This study used an *in silico* approach to evaluate the potential amino acid sequence similarity of the single mutated para-hydroxyphenylpyruvate dioxygenase (HPPD W336) protein with known toxins from public protein databases.

The overall amino acid sequence identity search was carried out by using BLASTP algorithm, which compared the complete amino acid sequence of the HPPD W336 protein with all protein sequences present in the following large reference databases: Uniprot_Swissprot, Uniprot_TrEMBL, PDB, DAD and GenPept. The scoring matrix used was BLOSUM62. The overconservative criterion for selecting similar proteins was a threshold E-value of 0.1. Matched sequence proteins were further examined for potential toxicity records in literature in order to assess their biological relevance.

As expected, the results showed similarities with other HPPD proteins from various origins. The list includes HPPD-like protein sequences annotated as toxins or putative toxins. However, a refined bioinformatics analysis demonstrated that these specific homologies were unlikely to be relevant. These matches are due to the presence, in the matching sequences, of a typical HPPD pattern that is extremely conserved amongst all known HPPDs from plants, animals, fungi and bacteria, and that explains the homology with HPPD W336. Since direct hemolytic activity of these matching proteins was not demonstrated, it is unlikely that these homologies are biologically relevant.

1. Material and methods

1.1. Amino acid query sequence

The 358 amino acid query sequence was coded using the one-letter code adopted by the Commission on Biochemical Nomenclature of the [IUPAC-IUB \(1984\)](#).

As described in the document number [M-228149-01-1 \(De Beuckeleer, 2004\)](#), the query sequence corresponding to the HPPD W336 protein is as follows:

```
MADLYENPMGLMGFEFIEFASPTPGTLEPIFEIMGFTKVATHRSKNVHLYRQGEINLILN  
NEPNSIASYFAAEHGPSVCGMAFRVKDSQKAYNRALELGAQPIHIDTGPMELNLPKGI  
GGAPLYLIDRFGEGSSIYDIDFVYLEGVERNVPVAGLKVVIDHLTHNVYRGRMVYWANFYE  
KLFNFREARYFDIKGEYTGLTSKAMSAPDGMIRIPLNEESSKGAGQIEEFLMQFNNGEQ  
HVAFLTDDLVTWDALKKIGMRFTAPPDTYYEMLEGRLPDHGEPVDQLQARGILLDGSS  
VEGDKRLLQLQIFSETLMGPVFFFEFIQRKGDDGFGEWNFKALFESIERDQVRRGVLTAD
```

Date of search: August 13, 2009.

1.2. Search design

The complete query sequence was compared with all the sequences available in the public reference databases using the BLASTP (standard Protein-protein Basic Local Alignment Search Tool) program.

The BLASTP program is a sequence comparison algorithm used to search sequence databases for optimal local alignments with a query sequence. BLASTP was developed and is maintained by the National Center for Biotechnology Information (NCBI) ([Altschul et al., 1997](#)). Version 2.2.20 (release February 08, 2009) was used in this study.

Comparisons were made in a pairwise fashion. The similarity was shown by local alignments of the two amino acid sequences that included only the most similar local region(s). This algorithm was combined with Karlin-Atschul statistics ([Karlin et al., 1990](#)). Each comparison was given a score reflecting the degree of similarity between the query and the comparing sequence. The scoring matrix used was BLOSUM62.

Discrimination between real and artefactual matches is done by using the Expect (E)-value, which describes an estimate of probability that the match might occur by chance when searching a database of a particular size. An E-value threshold of 0.1 was used. If the statistical significance ascribed to a match was greater than the E-value threshold, the match was not reported, *i.e.* scoring hits above E-value at 0.1 were not reported.

1.3. Protein databases

The sequence comparisons were carried out by using large publicly available databases as described below:

- Uniprot-Swissprot (release 57.4, 2009; 470 369 sequences). Uniprot-Swissprot is a protein sequence database that strives to provide a high level of annotations (e.g. protein function, post-translational modification, etc.), a minimal level of redundancy and a high level of integration with other databases, notably the EMBL, PROSITE pattern and NRL-3D databases. Uniprot-Swissprot has been developed by SIB (Swiss Institute of Bioinformatics) and EBI (European Bioinformatics Institute).
- Uniprot-TrEMBL (release 40.4, 2009; 8 594 382 sequences). Uniprot-TrEMBL is a computer-annotated supplement of Uniprot_Swissprot that contains all the translations of EMBL nucleotide sequence entries not yet integrated in Uniprot-Swissprot. Uniprot-TrEMBL has been developed by SIB and EBI.
- PDB (release 2009; 139 921 sequences). The PDB (Protein Data Bank) is the single international repository for public data on the 3-dimensional structures of biological macromolecules. The contents are primarily experimental data derived from X-ray crystallography and NMR experiments. This database is constantly updated as new structures are deposited by the international scientific community. It is also called NRL-3D.
- DAD (DDBJ Amino acid sequence Database) (release 47.0, 2009; 14 237 430 sequences). The DAD is a protein database translated from the DDBJ (DNA Data Bank of Japan) which is officially certified to collect DNA sequences from researchers and to issue the internationally recognized accession number to data submitters. This database exchanges the collected data with EMBL/EBI and GenBank/NCBI on a daily basis.
- GenPept (release 171, 2009; 6 809 291 sequences). The GenPept is an amino acid sequence database translated from the GenBank DNA sequence of the NCBI (National Center for Biotechnology Information) as a division of the National Library of Medicine (NLM) at the National Institutes of Health (NIH). The GenBank is built by individual laboratories and by data exchange with the international nucleotide sequence databases, EMBL and DDBJ. Arrangements with the U.S. Patent and Trademark Office enable the incorporation of patent sequence data. A powerful and unique feature of this database is the ability to retrieve references that are available through PubMed, a Web search interface that provides access to over 11 million journal citations in MEDLINE and contains links to full-text articles at participating publishers' Web sites.

1.4. Complementary analysis by multiple alignment

As similarity was identified between the HPPD W336 protein and the hemolytic VLLY protein, a refined bioinformatics analysis on this protein was performed by the Bioinformatics and BioAnalytics groups, Gent, Belgium, in order to interpret this similarity.

HPPD W336 sequence was compared to all other HPPD sequences extracted from the

HPPD W336 Protein
Amino acid sequence homology search with known toxins

Uniprot_Swissprot database in the multiple alignment using the ClustalW algorithm. The VLLY and legiolysin sequences were also compared in this multiple alignment.

This HPPD sequence dataset has been built by compiling all protein sequences referenced with the keyword "HPPD". The keyword "HPPD" was searched in all fields of the Uniprot_Swissprot entries (*i.e.* Keyword, Description, Comment, Title, References, *etc*). This compilation allowed to retrieve 42 protein sequences. Non relevant entries (*e.g.* HPPD-like, putative HPPD, uncharacterized HPPD) as well as legiolysin proteins were excluded. The final dataset was composed of 27 protein sequences. The proteins included in this HPPD dataset are listed in [Annex 1](#).

2. Results

The matching sequences for each of the protein databases are reported in [Tables 6.1](#) to [6.5](#).

Table Numbers	Database Names	Number of matches with E-value <0.1
6.1	Uniprot_Swissprot	37
6.2	Uniprot_TrEMBL	764
6.3	PDB	19
6.4	DAD	888
6.5	Genpept	530

The individual alignments between the HPPD W336 sequence and matched sequences from the databases are included in the raw data.

As expected, the query sequence matched with the 4-hydroxyphenylpyruvate dioxygenase (HPPD, also called HPPDase; MelA; enzyme classification E.C. 1.13.11.27) from various origins, including *Pseudomonas fluorescens*.

An identity of 54% (192 identical residues) was observed with the VLLY protein (Uniprot_SwissProt entry: O06695, [Figure 1](#)). It is described as a hemolysin from *Vibrio vulnificus*, a pathogenic bacterium present in seawaters and able to infect humans who consume seafood ([Chang *et al.*, 1997](#)). The VLLY protein is also annotated to belong to the HPPD family.

Because VLLY was annotated as an HPPD, the hypothesis was raised that the similarity between OTP-HPPD W336 and VLLY was caused by the presence of HPPD domains on the VLLY protein. To test this hypothesis, a multiple alignment of the HPPD W336, VLLY, and 27 HPPD sequences extracted from the Uniprot_Swissprot database from bacteria, plants, vertebrates, invertebrates and fungi was performed and a consensus HPPD sequence was obtained ([Figure 2](#)). The homology between HPPD W336 and VLLY appears to correspond to the conserved domains

HPPD W336 Protein
Amino acid sequence homology search with known toxins

among all HPPD proteins.

In addition, the similarities found between HPPD W336 and VLLY were systematically compared with the HPPD-conserved motifs. The results of this analysis are presented in [Table 1](#). Out of the 192 identical residues between HPPD-W336 and VLLY, only 53 line up with less than 4 HPPD entries on the HPPD multiple alignment. Of these 53 residues, 87% are distributed in short stretches of 1 or 2 amino acids. Such a distribution is not supportive of any specific biological function associated with these residues. The other 139 identical residues line up with 4 or more HPPD entries, among which 123 line up with more than 8 HPPD entries. Of those 139 residues, the vast majority are distributed in long stretches of consecutive amino acids: only 14% are distributed in stretches of 1 to 2 amino acids, whereas 27% are distributed in stretches of 3 to 7 amino acids, and 59% in stretches of 8 to 21 amino acids. The 41 residues that are strictly conserved amongst HPPDs are all part of the identical residues between HPPD-W336 and VLLY.

Table 1: Analysis of the distribution of the identical residues between OTP-W336 and VLLY

Distribution of the identical residues between OTP-HPPD W336 and VLLY	Number of residues	Distribution in stretches admitting gaps of 2 residues											
		Size of the stretch											
	192	1	2	3	4	5	8	9	10	12	14	21	
Identical residues that match with less than 4 HPPD entries	53	28	18	3	4								
		87%		13%			0%						
Identical residues that match with 4 or more HPPD entries	139	14	6	1 8	4	1 5	16	9	10	12	14	21	
		14%		27%			59%						

These observations support the hypothesis that the similarity between OTP-HPPD W336 and VLLY is caused by the presence of a typical HPPD structure shared by the HPPDs from all kingdoms in the sequence of VLLY.

Similarities with lower percentages of identity (49-50%) were also found between HPPD and legiolysins, also called LLY, from strains of *Legionella pneumophila* ([Figure 3](#)). Similar to the VLLY protein, the legiolysin is annotated as an HPPD protein and hemolysin, and the similarities between OTP-HPPD W336 and legiolysin are attributed to the HPPD domains, as shown by the multiple alignment between HPPD W336, VLLY and legiolysin ([Figure 2](#), last row).

These observations support the hypothesis that VLLY and LLY proteins are HPPDs and therefore, share typical HPPD structure with HPPD W336. This is corroborated by several authors who demonstrated the HPPD activity of the legiolysin ([Wintermeyer et al., 1994](#); [Steiner et al., 2001](#)). In addition, although VLLY or LLY protein expression was shown to be necessary for the hemolytic activity of bacteria, the direct hemolytic activity of these proteins was not observed ([Wintermeyer et al., 1994](#); [Chang et al., 1997](#); [Steinert et al., 2001](#)). It was shown that homogentisic acid, the product of HPPD enzymatic activity, forms spontaneously plasma soluble, toxic melanins that have hemolytic activity ([Hegedus and Nayak, 1994](#)). This supports the hypothesis that HPPD is not directly hemolytic.

3. Conclusion

The HPPD W336 is similar to other HPPD proteins from various origins. The list includes the HPPD-like hemolysin (e.g. from *Vibrio vulnificus*), which is described as a bacterial toxin. However, a refined bioinformatics analysis demonstrated that this specific homology was unlikely to be relevant. This match is due to the domains of proteins that possess the HPPD activity and that are conserved between all the HPPD proteins. Since direct hemolytic activity of these matching proteins was not demonstrated, it is unlikely that these homologies are biologically relevant.

4. References

DART #	References
M-222480-01-1	Altschul, S.F., Madden, S.F., Schaffer, A.A., Zhang, J., Zhang, Z., Miller, W., Lipman, D.J. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. <i>Nucleic Acid Res.</i> 25:3389-3402.
M-301840-01-1	Chang, TM, Chuang, YC, Su, JH, Chang, MC. 1997. Cloning and sequence analysis of a novel hemolysin gene (<i>vly</i>) from <i>Vibrio vulnificus</i> . <i>Applied and Environmental Microbiology</i> , 63:3851–3857.
M-232685-01-1	De Beuckeleer, M. 2004. Description of the amino acid sequence of the HPPDase W336 protein. Unpublished. Bayer Cropscience. 5 pages. Hegedus, Z.L. and Nayak, U. 1994. Homogentisic acid and structurally related compounds as intermediates in plasma soluble melanin formation and in tissue toxicities. <i>Arch. Int. Physiol. Biochim. Biophys.</i> 102:175-181.
M-264607-01-1	IUPAC-IUB. 1984. Joint Commission on Biochemical Nomenclature (JCBN). Nomenclature and symbolism for amino acids and peptides. Recommendations 1983. <i>Eur. J. Biochem.</i> 138: 9-37. http://www.chem.gmw.ac.uk/iupac/AminoAcid/
M-265204-01-1	Karlin, S., Altschul, S.F. 1990. Methods for assessing the statistical significance of molecular sequence features by using general scoring schemes. <i>Proc. Natl. Acad. Sci. USA.</i> 87:2264 2268.
M-301852-01-1	Steinert, M, Flügel, M, Schuppler, M, Helbig, JH, Supriyono, C, Proksch, P, Lück, C. 2001. The Lly protein is essential for <i>p</i> -hydroxyphenylpyruvate dioxygenase activity in <i>Legionella pneumophila</i> . <i>FEMS Letters.</i> 203:41-47.
M-301854-01-1	Wintermeyer, E, Flugel, M, Ott, M, Steinert, M, Rdest, U, Mann, KH, Hacker, J. 1994. Sequence determination and mutational analysis of the <i>lly</i> locus of <i>Legionella pneumophila</i> . <i>Infection and Immunity.</i> 62:1109-1117.

5. Acronyms and Abbreviations

%	Percent(age)
aa	Amino acid(s)
BLASTP	Standard basic local alignment search tool for proteins
DAD	DDBJ Amino acid sequence Database
DDBJ	DNA Data Bank of Japan
DNA	Desoxyribonucleic acid
E-Value.....	Expect(ed) value
E.C.	Enzyme classification
EBI.....	European Bioinformatics Institute
EMBL.....	European Molecular Biology Laboratory sequence database
HPPD or HPPDase....	para-hydroxyphenyl pyruvate dioxygenase
ID.....	Accession number
Ident.	Identity
JCBN	Joint Commission on Biochemical Nomenclature
MOL. NAME.....	Molecule name
NCBI	National Center for Biotechnology Information
NIH	National Institute of Health
NLM.....	National Library of Medicine
PDB	Protein Data Bank
SIB.....	Swiss Institute of Bioinformatics
TrEMBL	Translated sequences from the EMBL nucleotide sequence database

HPPD W336 Protein
Amino acid sequence homology search with known toxins

6. Tables

6.1. Table 1 - BLASTP sequence similarities of the HPPD W336 protein with proteins from the Uniprot_Swissprot database

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
1	HPPD_PSEUJ	P80064	357	0	330 \ 357	92	4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD; EC=1.13.11.27
2	HPPD_PSEAE	Q9I576	357	1.00E-104	186 \ 352	52	4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD; EC=1.13.11.27
3	VLLY_VIBVU	O06695	357	1.00E-103	192 \ 355	54	Hemolysin vIIY
4	LLY_LEGPC	P69053	348	2.00E-91	175 \ 349	50	4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD; EC=1.13.11.27; Legiolysin
5	LLY_LEGPH	Q5ZT84	348	4.00E-91	175 \ 349	50	4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD; EC=1.13.11.27; Legiolysin
6	MELA_SHECO	P23996	346	1.00E-79	154 \ 353	43	Protein melA
7	HPPD_STRAW	Q53586	381	3.00E-38	109 \ 297	36	4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD; EC=1.13.11.27
8	HPPD_STRCO	Q9S2F4	381	2.00E-36	105 \ 294	35	4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD; EC=1.13.11.27
9	HPPD1_ASPFU	Q4WHU1	403	2.00E-32	119 \ 364	32	Probable 4-hydroxyphenylpyruvate dioxygenase 1; Short=HPPDase 1; Short=4HPPD 1; Short=HPD 1; EC=1.13.11.27
10	HPPD_COCPO	Q00415	399	6.00E-31	112 \ 366	30	4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD; EC=1.13.11.27; T-cell reactive protein
11	HPPD_COCIM	Q1E803	399	9.00E-31	112 \ 366	30	4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD; EC=1.13.11.27; T-cell reactive protein
12	HPPD_MAGGR	Q96X22	419	1.00E-30	103 \ 308	33	4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD; EC=1.13.11.27
13	HPPD_DICDI	Q76NV5	367	1.00E-30	104 \ 304	34	4-hydroxyphenylpyruvate dioxygenase; EC=1.13.11.27; 4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD
14	HPPD_MYCGR	O42764	419	5.00E-30	104 \ 306	33	4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD; EC=1.13.11.27
15	HPPD2_ASPFU	Q4WPV8	406	2.00E-29	103 \ 310	33	Probable 4-hydroxyphenylpyruvate dioxygenase 2; Short=HPPDase 2; Short=4HPPD 2; Short=HPD 2; EC=1.13.11.27

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
16	HPPD_NEUCR	Q872T7	412	4.00E-29	98 \ 308	31	4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD; EC=1.13.11.27
17	HPPD_YARLI	Q6CDR5	394	1.00E-28	109 \ 356	30	4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD; EC=1.13.11.27
18	Y090_SYNY3	Q55810	339	2.00E-28	93 \ 307	30	Uncharacterized protein slr0090
19	HPPD_CAEEL	Q22633	393	4.00E-27	102 \ 339	30	4-hydroxyphenylpyruvate dioxygenase; EC=1.13.11.27; 4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD
20	HPPD_TETTH	Q27203	404	2.00E-26	94 \ 307	30	4-hydroxyphenylpyruvate dioxygenase; EC=1.13.11.27; 4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD; F-antigen homolog; TF-AG
21	HPPD_XENTR	Q5BKL0	394	3.00E-26	104 \ 332	31	4-hydroxyphenylpyruvate dioxygenase; EC=1.13.11.27; 4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD
22	HPPD_CAEBR	Q60Y65	393	4.00E-25	94 \ 306	30	4-hydroxyphenylpyruvate dioxygenase; EC=1.13.11.27; 4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD
23	HPPD_DANRE	Q6TGZ5	397	7.00E-25	107 \ 358	29	4-hydroxyphenylpyruvate dioxygenase; EC=1.13.11.27; 4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD
24	HPPD_PIG	Q02110	393	6.00E-23	99 \ 351	28	4-hydroxyphenylpyruvate dioxygenase; EC=1.13.11.27; 4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD
25	HPPD_BOVIN	Q5EA20	393	8.00E-23	98 \ 353	27	4-hydroxyphenylpyruvate dioxygenase; EC=1.13.11.27; 4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD
26	HPPD_RAT	P32755	393	1.00E-22	98 \ 355	27	4-hydroxyphenylpyruvate dioxygenase; EC=1.13.11.27; 4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD; F Alloantigen; Short=F protein
27	HPPD_HUMAN	P32754	393	1.00E-22	98 \ 355	27	4-hydroxyphenylpyruvate dioxygenase; EC=1.13.11.27; 4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD
28	HPPD_DAUCA	O23920	442	2.00E-22	92 \ 308	29	4-hydroxyphenylpyruvate dioxygenase; EC=1.13.11.27; 4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD
29	YBWL_CAEEL	Q18347	364	3.00E-22	97 \ 345	28	Putative protein C31H2.4
30	HPPD_MOUSE	P49429	393	1.00E-21	96 \ 350	27	4-hydroxyphenylpyruvate dioxygenase; EC=1.13.11.27; 4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD; F Alloantigen; Short=F protein
31	HPPD_ARATH	P93836	445	2.00E-20	90 \ 314	28	4-hydroxyphenylpyruvate dioxygenase; EC=1.13.11.27; 4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD
32	HPPD_SOLSC	Q9ARF9	436	8.00E-17	99 \ 350	28	4-hydroxyphenylpyruvate dioxygenase; EC=1.13.11.27; 4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD

HPPD W336 Protein
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HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
33	HPDL_MOUSE	Q8K248	371	4.00E-16	67 \ 231	29	4-hydroxyphenylpyruvate dioxygenase-like protein; Glyoxalase domain-containing protein 1
34	HPPD_HORVU	O48604	434	3.00E-15	94 \ 315	29	4-hydroxyphenylpyruvate dioxygenase; EC=1.13.11.27; 4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD
35	HPDL_HUMAN	Q96IR7	371	5.00E-15	83 \ 303	27	4-hydroxyphenylpyruvate dioxygenase-like protein; Glyoxalase domain-containing protein 1
36	HPDL_RAT	Q5XIH9	371	1.00E-14	46 \ 130	35	4-hydroxyphenylpyruvate dioxygenase-like protein; Glyoxalase domain-containing protein 1
37	HPDL_DICDI	Q557J8	494	3.00E-14	89 \ 380	23	Uncharacterized 4-hydroxyphenylpyruvate dioxygenase-like protein

HPPD W336 Protein
Amino acid sequence homology search with known toxins

6.2. Table 2 - BLASTP sequence similarities of the HPPD W336 protein with proteins from the Uniprot_TREMBL database

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
1	C3KA88_PSEFL	C3KA88	358	0	348 \ 358	97	Putative 4-hydroxyphenylpyruvate dioxygenase.
2	Q2HYA4_PSEFL	Q2HYA4	358	0	341 \ 358	95	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27. Flags: Fragment.
3	Q3KC47_PSEPF	Q3KC47	358	0	336 \ 358	93	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
4	Q4KB91_PSEF5	Q4KB91	358	0	332 \ 358	92	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
5	Q88HC7_PSEPK	Q88HC7	358	0	315 \ 358	87	4-hydroxyphenylpyruvate dioxygenase.
6	B0KRN7_PSEPG	B0KRN7	358	0	314 \ 358	87	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
7	Q4ZR60_PSEU2	Q4ZR60	358	0	312 \ 358	87	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
8	A5W2V8_PSEP1	A5W2V8	358	0	313 \ 358	87	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
9	Q87Z77_PSESM	Q87Z77	363	0	312 \ 357	87	4-hydroxyphenylpyruvate dioxygenase.
10	Q48GS3_PSE14	Q48GS3	358	0	312 \ 358	87	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
11	Q6EMJ1_PSEPU	Q6EMJ1	358	0	312 \ 358	87	P-hydroxyphenylpyruvate dioxygenase.
12	B1J895_PSEPW	B1J895	358	0	311 \ 355	87	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
13	Q1I954_PSEE4	Q1I954	357	1.00E-180	304 \ 358	84	4-hydroxyphenylpyruvate dioxygenase 4HPPD (HPD) (HPPDase). EC=1.13.11.27.
14	B1Y210_LEPCP	B1Y210	358	1.00E-177	298 \ 357	83	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
15	Q7X4L2_9BACT	Q7X4L2	301	1.00E-164	276 \ 301	91	4-hydroxyphenylpyruvate dioxygenase. Flags: Fragment.
16	Q46SN3_RALEJ	Q46SN3	359	1.00E-164	277 \ 358	77	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
17	Q0K2A0_RALEH	Q0K2A0	359	1.00E-162	275 \ 358	76	4-Hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
18	B3R9E4_CUPTR	B3R9E4	359	1.00E-161	273 \ 358	76	4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE PROTEIN. EC=1.13.11.27.
19	Q1LDI9_RALME	Q1LDI9	357	1.00E-161	271 \ 355	76	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
20	A1VLA8_POLNA	A1VLA8	360	1.00E-160	268 \ 358	74	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
21	B1XX63_LEPCP	B1XX63	358	1.00E-160	269 \ 358	75	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
22	Q7X4L1_9BACT	Q7X4L1	308	1.00E-157	267 \ 308	86	4-hydroxyphenylpyruvate dioxygenase. Flags: Fragment.
23	A9BM79_DELAS	A9BM79	364	1.00E-155	266 \ 360	73	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
24	A4BBT2_9GAMM	A4BBT2	365	1.00E-154	257 \ 355	72	4-hydroxyphenylpyruvate dioxygenase.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
25	A5P7N9_9SPHN	A5P7N9	373	1.00E-153	260 \ 362	71	4-hydroxyphenylpyruvate dioxygenase.
26	Q15WT7_PSEA6	Q15WT7	358	1.00E-150	255 \ 356	71	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
27	A1W3E5_ACISJ	A1W3E5	372	1.00E-150	260 \ 356	73	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
28	A5WE99_PSYWF	A5WE99	372	1.00E-149	257 \ 361	71	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
29	B9MCL6_DIAST	B9MCL6	372	1.00E-149	258 \ 356	72	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
30	B4RSS4_ALTMD	B4RSS4	357	1.00E-149	257 \ 356	72	4-hydroxyphenylpyruvate dioxygenase.
31	Q2NAB6_ERYLH	Q2NAB6	373	1.00E-148	251 \ 362	69	4-hydroxyphenylpyruvate dioxygenase.
32	A4ACB3_9GAMM	A4ACB3	361	1.00E-148	257 \ 356	72	4-hydroxyphenylpyruvate dioxygenase.
33	B7RYT6_9GAMM	B7RYT6	362	1.00E-148	251 \ 356	70	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
34	Q1GNF0_SPHAL	Q1GNF0	363	1.00E-147	247 \ 358	68	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
35	Q2GAS9_NOVAD	Q2GAS9	370	1.00E-146	249 \ 361	68	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
36	B8KHM2_9GAMM	B8KHM2	361	1.00E-144	259 \ 358	72	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
37	B7I282_ACIB5	B7I282	351	1.00E-144	241 \ 355	67	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
38	B7GUT4_ACIB3	B7GUT4	351	1.00E-144	241 \ 355	67	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
39	B2I2D6_ACIBC	B2I2D6	351	1.00E-144	241 \ 355	67	4-hydroxyphenylpyruvate dioxygenase.
40	B0V9Y4_ACIBY	B0V9Y4	351	1.00E-144	241 \ 355	67	4-hydroxyphenylpyruvate dioxygenase 4HPPD (HPPDase). EC=1.13.11.27.
41	A3MA63_ACIBT	A3MA63	351	1.00E-144	241 \ 355	67	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
42	Q0BY65_HYPNA	Q0BY65	366	1.00E-144	248 \ 363	68	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
43	B0VPW5_ACIBS	B0VPW5	351	1.00E-143	239 \ 355	67	4-hydroxyphenylpyruvate dioxygenase 4HPPD (HPPDase). EC=1.13.11.27.
44	Q0ASV8_MARMM	Q0ASV8	359	1.00E-143	236 \ 357	66	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
45	Q1QAH1_PSYCK	Q1QAH1	368	1.00E-142	249 \ 359	69	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
46	A3WGH0_9SPHN	A3WGH0	372	1.00E-141	246 \ 362	67	4-hydroxyphenylpyruvate dioxygenase.
47	A6VYX1_MARMS	A6VYX1	358	1.00E-141	245 \ 358	68	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
48	B6IWM9_RHOCS	B6IWM9	377	1.00E-122	224 \ 362	61	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
49	A7CAM9_BURPI	A7CAM9	368	1.00E-118	215 \ 364	59	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
50	B2UFE0_RALPJ	B2UFE0	368	1.00E-118	215 \ 364	59	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
51	B5SK30_RALSO	B5SK30	367	1.00E-117	215 \ 364	59	4-hydroxyphenylpyruvate dioxygenase protein. EC=1.13.11.27.
52	A3RR06_RALSO	A3RR06	367	1.00E-117	215 \ 364	59	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
53	Q7NZF3_CHRVO	Q7NZF3	358	1.00E-116	210 \ 361	58	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
54	Q8XUT2_RALSO	Q8XUT2	367	1.00E-116	213 \ 364	58	Probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein. EC=1.13.11.27.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
55	A1K4Q5_AZOSB	A1K4Q5	373	1.00E-116	215 \ 369	58	Probable 4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
56	A8TTE8_9PROT	A8TTE8	363	1.00E-115	210 \ 352	59	4-hydroxyphenylpyruvate dioxygenase.
57	B4R8C4_PHEZH	B4R8C4	374	1.00E-115	211 \ 357	59	4-hydroxyphenylpyruvate dioxygenase.
58	B5RZB9_RALSO	B5RZB9	358	1.00E-114	212 \ 360	58	4-hydroxyphenylpyruvate dioxygenase protein. EC=1.13.11.27.
59	Q2STZ8_BURTA	Q2STZ8	365	1.00E-114	207 \ 361	57	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
60	A1TUU3_ACIAC	A1TUU3	378	1.00E-114	215 \ 365	58	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
61	Q13TE2_BURXL	Q13TE2	365	1.00E-114	207 \ 361	57	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
62	Q7WFQ8_BORBR	Q7WFQ8	370	1.00E-113	206 \ 363	56	Putative hemolysin.
63	Q7W4A0_BORPA	Q7W4A0	370	1.00E-113	206 \ 363	56	Putative hemolysin.
64	B2JIJ2_BURP8	B2JIJ2	365	1.00E-113	203 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
65	B2T6N9_BURPP	B2T6N9	365	1.00E-113	206 \ 361	57	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
66	B7YTV0_VARPD	B7YTV0	375	1.00E-113	214 \ 367	58	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
67	A9I4P4_BORPD	A9I4P4	370	1.00E-113	205 \ 365	56	Putative 4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
68	Q63PY5_BURPS	Q63PY5	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
69	Q62GQ1_BURMA	Q62GQ1	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
70	Q3JYB9_BURP1	Q3JYB9	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
71	A3P0E5_BURP0	A3P0E5	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
72	A3NEK8_BURP6	A3NEK8	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
73	A3MS03_BURM7	A3MS03	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
74	A2S7M6_BURM9	A2S7M6	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
75	A1UZF6_BURMS	A1UZF6	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
76	C0XX28_BURPS	C0XX28	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
77	B7D0H7_BURPS	B7D0H7	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
78	B2H492_BURPS	B2H492	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
79	B1H4H6_BURPS	B1H4H6	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
80	A9K0E8_BURMA	A9K0E8	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
81	A8HLQ2_BURPS	A8HLQ2	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
82	A8EK77_BURPS	A8EK77	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
83	A5XQP2_BURMA	A5XQP2	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
84	A5J4Q0_BURMA	A5J4Q0	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
85	A4LVJ7_BURPS	A4LVJ7	365	1.00E-113	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
86	A2W5U6_9BURK	A2W5U6	365	1.00E-113	203 \ 361	56	4-hydroxyphenylpyruvate dioxygenase.
87	B1GAU4_9BURK	B1GAU4	365	1.00E-113	203 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
88	A4JAL3_BURVG	A4JAL3	365	1.00E-112	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
89	B9CJ72_9BURK	B9CJ72	365	1.00E-112	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
90	B9C086_9BURK	B9C086	365	1.00E-112	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
91	B9BBZ4_9BURK	B9BBZ4	365	1.00E-112	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
92	Q7VUN9_BORPE	Q7VUN9	370	1.00E-112	204 \ 363	56	Putative hemolysin.
93	Q1BRS2_BURCA	Q1BRS2	365	1.00E-112	202 \ 361	55	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
94	B1JTP1_BURCC	B1JTP1	365	1.00E-112	202 \ 361	55	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
95	A0K3J8_BURCH	A0K3J8	365	1.00E-112	202 \ 361	55	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
96	A2VUB1_9BURK	A2VUB1	365	1.00E-112	202 \ 361	55	4-hydroxyphenylpyruvate dioxygenase.
97	B5WHD6_9BURK	B5WHD6	365	1.00E-112	205 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
98	Q0BJ73_BURCM	Q0BJ73	365	1.00E-112	202 \ 361	55	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
99	A9AD93_BURM1	A9AD93	365	1.00E-112	202 \ 361	55	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
100	B1YRA2_BURA4	B1YRA2	365	1.00E-112	203 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
101	A5VD44_SPHWW	A5VD44	367	1.00E-112	199 \ 354	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
102	A4Z322_BRASO	A4Z322	372	1.00E-111	195 \ 355	54	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
103	B6C1V1_9GAMM	B6C1V1	363	1.00E-111	199 \ 355	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
104	A2SCL9_METPP	A2SCL9	370	1.00E-111	205 \ 364	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
105	B1T2A5_9BURK	B1T2A5	365	1.00E-111	202 \ 361	55	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
106	B1FGX2_9BURK	B1FGX2	365	1.00E-111	202 \ 361	55	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
107	B9Z224_9NEIS	B9Z224	360	1.00E-111	204 \ 361	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
108	B4E593_BURCJ	B4E593	365	1.00E-111	201 \ 361	55	4-hydroxyphenylpyruvic acid dioxygenase. EC=1.13.11.27.
109	Q39KJ4_BURS3	Q39KJ4	365	1.00E-111	201 \ 361	55	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
110	Q3JB70_NITOC	Q3JB70	351	1.00E-111	199 \ 355	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
111	B3QK03_RHOPT	B3QK03	372	1.00E-111	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
112	Q6NDU9_RHOPA	Q6NDU9	372	1.00E-111	190 \ 355	53	4-hydroxyphenylpyruvate dioxygenase.
113	Q2KVC6_BORA1	Q2KVC6	370	1.00E-110	204 \ 365	55	4-hydroxyphenylpyruvate dioxygenase Putative hemolysin. EC=1.13.11.27.
114	Q89XH5_BRAJA	Q89XH5	372	1.00E-110	190 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
115	A1WJS8_VEREI	A1WJS8	377	1.00E-110	204 \ 365	55	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
116	A5E9K4_BRASB	A5E9K4	372	1.00E-110	192 \ 355	54	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
117	Q124D7_POLSJ	Q124D7	376	1.00E-109	207 \ 367	56	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
118	Q2SND1_HAHCH	Q2SND1	365	1.00E-104	188 \ 362	51	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
119	B7WSE3_COMTE	B7WSE3	373	1.00E-104	196 \ 361	54	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
120	A1B2L7_PARDP	A1B2L7	370	1.00E-103	192 \ 355	54	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
121	Q02I25_PSEAB	Q02I25	357	1.00E-103	186 \ 352	52	4-hydroxyphenylpyruvate dioxygenase.
122	A3LMB2_PSEAE	A3LMB2	357	1.00E-103	186 \ 352	52	4-hydroxyphenylpyruvate dioxygenase.
123	A3L5C9_PSEAE	A3L5C9	357	1.00E-103	186 \ 352	52	4-hydroxyphenylpyruvate dioxygenase.
124	B7UY69_PSEA8	B7UY69	357	1.00E-103	186 \ 352	52	4-hydroxyphenylpyruvate dioxygenase.
125	A4XSZ4_PSEMY	A4XSZ4	360	1.00E-103	187 \ 355	52	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
126	A3Y5W8_9GAMM	A3Y5W8	363	1.00E-102	195 \ 355	54	4-hydroxyphenylpyruvate dioxygenase.
127	A8T1G9_9VIBR	A8T1G9	357	1.00E-102	194 \ 361	53	4-hydroxyphenylpyruvate dioxygenase.
128	A6CXY3_9VIBR	A6CXY3	357	1.00E-102	193 \ 355	54	4-hydroxyphenylpyruvate dioxygenase.
129	A3UE43_9RHOB	A3UE43	354	1.00E-102	191 \ 358	53	4-hydroxyphenylpyruvate dioxygenase.
130	A7MVT3_VIBHB	A7MVT3	357	1.00E-102	194 \ 361	53	Putative uncharacterized protein.
131	A6APV8_VIBHA	A6APV8	357	1.00E-102	194 \ 361	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
132	Q7MLD2_VIBVY	Q7MLD2	357	1.00E-102	192 \ 355	54	Putitive hemolysin.
133	Q1VDR3_VIBAL	Q1VDR3	357	1.00E-101	195 \ 361	54	4-hydroxyphenylpyruvate dioxygenase.
134	A7K0B8_9VIBR	A7K0B8	357	1.00E-101	195 \ 361	54	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
135	Q8VQC4_VIBAN	Q8VQC4	357	1.00E-101	192 \ 355	54	4-hydroxyphenylpyruvate dioxygenase.
136	B9QVK6_9RHOB	B9QVK6	378	1.00E-101	184 \ 355	51	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
137	B8K611_VIBPA	B8K611	357	1.00E-101	193 \ 355	54	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
138	A4VHW5_PSEU5	A4VHW5	361	1.00E-101	188 \ 354	53	4-hydroxyphenylpyruvate dioxygenase.
139	C1WB18_9GAMM	C1WB18	353	1.00E-101	188 \ 359	52	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
140	A3UNU9_VIBSP	A3UNU9	357	1.00E-100	192 \ 360	53	4-hydroxyphenylpyruvate dioxygenase.
141	B7VU48_VIBSL	B7VU48	357	1.00E-100	189 \ 354	53	4-hydroxyphenylpyruvate dioxygenase 4HPPD (Hemolysin).
142	A3XSJ5_9VIBR	A3XSJ5	357	1.00E-100	191 \ 360	53	4-hydroxyphenylpyruvate dioxygenase.
143	A0NXF2_9RHOB	A0NXF2	370	1.00E-100	182 \ 355	51	Probable 4-hydroxyphenylpyruvate dioxygenase protein.
144	Q87Q01_VIBPA	Q87Q01	357	1.00E-100	192 \ 361	53	4-hydroxyphenylpyruvate dioxygenase.
145	A6AYW8_VIBPA	A6AYW8	357	1.00E-100	192 \ 361	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
146	A5KW51_9GAMM	A5KW51	357	1.00E-100	189 \ 354	53	4-hydroxyphenylpyruvate dioxygenase.
147	C2I WV0_VIBCH	C2I WV0	369	1.00E-100	192 \ 355	54	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
148	Q15RI3_PSEA6	Q15RI3	360	1.00E-100	191 \ 361	52	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
149	A0KLM1_AERHH	A0KLM1	365	1.00E-100	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
150	B6R6M6_9RHOB	B6R6M6	370	1.00E-100	186 \ 353	52	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
151	C3M933_RHISN	C3M933	372	1.00E-100	183 \ 352	51	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
152	B8L7Z0_9GAMM	B8L7Z0	370	2.00E-99	181 \ 354	51	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
153	A9DH41_9RHIZ	A9DH41	369	2.00E-99	181 \ 353	51	Probable 4-hydroxyphenylpyruvate dioxygenase protein.
154	A6ABN4_VIBCH	A6ABN4	369	3.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
155	A6A1J5_VIBCH	A6A1J5	369	3.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
156	A2P5X9_VIBCH	A2P5X9	369	3.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
157	C2I5Q2_VIBCH	C2I5Q2	369	3.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
158	A6VAB1_PSEA7	A6VAB1	357	6.00E-99	185 \ 352	52	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
159	Q9RCH2_VIBCH	Q9RCH2	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. P-hydroxyphenylpyruvate dioxygenase.
160	A5F8H7_VIBC3	A5F8H7	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
161	C3NQU6_VIBCH	C3NQU6	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
162	C3LM39_VIBCH	C3LM39	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
163	C2J8N4_VIBCH	C2J8N4	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
164	C2II11_VIBCH	C2II11	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
165	C2HRM9_VIBCH	C2HRM9	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
166	C2CAV6_VIBCH	C2CAV6	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
167	B2D6T3_VIBCH	B2D6T3	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
168	A6Y286_VIBCH	A6Y286	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
169	A6XWB5_VIBCH	A6XWB5	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
170	A3GYV2_VIBCH	A3GYV2	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
171	A3GN89_VIBCH	A3GN89	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
172	A3EJ57_VIBCH	A3EJ57	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
173	A3EFS3_VIBCH	A3EFS3	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
174	A2PHM9_VIBCH	A2PHM9	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
175	A1F9C1_VIBCH	A1F9C1	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
176	A1EKH6_VIBCH	A1EKH6	369	6.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
177	A2PTY1_VIBCH	A2PTY1	357	8.00E-99	191 \ 355	53	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
178	B2FKN2_STRMK	B2FKN2	356	1.00E-98	181 \ 354	51	Putative 4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
179	A4SNS7_AERS4	A4SNS7	370	1.00E-98	190 \ 354	53	4-hydroxyphenylpyruvate dioxygenase.
180	B4SLG9_STRM5	B4SLG9	356	1.00E-98	181 \ 354	51	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
181	Q983J0_RHILO	Q983J0	371	4.00E-98	176 \ 355	49	4-hydroxyphenylpyruvate dioxygenase.
182	Q1MI53_RHIL3	Q1MI53	369	5.00E-98	179 \ 352	50	Putative 4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
183	Q09PG8_9BACT	Q09PG8	367	7.00E-98	179 \ 352	50	4-hydroxyphenylpyruvate dioxygenase.
184	B1PS46_9BACT	B1PS46	367	7.00E-98	179 \ 352	50	4-hydroxyphenylpyruvate dioxygenase.
185	Q2BWP1_9GAMM	Q2BWP1	356	9.00E-98	184 \ 356	51	Putative 4-hydroxyphenylpyruvate dioxygenase.
186	Q1ZUT8_9VIBR	Q1ZUT8	356	9.00E-98	186 \ 356	52	Putative 4-hydroxyphenylpyruvate dioxygenase.
187	C1DQI8_AZOVD	C1DQI8	359	2.00E-97	186 \ 352	52	4-hydroxyphenylpyruvate dioxygenase.
188	Q6LI28_PHOPR	Q6LI28	365	2.00E-97	190 \ 356	53	Putative 4-hydroxyphenylpyruvate dioxygenase.
189	B0J667_RHILT	B0J667	369	2.00E-97	178 \ 352	50	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
190	B0RMW9_XANCB	B0RMW9	371	5.00E-97	181 \ 354	51	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
191	Q8PDA4_XANCP	Q8PDA4	356	8.00E-97	181 \ 354	51	4-hydroxyphenylpyruvate dioxygenase.
192	Q4UZJ1_XANC8	Q4UZJ1	356	8.00E-97	181 \ 354	51	4-hydroxyphenylpyruvate dioxygenase.
193	Q2K9E6_RHIEC	Q2K9E6	369	8.00E-97	176 \ 352	50	Probable 4-hydroxyphenylpyruvate dioxygenase protein. EC=1.13.11.27.
194	Q1YYF4_PHOPR	Q1YYF4	356	9.00E-97	189 \ 356	53	Putative 4-hydroxyphenylpyruvate dioxygenase.
195	Q11EB4_MESSB	Q11EB4	369	9.00E-97	183 \ 352	51	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
196	A3JZN0_9RHOB	A3JZN0	364	2.00E-96	178 \ 355	50	4-hydroxyphenylpyruvate dioxygenase.
197	A6UDD6_SINMW	A6UDD6	370	3.00E-96	180 \ 353	50	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
198	Q92LT1_RHIME	Q92LT1	370	5.00E-96	179 \ 353	50	Putative 4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
199	B5ZZA7_RHILW	B5ZZA7	369	2.00E-95	173 \ 352	49	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
200	Q1D8M0_MYXXD	Q1D8M0	354	3.00E-95	184 \ 362	50	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
201	B3PWZ8_RHIE6	B3PWZ8	369	3.00E-95	173 \ 352	49	Probable 4-hydroxyphenylpyruvate dioxygenase protein. EC=1.13.11.27.
202	A3TX25_9RHOB	A3TX25	364	4.00E-95	177 \ 355	49	4-hydroxyphenylpyruvate dioxygenase.
203	A6F985_9GAMM	A6F985	362	6.00E-95	180 \ 354	50	4-hydroxyphenylpyruvate dioxygenase.
204	Q3BYF0_XANC5	Q3BYF0	356	1.00E-94	178 \ 354	50	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
205	A8W7V5_9BACT	A8W7V5	354	1.00E-94	182 \ 361	50	4-hydroxyphenylpyruvate dioxygenase.
206	A3JVK5_9RHOB	A3JVK5	373	2.00E-94	174 \ 353	49	Probable 4-hydroxyphenylpyruvate dioxygenase protein.
207	Q8PQ76_XANAC	Q8PQ76	356	2.00E-94	178 \ 354	50	4-hydroxyphenylpyruvate dioxygenase.
208	Q28M85_JANSC	Q28M85	363	3.00E-94	178 \ 352	50	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
209	A3WM93_9GAMM	A3WM93	357	5.00E-94	181 \ 360	50	4-hydroxyphenylpyruvate dioxygenase.
210	B2SM17_XANOP	B2SM17	371	5.00E-94	175 \ 354	49	4-hydroxyphenylpyruvate dioxygenase.
211	Q2NYM6_XANOM	Q2NYM6	356	5.00E-94	175 \ 354	49	4-hydroxyphenylpyruvate dioxygenase.
212	A3X9B5_9RHOB	A3X9B5	391	6.00E-94	177 \ 355	49	4-hydroxyphenylpyruvate dioxygenase.
213	Q5GVE8_XANOR	Q5GVE8	403	7.00E-94	175 \ 354	49	4-hydroxyphenylpyruvate dioxygenase.
214	A9E6M0_9RHOB	A9E6M0	364	7.00E-94	172 \ 352	48	4-hydroxyphenylpyruvate dioxygenase.
215	A3T1K1_9RHOB	A3T1K1	364	8.00E-94	171 \ 353	48	4-hydroxyphenylpyruvate dioxygenase.
216	B7QYV5_9RHOB	B7QYV5	366	1.00E-93	178 \ 355	50	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
217	Q5R0G8_IDILO	Q5R0G8	357	1.00E-93	183 \ 361	50	4-hydroxyphenylpyruvate dioxygenase.
218	A4F160_9RHOB	A4F160	366	1.00E-93	177 \ 355	49	4-hydroxyphenylpyruvate dioxygenase.
219	A3SC01_9RHOB	A3SC01	364	1.00E-93	171 \ 353	48	4-hydroxyphenylpyruvate dioxygenase.
220	Q9A5B7_CAUCR	Q9A5B7	357	2.00E-93	171 \ 354	48	4-hydroxyphenylpyruvate dioxygenase.
221	B8H073_CAUCN	B8H073	357	2.00E-93	171 \ 354	48	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
222	B6BAG9_9RHOB	B6BAG9	366	2.00E-93	177 \ 355	49	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
223	Q168Z7_ROSDO	Q168Z7	364	2.00E-93	170 \ 355	47	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
224	A9FCM3_9RHOB	A9FCM3	366	3.00E-93	176 \ 354	49	4-hydroxyphenylpyruvate dioxygenase.
225	A9GAM7_9RHOB	A9GAM7	366	3.00E-93	176 \ 355	49	4-hydroxyphenylpyruvate dioxygenase.
226	Q5LT18_SILPO	Q5LT18	366	5.00E-93	177 \ 355	49	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
227	Q7X4L3_9BACT	Q7X4L3	353	6.00E-93	173 \ 353	49	4-hydroxyphenylpyruvate dioxygenase.
228	Q1GJ51_SILST	Q1GJ51	366	9.00E-93	176 \ 355	49	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
229	A9GZ84_9RHOB	A9GZ84	364	1.00E-92	169 \ 355	47	4-hydroxyphenylpyruvate dioxygenase.
230	B7RP04_9RHOB	B7RP04	364	3.00E-91	166 \ 352	47	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
231	Q5WUG4_LEGPL	Q5WUG4	348	5.00E-90	175 \ 349	50	4-hydroxyphenylpyruvate dioxygenase Legiolysin.
232	Q5X304_LEGPA	Q5X304	348	1.00E-89	174 \ 349	49	4-hydroxyphenylpyruvate dioxygenase Legiolysin.
233	B4W7U3_9CAUL	B4W7U3	373	7.00E-89	173 \ 356	48	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
234	B9JHZ8_AGRRK	B9JHZ8	333	1.00E-88	165 \ 331	49	4-hydroxyphenylpyruvate dioxygenase.
235	B0T817_CAUSK	B0T817	353	6.00E-87	176 \ 357	49	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
236	Q1NF01_9SPHN	Q1NF01	355	3.00E-84	171 \ 355	48	4-hydroxyphenylpyruvate dioxygenase.
237	Q3IET4_PSEHT	Q3IET4	348	3.00E-83	163 \ 350	46	4-hydroxyphenylpyruvate dioxygenase 4HPPD (HPD) (HPPDase). EC=1.13.11.27.
238	A0XXD9_9GAMM	A0XXD9	348	1.00E-82	161 \ 349	46	4-hydroxyphenylpyruvate dioxygenase 4HPPD (HPD) (HPPDase).

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
239	A4C668_9GAMM	A4C668	348	8.00E-82	161 \ 350	46	4-hydroxyphenylpyruvate dioxygenase 4HPPD (HPD) (HPPDase).
240	B1KQH7_SHEWM	B1KQH7	346	1.00E-80	159 \ 353	45	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
241	B0TJH2_SHEHH	B0TJH2	346	1.00E-79	155 \ 350	44	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
242	A8H3Q9_SHEPA	A8H3Q9	346	6.00E-79	155 \ 353	43	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
243	Q080Z2_SHEFN	Q080Z2	346	7.00E-79	154 \ 349	44	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
244	A2V0K0_SHEPU	A2V0K0	346	7.00E-79	154 \ 351	43	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
245	A9L5W3_SHEB9	A9L5W3	346	7.00E-79	155 \ 351	44	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
246	A6WPQ0_SHEB8	A6WPQ0	346	7.00E-79	155 \ 351	44	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
247	A4Y612_SHEPC	A4Y612	346	9.00E-79	154 \ 351	43	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
248	B8E501_SHEB2	B8E501	346	1.00E-78	155 \ 351	44	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
249	A1RKI4_SHESW	A1RKI4	346	2.00E-78	154 \ 351	43	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
250	Q12M81_SHEDO	Q12M81	346	2.00E-78	154 \ 352	43	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
251	A8FWS1_SHESH	A8FWS1	346	2.00E-78	155 \ 353	43	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
252	A3D5U6_SHEB5	A3D5U6	346	2.00E-78	154 \ 351	43	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
253	Q6MHJ8_BDEBA	Q6MHJ8	352	4.00E-78	155 \ 358	43	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
254	A3QEX3_SHELP	A3QEX3	346	4.00E-78	153 \ 350	43	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
255	B8CPM1_SHEPW	B8CPM1	346	5.00E-78	152 \ 352	43	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
256	A9DJU6_9GAMM	A9DJU6	346	1.00E-77	155 \ 353	43	4-hydroxyphenylpyruvate dioxygenase.
257	A1S5W9_SHEAM	A1S5W9	345	4.00E-77	155 \ 352	44	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
258	Q8EFK9_SHEON	Q8EFK9	346	2.00E-76	151 \ 352	42	4-hydroxyphenylpyruvate dioxygenase.
259	Q0HU54_SHESR	Q0HU54	346	8.00E-76	151 \ 352	42	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
260	Q0HHV4_SHESM	Q0HHV4	346	8.00E-76	151 \ 352	42	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
261	A0KY42_SHESA	A0KY42	346	8.00E-76	151 \ 352	42	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27. Flags: Precursor.
262	C1WC63_9GAMM	C1WC63	356	8.00E-73	155 \ 367	42	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
263	Q0B913_BURCM	Q0B913	375	1.00E-69	147 \ 352	41	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
264	Q1BNE4_BURCA	Q1BNE4	375	6.00E-69	144 \ 352	40	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
265	A0B0F3_BURCH	A0B0F3	375	6.00E-69	144 \ 352	40	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
266	Q395X2_BURS3	Q395X2	375	6.00E-69	146 \ 352	41	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
267	A2VYU7_9BURK	A2VYU7	381	7.00E-69	144 \ 352	40	4-hydroxyphenylpyruvate dioxygenase.
268	B1FCL4_9BURK	B1FCL4	375	7.00E-69	145 \ 352	41	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
269	B1YWM6_BURA4	B1YWM6	375	9.00E-69	145 \ 352	41	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
270	B4EJL2_BURCJ	B4EJL2	375	2.00E-68	144 \ 352	40	Putative dioxygenase.
271	B1K5B9_BURCC	B1K5B9	375	2.00E-68	144 \ 352	40	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
272	C1DLB4_AZOVD	C1DLB4	345	2.00E-68	148 \ 349	42	4-hydroxyphenylpyruvate dioxygenase.
273	Q47YG2_COLP3	Q47YG2	351	2.00E-68	145 \ 357	40	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
274	B1T8K7_9BURK	B1T8K7	374	4.00E-68	144 \ 352	40	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
275	A4JNM5_BURVG	A4JNM5	375	1.00E-67	144 \ 352	40	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
276	Q2T5Y1_BURTA	Q2T5Y1	381	1.00E-66	144 \ 351	41	4-hydroxyphenylpyruvate dioxygenase.
277	B9C2D0_9BURK	B9C2D0	375	1.00E-66	143 \ 350	40	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
278	B9BIC5_9BURK	B9BIC5	375	1.00E-66	143 \ 350	40	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
279	B9B0B6_9BURK	B9B0B6	375	2.00E-66	142 \ 350	40	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
280	A2WEY2_9BURK	A2WEY2	415	2.00E-66	142 \ 352	40	4-hydroxyphenylpyruvate dioxygenase.
281	A9AKD4_BURM1	A9AKD4	375	2.00E-66	142 \ 350	40	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
282	B2UIJ5_RALPJ	B2UIJ5	357	5.00E-66	143 \ 348	41	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
283	A7CKG2_BURPI	A7CKG2	357	5.00E-66	143 \ 348	41	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
284	B1FVM6_9BURK	B1FVM6	377	1.00E-65	144 \ 353	40	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
285	B5WIM1_9BURK	B5WIM1	375	1.00E-65	142 \ 353	40	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
286	Q13RR7_BURXL	Q13RR7	377	3.00E-65	142 \ 356	39	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
287	Q46R58_RALEJ	Q46R58	357	3.00E-65	157 \ 355	44	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
288	B2JNR5_BURP8	B2JNR5	375	1.00E-64	144 \ 359	40	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
289	B2T9F0_BURPP	B2T9F0	377	2.00E-64	141 \ 356	39	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
290	B3D7I0_BURM1	B3D7I0	351	5.00E-64	138 \ 342	40	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
291	A8V9F5_9BURK	A8V9F5	377	5.00E-64	140 \ 356	39	4-hydroxyphenylpyruvate dioxygenase.
292	Q8XF91_RALSO	Q8XF91	361	4.00E-61	139 \ 349	39	Probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein. EC=1.13.11.27.
293	B5RY48_RALSO	B5RY48	322	5.00E-61	132 \ 336	39	4-hydroxyphenylpyruvate dioxygenase protein. EC=1.13.11.27.
294	A4VG06_PSEU5	A4VG06	641	6.00E-48	120 \ 345	34	4-hydroxyphenylpyruvate dioxygenase.
295	B8IUC4_METNO	B8IUC4	627	7.00E-47	115 \ 329	34	Xylose isomerase domain protein TIM barrel. EC=1.13.11.27.
296	B0UBQ8_METS4	B0UBQ8	637	2.00E-45	119 \ 329	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
297	Q2I3N2_PSECL	Q2I3N2	636	4.00E-45	123 \ 341	36	4-hydroxyphenylpyruvate dioxygenase.
298	Q4K5N0_PSEF5	Q4K5N0	636	3.00E-44	119 \ 340	35	4-hydroxyphenylpyruvate dioxygenase, putative.
299	B2UIK0_RALPJ	B2UIK0	628	4.00E-44	122 \ 348	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
300	A7CKF7_BURPI	A7CKF7	645	5.00E-44	122 \ 348	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
301	A6CLP8_9BACI	A6CLP8	378	7.00E-44	129 \ 347	37	4-hydroxyphenylpyruvate dioxygenase.
302	B4B0E7_9CHRO	B4B0E7	362	8.00E-44	124 \ 342	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
303	A3L0I2_PSEAE	A3L0I2	634	2.00E-43	121 \ 345	35	Putative uncharacterized protein.
304	Q3K6G2_PSEPF	Q3K6G2	633	8.00E-43	120 \ 352	34	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
305	C1DS77_AZOVD	C1DS77	632	1.00E-42	110 \ 327	33	4-hydroxyphenylpyruvate dioxygenase.
306	Q02UJ3_PSEAB	Q02UJ3	634	1.00E-42	122 \ 345	35	Putative 4-hydroxyphenylpyruvate dioxygenase.
307	A1ZF21_9SPHI	A1ZF21	365	2.00E-42	122 \ 355	34	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
308	Q9I6P6_PSEAE	Q9I6P6	634	2.00E-42	122 \ 345	35	Putative uncharacterized protein.
309	B7V2F3_PSEA8	B7V2F3	634	2.00E-42	122 \ 345	35	Putative 4-hydroxyphenylpyruvate dioxygenase.
310	A3LH51_PSEAE	A3LH51	634	3.00E-42	122 \ 345	35	Putative uncharacterized protein.
311	A7GKD6_BACCN	A7GKD6	372	1.00E-41	128 \ 347	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
312	A8TWA7_9PROT	A8TWA7	630	3.00E-41	117 \ 336	34	Putative glyoxalase/dioxygenase.
313	B1J7S2_PSEPW	B1J7S2	635	6.00E-41	108 \ 328	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
314	C3BEV2_9BACI	C3BEV2	372	7.00E-41	127 \ 347	36	4-hydroxyphenylpyruvate dioxygenase.
315	C3AYD8_BACMY	C3AYD8	372	7.00E-41	127 \ 347	36	4-hydroxyphenylpyruvate dioxygenase.
316	A9DQF2_9FLAO	A9DQF2	387	8.00E-41	113 \ 297	38	4-hydroxyphenylpyruvate dioxygenase.
317	B9LL20_CHLSY	B9LL20	365	1.00E-40	125 \ 367	34	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
318	A9WGC3_CHLAA	A9WGC3	365	1.00E-40	125 \ 367	34	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
319	Q1IBW8_PSEE4	Q1IBW8	634	1.00E-40	114 \ 343	33	Putative 4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
320	C2TAQ7_BACCE	C2TAQ7	385	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase.
321	Q81VG6_BACAN	Q81VG6	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase.
322	Q73EU8_BACC1	Q73EU8	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
323	Q6HPF2_BACHK	Q6HPF2	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
324	Q63GY1_BAC CZ	Q63GY1	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
325	B9J0M5_BACCQ	B9J0M5	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase.
326	B7JLD7_BACC0	B7JLD7	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
327	B7HRX9_BACC7	B7HRX9	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
328	C3PAS7_BACAN	C3PAS7	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
329	C3LK69_BACAN	C3LK69	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
330	C1EU86_BACC3	C1EU86	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
331	B9Z2U1_9NEIS	B9Z2U1	284	2.00E-40	91 \ 210	43	Glyoxalase/bleomycin resistance protein/dioxygenase.
332	B5V9G2_BACCE	B5V9G2	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
333	B3ZSP6_BACCE	B3ZSP6	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
334	B3ZDF9_BACCE	B3ZDF9	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
335	B3YZ40_BACCE	B3YZ40	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
336	B3J763_BACAN	B3J763	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
337	B1UTQ7_BACAN	B1UTQ7	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
338	B1GKB9_BACAN	B1GKB9	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
339	B1F273_BACAN	B1F273	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
340	B0QI74_BACAN	B0QI74	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
341	B0Q5G2_BACAN	B0Q5G2	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
342	B0ATU9_BACAN	B0ATU9	372	2.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
343	A6UY38_PSEA7	A6UY38	634	2.00E-40	119 \ 345	34	Putative uncharacterized protein.
344	C3HCS3_BACTU	C3HCS3	385	3.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase.
345	C3GDA4_BACTU	C3GDA4	385	3.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase.
346	C3FXF9_BACTU	C3FXF9	385	3.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase.
347	C2VN24_BACCE	C2VN24	385	3.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase.
348	C2RY10_BACCE	C2RY10	385	3.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase.
349	C2NC17_BACCE	C2NC17	385	3.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase.
350	C2MF68_BACCE	C2MF68	385	3.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase.
351	C3EW25_BACTU	C3EW25	385	3.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase.
352	A1ZPY8_9SPHI	A1ZPY8	375	3.00E-40	116 \ 328	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
353	B2JH32_BURP8	B2JH32	628	3.00E-40	106 \ 334	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
354	A0R8T9_BACAH	A0R8T9	389	3.00E-40	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
355	A2TRR3_9FLAO	A2TRR3	386	3.00E-40	127 \ 375	33	4-hydroxyphenylpyruvate dioxygenase.
356	C3K2G9_PSEFL	C3K2G9	633	3.00E-40	116 \ 340	34	Putative uncharacterized protein.
357	A2TY03_9FLAO	A2TY03	386	4.00E-40	120 \ 331	36	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
358	Q2K1Q9_RHIEC	Q2K1Q9	629	5.00E-40	113 \ 329	34	Putative 4-hydroxyphenylpyruvate dioxygenase protein. EC=1.13.11.27.
359	Q2B856_9BACI	Q2B856	371	6.00E-40	122 \ 333	36	4-hydroxyphenylpyruvate dioxygenase.
360	C0YT41_9FLAO	C0YT41	376	7.00E-40	122 \ 375	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
361	A8UIZ5_9FLAO	A8UIZ5	386	7.00E-40	117 \ 330	35	4-hydroxyphenylpyruvate dioxygenase.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
362	A0NW11_9RHOB	A0NW11	630	7.00E-40	107 \ 332	32	Putative 4-hydroxyphenylpyruvate dioxygenase protein.
363	C3BWQ0_BACTU	C3BWQ0	389	8.00E-40	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
364	C2QMD4_BACCE	C2QMD4	389	8.00E-40	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
365	A2WGL3_9BURK	A2WGL3	658	1.00E-39	111 \ 328	33	4-hydroxyphenylpyruvate dioxygenase.
366	B7YZ92_VARPD	B7YZ92	630	1.00E-39	109 \ 338	32	Xylose isomerase domain protein TIM barrel.
367	Q81IU6_BACCR	Q81IU6	372	1.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
368	B7HJR5_BACC4	B7HJR5	372	1.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
369	C3EF46_BACTK	C3EF46	385	1.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
370	C2Y509_BACCE	C2Y509	385	1.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
371	C2X684_BACCE	C2X684	385	1.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
372	C2U8C6_BACCE	C2U8C6	385	1.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
373	C2SVB8_BACCE	C2SVB8	385	1.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
374	C2RHH4_BACCE	C2RHH4	385	1.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
375	C2R2I1_BACCE	C2R2I1	385	1.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
376	C2NT95_BACCE	C2NT95	385	1.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
377	C2MV90_BACCE	C2MV90	385	1.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
378	B5UVV5_BACCE	B5UVV5	372	1.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
379	C3GVI4_BACTU	C3GVI4	385	1.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
380	C2W354_BACCE	C2W354	372	1.00E-39	128 \ 344	37	4-hydroxyphenylpyruvate dioxygenase.
381	Q4MPU8_BACCE	Q4MPU8	372	2.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
382	C3AGK2_BACMY	C3AGK2	303	2.00E-39	122 \ 314	38	4-hydroxyphenylpyruvate dioxygenase.
383	B1Z0T7_BURA4	B1Z0T7	630	2.00E-39	111 \ 331	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
384	C3HUP8_BACTU	C3HUP8	385	2.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
385	B7IU20_BACC2	B7IU20	372	2.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
386	C3IDU3_BACTU	C3IDU3	385	2.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
387	C3FEJ8_BACTB	C3FEJ8	385	2.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
388	C3DE48_BACTS	C3DE48	385	2.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
389	C3CW18_BACTU	C3CW18	385	2.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
390	C3CD20_BACTU	C3CD20	385	2.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
391	Q3EW31_BACTI	Q3EW31	389	2.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
392	Q2S2T7_SALRD	Q2S2T7	384	3.00E-39	119 \ 343	34	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
393	C2YL30_BACCE	C2YL30	385	3.00E-39	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase.
394	C2P9E0_BACCE	C2P9E0	385	3.00E-39	126 \ 348	36	4-hydroxyphenylpyruvate dioxygenase.
395	A3U5U2_9FLAO	A3U5U2	390	3.00E-39	116 \ 343	33	4-hydroxyphenylpyruvate dioxygenase.
396	C2Q6F4_BACCE	C2Q6F4	385	4.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
397	C2WY41_BACCE	C2WY41	385	4.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
398	C2UPX4_BACCE	C2UPX4	385	4.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
399	A4BXV0_9FLAO	A4BXV0	387	4.00E-39	116 \ 330	35	4-hydroxyphenylpyruvate dioxygenase.
400	C2V696_BACCE	C2V696	385	4.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
401	C2TRR7_BACCE	C2TRR7	385	4.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
402	C0ZI47_BREBN	C0ZI47	363	4.00E-39	118 \ 341	34	Probable 4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
403	B7RKL2_9RHOB	B7RKL2	628	4.00E-39	107 \ 330	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
404	A9AM73_BURM1	A9AM73	630	5.00E-39	107 \ 326	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
405	B9B2B1_9BURK	B9B2B1	630	5.00E-39	107 \ 326	32	4-hydroxyphenylpyruvate dioxygenase.
406	C3DXX9_BACTU	C3DXX9	385	5.00E-39	125 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
407	A5FM06_FLAJ1	A5FM06	386	5.00E-39	119 \ 336	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
408	Q46R51_RALEJ	Q46R51	632	6.00E-39	110 \ 327	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
409	Q0B6K7_BURCM	Q0B6K7	630	6.00E-39	110 \ 328	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
410	B0KJM6_PSEPG	B0KJM6	635	6.00E-39	109 \ 338	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
411	B0JAX8_RHILT	B0JAX8	631	6.00E-39	115 \ 340	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
412	A3XQC9_9FLAO	A3XQC9	386	6.00E-39	122 \ 348	35	4-hydroxyphenylpyruvate dioxygenase.
413	C1XKV3_MEIRU	C1XKV3	620	6.00E-39	110 \ 342	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
414	Q39AQ2_BURS3	Q39AQ2	630	9.00E-39	107 \ 329	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
415	A3VZD9_9RHOB	A3VZD9	628	9.00E-39	114 \ 330	34	Putative uncharacterized protein.
416	B9CFA4_9BURK	B9CFA4	630	9.00E-39	107 \ 326	32	4-hydroxyphenylpyruvate dioxygenase.
417	B9BU91_9BURK	B9BU91	630	9.00E-39	107 \ 326	32	AP endonuclease, family 2.
418	A3J2X0_9FLAO	A3J2X0	387	9.00E-39	123 \ 374	32	4-hydroxyphenylpyruvate dioxygenase.
419	Q883L0_PSESM	Q883L0	635	1.00E-38	105 \ 329	31	4-hydroxyphenylpyruvate dioxygenase, putative.
420	B8G5A1_CHLAD	B8G5A1	365	1.00E-38	122 \ 367	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
421	Q88JU3_PSEPK	Q88JU3	635	1.00E-38	110 \ 339	32	4-hydroxyphenylpyruvate dioxygenase, putative.
422	A5W579_PSEP1	A5W579	635	1.00E-38	110 \ 339	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
423	B9NUL1_9RHOB	B9NUL1	629	1.00E-38	109 \ 330	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
424	C3KMD4_RHISN	C3KMD4	629	1.00E-38	114 \ 331	34	Putative 4-hydroxyphenylpyruvate dioxygenase protein.
425	Q4ZUJ9_PSEU2	Q4ZUJ9	635	2.00E-38	105 \ 329	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
426	A9B1W0_HERA2	A9B1W0	373	2.00E-38	124 \ 371	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
427	Q01YY4_SOLUE	Q01YY4	375	2.00E-38	119 \ 356	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
428	Q09PG9_9BACT	Q09PG9	375	2.00E-38	122 \ 375	32	4-hydroxyphenylpyruvate dioxygenase.
429	B4EJ56_BURCJ	B4EJ56	630	2.00E-38	110 \ 328	33	Putative amino acid dioxygenase. Flags: Precursor.
430	Q26D67_9BACT	Q26D67	387	2.00E-38	117 \ 327	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
431	Q1MFD8_RHIL3	Q1MFD8	630	3.00E-38	113 \ 334	33	Putative glyoxalase/dioxygenase.
432	A9VQE1_BACWK	A9VQE1	372	3.00E-38	123 \ 347	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
433	B5HNX4_9ACTO	B5HNX4	381	3.00E-38	110 \ 297	37	4-hydroxyphenylpyruvate dioxygenase.
434	A4JJT7_BURVG	A4JJT7	630	3.00E-38	109 \ 328	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
435	C2XNG4_BACCE	C2XNG4	385	4.00E-38	123 \ 347	35	4-hydroxyphenylpyruvate dioxygenase.
436	C2SEH3_BACCE	C2SEH3	385	4.00E-38	123 \ 347	35	4-hydroxyphenylpyruvate dioxygenase.
437	Q48JV3_PSE14	Q48JV3	635	4.00E-38	104 \ 329	31	4-hydroxyphenylpyruvate dioxygenase, putative.
438	Q1VXT8_9FLAO	Q1VXT8	379	4.00E-38	115 \ 332	34	4-hydroxyphenylpyruvate dioxygenase.
439	A3VA67_9RHOB	A3VA67	627	4.00E-38	110 \ 348	31	Putative uncharacterized protein.
440	Q1BQZ7_BURCA	Q1BQZ7	630	4.00E-38	110 \ 328	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
441	A0B312_BURCH	A0B312	630	4.00E-38	110 \ 328	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
442	C2ZIV7_BACCE	C2ZIV7	385	4.00E-38	123 \ 347	35	4-hydroxyphenylpyruvate dioxygenase.
443	C2Z277_BACCE	C2Z277	385	4.00E-38	123 \ 347	35	4-hydroxyphenylpyruvate dioxygenase.
444	B1K5Q9_BURCC	B1K5Q9	630	5.00E-38	110 \ 328	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
445	A3HSH6_9SPHI	A3HSH6	364	5.00E-38	120 \ 360	33	4-hydroxyphenylpyruvate dioxygenase.
446	C2PQ90_BACCE	C2PQ90	385	5.00E-38	123 \ 347	35	4-hydroxyphenylpyruvate dioxygenase.
447	A0M669_GRAFK	A0M669	380	6.00E-38	116 \ 341	34	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
448	C3A0E5_BACMY	C3A0E5	385	6.00E-38	123 \ 347	35	4-hydroxyphenylpyruvate dioxygenase.
449	A6E759_9SPHI	A6E759	403	6.00E-38	121 \ 360	33	4-hydroxyphenylpyruvate dioxygenase.
450	Q1R0V3_CHRSD	Q1R0V3	615	6.00E-38	104 \ 323	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
451	C1A9I8_9BACT	C1A9I8	374	7.00E-38	118 \ 330	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
452	Q1M6W3_RHIL3	Q1M6W3	631	7.00E-38	114 \ 340	33	Putative dioxygenase.
453	B1SXM9_9BURK	B1SXM9	630	1.00E-37	108 \ 328	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
454	A8M7R7_SALAI	A8M7R7	401	2.00E-37	124 \ 386	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
455	A6W281_MARMS	A6W281	617	2.00E-37	108 \ 326	33	Xylose isomerase domain protein TIM barrel.
456	C1Z1L3_PEDHE	C1Z1L3	376	2.00E-37	122 \ 359	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
457	A3K1H7_9RHOB	A3K1H7	629	2.00E-37	110 \ 336	32	Putative uncharacterized protein.
458	A8EIQ5_BURPS	A8EIQ5	684	2.00E-37	108 \ 329	32	AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
459	A5EPE6_BRASB	A5EPE6	623	2.00E-37	104 \ 324	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
460	Q63NG0_BURPS	Q63NG0	684	2.00E-37	108 \ 329	32	Putative amino acid dioxygenase.
461	A3P2G3_BURP0	A3P2G3	684	2.00E-37	108 \ 329	32	AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
462	C0YEK9_BURPS	C0YEK9	684	2.00E-37	108 \ 329	32	AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
463	B1HBZ9_BURPS	B1HBZ9	684	2.00E-37	108 \ 329	32	AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
464	B2H5H1_BURPS	B2H5H1	684	2.00E-37	108 \ 329	32	AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
465	A3NGW1_BURP6	A3NGW1	687	2.00E-37	108 \ 329	32	4-hydroxyphenylpyruvate dioxygenase.
466	Q62CM9_BURMA	Q62CM9	684	2.00E-37	108 \ 329	32	Putative 4-hydroxyphenylpyruvate dioxygenase.
467	A3MCV3_BURM7	A3MCV3	684	2.00E-37	108 \ 329	32	AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
468	A2S228_BURM9	A2S228	684	2.00E-37	108 \ 329	32	Putative 4-hydroxyphenylpyruvate dioxygenase.
469	A1UZE1_BURMS	A1UZE1	684	2.00E-37	108 \ 329	32	Putative 4-hydroxyphenylpyruvate dioxygenase.
470	B7CTM4_BURPS	B7CTM4	683	2.00E-37	108 \ 329	32	AP endonuclease, family 2/putative 4-hydroxyphenylpyruvate dioxygenase.
471	A5XYF9_BURMA	A5XYF9	684	2.00E-37	108 \ 329	32	AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
472	A5XJI4_BURMA	A5XJI4	684	2.00E-37	108 \ 329	32	AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
473	A5TMH3_BURMA	A5TMH3	684	2.00E-37	108 \ 329	32	AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
474	A9LC58_BURMA	A9LC58	684	2.00E-37	108 \ 329	32	AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
475	A4LVC2_BURPS	A4LVC2	684	3.00E-37	108 \ 329	32	AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
476	B9Z034_9NEIS	B9Z034	645	3.00E-37	106 \ 309	34	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
477	Q3JHA2_BURP1	Q3JHA2	684	4.00E-37	108 \ 329	32	Putative amino acid dioxygenase.
478	A8KPI3_BURPS	A8KPI3	684	4.00E-37	108 \ 329	32	AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
479	A6END7_9BACT	A6END7	387	5.00E-37	114 \ 318	35	4-hydroxyphenylpyruvate dioxygenase.
480	A4CIN8_9FLAO	A4CIN8	380	5.00E-37	114 \ 332	34	4-hydroxyphenylpyruvate dioxygenase.
481	A4YZD8_BRASO	A4YZD8	623	5.00E-37	104 \ 327	31	Putative 4-hydroxyphenylpyruvate dioxygenase containing a TIM-barrel fold N-ter. EC=1.13.11.27.
482	A6GW69_FLAPJ	A6GW69	386	8.00E-37	118 \ 345	34	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
483	B5GJ98_9ACTO	B5GJ98	401	9.00E-37	112 \ 329	34	4-hydroxyphenylpyruvate dioxygenase.
484	Q0FG27_9RHOB	Q0FG27	580	9.00E-37	106 \ 331	32	Putative 4-hydroxyphenylpyruvate dioxygenase protein.
485	B4VCB6_9ACTO	B4VCB6	380	1.00E-36	105 \ 294	35	4-hydroxyphenylpyruvate dioxygenase.
486	Q6KZ98_PICTO	Q6KZ98	368	1.00E-36	116 \ 359	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
487	Q1IQ45_ACIBL	Q1IQ45	361	2.00E-36	116 \ 372	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
488	A8HX25_AZOC5	A8HX25	639	2.00E-36	114 \ 348	32	Putative 4-hydroxyphenylpyruvate dioxygenase protein.
489	B1MJ31_MYCA9	B1MJ31	401	2.00E-36	118 \ 360	32	Putative 4-hydroxyphenylpyruvate dioxygenase.
490	B1FGH7_9BURK	B1FGH7	312	3.00E-36	102 \ 304	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
491	A4XCM1_SALTO	A4XCM1	401	4.00E-36	120 \ 386	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
492	C1U810_9SPHI	C1U810	374	5.00E-36	106 \ 297	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
493	A4APX3_9FLAO	A4APX3	380	5.00E-36	112 \ 331	33	4-hydroxyphenylpyruvate dioxygenase.
494	A3V7V8_9RHOB	A3V7V8	628	6.00E-36	113 \ 332	34	Putative uncharacterized protein.
495	C1WMN3_9ACTO	C1WMN3	400	7.00E-36	107 \ 298	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
496	C1SA33_9SPHI	C1SA33	378	7.00E-36	117 \ 361	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
497	A6X7C4_OCHA4	A6X7C4	633	7.00E-36	111 \ 328	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
498	Q0SBW3_RHOSR	Q0SBW3	404	8.00E-36	124 \ 383	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
499	B0TJH7_SHEHH	B0TJH7	173	1.00E-35	80 \ 174	45	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
500	C1QZ16_9ACTO	C1QZ16	379	1.00E-35	118 \ 343	34	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
501	B5WQ29_9BURK	B5WQ29	630	2.00E-35	103 \ 338	30	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
502	C2A5X5_THECU	C2A5X5	355	2.00E-35	108 \ 322	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
503	Q2T3K2_BURTA	Q2T3K2	687	3.00E-35	106 \ 329	32	4-hydroxyphenylpyruvate dioxygenase, putative.
504	Q89VJ2_BRAJA	Q89VJ2	623	3.00E-35	104 \ 327	31	BlI1053 protein.
505	A9AUK4_HERA2	A9AUK4	366	3.00E-35	110 \ 328	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
506	C3KN89_RHISN	C3KN89	630	4.00E-35	108 \ 313	34	Putative 4-hydroxyphenylpyruvate dioxygenase protein.
507	C1F681_ACIC5	C1F681	374	4.00E-35	107 \ 355	30	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
508	B1VVT0_STRGG	B1VVT0	381	5.00E-35	105 \ 297	35	Putative 4-hydroxyphenylpyruvate dioxygenase.
509	A4F864_SACEN	A4F864	401	9.00E-35	113 \ 360	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
510	B9JJA0_AGRRK	B9JJA0	629	4.00E-34	114 \ 332	34	4-hydroxyphenylpyruvate dioxygenase.
511	C1AZ31_RHOOP	C1AZ31	402	5.00E-34	117 \ 337	34	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
512	B2TD26_BURPP	B2TD26	627	9.00E-34	107 \ 341	31	Xylose isomerase domain protein TIM barrel.
513	B1Y5P9_LEPCP	B1Y5P9	295	2.00E-33	91 \ 259	35	4-hydroxyphenylpyruvate dioxygenase.
514	C1D2E3_9DEIO	C1D2E3	618	2.00E-33	112 \ 348	32	Putative bifunctional protein : Xylose isomerase-like TIM barrel. 4-hydroxyphenylpyruvate dioxygenase.
515	C1B587_RHOOP	C1B587	401	2.00E-33	112 \ 358	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
516	C0ZQK1_RHOE4	C0ZQK1	401	2.00E-33	116 \ 375	30	Probable 4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
517	B1G9W8_9BURK	B1G9W8	627	2.00E-33	104 \ 331	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
518	C2FZV2_9SPHI	C2FZV2	375	2.00E-33	116 \ 332	34	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
519	Q8XQ86_RALSO	Q8XQ86	626	2.00E-33	114 \ 342	33	Probable 4-hydroxyphenylpyruvate dioxygenase-related protein.
520	Q0SF39_RHOSR	Q0SF39	402	2.00E-33	117 \ 337	34	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
521	C1ATW8_RHOOP	C1ATW8	401	3.00E-33	112 \ 358	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
522	C3JF61_RHOER	C3JF61	401	3.00E-33	115 \ 375	30	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
523	A3IMK6_9CHRO	A3IMK6	379	4.00E-33	112 \ 347	32	4-hydroxyphenylpyruvate dioxygenase.
524	C0U2M4_9ACTO	C0U2M4	401	4.00E-33	110 \ 311	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
525	B6A3Y9_RHILW	B6A3Y9	631	5.00E-33	109 \ 332	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
526	Q11K93_MESSB	Q11K93	630	5.00E-33	105 \ 332	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
527	Q0S6I1_RHOSR	Q0S6I1	401	7.00E-33	113 \ 364	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
528	A6TAD7_KLEP7	A6TAD7	617	7.00E-33	111 \ 334	33	Putative 4-hydroxyphenylpyruvate dioxygenase.
529	Q0SC92_RHOSR	Q0SC92	401	8.00E-33	113 \ 364	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
530	A1SG74_NOCSJ	A1SG74	397	8.00E-33	106 \ 333	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
531	B5GSL5_STRCL	B5GSL5	381	8.00E-33	110 \ 297	37	4-hydroxyphenylpyruvate dioxygenase.
532	B1WVS4_CYAA5	B1WVS4	386	9.00E-33	106 \ 317	33	4-hydroxyphenylpyruvate dioxygenase.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
533	C1Y383_ACTO	C1Y383	401	1.00E-32	122 \ 377	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
534	B7KCD4_CYAP7	B7KCD4	363	1.00E-32	107 \ 317	33	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
535	B5W8X3_SPIMA	B5W8X3	351	1.00E-32	110 \ 335	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
536	B5SBK5_RALSO	B5SBK5	626	2.00E-32	111 \ 335	33	4-hydroxyphenylpyruvate dioxygenase-related protein.
537	A3RZE9_RALSO	A3RZE9	626	2.00E-32	111 \ 335	33	3-dehydroshikimate dehydratase / 4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27. EC=4.2.1.-.
538	B0BZ81_ACAM1	B0BZ81	355	2.00E-32	110 \ 360	30	4-hydroxyphenylpyruvate dioxygenase.
539	Q13LG7_BURXL	Q13LG7	627	2.00E-32	105 \ 338	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
540	B5S3E5_RALSO	B5S3E5	626	2.00E-32	110 \ 330	33	4-hydroxyphenylpyruvate dioxygenase-related protein.
541	A0E6B4_PARTE	A0E6B4	390	2.00E-32	107 \ 341	31	Chromosome undetermined scaffold_8, whole genome shotgun sequence.
542	Q6BG80_PARTE	Q6BG80	390	2.00E-32	107 \ 341	31	4-hydroxyphenylpyruvate dioxygenase, putative. Chromosome undetermined scaffold_1, whole genome shotgun sequence.
543	Q10X37_TRIEI	Q10X37	353	2.00E-32	110 \ 347	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
544	C0T7Y5_9PSEU	C0T7Y5	386	2.00E-32	103 \ 297	34	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
545	B5XQI1_KLEP3	B5XQI1	617	4.00E-32	113 \ 336	33	AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase.
546	A1CEP1_ASPCL	A1CEP1	401	5.00E-32	122 \ 367	33	4-hydroxyphenylpyruvate dioxygenase, putative.
547	B9K124_AGRVS	B9K124	615	5.00E-32	106 \ 338	31	4-hydroxyphenylpyruvate dioxygenase.
548	B8LV58_TALSN	B8LV58	415	6.00E-32	123 \ 380	32	4-hydroxyphenylpyruvate dioxygenase, putative. EC=1.13.11.27.
549	A3TG27_9MICO	A3TG27	420	7.00E-32	114 \ 369	30	Putative 4-hydroxyphenylpyruvate dioxygenase.
550	Q2G7Z7_NOVAD	Q2G7Z7	621	7.00E-32	100 \ 332	30	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
551	Q3M423_ANAVT	Q3M423	344	8.00E-32	106 \ 336	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
552	Q1YHA4_MOBAS	Q1YHA4	628	9.00E-32	109 \ 356	30	4-hydroxyphenylpyruvate dioxygenase.
553	Q2ULZ5_ASPOR	Q2ULZ5	398	2.00E-31	119 \ 366	32	RIB40 genomic DNA, SC003.
554	C1X6M5_9MICO	C1X6M5	412	2.00E-31	105 \ 332	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
555	B8HQB5_CYAP4	B8HQB5	358	2.00E-31	119 \ 342	34	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
556	B8N2C6_ASPFN	B8N2C6	398	3.00E-31	119 \ 366	32	4-hydroxyphenylpyruvate dioxygenase, putative.
557	B0XV11_ASPFC	B0XV11	403	3.00E-31	119 \ 364	32	4-hydroxyphenylpyruvate dioxygenase, putative.
558	Q5YPF8_NOCFA	Q5YPF8	392	4.00E-31	111 \ 330	33	Putative 4-hydroxyphenylpyruvate dioxygenase.
559	A6AKU9_VIBHA	A6AKU9	607	4.00E-31	99 \ 338	29	4-hydroxyphenylpyruvate dioxygenase.
560	Q12CF6_POLSJ	Q12CF6	301	6.00E-31	93 \ 261	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
561	B6QEH2_PENMQ	B6QEH2	407	6.00E-31	113 \ 306	36	4-hydroxyphenylpyruvate dioxygenase, putative.
562	A4EVQ2_9RHOB	A4EVQ2	627	1.00E-30	102 \ 351	29	Putative 4-hydroxyphenylpyruvate dioxygenase protein.
563	A6R9T1_AJECN	A6R9T1	402	3.00E-30	118 \ 372	31	4-hydroxyphenylpyruvate dioxygenase.
564	A2QVP8_ASPNC	A2QVP8	403	4.00E-30	113 \ 366	30	Catalytic activity: 4-hydroxyphenylpyruvate + O ₂ = homogentisate + CO(2).
565	B1XX47_LEPCP	B1XX47	635	4.00E-30	98 \ 331	29	Xylose isomerase domain protein TIM barrel.
566	Q06Z04_9ACTO	Q06Z04	356	4.00E-30	105 \ 349	30	4-hydroxyphenylpyruvate dioxygenase.
567	Q0V354_PHANO	Q0V354	406	5.00E-30	114 \ 363	31	Putative uncharacterized protein.
568	Q7WZ89_9ACTO	Q7WZ89	356	6.00E-30	108 \ 339	31	Putative hydroxymandelate synthase.
569	A1DFJ8_NEOFI	A1DFJ8	403	6.00E-30	117 \ 364	32	4-hydroxyphenylpyruvate dioxygenase, putative.
570	Q0CK63_ASPTN	Q0CK63	403	9.00E-30	113 \ 367	30	4-hydroxyphenylpyruvate dioxygenase.
571	A7EQM8_SCLS1	A7EQM8	422	1.00E-29	103 \ 310	33	4-hydroxyphenylpyruvate dioxygenase.
572	C0NJZ8_AJECG	C0NJZ8	428	1.00E-29	108 \ 333	32	4-hydroxyphenylpyruvate dioxygenase.
573	B6GYX3_PENCW	B6GYX3	403	1.00E-29	112 \ 367	30	Pc12g09060 protein.
574	A6QWC6_AJECN	A6QWC6	428	2.00E-29	109 \ 332	32	4-hydroxyphenylpyruvate dioxygenase.
575	C0NI55_AJECG	C0NI55	402	2.00E-29	117 \ 373	31	T-cell reactive protein.
576	B6Q562_PENMQ	B6Q562	415	2.00E-29	103 \ 312	33	4-hydroxyphenylpyruvate dioxygenase, putative.
577	A2VD78_XENLA	A2VD78	383	2.00E-29	108 \ 338	31	LOC100037181 protein.
578	A8L2Y6_FRASN	A8L2Y6	401	3.00E-29	108 \ 301	35	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
579	Q7CV67_AGRT5	Q7CV67	633	4.00E-29	110 \ 334	32	Putative uncharacterized protein.
580	Q8YYS5_ANASP	Q8YYS5	344	5.00E-29	96 \ 296	32	4-hydroxyphenylpyruvate dioxygenase.
581	B4VLV0_9CYAN	B4VLV0	431	5.00E-29	76 \ 202	37	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
582	A6RRU5_BOTFB	A6RRU5	422	1.00E-28	99 \ 306	32	Putative uncharacterized protein.
583	A6UH79_SINMW	A6UH79	629	1.00E-28	103 \ 336	30	Xylose isomerase domain protein TIM barrel. Flags: Precursor.
584	C1HBM5_PARBR	C1HBM5	403	2.00E-28	112 \ 368	30	4-hydroxyphenylpyruvate dioxygenase.
585	C1GMI2_PARBR	C1GMI2	404	2.00E-28	112 \ 367	30	4-hydroxyphenylpyruvate dioxygenase.
586	B0Y6P8_ASPFC	B0Y6P8	406	2.00E-28	103 \ 310	33	4-hydroxyphenylpyruvate dioxygenase, putative.
587	A9C0K0_DELAS	A9C0K0	294	4.00E-28	70 \ 180	38	4-hydroxyphenylpyruvate dioxygenase.
588	Q1WCM4_9PSED	Q1WCM4	294	4.00E-28	70 \ 180	38	Probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein.
589	Q16FX9_AEDAE	Q16FX9	381	5.00E-28	109 \ 353	30	4-hydroxyphenylpyruvate dioxygenase.
590	A8YLT7_MICAE	A8YLT7	361	5.00E-28	98 \ 320	30	Similar to tr Q4C4V8 Q4C4V8_CROWT 4-hydroxyphenylpyruvate dioxygenase.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
591	Q8KLK2_STRTO	Q8KLK2	369	5.00E-28	101 \ 333	30	HmaS.
592	Q123B0_POLSJ	Q123B0	638	5.00E-28	97 \ 349	27	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27. Flags: Precursor.
593	A0ZMC8_NODSP	A0ZMC8	343	5.00E-28	101 \ 337	29	4-hydroxyphenylpyruvate dioxygenase.
594	Q92TL8_RHIME	Q92TL8	629	6.00E-28	102 \ 337	30	Putative 4-hydroxyphenylpyruvate dioxygenase protein. EC=1.13.11.27.
595	C0SII0_PARBP	C0SII0	385	6.00E-28	113 \ 368	30	4-hydroxyphenylpyruvate dioxygenase.
596	Q16SY0_AEDAE	Q16SY0	378	6.00E-28	109 \ 351	31	4-hydroxyphenylpyruvate dioxygenase. Flags: Fragment.
597	B0JW83_MICAN	B0JW83	361	7.00E-28	96 \ 319	30	4-hydroxyphenylpyruvate dioxygenase.
598	B3SAN2_TRIAD	B3SAN2	403	7.00E-28	102 \ 306	33	Putative uncharacterized protein.
599	A1CWQ6_NEOFI	A1CWQ6	406	7.00E-28	104 \ 310	33	4-hydroxyphenylpyruvate dioxygenase, putative.
600	A8E618_XENLA	A8E618	383	1.00E-27	112 \ 355	31	LOC100126650 protein.
601	Q4C4V8_CROWT	Q4C4V8	386	1.00E-27	100 \ 308	32	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
602	B2B0A4_PODAN	B2B0A4	418	2.00E-27	99 \ 306	32	Predicted CDS Pa_3_8470.
603	B6HQB0_PENCW	B6HQB0	407	2.00E-27	103 \ 310	33	Pc22g07130 protein.
604	A9UYG6_MONBE	A9UYG6	385	2.00E-27	110 \ 356	30	Predicted protein.
605	B7K095_CYAP8	B7K095	363	4.00E-27	92 \ 342	26	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
606	B4C120_9CHRO	B4C120	388	4.00E-27	92 \ 342	26	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
607	C1G3X0_PARBR	C1G3X0	427	5.00E-27	103 \ 323	31	4-hydroxyphenylpyruvate dioxygenase.
608	C1GVS0_PARBR	C1GVS0	427	6.00E-27	103 \ 324	31	4-hydroxyphenylpyruvate dioxygenase.
609	A1VMU1_POLNA	A1VMU1	300	6.00E-27	91 \ 265	34	4-hydroxyphenylpyruvate dioxygenase.
610	A1VMJ6_POLNA	A1VMJ6	632	9.00E-27	92 \ 330	27	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27. Flags: Precursor.
611	A4X7T6_SALTO	A4X7T6	389	1.00E-26	96 \ 316	30	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
612	Q2GVU5_CHAGB	Q2GVU5	413	1.00E-26	98 \ 310	31	Putative uncharacterized protein.
613	B7T1A2_9BACT	B7T1A2	357	1.00E-26	99 \ 324	30	Veg30.
614	B2J7N7_NOSP7	B2J7N7	361	2.00E-26	104 \ 345	30	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
615	Q0IY1_XENTR	Q0IY1	393	2.00E-26	106 \ 354	29	4-hydroxyphenylpyruvate dioxygenase.
616	Q6ZZG5_ACTTI	Q6ZZG5	353	3.00E-26	89 \ 304	29	HmaS protein.
617	Q70AX1_ACTTI	Q70AX1	351	3.00E-26	89 \ 304	29	HmaS protein.
618	B2W0P7_PYRTR	B2W0P7	405	4.00E-26	114 \ 365	31	4-hydroxyphenylpyruvate dioxygenase.
619	Q6PA53_XENLA	Q6PA53	313	7.00E-26	100 \ 305	32	MGC68535 protein.
620	B4H7M3_DROPE	B4H7M3	350	1.00E-25	98 \ 306	32	GL12777.
621	Q29DD3_DROPS	Q29DD3	381	1.00E-25	98 \ 306	32	GA11203.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
622	A2QHW5_ASPNC	A2QHW5	511	1.00E-25	101 \ 303	33	Contig An04c0070, complete genome.. EC=1.13.11.27. Flags: Fragment.
623	C3KIF6_9PERC	C3KIF6	395	2.00E-25	110 \ 352	31	4-hydroxyphenylpyruvate dioxygenase.
624	Q6BMX4_DEBHA	Q6BMX4	473	2.00E-25	102 \ 356	28	DEHA2F01892p.
625	A3LW07_PICST	A3LW07	530	3.00E-25	106 \ 323	32	4-hydroxyphenylpyruvate dioxygenase 4HPPD (HPD) (HPPDase). EC=1.13.11.27. Flags: Fragment.
626	B3M9A0_DROAN	B3M9A0	402	3.00E-25	98 \ 306	32	GF24132.
627	Q9Z4X7_STRCO	Q9Z4X7	371	3.00E-25	95 \ 344	27	Putative 4-hydroxyphenylpyruvic acid dioxygenase.
628	B9YRC2_ANAAZ	B9YRC2	381	3.00E-25	95 \ 338	28	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
629	Q7NC88_GLOVI	Q7NC88	344	4.00E-25	74 \ 205	36	4-hydroxyphenylpyruvate dioxygenase.
630	Q2JA71_FRASC	Q2JA71	355	4.00E-25	96 \ 320	30	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
631	Q5XHD8_XENLA	Q5XHD8	393	4.00E-25	94 \ 308	30	LOC495029 protein.
632	Q961W1_DROME	Q961W1	294	6.00E-25	96 \ 306	31	CG11796, isoform B. EC=1.13.11.27. GH03058p.
633	B3NIM3_DROER	B3NIM3	380	6.00E-25	106 \ 356	29	GG13309.
634	B4QRZ7_DROSI	B4QRZ7	380	7.00E-25	106 \ 356	29	GD12185.
635	B0WBB9_CULQU	B0WBB9	388	7.00E-25	79 \ 209	37	4-hydroxyphenylpyruvate dioxygenase.
636	Q5BC31_EMENI	Q5BC31	169	7.00E-25	69 \ 169	40	Putative uncharacterized protein.
637	Q9VPF3_DROME	Q9VPF3	380	7.00E-25	106 \ 356	29	CG11796, isoform A. EC=1.13.11.27. GH11957p.
638	B4IAB1_DROSE	B4IAB1	380	9.00E-25	106 \ 356	29	GM22213.
639	B4IUG7_DROYA	B4IUG7	380	1.00E-24	106 \ 356	29	GE22742.
640	Q939Y0_9PSEU	Q939Y0	356	1.00E-24	102 \ 329	31	Putative hydroxyphenyl pyruvate dioxygenase.
641	B4KY40_DROMO	B4KY40	402	1.00E-24	107 \ 356	30	GI11911.
642	A2QMF4_ASPNC	A2QMF4	409	2.00E-24	99 \ 310	31	Putative sequencing error. EC=1.13.11.27.
643	B4N6M5_DROWI	B4N6M5	380	2.00E-24	102 \ 351	29	GK12342.
644	B1XM12_SYNP2	B1XM12	337	2.00E-24	85 \ 220	38	Glyoxalase family protein.
645	B4UBP2_ANASK	B4UBP2	393	3.00E-24	105 \ 340	30	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
646	B8J606_ANAD2	B8J606	395	4.00E-24	104 \ 340	30	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
647	C0S557_PARBP	C0S557	366	4.00E-24	74 \ 203	36	4-hydroxyphenylpyruvate dioxygenase.
648	Q59P37_CANAL	Q59P37	572	4.00E-24	105 \ 334	31	Putative uncharacterized protein HPD99.
649	Q7ZUY6_DANRE	Q7ZUY6	387	1.00E-23	107 \ 358	29	Zgc:56326.
650	A8R3H6_BLEJA	A8R3H6	382	2.00E-23	92 \ 322	28	4-hydroxyphenylpyruvate dioxygenase homolog.
651	Q7Q2T3_ANOGA	Q7Q2T3	381	2.00E-23	78 \ 211	36	AGAP004802-PA.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
652	B9WBT3_CANDC	B9WBT3	570	2.00E-23	105 \ 331	31	4-hydroxyphenylpyruvate dioxygenase, putative. EC=1.13.11.27.
653	B6NIX0_BRAFL	B6NIX0	382	2.00E-23	100 \ 331	30	Putative uncharacterized protein.
654	Q2IF31_ANADE	Q2IF31	393	3.00E-23	99 \ 313	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
655	B6NBV5_BRAFL	B6NBV5	291	4.00E-23	94 \ 299	31	Putative uncharacterized protein.
656	Q6AZV8_DANRE	Q6AZV8	393	5.00E-23	103 \ 354	29	4-hydroxyphenylpyruvate dioxygenase.
657	Q0ZRG4_NEMVE	Q0ZRG4	873	5.00E-23	85 \ 235	36	HNF-HNF class homeobox protein.
658	A4X8H1_SALTO	A4X8H1	358	5.00E-23	90 \ 294	30	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
659	A7HG21_ANADF	A7HG21	391	5.00E-23	107 \ 337	31	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27. Flags: Precursor.
660	B7PHP6_IXOSC	B7PHP6	381	6.00E-23	80 \ 211	37	4-hydroxyphenylpyruvate dioxygenase, putative. EC=1.13.11.27.
661	Q93N78_STRLA	Q93N78	338	6.00E-23	100 \ 331	30	Hydroxyphenyl pyruvate dioxygenase.
662	B4IYZ9_DROGR	B4IYZ9	387	8.00E-23	95 \ 305	31	GH17018.
663	B4LGD0_DROVI	B4LGD0	380	8.00E-23	102 \ 352	28	GJ13785.
664	B5X472_SALSA	B5X472	386	1.00E-22	104 \ 350	29	4-hydroxyphenylpyruvate dioxygenase.
665	O52791_AMYOR	O52791	357	2.00E-22	94 \ 324	29	PCZA361.1.
666	A8M4U2_SALAI	A8M4U2	369	2.00E-22	96 \ 325	29	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
667	C1UKR8_9DELT	C1UKR8	384	4.00E-22	106 \ 369	28	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
668	B6PBX0_BRAFL	B6PBX0	213	7.00E-22	75 \ 211	35	Putative uncharacterized protein.
669	Q4SLF2_TETNG	Q4SLF2	255	1.00E-21	79 \ 227	34	Chromosome 7 SCAF14557, whole genome shotgun sequence.. Flags: Fragment.
670	B3KQ63_HUMAN	B3KQ63	354	1.00E-21	98 \ 355	27	cDNA FLJ32948 fis, clone TESTI2008014, highly similar to 4-hydroxyphenylpyruvate dioxygenase EC 1.13.11.27.
671	A8K461_HUMAN	A8K461	393	1.00E-21	98 \ 355	27	cDNA FLJ76150, highly similar to Homo sapiens 4-hydroxyphenylpyruvate dioxygenase HPD, mRNA. 4-hydroxyphenylpyruvate dioxygenase, isoform CRA_b.
672	C1ULH3_9DELT	C1ULH3	382	2.00E-21	104 \ 361	28	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
673	Q2WBX9_PLADU	Q2WBX9	287	2.00E-21	75 \ 212	35	4-hydroxyphenylpyruvate dioxygenase protein. Flags: Fragment.
674	Q5J1Q8_9NOCA	Q5J1Q8	345	3.00E-21	90 \ 324	27	NocF.
675	C0T2G1_9PSEU	C0T2G1	345	3.00E-21	90 \ 324	27	4-hydroxyphenylpyruvate dioxygenase.
676	C1WG10_9ACTO	C1WG10	357	4.00E-21	88 \ 316	27	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
677	Q2JX04_SYNJA	Q2JX04	350	5.00E-21	79 \ 215	36	Putative 4-hydroxyphenylpyruvate dioxygenase.
678	A7BG64_COPJA	A7BG64	430	6.00E-21	96 \ 332	28	Hydroxyphenylpyruvate dioxygenase.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
679	Q6GPB7_XENLA	Q6GPB7	391	7.00E-21	86 \ 305	28	MGC80543 protein.
680	B9S300_RICCO	B9S300	441	9.00E-21	91 \ 309	29	4-hydroxyphenylpyruvate dioxygenase, putative. EC=1.13.11.27.
681	B5FX47_HUMAN	B5FX47	377	1.00E-20	96 \ 352	27	Liver F protein. Flags: Fragment.
682	B4WLD7_9SYNE	B4WLD7	387	2.00E-20	89 \ 330	26	Glyoxalase family protein.
683	A5DG82_PICGU	A5DG82	309	3.00E-20	75 \ 220	34	Putative uncharacterized protein.
684	Q2JPN8_SYNJB	Q2JPN8	359	7.00E-20	69 \ 202	34	4-hydroxyphenylpyruvate dioxygenase, putative.
685	A5ADC8_VITVI	A5ADC8	445	9.00E-20	93 \ 320	29	Putative uncharacterized protein.
686	Q8L7E8_ARATH	Q8L7E8	473	1.00E-19	90 \ 314	28	4-hydroxyphenylpyruvate dioxygenase HPD.
687	B7X935_HEVBR	B7X935	445	4.00E-19	89 \ 315	28	4-hydroxyphenylpyruvate dioxygenase.
688	O82449_ARATH	O82449	419	5.00E-19	81 \ 282	28	P-hydroxyphenylpyruvate dioxygenase.
689	Q9R668_SHECO	Q9R668	151	6.00E-19	61 \ 139	43	P-hydroxyphenylpyruvate DIOXYGENASE=MELA product. Flags: Fragments.
690	Q1J3W8_DEIGD	Q1J3W8	477	6.00E-19	69 \ 198	34	Xylose isomerase-like protein TIM barrel. Flags: Precursor.
691	A8PTJ2_BRUMA	A8PTJ2	403	7.00E-19	71 \ 207	34	4-hydroxyphenylpyruvate dioxygenase family protein.
692	A0YK40_9CYAN	A0YK40	363	7.00E-19	98 \ 370	26	4-hydroxyphenylpyruvate dioxygenase.
693	A4RUQ4_OSTLU	A4RUQ4	427	1.00E-18	90 \ 318	28	Predicted protein.
694	A9RV71_PHYP	A9RV71	432	1.00E-18	90 \ 313	28	Predicted protein.
695	C1BKE9_OSMO	C1BKE9	451	1.00E-18	87 \ 324	26	4-hydroxyphenylpyruvate dioxygenase.
696	C1JC81_HYPNO	C1JC81	175	2.00E-18	62 \ 167	37	4-hydroxyphenylpyruvate dioxygenase. Flags: Fragment.
697	C1RBY6_9ACTO	C1RBY6	367	3.00E-18	90 \ 337	26	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
698	B1WAT4_XENTR	B1WAT4	386	3.00E-18	80 \ 300	26	HpdI protein.
699	A9RPY0_PHYP	A9RPY0	433	5.00E-18	89 \ 315	28	Predicted protein.
700	Q56H33_MEDTR	Q56H33	437	5.00E-18	87 \ 319	27	4-hydroxyphenylpyruvate dioxygenase.
701	B9GT13_POPTR	B9GT13	444	6.00E-18	87 \ 317	27	Predicted protein.
702	A8XKB1_CAEBR	A8XKB1	380	7.00E-18	74 \ 242	30	Putative uncharacterized protein.
703	A9GC61_SORC5	A9GC61	382	7.00E-18	66 \ 167	39	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
704	A7MC29_DANRE	A7MC29	420	9.00E-18	101 \ 383	26	Zgc:171978 protein.
705	Q6H4V1_ORYSJ	Q6H4V1	446	1.00E-17	93 \ 311	29	Putative 4-hydroxyphenylpyruvate dioxygenase.
706	A3A3J1_ORYSJ	A3A3J1	447	1.00E-17	93 \ 311	29	Putative uncharacterized protein.
707	B8AIH6_ORYSI	B8AIH6	601	1.00E-17	93 \ 311	29	Putative uncharacterized protein.
708	A9FJX5_SORC5	A9FJX5	383	1.00E-17	74 \ 217	34	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
709	Q01CD2_OSTTA	Q01CD2	432	3.00E-17	89 \ 324	27	P-hydroxyphenylpyruvate dioxygenase ISS.
710	B8BU80_THAPS	B8BU80	418	4.00E-17	92 \ 337	27	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27. Flags: Fragment.
711	A5Z1N7_SOYBN	A5Z1N7	443	2.00E-16	91 \ 318	28	4-hydroxyphenylpyruvate dioxygenase.
712	Q09JZ2_BRARP	Q09JZ2	443	3.00E-16	86 \ 307	28	4-hydroxyphenylpyruvate dioxygenase.
713	Q8H1T5_ABUTH	Q8H1T5	363	4.00E-16	81 \ 302	26	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27. Flags: Fragment.
714	Q1E7J7_COCIM	Q1E7J7	345	5.00E-16	56 \ 135	41	Putative uncharacterized protein.
715	Q08WC1_STIAU	Q08WC1	386	2.00E-15	71 \ 221	32	Glyoxalase family protein.
716	B8H805_ARTCA	B8H805	624	5.00E-15	92 \ 350	26	Xylose isomerase domain protein TIM barrel.
717	A2AGE4_MOUSE	A2AGE4	371	6.00E-15	67 \ 231	29	4-hydroxyphenylpyruvate dioxygenase-like. Glyoxalase domain containing 1.
718	A1RBV1_ARTAT	A1RBV1	628	6.00E-15	86 \ 348	24	Putative 4-hydroxyphenylpyruvate dioxygenase.
719	Q2HR40_9ACTO	Q2HR40	626	6.00E-15	101 \ 368	27	Putative 4-hydroxyphenyl pyruvate dioxygenase.
720	C1DZE9_9CHLO	C1DZE9	441	2.00E-14	89 \ 325	27	Predicted protein.
721	Q4RE46_TETNG	Q4RE46	418	2.00E-14	85 \ 322	26	Chromosome 2 SCAF15135, whole genome shotgun sequence.. Flags: Fragment.
722	Q45FE8_WHEAT	Q45FE8	436	3.00E-14	94 \ 319	29	4-hydroxyphenylpyruvate dioxygenase.
723	A0K2D4_ARTS2	A0K2D4	629	7.00E-14	87 \ 352	24	Xylose isomerase domain protein TIM barrel.
724	B2R9B0_HUMAN	B2R9B0	371	7.00E-14	83 \ 303	27	Glyoxalase domain containing 1. cDNA, FLJ94307.
725	A8J0K1_CHLRE	A8J0K1	372	2.00E-13	88 \ 322	27	4-hydroxyphenylpyruvate dioxygenase.
726	A9P1M2_PICSI	A9P1M2	263	2.00E-13	69 \ 230	30	Putative uncharacterized protein.
727	Q9C0R9_AUXZU	Q9C0R9	130	5.00E-13	47 \ 131	35	T-cell reactive protein. Flags: Fragment.
728	Q70ZL8_CHLRE	Q70ZL8	432	5.00E-13	85 \ 314	27	4-hydroxyphenylpyruvate dioxygenase. P-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27. Flags: Fragment.
729	B6MR21_BRAFL	B6MR21	429	6.00E-13	84 \ 322	26	Putative uncharacterized protein.
730	C2WGY7_BACCE	C2WGY7	92	7.00E-13	48 \ 97	49	Putative uncharacterized protein.
731	C0M659_CHLRE	C0M659	432	1.00E-12	84 \ 314	26	p-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
732	Q9C0Q2_9EURO	Q9C0Q2	130	1.00E-12	45 \ 131	34	T-cell reactive protein. Flags: Fragment.
733	A7WK82_WHEAT	A7WK82	381	2.00E-12	78 \ 268	29	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
734	B6PID2_BRAFL	B6PID2	428	2.00E-12	84 \ 321	26	Putative uncharacterized protein.
735	Q9C0U2_9EURO	Q9C0U2	130	3.00E-12	44 \ 131	33	T-cell reactive protein. Flags: Fragment.
736	B5I5I3_9ACTO	B5I5I3	592	3.00E-12	84 \ 332	25	Sugar phosphate isomerase/epimerase.
737	A5PJL0_BOVIN	A5PJL0	390	3.00E-12	44 \ 136	32	HPDL protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
738	Q9C160_AUXZU	Q9C160	130	3.00E-12	46 \ 131	35	T-cell reactive protein. Flags: Fragment.
739	Q0E3L4_ORYSJ	Q0E3L4	239	3.00E-12	67 \ 224	29	Os02g0168100 protein. Flags: Fragment.
740	Q82M84_STRAW	Q82M84	601	6.00E-12	88 \ 334	26	Putative sugar phosphate isomerase/epimerase.
741	C1Y801_9ACTO	C1Y801	675	6.00E-12	88 \ 333	26	4-hydroxyphenylpyruvate dioxygenase/hemolysin-like protein.
742	C0PMF6_MAIZE	C0PMF6	426	9.00E-12	85 \ 305	27	Putative uncharacterized protein.
743	B3S1B3_TRIAD	B3S1B3	388	1.00E-11	65 \ 224	29	Putative uncharacterized protein.
744	A4QB63_CORGB	A4QB63	618	2.00E-11	78 \ 325	24	Putative uncharacterized protein.
745	B9H843_POPTR	B9H843	343	3.00E-11	73 \ 297	24	Predicted protein.
746	Q8NT86_CORGL	Q8NT86	618	4.00E-11	78 \ 325	24	Sugar phosphate isomerases/epimerases. EC=4.2.1.-. Phosphate isomerase/epimerase.
747	A7SLZ3_NEMVE	A7SLZ3	330	1.00E-10	62 \ 236	26	Predicted protein. Flags: Fragment.
748	A7PJT5_VITVI	A7PJT5	164	5.00E-10	54 \ 151	35	Chromosome chr12 scaffold_18, whole genome shotgun sequence.
749	A1CI04_ASPCL	A1CI04	132	9.00E-10	47 \ 104	45	Putative uncharacterized protein.
750	C1MJF3_9CHLO	C1MJF3	447	1.00E-09	59 \ 200	29	Predicted protein.
751	A6W826_KINRD	A6W826	596	1.00E-09	79 \ 330	23	Xylose isomerase domain protein TIM barrel.
752	C1AVQ1_RHOOP	C1AVQ1	644	7.00E-09	81 \ 335	24	Putative 4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27.
753	A7PC29_VITVI	A7PC29	196	8.00E-09	52 \ 187	27	Chromosome chr2 scaffold_11, whole genome shotgun sequence.
754	Q8FSF2_COREF	Q8FSF2	622	1.00E-08	82 \ 333	24	Putative uncharacterized protein.
755	Q0SGZ5_RHOSR	Q0SGZ5	644	2.00E-08	82 \ 335	24	Dehydroshikimate dehydratase.
756	A1F9J3_VIBCH	A1F9J3	38	3.00E-08	30 \ 36	83	4-hydroxyphenylpyruvate dioxygenase. EC=1.13.11.27. Flags: Fragment.
757	C1A1N0_RHOE4	C1A1N0	637	7.00E-07	78 \ 321	24	Putative uncharacterized protein.
758	C3JRU0_RHOER	C3JRU0	637	2.00E-06	79 \ 321	24	Dehydroshikimate dehydratase.
759	C0UHV6_9ACTO	C0UHV6	182	8.00E-06	48 \ 163	29	4-hydroxyphenylpyruvate dioxygenase/hemolysin-like protein.
760	Q1LGU9_RALME	Q1LGU9	207	1.00E-04	24 \ 32	75	Endoribonuclease L-PSP.
761	Q1J3W5_DEIGD	Q1J3W5	149	5.00E-04	30 \ 98	30	Hemolysin-like protein, 4-hydroxyphenylpyruvate dioxygenase related.
762	Q5BS34_SCHJA	Q5BS34	98	0.001	38 \ 93	40	SJCHGC06518 protein.
763	C0UCB8_9ACTO	C0UCB8	183	0.001	40 \ 161	24	4-hydroxyphenylpyruvate dioxygenase/hemolysin-like protein.
764	Q4RE47_TETNG	Q4RE47	199	0.015	27 \ 81	33	Chromosome 2 SCAF15135, whole genome shotgun sequence.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

6.3. Table 3 - BLASTP sequence similarities of the HPPD W336 protein with proteins from the PDB database

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
1	1CJX_D	1CJX_D	357	0	354 \ 357	99	Crystal structure of <i>Pseudomonas fluorescens</i> HPPD
2	1CJX_C	1CJX_C	357	0	354 \ 357	99	Crystal structure of <i>Pseudomonas fluorescens</i> HPPD
3	1CJX_B	1CJX_B	357	0	354 \ 357	99	Crystal structure of <i>Pseudomonas fluorescens</i> HPPD
4	1CJX_A	1CJX_A	357	0	354 \ 357	99	Crystal structure of <i>Pseudomonas fluorescens</i> HPPD
5	1T47_B	1T47_B	381	4.00E-39	109 \ 297	36	Structure of fe2-HPPD bound to NTBC
6	1T47_A	1T47_A	381	4.00E-39	109 \ 297	36	Structure of fe2-HPPD bound to NTBC
7	2R5V_B	2R5V_B	357	2.00E-24	94 \ 324	29	Hydroxymandelate synthase crystal structure
8	2R5V_A	2R5V_A	357	2.00E-24	94 \ 324	29	Hydroxymandelate synthase crystal structure
9	1SQI_B	1SQI_B	393	2.00E-23	98 \ 355	27	Structural basis for inhibitor selectivity revealed by crystal structures of plant and mammalian 4-hydroxyphenylpyruvate dioxygenases
10	1SQI_A	1SQI_A	393	2.00E-23	98 \ 355	27	Structural basis for inhibitor selectivity revealed by crystal structures of plant and mammalian 4-hydroxyphenylpyruvate dioxygenases
11	1SP9_B	1SP9_B	445	3.00E-21	90 \ 314	28	4-hydroxyphenylpyruvate dioxygenase
12	1SP9_A	1SP9_A	445	3.00E-21	90 \ 314	28	4-hydroxyphenylpyruvate dioxygenase
13	1TG5_A	1TG5_A	424	3.00E-21	90 \ 314	28	Crystal structures of plant 4-hydroxyphenylpyruvate dioxygenases complexed with das645
14	1TFZ_A	1TFZ_A	424	3.00E-21	90 \ 314	28	Structural basis for herbicidal inhibitor selectivity revealed by comparison of crystal structures of plant and mammalian 4-hydroxyphenylpyruvate dioxygenases
15	1SQD_A	1SQD_A	424	3.00E-21	90 \ 314	28	Structural basis for inhibitor selectivity revealed by crystal structures of plant and mammalian 4- hydroxyphenylpyruvate dioxygenases
16	1SP8_D	1SP8_D	418	1.00E-15	88 \ 309	28	4-hydroxyphenylpyruvate dioxygenase
17	1SP8_C	1SP8_C	418	1.00E-15	88 \ 309	28	4-hydroxyphenylpyruvate dioxygenase
18	1SP8_B	1SP8_B	418	1.00E-15	88 \ 309	28	4-hydroxyphenylpyruvate dioxygenase
19	1SP8_A	1SP8_A	418	1.00E-15	88 \ 309	28	4-hydroxyphenylpyruvate dioxygenase

HPPD W336 Protein
Amino acid sequence homology search with known toxins

6.4. Table 4 - BLASTP sequence similarities of the HPPD W336 protein with proteins from the DAD database

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
1	ABF50058.1	DQ459070-1	358	0	357 \ 358	99	Plastid transformation vector pCLT323 4-hydroxyphenylpyruvate dioxygenase protein.
2	ABF50055.1	DQ459069-2	358	0	357 \ 358	99	Plastid transformation vector pCLT111 4-hydroxyphenylpyruvate dioxygenase protein.
3	CAH04016.1	CQ830293-1	358	0	357 \ 358	99	Synthetic construct protein Sequence 7 from Patent WO2004055191.
4	CAH04015.1	CQ830291-1	358	0	357 \ 358	99	Synthetic construct protein Sequence 5 from Patent WO2004055191.
5	EDF36983.1	EP674944-2	358	0	346 \ 358	96	Marine metagenome hypothetical protein.
6	CAL91816.1	CS456037-1	358	0	345 \ 358	96	<i>Pseudomonas fluorescens</i> protein Sequence 3 from Patent EP1728868.
7	CAB69499.1	A92169-1	358	0	345 \ 358	96	<i>Pseudomonas fluorescens</i> protein Sequence 3 from Patent WO9820144.
8	ABC88387.2	DQ364627-1	358	0	341 \ 358	95	<i>Pseudomonas fluorescens</i> 4-hydroxyphenylpyruvate dioxygenase protein.
9	ABA74658.1	CP000094-2915	358	0	336 \ 358	93	<i>Pseudomonas fluorescens</i> Pf0-1 4-hydroxyphenylpyruvate dioxygenase protein.
10	AAV92656.1	CP000076-3340	358	0	332 \ 358	92	<i>Pseudomonas fluorescens</i> Pf-5 4-hydroxyphenylpyruvate dioxygenase protein.
11	AAN69035.1	AE015451-3401	358	0	315 \ 358	87	<i>Pseudomonas putida</i> KT2440 4-hydroxyphenylpyruvate dioxygenase protein.
12	ABY98401.1	CP000926-2485	358	0	314 \ 358	87	<i>Pseudomonas putida</i> GB-1 4-hydroxyphenylpyruvate dioxygenase protein.
13	AAV38362.1	CP000075-3329	358	0	312 \ 358	87	<i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a 4-hydroxyphenylpyruvate dioxygenase protein.
14	ABQ78468.1	CP000712-2291	358	0	313 \ 358	87	<i>Pseudomonas putida</i> F1 4-hydroxyphenylpyruvate dioxygenase protein.
15	AAO57028.1	AE016853-3474	363	0	312 \ 357	87	<i>Pseudomonas syringae</i> pv. tomato str. DC3000 4-hydroxyphenylpyruvate dioxygenase protein.
16	AAZ36778.1	CP000058-3098	358	0	312 \ 358	87	<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A 4-hydroxyphenylpyruvate dioxygenase protein.
17	AAO12525.1	AY168854-1	358	0	312 \ 358	87	<i>Pseudomonas putida</i> p-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
18	ACA72940.1	CP000949-2434	358	0	311 \ 355	87	<i>Pseudomonas putida</i> W619 4-hydroxyphenylpyruvate dioxygenase protein.
19	CAK15824.1	CT573326-2827	357	1.00E-180	304 \ 358	84	<i>Pseudomonas entomophila</i> L48 4-hydroxyphenylpyruvate dioxygenase 4HPPD (HPD) (HPPDase) protein.
20	ACB34309.1	CP001013-2033	358	1.00E-176	298 \ 357	83	<i>Leptothrix cholodnii</i> SP-6 4-hydroxyphenylpyruvate dioxygenase protein.
21	AAP47153.1	AF511571-1	301	1.00E-164	276 \ 301	91	Uncultured soil bacterium 4-hydroxyphenylpyruvate dioxygenase protein.
22	AAZ63851.1	CP000091-1030	359	1.00E-164	277 \ 358	77	<i>Ralstonia eutropha</i> JMP134 4-hydroxyphenylpyruvate dioxygenase protein.
23	CAJ95874.1	AM260480-1068	359	1.00E-162	275 \ 358	76	<i>Ralstonia eutropha</i> H16 4-Hydroxyphenylpyruvate dioxygenase protein.
24	CAQ71519.1	CU633750-885	359	1.00E-161	273 \ 358	76	<i>Cupriavidus taiwanensis</i> 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE Protein.
25	ABF11787.1	CP000353-1300	357	1.00E-161	271 \ 355	76	<i>Ralstonia metallidurans</i> CH34 4-hydroxyphenylpyruvate dioxygenase protein.
26	ABM36436.1	CP000529-1109	360	1.00E-160	268 \ 358	74	<i>Polaromonas naphthalenivorans</i> CJ2 4-hydroxyphenylpyruvate dioxygenase protein.
27	ACB32709.1	CP001013-433	358	1.00E-160	269 \ 358	75	<i>Leptothrix cholodnii</i> SP-6 4-hydroxyphenylpyruvate dioxygenase protein.
28	AAP47154.1	AF511572-1	308	1.00E-157	267 \ 308	86	Uncultured soil bacterium 4-hydroxyphenylpyruvate dioxygenase protein.
29	ABX37424.1	CP000884-4777	364	1.00E-155	266 \ 360	73	<i>Delftia acidovorans</i> SPH-1 4-hydroxyphenylpyruvate dioxygenase protein.
30	EBM31344.1	EN857387-1	359	1.00E-153	260 \ 355	73	Marine metagenome hypothetical protein.
31	ABG39651.1	CP000388-1118	358	1.00E-150	255 \ 356	71	<i>Pseudoalteromonas atlantica</i> T6c 4-hydroxyphenylpyruvate dioxygenase protein.
32	ABM40770.1	CP000539-514	372	1.00E-150	260 \ 356	73	<i>Acidovorax</i> sp. JS42 4-hydroxyphenylpyruvate dioxygenase protein.
33	ABQ93990.1	CP000713-1030	372	1.00E-149	257 \ 361	71	<i>Psychrobacter</i> sp. PRwf-1 4-hydroxyphenylpyruvate dioxygenase protein.
34	ACM32016.1	CP001392-527	372	1.00E-149	258 \ 356	72	<i>Diaphorobacter</i> sp. TPSY 4-hydroxyphenylpyruvate dioxygenase protein.
35	ACG66837.1	CP001103-2517	357	1.00E-149	257 \ 356	72	<i>Alteromonas macleodii</i> Deep ecotype' 4-hydroxyphenylpyruvate dioxygenase protein.
36	ABC63375.1	CP000157-1283	373	1.00E-148	251 \ 362	69	<i>Erythrobacter litoralis</i> HTCC2594 4-hydroxyphenylpyruvate dioxygenase protein.
37	EEB78396.1	DS999228-74	362	1.00E-148	251 \ 356	70	Marine gamma proteobacterium HTCC2148 4-hydroxyphenylpyruvate dioxygenase protein.
38	ABF54822.1	CP000356-3096	363	1.00E-147	247 \ 358	68	<i>Sphingopyxis alaskensis</i> RB2256 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
39	ABD25044.1	CP000248-595	370	1.00E-145	249 \ 361	68	<i>Novosphingobium aromaticivorans</i> DSM 12444 4-hydroxyphenylpyruvate dioxygenase protein.
40	EED33338.1	DS999405-982	361	1.00E-144	259 \ 358	72	Gamma proteobacterium NOR5-3 4-hydroxyphenylpyruvate dioxygenase protein.
41	CAM85052.1	CU459141-60	351	1.00E-144	241 \ 355	67	<i>Acinetobacter baumannii</i> 4-hydroxyphenylpyruvate dioxygenase 4HPPD (HPPDase) protein.
42	ACJ43222.1	CP001182-3743	351	1.00E-144	241 \ 355	67	<i>Acinetobacter baumannii</i> AB0057 4-hydroxyphenylpyruvate dioxygenase protein.
43	ACJ59060.1	CP001172-63	351	1.00E-144	241 \ 355	67	<i>Acinetobacter baumannii</i> AB307-0294 4-hydroxyphenylpyruvate dioxygenase protein.
44	ACC58923.1	CP000863-3611	351	1.00E-144	241 \ 355	67	<i>Acinetobacter baumannii</i> ACICU 4-hydroxyphenylpyruvate dioxygenase protein.
45	ABO13807.2	CP000521-3738	351	1.00E-144	241 \ 355	67	<i>Acinetobacter baumannii</i> ATCC 17978 4-hydroxyphenylpyruvate dioxygenase protein.
46	ABI76867.1	CP000158-2844	366	1.00E-144	248 \ 363	68	<i>Hyphomonas neptunium</i> ATCC 15444 4-hydroxyphenylpyruvate dioxygenase protein.
47	CAP02856.1	CU468230-3432	351	1.00E-143	239 \ 355	67	<i>Acinetobacter baumannii</i> 4-hydroxyphenylpyruvate dioxygenase 4HPPD (HPPDase) protein.
48	ABI64629.1	CP000449-333	359	1.00E-143	236 \ 357	66	<i>Maricaulis maris</i> MCS10 4-hydroxyphenylpyruvate dioxygenase protein.
49	ABE75332.1	CP000323-1548	368	1.00E-142	249 \ 359	69	<i>Psychrobacter cryohalolentis</i> K5 4-hydroxyphenylpyruvate dioxygenase protein.
50	ABR71650.1	CP000749-2707	358	1.00E-141	245 \ 358	68	<i>Marinomonas</i> sp. MWYL1 4-hydroxyphenylpyruvate dioxygenase protein.
51	EDH19313.1	EP606139-1	333	1.00E-138	239 \ 331	72	Marine metagenome hypothetical protein.
52	EBQ04394.1	EN661398-1	361	1.00E-138	237 \ 348	68	Marine metagenome hypothetical protein.
53	EDA10818.1	EP908841-2	308	1.00E-126	220 \ 307	71	Marine metagenome hypothetical protein.
54	ACJ00703.1	CP000613-3271	377	1.00E-122	224 \ 362	61	<i>Rhodospirillum centenum</i> SW 4-hydroxyphenylpyruvate dioxygenase protein.
55	ACD28509.1	CP001068-3342	368	1.00E-118	215 \ 364	59	<i>Ralstonia pickettii</i> 12J 4-hydroxyphenylpyruvate dioxygenase protein.
56	EBH05176.1	EP150084-4	282	1.00E-117	204 \ 282	72	Marine metagenome hypothetical protein.
57	CAQ62975.1	CU914168-2846	367	1.00E-117	215 \ 364	59	<i>Ralstonia solanacearum</i> IPO1609 4-hydroxyphenylpyruvate dioxygenase protein.
58	AAQ58643.1	AE016825-969	358	1.00E-116	210 \ 361	58	<i>Chromobacterium violaceum</i> ATCC 12472 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
59	CAD16812.1	AL646052-3101	367	1.00E-116	213 \ 364	58	<i>Ralstonia solanacearum</i> GMI1000 probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein.
60	CAL93810.1	AM406670-1192	373	1.00E-116	215 \ 369	58	<i>Azoarcus</i> sp. BH72 probable 4-hydroxyphenylpyruvate dioxygenase protein.
61	ECY16948.1	EP986854-2	304	1.00E-116	208 \ 304	68	Marine metagenome hypothetical protein.
62	ACG79242.1	CP000747-2828	374	1.00E-115	211 \ 357	59	<i>Phenylobacterium zucineum</i> HLK1 4-hydroxyphenylpyruvate dioxygenase protein.
63	CAQ18565.1	CU694394-79	358	1.00E-114	212 \ 360	58	<i>Ralstonia solanacearum</i> 4-hydroxyphenylpyruvate dioxygenase protein.
64	ABC37897.1	CP000086-3041	365	1.00E-114	207 \ 361	57	<i>Burkholderia thailandensis</i> E264 4-hydroxyphenylpyruvate dioxygenase protein.
65	ABM34731.1	CP000512-4113	378	1.00E-114	215 \ 365	58	<i>Acidovorax avenae</i> subsp. citrulli AAC00-1 4-hydroxyphenylpyruvate dioxygenase protein.
66	ABE32647.1	CP000270-4109	365	1.00E-114	207 \ 361	57	<i>Burkholderia xenovorans</i> LB400 4-hydroxyphenylpyruvate dioxygenase protein.
67	CAE34577.1	BX640449-283	370	1.00E-113	206 \ 363	56	<i>Bordetella bronchiseptica</i> putative hemolysin protein.
68	CAE39050.1	BX640434-224	370	1.00E-113	206 \ 363	56	<i>Bordetella parapertussis</i> putative hemolysin protein.
69	ACC72038.1	CP001043-2841	365	1.00E-113	203 \ 361	56	<i>Burkholderia phymatum</i> STM815 4-hydroxyphenylpyruvate dioxygenase protein.
70	ACD18061.1	CP001052-3608	365	1.00E-113	206 \ 361	57	<i>Burkholderia phytofirmans</i> PsJN 4-hydroxyphenylpyruvate dioxygenase protein.
71	CAP41013.1	AM902716-682	370	1.00E-113	205 \ 365	56	<i>Bordetella petrii</i> putative 4-hydroxyphenylpyruvate dioxygenase protein.
72	EDS82090.1	CH899758-13	365	1.00E-113	204 \ 361	56	<i>Burkholderia pseudomallei</i> S13 4-hydroxyphenylpyruvate dioxygenase protein.
73	EDO86976.1	CH899735-10	365	1.00E-113	204 \ 361	56	<i>Burkholderia pseudomallei</i> 406e 4-hydroxyphenylpyruvate dioxygenase protein.
74	EDU09869.1	CH899714-10	365	1.00E-113	204 \ 361	56	<i>Burkholderia pseudomallei</i> 1655 4-hydroxyphenylpyruvate dioxygenase protein.
75	EDP86195.1	CH899680-10	365	1.00E-113	204 \ 361	56	<i>Burkholderia mallei</i> ATCC 10399 4-hydroxyphenylpyruvate dioxygenase protein.
76	EDO95300.1	DS496054-5	365	1.00E-113	204 \ 361	56	<i>Burkholderia pseudomallei</i> Pasteur 52237 4-hydroxyphenylpyruvate dioxygenase protein.
77	EDK59140.1	DS264108-8	365	1.00E-113	204 \ 361	56	<i>Burkholderia mallei</i> JHU 4-hydroxyphenylpyruvate dioxygenase protein.
78	EDK54161.1	DS264096-8	365	1.00E-113	204 \ 361	56	<i>Burkholderia mallei</i> FMH 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
79	ABN92248.1	CP000572-3781	365	1.00E-113	204 \ 361	56	<i>Burkholderia pseudomallei</i> 1106a 4-hydroxyphenylpyruvate dioxygenase protein.
80	ABN82765.1	CP000570-3724	365	1.00E-113	204 \ 361	56	<i>Burkholderia pseudomallei</i> 668 4-hydroxyphenylpyruvate dioxygenase protein.
81	ABO06919.1	CP000548-3456	365	1.00E-113	204 \ 361	56	<i>Burkholderia mallei</i> NCTC 10247 4-hydroxyphenylpyruvate dioxygenase protein.
82	ABN02465.1	CP000546-1936	365	1.00E-113	204 \ 361	56	<i>Burkholderia mallei</i> NCTC 10229 4-hydroxyphenylpyruvate dioxygenase protein.
83	ABM49903.1	CP000526-3052	365	1.00E-113	204 \ 361	56	<i>Burkholderia mallei</i> SAVP1 4-hydroxyphenylpyruvate dioxygenase protein.
84	ABM51806.1	CP000526-3	365	1.00E-113	204 \ 361	56	<i>Burkholderia mallei</i> SAVP1 4-hydroxyphenylpyruvate dioxygenase protein.
85	ABA50777.1	CP000124-11	365	1.00E-113	204 \ 361	56	<i>Burkholderia pseudomallei</i> 1710b 4-hydroxyphenylpyruvate dioxygenase protein.
86	AAU48238.1	CP000010-2259	365	1.00E-113	204 \ 361	56	<i>Burkholderia mallei</i> ATCC 23344 4-hydroxyphenylpyruvate dioxygenase protein.
87	CAH37250.1	BX571965-3267	365	1.00E-113	204 \ 361	56	<i>Burkholderia pseudomallei</i> K96243 4-hydroxyphenylpyruvate dioxygenase protein.
88	EAY67342.1	CH482380-11	365	1.00E-112	203 \ 361	56	<i>Burkholderia dolosa</i> AUO158 4-hydroxyphenylpyruvate dioxygenase protein.
89	ABO53316.1	CP000614-288	365	1.00E-112	204 \ 361	56	<i>Burkholderia vietnamiensis</i> G4 4-hydroxyphenylpyruvate dioxygenase protein.
90	CAE43309.1	BX640420-96	370	1.00E-112	204 \ 363	56	<i>Bordetella pertussis</i> putative hemolysin protein.
91	EAY63307.1	CH482377-1511	365	1.00E-112	202 \ 361	55	<i>Burkholderia cenocepacia</i> PC184 4-hydroxyphenylpyruvate dioxygenase protein.
92	ACA89481.1	CP000958-300	365	1.00E-112	202 \ 361	55	<i>Burkholderia cenocepacia</i> MC0-3 4-hydroxyphenylpyruvate dioxygenase protein.
93	ABK07075.1	CP000458-321	365	1.00E-112	202 \ 361	55	<i>Burkholderia cenocepacia</i> HI2424 4-hydroxyphenylpyruvate dioxygenase protein.
94	ABF77683.1	CP000378-2767	365	1.00E-112	202 \ 361	55	<i>Burkholderia cenocepacia</i> AU 1054 4-hydroxyphenylpyruvate dioxygenase protein.
95	ABI85800.1	CP000440-237	365	1.00E-112	202 \ 361	55	<i>Burkholderia ambifaria</i> AMMD 4-hydroxyphenylpyruvate dioxygenase protein.
96	ABX13918.1	CP000868-223	365	1.00E-112	202 \ 361	55	<i>Burkholderia multivorans</i> ATCC 17616 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
97	BAG44916.1	AP009385-2974	365	1.00E-112	202 \ 361	55	<i>Burkholderia multivorans</i> ATCC 17616 4-hydroxyphenylpyruvate dioxygenase protein.
98	ECV30391.1	EQ081423-13	424	1.00E-112	201 \ 361	55	Marine metagenome hypothetical protein.
99	ACB62749.1	CP001025-246	365	1.00E-112	203 \ 361	56	<i>Burkholderia ambifaria</i> MC40-6 4-hydroxyphenylpyruvate dioxygenase protein.
100	ABQ70210.1	CP000699-3837	367	1.00E-111	199 \ 354	56	<i>Sphingomonas wittichii</i> RW1 4-hydroxyphenylpyruvate dioxygenase protein.
101	CAL80548.1	CU234118-6575	372	1.00E-111	195 \ 355	54	<i>Bradyrhizobium</i> sp. ORS278 4-hydroxyphenylpyruvate dioxygenase protein.
102	EDZ66931.1	DS995300-746	363	1.00E-111	199 \ 355	56	<i>Nitrosococcus oceani</i> AFC27 4-hydroxyphenylpyruvate dioxygenase protein.
103	ABM93308.1	CP000555-346	370	1.00E-111	205 \ 364	56	<i>Methylibium petroleiphilum</i> PM1 4-hydroxyphenylpyruvate dioxygenase protein.
104	CAR50518.1	AM747720-213	365	1.00E-111	201 \ 361	55	<i>Burkholderia cenocepacia</i> J2315 4-hydroxyphenylpyruvic acid dioxygenase protein.
105	ABB07022.1	CP000151-239	365	1.00E-111	201 \ 361	55	<i>Burkholderia</i> sp. 383 4-hydroxyphenylpyruvate dioxygenase protein.
106	ABA57926.1	CP000127-1370	351	1.00E-111	199 \ 355	56	<i>Nitrosococcus oceani</i> ATCC 19707 4-hydroxyphenylpyruvate dioxygenase protein.
107	ACE98567.1	CP001096-5	372	1.00E-111	191 \ 355	53	<i>Rhodopseudomonas palustris</i> TIE-1 4-hydroxyphenylpyruvate dioxygenase protein.
108	CAE25449.1	BX572593-5	372	1.00E-111	190 \ 355	53	<i>Rhodopseudomonas palustris</i> CGA009 4-hydroxyphenylpyruvate dioxygenase protein.
109	CAJ50504.1	AM167904-2891	370	1.00E-110	204 \ 365	55	<i>Bordetella avium</i> 197N 4-hydroxyphenylpyruvate dioxygenase putative hemolysin protein.
110	BAC45604.1	BA000040-339	372	1.00E-110	190 \ 355	53	<i>Bradyrhizobium japonicum</i> USDA 110 4-hydroxyphenylpyruvate dioxygenase protein.
111	ABM57885.1	CP000542-2092	377	1.00E-110	204 \ 365	55	<i>Verminephrobacter eiseniae</i> EF01-2 4-hydroxyphenylpyruvate dioxygenase protein.
112	ABQ32848.1	CP000494-543	372	1.00E-110	192 \ 355	54	<i>Bradyrhizobium</i> sp. BTAi1 4-hydroxyphenylpyruvate dioxygenase protein.
113	ABE46105.1	CP000316-4138	376	1.00E-109	207 \ 367	56	<i>Polaromonas</i> sp. JS666 4-hydroxyphenylpyruvate dioxygenase protein.
114	ABC27843.1	CP000155-920	365	1.00E-104	188 \ 362	51	<i>Hahella chejuensis</i> KCTC 2396 4-hydroxyphenylpyruvate dioxygenase protein.
115	ABL69761.1	CP000489-1644	370	1.00E-103	192 \ 355	54	<i>Paracoccus denitrificans</i> PD1222 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
116	ABJ10025.1	CP000438-4256	357	1.00E-103	186 \ 352	52	<i>Pseudomonas aeruginosa</i> UCBPP-PA14 4-hydroxyphenylpyruvate dioxygenase protein.
117	EAZ62593.1	CH482384-5764	357	1.00E-103	186 \ 352	52	<i>Pseudomonas aeruginosa</i> 2192 4-hydroxyphenylpyruvate dioxygenase protein.
118	EAZ56660.1	CH482383-5052	357	1.00E-103	186 \ 352	52	<i>Pseudomonas aeruginosa</i> C3719 4-hydroxyphenylpyruvate dioxygenase protein.
119	AAG04254.1	AE004091-867	357	1.00E-103	186 \ 352	52	<i>Pseudomonas aeruginosa</i> PAO1 4-hydroxyphenylpyruvate dioxygenase protein.
120	CAW29206.1	FM209186-4452	357	1.00E-102	186 \ 352	52	<i>Pseudomonas aeruginosa</i> LESB58 4-hydroxyphenylpyruvate dioxygenase protein.
121	ABP84460.1	CP000680-1685	360	1.00E-102	187 \ 355	52	<i>Pseudomonas mendocina</i> ymp 4-hydroxyphenylpyruvate dioxygenase protein.
122	ABU71142.1	CP000789-2081	357	1.00E-102	194 \ 361	53	<i>Vibrio harveyi</i> ATCC BAA-1116 hypothetical protein.
123	BAC94259.1	BA000037-1495	357	1.00E-101	192 \ 355	54	<i>Vibrio vulnificus</i> YJ016 putitive hemolysin protein.
124	AAO11111.1	AE016795-2567	357	1.00E-101	192 \ 355	54	<i>Vibrio vulnificus</i> CMCP6 4-hydroxyphenylpyruvate dioxygenase protein.
125	EDN57982.1	DS267813-68	357	1.00E-101	195 \ 361	54	<i>Vibrio</i> sp. Ex25 4-hydroxyphenylpyruvate dioxygenase protein.
126	EEE46022.1	EQ973121-2542	378	1.00E-101	184 \ 355	51	<i>Labrenzia alexandrii</i> DFL-11 4-hydroxyphenylpyruvate dioxygenase protein.
127	AAL59614.1	AF457645-1	357	1.00E-101	192 \ 355	54	<i>Listonella anguillarum</i> 4-hydroxyphenylpyruvate dioxygenase protein.
128	EED27710.1	DS999329-91	357	1.00E-101	193 \ 355	54	<i>Vibrio parahaemolyticus</i> 16 4-hydroxyphenylpyruvate dioxygenase protein.
129	ABP78566.1	CP000304-858	361	1.00E-101	188 \ 354	53	<i>Pseudomonas stutzeri</i> A1501 4-hydroxyphenylpyruvate dioxygenase protein.
130	EBC17436.1	EP434888-1	260	1.00E-100	173 \ 265	65	Marine metagenome hypothetical protein.
131	CAV27734.1	FM954973-1474	357	1.00E-100	189 \ 354	53	<i>Vibrio splendidus</i> LGP32 4-hydroxyphenylpyruvate dioxygenase 4HPPD (hemolysin) protein.
132	BAC59612.1	BA000031-1349	357	1.00E-100	192 \ 361	53	<i>Vibrio parahaemolyticus</i> RIMD 2210633 4-hydroxyphenylpyruvate dioxygenase protein.
133	ABG41505.1	CP000388-2972	360	1.00E-100	191 \ 361	52	<i>Pseudoalteromonas atlantica</i> T6c 4-hydroxyphenylpyruvate dioxygenase protein.
134	ABK39516.1	CP000462-2590	365	1.00E-100	191 \ 355	53	<i>Aeromonas hydrophila</i> subsp. <i>hydrophila</i> ATCC 7966 4-hydroxyphenylpyruvate dioxygenase protein.
135	EEA92947.1	DS996812-18	370	1.00E-100	186 \ 353	52	Pseudo <i>Vibrio</i> sp. JE062 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
136	EED37592.1	DS999412-701	370	2.00E-99	181 \ 354	51	<i>Stenotrophomonas</i> sp. SKA14 4-hydroxyphenylpyruvate dioxygenase protein.
137	ECY20143.1	EP985667-3	235	6.00E-99	174 \ 233	74	Marine metagenome hypothetical protein.
138	ABR84894.1	CP000744-4600	357	7.00E-99	185 \ 352	52	<i>Pseudomonas aeruginosa</i> PA7 4-hydroxyphenylpyruvate dioxygenase protein.
139	EDN13204.1	DS265364-22	369	7.00E-99	191 \ 355	53	<i>Vibrio cholerae</i> RC385 4-hydroxyphenylpyruvate dioxygenase protein.
140	EDN15260.1	DS265235-13	369	7.00E-99	191 \ 355	53	<i>Vibrio cholerae</i> AM-19226 4-hydroxyphenylpyruvate dioxygenase protein.
141	EAZ50521.1	DS179718-101	369	7.00E-99	191 \ 355	53	<i>Vibrio cholerae</i> V51 4-hydroxyphenylpyruvate dioxygenase protein.
142	AAF21216.1	U31553-1	369	7.00E-99	191 \ 355	53	<i>Vibrio cholerae</i> p-hydroxyphenylpyruvate dioxygenase protein.
143	ABQ19482.1	CP000627-932	369	7.00E-99	191 \ 355	53	<i>Vibrio cholerae</i> O395 4-hydroxyphenylpyruvate dioxygenase protein.
144	AAF94502.1	AE003852-1324	369	7.00E-99	191 \ 355	53	<i>Vibrio cholerae</i> O1 biovar El Tor str. N16961 4-hydroxyphenylpyruvate dioxygenase protein.
145	CAQ47715.1	AM743169-4097	356	1.00E-98	181 \ 354	51	<i>Stenotrophomonas maltophilia</i> K279a putative 4-hydroxyphenylpyruvate dioxygenase protein.
146	ABO90549.1	CP000644-2332	370	1.00E-98	190 \ 354	53	<i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i> A449 4-hydroxyphenylpyruvate dioxygenase protein.
147	ACF53438.1	CP001111-3733	356	1.00E-98	181 \ 354	51	<i>Stenotrophomonas maltophilia</i> R551-3 4-hydroxyphenylpyruvate dioxygenase protein.
148	BAB53891.1	BA000012-6535	371	4.00E-98	176 \ 355	49	<i>Mesorhizobium loti</i> MAFF303099 4-hydroxyphenylpyruvate dioxygenase protein.
149	CAK07357.1	AM236080-1869	369	6.00E-98	179 \ 352	50	<i>Rhizobium leguminosarum</i> bv. <i>viciae</i> 3841 putative 4-hydroxyphenylpyruvate dioxygenase protein.
150	ACA62760.1	EU489065-2	367	8.00E-98	179 \ 352	50	Uncultured soil bacterium 4-hydroxyphenylpyruvate dioxygenase protein.
151	ABI53729.1	DQ849081-1	367	8.00E-98	179 \ 352	50	Uncultured bacterium 4-hydroxyphenylpyruvate dioxygenase protein.
152	CAG23052.1	CR378678-279	365	3.00E-97	190 \ 356	53	<i>Photobacterium profundum</i> putative 4-hydroxyphenylpyruvate dioxygenase protein.
153	CAP49804.1	AM920689-476	371	6.00E-97	181 \ 354	51	<i>Xanthomonas campestris</i> pv. <i>campestris</i> 4-hydroxyphenylpyruvate dioxygenase protein.
154	AAY47532.1	CP000050-438	356	9.00E-97	181 \ 354	51	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. 8004 4-hydroxyphenylpyruvate dioxygenase protein.
155	AAM39754.1	AE012141-5	356	9.00E-97	181 \ 354	51	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
156	ABC90540.1	CP000133-1718	369	1.00E-96	176 \ 352	50	<i>Rhizobium etli</i> CFN 42 probable 4-hydroxyphenylpyruvate dioxygenase protein.
157	ABG64261.1	CP000390-2856	369	1.00E-96	183 \ 352	51	<i>Mesorhizobium</i> sp. BNC1 4-hydroxyphenylpyruvate dioxygenase protein.
158	ABR61666.1	CP000738-2806	370	4.00E-96	180 \ 353	50	<i>Sinorhizobium medicae</i> WSM419 4-hydroxyphenylpyruvate dioxygenase protein.
159	CAC47521.1	AL591688-2951	370	6.00E-96	179 \ 353	50	<i>Sinorhizobium meliloti</i> 1021 Putative 4-hydroxyphenylpyruvate dioxygenase protein.
160	ACI54700.1	CP001191-1397	369	2.00E-95	173 \ 352	49	<i>Rhizobium leguminosarum</i> bv. trifolii WSM2304 4-hydroxyphenylpyruvate dioxygenase protein.
161	ABF89344.1	CP000113-2717	354	4.00E-95	184 \ 362	50	<i>Myxococcus xanthus</i> DK 1622 4-hydroxyphenylpyruvate dioxygenase protein.
162	ACE90796.1	CP001074-1798	369	4.00E-95	173 \ 352	49	<i>Rhizobium etli</i> CIAT 652 probable 4-hydroxyphenylpyruvate dioxygenase protein.
163	CAJ22113.1	AM039952-482	356	1.00E-94	178 \ 354	50	<i>Xanthomonas euvesicatoria</i> 4-hydroxyphenylpyruvate dioxygenase protein.
164	ABW76439.1	EU196552-2	354	2.00E-94	182 \ 361	50	Uncultured bacterium 4-hydroxyphenylpyruvate dioxygenase protein.
165	AAM35343.1	AE011672-5	356	2.00E-94	178 \ 354	50	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306 4-hydroxyphenylpyruvate dioxygenase protein.
166	ABD56177.1	CP000264-3260	363	3.00E-94	178 \ 352	50	<i>Jannaschia</i> sp. CCS1 4-hydroxyphenylpyruvate dioxygenase protein.
167	ACD57433.1	CP000967-766	371	6.00E-94	175 \ 354	49	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A 4-hydroxyphenylpyruvate dioxygenase protein.
168	BAE70601.1	AP008229-3846	356	6.00E-94	175 \ 354	49	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> MAFF 311018 4-hydroxyphenylpyruvate dioxygenase protein.
169	AAW77325.1	AE013598-3980	403	8.00E-94	175 \ 354	49	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> KACC10331 4-hydroxyphenylpyruvate dioxygenase protein.
170	EEB70684.1	DS999054-6	366	1.00E-93	178 \ 355	50	<i>Ruegeria</i> sp. R11 4-hydroxyphenylpyruvate dioxygenase protein.
171	AAV81563.1	AE017340-719	357	1.00E-93	183 \ 361	50	<i>Idiomarina loihiensis</i> L2TR 4-hydroxyphenylpyruvate dioxygenase protein.
172	ACL96081.1	CP001340-2614	357	2.00E-93	171 \ 354	48	<i>Caulobacter crescentus</i> NA1000 4-hydroxyphenylpyruvate dioxygenase protein.
173	AAK24504.1	AE005673-2516	357	2.00E-93	171 \ 354	48	<i>Caulobacter crescentus</i> CB15 4-hydroxyphenylpyruvate dioxygenase protein.
174	EDZ48031.1	DS995281-822	366	2.00E-93	177 \ 355	49	<i>Rhodobacterales</i> bacterium Y4I 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
175	ABG31446.1	CP000362-1709	364	2.00E-93	170 \ 355	47	<i>Roseobacter denitrificans</i> OCh 114 4-hydroxyphenylpyruvate dioxygenase protein.
176	AAC45755.1	U97357-1	357	4.00E-93	182 \ 355	51	<i>Vibrio vulnificus</i> hemolysin protein.
177	AAV94713.1	CP000031-1394	366	6.00E-93	177 \ 355	49	<i>Silicibacter pomeroyi</i> DSS-3 4-hydroxyphenylpyruvate dioxygenase protein.
178	AAP47152.1	AF511570-1	353	7.00E-93	173 \ 353	49	Uncultured soil bacterium 4-hydroxyphenylpyruvate dioxygenase protein.
179	ABF63315.1	CP000377-582	366	1.00E-92	176 \ 355	49	<i>Silicibacter</i> sp. TM1040 4-hydroxyphenylpyruvate dioxygenase protein.
180	EEB84524.1	DS999213-4	364	3.00E-91	166 \ 352	47	<i>Roseobacter</i> sp. GAI101 4-hydroxyphenylpyruvate dioxygenase protein.
181	ABQ55683.1	CP000675-1683	348	3.00E-90	175 \ 349	50	<i>Legionella pneumophila</i> str. Corby 4-hydroxyphenylpyruvate dioxygenase protein.
182	AAU28343.1	AE017354-2235	361	6.00E-90	175 \ 349	50	<i>Legionella pneumophila</i> subsp. pneumophila str. Philadelphia 1 4-hydroxyphenylpyruvate dioxygenase protein.
183	CAH16444.1	CR628337-2214	348	6.00E-90	175 \ 349	50	<i>Legionella pneumophila</i> str. Lens 4-hydroxyphenylpyruvate dioxygenase legiolysin protein.
184	AAC32843.1	AF075724-3	348	6.00E-90	175 \ 349	50	<i>Legionella pneumophila</i> legiolysin protein.
185	CAH13384.1	CR628336-2236	348	1.00E-89	174 \ 349	49	<i>Legionella pneumophila</i> str. Paris 4-hydroxyphenylpyruvate dioxygenase legiolysin protein.
186	CAA04693.1	AJ001357-1	348	1.00E-89	175 \ 349	50	<i>Legionella pneumophila</i> legiolysin protein.
187	EDX79982.1	DS989898-378	373	8.00E-89	173 \ 356	48	<i>Brevundimonas</i> sp. BAL3 4-hydroxyphenylpyruvate dioxygenase protein.
188	ACM29540.1	CP000629-952	333	1.00E-88	165 \ 331	49	<i>Agrobacterium radiobacter</i> K84 4-hydroxyphenylpyruvate dioxygenase protein.
189	EBG36881.1	EP192185-1	277	3.00E-88	172 \ 280	61	Marine metagenome hypothetical protein.
190	ECF36766.1	EM640294-2	229	8.00E-88	160 \ 229	69	Marine metagenome hypothetical protein.
191	ABZ72780.1	CP000927-3642	353	7.00E-87	176 \ 357	49	<i>Caulobacter</i> sp. K31 4-hydroxyphenylpyruvate dioxygenase protein.
192	EDJ40324.1	EP835254-1	211	2.00E-85	146 \ 211	69	Marine metagenome hypothetical protein.
193	CAI87224.1	CR954246-2110	348	3.00E-83	163 \ 350	46	<i>Pseudoalteromonas haloplanktis</i> TAC125 4-hydroxyphenylpyruvate dioxygenase 4HPPD (HPD) (HPPDase) protein.
194	ACA86216.1	CP000961-1915	346	1.00E-80	159 \ 353	45	<i>Shewanella woodyi</i> ATCC 51908 4-hydroxyphenylpyruvate dioxygenase protein.
195	ABZ76968.1	CP000931-2392	346	1.00E-79	155 \ 350	44	<i>Shewanella halifaxensis</i> HAW-EB4 4-hydroxyphenylpyruvate dioxygenase protein.
196	EBF86711.1	EP224084-2	251	3.00E-79	146 \ 246	59	Marine metagenome hypothetical protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
197	EDA40061.1	EP897660-2	301	4.00E-79	148 \ 272	54	Marine metagenome hypothetical protein.
198	ABV87196.1	CP000851-1867	346	7.00E-79	155 \ 353	43	<i>Shewanella pealeana</i> ATCC 700345 4-hydroxyphenylpyruvate dioxygenase protein.
199	ABI72173.1	CP000447-2310	346	8.00E-79	154 \ 349	44	<i>Shewanella frigidimarina</i> NCIMB 400 4-hydroxyphenylpyruvate dioxygenase protein.
200	ABX49897.1	CP000891-2715	346	8.00E-79	155 \ 351	44	<i>Shewanella baltica</i> OS195 4-hydroxyphenylpyruvate dioxygenase protein.
201	ABS08789.1	CP000753-2616	346	8.00E-79	155 \ 351	44	<i>Shewanella baltica</i> OS185 4-hydroxyphenylpyruvate dioxygenase protein.
202	ABP75395.1	CP000681-1659	346	1.00E-78	154 \ 351	43	<i>Shewanella putrefaciens</i> CN-32 4-hydroxyphenylpyruvate dioxygenase protein.
203	ACK46236.1	CP001252-1692	346	1.00E-78	155 \ 351	44	<i>Shewanella baltica</i> OS223 4-hydroxyphenylpyruvate dioxygenase protein.
204	ABM25179.1	CP000503-2326	346	2.00E-78	154 \ 351	43	<i>Shewanella</i> sp. W3-18-1 4-hydroxyphenylpyruvate dioxygenase protein.
205	AAA26510.1	M59289-1	346	2.00E-78	154 \ 353	43	<i>Shewanella colwelliana</i> melA protein.
206	ABV37294.1	CP000821-2681	346	3.00E-78	155 \ 353	43	<i>Shewanella sediminis</i> HAW-EB3 4-hydroxyphenylpyruvate dioxygenase protein.
207	ABE55445.1	CP000302-2148	346	3.00E-78	154 \ 352	43	<i>Shewanella denitrificans</i> OS217 4-hydroxyphenylpyruvate dioxygenase protein.
208	ECL90326.1	EM342390-2	298	3.00E-78	147 \ 290	50	Marine metagenome hypothetical protein.
209	ABN62109.1	CP000563-2572	346	3.00E-78	154 \ 351	43	<i>Shewanella baltica</i> OS155 4-hydroxyphenylpyruvate dioxygenase protein.
210	CAE78334.1	BX842655-312	352	4.00E-78	155 \ 358	43	<i>BdelloVibrio bacteriovorus</i> 4-hydroxyphenylpyruvate dioxygenase protein.
211	ABO24021.1	CP000606-2148	346	5.00E-78	153 \ 350	43	<i>Shewanella loihica</i> PV-4 4-hydroxyphenylpyruvate dioxygenase protein.
212	ACJ29597.1	CP000472-2748	346	5.00E-78	152 \ 352	43	<i>Shewanella piezotolerans</i> WP3 4-hydroxyphenylpyruvate dioxygenase protein.
213	EDA80983.1	EP883697-1	278	4.00E-77	154 \ 280	55	Marine metagenome hypothetical protein.
214	ABL99775.1	CP000507-1563	345	4.00E-77	155 \ 352	44	<i>Shewanella amazonensis</i> SB2B 4-hydroxyphenylpyruvate dioxygenase protein.
215	ECV29884.1	EQ081469-26	353	1.00E-76	150 \ 351	42	Marine metagenome hypothetical protein.
216	AAN55013.1	AE014299-1926	346	3.00E-76	151 \ 352	42	<i>Shewanella oneidensis</i> MR-1 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
217	ECT85384.1	EM694439-1	269	6.00E-76	143 \ 252	56	Marine metagenome hypothetical protein.
218	ECV09867.1	EQ085153-98	353	8.00E-76	151 \ 352	42	Marine metagenome hypothetical protein.
219	ABK48711.1	CP000469-2466	346	9.00E-76	151 \ 352	42	<i>Shewanella</i> sp. ANA-3 4-hydroxyphenylpyruvate dioxygenase protein.
220	ABI39363.1	CP000446-2281	346	9.00E-76	151 \ 352	42	<i>Shewanella</i> sp. MR-4 4-hydroxyphenylpyruvate dioxygenase protein.
221	ABI43351.1	CP000444-2345	346	9.00E-76	151 \ 352	42	<i>Shewanella</i> sp. MR-7 4-hydroxyphenylpyruvate dioxygenase protein.
222	ECL28439.1	EM370994-1	293	5.00E-75	140 \ 289	48	Marine metagenome hypothetical protein.
223	EDA72576.1	EP886536-4	253	3.00E-74	142 \ 254	55	Marine metagenome hypothetical protein.
224	EBD97270.1	EP322668-2	266	5.00E-73	141 \ 269	52	Marine metagenome hypothetical protein.
225	EBF09645.1	EP267376-1	295	7.00E-70	135 \ 261	51	Marine metagenome hypothetical protein.
226	ABI89360.1	CP000441-586	375	1.00E-69	147 \ 352	41	<i>Burkholderia ambifaria</i> AMMD 4-hydroxyphenylpyruvate dioxygenase protein.
227	ECV11256.1	EQ085150-1422	393	5.00E-69	146 \ 352	41	Marine metagenome hypothetical protein.
228	ECG50802.1	EM586851-2	263	6.00E-69	135 \ 251	53	Marine metagenome hypothetical protein.
229	ABK11129.1	CP000459-1216	375	7.00E-69	144 \ 352	40	<i>Burkholderia cenocepacia</i> HI2424 4-hydroxyphenylpyruvate dioxygenase protein.
230	ABF78861.1	CP000379-980	375	7.00E-69	144 \ 352	40	<i>Burkholderia cenocepacia</i> AU 1054 4-hydroxyphenylpyruvate dioxygenase protein.
231	ABB11739.1	CP000152-1622	375	7.00E-69	146 \ 352	41	<i>Burkholderia</i> sp. 383 4-hydroxyphenylpyruvate dioxygenase protein.
232	EAY64893.1	CH482378-305	381	8.00E-69	144 \ 352	40	<i>Burkholderia cenocepacia</i> PC184 4-hydroxyphenylpyruvate dioxygenase protein.
233	ACB66738.1	CP001026-1161	375	1.00E-68	145 \ 352	41	<i>Burkholderia ambifaria</i> MC40-6 4-hydroxyphenylpyruvate dioxygenase protein.
234	ACA95081.1	CP000959-2740	375	2.00E-68	144 \ 352	40	<i>Burkholderia cenocepacia</i> MC0-3 4-hydroxyphenylpyruvate dioxygenase protein.
235	CAR55376.1	AM747721-1523	375	2.00E-68	144 \ 352	40	<i>Burkholderia cenocepacia</i> J2315 putative dioxygenase protein.
236	AAZ27789.1	CP000083-3376	351	3.00E-68	145 \ 357	40	<i>Colwellia psychrerythraea</i> 34H 4-hydroxyphenylpyruvate dioxygenase protein.
237	EBU41282.1	EN334861-1	270	3.00E-68	130 \ 246	52	Marine metagenome hypothetical protein.
238	ABO57878.1	CP000615-1576	375	1.00E-67	144 \ 352	40	<i>Burkholderia vietnamiensis</i> G4 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
239	ABC34571.1	CP000085-1216	381	1.00E-66	144 \ 351	41	<i>Burkholderia thailandensis</i> E264 4-hydroxyphenylpyruvate dioxygenase protein.
240	EAY70528.1	CH482381-509	415	2.00E-66	142 \ 352	40	<i>Burkholderia dolosa</i> AUO158 4-hydroxyphenylpyruvate dioxygenase protein.
241	ABX17907.1	CP000869-1066	375	3.00E-66	142 \ 350	40	<i>Burkholderia multivorans</i> ATCC 17616 4-hydroxyphenylpyruvate dioxygenase protein.
242	ACD29396.1	CP001069-520	357	5.00E-66	143 \ 348	41	<i>Ralstonia pickettii</i> 12J 4-hydroxyphenylpyruvate dioxygenase protein.
243	ABE33222.1	CP000271-254	377	3.00E-65	142 \ 356	39	<i>Burkholderia xenovorans</i> LB400 4-hydroxyphenylpyruvate dioxygenase protein.
244	AAZ64376.1	CP000091-1555	357	4.00E-65	157 \ 355	44	<i>Ralstonia eutropha</i> JMP134 4-hydroxyphenylpyruvate dioxygenase protein.
245	ACC73016.1	CP001044-747	375	1.00E-64	144 \ 359	40	<i>Burkholderia phymatum</i> STM815 4-hydroxyphenylpyruvate dioxygenase protein.
246	ACD21052.1	CP001053-2678	377	2.00E-64	141 \ 356	39	<i>Burkholderia phytofirmans</i> PsJN 4-hydroxyphenylpyruvate dioxygenase protein.
247	BAG46137.1	AP009386-1083	351	5.00E-64	138 \ 342	40	<i>Burkholderia multivorans</i> ATCC 17616 4-hydroxyphenylpyruvate dioxygenase protein.
248	ABW22850.1	EU165546-8	377	6.00E-64	140 \ 356	39	<i>Burkholderia</i> sp. NCIMB 10467 4-hydroxyphenylpyruvate dioxygenase protein.
249	EBZ10531.1	EM962029-2	169	5.00E-62	115 \ 164	70	Marine metagenome hypothetical protein.
250	CAD18498.1	AL646053-1348	361	4.00E-61	139 \ 349	39	<i>Ralstonia solanacearum</i> GMI1000 probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein.
251	CAD18467.1	AL646053-1317	361	4.00E-61	139 \ 349	39	<i>Ralstonia solanacearum</i> GMI1000 probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein.
252	CAQ18125.1	CU694393-146	322	6.00E-61	132 \ 336	39	<i>Ralstonia solanacearum</i> 4-hydroxyphenylpyruvate dioxygenase protein.
253	ECP31079.1	EM186947-2	205	2.00E-59	117 \ 203	57	Marine metagenome hypothetical protein.
254	EBM82315.1	EN832079-1	393	7.00E-59	142 \ 359	39	Marine metagenome hypothetical protein.
255	EBL94723.1	EN875974-3	253	4.00E-57	112 \ 238	47	Marine metagenome hypothetical protein.
256	ECB70543.1	EM843631-2	243	1.00E-56	107 \ 195	54	Marine metagenome hypothetical protein.
257	ECS18179.1	EM029396-2	146	5.00E-55	107 \ 145	73	Marine metagenome hypothetical protein.
258	EBK12314.1	EN966601-1	155	5.00E-54	100 \ 155	64	Marine metagenome hypothetical protein.
259	EBZ10533.1	EM962029-3	163	5.00E-50	95 \ 149	63	Marine metagenome hypothetical protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
260	ECI27444.1	EM506498-1	265	1.00E-49	101 \ 260	38	Marine metagenome hypothetical protein.
261	ECA33540.1	EM904759-1	190	3.00E-49	99 \ 186	53	Marine metagenome hypothetical protein.
262	ECC16417.1	EM821664-1	206	2.00E-48	96 \ 207	46	Marine metagenome hypothetical protein.
263	ECC40935.1	EM811068-1	146	3.00E-48	101 \ 146	69	Marine metagenome hypothetical protein.
264	ABP77907.1	CP000304-199	641	7.00E-48	120 \ 345	34	<i>Pseudomonas stutzeri</i> A1501 4-hydroxyphenylpyruvate dioxygenase protein.
265	EBT60672.1	EN400035-1	288	1.00E-47	109 \ 274	39	Marine metagenome hypothetical protein.
266	EBG32671.1	EP195127-1	284	7.00E-47	106 \ 259	40	Marine metagenome hypothetical protein.
267	ACL55169.1	CP001349-117	627	9.00E-47	115 \ 329	34	<i>Methylobacterium nodulans</i> ORS 2060 Xylose isomerase domain protein TIM barrel protein.
268	ECR36957.1	EM066443-1	273	3.00E-46	109 \ 271	40	Marine metagenome hypothetical protein.
269	EDA70829.1	EP887109-1	221	2.00E-45	93 \ 181	51	Marine metagenome hypothetical protein.
270	ACA19085.1	CP000943-4497	637	2.00E-45	119 \ 329	36	<i>Methylobacterium</i> sp. 4-46 4-hydroxyphenylpyruvate dioxygenase protein.
271	EBU47469.1	EN328922-2	131	3.00E-45	89 \ 122	72	Marine metagenome hypothetical protein.
272	ABC42332.1	DQ311664-1	636	5.00E-45	123 \ 341	36	<i>Pseudomonas chlororaphis</i> 4-hydroxyphenylpyruvate dioxygenase protein.
273	EDE21720.1	EP718946-4	328	1.00E-44	122 \ 337	36	Marine metagenome hypothetical protein.
274	ECS48530.1	EM016804-1	157	2.00E-44	94 \ 157	59	Marine metagenome hypothetical protein.
275	AAY94595.1	CP000076-5302	636	4.00E-44	119 \ 340	35	<i>Pseudomonas fluorescens</i> Pf-5 4-hydroxyphenylpyruvate dioxygenase, putative protein.
276	EDB37406.1	EP863751-1	572	4.00E-44	117 \ 332	35	Marine metagenome hypothetical protein.
277	ACD29401.1	CP001069-525	628	5.00E-44	122 \ 348	35	<i>Ralstonia pickettii</i> 12J 4-hydroxyphenylpyruvate dioxygenase protein.
278	EBG19045.1	EP204722-1	120	1.00E-43	85 \ 120	70	Marine metagenome hypothetical protein.
279	EBG53799.1	EP180382-2	211	2.00E-43	94 \ 207	45	Marine metagenome hypothetical protein.
280	EAZ54963.1	CH482383-3355	634	3.00E-43	121 \ 345	35	<i>Pseudomonas aeruginosa</i> C3719 hypothetical protein.
281	EBG29950.1	EP197036-2	263	3.00E-43	97 \ 206	47	Marine metagenome hypothetical protein.
282	ABA76642.1	CP000094-4900	633	1.00E-42	120 \ 352	34	<i>Pseudomonas fluorescens</i> Pf0-1 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
283	ECF85937.1	EM617389-3	318	1.00E-42	119 \ 325	36	Marine metagenome hypothetical protein.
284	ABJ15191.1	CP000438-238	634	1.00E-42	122 \ 345	35	<i>Pseudomonas aeruginosa</i> UCBPP-PA14 putative 4-hydroxyphenylpyruvate dioxygenase protein.
285	CAW24966.1	FM209186-239	634	3.00E-42	122 \ 345	35	<i>Pseudomonas aeruginosa</i> LESB58 putative 4-hydroxyphenylpyruvate dioxygenase protein.
286	AAG03631.1	AE004091-243	634	3.00E-42	122 \ 345	35	<i>Pseudomonas aeruginosa</i> PAO1 hypothetical protein.
287	EAZ60782.1	CH482384-3953	634	4.00E-42	122 \ 345	35	<i>Pseudomonas aeruginosa</i> 2192 hypothetical protein.
288	ECX86630.1	EP997128-1	498	1.00E-41	114 \ 332	34	Marine metagenome hypothetical protein.
289	ABS20594.1	CP000764-218	372	1.00E-41	128 \ 347	36	<i>Bacillus cereus</i> subsp. <i>cytotoxis</i> NVH 391-98 4-hydroxyphenylpyruvate dioxygenase protein.
290	ACA72725.1	CP000949-2219	635	6.00E-41	108 \ 328	32	<i>Pseudomonas putida</i> W619 4-hydroxyphenylpyruvate dioxygenase protein.
291	EBO05124.1	EN774514-1	113	1.00E-40	76 \ 109	69	Marine metagenome hypothetical protein.
292	ACM52301.1	CP001364-855	365	1.00E-40	125 \ 367	34	<i>Chloroflexus</i> sp. Y-400-fl 4-hydroxyphenylpyruvate dioxygenase protein.
293	ABY34044.1	CP000909-786	365	1.00E-40	125 \ 367	34	<i>Chloroflexus aurantiacus</i> J-10-fl 4-hydroxyphenylpyruvate dioxygenase protein.
294	CAK14847.1	CT573326-1850	634	2.00E-40	114 \ 343	33	<i>Pseudomonas entomophila</i> L48 putative 4-hydroxyphenylpyruvate dioxygenase protein.
295	EBN11607.1	EN818507-1	386	2.00E-40	115 \ 329	34	Marine metagenome hypothetical protein.
296	ECV18614.1	EQ083594-2	380	2.00E-40	127 \ 375	33	Marine metagenome hypothetical protein.
297	EDG17800.1	EP645468-2	322	2.00E-40	118 \ 328	35	Marine metagenome hypothetical protein.
298	ACK91608.1	CP001283-228	372	3.00E-40	126 \ 348	36	<i>Bacillus cereus</i> AH820 4-hydroxyphenylpyruvate dioxygenase protein.
299	ACJ77205.1	CP001177-221	372	3.00E-40	126 \ 348	36	<i>Bacillus cereus</i> AH187 4-hydroxyphenylpyruvate dioxygenase protein.
300	ACM10759.1	CP000227-230	372	3.00E-40	126 \ 348	36	<i>Bacillus cereus</i> Q1 4-hydroxyphenylpyruvate dioxygenase protein.
301	AAU20018.1	CP000001-211	372	3.00E-40	126 \ 348	36	<i>Bacillus cereus</i> E33L 4-hydroxyphenylpyruvate dioxygenase protein.
302	AAT61344.1	AE017355-208	372	3.00E-40	126 \ 348	36	<i>Bacillus thuringiensis</i> serovar konkukian str. 97-27 4-hydroxyphenylpyruvate dioxygenase protein.
303	AAT29321.1	AE017334-222	372	3.00E-40	126 \ 348	36	<i>Bacillus anthracis</i> str. Ames Ancestor' 4-hydroxyphenylpyruvate dioxygenase protein.
304	AAT52562.1	AE017225-220	372	3.00E-40	126 \ 348	36	<i>Bacillus anthracis</i> str. Sterne 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
305	AAS39196.1	AE017194-260	372	3.00E-40	126 \ 348	36	<i>Bacillus cereus</i> ATCC 10987 4-hydroxyphenylpyruvate dioxygenase protein.
306	AAP24280.1	AE016879-222	372	3.00E-40	126 \ 348	36	<i>Bacillus anthracis</i> str. Ames 4-hydroxyphenylpyruvate dioxygenase protein.
307	ECY55382.1	EP972053-6	398	3.00E-40	121 \ 344	35	Marine metagenome hypothetical protein.
308	ABR84446.1	CP000744-327	634	3.00E-40	119 \ 345	34	<i>Pseudomonas aeruginosa</i> PA7 hypothetical protein.
309	ACC70270.1	CP001043-1073	628	3.00E-40	106 \ 334	31	<i>Burkholderia phymatum</i> STM815 4-hydroxyphenylpyruvate dioxygenase protein.
310	ABK83632.1	CP000485-210	389	3.00E-40	126 \ 348	36	<i>Bacillus thuringiensis</i> str. Al Hakam 4-hydroxyphenylpyruvate dioxygenase protein.
311	EDC86364.1	EP771255-1	380	4.00E-40	126 \ 375	33	Marine metagenome hypothetical protein.
312	EAQ42921.1	CH902588-1825	386	5.00E-40	120 \ 331	36	<i>Polaribacter</i> sp. MED152 4-hydroxyphenylpyruvate dioxygenase protein.
313	ABC93421.1	CP000136-215	629	5.00E-40	113 \ 329	34	<i>Rhizobium etli</i> CFN 42 putative 4-hydroxyphenylpyruvate dioxygenase protein.
314	EDA87252.1	EP881731-4	417	6.00E-40	111 \ 338	32	Marine metagenome hypothetical protein.
315	EDF67561.1	EP663852-1	315	7.00E-40	119 \ 327	36	Marine metagenome hypothetical protein.
316	EDC51166.1	EP784110-1	378	7.00E-40	119 \ 344	34	Marine metagenome hypothetical protein.
317	EBG20097.1	EP203962-1	222	7.00E-40	93 \ 205	45	Marine metagenome hypothetical protein.
318	EBT54351.1	EN405047-1	152	9.00E-40	82 \ 153	53	Marine metagenome hypothetical protein.
319	EAY71109.1	CH482381-1090	658	1.00E-39	111 \ 328	33	<i>Burkholderia dolosa</i> AUO158 4-hydroxyphenylpyruvate dioxygenase protein.
320	ECV73688.1	EQ070211-3	386	1.00E-39	125 \ 358	34	Marine metagenome hypothetical protein.
321	ACK62105.1	CP001176-212	372	1.00E-39	125 \ 348	35	<i>Bacillus cereus</i> B4264 4-hydroxyphenylpyruvate dioxygenase protein.
322	AAP07321.1	AE016877-211	372	1.00E-39	125 \ 348	35	<i>Bacillus cereus</i> ATCC 14579 4-hydroxyphenylpyruvate dioxygenase protein.
323	EDI64406.1	EP548370-2	386	2.00E-39	119 \ 330	36	Marine metagenome hypothetical protein.
324	EDJ19476.1	EP842656-2	423	2.00E-39	116 \ 325	35	Marine metagenome hypothetical protein.
325	ACB67639.1	CP001026-2062	630	2.00E-39	111 \ 331	33	<i>Burkholderia ambifaria</i> MC40-6 4-hydroxyphenylpyruvate dioxygenase protein.
326	ACK95428.1	CP001186-211	372	2.00E-39	125 \ 348	35	<i>Bacillus cereus</i> G9842 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
327	EBO57524.1	EN745911-2	327	3.00E-39	116 \ 325	35	Marine metagenome hypothetical protein.
328	ABC46078.1	CP000159-1336	384	3.00E-39	119 \ 343	34	<i>Salinibacter ruber</i> DSM 13855 4-hydroxyphenylpyruvate dioxygenase protein.
329	EDG75161.1	EP622856-1	342	5.00E-39	114 \ 325	35	Marine metagenome hypothetical protein.
330	EEB86421.1	DS999213-2069	628	5.00E-39	107 \ 330	32	<i>Roseobacter</i> sp. GAI101 4-hydroxyphenylpyruvate dioxygenase protein.
331	ABX17102.1	CP000869-261	630	6.00E-39	107 \ 326	32	<i>Burkholderia multivorans</i> ATCC 17616 4-hydroxyphenylpyruvate dioxygenase protein.
332	BAG46949.1	AP009386-1907	630	6.00E-39	107 \ 326	32	<i>Burkholderia multivorans</i> ATCC 17616 4-hydroxyphenylpyruvate dioxygenase protein.
333	ABQ03764.1	CP000685-726	386	6.00E-39	119 \ 336	35	<i>Flavobacterium johnsoniae</i> UW101 4-hydroxyphenylpyruvate dioxygenase protein.
334	AAZ64383.1	CP000091-1562	632	6.00E-39	110 \ 327	33	<i>Ralstonia eutropha</i> JMP134 4-hydroxyphenylpyruvate dioxygenase protein.
335	ABI90216.1	CP000441-1442	630	7.00E-39	110 \ 328	33	<i>Burkholderia ambifaria</i> AMMD 4-hydroxyphenylpyruvate dioxygenase protein.
336	ABY99254.1	CP000926-3338	635	7.00E-39	109 \ 338	32	<i>Pseudomonas putida</i> GB-1 4-hydroxyphenylpyruvate dioxygenase protein.
337	EDB27371.1	EP867538-1	348	9.00E-39	114 \ 329	34	Marine metagenome hypothetical protein.
338	ABB10459.1	CP000152-342	630	1.00E-38	107 \ 329	32	<i>Burkholderia</i> sp. 383 4-hydroxyphenylpyruvate dioxygenase protein.
339	AAO55858.1	AE016853-2303	635	1.00E-38	105 \ 329	31	<i>Pseudomonas syringae</i> pv. tomato str. DC3000 4-hydroxyphenylpyruvate dioxygenase, putative protein.
340	ACL25607.1	CP001337-2654	365	1.00E-38	122 \ 367	33	<i>Chloroflexus aggregans</i> DSM 9485 4-hydroxyphenylpyruvate dioxygenase protein.
341	EBF32952.1	EP254156-2	137	1.00E-38	80 \ 135	59	Marine metagenome hypothetical protein.
342	EEE38379.1	DS999531-1348	629	2.00E-38	109 \ 330	33	<i>Rhodobacteraceae bacterium</i> KLH11 4-hydroxyphenylpyruvate dioxygenase protein.
343	ABQ79289.1	CP000712-3112	635	2.00E-38	110 \ 339	32	<i>Pseudomonas putida</i> F1 4-hydroxyphenylpyruvate dioxygenase protein.
344	AAN68163.1	AE015451-2529	635	2.00E-38	110 \ 339	32	<i>Pseudomonas putida</i> KT2440 4-hydroxyphenylpyruvate dioxygenase, putative protein.
345	ECV29457.1	EQ081474-15	661	2.00E-38	109 \ 331	32	Marine metagenome hypothetical protein.
346	ECV75010.1	EQ069695-2	372	2.00E-38	121 \ 344	35	Marine metagenome hypothetical protein.
347	AAY37173.1	CP000075-2129	635	2.00E-38	105 \ 329	31	<i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
348	ABX05402.1	CP000875-2750	373	2.00E-38	124 \ 371	33	<i>Herpetosiphon aurantiacus</i> ATCC 23779 4-hydroxyphenylpyruvate dioxygenase protein.
349	ABJ85131.1	CP000473-4115	375	2.00E-38	119 \ 356	33	<i>Solibacter usitatus</i> Ellin6076 4-hydroxyphenylpyruvate dioxygenase protein.
350	ABI53728.2	DQ849080-1	375	2.00E-38	122 \ 375	32	uncultured bacterium 4-hydroxyphenylpyruvate dioxygenase protein.
351	CAR56368.1	AM747721-2515	630	3.00E-38	110 \ 328	33	<i>Burkholderia cenocepacia</i> J2315 putative amino acid dioxygenase protein.
352	CAK08336.1	AM236080-2848	630	3.00E-38	113 \ 334	33	<i>Rhizobium leguminosarum</i> bv. <i>viciae</i> 3841 putative glyoxalase/dioxygenase protein.
353	EDY54529.1	DS570906-241	381	4.00E-38	110 \ 297	37	<i>Streptomyces sviveus</i> ATCC 29083 4-hydroxyphenylpyruvate dioxygenase protein.
354	ABY41487.1	CP000903-218	372	4.00E-38	123 \ 347	35	<i>Bacillus weihenstephanensis</i> KBAB4 4-hydroxyphenylpyruvate dioxygenase protein.
355	ABO56540.1	CP000615-238	630	4.00E-38	109 \ 328	33	<i>Burkholderia vietnamiensis</i> G4 4-hydroxyphenylpyruvate dioxygenase protein.
356	ECU54802.1	EM170165-3	314	4.00E-38	97 \ 316	30	Marine metagenome hypothetical protein.
357	AAZ36848.1	CP000058-2012	635	5.00E-38	104 \ 329	31	<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A 4-hydroxyphenylpyruvate dioxygenase, putative protein.
358	EBT43156.1	EN413945-1	208	5.00E-38	85 \ 202	42	Marine metagenome hypothetical protein.
359	ABK12038.1	CP000459-2125	630	5.00E-38	110 \ 328	33	<i>Burkholderia cenocepacia</i> HI2424 4-hydroxyphenylpyruvate dioxygenase protein.
360	ABF77958.1	CP000379-77	630	5.00E-38	110 \ 328	33	<i>Burkholderia cenocepacia</i> AU 1054 4-hydroxyphenylpyruvate dioxygenase protein.
361	ACA94093.1	CP000959-1752	630	6.00E-38	110 \ 328	33	<i>Burkholderia cenocepacia</i> MC0-3 4-hydroxyphenylpyruvate dioxygenase protein.
362	CAL68114.1	CU207366-3123	380	6.00E-38	116 \ 341	34	<i>Gramella forsetii</i> KT0803 4-hydroxyphenylpyruvate dioxygenase protein.
363	ABE57655.1	CP000285-290	615	7.00E-38	104 \ 323	32	<i>Chromohalobacter salexigens</i> DSM 3043 4-hydroxyphenylpyruvate dioxygenase protein.
364	CAK03016.1	AM236085-74	631	8.00E-38	114 \ 340	33	<i>Rhizobium leguminosarum</i> bv. <i>viciae</i> 3841 putative dioxygenase protein.
365	EBL05809.1	EN920846-1	377	1.00E-37	109 \ 303	35	Marine metagenome hypothetical protein.
366	ABW00434.1	CP000850-4497	401	2.00E-37	124 \ 386	32	<i>Salinispora arenicola</i> CNS-205 4-hydroxyphenylpyruvate dioxygenase protein.
367	ABR72810.1	CP000749-3867	617	2.00E-37	108 \ 326	33	<i>Marinomonas</i> sp. MWYL1 Xylose isomerase domain protein TIM barrel protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
368	EDO86499.1	CH899733-13	684	2.00E-37	108 \ 329	32	<i>Burkholderia pseudomallei</i> 406e AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase protein.
369	ABQ38040.1	CP000494-5735	623	2.00E-37	104 \ 324	32	<i>Bradyrhizobium</i> sp. BTAi1 4-hydroxyphenylpyruvate dioxygenase protein.
370	EDS84917.1	CH899767-342	684	3.00E-37	108 \ 329	32	<i>Burkholderia pseudomallei</i> S13 AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase protein.
371	ABN94825.1	CP000573-481	684	3.00E-37	108 \ 329	32	<i>Burkholderia pseudomallei</i> 1106a AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase protein.
372	CAH37787.1	BX571966-344	684	3.00E-37	108 \ 329	32	<i>Burkholderia pseudomallei</i> K96243 putative amino acid dioxygenase protein.
373	EDU10248.1	CH899717-11	684	3.00E-37	108 \ 329	32	<i>Burkholderia pseudomallei</i> 1655 AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase protein.
374	ABN85976.1	CP000571-576	687	3.00E-37	108 \ 329	32	<i>Burkholderia pseudomallei</i> 668 4-hydroxyphenylpyruvate dioxygenase protein.
375	EDK86092.1	CH899695-12	684	3.00E-37	108 \ 329	32	<i>Burkholderia mallei</i> 2002721280 AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase protein.
376	EDK57546.1	DS264112-270	684	3.00E-37	108 \ 329	32	<i>Burkholderia mallei</i> JHU AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase protein.
377	EDK51874.1	DS264103-18	684	3.00E-37	108 \ 329	32	<i>Burkholderia mallei</i> FMH AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase protein.
378	ABO02512.1	CP000547-882	684	3.00E-37	108 \ 329	32	<i>Burkholderia mallei</i> NCTC 10247 AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase protein.
379	ABM99485.1	CP000545-2165	684	3.00E-37	108 \ 329	32	<i>Burkholderia mallei</i> NCTC 10229 putative 4-hydroxyphenylpyruvate dioxygenase protein.
380	ABM48672.1	CP000525-1722	684	3.00E-37	108 \ 329	32	<i>Burkholderia mallei</i> SAVP1 putative 4-hydroxyphenylpyruvate dioxygenase protein.
381	AAU47111.1	CP000011-808	684	3.00E-37	108 \ 329	32	<i>Burkholderia mallei</i> ATCC 23344 putative 4-hydroxyphenylpyruvate dioxygenase protein.
382	EDP84482.1	DS544751-79	684	3.00E-37	108 \ 329	32	<i>Burkholderia mallei</i> ATCC 10399 AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase protein.
383	EDI55974.1	EP551342-2	312	3.00E-37	116 \ 324	35	Marine metagenome hypothetical protein.
384	EBP87853.1	EN670074-2	273	3.00E-37	95 \ 228	41	Marine metagenome hypothetical protein.
385	CAD35423.1	AX417724-1	381	4.00E-37	109 \ 297	36	Synthetic construct protein Sequence 15 from Patent WO0231173.
386	CAC34022.1	AX085149-1	381	4.00E-37	109 \ 297	36	Synthetic construct protein Sequence 14 from Patent WO0112827.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
387	BAC72861.1	BA000030-5156	381	4.00E-37	109 \ 297	36	<i>Streptomyces avermitilis</i> MA-4680 4-hydroxyphenylpyruvate dioxygenase protein.
388	BAB69150.1	AB070935-2	381	4.00E-37	109 \ 297	36	<i>Streptomyces avermitilis</i> 4-hydroxyphenylpyruvate dioxygenase protein.
389	EDO92693.1	CH899748-11	684	4.00E-37	108 \ 329	32	<i>Burkholderia pseudomallei</i> Pasteur 52237 AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase protein.
390	ABA51974.1	CP000125-1892	684	4.00E-37	108 \ 329	32	<i>Burkholderia pseudomallei</i> 1710b putative amino acid dioxygenase protein.
391	EDE30458.1	EP715656-1	239	5.00E-37	101 \ 246	41	Marine metagenome hypothetical protein.
392	AAA50231.1	U11864-1	380	5.00E-37	109 \ 297	36	<i>Streptomyces avermitilis</i> 4-hydroxyphenylpyruvate acid dioxygenase protein.
393	CAL79264.1	CU234118-5291	623	6.00E-37	104 \ 327	31	<i>Bradyrhizobium</i> sp. ORS278 putative 4-hydroxyphenylpyruvate dioxygenase containing a TIM-barrel fold N-ter protein.
394	EBU88201.1	EN263343-1	281	6.00E-37	108 \ 290	37	Marine metagenome hypothetical protein.
395	ECT78614.1	EM697376-4	212	7.00E-37	92 \ 215	42	Marine metagenome hypothetical protein.
396	ECY37026.1	EP979861-1	315	8.00E-37	104 \ 322	32	Marine metagenome hypothetical protein.
397	ECU86201.1	EQ086505-20	363	9.00E-37	117 \ 369	31	Marine metagenome hypothetical protein.
398	CAL42342.1	AM398681-223	386	9.00E-37	118 \ 345	34	<i>Flavobacterium psychrophilum</i> JIP02/86 4-hydroxyphenylpyruvate dioxygenase protein.
399	EDY46394.1	DS570576-8	401	1.00E-36	112 \ 329	34	<i>Streptomyces</i> sp. SPB74 4-hydroxyphenylpyruvate dioxygenase protein.
400	EBE87724.1	EP277951-1	284	1.00E-36	110 \ 296	37	Marine metagenome hypothetical protein.
401	EDX25603.1	DS570429-38	380	1.00E-36	105 \ 294	35	<i>Streptomyces</i> sp. Mg1 4-hydroxyphenylpyruvate dioxygenase protein.
402	AAT43954.1	AE017261-1369	368	2.00E-36	116 \ 359	32	<i>Picrophilus torridus</i> DSM 9790 4-hydroxyphenylpyruvate dioxygenase protein.
403	EBI58388.1	EP069871-1	304	2.00E-36	109 \ 298	36	Marine metagenome hypothetical protein.
404	ABF41005.1	CP000360-2000	361	3.00E-36	116 \ 372	31	<i>Acidobacteria bacterium</i> Ellin345 4-hydroxyphenylpyruvate dioxygenase protein.
405	BAF87452.1	AP009384-1454	639	3.00E-36	114 \ 348	32	<i>Azorhizobium caulinodans</i> ORS 571 putative 4-hydroxyphenylpyruvate dioxygenase protein.
406	CAM60987.1	CU458896-884	401	3.00E-36	118 \ 360	32	<i>Mycobacterium abscessus</i> Putative 4-hydroxyphenylpyruvate dioxygenase protein.
407	ABP56678.1	CP000667-4193	401	5.00E-36	120 \ 386	31	<i>Salinispora tropica</i> CNB-440 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
408	ABS17128.1	CP000759-1665	633	9.00E-36	111 \ 328	33	<i>Ochrobactrum anthropi</i> ATCC 49188 4-hydroxyphenylpyruvate dioxygenase protein.
409	ABG94973.1	CP000431-3137	404	9.00E-36	124 \ 383	32	<i>Rhodococcus jostii</i> RHA1 4-hydroxyphenylpyruvate dioxygenase protein.
410	EBC56881.1	EP408385-2	247	1.00E-35	94 \ 228	41	Marine metagenome hypothetical protein.
411	ABZ76973.1	CP000931-2397	173	2.00E-35	80 \ 174	45	<i>Shewanella halifaxensis</i> HAW-EB4 4-hydroxyphenylpyruvate dioxygenase protein.
412	EDJ59529.1	EP828549-1	619	2.00E-35	102 \ 336	30	Marine metagenome hypothetical protein.
413	CAB51008.1	AL939114-146	381	2.00E-35	105 \ 294	35	<i>Streptomyces coelicolor</i> putative 4-hydroxyphenylpyruvate dioxygenase protein.
414	ABC36215.1	CP000085-2045	687	3.00E-35	106 \ 329	32	<i>Burkholderia thailandensis</i> E264 4-hydroxyphenylpyruvate dioxygenase, putative protein.
415	BAC46318.1	BA000040-1053	623	4.00E-35	104 \ 327	31	<i>Bradyrhizobium japonicum</i> USDA 110 bll1053 protein.
416	ABX04531.1	CP000875-1879	366	4.00E-35	110 \ 328	33	<i>Herpetosiphon aurantiacus</i> ATCC 23779 4-hydroxyphenylpyruvate dioxygenase protein.
417	BAG21441.1	AP009493-4612	381	5.00E-35	105 \ 297	35	<i>Streptomyces griseus</i> subsp. <i>griseus</i> NBRC 13350 putative 4-hydroxyphenylpyruvate dioxygenase protein.
418	CAM00239.1	AM420293-884	401	1.00E-34	113 \ 360	31	<i>Saccharopolyspora erythraea</i> NRRL 2338 4-hydroxyphenylpyruvate dioxygenase protein.
419	EBW54263.1	EN129526-1	228	1.00E-34	90 \ 210	42	Marine metagenome hypothetical protein.
420	ECY26509.1	EP983322-4	498	2.00E-34	104 \ 328	31	Marine metagenome hypothetical protein.
421	EBP17169.1	EN712222-1	168	2.00E-34	80 \ 174	45	Marine metagenome hypothetical protein.
422	EDH88356.1	EP579131-1	550	2.00E-34	107 \ 348	30	Marine metagenome hypothetical protein.
423	ECZ11395.1	EP949625-4	373	3.00E-34	116 \ 370	31	Marine metagenome hypothetical protein.
424	EBP88309.1	EN669833-3	358	3.00E-34	105 \ 332	31	Marine metagenome hypothetical protein.
425	EDB46797.1	EP860423-1	631	3.00E-34	106 \ 343	30	Marine metagenome hypothetical protein.
426	EBI88118.1	EP051537-1	228	3.00E-34	92 \ 224	41	Marine metagenome hypothetical protein.
427	ACM29992.1	CP000629-1404	629	5.00E-34	114 \ 332	34	<i>Agrobacterium radiobacter</i> K84 4-hydroxyphenylpyruvate dioxygenase protein.
428	ECU49612.1	EM172525-3	200	5.00E-34	89 \ 205	43	Marine metagenome hypothetical protein.
429	EDA07090.1	EP910358-1	328	5.00E-34	110 \ 327	33	Marine metagenome hypothetical protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
430	ACD18940.1	CP001053-565	627	1.00E-33	107 \ 341	31	<i>Burkholderia phytofirmans</i> PsJN Xylose isomerase domain protein TIM barrel protein.
431	ECN30387.1	EM279690-2	310	2.00E-33	98 \ 317	30	Marine metagenome hypothetical protein.
432	ACB35945.1	CP001013-3669	295	2.00E-33	91 \ 259	35	<i>Leptothrix cholodnii</i> SP-6 4-hydroxyphenylpyruvate dioxygenase protein.
433	CAD18551.1	AL646053-1401	626	2.00E-33	114 \ 342	33	<i>Ralstonia solanacearum</i> GMI1000 probable 4-hydroxyphenylpyruvate dioxygenase-related protein.
434	ABG93847.1	CP000431-2011	402	3.00E-33	117 \ 337	34	<i>Rhodococcus jostii</i> RHA1 4-hydroxyphenylpyruvate dioxygenase protein.
435	ECO15483.1	EM241014-2	217	3.00E-33	88 \ 211	41	Marine metagenome hypothetical protein.
436	EBP17838.1	EN711845-1	244	5.00E-33	90 \ 224	40	Marine metagenome hypothetical protein.
437	ACI59122.1	CP001193-333	631	5.00E-33	109 \ 332	32	<i>Rhizobium leguminosarum</i> bv. trifolii WSM2304 4-hydroxyphenylpyruvate dioxygenase protein.
438	ABG62182.1	CP000390-777	630	6.00E-33	105 \ 332	31	<i>Mesorhizobium</i> sp. BNC1 4-hydroxyphenylpyruvate dioxygenase protein.
439	ABG96855.1	CP000431-5019	401	8.00E-33	113 \ 364	31	<i>Rhodococcus jostii</i> RHA1 4-hydroxyphenylpyruvate dioxygenase protein.
440	ABR77558.1	CP000647-2097	617	9.00E-33	111 \ 334	33	<i>Klebsiella pneumoniae</i> subsp. pneumoniae MGH 78578 putative 4-hydroxyphenylpyruvate dioxygenase protein.
441	ABG94844.1	CP000431-3008	401	9.00E-33	113 \ 364	31	<i>Rhodococcus jostii</i> RHA1 4-hydroxyphenylpyruvate dioxygenase protein.
442	EBM48072.1	EN848684-1	257	9.00E-33	89 \ 215	41	Marine metagenome hypothetical protein.
443	ABL80809.1	CP000509-1259	397	9.00E-33	106 \ 333	31	<i>Nocardioides</i> sp. JS614 4-hydroxyphenylpyruvate dioxygenase protein.
444	EDY49311.1	DS570639-36	381	1.00E-32	110 \ 297	37	<i>Streptomyces clavuligerus</i> ATCC 27064 4-hydroxyphenylpyruvate dioxygenase protein.
445	ACB50661.1	CP000806-1309	386	1.00E-32	106 \ 317	33	<i>Cyanothece</i> sp. ATCC 51142 4-hydroxyphenylpyruvate dioxygenase protein.
446	ACK70239.1	CP001291-1765	363	1.00E-32	107 \ 317	33	<i>Cyanothece</i> sp. PCC 7424 4-hydroxyphenylpyruvate dioxygenase protein.
447	CAQ59119.1	CU914166-434	626	2.00E-32	111 \ 335	33	<i>Ralstonia solanacearum</i> 4-hydroxyphenylpyruvate dioxygenase- related protein.
448	ABW29525.1	CP000828-4438	355	2.00E-32	110 \ 360	30	<i>Acaryochloris marina</i> MBIC11017 4-hydroxyphenylpyruvate dioxygenase protein.
449	CAQ37197.1	CU695240-822	626	2.00E-32	110 \ 330	33	<i>Ralstonia solanacearum</i> 4-hydroxyphenylpyruvate dioxygenase- related protein.
450	ABE35072.1	CP000271-2104	627	2.00E-32	105 \ 338	31	<i>Burkholderia xenovorans</i> LB400 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
451	CAK90831.1	CT868660-317	390	2.00E-32	107 \ 341	31	<i>Paramecium tetraurelia</i> protein <i>Paramecium tetraurelia</i> chromosome undetermined scaffold_8, whole genome shotgun sequence.
452	CAH03340.1	CR548612-143	390	2.00E-32	107 \ 341	31	<i>Paramecium tetraurelia</i> 4-hydroxyphenylpyruvate dioxygenase, putative protein.
453	CAK55954.1	CT867985-389	390	2.00E-32	107 \ 341	31	<i>Paramecium tetraurelia</i> protein <i>Paramecium tetraurelia</i> chromosome undetermined scaffold_1, whole genome shotgun sequence.
454	ABG53187.1	CP000393-3657	353	2.00E-32	110 \ 347	31	<i>Trichodesmium erythraeum</i> IMS101 4-hydroxyphenylpyruvate dioxygenase protein.
455	EDA44121.1	EP896268-1	374	2.00E-32	103 \ 320	32	Marine metagenome hypothetical protein.
456	ECM26259.1	EM326809-1	219	4.00E-32	83 \ 214	38	Marine metagenome hypothetical protein.
457	ACI11288.1	CP000964-2144	617	4.00E-32	113 \ 336	33	<i>Klebsiella pneumoniae</i> 342 AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase protein.
458	ECZ26339.1	EP943095-1	278	5.00E-32	100 \ 291	34	Marine metagenome hypothetical protein.
459	EAW11340.1	DS027052-223	401	5.00E-32	122 \ 367	33	<i>Aspergillus clavatus</i> NRRL 1 4-hydroxyphenylpyruvate dioxygenase, putative protein.
460	ACM38572.1	CP000634-370	615	6.00E-32	106 \ 338	31	<i>Agrobacterium vitis</i> S4 4-hydroxyphenylpyruvate dioxygenase protein.
461	EED23108.1	EQ962652-635	415	7.00E-32	123 \ 380	32	<i>Talaromyces stipitatus</i> ATCC 10500 4-hydroxyphenylpyruvate dioxygenase, putative protein.
462	ECD29267.1	EM771148-1	188	7.00E-32	76 \ 181	41	Marine metagenome hypothetical protein.
463	ABD26026.1	CP000248-1577	621	9.00E-32	100 \ 332	30	<i>Novosphingobium aromaticivorans</i> DSM 12444 4-hydroxyphenylpyruvate dioxygenase protein.
464	ABA24263.1	CP000117-4637	344	9.00E-32	106 \ 336	31	<i>Anabaena variabilis</i> ATCC 29413 4-hydroxyphenylpyruvate dioxygenase protein.
465	ECZ42331.1	EP936364-2	283	1.00E-31	100 \ 292	34	Marine metagenome hypothetical protein.
466	BAE57420.1	AP007155-180	398	2.00E-31	119 \ 366	32	<i>Aspergillus oryzae</i> protein <i>Aspergillus oryzae</i> RIB40 genomic DNA, SC003.
467	ACL47512.1	CP001344-4919	358	3.00E-31	119 \ 342	34	<i>Cyanotheca</i> sp. PCC 7425 4-hydroxyphenylpyruvate dioxygenase protein.
468	EED56339.1	EQ963473-1321	398	3.00E-31	119 \ 366	32	<i>Aspergillus flavus</i> NRRL3357 4-hydroxyphenylpyruvate dioxygenase, putative protein.
469	EDP54077.1	DS499595-401	403	4.00E-31	119 \ 364	32	<i>Aspergillus fumigatus</i> A1163 4-hydroxyphenylpyruvate dioxygenase, putative protein.
470	BAD59933.1	AP006618-5101	392	5.00E-31	111 \ 330	33	<i>Nocardia farcinica</i> IFM 10152 putative 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
471	ABE43786.1	CP000316-1819	301	7.00E-31	93 \ 261	35	<i>Polaromonas</i> sp. JS666 4-hydroxyphenylpyruvate dioxygenase protein.
472	EEA24946.1	DS995901-1299	407	7.00E-31	113 \ 306	36	<i>Penicillium marneffei</i> ATCC 18224 4-hydroxyphenylpyruvate dioxygenase, putative protein.
473	EDI34065.1	EP559780-4	187	1.00E-30	83 \ 189	43	Marine metagenome hypothetical protein.
474	EBM05344.1	EN871047-1	274	2.00E-30	91 \ 268	33	Marine metagenome hypothetical protein.
475	ECI81940.1	EM483275-2	298	2.00E-30	84 \ 235	35	Marine metagenome hypothetical protein.
476	EDN09916.1	CH476661-66	402	4.00E-30	118 \ 372	31	<i>Ajellomyces capsulatus</i> NAm1 4-hydroxyphenylpyruvate dioxygenase protein.
477	ECE50154.1	EM679381-4	183	4.00E-30	80 \ 187	42	Marine metagenome hypothetical protein.
478	CAK40580.1	AM270224-11	403	4.00E-30	113 \ 366	30	<i>Aspergillus niger</i> protein <i>Aspergillus niger</i> contig An11c0070, complete genome.
479	ACB32693.1	CP001013-417	635	5.00E-30	98 \ 331	29	<i>Leptothrix cholodnii</i> SP-6 Xylose isomerase domain protein TIM barrel protein.
480	ABD65945.1	DQ403252-25	356	5.00E-30	105 \ 349	30	<i>Streptomyces fungicidicus</i> 4-hydroxyphenylpyruvate dioxygenase protein.
481	EAT91209.2	CH445326-420	406	6.00E-30	114 \ 363	31	<i>Phaeosphaeria nodorum</i> SN15 hypothetical protein.
482	ECB13322.1	EM867834-1	212	6.00E-30	83 \ 208	39	Marine metagenome hypothetical protein.
483	CAD91197.1	AJ561198-8	356	7.00E-30	108 \ 339	31	<i>Nonomuraea</i> sp. ATCC 39727 putative hydroxymandelate synthase protein.
484	EAW18155.1	DS027696-863	403	7.00E-30	117 \ 364	32	<i>Neosartorya fischeri</i> NRRL 181 4-hydroxyphenylpyruvate dioxygenase, putative protein.
485	ECF88502.1	EM616353-2	211	7.00E-30	84 \ 213	39	Marine metagenome hypothetical protein.
486	ECV40631.1	EQ079249-2	202	7.00E-30	83 \ 204	40	Marine metagenome hypothetical protein.
487	EBX85518.1	EN023254-1	334	8.00E-30	99 \ 293	33	Marine metagenome hypothetical protein.
488	AAA82574.1	L38493-1	399	9.00E-30	112 \ 366	30	<i>Coccidioides posadasii</i> T-cell reactive protein.
489	EAU33682.1	CH476601-295	403	1.00E-29	113 \ 367	30	<i>Aspergillus terreus</i> NIH2624 4-hydroxyphenylpyruvate dioxygenase protein.
490	EDC19903.1	EP795409-4	521	1.00E-29	90 \ 327	27	Marine metagenome hypothetical protein.
491	EAS35956.1	CH476726-1309	399	1.00E-29	112 \ 366	30	<i>Coccidioides immitis</i> RS 4-hydroxyphenylpyruvate dioxygenase protein.
492	EDN91770.1	CH476630-97	422	2.00E-29	103 \ 310	33	<i>Sclerotinia sclerotiorum</i> 1980 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
493	CAP80533.1	AM920427-906	403	2.00E-29	112 \ 367	30	<i>Penicillium chrysogenum</i> Wisconsin 54-1255 Pc12g09060 protein.
494	ECT48794.1	EM709817-2	228	2.00E-29	85 \ 210	40	Marine metagenome hypothetical protein.
495	AAK48714.1	AF325533-1	419	2.00E-29	103 \ 308	33	<i>Magnaporthe grisea</i> 4-hydroxyphenylpyruvate dioxygenase protein.
496	EDJ98433.1	CH476830-697	419	2.00E-29	103 \ 308	33	<i>Magnaporthe grisea</i> 70-15 hypothetical protein.
497	AAS38823.1	AC117081-20	367	2.00E-29	104 \ 304	34	<i>Dictyostelium discoideum</i> hypothetical protein.
498	EDN03818.1	CH476655-1682	428	2.00E-29	109 \ 332	32	<i>Ajellomyces capsulatus</i> NAm1 4-hydroxyphenylpyruvate dioxygenase protein.
499	ECB70545.1	EM843631-3	113	2.00E-29	65 \ 113	57	Marine metagenome hypothetical protein.
500	EEA28381.1	DS995899-1770	415	3.00E-29	103 \ 312	33	<i>Penicillium marneffei</i> ATCC 18224 4-hydroxyphenylpyruvate dioxygenase, putative protein.
501	AAI29580.1	BC129579-1	383	3.00E-29	108 \ 338	31	<i>Xenopus laevis</i> LOC100037181 protein.
502	ABW13179.1	CP000820-3710	401	4.00E-29	108 \ 301	35	<i>Frankia</i> sp. EAN1pec 4-hydroxyphenylpyruvate dioxygenase protein.
503	EBS45386.1	EN490617-1	314	4.00E-29	102 \ 321	31	Marine metagenome hypothetical protein.
504	AAK88914.2	AE007870-1490	633	5.00E-29	110 \ 334	32	<i>Agrobacterium tumefaciens</i> str. C58 conserved hypothetical protein.
505	ECP93114.1	EM132508-2	248	5.00E-29	86 \ 249	34	Marine metagenome hypothetical protein.
506	BAB72728.1	BA000019-769	344	5.00E-29	96 \ 296	32	<i>Nostoc</i> sp. PCC 7120 4-hydroxyphenylpyruvate dioxygenase protein.
507	EBT35093.1	EN420251-2	314	6.00E-29	86 \ 276	31	Marine metagenome hypothetical protein.
508	EDX77401.1	DS989844-43	431	6.00E-29	76 \ 202	37	<i>Microcoleus chthonoplastes</i> PCC 7420 4-hydroxyphenylpyruvate dioxygenase protein.
509	AAC15884.1	AF038152-1	419	8.00E-29	104 \ 306	33	<i>Mycosphaerella graminicola</i> 4-hydroxyphenylpyruvate dioxygenase protein.
510	EDN18823.1	CH476852-108	422	1.00E-28	99 \ 306	32	<i>Botryotinia fuckeliana</i> B05.10 hypothetical protein.
511	EBS22038.1	EN508845-1	215	1.00E-28	84 \ 208	40	Marine metagenome hypothetical protein.
512	ABR63009.1	CP000739-620	629	1.00E-28	103 \ 336	30	<i>Sinorhizobium medicae</i> WSM419 Xylose isomerase domain protein TIM barrel protein.
513	EDP50433.1	DS499598-476	406	3.00E-28	103 \ 310	33	<i>Aspergillus fumigatus</i> A1163 4-hydroxyphenylpyruvate dioxygenase, putative protein.
514	EBA65828.1	EP534593-1	309	4.00E-28	77 \ 248	31	Marine metagenome hypothetical protein.
515	EBD81862.1	EP330527-2	187	4.00E-28	77 \ 190	40	Marine metagenome hypothetical protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
516	ABD84015.1	DQ397304-5	294	5.00E-28	70 \ 180	38	<i>Pseudomonas</i> sp. K82 probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein.
517	ABX37073.1	CP000884-4426	294	5.00E-28	70 \ 180	38	<i>Delftia acidovorans</i> SPH-1 4-hydroxyphenylpyruvate dioxygenase protein.
518	EAT33142.1	CH478368-1	381	6.00E-28	109 \ 353	30	<i>Aedes aegypti</i> 4-hydroxyphenylpyruvate dioxygenase protein.
519	CAO91156.1	AM778957-7	361	6.00E-28	98 \ 320	30	<i>Microcystis aeruginosa</i> PCC 7806 protein <i>Microcystis aeruginosa</i> PCC 7806 genome sequencing data, contig C327.gene (partial), tRNA-Ile gene, tRNA-Ala gene and ITS1.
520	CAD70479.1	BX284754-17	412	6.00E-28	98 \ 308	31	<i>Neurospora crassa</i> probable 4-hydroxyphenylpyruvate dioxygenase protein.
521	AAM80551.1	U82965-25	369	6.00E-28	101 \ 333	30	<i>Streptomyces toyocaensis</i> HmaS protein.
522	ABE46382.1	CP000316-4415	638	6.00E-28	97 \ 349	27	<i>Polaromonas</i> sp. JS666 4-hydroxyphenylpyruvate dioxygenase protein.
523	CAC49893.1	AL591985-1505	629	7.00E-28	102 \ 337	30	<i>Sinorhizobium meliloti</i> 1021 putative 4-hydroxyphenylpyruvate dioxygenase protein.
524	EAT37578.1	CH477663-14	378	8.00E-28	109 \ 351	31	<i>Aedes aegypti</i> 4-hydroxyphenylpyruvate dioxygenase protein.
525	BAG01563.1	AP009552-1740	361	8.00E-28	96 \ 319	30	<i>Microcystis aeruginosa</i> NIES-843 4-hydroxyphenylpyruvate dioxygenase protein.
526	EDV20132.1	DS985262-16	403	8.00E-28	102 \ 306	33	<i>Trichoplax adhaerens</i> expressed hypothetical protein.
527	EAU25058.1	DS027685-423	406	8.00E-28	104 \ 310	33	<i>Neosartorya fischeri</i> NRRL 181 4-hydroxyphenylpyruvate dioxygenase, putative protein.
528	AAI53802.1	BC153801-1	383	1.00E-27	112 \ 355	31	<i>Xenopus laevis</i> LOC100126650 protein.
529	EBI20210.1	EP091471-3	125	1.00E-27	58 \ 90	64	Marine metagenome hypothetical protein.
530	CAG83450.1	CR382128-876	394	2.00E-27	109 \ 356	30	<i>Yarrowia lipolytica</i> YALI0B21846p protein.
531	EBQ17655.1	EN654487-2	211	2.00E-27	78 \ 197	39	Marine metagenome hypothetical protein.
532	CAP70785.1	CU638743-699	418	2.00E-27	99 \ 306	32	<i>Podospora anserina</i> protein <i>Podospora anserina</i> genomic DNA chromosome 3, supercontig 2.
533	CAP98001.1	AM920437-713	407	2.00E-27	103 \ 310	33	<i>Penicillium chrysogenum</i> Wisconsin 54-1255 Pc22g07130 protein.
534	EDQ89603.1	CH991550-49	385	3.00E-27	110 \ 356	30	<i>Monosiga brevicollis</i> MX1 predicted protein.
535	CAL91815.1	CS456035-1	339	4.00E-27	93 \ 307	30	<i>Synechocystis</i> sp. PCC 6803 protein Sequence 1 from Patent EP1728868.
536	CAB69498.1	A92167-1	339	4.00E-27	93 \ 307	30	<i>Synechocystis</i> sp. PCC 6803 protein Sequence 1 from Patent WO9820144.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
537	BAA10563.1	BA000022-2594	339	4.00E-27	93 \ 307	30	<i>Synechocystis</i> sp. PCC 6803 4-hydroxyphenylpyruvic acid dioxygenase protein.
538	ECG42393.1	EM590533-3	231	5.00E-27	79 \ 215	36	Marine metagenome hypothetical protein.
539	ACK67379.1	CP001287-3272	363	5.00E-27	92 \ 342	26	<i>Cyanotheca</i> sp. PCC 8801 4-hydroxyphenylpyruvate dioxygenase protein.
540	ABM36969.1	CP000529-1642	300	8.00E-27	91 \ 265	34	<i>Polaromonas naphthalenivorans</i> CJ2 4-hydroxyphenylpyruvate dioxygenase protein.
541	ABM36874.1	CP000529-1547	632	1.00E-26	92 \ 330	27	<i>Polaromonas naphthalenivorans</i> CJ2 4-hydroxyphenylpyruvate dioxygenase protein.
542	ABP54936.1	CP000667-2451	389	1.00E-26	96 \ 316	30	<i>Salinispora tropica</i> CNB-440 4-hydroxyphenylpyruvate dioxygenase protein.
543	EAQ86656.1	CH408033-1090	413	2.00E-26	98 \ 310	31	<i>Chaetomium globosum</i> CBS 148.51 hypothetical protein.
544	ACJ60972.1	EU874252-30	357	2.00E-26	99 \ 324	30	Uncultured soil bacterium Veg30 protein.
545	ECG20187.1	EM602391-1	185	2.00E-26	76 \ 190	40	Marine metagenome hypothetical protein.
546	ACC82482.1	CP001037-3679	361	2.00E-26	104 \ 345	30	<i>Nostoc punctiforme</i> PCC 73102 4-hydroxyphenylpyruvate dioxygenase protein.
547	AAI21487.1	BC121486-1	393	2.00E-26	106 \ 354	29	<i>Xenopus Silurana tropicalis</i> 4-hydroxyphenylpyruvate dioxygenase protein.
548	EBS11229.1	EN517924-1	273	2.00E-26	86 \ 270	31	Marine metagenome hypothetical protein.
549	EBE70030.1	EP286314-1	320	3.00E-26	90 \ 288	31	Marine metagenome hypothetical protein.
550	ECS11955.1	EM032138-2	247	3.00E-26	83 \ 242	34	Marine metagenome hypothetical protein.
551	CAG15040.1	AJ632270-43	353	4.00E-26	89 \ 304	29	<i>Actinoplanes teichomyceticus</i> HmaS protein.
552	CAE53378.1	AJ605139-46	351	4.00E-26	89 \ 304	29	<i>Actinoplanes teichomyceticus</i> HmaS protein.
553	ECO52878.1	EM223102-1	158	4.00E-26	72 \ 163	44	Marine metagenome hypothetical protein.
554	EDU46870.1	DS231617-625	405	5.00E-26	114 \ 365	31	<i>Pyrenophora tritici-repentis</i> Pt-1C-BFP 4-hydroxyphenylpyruvate dioxygenase protein.
555	CAA90315.1	Z50016-8	393	6.00E-26	102 \ 339	30	<i>Caenorhabditis elegans</i> C. <i>elegans</i> protein T21C12.2, confirmed by transcript evidence protein.
556	AAH60451.1	BC060451-1	313	8.00E-26	100 \ 305	32	<i>Xenopus laevis</i> MGC68535 protein.
557	EDW34663.1	CH479219-10	350	1.00E-25	98 \ 306	32	<i>Drosophila persimilis</i> GL12777 protein.
558	ECA89280.1	EM880517-2	262	1.00E-25	85 \ 267	31	Marine metagenome hypothetical protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
559	EAL30481.2	CH379070-907	381	2.00E-25	98 \ 306	32	<i>Drosophila pseudoobscura pseudoobscura</i> GA11203 protein.
560	EBX46258.1	EN055244-2	191	2.00E-25	74 \ 192	38	Marine metagenome hypothetical protein.
561	ECW53067.1	EQ044471-1	498	2.00E-25	71 \ 223	31	Marine metagenome hypothetical protein.
562	CAK38585.1	AM270068-22	511	2.00E-25	101 \ 303	33	<i>Aspergillus niger</i> protein <i>Aspergillus niger</i> contig An04c0070, complete genome.
563	CAG88753.1	CR382138-79	473	3.00E-25	102 \ 356	28	<i>Debaryomyces hansenii</i> DEHA2F01892p protein.
564	AAA96492.1	M59429-1	404	3.00E-25	94 \ 307	30	<i>Tetrahymena thermophila</i> F-antigen protein.
565	EAS07560.1	CH445401-34	404	3.00E-25	94 \ 307	30	<i>Tetrahymena thermophila</i> SB210 4-hydroxyphenylpyruvate dioxygenase family protein.
566	ABN66879.2	CP000499-465	530	3.00E-25	106 \ 323	32	<i>Pichia stipitis</i> CBS 6054 4-hydroxyphenylpyruvate dioxygenase 4HPPD (HPD) (HPPDase) protein.
567	EDV40084.1	CH902618-1435	402	3.00E-25	98 \ 306	32	<i>Drosophila ananassae</i> GF24132 protein.
568	CAB38519.1	AL939115-176	371	3.00E-25	95 \ 344	27	<i>Streptomyces coelicolor</i> putative 4-hydroxyphenylpyruvic acid dioxygenase protein.
569	ECK51425.1	EM406400-4	174	4.00E-25	69 \ 167	41	Marine metagenome hypothetical protein.
570	AAH91035.1	BC091035-1	394	4.00E-25	104 \ 332	31	<i>Xenopus Silurana tropicalis</i> hpd protein.
571	BAC91032.1	BA000045-3091	344	5.00E-25	74 \ 205	36	<i>Gloeobacter violaceus</i> PCC 7421 4-hydroxyphenylpyruvate dioxygenase protein.
572	ABD11821.1	CP000249-2426	355	5.00E-25	96 \ 320	30	<i>Frankia</i> sp. Ccl3 4-hydroxyphenylpyruvate dioxygenase protein.
573	AAH84120.1	BC084120-1	393	5.00E-25	94 \ 308	30	<i>Xenopus laevis</i> LOC495029 protein.
574	ACL90096.1	FJ635837-1	294	7.00E-25	96 \ 306	31	Synthetic construct CG11796-PB protein.
575	ACL85188.1	FJ630929-1	294	7.00E-25	96 \ 306	31	Synthetic construct CG11796-PB protein.
576	AAK77255.1	AY047523-1	294	7.00E-25	96 \ 306	31	<i>Drosophila melanogaster</i> GH03058p protein.
577	AAF51602.1	AE014296-3564	294	7.00E-25	96 \ 306	31	<i>Drosophila melanogaster</i> CG11796, isoform B protein.
578	EDV52519.1	CH954178-2528	380	7.00E-25	106 \ 356	29	<i>Drosophila erecta</i> GG13309 protein.
579	ECP36457.1	EM158848-1	297	8.00E-25	68 \ 169	40	Marine metagenome hypothetical protein.
580	EDX11243.1	CM000363-2575	380	8.00E-25	106 \ 356	29	<i>Drosophila simulans</i> GD12185 protein.
581	EDS42263.1	DS231878-30	388	9.00E-25	79 \ 209	37	<i>Culex quinquefasciatus</i> 4-hydroxyphenylpyruvate dioxygenase protein.
582	ACL92412.1	FJ638153-1	380	9.00E-25	106 \ 356	29	Synthetic construct CG11796-PA protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
583	ACL88267.1	FJ634008-1	380	9.00E-25	106 \ 356	29	Synthetic construct CG11796-PA protein.
584	AAS77442.1	BT012317-1	380	9.00E-25	106 \ 356	29	<i>Drosophila melanogaster</i> GH11957p protein.
585	AAF51601.1	AE014296-3563	380	9.00E-25	106 \ 356	29	<i>Drosophila melanogaster</i> CG11796, isoform A protein.
586	EBI46437.1	EP076690-1	174	1.00E-24	70 \ 167	41	Marine metagenome hypothetical protein.
587	EDW44224.1	CH480826-73	380	1.00E-24	106 \ 356	29	<i>Drosophila sechellia</i> GM22213 protein.
588	EDB75455.1	EP813508-1	538	1.00E-24	76 \ 254	29	Marine metagenome hypothetical protein.
589	EDX00031.1	CH891904-1	380	1.00E-24	106 \ 356	29	<i>Drosophila yakuba</i> GE22742 protein.
590	CAC48371.1	Y16952-25	356	1.00E-24	102 \ 329	31	<i>Amycolatopsis balhimycina</i> putative hydroxyphenyl pyruvate dioxygenase protein.
591	EDW18742.1	CH933809-1327	402	1.00E-24	107 \ 356	30	<i>Drosophila mojavensis</i> GI11911 protein.
592	EBE79806.1	EP281706-1	146	2.00E-24	68 \ 150	45	Marine metagenome hypothetical protein.
593	CAK48092.1	AM270121-9	409	2.00E-24	99 \ 310	31	<i>Aspergillus niger</i> protein <i>Aspergillus niger</i> contig An07c0030, complete genome.
594	EDW80014.1	CH964161-49	380	2.00E-24	102 \ 351	29	<i>Drosophila willistoni</i> GK12342 protein.
595	ACB00686.1	CP000951-2667	337	2.00E-24	85 \ 220	38	<i>Synechococcus</i> sp. PCC 7002 glyoxalase family protein.
596	EBW30019.1	EN147596-1	168	3.00E-24	69 \ 167	41	Marine metagenome hypothetical protein.
597	ECD95679.1	EM740454-1	297	3.00E-24	91 \ 302	30	Marine metagenome hypothetical protein.
598	ECD46977.1	EM763674-2	258	4.00E-24	76 \ 231	32	Marine metagenome hypothetical protein.
599	ACG74716.1	CP001131-3473	393	4.00E-24	105 \ 340	30	<i>Anaeromyxobacter</i> sp. K 4-hydroxyphenylpyruvate dioxygenase protein.
600	ACL66901.1	CP001359-3540	395	4.00E-24	104 \ 340	30	<i>Anaeromyxobacter dehalogenans</i> 2CP-1 4-hydroxyphenylpyruvate dioxygenase protein.
601	ECY32995.1	EP981222-1	535	5.00E-24	69 \ 207	33	Marine metagenome hypothetical protein.
602	AAQ97794.1	AY398361-1	397	1.00E-23	107 \ 358	29	<i>Danio rerio</i> 4-hydroxyphenylpyruvate dioxygenase protein.
603	AAH46075.1	BC046075-1	387	1.00E-23	107 \ 358	29	<i>Danio rerio</i> zgc:56326 protein.
604	ECH97797.1	EM521405-3	244	1.00E-23	68 \ 177	38	Marine metagenome hypothetical protein.
605	BAF91881.1	AB325671-1	382	2.00E-23	92 \ 322	28	<i>Blepharisma japonicum</i> 4-hydroxyphenylpyruvate dioxygenase homolog protein.
606	CAX43855.1	FM992689-576	570	2.00E-23	105 \ 331	31	<i>Candida dubliniensis</i> CD36 4-hydroxyphenylpyruvate dioxygenase, putative protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
607	EEA47398.1	DS986965-2	382	3.00E-23	100 \ 331	30	<i>Branchiostoma floridae</i> hypothetical protein.
608	EDE32430.1	EP714952-3	225	3.00E-23	68 \ 167	40	Marine metagenome hypothetical protein.
609	ECA76288.1	EM886410-2	161	3.00E-23	65 \ 166	39	Marine metagenome hypothetical protein.
610	ABC83189.1	CP000251-3411	393	4.00E-23	99 \ 313	31	<i>Anaeromyxobacter dehalogenans</i> 2CP-C 4-hydroxyphenylpyruvate dioxygenase protein.
611	EEA49942.1	DS986928-53	291	5.00E-23	94 \ 299	31	<i>Branchiostoma floridae</i> hypothetical protein.
612	AAI65880.1	BC165880-1	393	5.00E-23	103 \ 354	29	<i>Danio rerio</i> hpd protein.
613	AAH77167.1	BC077167-1	393	5.00E-23	103 \ 354	29	<i>Danio rerio</i> 4-hydroxyphenylpyruvate dioxygenase protein.
614	ECH56198.1	EM539447-1	114	6.00E-23	55 \ 98	56	Marine metagenome hypothetical protein.
615	ABB86496.1	DQ206332-1	873	6.00E-23	85 \ 235	36	<i>Nematostella vectensis</i> HNF-HNF class homeobox protein.
616	ABP55171.1	CP000667-2686	358	6.00E-23	90 \ 294	30	<i>Salinispora tropica</i> CNB-440 4-hydroxyphenylpyruvate dioxygenase protein.
617	ABS27667.1	CP000769-3447	391	6.00E-23	107 \ 337	31	<i>Anaeromyxobacter</i> sp. Fw109-5 4-hydroxyphenylpyruvate dioxygenase protein.
618	EEC06118.1	DS714433-5	381	7.00E-23	80 \ 211	37	<i>Ixodes scapularis</i> 4-hydroxyphenylpyruvate dioxygenase, putative protein.
619	AAK81835.1	AF386507-14	338	7.00E-23	100 \ 331	30	<i>Streptomyces lavendulae</i> hydroxyphenyl pyruvate dioxygenase protein.
620	EDV97707.1	CH916366-2203	387	9.00E-23	95 \ 305	31	<i>Drosophila grimshawi</i> GH17018 protein.
621	EDW70459.1	CH940647-2031	380	1.00E-22	102 \ 352	28	<i>Drosophila virilis</i> GJ13785 protein.
622	ECD42669.1	EM765572-1	151	1.00E-22	66 \ 156	42	Marine metagenome hypothetical protein.
623	ACI34103.1	BT045841-1	386	2.00E-22	104 \ 350	29	<i>Salmo salar</i> 4-hydroxyphenylpyruvate dioxygenase protein.
624	ECC16418.1	EM821664-2	88	2.00E-22	54 \ 87	62	Marine metagenome hypothetical protein.
625	CAA11761.1	AJ223998-1	357	2.00E-22	94 \ 324	29	<i>Amycolatopsis orientalis</i> PCZA361.1 protein.
626	ABV98510.1	CP000850-2574	369	2.00E-22	96 \ 325	29	<i>Salinispora arenicola</i> CNS-205 4-hydroxyphenylpyruvate dioxygenase protein.
627	EBC51105.1	EP412306-1	329	6.00E-22	91 \ 340	26	Marine metagenome hypothetical protein.
628	ECJ38192.1	EM457290-1	259	7.00E-22	79 \ 257	30	Marine metagenome hypothetical protein.
629	EBK71594.1	EN937350-2	290	8.00E-22	85 \ 283	30	Marine metagenome hypothetical protein.
630	EEA37616.1	DS987179-11	213	8.00E-22	75 \ 211	35	<i>Branchiostoma floridae</i> hypothetical protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
631	BAA02660.1	D13390-1	393	9.00E-22	99 \ 351	28	<i>Sus scrofa</i> 4-hydroxyphenylpyruvic acid dioxygenase protein.
632	EDE60285.1	EP704321-3	147	9.00E-22	64 \ 150	42	Marine metagenome hypothetical protein.
633	AAX08766.1	BT020749-1	393	1.00E-21	98 \ 353	27	<i>Bos taurus</i> 4-hydroxyphenylpyruvate dioxygenase protein.
634	AAI05226.1	BC105225-1	393	1.00E-21	98 \ 353	27	<i>Bos taurus</i> 4-hydroxyphenylpyruvate dioxygenase protein.
635	EBT79806.1	EN385157-2	86	1.00E-21	52 \ 88	59	Marine metagenome hypothetical protein.
636	BAG51925.1	AK057510-1	354	1.00E-21	98 \ 355	27	<i>Homo sapiens</i> protein <i>Homo sapiens</i> cDNA FLJ32948 fis, clone TESTI2008014, highly similar to 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27).
637	EDM13651.1	CH473973-422	354	2.00E-21	98 \ 355	27	<i>Rattus norvegicus</i> 4-hydroxyphenylpyruvic acid dioxygenase protein.
638	AAH81819.1	BC081819-1	393	2.00E-21	98 \ 355	27	<i>Rattus norvegicus</i> 4-hydroxyphenylpyruvic acid dioxygenase protein.
639	AAC32387.1	AF082834-1	393	2.00E-21	98 \ 355	27	<i>Rattus norvegicus</i> 4-hydroxyphenylpyruvate dioxygenase protein.
640	AAC73008.1	U29895-1	393	2.00E-21	98 \ 355	27	<i>Homo sapiens</i> 4-hydroxyphenylpyruvate-dioxygenase protein.
641	ABM87048.1	DQ896049-1	393	2.00E-21	98 \ 355	27	Synthetic construct 4-hydroxyphenylpyruvate dioxygenase protein.
642	ABM83590.1	DQ892664-1	393	2.00E-21	98 \ 355	27	Synthetic construct 4-hydroxyphenylpyruvate dioxygenase protein.
643	CAA51082.1	X72389-1	393	2.00E-21	98 \ 355	27	<i>Homo sapiens</i> 4-hydroxyphenylpyruvate dioxygenase protein.
644	BAA06498.1	D31628-1	393	2.00E-21	98 \ 355	27	<i>Homo sapiens</i> 4-hydroxyphenylpyruvic acid dioxygenase protein.
645	AAH24287.1	BC024287-1	393	2.00E-21	98 \ 355	27	<i>Homo sapiens</i> 4-hydroxyphenylpyruvate dioxygenase protein.
646	BAF83515.1	AK290826-1	393	2.00E-21	98 \ 355	27	<i>Homo sapiens</i> protein <i>Homo sapiens</i> cDNA FLJ76150 complete cds, highly similar to <i>Homo sapiens</i> 4-hydroxyphenylpyruvate dioxygenase (HPD), mRNA.
647	EAU98292.1	CH471054-1670	393	2.00E-21	98 \ 355	27	<i>Homo sapiens</i> 4-hydroxyphenylpyruvate dioxygenase, isoform CRA_b protein.
648	EBB52473.1	EP479065-1	309	2.00E-21	61 \ 184	33	Marine metagenome hypothetical protein.
649	EBU70535.1	EN276866-1	288	2.00E-21	78 \ 250	31	Marine metagenome hypothetical protein.
650	CAJ38798.1	AM114773-1	287	2.00E-21	75 \ 212	35	<i>Platynereis dumerilii</i> 4-hydroxyphenylpyruvate dioxygenase protein.
651	EBX13490.1	EN084502-2	132	2.00E-21	63 \ 136	46	Marine metagenome hypothetical protein.
652	EDC72320.1	EP776372-3	153	4.00E-21	62 \ 157	39	Marine metagenome hypothetical protein.
653	AAC49815.1	U87257-1	442	4.00E-21	92 \ 308	29	<i>Daucus carota</i> 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
654	CAD42448.1	AX467199-1	345	4.00E-21	90 \ 324	27	<i>Nocardia uniformis</i> protein Sequence 9 from Patent WO0234921.
655	AAT09803.1	AY541063-9	345	4.00E-21	90 \ 324	27	<i>Nocardia uniformis</i> subsp. <i>tsuyamanensis</i> NocF protein.
656	AAA83338.1	U41748-5	364	5.00E-21	97 \ 345	28	<i>Caenorhabditis elegans</i> Hypothetical protein C31H2.4 protein.
657	ABC98696.1	CP000239-460	350	6.00E-21	79 \ 215	36	<i>Synechococcus</i> sp. JA-3-3Ab putative 4-hydroxyphenylpyruvate dioxygenase protein.
658	BAF74636.1	AB267400-1	430	7.00E-21	96 \ 332	28	<i>Coptis japonica</i> var. <i>dissecta</i> hydroxyphenylpyruvate dioxygenase protein.
659	AAH73224.1	BC073224-1	391	9.00E-21	86 \ 305	28	<i>Xenopus laevis</i> MGC80543 protein.
660	ECR96773.1	EM040759-3	260	1.00E-20	63 \ 203	31	Marine metagenome hypothetical protein.
661	EEF41985.1	EQ973855-6	441	1.00E-20	91 \ 309	29	<i>Ricinus communis</i> 4-hydroxyphenylpyruvate dioxygenase, putative protein.
662	ECG36009.1	EM593395-2	312	1.00E-20	88 \ 309	28	Marine metagenome hypothetical protein.
663	AAA40740.1	M18405-1	376	1.00E-20	96 \ 352	27	<i>Rattus norvegicus</i> protein Rat F alloantigen mRNA, 3' end.
664	ABA03141.1	DQ188836-1	377	1.00E-20	96 \ 352	27	<i>Homo sapiens</i> liver F protein.
665	EBX70874.1	EN034883-1	276	1.00E-20	63 \ 203	31	Marine metagenome hypothetical protein.
666	AAH13343.1	BC013343-1	393	2.00E-20	96 \ 350	27	<i>Mus musculus</i> 4-hydroxyphenylpyruvic acid dioxygenase protein.
667	EDL19647.1	CH466529-719	393	2.00E-20	96 \ 350	27	<i>Mus musculus</i> 4-hydroxyphenylpyruvic acid dioxygenase protein.
668	EBO18306.1	EN767288-2	245	2.00E-20	54 \ 144	37	Marine metagenome hypothetical protein.
669	BAE28861.1	AK149416-1	393	2.00E-20	96 \ 352	27	<i>Mus musculus</i> protein <i>Mus musculus</i> adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730007B19 product:4-hydroxyphenylpyruvic acid dioxygenase, full insert sequence.
670	EDX83703.1	DS989904-2721	387	2.00E-20	89 \ 330	26	<i>Synechococcus</i> sp. PCC 7335 glyoxalase family protein.
671	EDD96318.1	EP728889-2	477	3.00E-20	61 \ 189	32	Marine metagenome hypothetical protein.
672	EDK38185.2	CH408156-1079	309	4.00E-20	75 \ 220	34	<i>Pichia guilliermondii</i> ATCC 6260 hypothetical protein.
673	EBX09619.1	EN087416-1	250	5.00E-20	77 \ 242	31	Marine metagenome hypothetical protein.
674	BAA06267.1	D29987-1	393	7.00E-20	96 \ 350	27	<i>Mus musculus</i> 4-hydroxyphenylpyruvate dioxygenase protein.
675	ECK38384.1	EM411877-2	287	8.00E-20	73 \ 283	25	Marine metagenome hypothetical protein.
676	ABD01244.1	CP000240-242	359	9.00E-20	69 \ 202	34	<i>Synechococcus</i> sp. JA-2-3Ba(2-13) 4-hydroxyphenylpyruvate dioxygenase, putative protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
677	CAN71143.1	AM423697-2	445	1.00E-19	93 \ 320	29	<i>Vitis vinifera</i> hypothetical protein.
678	CAA42111.1	X59530-1	379	1.00E-19	94 \ 347	27	<i>Mus musculus</i> F1 protein.
679	EBL62910.1	EN890937-3	131	2.00E-19	55 \ 132	41	Marine metagenome hypothetical protein.
680	AAM96960.1	AY136294-1	473	2.00E-19	90 \ 314	28	<i>Arabidopsis thaliana</i> 4-hydroxyphenylpyruvate dioxygenase HPD protein.
681	AAF24813.1	AC007592-9	473	2.00E-19	90 \ 314	28	<i>Arabidopsis thaliana</i> F12K11.9 protein.
682	ECE30173.1	EM725742-1	224	2.00E-19	65 \ 211	30	Marine metagenome hypothetical protein.
683	AAB70025.1	U89267-1	445	2.00E-19	90 \ 314	28	<i>Arabidopsis thaliana</i> p-hydroxyphenylpyruvate dioxygenase protein.
684	AAM91145.1	AY128745-1	445	2.00E-19	90 \ 314	28	<i>Arabidopsis thaliana</i> 4-hydroxyphenylpyruvate dioxygenase HPD protein.
685	AAL61936.1	AY072329-1	445	2.00E-19	90 \ 314	28	<i>Arabidopsis thaliana</i> 4-hydroxyphenylpyruvate dioxygenase HPD protein.
686	AAL16215.1	AF428446-1	445	2.00E-19	90 \ 314	28	<i>Arabidopsis thaliana</i> At1g06570/F12K11_12 protein.
687	AAC15697.1	AF047834-1	445	2.00E-19	90 \ 314	28	<i>Arabidopsis thaliana</i> 4-hydroxyphenylpyruvate dioxygenase protein.
688	AAB58404.1	AF000228-1	445	2.00E-19	90 \ 314	28	<i>Arabidopsis thaliana</i> p-hydroxyphenylpyruvate dioxygenase protein.
689	CAD60074.1	AX575735-1	445	2.00E-19	90 \ 314	28	<i>Arabidopsis thaliana</i> protein Sequence 13 from Patent WO02072848.
690	ECT13066.1	EN314147-2	87	3.00E-19	50 \ 80	62	Marine metagenome hypothetical protein.
691	EBF09646.1	EP267376-2	87	3.00E-19	50 \ 85	58	Marine metagenome hypothetical protein.
692	EBH05175.1	EP150084-3	108	4.00E-19	47 \ 63	74	Marine metagenome hypothetical protein.
693	BAH10638.1	AB376089-1	445	4.00E-19	89 \ 315	28	<i>Hevea brasiliensis</i> 4-hydroxyphenylpyruvate dioxygenase protein.
694	ECM62258.1	EM308888-3	236	5.00E-19	68 \ 227	29	Marine metagenome hypothetical protein.
695	AAC62457.1	AF060481-1	419	6.00E-19	81 \ 282	28	<i>Arabidopsis thaliana</i> p-hydroxyphenylpyruvate dioxygenase protein.
696	ABF43810.1	CP000358-102	477	7.00E-19	69 \ 198	34	<i>Deinococcus geothermalis</i> DSM 11300 Xylose isomerase-like protein TIM barrel protein.
697	EDP32906.1	DS239400-78	403	8.00E-19	71 \ 207	34	<i>Brugia malayi</i> 4-hydroxyphenylpyruvate dioxygenase family protein.
698	ABO95005.1	CP000583-371	427	1.00E-18	90 \ 318	28	<i>Ostreococcus lucimarinus</i> CCE9901 predicted protein.
699	EBQ38388.1	EN644215-3	80	1.00E-18	44 \ 71	61	Marine metagenome hypothetical protein.
700	EDQ77182.1	DS544919-132	432	2.00E-18	90 \ 313	28	<i>Physcomitrella patens</i> subsp. <i>patens</i> predicted protein.
701	ECY33059.1	EP981199-3	139	2.00E-18	42 \ 97	43	Marine metagenome hypothetical protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
702	EBD67562.1	EP338536-1	436	2.00E-18	56 \ 154	36	Marine metagenome hypothetical protein.
703	EBV04788.1	EN250358-1	119	2.00E-18	55 \ 122	45	Marine metagenome hypothetical protein.
704	ECU73963.1	EM161995-2	255	2.00E-18	68 \ 219	31	Marine metagenome hypothetical protein.
705	EBM96457.1	EN825314-1	303	2.00E-18	77 \ 298	25	Marine metagenome hypothetical protein.
706	EBE22254.1	EP309995-2	287	3.00E-18	72 \ 219	32	Marine metagenome hypothetical protein.
707	AAI61492.1	BC161492-1	386	4.00E-18	80 \ 300	26	<i>Xenopus Silurana tropicalis</i> hpdI protein.
708	EDQ78952.1	DS544910-92	433	6.00E-18	89 \ 315	28	<i>Physcomitrella patens</i> subsp. <i>patens</i> predicted protein.
709	AAX59006.1	AY957391-1	437	6.00E-18	87 \ 319	27	<i>Medicago truncatula</i> 4-hydroxyphenylpyruvate dioxygenase protein.
710	EEE80140.1	CM000338-546	444	7.00E-18	87 \ 317	27	<i>Populus trichocarpa</i> predicted protein.
711	CAN96143.1	AM746676-5987	382	9.00E-18	66 \ 167	39	<i>Sorangium cellulosum</i> So ce 56' 4-hydroxyphenylpyruvate dioxygenase protein.
712	AAI52022.1	BC152021-1	420	1.00E-17	101 \ 383	26	<i>Danio rerio</i> zgc:171978 protein.
713	BAD26248.1	AP005804-30	446	1.00E-17	93 \ 311	29	<i>Oryza sativa Japonica</i> Group putative 4-hydroxyphenylpyruvate dioxygenase protein.
714	BAD25710.1	AP005071-3	446	1.00E-17	93 \ 311	29	<i>Oryza sativa Japonica</i> Group putative 4-hydroxyphenylpyruvate dioxygenase protein.
715	EAZ21880.1	CM000139-515	447	1.00E-17	93 \ 311	29	<i>Oryza sativa Japonica</i> Group hypothetical protein.
716	EEC72567.1	CM000127-548	601	2.00E-17	93 \ 311	29	<i>Oryza sativa Indica</i> Group hypothetical protein.
717	CAN95056.1	AM746676-4900	383	2.00E-17	74 \ 217	34	<i>Sorangium cellulosum</i> So ce 56' 4-hydroxyphenylpyruvate dioxygenase protein.
718	EBF14667.1	EP264539-1	212	2.00E-17	65 \ 187	34	Marine metagenome hypothetical protein.
719	EAW98291.1	CH471054-1671	375	2.00E-17	90 \ 345	26	<i>Homo sapiens</i> 4-hydroxyphenylpyruvate dioxygenase, isoform CRA_a protein.
720	ECF71409.1	EM623644-2	259	3.00E-17	50 \ 186	26	Marine metagenome hypothetical protein.
721	CAL53021.1	CR954203-369	432	3.00E-17	89 \ 324	27	<i>Ostreococcus tauri</i> p-hydroxyphenylpyruvate dioxygenase ISS protein.
722	CAD35421.1	AX417719-1	400	3.00E-17	75 \ 267	28	<i>Arabidopsis thaliana</i> protein Sequence 10 from Patent WO0231173.
723	EBQ20111.1	EN653098-2	290	3.00E-17	79 \ 272	29	Marine metagenome hypothetical protein.
724	EED94715.1	CM000639-352	418	4.00E-17	92 \ 337	27	<i>Thalassiosira pseudonana</i> CCMP1335 4-hydroxyphenylpyruvate dioxygenase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
725	EDE59592.1	EP704610-3	117	7.00E-17	57 \ 122	46	Marine metagenome hypothetical protein.
726	ECF48311.1	EM633300-2	302	1.00E-16	80 \ 303	26	Marine metagenome hypothetical protein.
727	EBD53302.1	EP346436-1	288	1.00E-16	81 \ 290	27	Marine metagenome hypothetical protein.
728	EBZ51619.1	EM942315-1	95	2.00E-16	41 \ 85	48	Marine metagenome hypothetical protein.
729	ABQ96868.1	EF608178-1	443	3.00E-16	91 \ 318	28	<i>Glycine max</i> 4-hydroxyphenylpyruvate dioxygenase protein.
730	EBX64698.1	EN039748-1	279	3.00E-16	62 \ 198	31	Marine metagenome hypothetical protein.
731	ABI63586.1	DQ886526-1	443	3.00E-16	86 \ 307	28	<i>Brassica rapa</i> subsp. <i>pekinensis</i> 4-hydroxyphenylpyruvate dioxygenase protein.
732	EBZ18622.1	EM958358-2	263	3.00E-16	72 \ 235	30	Marine metagenome hypothetical protein.
733	AAN28922.1	AY138969-1	363	4.00E-16	81 \ 302	26	Abutilon theophrasti 4-hydroxyphenylpyruvate dioxygenase protein.
734	EBP15365.1	EN713243-2	61	4.00E-16	40 \ 57	70	Marine metagenome hypothetical protein.
735	ECA33541.1	EM904759-2	138	6.00E-16	41 \ 86	47	Marine metagenome hypothetical protein.
736	EAS36112.1	CH476726-1465	345	6.00E-16	56 \ 135	41	<i>Coccidioides immitis</i> RS hypothetical protein.
737	EBP42697.1	EN696464-1	301	1.00E-15	76 \ 274	27	Marine metagenome hypothetical protein.
738	CAC37394.1	AJ309203-1	436	1.00E-15	99 \ 350	28	<i>Solenostemon scutellarioides</i> 4-hydroxyphenylpyruvate dioxygenase protein.
739	EEB11881.1	DS235096-5	406	2.00E-15	93 \ 322	28	<i>Pediculus humanus corporis</i> 4-hydroxyphenylpyruvate dioxygenase, putative protein.
740	EBP68994.1	EN680073-1	291	2.00E-15	66 \ 226	29	Marine metagenome hypothetical protein.
741	EBP77673.1	EN675483-1	70	4.00E-15	42 \ 63	66	Marine metagenome hypothetical protein.
742	ACL41808.1	CP001341-3805	624	6.00E-15	92 \ 350	26	<i>Arthrobacter chlorophenolicus</i> A6 Xylose isomerase domain protein TIM barrel protein.
743	AAH34099.1	BC034099-1	371	7.00E-15	67 \ 231	29	<i>Mus musculus</i> 4-hydroxyphenylpyruvate dioxygenase-like protein.
744	CAM13544.1	AL683847-17	371	7.00E-15	67 \ 231	29	<i>Mus musculus</i> 4-hydroxyphenylpyruvate dioxygenase-like protein.
745	BAC37467.1	AK078929-1	371	7.00E-15	67 \ 231	29	<i>Mus musculus</i> protein <i>Mus musculus</i> adult male cecum cDNA, RIKEN full-length enriched library, clone:9130202117 product: hypothetical Glyoxalase/Bleomycin resistance protein/Dihydroxybiphen yl dioxygenase structure containing protein, full insert sequence.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
746	BAC33615.1	AK049217-1	371	7.00E-15	67 \ 231	29	<i>Mus musculus</i> protein <i>Mus musculus</i> ES cells cDNA, RIKEN full-length enriched library, clone:C330013N21 product: hypothetical Glyoxalase/Bleomycin resistance protein/Dihydroxybiphen yl dioxygenase structure containing protein, full insert sequence.
747	BAC31697.1	AK043902-1	371	7.00E-15	67 \ 231	29	<i>Mus musculus</i> protein <i>Mus musculus</i> 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830048M07 product: hypothetical Glyoxalase/Bleomycin resistance protein/ Dihydroxybiphenyl dioxygenase structure containing protein, full insert sequence.
748	EDL30580.1	CH466552-94	371	7.00E-15	67 \ 231	29	<i>Mus musculus</i> glyoxalase domain containing 1 protein.
749	ABM08434.1	CP000474-3880	628	7.00E-15	86 \ 348	24	<i>Arthrobacter aureus</i> TC1 putative 4-hydroxyphenylpyruvate dioxygenase protein.
750	CAH10097.1	AJ628018-6	626	7.00E-15	101 \ 368	27	<i>Streptomyces</i> sp. SCC 2136 putative 4-hydroxyphenyl pyruvate dioxygenase protein.
751	ECL26640.1	EM371805-1	100	1.00E-14	43 \ 87	49	Marine metagenome hypothetical protein.
752	AAZ67144.1	DQ139267-1	436	4.00E-14	94 \ 319	29	<i>Triticum aestivum</i> 4-hydroxyphenylpyruvate dioxygenase protein.
753	ECC57142.1	EM804381-2	196	4.00E-14	64 \ 198	32	Marine metagenome hypothetical protein.
754	CAA04245.1	AJ000693-1	434	4.00E-14	94 \ 315	29	<i>Hordeum vulgare</i> 4-hydroxyphenylpyruvate dioxygenase protein.
755	CAB69192.1	A81449-1	434	4.00E-14	94 \ 315	29	unidentified protein Sequence 1 from Patent WO9904021.
756	EBD94904.1	EP323824-1	265	4.00E-14	63 \ 212	29	Marine metagenome hypothetical protein.
757	ABK05454.1	CP000454-4053	629	8.00E-14	87 \ 352	24	<i>Arthrobacter</i> sp. FB24 Xylose isomerase domain protein TIM barrel protein.
758	EBG36882.1	EP192185-2	120	9.00E-14	35 \ 64	54	Marine metagenome hypothetical protein.
759	AAH07293.1	BC007293-1	371	9.00E-14	83 \ 303	27	<i>Homo sapiens</i> 4-hydroxyphenylpyruvate dioxygenase-like protein.
760	CAI21712.1	AL359540-1	371	9.00E-14	83 \ 303	27	<i>Homo sapiens</i> 4-hydroxyphenylpyruvate dioxygenase-like protein.
761	BAG36457.1	AK313714-1	371	9.00E-14	83 \ 303	27	<i>Homo sapiens</i> protein <i>Homo sapiens</i> cDNA, FLJ94307.
762	EAX07002.1	CH471059-877	371	9.00E-14	83 \ 303	27	<i>Homo sapiens</i> glyoxalase domain containing 1 protein.
763	EBX70575.1	EN035126-1	294	1.00E-13	47 \ 133	35	Marine metagenome hypothetical protein.
764	CAG25475.1	AJ634707-1	444	2.00E-13	88 \ 309	28	<i>Zea mays</i> putative p-hydroxyphenylpyruvate dioxygenase protein.
765	ECF27816.1	EM644089-3	281	2.00E-13	39 \ 90	43	Marine metagenome hypothetical protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
766	EDP02306.1	DS496130-159	372	2.00E-13	88 \ 322	27	<i>Chlamydomonas reinhardtii</i> 4-hydroxyphenylpyruvate dioxygenase protein.
767	ABK26783.1	EF087545-1	263	2.00E-13	69 \ 230	30	<i>Picea sitchensis</i> unknown protein.
768	ECV16927.1	EQ083978-4	271	2.00E-13	71 \ 250	28	Marine metagenome hypothetical protein.
769	ECU09822.1	EM683971-2	253	2.00E-13	67 \ 245	27	Marine metagenome hypothetical protein.
770	AAH83702.1	BC083702-1	371	2.00E-13	46 \ 130	35	<i>Rattus norvegicus</i> 4-hydroxyphenylpyruvate dioxygenase-like protein.
771	EDL90243.1	CH474008-240	371	2.00E-13	46 \ 130	35	<i>Rattus norvegicus</i> glyoxalase domain containing 1 protein.
772	EDA72580.1	EP886536-3	75	2.00E-13	37 \ 64	57	Marine metagenome hypothetical protein.
773	EBF37884.1	EP251348-1	110	5.00E-13	48 \ 115	41	Marine metagenome hypothetical protein.
774	EBO02389.1	EN776043-1	304	5.00E-13	80 \ 286	27	Marine metagenome hypothetical protein.
775	EBU77987.1	EN271172-1	260	5.00E-13	64 \ 218	29	Marine metagenome hypothetical protein.
776	CAC35131.1	AJ291979-1	130	6.00E-13	47 \ 131	35	<i>Auxarthron zuffianum</i> human T-cell reactive protein.
777	CAC35130.1	AJ291978-1	130	6.00E-13	47 \ 131	35	<i>Auxarthron zuffianum</i> human T-cell reactive protein.
778	CAC35128.1	AJ291976-1	130	6.00E-13	47 \ 131	35	<i>Auxarthron zuffianum</i> human T-cell reactive protein.
779	CAC35127.1	AJ291975-1	130	6.00E-13	47 \ 131	35	<i>Auxarthron zuffianum</i> human T-cell reactive protein.
780	CAD24031.1	AJ431261-1	432	6.00E-13	85 \ 314	27	<i>Chlamydomonas reinhardtii</i> p-hydroxyphenylpyruvate dioxigenase protein.
781	EDP02307.1	DS496130-160	432	6.00E-13	85 \ 314	27	<i>Chlamydomonas reinhardtii</i> 4-hydroxyphenylpyruvate dioxygenase protein.
782	AAO51054.1	AC116330-31	637	6.00E-13	89 \ 380	23	<i>Dictyostelium discoideum</i> hypothetical protein.
783	EBC86862.1	EP387059-2	314	6.00E-13	82 \ 323	25	Marine metagenome hypothetical protein.
784	EEA57207.1	DS986836-41	429	7.00E-13	84 \ 322	26	<i>Branchiostoma floridae</i> hypothetical protein.
785	CAR47957.1	FM202438-1	432	2.00E-12	84 \ 314	26	<i>Chlamydomonas reinhardtii</i> p-hydroxyphenylpyruvate dioxygenase protein.
786	CAC35133.1	AJ291974-1	130	2.00E-12	45 \ 131	34	<i>Uncinocarpus reesii</i> human T-cell reactive protein.
787	CAC35137.1	AJ291972-1	130	2.00E-12	45 \ 131	34	<i>Uncinocarpus reesii</i> human T-cell reactive protein.
788	CAC35136.1	AJ291971-1	130	2.00E-12	45 \ 131	34	<i>Uncinocarpus reesii</i> human T-cell reactive protein.
789	CAC35135.1	AJ291970-1	130	2.00E-12	45 \ 131	34	<i>Uncinocarpus reesii</i> human T-cell reactive protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
790	ECR94569.1	EM041703-2	290	2.00E-12	62 \ 235	26	Marine metagenome hypothetical protein.
791	CAJ29893.1	AM084898-1	381	2.00E-12	78 \ 268	29	<i>Triticum aestivum</i> 4-hydroxyphenylpyruvate dioxygenase protein.
792	ECQ19986.1	EM120910-2	196	2.00E-12	55 \ 186	29	Marine metagenome hypothetical protein.
793	EEA35361.1	DS987265-3	428	2.00E-12	84 \ 321	26	<i>Branchiostoma floridae</i> hypothetical protein.
794	CAC35138.1	AJ291973-1	130	3.00E-12	44 \ 131	33	<i>Uncinocarpus reesii</i> human T-cell reactive protein.
795	EDY60338.1	DS570958-46	592	3.00E-12	84 \ 332	25	<i>Streptomyces sviveus</i> ATCC 29083 sugar phosphate isomerase/epimerase protein.
796	AAI42155.1	BC142154-1	390	3.00E-12	44 \ 136	32	<i>Bos taurus</i> HPDL protein.
797	CAC35134.1	AJ291969-1	130	4.00E-12	45 \ 131	34	<i>Coccidioides immitis</i> human T-cell reactive protein.
798	CAC35132.1	AJ291968-1	130	4.00E-12	45 \ 131	34	<i>Coccidioides immitis</i> human T-cell reactive protein.
799	ECO46491.1	EM225601-1	301	4.00E-12	71 \ 308	23	Marine metagenome hypothetical protein.
800	EBU54862.1	EN289718-1	227	4.00E-12	42 \ 113	37	Marine metagenome hypothetical protein.
801	CAC35129.1	AJ291977-1	130	4.00E-12	46 \ 131	35	<i>Auxarthron zuffianum</i> human T-cell reactive protein.
802	BAF07924.1	AP008208-432	239	4.00E-12	67 \ 224	29	<i>Oryza sativa Japonica</i> cultivar-group Os02g0168100 protein.
803	BAC69487.1	BA000030-1782	601	7.00E-12	88 \ 334	26	<i>Streptomyces avermitilis</i> MA-4680 putative sugar phosphate isomerase/epimerase protein.
804	EBC61936.1	EP404880-2	213	1.00E-11	59 \ 205	28	Marine metagenome hypothetical protein.
805	ECQ41976.1	EM109472-1	279	1.00E-11	68 \ 258	26	Marine metagenome hypothetical protein.
806	ACN36372.1	BT069475-1	426	1.00E-11	85 \ 305	27	<i>Zea mays</i> unknown protein.
807	EDV23532.1	DS985247-457	388	1.00E-11	65 \ 224	29	<i>Trichoplax adhaerens</i> hypothetical protein.
808	ECE82307.1	EM663629-2	231	2.00E-11	57 \ 225	25	Marine metagenome hypothetical protein.
809	BAF53460.1	AP009044-499	618	3.00E-11	78 \ 325	24	<i>Corynebacterium glutamicum</i> R hypothetical protein.
810	EEE94558.1	CM000341-1132	343	3.00E-11	73 \ 297	24	<i>Populus trichocarpa</i> predicted protein.
811	CAL31762.1	CS360397-1	618	5.00E-11	78 \ 325	24	<i>Corynebacterium glutamicum</i> protein Sequence 395 from Patent EP1683859.
812	CAC26265.1	AX066051-1	618	5.00E-11	78 \ 325	24	<i>Corynebacterium glutamicum</i> protein Sequence 395 from Patent WO0100842.
813	CAF19138.1	BX927149-93	618	5.00E-11	78 \ 325	24	<i>Corynebacterium glutamicum</i> ATCC 13032 phosphate isomerase/epimerase protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
814	BAB97815.1	BA000036-422	618	5.00E-11	78 \ 325	24	<i>Corynebacterium glutamicum</i> ATCC 13032 Sugar phosphate isomerases/epimerases protein.
815	EDO35286.1	DS469703-21	330	1.00E-10	62 \ 236	26	<i>Nematostella vectensis</i> predicted protein.
816	BAE20327.1	AB232882-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> dioxygenase protein.
817	BAE20326.1	AB232881-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> dioxygenase protein.
818	BAE20325.1	AB232880-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> dioxygenase protein.
819	BAE20324.1	AB232879-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> dioxygenase protein.
820	BAE20323.1	AB232878-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides immitis</i> dioxygenase protein.
821	BAE20322.1	AB232877-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> dioxygenase protein.
822	BAE20321.1	AB232876-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> dioxygenase protein.
823	BAE20320.1	AB232875-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides immitis</i> dioxygenase protein.
824	BAE20319.1	AB232874-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides immitis</i> dioxygenase protein.
825	BAE20317.1	AB232872-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides immitis</i> dioxygenase protein.
826	BAE20316.1	AB232871-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides immitis</i> dioxygenase protein.
827	BAE20315.1	AB232870-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> dioxygenase protein.
828	BAE20314.1	AB232869-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> dioxygenase protein.
829	BAE20313.1	AB232868-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> dioxygenase protein.
830	BAE20312.1	AB232867-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> dioxygenase protein.
831	BAE20311.1	AB232866-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> dioxygenase protein.
832	BAE20310.1	AB232865-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> dioxygenase protein.
833	BAE20309.1	AB232864-1	147	2.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> dioxygenase protein.
834	ECP31077.1	EM186947-3	77	2.00E-10	34 \ 68	50	Marine metagenome hypothetical protein.
835	BAE20318.1	AB232873-1	147	3.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> dioxygenase protein.
836	EBZ04618.1	EM964820-1	264	3.00E-10	58 \ 199	29	Marine metagenome hypothetical protein.
837	EBW70085.1	EN117759-2	104	4.00E-10	45 \ 109	41	Marine metagenome hypothetical protein.
838	EBR99421.1	EN527175-1	253	5.00E-10	63 \ 228	27	Marine metagenome hypothetical protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
839	CAO69988.1	CU459235-273	164	6.00E-10	54 \ 151	35	<i>Vitis vinifera</i> protein <i>Vitis vinifera</i> chromosome chr12 scaffold_18, whole genome shotgun sequence.
840	EBP16467.1	EN712623-1	86	7.00E-10	44 \ 90	48	Marine metagenome hypothetical protein.
841	ECM56844.1	EM311274-1	225	7.00E-10	61 \ 233	26	Marine metagenome hypothetical protein.
842	ECI52254.1	EM496253-1	255	9.00E-10	64 \ 234	27	Marine metagenome hypothetical protein.
843	EAW10509.1	DS027054-467	132	1.00E-09	47 \ 104	45	<i>Aspergillus clavatus</i> NRRL 1 hypothetical protein.
844	ABS02965.1	CP000750-740	596	2.00E-09	79 \ 330	23	<i>Kineococcus radiotolerans</i> SRS30216 Xylose isomerase domain protein TIM barrel protein.
845	ECK69403.1	EM398094-1	179	2.00E-09	53 \ 161	32	Marine metagenome hypothetical protein.
846	ECE07777.1	EM735613-1	257	2.00E-09	55 \ 185	29	Marine metagenome hypothetical protein.
847	ECP37497.1	EM158063-2	155	4.00E-09	48 \ 143	33	Marine metagenome hypothetical protein.
848	ECF27814.1	EM644089-2	159	6.00E-09	49 \ 143	34	Marine metagenome hypothetical protein.
849	ECC24957.1	EM818089-1	89	9.00E-09	39 \ 90	43	Marine metagenome hypothetical protein.
850	CAO63348.1	CU459228-72	196	1.00E-08	52 \ 187	27	<i>Vitis vinifera</i> protein <i>Vitis vinifera</i> chromosome chr2 scaffold_11, whole genome shotgun sequence.
851	ECE79704.1	EM664652-2	301	1.00E-08	67 \ 248	27	Marine metagenome hypothetical protein.
852	BAC17251.1	BA000035-441	622	2.00E-08	82 \ 333	24	<i>Corynebacterium efficiens</i> YS-314 conserved hypothetical protein.
853	ECO08079.1	EM244557-1	278	2.00E-08	30 \ 84	35	Marine metagenome hypothetical protein.
854	ABG93191.1	CP000431-1355	644	2.00E-08	82 \ 335	24	<i>Rhodococcus jostii</i> RHA1 dehydroshikimate dehydratase protein.
855	EDH15564.1	EP607454-2	72	3.00E-08	38 \ 74	51	Marine metagenome hypothetical protein.
856	ECN80939.1	EM256371-1	204	3.00E-08	47 \ 182	25	Marine metagenome hypothetical protein.
857	ECL85783.1	EM344257-2	78	5.00E-08	37 \ 80	46	Marine metagenome hypothetical protein.
858	ECI61629.1	EM492002-1	203	2.00E-07	38 \ 110	34	Marine metagenome hypothetical protein.
859	ECF22847.1	EM646189-1	171	3.00E-07	45 \ 167	26	Marine metagenome hypothetical protein.
860	ECL85781.1	EM344257-3	217	5.00E-07	56 \ 216	25	Marine metagenome hypothetical protein.
861	EBR91108.1	EN533498-2	70	5.00E-07	35 \ 74	47	Marine metagenome hypothetical protein.
862	ECZ05324.1	EP952211-1	214	5.00E-07	62 \ 212	29	Marine metagenome hypothetical protein.
863	EDC18152.1	EP796066-1	144	7.00E-07	42 \ 115	36	Marine metagenome hypothetical protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
864	EBM71625.1	EN837192-1	479	1.00E-06	49 \ 190	25	Marine metagenome hypothetical protein.
865	EBR57064.1	EN559896-2	231	2.00E-06	59 \ 228	25	Marine metagenome hypothetical protein.
866	EBQ53501.1	EN636597-3	67	2.00E-06	35 \ 69	50	Marine metagenome hypothetical protein.
867	AAC60567.2	S69110-1	73	3.00E-06	24 \ 70	34	<i>Coccidioides immitis</i> fusion protein T-cell stimulating antigen protein.
868	EBR98670.1	EN527769-1	192	4.00E-06	51 \ 193	26	Marine metagenome hypothetical protein.
869	ECX35642.1	EQ015294-1	237	4.00E-06	54 \ 223	24	Marine metagenome hypothetical protein.
870	EDH79599.1	EP582663-1	331	4.00E-06	32 \ 78	41	Marine metagenome hypothetical protein.
871	AAA33047.1	M77190-1	69	6.00E-06	24 \ 69	34	<i>Coccidioides posadasii</i> T-cell reactive fusion protein.
872	EBW84121.1	EN106907-2	77	6.00E-06	37 \ 81	45	Marine metagenome hypothetical protein.
873	EBG20098.1	EP203962-2	143	3.00E-05	36 \ 125	28	Marine metagenome hypothetical protein.
874	ECQ19988.1	EM120910-3	254	3.00E-05	29 \ 71	40	Marine metagenome hypothetical protein.
875	CAA43931.1	X61929-1	66	4.00E-05	23 \ 66	34	<i>Coccidioides immitis</i> T-cell reactive fusion protein.
876	ECD69930.1	EM751433-3	238	4.00E-05	56 \ 234	23	Marine metagenome hypothetical protein.
877	ECC45646.1	EM808975-1	270	4.00E-05	62 \ 264	23	Marine metagenome hypothetical protein.
878	ABF10627.1	CP000353-140	207	1.00E-04	24 \ 32	75	<i>Ralstonia metallidurans</i> CH34 Endoribonuclease L-PSP protein.
879	ECH37372.1	EM547246-1	131	1.00E-04	37 \ 130	28	Marine metagenome hypothetical protein.
880	EBC68193.1	EP400328-2	173	2.00E-04	40 \ 144	27	Marine metagenome hypothetical protein.
881	ECN80938.1	EM256371-2	259	5.00E-04	26 \ 74	35	Marine metagenome hypothetical protein.
882	ABF43813.1	CP000358-99	149	6.00E-04	30 \ 98	30	<i>Deinococcus geothermalis</i> DSM 11300 Hemolysin-like protein, 4-hydroxyphenylpyruvate dioxygenase related protein.
883	AAX30651.1	AY915430-1	98	0.001	38 \ 93	40	<i>Schistosoma japonicum</i> SJCHGC06518 protein.
884	ECJ14682.1	EM466849-2	150	0.003	38 \ 127	29	Marine metagenome hypothetical protein.
885	EBS28217.1	EN504088-1	181	0.004	40 \ 136	29	Marine metagenome hypothetical protein.
886	EDG47819.1	EP633652-1	218	0.009	49 \ 216	22	Marine metagenome hypothetical protein.
887	EDD44004.1	EP749214-3	224	0.016	48 \ 188	25	Marine metagenome hypothetical protein.
888	ECN72855.1	EM259588-1	108	0.06	29 \ 111	26	Marine metagenome hypothetical protein.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

6.5. Table 5 - BLASTP sequence similarities of the HPPD W336 protein with proteins from the GenPept database

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
1	94982486	DQ459070	358	0	357 \ 358	99	Plastid transformation vector pCLT323, partial sequence.
2	94982482	DQ459069	358	0	357 \ 358	99	Plastid transformation vector pCLT111, partial sequence.
3	50250787	CQ830293	358	0	357 \ 358	99	Sequence 7 from Patent WO2004055191.
4	50250785	CQ830291	358	0	357 \ 358	99	Sequence 5 from Patent WO2004055191.
5	119358722	CS456037	358	0	345 \ 358	96	Sequence 3 from Patent EP1728868.
6	6740966	A92169	358	0	345 \ 358	96	Sequence 3 from Patent WO9820144.
7	94449351	DQ364627	358	0	341 \ 358	95	<i>Pseudomonas fluorescens</i> strain DSMZ 4358 4-hydroxyphenylpyruvate dioxygenase gene, partial cds.
8	77383145	CP000094	358	0	336 \ 358	93	<i>Pseudomonas fluorescens</i> Pf0-1, complete genome.
9	68345050	CP000076	358	0	332 \ 358	92	<i>Pseudomonas fluorescens</i> Pf-5, complete genome.
10	24985082	AE015451	358	0	315 \ 358	87	<i>Pseudomonas putida</i> KT2440 complete genome.
11	166859994	CP000926	358	0	314 \ 358	87	<i>Pseudomonas putida</i> GB-1, complete genome.
12	63257266	CP000075	358	0	312 \ 358	87	<i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a, complete genome.
13	148511608	CP000712	358	0	313 \ 358	87	<i>Pseudomonas putida</i> F1, complete genome.
14	28853962	AE016853	363	0	312 \ 357	87	<i>Pseudomonas syringae</i> pv. tomato str. DC3000, complete genome.
15	71557567	CP000058	358	0	312 \ 358	87	<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A, complete genome.
16	37727200	AY168854	358	0	312 \ 358	87	<i>Pseudomonas putida</i> p-hydroxyphenylpyruvate dioxygenase hpd gene, complete cds.
17	169759624	CP000949	358	0	311 \ 355	87	<i>Pseudomonas putida</i> W619, complete genome.
18	95111104	CT573326	357	1.00E-180	304 \ 358	84	<i>Pseudomonas entomophila</i> str. L48 chromosome, complete sequence.
19	170776170	CP001013	358	1.00E-177	298 \ 357	83	<i>Leptothrix cholodnii</i> SP-6, complete genome.
20	31324016	AF511571	301	1.00E-164	276 \ 301	91	Uncultured soil bacterium clone 214D2 4-hydroxyphenylpyruvate dioxygenase gene, partial cds.
21	72121665	CP000091	359	1.00E-164	277 \ 358	77	<i>Ralstonia eutropha</i> JMP134 chromosome 2, complete sequence.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
22	113529527	AM260480	359	1.00E-162	275 \ 358	76	<i>Ralstonia eutropha</i> H16 chromosome 2.
23	193225573	CU633750	359	1.00E-161	273 \ 358	76	<i>Cupriavidus taiwanensis</i> str. LMG19424 chromosome 2, complete genome.
24	93357699	CP000353	357	1.00E-161	271 \ 355	76	<i>Ralstonia metallidurans</i> CH34 megaplasmid, complete sequence.
25	120592997	CP000529	360	1.00E-160	268 \ 358	74	<i>Polaromonas naphthalenivorans</i> CJ2, complete genome.
26	170774570	CP001013	358	1.00E-160	269 \ 358	75	<i>Leptothrix cholodnii</i> SP-6, complete genome.
27	31324018	AF511572	308	1.00E-157	267 \ 308	86	Uncultured soil bacterium clone 89C8 4-hydroxyphenylpyruvate dioxygenase gene, partial cds.
28	160365811	CP000884	364	1.00E-155	266 \ 360	73	<i>Delftia acidovorans</i> SPH-1, complete genome.
29	109699731	CP000388	358	1.00E-150	255 \ 356	71	<i>Pseudoalteromonas atlantica</i> T6c, complete genome.
30	120605030	CP000539	372	1.00E-150	260 \ 356	73	<i>Acidovorax</i> sp. JS42, complete genome.
31	148571931	CP000713	372	1.00E-149	257 \ 361	71	<i>Psychrobacter</i> sp. PRwf-1, complete genome.
32	221729196	CP001392	372	1.00E-149	258 \ 356	72	<i>Diaphorobacter</i> sp. TPSY, complete genome.
33	196113121	CP001103	357	1.00E-149	257 \ 356	72	<i>Alteromonas macleodii</i> Deep ecotype', complete genome.
34	84787193	CP000157	373	1.00E-149	251 \ 362	69	<i>Erythrobacter litoralis</i> HTCC2594, complete genome.
35	98978671	CP000356	363	1.00E-147	247 \ 358	68	<i>Sphingopyxis alaskensis</i> RB2256, complete genome.
36	87134302	CP000248	370	1.00E-146	249 \ 361	68	<i>Novosphingobium aromaticivorans</i> DSM 12444, complete genome.
37	169147193	CU459141	351	1.00E-144	241 \ 355	67	<i>Acinetobacter baumannii</i> str. AYE, complete genome.
38	213058320	CP001182	351	1.00E-144	241 \ 355	67	<i>Acinetobacter baumannii</i> AB0057, complete genome.
39	213988761	CP001172	351	1.00E-144	241 \ 355	67	<i>Acinetobacter baumannii</i> AB307-0294, complete genome.
40	183211525	CP000863	351	1.00E-144	241 \ 355	67	<i>Acinetobacter baumannii</i> ACICU, complete genome.
41	193078735	CP000521	351	1.00E-144	241 \ 355	67	<i>Acinetobacter baumannii</i> ATCC 17978, complete genome.
42	114738742	CP000158	366	1.00E-144	248 \ 363	68	<i>Hyphomonas neptunium</i> ATCC 15444, complete genome.
43	169153662	CU468230	351	1.00E-143	239 \ 355	67	<i>Acinetobacter baumannii</i> str. SDF, complete genome.
44	114339349	CP000449	359	1.00E-143	236 \ 357	66	<i>Maricaulis maris</i> MCS10, complete genome.
45	92394057	CP000323	368	1.00E-142	249 \ 359	69	<i>Psychrobacter cryohalolentis</i> K5, complete genome.
46	150837674	CP000749	358	1.00E-141	245 \ 358	68	<i>Marinomonas</i> sp. MWYL1, complete genome.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
47	209960066	CP000613	377	1.00E-122	224 \ 362	61	<i>Rhodospirillum centenum</i> SW, complete genome.
48	187727344	CP001068	368	1.00E-118	215 \ 364	59	<i>Ralstonia pickettii</i> 12J chromosome 1, complete sequence.
49	206596048	CU914168	367	1.00E-117	215 \ 364	59	<i>Ralstonia solanacearum</i> strain IPO1609 Genome Draft.
50	34102277	AE016825	358	1.00E-116	210 \ 361	58	<i>Chromobacterium violaceum</i> ATCC 12472, complete genome.
51	17430127	AL646052	367	1.00E-116	213 \ 364	58	<i>Ralstonia solanacearum</i> GMI1000 chromosome complete sequence.
52	119669897	AM406670	373	1.00E-116	215 \ 369	58	<i>Azoarcus</i> sp. BH72, complete genome.
53	196479714	CP000747	374	1.00E-115	211 \ 357	59	<i>Phenylobacterium zucineum</i> HLK1, complete genome.
54	206587984	CU694394	358	1.00E-115	212 \ 360	58	<i>Ralstonia solanacearum</i> strain MolK2 Genome Draft.
55	83653834	CP000086	365	1.00E-114	207 \ 361	57	<i>Burkholderia thailandensis</i> E264 chromosome I, complete sequence.
56	120591291	CP000512	378	1.00E-114	215 \ 365	58	<i>Acidovorax avenae</i> subsp. citrulli AAC00-1, complete genome.
57	91689447	CP000270	365	1.00E-114	207 \ 361	57	<i>Burkholderia xenovorans</i> LB400 chromosome 1, complete sequence.
58	33568819	BX640449	370	1.00E-114	206 \ 363	56	<i>Bordetella bronchiseptica</i> strain RB50, complete genome; segment 13/16.
59	33566835	BX640434	370	1.00E-114	206 \ 363	56	<i>Bordetella parapertussis</i> strain 12822, complete genome; segment 12/14.
60	184194073	CP001043	365	1.00E-113	203 \ 361	56	<i>Burkholderia phymatum</i> STM815 chromosome 1, complete sequence.
61	187716837	CP001052	365	1.00E-113	206 \ 361	57	<i>Burkholderia phytofirmans</i> PsJN chromosome 1, complete sequence.
62	163258714	AM902716	370	1.00E-113	205 \ 365	56	<i>Bordetella petrii</i> strain DSM 12804, complete genome.
63	126228708	CP000572	365	1.00E-113	204 \ 361	56	<i>Burkholderia pseudomallei</i> 1106a chromosome I, complete sequence.
64	126219259	CP000570	365	1.00E-113	204 \ 361	56	<i>Burkholderia pseudomallei</i> 668 chromosome I, complete sequence.
65	126243826	CP000548	365	1.00E-113	204 \ 361	56	<i>Burkholderia mallei</i> NCTC 10247 chromosome I, complete sequence.
66	124293196	CP000546	365	1.00E-113	204 \ 361	56	<i>Burkholderia mallei</i> NCTC 10229 chromosome I, complete sequence.
67	121227385	CP000526	365	1.00E-113	204 \ 361	56	<i>Burkholderia mallei</i> SAVP1 chromosome I, complete sequence.
68	121229288	CP000526	365	1.00E-113	204 \ 361	56	<i>Burkholderia mallei</i> SAVP1 chromosome I, complete sequence.
69	76581302	CP000124	365	1.00E-113	204 \ 361	56	<i>Burkholderia pseudomallei</i> 1710b chromosome I, complete sequence.
70	52427645	CP000010	365	1.00E-113	204 \ 361	56	<i>Burkholderia mallei</i> ATCC 23344 chromosome 1, complete sequence.
71	52211261	BX571965	365	1.00E-113	204 \ 361	56	<i>Burkholderia pseudomallei</i> strain K96243, chromosome 1, complete sequence.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
72	134137573	CP000614	365	1.00E-113	204 \ 361	56	<i>Burkholderia vietnamiensis</i> G4 chromosome 1, complete sequence.
73	33564043	BX640420	370	1.00E-112	204 \ 363	56	<i>Bordetella pertussis</i> strain Tohama I, complete genome; segment 10/12.
74	169814898	CP000958	365	1.00E-112	202 \ 361	55	<i>Burkholderia cenocepacia</i> MC0-3 chromosome 1, complete sequence.
75	116646434	CP000458	365	1.00E-112	202 \ 361	55	<i>Burkholderia cenocepacia</i> HI2424 chromosome 1, complete sequence.
76	105894518	CP000378	365	1.00E-112	202 \ 361	55	<i>Burkholderia cenocepacia</i> AU 1054 chromosome 1, complete sequence.
77	115280283	CP000440	365	1.00E-112	202 \ 361	55	<i>Burkholderia ambifaria</i> AMMD chromosome 1, complete sequence.
78	160340832	CP000868	365	1.00E-112	202 \ 361	55	<i>Burkholderia multivorans</i> ATCC 17616 chromosome 1, complete sequence.
79	189335846	AP009385	365	1.00E-112	202 \ 361	55	<i>Burkholderia multivorans</i> ATCC 17616 DNA, complete genome, chromosome 1.
80	171991830	CP001025	365	1.00E-112	203 \ 361	56	<i>Burkholderia ambifaria</i> MC40-6 chromosome 1, complete sequence.
81	148501956	CP000699	367	1.00E-112	199 \ 354	56	<i>Sphingomonas wittichii</i> RW1, complete genome.
82	146196521	CU234118	372	1.00E-112	195 \ 355	54	<i>Bradyrhizobium</i> sp. ORS278, complete sequence.
83	124258314	CP000555	370	1.00E-111	205 \ 364	56	<i>Methylibium petroleiphilum</i> PM1, complete genome.
84	198034651	AM747720	365	1.00E-111	201 \ 361	55	<i>Burkholderia cenocepacia</i> J2315 chromosome 1, complete genome.
85	77965642	CP000151	365	1.00E-111	201 \ 361	55	<i>Burkholderia</i> sp. 383 chromosome 1, complete sequence.
86	76883245	CP000127	351	1.00E-111	199 \ 355	56	<i>Nitrosococcus oceani</i> ATCC 19707, complete genome.
87	192282187	CP001096	372	1.00E-111	191 \ 355	53	<i>RhodoPseudomonas palustris</i> TIE-1, complete genome.
88	39652710	BX572593	372	1.00E-111	190 \ 355	53	<i>RhodoPseudomonas palustris</i> CGA009 complete genome; segment 1/16.
89	115423952	AM167904	370	1.00E-111	204 \ 365	55	<i>Bordetella avium</i> 197N complete genome.
90	27348587	BA000040	372	1.00E-110	190 \ 355	53	<i>Bradyrhizobium japonicum</i> USDA 110 DNA, complete genome.
91	121553736	CP000542	377	1.00E-110	204 \ 365	55	<i>Verminephrobacter eiseniae</i> EF01-2, complete genome.
92	146404342	CP000494	372	1.00E-110	192 \ 355	54	<i>Bradyrhizobium</i> sp. BTAi1, complete genome.
93	91699276	CP000316	376	1.00E-109	207 \ 367	56	<i>Polaromonas</i> sp. JS666, complete genome.
94	83631876	CP000155	365	1.00E-104	188 \ 362	51	<i>Hahella chejuensis</i> KCTC 2396, complete genome.
95	119374168	CP000489	370	1.00E-104	192 \ 355	54	<i>Paracoccus denitrificans</i> PD1222 chromosome 1, complete sequence.
96	115584010	CP000438	357	1.00E-103	186 \ 352	52	<i>Pseudomonas aeruginosa</i> UCBPP-PA14, complete genome.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
97	9946763	AE004091	357	1.00E-103	186 \ 352	52	<i>Pseudomonas aeruginosa</i> PAO1, complete genome.
98	218773394	FM209186	357	1.00E-103	186 \ 352	52	<i>Pseudomonas aeruginosa</i> LESB58 complete genome sequence.
99	145574928	CP000680	360	1.00E-103	187 \ 355	52	<i>Pseudomonas mendocina</i> ymp, complete genome.
100	156526056	CP000789	357	1.00E-102	194 \ 361	53	<i>Vibrio harveyi</i> ATCC BAA-1116 chromosome I, complete sequence.
101	27362256	AE016795	357	1.00E-102	192 \ 355	54	<i>Vibrio vulnificus</i> CMCP6 chromosome I complete sequence.
102	37198424	BA000037	357	1.00E-102	192 \ 355	54	<i>Vibrio vulnificus</i> YJ016 DNA, chromosome I, complete sequence.
103	18104608	AF457645	357	1.00E-101	192 \ 355	54	<i>Listonella anguillarum</i> 4-hydroxyphenylpyruvate dioxygenase hpdA gene, complete cds; and homogentisic acid oxidase (hmgA) gene, partial cds.
104	145569460	CP000304	361	1.00E-101	188 \ 354	53	<i>Pseudomonas stutzeri</i> A1501, complete genome.
105	218325528	FM954973	357	1.00E-100	189 \ 354	53	<i>Vibrio splendidus</i> LGP32 chromosome 2.
106	28806337	BA000031	357	1.00E-100	192 \ 361	53	<i>Vibrio parahaemolyticus</i> RIMD 2210633 DNA, chromosome 1, complete sequence.
107	109701585	CP000388	360	1.00E-100	191 \ 361	52	<i>Pseudoalteromonas atlantica</i> T6c, complete genome.
108	117562568	CP000462	365	1.00E-100	191 \ 355	53	<i>Aeromonas hydrophila</i> subsp. <i>hydrophila</i> ATCC 7966, complete genome.
109	150962869	CP000744	357	5.00E-99	185 \ 352	52	<i>Pseudomonas aeruginosa</i> PA7, complete genome.
110	6648538	U31553	369	5.00E-99	191 \ 355	53	<i>Vibrio cholerae</i> p-hydroxyphenylpyruvate dioxygenase ppdA and ORF2 protein genes, complete cds.
111	146314943	CP000627	369	5.00E-99	191 \ 355	53	<i>Vibrio cholerae</i> O395 chromosome 2, complete genome.
112	9655836	AE003852	369	5.00E-99	191 \ 355	53	<i>Vibrio cholerae</i> O1 biovar eltor str. N16961 chromosome I, complete sequence.
113	190014075	AM743169	356	7.00E-99	181 \ 354	51	<i>Stenotrophomonas maltophilia</i> K279a complete genome, strain K279a.
114	142852228	CP000644	370	7.00E-99	190 \ 354	53	<i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i> A449, complete genome.
115	194350315	CP001111	356	9.00E-99	181 \ 354	51	<i>Stenotrophomonas maltophilia</i> R551-3, complete genome.
116	14027622	BA000012	371	3.00E-98	176 \ 355	49	<i>Mesorhizobium loti</i> MAFF303099 DNA, complete genome.
117	115256276	AM236080	369	4.00E-98	179 \ 352	50	<i>Rhizobium leguminosarum</i> bv. <i>viciae</i> chromosome complete genome, strain 3841.
118	114177171	DQ849081	367	5.00E-98	179 \ 352	50	Uncultured bacterium clone pYS103B 4-hydroxyphenylpyruvate dioxygenase HPPD gene, complete cds.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
119	169655858	EU489065	367	5.00E-98	179 \ 352	50	Uncultured soil bacterium clone pYS107D di-tripeptide transporter gene, partial cds; and 4-hydroxyphenylpyruvate dioxygenase and putative homogentisate dioxygenase genes, complete cds.
120	46916283	CR378678	365	2.00E-97	190 \ 356	53	<i>Photobacterium profundum</i> SS9 chromosome 2; segment 4/7.
121	167731626	AM920689	371	4.00E-97	181 \ 354	51	<i>Xanthomonas campestris</i> pv. <i>campestris</i> complete genome, strain B100.
122	21111421	AE008922	356	6.00E-97	181 \ 354	51	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913, complete genome.
123	66572122	CP000050	356	6.00E-97	181 \ 354	51	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. 8004, complete genome.
124	86281477	CP000133	369	6.00E-97	176 \ 352	50	<i>Rhizobium etli</i> CFN 42, complete genome.
125	110286202	CP000390	369	7.00E-97	183 \ 352	51	<i>Mesorhizobium</i> sp. BNC1, complete genome.
126	150029549	CP000738	370	2.00E-96	180 \ 353	50	<i>Sinorhizobium medicae</i> WSM419, complete genome.
127	15075967	AL591688	370	4.00E-96	179 \ 353	50	<i>Sinorhizobium meliloti</i> 1021 complete chromosome.
128	209534765	CP001191	369	1.00E-95	173 \ 352	49	<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM2304, complete genome.
129	108464159	CP000113	354	2.00E-95	184 \ 362	50	<i>Myxococcus xanthus</i> DK 1622, complete genome.
130	190696711	CP001074	369	3.00E-95	173 \ 352	49	<i>Rhizobium etli</i> CIAT 652, complete genome.
131	78034468	AM039952	356	8.00E-95	178 \ 354	50	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> complete genome.
132	158667951	EU196552	354	1.00E-94	182 \ 361	50	Uncultured bacterium clone fSS61 putative homogentisate 1,2-dioxygenase gene, partial cds; and 4-hydroxyphenylpyruvate dioxygenase, putative aromatic amino acid metabolism transcriptional regulator, and putative pterin-4-alpha-carbinolamine dehydratase genes, complete cds.
133	21106538	AE008923	356	1.00E-94	178 \ 354	50	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306, complete genome.
134	88865300	CP000264	363	2.00E-94	178 \ 352	50	<i>Jannaschia</i> sp. CCS1, complete genome.
135	188519488	CP000967	371	4.00E-94	175 \ 354	49	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A, complete genome.
136	84369443	AP008229	356	4.00E-94	175 \ 354	49	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> MAFF 311018 DNA, complete genome.
137	58428288	AE013598	403	5.00E-94	175 \ 354	49	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> KACC10331, complete genome.
138	56178841	AE017340	357	7.00E-94	183 \ 361	50	<i>Idiomarina loihiensis</i> L2TR, complete genome.
139	220964725	CP001340	357	1.00E-93	171 \ 354	48	<i>Caulobacter crescentus</i> NA1000, complete genome.
140	13424094	AE005673	357	1.00E-93	171 \ 354	48	<i>Caulobacter crescentus</i> CB15, complete genome.
141	109455241	CP000362	364	1.00E-93	170 \ 355	47	<i>Roseobacter denitrificans</i> OCh 114, complete genome.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
142	2108220	U97357	357	2.00E-93	182 \ 355	51	<i>Vibrio vulnificus</i> hemolysin vly gene, complete cds.
143	56678047	CP000031	366	4.00E-93	177 \ 355	49	<i>Ruegeria pomeroyi</i> DSS-3, complete genome.
144	31324014	AF511570	353	4.00E-93	173 \ 353	49	Uncultured soil bacterium clone 57G4 4-hydroxyphenylpyruvate dioxygenase gene, complete cds.
145	99036703	CP000377	366	6.00E-93	176 \ 355	49	<i>Silicibacter</i> sp. TM1040, complete genome.
146	148281595	CP000675	348	2.00E-90	175 \ 349	50	<i>Legionella pneumophila</i> str. Corby, complete genome.
147	52629602	AE017354	361	4.00E-90	175 \ 349	50	<i>Legionella pneumophila</i> subsp. pneumophila str. Philadelphia 1, complete genome.
148	3452358	AF075724	348	4.00E-90	175 \ 349	50	<i>Legionella pneumophila</i> legiolysin lly gene, complete cds; and unknown genes.
149	53754956	CR628337	348	4.00E-90	175 \ 349	50	<i>Legionella pneumophila</i> str. Lens complete genome.
150	53751960	CR628336	348	8.00E-90	174 \ 349	49	<i>Legionella pneumophila</i> str. Paris complete genome.
151	2632111	AJ001357	348	9.00E-90	175 \ 349	50	<i>Legionella pneumophila</i> strain Corby DNA for Legiolysin.
152	221726451	CP000629	333	8.00E-89	165 \ 331	49	<i>Agrobacterium radiobacter</i> K84 chromosome 2, complete sequence.
153	167350045	CP000927	353	4.00E-87	176 \ 357	49	<i>Caulobacter</i> sp. K31, complete genome.
154	76876002	CR954246	348	2.00E-83	163 \ 350	46	<i>Pseudoalteromonas haloplanktis</i> str. TAC125 chromosome I, complete sequence.
155	169811632	CP000961	346	9.00E-81	159 \ 353	45	<i>Shewanella woodyi</i> ATCC 51908, complete genome.
156	167354355	CP000931	346	9.00E-80	155 \ 350	44	<i>Shewanella halifaxensis</i> HAW-EB4, complete genome.
157	157846697	CP000851	346	4.00E-79	155 \ 353	43	<i>Shewanella pealeana</i> ATCC 700345, complete genome.
158	114334791	CP000447	346	5.00E-79	154 \ 349	44	<i>Shewanella frigidimarina</i> NCIMB 400, complete genome.
159	160861363	CP000891	346	5.00E-79	155 \ 351	44	<i>Shewanella baltica</i> OS195, complete genome.
160	151365789	CP000753	346	5.00E-79	155 \ 351	44	<i>Shewanella baltica</i> OS185, complete genome.
161	145564460	CP000681	346	6.00E-79	154 \ 351	43	<i>Shewanella putrefaciens</i> CN-32, complete genome.
162	217498043	CP001252	346	8.00E-79	155 \ 351	44	<i>Shewanella baltica</i> OS223, complete genome.
163	120559252	CP000503	346	1.00E-78	154 \ 351	43	<i>Shewanella</i> sp. W3-18-1, complete genome.
164	152722	M59289	346	1.00E-78	154 \ 353	43	<i>S. colwelliana</i> melA protein gene, complete cds.
165	157318196	CP000821	346	2.00E-78	155 \ 353	43	<i>Shewanella sediminis</i> HAW-EB3, complete genome.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
166	91715519	CP000302	346	2.00E-78	154 \ 352	43	<i>Shewanella denitrificans</i> OS217, complete genome.
167	125998034	CP000563	346	2.00E-78	154 \ 351	43	<i>Shewanella baltica</i> OS155, complete genome.
168	39577105	BX842655	352	3.00E-78	155 \ 358	43	<i>BdelloVibrio bacteriovorus</i> complete genome, strain HD100; segment 10/11.
169	126638378	CP000606	346	3.00E-78	153 \ 350	43	<i>Shewanella loihica</i> PV-4, complete genome.
170	212557143	CP000472	346	3.00E-78	152 \ 352	43	<i>Shewanella piezotolerans</i> WP3, complete genome.
171	119767205	CP000507	345	3.00E-77	155 \ 352	44	<i>Shewanella amazonensis</i> SB2B, complete genome.
172	24347835	AE014299	346	2.00E-76	151 \ 352	42	<i>Shewanella oneidensis</i> MR-1, complete genome.
173	117613257	CP000469	346	6.00E-76	151 \ 352	42	<i>Shewanella</i> sp. ANA-3, complete genome.
174	113885311	CP000446	346	6.00E-76	151 \ 352	42	<i>Shewanella</i> sp. MR-4, complete genome.
175	113889300	CP000444	346	6.00E-76	151 \ 352	42	<i>Shewanella</i> sp. MR-7, complete genome.
176	115283844	CP000441	375	9.00E-70	147 \ 352	41	<i>Burkholderia ambifaria</i> AMMD chromosome 2, complete sequence.
177	116650489	CP000459	375	4.00E-69	144 \ 352	40	<i>Burkholderia cenocepacia</i> HI2424 chromosome 2, complete sequence.
178	105895697	CP000379	375	4.00E-69	144 \ 352	40	<i>Burkholderia cenocepacia</i> AU 1054 chromosome 2, complete sequence.
179	77970360	CP000152	375	4.00E-69	146 \ 352	41	<i>Burkholderia</i> sp. 383 chromosome 2, complete sequence.
180	171995820	CP001026	375	7.00E-69	145 \ 352	41	<i>Burkholderia ambifaria</i> MC40-6 chromosome 2, complete sequence.
181	198039410	AM747721	375	1.00E-68	144 \ 352	40	<i>Burkholderia cenocepacia</i> J2315 chromosome 2, complete genome.
182	169820499	CP000959	375	1.00E-68	144 \ 352	40	<i>Burkholderia cenocepacia</i> MC0-3 chromosome 2, complete sequence.
183	71147316	CP000083	351	2.00E-68	145 \ 357	40	<i>Colwellia psychrerythraea</i> 34H, complete genome.
184	134136764	CP000615	375	9.00E-68	144 \ 352	40	<i>Burkholderia vietnamiensis</i> G4 chromosome 2, complete sequence.
185	83650507	CP000085	381	7.00E-67	144 \ 351	41	<i>Burkholderia thailandensis</i> E264 chromosome II, complete sequence.
186	160344822	CP000869	375	2.00E-66	142 \ 350	40	<i>Burkholderia multivorans</i> ATCC 17616 chromosome 2, complete sequence.
187	187728232	CP001069	357	3.00E-66	143 \ 348	41	<i>Ralstonia pickettii</i> 12J chromosome 2, complete sequence.
188	91690024	CP000271	377	2.00E-65	142 \ 356	39	<i>Burkholderia xenovorans</i> LB400 chromosome 2, complete sequence.
189	72122190	CP000091	357	2.00E-65	157 \ 355	44	<i>Ralstonia eutropha</i> JMP134 chromosome 2, complete sequence.
190	184195052	CP001044	375	8.00E-65	144 \ 359	40	<i>Burkholderia phymatum</i> STM815 chromosome 2, complete sequence.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
191	187719829	CP001053	377	1.00E-64	141 \ 356	39	<i>Burkholderia phytofirmans</i> PsJN chromosome 2, complete sequence.
192	189337068	AP009386	351	3.00E-64	138 \ 342	40	<i>Burkholderia multivorans</i> ATCC 17616 genomic DNA, complete genome, chromosome 2.
193	158187231	EU165546	377	4.00E-64	140 \ 356	39	<i>Burkholderia</i> sp. NCIMB 10467 hypothetical protein gene, partial cds; and hypothetical protein, putative amino acid efflux pump <i>pcaE</i> , hypothetical protein, protocatechuate 3,4-dioxygenase alpha subunit (<i>pcaG</i>), protocatechuate 3,4-dioxygenase beta subunit (<i>pcaH</i>), LysR-like transcriptional regulator (<i>pcaR</i>), 4-hydroxyphenylpyruvate dioxygenase (<i>hpd</i>), LysR-like transcriptional regulator (<i>pcaR'</i>), hypothetical protein, and putative FAD-dependent oxidoreductase genes, complete cds.
194	17431820	AL646053	361	3.00E-61	139 \ 349	39	<i>Ralstonia solanacearum</i> GMI1000 megaplasmid complete sequence.
195	17431789	AL646053	361	3.00E-61	139 \ 349	39	<i>Ralstonia solanacearum</i> GMI1000 megaplasmid complete sequence.
196	206587543	CU694393	322	4.00E-61	132 \ 336	39	<i>Ralstonia solanacearum</i> strain MolK2 Genome Draft.
197	145568801	CP000304	641	4.00E-48	120 \ 345	34	<i>Pseudomonas stutzeri</i> A1501, complete genome.
198	219944777	CP001349	627	5.00E-47	115 \ 329	34	<i>Methylobacterium nodulans</i> ORS 2060, complete genome.
199	168197138	CP000943	637	1.00E-45	119 \ 329	36	<i>Methylobacterium</i> sp. 4-46, complete genome.
200	83744141	DQ311664	636	3.00E-45	123 \ 341	36	<i>Pseudomonas chlororaphis</i> 4-hydroxyphenylpyruvate dioxygenase, phenazine inducing protein <i>pip</i> , and transcriptional regulator genes, complete cds.
201	68346989	CP000076	636	2.00E-44	119 \ 340	35	<i>Pseudomonas fluorescens</i> Pf-5, complete genome.
202	187728237	CP001069	628	3.00E-44	122 \ 348	35	<i>Ralstonia pickettii</i> 12J chromosome 2, complete sequence.
203	77385129	CP000094	633	6.00E-43	120 \ 352	34	<i>Pseudomonas fluorescens</i> Pf0-1, complete genome.
204	115589176	CP000438	634	9.00E-43	122 \ 345	35	<i>Pseudomonas aeruginosa</i> UCBPP-PA14, complete genome.
205	218769206	FM209186	634	2.00E-42	122 \ 345	35	<i>Pseudomonas aeruginosa</i> LESB58 complete genome sequence.
206	9946081	AE004091	634	2.00E-42	122 \ 345	35	<i>Pseudomonas aeruginosa</i> PAO1, complete genome.
207	152022824	CP000764	372	8.00E-42	128 \ 347	36	<i>Bacillus cereus</i> subsp. <i>cytotoxis</i> NVH 391-98, complete genome.
208	169759409	CP000949	635	4.00E-41	108 \ 328	32	<i>Pseudomonas putida</i> W619, complete genome.
209	222448035	CP001364	365	9.00E-41	125 \ 367	34	<i>Chloroflexus</i> sp. Y-400-fl, complete genome.
210	163667678	CP000909	365	9.00E-41	125 \ 367	34	<i>Chloroflexus aurantiacus</i> J-10-fl, complete genome.
211	95110140	CT573326	634	9.00E-41	114 \ 343	33	<i>Pseudomonas entomophila</i> str. L48 chromosome, complete sequence.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
212	49330698	AE017355	372	2.00E-40	126 \ 348	36	<i>Bacillus thuringiensis</i> serovar konkukian str. 97-27, complete genome.
213	47500645	AE017334	372	2.00E-40	126 \ 348	36	<i>Bacillus anthracis</i> str. Ames Ancestor', complete genome.
214	49177186	AE017225	372	2.00E-40	126 \ 348	36	<i>Bacillus anthracis</i> str. Sterne, complete genome.
215	42735256	AE017194	372	2.00E-40	126 \ 348	36	<i>Bacillus cereus</i> ATCC 10987, complete genome.
216	225789585	CP001407	372	2.00E-40	126 \ 348	36	<i>Bacillus cereus</i> 03BB102, complete genome.
217	218539210	CP001283	372	2.00E-40	126 \ 348	36	<i>Bacillus cereus</i> AH820, complete genome.
218	217062955	CP001177	372	2.00E-40	126 \ 348	36	<i>Bacillus cereus</i> AH187, complete genome.
219	30253738	AE016879	372	2.00E-40	126 \ 348	36	<i>Bacillus anthracis</i> str. Ames, complete genome.
220	221238049	CP000227	372	2.00E-40	126 \ 348	36	<i>Bacillus cereus</i> Q1, complete genome.
221	51978468	CP000001	372	2.00E-40	126 \ 348	36	<i>Bacillus cereus</i> E33L, complete genome.
222	150962421	CP000744	634	2.00E-40	119 \ 345	34	<i>Pseudomonas aeruginosa</i> PA7, complete genome.
223	184192305	CP001043	628	2.00E-40	106 \ 334	31	<i>Burkholderia phymatum</i> STM815 chromosome 1, complete sequence.
224	118415213	CP000485	389	2.00E-40	126 \ 348	36	<i>Bacillus thuringiensis</i> str. Al Hakam, complete genome.
225	86284361	CP000136	629	3.00E-40	113 \ 329	34	<i>Rhizobium etli</i> CFN 42 plasmid p42c, complete sequence.
226	218162113	CP001176	372	9.00E-40	125 \ 348	35	<i>Bacillus cereus</i> B4264, complete genome.
227	29894029	AE016877	372	9.00E-40	125 \ 348	35	<i>Bacillus cereus</i> ATCC 14579, complete genome.
228	171996721	CP001026	630	1.00E-39	111 \ 331	33	<i>Burkholderia ambifaria</i> MC40-6 chromosome 2, complete sequence.
229	218543034	CP001186	372	2.00E-39	125 \ 348	35	<i>Bacillus cereus</i> G9842, complete genome.
230	83757965	CP000159	384	2.00E-39	119 \ 343	34	<i>Salinibacter ruber</i> DSM 13855, complete genome.
231	226096879	AP008955	363	3.00E-39	118 \ 341	34	<i>Brevibacillus brevis</i> NBRC 100599 DNA, complete genome.
232	160344017	CP000869	630	4.00E-39	107 \ 326	32	<i>Burkholderia multivorans</i> ATCC 17616 chromosome 2, complete sequence.
233	189337880	AP009386	630	4.00E-39	107 \ 326	32	<i>Burkholderia multivorans</i> ATCC 17616 genomic DNA, complete genome, chromosome 2.
234	146152910	CP000685	386	4.00E-39	119 \ 336	35	<i>Flavobacterium johnsoniae</i> UW101, complete genome.
235	72122197	CP000091	632	4.00E-39	110 \ 327	33	<i>Ralstonia eutropha</i> JMP134 chromosome 2, complete sequence.
236	115284700	CP000441	630	4.00E-39	110 \ 328	33	<i>Burkholderia ambifaria</i> AMMD chromosome 2, complete sequence.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
237	166860847	CP000926	635	4.00E-39	109 \ 338	32	<i>Pseudomonas putida</i> GB-1, complete genome.
238	77969080	CP000152	630	6.00E-39	107 \ 329	32	<i>Burkholderia</i> sp. 383 chromosome 2, complete sequence.
239	28852786	AE016853	635	8.00E-39	105 \ 329	31	<i>Pseudomonas syringae</i> pv. tomato str. DC3000, complete genome.
240	219543869	CP001337	365	9.00E-39	122 \ 367	33	<i>Chloroflexus aggregans</i> DSM 9485, complete genome.
241	24984122	AE015451	635	9.00E-39	110 \ 339	32	<i>Pseudomonas putida</i> KT2440 complete genome.
242	148512429	CP000712	635	9.00E-39	110 \ 339	32	<i>Pseudomonas putida</i> F1, complete genome.
243	63256077	CP000075	635	1.00E-38	105 \ 329	31	<i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a, complete genome.
244	159892322	CP000875	373	1.00E-38	124 \ 371	33	<i>Herpetosiphon aurantiacus</i> ATCC 23779, complete genome.
245	116226422	CP000473	375	1.00E-38	119 \ 356	33	<i>Solibacter usitatus</i> Ellin6076, complete genome.
246	145314566	DQ849080	375	1.00E-38	122 \ 375	32	Uncultured bacterium clone pYS85C 4-hydroxyphenylpyruvate dioxygenase HPPD gene, complete cds.
247	198040383	AM747721	630	2.00E-38	110 \ 328	33	<i>Burkholderia cenocepacia</i> J2315 chromosome 2, complete genome.
248	115257241	AM236080	630	2.00E-38	113 \ 334	33	<i>Rhizobium leguminosarum</i> bv. <i>viciae</i> chromosome complete genome, strain 3841.
249	163860428	CP000903	372	2.00E-38	123 \ 347	35	<i>Bacillus weihenstephanensis</i> KBAB4, complete genome.
250	134135426	CP000615	630	2.00E-38	109 \ 328	33	<i>Burkholderia vietnamiensis</i> G4 chromosome 2, complete sequence.
251	71557637	CP000058	635	3.00E-38	104 \ 329	31	<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A, complete genome.
252	116651398	CP000459	630	3.00E-38	110 \ 328	33	<i>Burkholderia cenocepacia</i> HI2424 chromosome 2, complete sequence.
253	105894794	CP000379	630	3.00E-38	110 \ 328	33	<i>Burkholderia cenocepacia</i> AU 1054 chromosome 2, complete sequence.
254	169819511	CP000959	630	3.00E-38	110 \ 328	33	<i>Burkholderia cenocepacia</i> MC0-3 chromosome 2, complete sequence.
255	117579645	CU207366	380	4.00E-38	116 \ 341	34	<i>Gramella forsetii</i> KT0803 complete circular genome.
256	91795516	CP000285	615	4.00E-38	104 \ 323	32	<i>Chromohalobacter salexigens</i> DSM 3043, complete genome.
257	226090720	AP009153	374	5.00E-38	118 \ 330	35	Gemmatimonas aurantiaca T-27 DNA, complete genome.
258	115259922	AM236085	631	5.00E-38	114 \ 340	33	<i>Rhizobium leguminosarum</i> bv. <i>viciae</i> plasmid pRL11 complete genome, strain 3841.
259	157919006	CP000850	401	1.00E-37	124 \ 386	32	<i>Salinispora arenicola</i> CNS-205, complete genome.
260	150838834	CP000749	617	1.00E-37	108 \ 326	33	<i>Marinomonas</i> sp. MWYL1, complete genome.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
261	146409534	CP000494	623	1.00E-37	104 \ 324	32	<i>Bradyrhizobium</i> sp. BTAi1, complete genome.
262	126231412	CP000573	684	2.00E-37	108 \ 329	32	<i>Burkholderia pseudomallei</i> 1106a chromosome II, complete sequence.
263	52211788	BX571966	684	2.00E-37	108 \ 329	32	<i>Burkholderia pseudomallei</i> strain K96243, chromosome 2, complete sequence.
264	126222471	CP000571	687	2.00E-37	108 \ 329	32	<i>Burkholderia pseudomallei</i> 668 chromosome II, complete sequence.
265	126239400	CP000547	684	2.00E-37	108 \ 329	32	<i>Burkholderia mallei</i> NCTC 10247 chromosome II, complete sequence.
266	124290216	CP000545	684	2.00E-37	108 \ 329	32	<i>Burkholderia mallei</i> NCTC 10229 chromosome II, complete sequence.
267	121225141	CP000525	684	2.00E-37	108 \ 329	32	<i>Burkholderia mallei</i> SAVP1 chromosome II, complete sequence.
268	52423541	CP000011	684	2.00E-37	108 \ 329	32	<i>Burkholderia mallei</i> ATCC 23344 chromosome 2, complete sequence.
269	21522871	AX417724	381	3.00E-37	109 \ 297	36	Sequence 15 from Patent WO0231173.
270	13275243	AX085149	381	3.00E-37	109 \ 297	36	Sequence 14 from Patent WO0112827.
271	29608808	BA000030	381	3.00E-37	109 \ 297	36	<i>Streptomyces avermitilis</i> MA-4680 DNA, complete genome.
272	15823928	AB070935	381	3.00E-37	109 \ 297	36	<i>Streptomyces avermitilis</i> ochronotic pigment bioSynthetic gene cluster.
273	76582500	CP000125	684	3.00E-37	108 \ 329	32	<i>Burkholderia pseudomallei</i> 1710b chromosome II, complete sequence.
274	555806	U11864	380	3.00E-37	109 \ 297	36	<i>Streptomyces avermitilis</i> ATCC 31272 4-hydroxyphenylpyruvate acid dioxygenase gene, complete cds.
275	146195239	CU234118	623	4.00E-37	104 \ 327	31	<i>Bradyrhizobium</i> sp. ORS278, complete sequence.
276	149770877	AM398681	386	6.00E-37	118 \ 345	34	<i>Flavobacterium psychrophilum</i> JIP02/86 complete genome.
277	48431089	AE017261	368	1.00E-36	116 \ 359	32	<i>Picrophilus torridus</i> DSM 9790, complete genome.
278	94551081	CP000360	361	2.00E-36	116 \ 372	31	<i>Acidobacteria bacterium</i> Ellin345, complete genome.
279	158329967	AP009384	639	2.00E-36	114 \ 348	32	<i>Azorhizobium caulinodans</i> ORS 571 DNA, complete genome.
280	169239959	CU458896	401	2.00E-36	118 \ 360	32	<i>Mycobacterium abscessus</i> chromosome, complete sequence.
281	145306096	CP000667	401	3.00E-36	120 \ 386	31	<i>Salinispora tropica</i> CNB-440, complete genome.
282	151563631	CP000759	633	5.00E-36	111 \ 328	33	<i>Ochrobactrum anthropi</i> ATCC 49188 chromosome 2, complete sequence.
283	110819689	CP000431	404	6.00E-36	124 \ 383	32	<i>Rhodococcus jostii</i> RHA1, complete genome.
284	167354360	CP000931	173	1.00E-35	80 \ 174	45	<i>Shewanella halifaxensis</i> HAW-EB4, complete genome.
285	5531376	AL939114	381	2.00E-35	105 \ 294	35	<i>Streptomyces coelicolor</i> A32 complete genome; segment 11/29.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
286	83652151	CP000085	687	2.00E-35	106 \ 329	32	<i>Burkholderia thailandensis</i> E264 chromosome II, complete sequence.
287	27349303	BA000040	623	2.00E-35	104 \ 327	31	<i>Bradyrhizobium japonicum</i> USDA 110 DNA, complete genome.
288	159891451	CP000875	366	2.00E-35	110 \ 328	33	<i>Herpetosiphon aurantiacus</i> ATCC 23779, complete genome.
289	225792460	CP001472	374	3.00E-35	107 \ 355	30	<i>Acidobacterium capsulatum</i> ATCC 51196, complete genome.
290	178466921	AP009493	381	3.00E-35	105 \ 297	35	<i>Streptomyces griseus</i> subsp. <i>griseus</i> NBRC 13350 DNA, complete genome.
291	133910126	AM420293	401	7.00E-35	113 \ 360	31	<i>Saccharopolyspora erythraea</i> NRRL2338 complete genome.
292	221726903	CP000629	629	3.00E-34	114 \ 332	34	<i>Agrobacterium radiobacter</i> K84 chromosome 2, complete sequence.
293	226239611	AP011115	402	3.00E-34	117 \ 337	34	<i>Rhodococcus opacus</i> B4 DNA, complete genome.
294	187717717	CP001053	627	7.00E-34	107 \ 341	31	<i>Burkholderia phytofirmans</i> PsJN chromosome 2, complete sequence.
295	170777806	CP001013	295	1.00E-33	91 \ 259	35	<i>Leptothrix cholodnii</i> SP-6, complete genome.
296	226319587	CP001115	618	1.00E-33	112 \ 348	32	<i>Deinococcus deserti</i> VCD115 plasmid 1, complete sequence.
297	226240665	AP011115	401	1.00E-33	112 \ 358	31	<i>Rhodococcus opacus</i> B4 DNA, complete genome.
298	226187665	AP008957	401	1.00E-33	116 \ 375	30	<i>Rhodococcus erythropolis</i> PR4 DNA, complete genome.
299	17431873	AL646053	626	2.00E-33	114 \ 342	33	<i>Ralstonia solanacearum</i> GMI1000 megaplasmid complete sequence.
300	110818563	CP000431	402	2.00E-33	117 \ 337	34	<i>Rhodococcus jostii</i> RHA1, complete genome.
301	226243034	AP011115	401	2.00E-33	112 \ 358	31	<i>Rhodococcus opacus</i> B4 DNA, complete genome.
302	209539189	CP001193	631	3.00E-33	109 \ 332	32	<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM2304 plasmid pRLG202, complete sequence.
303	110284123	CP000390	630	4.00E-33	105 \ 332	31	<i>Mesorhizobium</i> sp. BNC1, complete genome.
304	110821571	CP000431	401	5.00E-33	113 \ 364	31	<i>Rhodococcus jostii</i> RHA1, complete genome.
305	150955528	CP000647	617	5.00E-33	111 \ 334	33	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> MGH 78578, complete sequence.
306	110819560	CP000431	401	6.00E-33	113 \ 364	31	<i>Rhodococcus jostii</i> RHA1, complete genome.
307	119536192	CP000509	397	6.00E-33	106 \ 333	31	<i>Nocardioides</i> sp. JS614, complete genome.
308	171697680	CP000806	386	6.00E-33	106 \ 317	33	<i>Cyanothece</i> sp. ATCC 51142 circular chromosome, complete sequence.
309	218171506	CP001291	363	8.00E-33	107 \ 317	33	<i>Cyanothece</i> sp. PCC 7424, complete genome.
310	206592213	CU914166	626	1.00E-32	111 \ 335	33	<i>Ralstonia solanacearum</i> strain IPO1609 Genome Draft.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
311	158307908	CP000828	355	1.00E-32	110 \ 360	30	<i>Acaryochloris marina</i> MBIC11017, complete genome.
312	206590236	CU695240	626	1.00E-32	110 \ 330	33	<i>Ralstonia solanacearum</i> strain MolK2 Genome Draft.
313	91691874	CP000271	627	1.00E-32	105 \ 338	31	<i>Burkholderia xenovorans</i> LB400 chromosome 2, complete sequence.
314	50057356	CR548612	390	1.00E-32	107 \ 341	31	<i>Paramecium tetraurelia</i> macronuclear largest chromosome, complete sequence.
315	110168647	CP000393	353	1.00E-32	110 \ 347	31	<i>Trichodesmium erythraeum</i> IMS101, complete genome.
316	206569512	CP000964	617	3.00E-32	113 \ 336	33	<i>Klebsiella pneumoniae</i> 342, complete genome.
317	221737676	CP000634	615	4.00E-32	106 \ 338	31	<i>Agrobacterium vitis</i> S4 chromosome 2, complete sequence.
318	87135284	CP000248	621	5.00E-32	100 \ 332	30	<i>Novosphingobium aromaticivorans</i> DSM 12444, complete genome.
319	75704587	CP000117	344	6.00E-32	106 \ 336	31	<i>Anabaena variabilis</i> ATCC 29413, complete genome.
320	83767281	AP007155	398	1.00E-31	119 \ 366	32	<i>Aspergillus oryzae</i> RIB40 genomic DNA, SC003.
321	219867173	CP001344	358	2.00E-31	119 \ 342	34	<i>Cyanothece</i> sp. PCC 7425, complete genome.
322	54018563	AP006618	392	3.00E-31	111 \ 330	33	<i>Nocardia farcinica</i> IFM 10152 DNA, complete genome.
323	91696957	CP000316	301	4.00E-31	93 \ 261	35	<i>Polaromonas</i> sp. JS666, complete genome.
324	134078895	AM270224	403	3.00E-30	113 \ 366	30	<i>Aspergillus niger</i> contig An11c0070, complete genome.
325	170774554	CP001013	635	3.00E-30	98 \ 331	29	<i>Leptothrix cholodnii</i> SP-6, complete genome.
326	89274982	DQ403252	356	3.00E-30	105 \ 349	30	<i>Streptomyces fungicidicus</i> DXP synthase 2 gene, partial cds; cationic amino acid transporter, transcriptional regulator, glycosyltransferase, fatty acid oxidation complex alpha-subunit, acetyl-CoA acetyltransferase, transcriptional regulator, beta-mannosidase, probable sugar transport system sugar-binding lipoprotein, sugar transport system permease proteins, ribonuclease D, two-component response regulator, uroporphyrinogen decarboxylase, and PAS protein phosphatase 2C-like protein genes, complete cds; peptide antibiotic enduracidin bioSynthetic gene cluster, complete sequence; and unknown genes.
327	32487230	AJ561198	356	4.00E-30	108 \ 339	31	<i>Actinomadura</i> sp. ATCC 39727 gene cluster for biosynthesis of glycopeptide antibiotic A40926, strain ATCC 39727.
328	601846	L38493	399	6.00E-30	112 \ 366	30	<i>Coccidioides immitis</i> T-cell reactive protein trcP gene exons 1-4, complete cds.
329	211582353	AM920427	403	1.00E-29	112 \ 367	30	<i>Penicillium chrysogenum</i> Wisconsin 54-1255 complete genome, contig Pc00c12.
330	13898392	AF325533	419	1.00E-29	103 \ 308	33	<i>Magnaporthe grisea</i> 4-hydroxyphenylpyruvate dioxygenase HPD4 gene, complete cds.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
331	42733908	AC117081	367	1.00E-29	104 \ 304	34	<i>Dictyostelium discoideum</i> chromosome 2 map 5862124-6045772 strain AX4, complete sequence.
332	125858898	BC129579	383	2.00E-29	108 \ 338	31	<i>Xenopus laevis</i> hypothetical protein LOC100037181, mRNA cDNA clone MGC:160250 IMAGE:8527600, complete cds.
333	158110982	CP000820	401	2.00E-29	108 \ 301	35	<i>Frankia</i> sp. EAN1pec, complete genome.
334	159141337	AE007870	633	3.00E-29	110 \ 334	32	<i>Agrobacterium tumefaciens</i> str. C58 linear chromosome, complete sequence.
335	17130116	BA000019	344	3.00E-29	96 \ 296	32	<i>Nostoc</i> sp. PCC 7120 DNA, complete genome.
336	2708690	AF038152	419	5.00E-29	104 \ 306	33	<i>Mycosphaerella graminicola</i> 4-hydroxyphenylpyruvate dioxygenase HPPD gene, complete cds.
337	150030893	CP000739	629	9.00E-29	103 \ 336	30	<i>Sinorhizobium medicae</i> WSM419 plasmid pSMED01, complete genome.
338	90018520	DQ397304	294	3.00E-28	70 \ 180	38	<i>Pseudomonas</i> sp. K82 pca gene cluster, partial sequence; and probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein, probable 4-hydroxyphenylpyruvate dioxygenase, and probable aldo/keto reductase precursor, genes, complete cds.
339	160365460	CP000884	294	3.00E-28	70 \ 180	38	<i>Delftia acidovorans</i> SPH-1, complete genome.
340	159030261	AM778957	361	4.00E-28	98 \ 320	30	<i>Microcystis aeruginosa</i> PCC 7806 genome sequencing data, contig C327.
341	28881241	BX284754	412	4.00E-28	98 \ 308	31	<i>Neurospora crassa</i> DNA linkage group II BAC contig B23G1.
342	21911428	U82965	369	4.00E-28	101 \ 333	30	<i>Streptomyces toyocaensis</i> strain NRRL 15009 bioSynthetic gene cluster A47934, complete sequence.
343	91699553	CP000316	638	4.00E-28	97 \ 349	27	<i>Polaromonas</i> sp. JS666, complete genome.
344	15141381	AL591985	629	4.00E-28	102 \ 337	30	<i>Sinorhizobium meliloti</i> 1021 plasmid pSymB.
345	166086855	AP009552	361	5.00E-28	96 \ 319	30	<i>Microcystis aeruginosa</i> NIES-843 DNA, complete genome.
346	157422999	BC153801	383	7.00E-28	112 \ 355	31	<i>Xenopus laevis</i> hypothetical protein LOC100126650, mRNA cDNA clone MGC:181745 IMAGE:8824637, complete cds.
347	49647063	CR382128	394	1.00E-27	109 \ 356	30	<i>Yarrowia lipolytica</i> strain CLIB122 chromosome B complete sequence.
348	170944674	CU638743	418	1.00E-27	99 \ 306	32	<i>Podospora anserina</i> genomic DNA chromosome 3, supercontig 2.
349	211591755	AM920437	407	1.00E-27	103 \ 310	33	<i>Penicillium chrysogenum</i> Wisconsin 54-1255 complete genome, contig Pc00c22.
350	119358720	CS456035	339	2.00E-27	93 \ 307	30	Sequence 1 from Patent EP1728868.
351	6740964	A92167	339	2.00E-27	93 \ 307	30	Sequence 1 from Patent WO9820144.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
352	1001726	BA000022	339	2.00E-27	93 \ 307	30	<i>Synechocystis</i> sp. PCC 6803 DNA, complete genome.
353	218168642	CP001287	363	3.00E-27	92 \ 342	26	<i>Cyanothece</i> sp. PCC 8801, complete genome.
354	120593530	CP000529	300	5.00E-27	91 \ 265	34	<i>Polaromonas naphthalenivorans</i> CJ2, complete genome.
355	120593435	CP000529	632	7.00E-27	92 \ 330	27	<i>Polaromonas naphthalenivorans</i> CJ2, complete genome.
356	145304354	CP000667	389	8.00E-27	96 \ 316	30	<i>Salinispora tropica</i> CNB-440, complete genome.
357	214003852	EU874252	357	1.00E-26	99 \ 324	30	Uncultured soil bacterium clone B128 VEG gene cluster, complete sequence.
358	186466681	CP001037	361	1.00E-26	104 \ 345	30	<i>Nostoc punctiforme</i> PCC 73102, complete genome.
359	113197875	BC121486	393	1.00E-26	106 \ 354	29	<i>Xenopus tropicalis</i> 4-hydroxyphenylpyruvate dioxygenase, mRNA cDNA clone MGC:146689 IMAGE:7668286, complete cds.
360	45580880	AJ632270	353	2.00E-26	89 \ 304	29	<i>Actinoplanes teichomyceticus</i> teicoplanin gene cluster.
361	40713178	AJ605139	351	3.00E-26	89 \ 304	29	<i>Actinoplanes teichomyceticus</i> gene cluster for biosynthesis of glycopeptide antibiotic teicoplanin.
362	3880060	Z50016	393	4.00E-26	102 \ 339	30	<i>Caenorhabditis elegans</i> Cosmid T21C12, complete sequence.
363	38014668	BC060451	313	5.00E-26	100 \ 305	32	<i>Xenopus laevis</i> hypothetical protein MGC68535, mRNA cDNA clone MGC:68535 IMAGE:4031049, complete cds.
364	134058400	AM270068	511	1.00E-25	101 \ 303	33	<i>Aspergillus niger</i> contig An04c0070, complete genome.
365	49656115	CR382138	473	2.00E-25	102 \ 356	28	<i>Debaryomyces hansenii</i> strain CBS767 chromosome F complete sequence.
366	161863	M59429	404	2.00E-25	94 \ 307	30	<i>T. thermophila</i> F-antigen tfa gene, complete cds.
367	149386872	CP000499	530	2.00E-25	106 \ 323	32	<i>Pichia stipitis</i> CBS 6054 chromosome 5, complete sequence.
368	4481935	AL939115	371	2.00E-25	95 \ 344	27	<i>Streptomyces coelicolor</i> A32 complete genome; segment 12/29.
369	60552039	BC091035	394	3.00E-25	104 \ 332	31	<i>Xenopus tropicalis</i> hpd protein, mRNA cDNA clone MGC:107914 IMAGE:7024220, complete cds.
370	35213661	BA000045	344	3.00E-25	74 \ 205	36	<i>Gloeobacter violaceus</i> PCC 7421 DNA, complete genome.
371	86568012	CP000249	355	3.00E-25	96 \ 320	30	<i>Frankia</i> sp. Ccl3, complete genome.
372	54035226	BC084120	393	3.00E-25	94 \ 308	30	<i>Xenopus laevis</i> hypothetical LOC495029, mRNA cDNA clone MGC:85321 IMAGE:6875780, complete cds.
373	220955106	FJ635837	294	5.00E-25	96 \ 306	31	Synthetic construct <i>Drosophila melanogaster</i> clone BS07387 encodes CG11796-RB.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
374	220945290	FJ630929	294	5.00E-25	96 \ 306	31	Synthetic construct <i>Drosophila melanogaster</i> clone BO07787 encodes CG11796-RB.
375	15010414	AY047523	294	5.00E-25	96 \ 306	31	<i>Drosophila melanogaster</i> GH03058 full length cDNA.
376	7296312	AE014296	294	5.00E-25	96 \ 306	31	<i>Drosophila melanogaster</i> chromosome 3L, complete sequence.
377	220959738	FJ638153	380	5.00E-25	106 \ 356	29	Synthetic construct <i>Drosophila melanogaster</i> clone BS16504 encodes CG11796-RA.
378	220951448	FJ634008	380	5.00E-25	106 \ 356	29	Synthetic construct <i>Drosophila melanogaster</i> clone BO17004 encodes CG11796-RA.
379	45825069	BT012317	380	5.00E-25	106 \ 356	29	<i>Drosophila melanogaster</i> GH11957 full insert cDNA.
380	7296311	AE014296	380	5.00E-25	106 \ 356	29	<i>Drosophila melanogaster</i> chromosome 3L, complete sequence.
381	15131503	Y16952	356	9.00E-25	102 \ 329	31	<i>Amycolatopsis balhimycina</i> bioSynthetic gene cluster for balhimycin, strain DSM 5908.
382	134075744	AM270121	409	1.00E-24	99 \ 310	31	<i>Aspergillus niger</i> contig An07c0030, complete genome.
383	169886972	CP000951	337	1.00E-24	85 \ 220	38	<i>Synechococcus</i> sp. PCC 7002, complete genome.
384	196173743	CP001131	393	2.00E-24	105 \ 340	30	<i>Anaeromyxobacter</i> sp. K, complete genome.
385	219956517	CP001359	395	3.00E-24	104 \ 340	30	<i>Anaeromyxobacter dehalogenans</i> 2CP-1, complete genome.
386	37681833	AY398361	397	7.00E-24	107 \ 358	29	<i>Danio rerio</i> clone RK355A3C10 4-hydroxyphenylpyruvate dioxygenase HPD mRNA, complete cds.
387	28374346	BC046075	387	7.00E-24	107 \ 358	29	<i>Danio rerio</i> zgc:56326, mRNA cDNA clone MGC:56326 IMAGE:5603649, complete cds.
388	159031819	AB325671	382	1.00E-23	92 \ 322	28	<i>Blepharisma japonicum</i> Bj4HPPD mRNA for 4-hydroxyphenylpyruvate dioxygenase homolog, complete cds.
389	223641892	FM992689	570	1.00E-23	105 \ 331	31	<i>Candida dubliniensis</i> CD36 chromosome 2, complete sequence.
390	85776352	CP000251	393	2.00E-23	99 \ 313	31	<i>Anaeromyxobacter dehalogenans</i> 2CP-C, complete genome.
391	182889970	BC165880	393	3.00E-23	103 \ 354	29	<i>Danio rerio</i> 4-hydroxyphenylpyruvate dioxygenase, mRNA cDNA clone MGC:192968 IMAGE:100061460, complete cds.
392	50603845	BC077167	393	3.00E-23	103 \ 354	29	<i>Danio rerio</i> 4-hydroxyphenylpyruvate dioxygenase, mRNA cDNA clone MGC:92456 IMAGE:7042062, complete cds.
393	93209319	DQ206332	873	4.00E-23	85 \ 235	36	<i>Nematostella vectensis</i> HNF-HNF class homeobox protein gene, complete cds.
394	145304589	CP000667	358	4.00E-23	90 \ 294	30	<i>Salinispora tropica</i> CNB-440, complete genome.
395	152029899	CP000769	391	4.00E-23	107 \ 337	31	<i>Anaeromyxobacter</i> sp. Fw109-5, complete genome.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
396	15029330	AF386507	338	5.00E-23	100 \ 331	30	<i>Streptomyces lavendulae</i> complestatin bioSynthetic gene cluster, complete sequence.
397	209155742	BT045841	386	1.00E-22	104 \ 350	29	<i>Salmo salar</i> clone ssal-rgf-534-157 4-hydroxyphenylpyruvate dioxygenase putative mRNA, complete cds.
398	2894154	AJ223998	357	1.00E-22	94 \ 324	29	<i>Amycolatopsis orientalis</i> cosmid PCZA361.
399	157917083	CP000850	369	2.00E-22	96 \ 325	29	<i>Salinispora arenicola</i> CNS-205, complete genome.
400	217692	D13390	393	6.00E-22	99 \ 351	28	<i>Sus scrofa</i> HPD mRNA for 4-hydroxyphenylpyruvic acid dioxygenase, complete cds.
401	59857863	BT020749	393	8.00E-22	98 \ 353	27	<i>Bos taurus</i> 4-hydroxyphenylpyruvate dioxygenase HPD, mRNA, complete cds.
402	75948304	BC105225	393	8.00E-22	98 \ 353	27	<i>Bos taurus</i> 4-hydroxyphenylpyruvate dioxygenase, mRNA cDNA clone MGC:128788 IMAGE:7989260, complete cds.
403	193786602	AK057510	354	8.00E-22	98 \ 355	27	<i>Homo sapiens</i> cDNA FLJ32948 fis, clone TESTI2008014, highly similar to 4-hydroxyphenylpyruvate dioxygenase EC 1.13.11.27.
404	51980500	BC081819	393	1.00E-21	98 \ 355	27	<i>Rattus norvegicus</i> 4-hydroxyphenylpyruvate dioxygenase, mRNA cDNA clone MGC:93530 IMAGE:7107086, complete cds.
405	3435296	AF082834	393	1.00E-21	98 \ 355	27	<i>Rattus norvegicus</i> 4-hydroxyphenylpyruvate dioxygenase HPPD mRNA, complete cds.
406	3860238	U29895	393	1.00E-21	98 \ 355	27	Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds.
407	123998839	DQ896049	393	1.00E-21	98 \ 355	27	Synthetic construct <i>Homo sapiens</i> clone IMAGE:100010509; FLH189851.01L; RZPD0839B1165D 4-hydroxyphenylpyruvate dioxygenase HPD gene, encodes complete protein.
408	123984489	DQ892664	393	1.00E-21	98 \ 355	27	Synthetic construct clone IMAGE:100005294; FLH189855.01X; RZPD0839B1175D 4-hydroxyphenylpyruvate dioxygenase HPD gene, encodes complete protein.
409	288105	X72389	393	1.00E-21	98 \ 355	27	<i>H. sapiens</i> mRNA for 4-hydroxyphenylpyruvate dioxygenase.
410	1100256	D31628	393	1.00E-21	98 \ 355	27	<i>Homo sapiens</i> gene for 4-hydroxyphenylpyruvic acid dioxgenase, complete cds.
411	18999511	BC024287	393	1.00E-21	98 \ 355	27	<i>Homo sapiens</i> 4-hydroxyphenylpyruvate dioxygenase, mRNA cDNA clone MGC:39261 IMAGE:5087393, complete cds.
412	158255088	AK290826	393	1.00E-21	98 \ 355	27	<i>Homo sapiens</i> cDNA FLJ76150 complete cds, highly similar to <i>Homo sapiens</i> 4-hydroxyphenylpyruvate dioxygenase HPD, mRNA.
413	83318921	AM114773	287	1.00E-21	75 \ 212	35	<i>Platynereis dumerilii</i> partial mRNA for 4-hydroxyphenylpyruvate dioxygenase protein hppd gene.
414	2231615	U87257	442	2.00E-21	92 \ 308	29	<i>Daucus carota</i> 4-hydroxyphenylpyruvate dioxygenase mRNA, complete cds.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
415	21900482	AX467199	345	2.00E-21	90 \ 324	27	Sequence 9 from Patent WO0234921.
416	47078310	AY541063	345	2.00E-21	90 \ 324	27	<i>Nocardia uniformis</i> subsp. <i>tsuyamanensis</i> monocyclic beta-lactam antibiotic nocardicin A biosynthesis gene cluster, partial sequence.
417	1118143	U41748	364	3.00E-21	97 \ 345	28	<i>Caenorhabditis elegans</i> cosmid C31H2, complete sequence.
418	86553738	CP000239	350	4.00E-21	79 \ 215	36	<i>Synechococcus</i> sp. JA-3-3Ab, complete genome.
419	154240639	AB267400	430	4.00E-21	96 \ 332	28	<i>Coptis Japonica</i> var. <i>dissecta</i> hppd mRNA for hydroxyphenylpyruvate dioxygenase, complete cds.
420	49119225	BC073224	391	5.00E-21	86 \ 305	28	<i>Xenopus laevis</i> MGC80543 protein, mRNA cDNA clone MGC:80543 IMAGE:5161849, complete cds.
421	202924	M18405	376	7.00E-21	96 \ 352	27	Rat F alloantigen mRNA, 3 end.
422	74418655	DQ188836	377	8.00E-21	96 \ 352	27	<i>Homo sapiens</i> liver F protein mRNA, partial cds.
423	15426479	BC013343	393	1.00E-20	96 \ 350	27	<i>Mus musculus</i> 4-hydroxyphenylpyruvic acid dioxygenase, mRNA cDNA clone MGC:14040 IMAGE:4193670, complete cds.
424	74143620	AK149416	393	1.00E-20	96 \ 352	27	<i>Mus musculus</i> adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730007B19 product:4-hydroxyphenylpyruvic acid dioxygenase, full insert sequence.
425	849053	D29987	393	4.00E-20	96 \ 350	27	<i>Mus musculus</i> mRNA for 4-hydroxyphenylpyruvate dioxygenase, complete cds.
426	86556287	CP000240	359	5.00E-20	69 \ 202	34	<i>Synechococcus</i> sp. JA-2-3Ba(2-13), complete genome.
427	147787057	AM423697	445	7.00E-20	93 \ 320	29	<i>Vitis vinifera</i> contig VV78X073408.8, whole genome shotgun sequence.
428	1841443	X59530	379	8.00E-20	94 \ 347	27	M.musculus mRNA for F protein.
429	22530912	AY136294	473	1.00E-19	90 \ 314	28	<i>Arabidopsis thaliana</i> 4-hydroxyphenylpyruvate dioxygenase HPD At1g06570 mRNA, complete cds.
430	6692679	AC007592	473	1.00E-19	90 \ 314	28	Genomic sequence for <i>Arabidopsis thaliana</i> BAC F12K11 from chromosome I, complete sequence.
431	16226618	AF428446	445	2.00E-19	90 \ 314	28	<i>Arabidopsis thaliana</i> At1g06570/F12K11_12 mRNA, complete cds.
432	3098559	AF047834	445	2.00E-19	90 \ 314	28	<i>Arabidopsis thaliana</i> 4-hydroxyphenylpyruvate dioxygenase mRNA, complete cds.
433	2145039	AF000228	445	2.00E-19	90 \ 314	28	<i>Arabidopsis thaliana</i> p-hydroxyphenylpyruvate dioxygenase mRNA, complete cds.
434	2392518	U89267	445	2.00E-19	90 \ 314	28	<i>Arabidopsis thaliana</i> p-hydroxyphenylpyruvate dioxygenase HPD mRNA, complete cds.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
435	22136134	AY128745	445	2.00E-19	90 \ 314	28	<i>Arabidopsis thaliana</i> 4-hydroxyphenylpyruvate dioxygenase HPD (At1g06570) mRNA, complete cds.
436	18252207	AY072329	445	2.00E-19	90 \ 314	28	<i>Arabidopsis thaliana</i> 4-hydroxyphenylpyruvate dioxygenase HPD (At1g06570) mRNA, complete cds.
437	27552225	AX575735	445	2.00E-19	90 \ 314	28	Sequence 13 from Patent WO02072848.
438	219842162	AB376089	445	3.00E-19	89 \ 315	28	<i>Hevea brasiliensis</i> hppd mRNA for 4-hydroxyphenylpyruvate dioxygenase, complete cds.
439	3694811	AF060481	419	4.00E-19	81 \ 282	28	<i>Arabidopsis thaliana</i> p-hydroxyphenylpyruvate dioxygenase pds1 gene, complete cds.
440	94553895	CP000358	477	5.00E-19	69 \ 198	34	<i>Deinococcus geothermalis</i> DSM 11300 plasmid pDGEO01, complete sequence.
441	144576938	CP000583	427	8.00E-19	90 \ 318	28	<i>Ostreococcus lucimarinus</i> CCE9901 chromosome 3, complete sequence.
442	225707312	BT075078	451	1.00E-18	87 \ 324	26	<i>Osmerus mordax</i> clone omor-eva-520-127 4-hydroxyphenylpyruvate dioxygenase putative mRNA, complete cds.
443	226358517	FJ501992	175	2.00E-18	62 \ 167	37	<i>Aristichthys nobilis</i> clone A21 4-hydroxyphenylpyruvate dioxygenase mRNA, partial cds.
444	171846301	BC161492	386	2.00E-18	80 \ 300	26	<i>Xenopus tropicalis</i> 4-hydroxyphenylpyruvate dioxygenase-like, mRNA cDNA clone MGC:135498 IMAGE:7556732, complete cds.
445	62003087	AY957391	437	4.00E-18	87 \ 319	27	<i>Medicago truncatula</i> 4-hydroxyphenylpyruvate dioxygenase HPD mRNA, complete cds.
446	161164838	AM746676	382	5.00E-18	66 \ 167	39	<i>Sorangium cellulosum</i> So ce 56' complete genome.
447	156230369	BC152021	420	7.00E-18	101 \ 383	26	<i>Danio rerio</i> zgc:171978, mRNA cDNA clone MGC:171978 IMAGE:8109900, complete cds.
448	49387760	AP005804	446	9.00E-18	93 \ 311	29	<i>Oryza sativa Japonica</i> Group genomic DNA, chromosome 2, BAC clone:OSJNBa0085K21.
449	49388595	AP005071	446	9.00E-18	93 \ 311	29	<i>Oryza sativa Japonica</i> Group genomic DNA, chromosome 2, PAC clone:P0669G09.
450	161163751	AM746676	383	1.00E-17	74 \ 217	34	<i>Sorangium cellulosum</i> So ce 56' complete genome.
451	116056732	CR954203	432	2.00E-17	89 \ 324	27	<i>Ostreococcus tauri</i> strain OTTH0595, *** SEQUENCING IN PROGRESS ***.
452	21522866	AX417719	400	2.00E-17	75 \ 267	28	Sequence 10 from Patent WO0231173.
453	148616206	EF608178	443	2.00E-16	91 \ 318	28	<i>Glycine max</i> 4-hydroxyphenylpyruvate dioxygenase mRNA, complete cds.
454	114324487	DQ886526	443	2.00E-16	86 \ 307	28	<i>Brassica rapa</i> subsp. <i>pekinensis</i> 4-hydroxyphenylpyruvate dioxygenase mRNA, complete cds.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
455	23505684	AY138969	363	3.00E-16	81 \ 302	26	<i>Abutilon theophrasti</i> 4-hydroxyphenylpyruvate dioxygenase HPPD gene, partial cds.
456	13810184	AJ309203	436	8.00E-16	99 \ 350	28	<i>Coleus blumei</i> mRNA for 4-hydroxyphenylpyruvate dioxygenase hppd_SOLSC gene.
457	219861466	CP001341	624	4.00E-15	92 \ 350	26	<i>Arthrobacter chlorophenolicus</i> A6, complete genome.
458	21706602	BC034099	371	4.00E-15	67 \ 231	29	<i>Mus musculus</i> 4-hydroxyphenylpyruvate dioxygenase-like, mRNA cDNA clone MGC:31514 IMAGE:4489103, complete cds.
459	122889970	AL683847	371	4.00E-15	67 \ 231	29	Mouse DNA sequence from clone RP23-109A3 on chromosome 4 Contains the 5' end of a novel gene (1810037K07Rik), a novel gene (0610037D15Rik), the <i>Tesk2</i> gene for testis-specific kinase 2, a novel gene (4930584N22Rik), the <i>Mutyh</i> gene for mutY homolog (<i>E. coli</i>), two novel genes, a ribosomal protein L36 (Rpl36) pseudogene, a tumor protein translationally-controlled 1 (Tpt1) pseudogene, a U1 small nuclear ribonucleoprotein 1C (Snrp1c) pseudogene, the 5' end of the <i>Zswim5</i> gene for zinc finger SWIM domain containing 5 (<i>Zswim5</i>) and four CpG islands, complete sequence.
460	26347637	AK078929	371	4.00E-15	67 \ 231	29	<i>Mus musculus</i> adult male cecum cDNA, RIKEN full-length enriched library, clone:9130202117 product:hypothetical Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase structure containing protein, full insert sequence.
461	26339904	AK049217	371	4.00E-15	67 \ 231	29	<i>Mus musculus</i> ES cells cDNA, RIKEN full-length enriched library, clone:C330013N21 product:hypothetical Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase structure containing protein, full insert sequence.
462	26335998	AK043902	371	4.00E-15	67 \ 231	29	<i>Mus musculus</i> 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830048M07 product:hypothetical Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase structure containing protein, full insert sequence.
463	119949523	CP000474	628	4.00E-15	86 \ 348	24	<i>Arthrobacter aurescens</i> TC1, complete genome.
464	88319761	AJ628018	626	5.00E-15	101 \ 368	27	<i>Streptomyces</i> sp. SCC 2136 deoxysugar bioSynthetic gene cluster.
465	226514643	CP001323	441	1.00E-14	89 \ 325	27	<i>Micromonas</i> sp. RCC299 chromosome 2, complete sequence.
466	72256523	DQ139267	436	2.00E-14	94 \ 319	29	<i>Triticum aestivum</i> 4-hydroxyphenylpyruvate dioxygenase mRNA, complete cds.
467	2695710	AJ000693	434	3.00E-14	94 \ 315	29	<i>Hordeum vulgare</i> mRNA for 4-hydroxyphenylpyruvate dioxygenase.
468	6731754	A81449	434	3.00E-14	94 \ 315	29	Sequence 1 from Patent WO9904021.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
469	116612730	CP000454	629	5.00E-14	87 \ 352	24	<i>Arthrobacter</i> sp. FB24, complete genome.
470	13938327	BC007293	371	5.00E-14	83 \ 303	27	<i>Homo sapiens</i> 4-hydroxyphenylpyruvate dioxygenase-like, mRNA cDNA clone MGC:15668 IMAGE:3349473, complete cds.
471	56205982	AL359540	371	5.00E-14	83 \ 303	27	Human DNA sequence from clone RP4-534D1 on chromosome 1p34.1-35.3 Contains the 5 end of one variant of the ZSWIM5 gene for zinc finger SWIM domain containing 5, a novel gene (MGC15668), the MUTYH gene for mutY homolog (<i>E. coli</i>), the TOE1 gene for target of EGR1 member 1 (nuclear) and the 3' end of the TESK2 gene for testis-specific kinase 2, complete sequence.
472	189053950	AK313714	371	5.00E-14	83 \ 303	27	<i>Homo sapiens</i> cDNA, FLJ94307.
473	62989586	AJ634707	444	1.00E-13	88 \ 309	28	<i>Zea mays</i> mRNA for putative p-hydroxyphenylpyruvate dioxygenase hppd gene.
474	116793541	EF087545	263	1.00E-13	69 \ 230	30	<i>Picea sitchensis</i> clone WS02751_M23 unknown mRNA.
475	53733502	BC083702	371	1.00E-13	46 \ 130	35	<i>Rattus norvegicus</i> 4-hydroxyphenylpyruvate dioxygenase-like, mRNA cDNA clone MGC:94580 IMAGE:7190108, complete cds.
476	13508705	AJ291979	130	4.00E-13	47 \ 131	35	<i>Auxarthron zuffianum</i> partial tcrP gene for human T-cell reactive protein, strain UAMH 4082, exons 1-3.
477	13508703	AJ291978	130	4.00E-13	47 \ 131	35	<i>Auxarthron zuffianum</i> partial tcrP gene for human T-cell reactive protein, strain UAMH 3135, exons 1-3.
478	13508699	AJ291976	130	4.00E-13	47 \ 131	35	<i>Auxarthron zuffianum</i> partial tcrP gene for human T-cell reactive protein, strain UAMH 2653, exons 1-3.
479	13508697	AJ291975	130	4.00E-13	47 \ 131	35	<i>Auxarthron zuffianum</i> partial tcrP gene for human T-cell reactive protein, strain UAMH 1875, exons 1-3.
480	42600537	AJ431261	432	4.00E-13	85 \ 314	27	<i>Chlamydomonas reinhardtii</i> partial mRNA for p-hydroxyphenylpyruvate dioxygenase hppd1 gene.
481	28828436	AC116330	637	4.00E-13	89 \ 380	23	<i>Dictyostelium discoideum</i> chromosome 2 map 3191214-3323468 strain AX4, complete sequence.
482	13508833	AJ291974	130	1.00E-12	45 \ 131	34	<i>Uncinocarpus reesii</i> partial tcrP gene for human T-cell reactive protein, strain UAMH 2862, exons 1-3.
483	13508829	AJ291972	130	1.00E-12	45 \ 131	34	<i>Uncinocarpus reesii</i> partial tcrP gene for human T-cell reactive protein, strain UAMH 2847, exons 1-3.
484	13508827	AJ291971	130	1.00E-12	45 \ 131	34	<i>Uncinocarpus reesii</i> partial tcrP gene for human T-cell reactive protein, strain UAMH 1706, exons 1-3.
485	13508825	AJ291970	130	1.00E-12	45 \ 131	34	<i>Uncinocarpus reesii</i> partial tcrP gene for human T-cell reactive protein, strain UAMH 160, exons 1-3.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
486	223717664	FM202438	432	1.00E-12	84 \ 314	26	<i>Chlamydomonas reinhardtii</i> hppd1 gene for p-hydroxyphenylpyruvate dioxygenase, strain 6145c.
487	157040846	AM084898	381	1.00E-12	78 \ 268	29	<i>Triticum aestivum</i> mRNA for 4-hydroxyphenylpyruvate dioxygenase hppd gene, cultivar CPAN 1676.
488	13508831	AJ291973	130	2.00E-12	44 \ 131	33	<i>Uncinocarpus reesii</i> partial tcrP gene for human T-cell reactive protein, strain UAMH 1704, exons 1-3.
489	148744249	BC142154	390	2.00E-12	44 \ 136	32	<i>Bos taurus</i> 4-hydroxyphenylpyruvate dioxygenase-like, mRNA cDNA clone MGC:160069 IMAGE:8513837, complete cds.
490	13508695	AJ291969	130	2.00E-12	45 \ 131	34	<i>Coccidioides immitis</i> partial tcrP gene for human T-cell reactive protein, strain RMSCC 2267, exons 1-3.
491	13508693	AJ291968	130	2.00E-12	45 \ 131	34	<i>Coccidioides immitis</i> partial tcrP gene for human T-cell reactive protein, strain RMSCC 757, exons 1-3.
492	13508701	AJ291977	130	2.00E-12	46 \ 131	35	<i>Auxarthron zuffianum</i> partial tcrP gene for human T-cell reactive protein, strain UAMH 3079, exons 1-3.
493	113535541	AP008208	239	3.00E-12	67 \ 224	29	<i>Oryza sativa Japonica</i> cultivar-group genomic DNA, chromosome 2.
494	29605421	BA000030	601	4.00E-12	88 \ 334	26	<i>Streptomyces avermitilis</i> MA-4680 DNA, complete genome.
495	224034593	BT069475	426	7.00E-12	85 \ 305	27	<i>Zea mays</i> full-length cDNA clone ZM_BFb0142O19 mRNA, complete cds.
496	140844461	AP009044	618	2.00E-11	78 \ 325	24	<i>Corynebacterium glutamicum</i> R DNA, complete genome.
497	12543764	AX066051	618	3.00E-11	78 \ 325	24	Sequence 395 from Patent WO0100842.
498	111921098	CS360397	618	3.00E-11	78 \ 325	24	Sequence 395 from Patent EP1683859.
499	41324656	BX927149	618	3.00E-11	78 \ 325	24	<i>Corynebacterium glutamicum</i> ATCC 13032, IS fingerprint type 4-5, complete genome; segment 2/10.
500	21323187	BA000036	618	3.00E-11	78 \ 325	24	<i>Corynebacterium glutamicum</i> ATCC 13032 DNA, complete genome.
501	73912494	AB232882	147	1.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> gene for dioxygenase, partial cds, strain: IFM 54196.
502	73912492	AB232881	147	1.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> gene for dioxygenase, partial cds, strain: IFM 54195.
503	73912490	AB232880	147	1.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> gene for dioxygenase, partial cds, strain: IFM 54194.
504	73912488	AB232879	147	1.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> gene for dioxygenase, partial cds, strain: IFM 51112.
505	73912486	AB232878	147	1.00E-10	41 \ 124	33	<i>Coccidioides immitis</i> gene for dioxygenase, partial cds, strain: IFM 50995.
506	73912484	AB232877	147	1.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> gene for dioxygenase, partial cds, strain: IFM 50994.
507	73912482	AB232876	147	1.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> gene for dioxygenase, partial cds, strain: IFM 50993.

HPPD W336 Protein
Amino acid sequence homology search with known toxins

HIT	MOL. NAME	LOCUS	LENGTH	EXPECT	IDENT.	% IDENT.	DESCRIPTION
508	73912480	AB232875	147	1.00E-10	41 \ 124	33	<i>Coccidioides immitis</i> gene for dioxygenase, partial cds, strain: IFM 50992.
509	73912478	AB232874	147	1.00E-10	41 \ 124	33	<i>Coccidioides immitis</i> gene for dioxygenase, partial cds, strain: IFM 46868.
510	73912474	AB232872	147	1.00E-10	41 \ 124	33	<i>Coccidioides immitis</i> gene for dioxygenase, partial cds, strain: IFM 45816.
511	73912472	AB232871	147	1.00E-10	41 \ 124	33	<i>Coccidioides immitis</i> gene for dioxygenase, partial cds, strain: IFM 45815.
512	73912470	AB232870	147	1.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> gene for dioxygenase, partial cds, strain: IFM 45813.
513	73912468	AB232869	147	1.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> gene for dioxygenase, partial cds, strain: IFM 45812.
514	73912466	AB232868	147	1.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> gene for dioxygenase, partial cds, strain: IFM 45811.
515	73912464	AB232867	147	1.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> gene for dioxygenase, partial cds, strain: IFM 45810.
516	73912462	AB232866	147	1.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> gene for dioxygenase, partial cds, strain: IFM 45809.
517	73912460	AB232865	147	1.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> gene for dioxygenase, partial cds, strain: IFM 4945.
518	73912458	AB232864	147	1.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> gene for dioxygenase, partial cds, strain: IFM 4935.
519	73912476	AB232873	147	2.00E-10	41 \ 124	33	<i>Coccidioides posadasii</i> gene for dioxygenase, partial cds, strain: IFM 45817.
520	151359962	CP000750	596	1.00E-09	79 \ 330	23	<i>Kineococcus radiotolerans</i> SRS30216, complete genome.
521	226238983	AP011115	644	5.00E-09	81 \ 335	24	<i>Rhodococcus opacus</i> B4 DNA, complete genome.
522	23492277	BA000035	622	1.00E-08	82 \ 333	24	<i>Corynebacterium efficiens</i> YS-314 DNA, complete genome.
523	110817907	CP000431	644	1.00E-08	82 \ 335	24	<i>Rhodococcus jostii</i> RHA1, complete genome.
524	226186411	AP008957	637	5.00E-07	78 \ 321	24	<i>Rhodococcus erythropolis</i> PR4 DNA, complete genome.
525	7705186	S69110	73	2.00E-06	24 \ 70	34	Fusion protein T-cell stimulating antigen [<i>Coccidioides immitis</i> , mRNA Partial, 220 nt].
526	387590	M77190	69	4.00E-06	24 \ 69	34	<i>C.immitis</i> T-cell reactive fusion protein mRNA, partial cds.
527	2592	X61929	66	2.00E-05	23 \ 66	34	<i>C. immitis</i> mRNA for T-cell reactive fusion protein, partial.
528	93356539	CP000353	207	8.00E-05	24 \ 32	75	<i>Ralstonia metallidurans</i> CH34 megaplasmid, complete sequence.
529	94553898	CP000358	149	4.00E-04	30 \ 98	30	<i>Deinococcus geothermalis</i> DSM 11300 plasmid pDGEO01, complete sequence.
530	60692862	AY915430	98	9.00E-04	38 \ 93	40	<i>Schistosoma japonicum</i> SJCHGC06518 protein mRNA, complete cds.

7. Figures

7.1. Figure 1 – Alignment of the HPPD W336 sequence with the VLLY sequence

Uniprot_Swissprot:VLLY_VIBVU |O06695|VLLY_VIBVU|Hemolysin vllY; |*Vibrio vulnificus*. |AA|357
Length = 357

Score = 374 bits (959), Expect = e-103, Method: Compositional matrix adjust.
Identities = 192/355 (54%), Positives = 253/355 (71%), Gaps = 10/355 (2%)

```
Query: 7   NPMGLMGFEFIEF-ASPTPG--TLEPIFEIMGFTKVATHRSKNVHLYRQGEINLILNNEP 63
          NP+G GFEF+E+ A+   G   L+ +F +GF +VA HRSK   LYRQG+IN ++N +P
Sbjct: 6   NPLGTDGFEFVEYTAADNTGIEQLKHLFSSLGFAEVAKHRSKEAWLYRQGDINFVVNAQP 65

Query: 64  NSIASYFAAEHGPSVCGMAFRVKDSQKAYNRALELGAQPIHIDTGPMEINLPAIKGIGGA 123
          +S A FA HGPSVCGMAFRV+D+ A   AL GA+   + GPMEL++PA+ GIGG+
Sbjct: 66  HSQAEEFAKVHGPSVCGMAFRVQDAASALKHALTNGAEEYKTEIGPMELSIPAVYGIGGS 125

Query: 124 PLYLIDRFEGEGSSIIDIDFVYLEGVERNVPVGA--GLKVIDHLTHNVYGRMVYWANFYEK 181
          LY +DR+G+ SIYD+DF + +   +   + GL IDHLTHNV RG M WA FYE+
Sbjct: 126 LLYFVDTRYGK-QSIYDVDFRFYDDAAQRLAKSDVGLYEIDHLTHNVKRGNMMDTWAGFYER 184

Query: 182 LFNFREARYFDIKGEYTGLTSKAMSAPDGMIRIPLNEESSKGAGQIEEFLMQFNAGEGIQH 241
          + NFRE RYFDI+G+ TGL S+AM+AP G IRIP+N ESS   QIEEF+ ++NGEGIQH
Sbjct: 185 IGNFREIRYFDIEGKLTGLVSRAMTAPCGKIRIPIN-ESSDDKSQIEEFIREYNGEGIQH 243

Query: 242 VAFLLTDDLVTWDALKKIGMRFMTAPPDTYYEMLEGRLPDHGEPVDQLQARGILLDGSSV 301
          +A TDD+ +T   L+   GM FM   PDTYY+ ++ R+   H E V +L+   IL+DG+ +
Sbjct: 244 IALTDDDIYQTVQTLRDRGMDFMPT-PDTYYDKVDSRVEGHKEDVSRLRDLRILIDGAPL 302

Query: 302 EGDKRLLLQIFSETLMGPVFFFEFIQRKGDDGFGGEWNFKALFESIERDQVRRGVLT 356
          +   +LLQIF++T++GPVFFE IQRKG++GFGE NFKALFESIE DQ+RRGVL
Sbjct: 303 KDG--ILLQIFTQTVIGPVFFFEIIQRKGNEGFGEKNFKALFESIEEDQIRRGVLN 355
```

7.2. Figure 2 – Alignment of the HPPD W336 and VLLY sequences with a dataset of HPPD extracted from Uniprot_Swissprot



HPPD W336 Protein Amino acid sequence homology search with known toxins

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                                101                                200
HPPD-W336 (55) INLILNNE--PNS-----IASYFAAEHGPSVCGMAFRVK--DSQKAYNRALELGAQPIIHIDTGMELN-----LPA--TKG-
Blast identities IN ++N +- P+S          A FA HGPSVCGMAFRV+ D+ A AL GA+ + GPMEL+ +PA+ G-
VLLY (57) INFVVNAQ--PNS-----QAEFFAKVHGPSVCGMAFRVQ--DAASALKHAI TNCAEEYKTEIGMELIS-----IPA--VYG-

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HPPD multiple alignment

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b P80064 (54) INLILNNE--PNS-----VASYFAAEHGPSVCGMAFRVK--DSQKAYKRALELGAQPIIHETGMELN-----LPA--TKG-
b Q9I576 (62) INIVLNGS--PTG-----HVHEFALKHGPSACAMAFRVK--NASQAAAYAESQAKLVGSHANFGELN-----IPS--LEG-
p O23920 (94) LSFVFTA---PSPSTTTSSG-----SAAIPSFASGFSFAAKHGLAVRAIALEVA--DVAAAFEASVARGARPASA---PVELDD---QAWLAEVEL-
p Q9ARF9 (87) LSFVFTA---PSPSLAEPS-----SASIPTFSFSDHRAFTSSHGLAVRAVAIQVD--SASSAYSAAVSRGAKPVSP---PVVLAD---CETAIAEVHL-
p P93836 (95) LRFLFTA---PSPSLSAGEIKPT-TTASIPSFHDHGSCRSFFSSHGLGVRVAIEVE--DAESAFSISVANCAIPSSP---PIVLNE---AVTIAEVKL-
p O48604 (90) LAFLFTA---PYANGCDAAT-----ASLPSFSADAARRESADHGIAVRSVALRVA--DAAEAFRASRRRGARPAPA---PVDLGR---GFAFAEVEL-
v P32754 (67) IVFVLSSALNPWNK-----EMGDHLVKHGDGVKDIAFEVE--DCDYIVQKARERGAKIMRE---PWVEQD--KFGKVKFAVLQT-
v Q5EA20 (67) IVFVFSSALNPWNK-----EMGDHLVKHGDGVKDIAFEVE--DCDYIVQKARERGAKIVRE---PWVEQD--KLGKVKFAVLQT-
v P32755 (67) IVFVLCSALNPWNK-----EMGDHLVKHGDGVKDIAFEVE--DCDHIVQKARERGAKIVRE---PWVEED--KFGKVKFAVLQT-
v P49429 (67) IVFVLCSALNPWNK-----EMGDHLVKHGDGVKDIAFEVE--DCDHIVQKARERGAKIVRE---PWVEQD--KFGKVKFAVLQT-
v Q02110 (67) IVFVFSSALNPWNK-----EMGDHLVKHGDGVKDIAFEVE--DCDYIVQKARERGAIIIVRE---EVCCAA--DVRGHHTPLDRA-
v Q5BKL0 (67) IIFVFQSPLENGNQ-----EMGQHMIKHGDGVKDVAFQVE--DCDFLFQKAKDHGAVVVRE---PWIEED--EGGKVKYAVLQT-
v Q6TGZ5 (67) IIFVFESALNPNE-----EMGEHMIKHGDGVKDVAFLEVE--DCDFLVKKAKERGAAVLKE---PWVEQD--AGGKVKYAIIVQT-
i Q22633 (66) IVFIFESALLEDNS-----ELGNHLVQHGDGVKDVCFEVE--DLDSIIAHAKAAGATIVHD---ITEESD--ADGSIRYATLRT-
i Q60Y65 (66) IVFVFESALLEPNT-----ELGEHLVQHGDGVKDVCFEVE--DLDSIVAHAKAAGATIVRD---ITEESD--ENGSVRFATLRT-
i Q27203 (78) VTLAFST---PYGNDKDN-----QREMNHQSLHGDGVKDVAFAVE--DCHSIYNKAIQRCAKCAYP---PQDLKD--EHGVTIAAVHT-
f Q53586 (71) ARFVLTSVIKEATPWG-----HFLADHVAEHGDGVVDLAIIEVP--DARAAHAYATIEHGARSVAE---PYELKD--EHGTVVLAATAT-
f Q9S2F4 (71) ARFVFTSVIKPSTDWG-----TFLAQHVAEHGDGVVDLAIIEVP--DARAAHAYAVEHGARSVAE---PHEVKD--EHGTVVLAATAT-
f Q76NV5 (52) IMAFTS---PLTGDNK-----DYADHMMRHGDGVKDIAFNVK--DVQHIYDEAVKAGQSVKE---PHQIKD--EHGIVTLATIMSP-
f Q4WPV8 (71) AIFVLTS---PIRSMAGTGAYDDDPDVTKADRRLLEEIHNLHLEKHGDGVKDVAFRIE--DIEAVWKRAVDHGAAPVAA---PTTLKDDRHSITLATIGT-
f Q872T7 (80) VRFVFTS---PIRSQK---CLPEEPIISDADRKLLECHEHLEKHGDGVKDVAFVEVD--NVDGVFHKAVAAGADVVE---PTTLTDKMHGSVRTAVIRT-
f Q96X22 (86) VRFVFTS---PIRSHV---HLPEDEPISDEDRAALLKEMHAHLEKHGDGVKDVCFEVD--NVQGVYERAVQQCAVSIAP---PKTSLDKHGSVTMAVIQT-
f O42764 (90) VRFVFTS---PVRSSA---RQ-TLKAAPLADQARLDEMYDHLDKHGDGVKDVAFVEVD--DVLAVYENAVANGAESVSS---PHTDSC--DEGDVISAIAKT-
f Q00415 (72) ITFILTS---PLRSVE---QA-SRFP---EDEALLKEIHAEHLERHGDGVKDVAFVEVD--CVESVFSAAVRNGAEVVS---VRTVED--EDGQIKMATIRT-
f Q1E803 (72) ITFILTS---PLRSVE---QA-SRFP---EDEALLKEIHAEHLERHGDGVKDVAFVEVD--CVESVFSAAVRNGAEVVS---VRTVED--EDGQIKMATIRT-
f Q4WHU1 (74) ITFILTS---PLRSLD---QV-DRFPP---EEQELLKEIHAEHLERHGDGVKDVAFVEVD--SVDSVFYAATNNGAKIVSQ---PRTLED--DNGQVRVATIQT-
f Q6CDR5 (76) VREAFSS---ALR-----T-----GEPQADEIHAEHLVVKHGDGVKDVAFVEVD--NVEQLFSAAVKKGVRISE---PKVLKD--AHGSVTYAVIST-
HPPDconsens. (101) I FVFTS P EM HL KHGDGVKDVAFVEVE D D IF AV GA IV E P L D G V A I T

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LLY_LEGPC (53) IQFIVNAA-----SHCQAEHAH--STHGPAGACAMGFKVK--DAKAAFQHAIAHGGIAFQD--APHANHG-----LPA--IQA-

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HPPD W336 Protein

Amino acid sequence homology search with known toxins

201 300

HPPD-W336 (120) IGGAPLYLIDRFEGEG--SSIVDIDFVYLEG----VERNPVGAGLKVIIDHLTHNVYRGRMVYWANFYEKLENE--REARYFD--IKGEYTGLTSKAMSPDGG

Blast identities IGG+ LY +DR+G+ -- SIYD+DF + + -- + GL IDHLTHNV RG M WA FYE++ NE-RE RYFD--I+G+ TGL S+AM+AP G

VLLY (122) IGGSLLYFVDRYVGK---QSIYDVDFRFYDDA--AORLAKSDVGLYEIDHLTHNVKRGNMWTWAGFYERIGNE--REIRYFD--IEGKLTGLVSRAMTAPCG

HPPD multiple alignment

b P80064 (119) IGGAPLYLIDRFEGEG--SSIVDIDFVYLEG----VDRHPVGAGLKIIIDHLTHNVYRGRMAYWANFYEKLENE--REIRYFD--IKGEYTGLTSKAMTAPDGG

b Q9I576 (127) IGGSLLYLVDRYGD---RSIYDVDFEFIE---GRSANDNSVGLTYIDHLTHNVKRGQMDVWSGFYERIANF--REIRYFD--IEGKLTGLFSRAMTAPCG

p Q23920 (177) YGDVVLRFVSFGR---EEGLFLPGFEAVE---GTASFPDLDYGIIRRLDHAVGN--VTELGPVVEYIKGFTGEHEFAEFTAEDVGTLESGLNSVVLANNEE

p Q9ARF9 (170) YGDTVLRVSVSCGSG--ADGWFLPGFEVVG---DGVSCQELDYGIIRRLDHAVGN--VPKLEPVVDYLKFTGGEHEFAEFTAEDVGTAEGLNSVVLANNNE

p P93836 (182) YGDVVLRYVSYKAEDTEKSEFLPGFERVE---DASSFP-LDYGIIRRLDHAVGN--VPELGPALTYVAGFTGGEHQFAEFTADDVGTAEGLNSAVLASNDE

p Q48604 (171) YGDVVLRFVSHPDG--TDVPFLPGFEVGT---NPDAVD---YGLTRFDHVVG--VPELAPAAAYIAGFTGGEHEFAEFTAEDVGTTEGLNSVVLANNSE

v P32754 (139) YGDTTHTLVEKMN---YIGQFLPGYEAPA-FMDPLLPKLPKCSLEMIIDHIVGNOPDQEMVSASEWYLKNIQEHFRFWSVDDTQVHTEYSSLSRSIVVANYEE

v Q5EA20 (139) YGDTTHTLVEKMN---YTGRFLPGFEAPP-FMDPQLSKLPSCSLEIIDHIVGNOPDQEMVSASEWYLKNIQEHFRFWSVDDTQVHTEYSSLSRSVVVANYEE

v P32755 (139) YGDTTHTLVEKIN---YTGRFLPGFEAPT-YKDTLLPKLPKCSLEIIDHIVGNOPDQEMVSASEWYLKNIQEHFRFWSVDDTQVHTEYSSLSRSIVVANYEE

v P49429 (139) YGDTTHTLVEKIN---YTGRFLPGFEAPT-YKDTLLPKLPKCSLEIIDHIVGNOPDQEMVSASEWYLKNIQEHFRFWSVDDTQVHTEYSSLSRSIVVANYEE

v Q02110 (139) RQVWEGTLVEKMT---FCLDSRFQPSQTL-LHRLLLSKLPKCGLEIIDHIVGNOPDQEMVSASEWYLKNIQEHFRFWSVDDTQVHTEYSSLSRSIVVANYEE

v Q5BKL0 (139) YGDTTHTLLEYLGP--YRGVFLPGYKEPL-FRDPLLPKLPKCSLEIIDHIVGNOPDQEMVSASEWYLKNIQEHFRFWSVDDTQVHTEYSSLSRSIVVANYEE

v Q6TGZ5 (139) YGDTTHTFVEYLGP--YKGLFLPGYKEPL-FRDPLLPKLPKCSLEIIDHIVGNOPDQEMVSASEWYLKNIQEHFRFWSVDDTQVHTEYSSLSRSIVVANYEE

i Q22633 (138) YGETDHTLLEKKN---YRGAFPLPGFKAHP-MPATFFKTLPRVGLNFDHICVGNOPDLQMDSAVQWYKVLKEHFRFWSVDDSMIHTEYSALRSIVVTNFEE

i Q60Y65 (138) YGETDHTLLEKKN---YKGAFLPGFKPHP-MPPTFFHSLPRVGLNFDHICVGNOPDLQMDSAVQWYKVLKEHFRFWSVDDSMIHTEYSALRSIVVTNFEE

i Q27203 (153) YGEVIHTFIQRND---YKGFMPGPFVAHP-LKDPINNVLDPDISYNYVDHICVGNOPDLQMDSAVQWYKVLKEHFRFWSVDDSMIHTEYSALRSIVVTNFEE

f Q53586 (146) YGKTRHTLVDRGTG---YDGPYLPGYVAAA---PIVEPPAHRFTQADHICVGNVDELGRMNEWVGFYKVMGFTNMKEFVGDDIATEYSALMSKVVADGTL

f Q9S2F4 (146) YGETRHTLVERTG---YDGPYLPGYVAAK---PMVAPPAQRVFGAVDHCVGNVDELGRMNEWVGFYKVMGFTNMKEFVGDDIATEYSALMSKVVADGTL

f Q76NV5 (125) YGETTHTFVDRSQ---YKGAFLPGFTYKV-ASDPLSNITEPVGLNLDHIVVSNHADKMMEPVVQWYKVLKEHFRFWSVDDKTHTHTEYSSLSRSVVVADKSE

f Q4WPV8 (164) YEDTVHSLINRHD---YSGPFLPGYEVVT-DDDPIINRLPSIDFIEIDHICVGNOPWNGVDPIVKYEDCLNHFHRYWTVDLNMCGEYSAMRSIVVASPNE

f Q872T7 (169) YGDTTHTLISRAD---YNGPFLPGFRTAA-PS-SATVQLPSVPLARIDHICVGNQDWNEMVSACAFYEQCLSEHFRFWSVDDSQICTEFSALNSIVMASENN

f Q96X22 (175) YGDTTHTLISRDN---FRGTFLPGFRDVN-RQPAAYSALAPVPLQRIDHICVGNQDWDMMRAACDFYERCLSEHFRFWSVDDNQISTDFSALNSIVMASPNN

f Q42764 (177) YGDTTHTFIQRTT---YTGPFLPGYRSCT-TVDSANKFLFPVNLEAIDHICVGNQDWDDEMSDACDFYERCLSEHFRFWSVDDKDICTEFSALKSIVMSSPNQ

f Q00415 (156) YGETTHTLIERSG---YRGGFMPGYRMES-NADATSKFLPKVVLERIDHICVGNQDWDDEMERVCDDYEEKILGEHFRFWSVDDKDICTEFSALKSIVMASPND

f Q1E803 (156) YGETTHTLIERSG---YRGGFMPGYRMES-NADATSKFLPKVVLERIDHICVGNQDWDDEMERVCDDYEEKILGEHFRFWSVDDKDICTEFSALKSIVMASPND

f Q4WHU1 (159) YGETTHTLVERGS---YHGAFLPGYRMETGVEDPISQLLPVGLNRLDHCVGNQDWDDEMDKVCYEEKALGEHFRFWSVDDKDICTEYSALKSIVMASPNE

f Q6CDR5 (151) YGDTTHTLIERGS---YEGAFPLPGFVDTSAKNDPIAFAFLNIELMHIDHCVGNQDWNEMDNACKYEEETLGEHFRFWSVDDKDICTEFSALKSIVMASPNE

HPPDconsens. (201) YGDT HTLVER Y G FLPGF D L LP L IDH VGNQ EM EWYK L FHRFWSVDD I TEYSALRSIVMA E

LLY_LEGPC (117) IGGSVIYFVDEEH--QPFSEHWNITS-----SEP-V-VGN---GLTAIDHLTHNVYRGNMDKWASFYASIFNEQ---EIRFFNIGKMTGLVSRALGSPCG

HPPD W336 Protein Amino acid sequence homology search with known toxins

301 400

HPPD-W336 (211) MIRIPLNEES SKGAG---QIEEF LMQFN EGIQH VAF L TDD L V K I T W D A L K K I ---G M R F M T A P P D T Y Y E M I E G R L P D H G -----E P V D Q L Q A R G I L L

Blast identities IRIP+NE-SS ---QIEEF+ ++NGEGIOH+A TDD+ +T L+ ---GM FM P DTY+ ++ R+ H ---E V +L+ IL+

VLLY (214) KIRIPINE-SSDDKS---QIEEF IREYNGEGIOH IAL T TDD I Y Q T V Q T L R D R ---G M D F M P T P D T Y Y E K V D S R V E G H K -----E D V S R L R D L R L I L

HPPD multiple alignment

b P80064 (210) MIRIPLNEES SKGAG---QIEEF LMQFN EGIQH VAF L TDD L V K I T W D H L K S I ---G M R F M T A P P D T Y Y E M I E G R L P N H G -----E P V G E L Q A R G I L L

b Q9I576 (217) KIRIPINE-SADDT---QIEEF IREYHGE G I Q H I A L T T D D I Y A T V R K L R D N ---G V K F M S T P D T Y Y E K V D T R V A G H G -----E P L E Q L R E L N L L I

p O23920 (269) MVLLPLNEPVYGTGR-KS Q I Q T Y L E H N E G A G V Q H L A L V S E D I F R T L R E M R K R S C L G G F E F M P S P P P T Y Y K N L K N R V G D V L S -----D E Q I K E C E D L G L I V

p Q9ARF9 (263) NVLEPLNEPVYGTGR-KS Q I Q T Y L D H N E G A G V Q H L A L I T E D I F R T L R E M R K R S E V G G F E F M P S P P P T Y Y R N L K S R A G D V L S -----D E Q I E C E K L G L I L

p P93836 (276) MVLLPLNEPVHGTGR-KS Q I Q T Y L E H N E G A G I Q H L A L M S E D I F R T L R E M R K R S S I G G F D F M P S P P P T Y Y Q N L K K R V G D V L S -----D D Q I K E C E E L G L I V

p O48604 (261) GVLLPLNEPVHGTGR-RS Q I Q T F L E H H G G P G V Q H I A V A S S D V I R T L R K M R A R S A M G G F D F L P P P L P K Y Y E G V R R L A G D V L S -----E A Q I K E C Q E L G V L V

v P32754 (235) SIKMPINEPAPGKK--KS Q I Q E Y V D Y N G G A G V Q H I A L K T E D I I T A I R H L R E R ---G L E F L S V P S T Y Y K Q L R E K L K T A K ---I K V K E N I D A L E E L K I L V

v Q5EA20 (235) SIKMPINEPAPGKK--KS Q I Q E Y V D Y N G G A G V Q H I A L K T K D I I T A I R H L R E R ---G V F L A V P S T Y Y K Q L R E K L K M A K ---I R V K E N I D I L E E L K I L V

v P32755 (235) SIKMPINEPAPGKK--KS Q I Q E Y V D Y N G G A G V Q H I A L R T E D I I T T I R H L R E R ---G M E F L A V P S S Y Y R L L R E N L K T S K ---I Q V K E N M D V L E E L K I L V

v P49429 (235) SIKMPINEPAPGKK--KS Q I Q E Y V D Y N G G A G V Q H I A L K T E D I I T A I R H L R E R ---G T E F L A A P S S Y Y K L L R E N L K S A K ---I Q V K E S M D V L E E L H I L V

v Q02110 (235) SIKMPINEPAPGKK--KS Q I Q E Y V D Y N G G A G V Q H I A L K T E D I I T A I R S L R E R ---G V E F L A V P F T Y Y K Q L Q E K L K S A K ---I R V K E S I D V L E E L K I L V

v Q5BKL0 (236) TIKMPINEPAGKK--KS Q I Q E Y V D Y Y G S A G V Q H I A L N T S N I I K A V K N L K S R ---G I E F L S A P D T Y Y E L R K K L K T A K ---I T V K E D L N V L Q E L K I L V

v Q6TGZ5 (236) TIKMPINEPAGKK--KS Q I Q E Y I D Y N G G P G V Q H I A L N T S N I I Q A I V N L R A R ---G L E F L S A P D N Y Y E S L R E K L K T A K ---I K V K E D L K T L Q E L K I L V

i Q22633 (234) TIKMPINEPATSDKKAIS Q I Q E Y V D Y Y G G S G V Q H I A L N T S D I I T A I E A L R A R ---G C E F L S I P S S Y Y D N L K E R L A A S S ---M V V K E D M D R L Q K L H I L V

i Q60Y65 (234) TIKMPINEPASSNKKAVS Q I Q E F V D Y Y G G S G V Q H I A L N T D I I T A I E A L R A R ---G C E F L S I P S S Y Y D N L R Q R L S V S S ---M K I K E D M D R L Q K L H I L V

i Q27203 (249) KIKMPINEPADGKR--KS Q I Q E Y I D F Y A G P G V Q H I A L N T S D V I N T V E G L R A R ---G V E F L S I P T S Y Y D N L R K A L T A Q T ---S I T V K E D L D V L Q K N H I L V

f Q53586 (239) KVKFPINEPALAKK--KS Q I D E Y L E F Y G G A G V Q H I A L N T G D I V E T V R T M R A A ---G V Q F L D T P D S Y Y D T L G E W V G D T R -----V P -V D T L R E L K I L A

f Q9S2F4 (239) KVKFPINEPAIAKK--KS Q I D E Y L E F Y G G A G V Q H I A L N T D I V A T V R A M R A A ---G V E F L D T P D S Y Y D T L G E W A G E T R -----V P -V D V L R E L K I L V

f Q76NV5 (221) KVKLPINEPANGIR--KS Q I Q E Y V D F Y N G A G V Q H I A L K T D N I I D A I S K L R S R ---G V S F L T V P K T Y Y T S L R E K L Q H S S ---L E I T K E D L D T L E K L H I L I

f Q4WPV8 (260) VIKMPMNEPAQGKK--KS Q I E E F V N Y Y N G A G V Q H I A F R T H D I V T A V T R L R E R ---G V S F L E V P S A Y Y S D L R Q R L S H T ---G L T L E E D I A V L E K L H I L V

f Q872T7 (264) LVKMPINEPAPGKK--KS Q I E E Y V V F N S G A G V Q H I A L L T P D I I S T V S A M R A R ---G V E F L N V P S T Y Y D T I R Q R L K T E K R G ---W E L K E D L D T I Q K L N L I L

f Q96X22 (271) VVKMPINEPAGKK--RS Q I E E Y V T F N S G A G V Q H I A L L T S D I I T T V E A M R S R ---G V E F L E V P H T Y Y D T M R R R L K T E K R D ---W E L Q E D F D R L V R N N L I L

f O42764 (273) VVKMPINEPAGKK--KS Q I E E Y V D F Y N G P G V Q H I A L R T P N I I E A V S N L R S R ---G V E F L S V P D T Y Y E N M R L R L K A A ---G M K L E E S F D I I Q K L N L I L

f Q00415 (252) IVKMPINEPAGKK--QS Q I E E Y V D F Y N G A G V Q H I A L R T N N I I D A I T N L K A R ---G T E F L K V P E T Y Y E D M K I R L K R Q ---G L V L D E D F E T L K S L D I L I

f Q1E803 (252) IVKMPINEPAGKK--QS Q I E E Y V D F Y N G A G V Q H I A L R T N N I I D A I T N L K A R ---G T E F L K V P E T Y Y E D M K I R L K R Q ---G L V L D E D F E T L K S L D I L I

f Q4WHU1 (256) VVKMPINEPAGKK--QS Q I E E Y V D F Y N G A G V Q H I A L L T D D I I R D I T N L K A R ---G V E F L K V P D T Y Y E D I K V R L K A A ---G L T L H E D F E T I R S L D I L I

f Q6CDR5 (248) KIKMPVNEPAVGKK--KS Q I E E Y I D F Y D G P G I Q H I A L R T D C I L D T V R D L R A R ---G V E F L S V P G S Y Y E N M K E R L A K S ---S L K L E E K F E D I Q A L N L I L

HPPDconsens. (301) IKMPINEPAGKK KSQIQEYVDFY GAGVQHIAL T DII TI LRAR GVEFL VP TYYE LR RL I V E I D L L ILV

LLY_LEGPC (203) KIKIPLNE-SKDDL---QIEEF LHEYHGE G I Q H I A L N T N D I Y K T V N G L R K Q ---G V K F L D V P D T Y Y E M I N D R I P W H K -----E P L N Q L H A E K I L I

HPPD W336 Protein

Amino acid sequence homology search with known toxins

401 496

HPPD-W336 (297) DGSSVEGDKRLLLQIFSETLMG-P-VFFEFIOR-----K-GDDGFGGEWNFKALFESIERDQVRRGVLSTAD-----

Blast identities DG+ ++ +LLQIF++T++G-P-VFFE-IQR-----K-G++GFGG NFKALFESIE DQ+RRGVL

VLLY (298) DGAPLKD--GILLQIFTQTIVIG-P-VFFEFIOR-----K-GNEGFGGEGNFKALFESIEEDQIRRGVLNNA-----SY-M

HPPD multiple alignment

b P80064 (296) DGSSSESGDKRLLLQIFSETLMG-P-VFFEFIOR-----K-GDDGFGGEGNFKALFESIERDQVRRGVLSTD-----RIC-

b Q9I576 (301) DG--APGDDGILLQIFTDTVIG-P-IFFEIIOR-----K-GNQGFGGEGNFKALFESIEEDQIRRGVI-----ERYT

p O23920 (363) DRD----DQGTLLQIFTKPVGDRPTLFIETIQRVGCMLKDDAGQMYQKGGCGGFGKGNFSELFKSIIEYEKTLQAKQITGSAAA-----DDW

p Q9ARF9 (357) DRD----DQGTLLQIFTKPVGDRPTLFIETIQRVGCMMKDEEGKMYQKGGCGGFGKGNFSELFKSIIEYEKMLQSKLVTKTAMA-----L---

p P93836 (370) DRD----DQGTLLQIFTKPIGDRPTIFIEIIRVGCMMKDEEGKAYQSGGCGGFGKGNFSELFKSIIEYEKTLQAKQLVG-----BICT

p O48604 (355) DRD----DQGVLLQIFTKPVGDRPTLFLFLEVIORIGCMKDERGEEYQKGGCGGFGKGNFSELFKSIIEYEKSLEAKQSAVQGS-S-IP-

v P32754 (325) DYD----EKGYLLQIFTKPVQDRPTLFLFLEVIORH-----NHQFGGAGNFSLFKAFEEEEQNLRGNLTNMETNGVVPGM-----

v Q5EA20 (325) DYD----EKGYLLQIFTKPMQDRPTLFLFLEVIORH-----NHQFGGAGNFSLFKAFEEEEQDLRGNLTDMEPNGVVSVM-----

v P32755 (325) DYD----EKGYLLQIFTKPMQDRPTLFLFLEVIORH-----NHQFGGAGNFSLFKAFEEEEQALRGNLTDLETNGVRSVM-----

v P49429 (325) DYD----EKGYLLQIFTKPMQDRPTLFLFLEVIORH-----NHQFGGAGNFSLFKAFEEEEQALRGNLTDLEPNGVRSVM-----

v Q02110 (325) DYD----EKGYLLQIFTKPMQDRPTVFLFLEVIORN-----NHQFGGAGNFSLFKAFEEEEQELRGNLTDTPNGVPFRL-----

v Q5BKL0 (326) DYD----DKGYLLQIFTKPMQDRPTLFLFLEVIORY-----NHFGGAGNFKSLFEAIEETDQDARGNLTIIYAANGEHQVL-----

v Q6TGZ5 (326) DFD----DKGYLLQIFTKPVQDRPTLFLFLEVIORN-----NHFGGAGNFKSLFEAIEKDQDARGNLTVLTQNGSVSKAFQ--

i Q22633 (326) DFD----ENGYYLLQIFSKPCQDRPTLFLFLEVIORQ-----NHEGFGAGNFKALFESIELEQTKRGNLFYDNVKGDNK-----

i Q60Y65 (326) DFD----ENGYYLLQIFSKPCQDRPTLFLFLEVIORQ-----NHQFGGAGNFKALFESIELEQTKRGNLFYENVKDGQHK-----

i Q27203 (340) DYD----EKGYLLQIFTKPVDRPTLFIETIORN-----NHQFGGAGNFKSLFVSLELEQEKRGNLTIIVKNIY-----

f Q53586 (325) DRD----EDGYLLQIFTKPVQDRPTVFFEFIERH-----GSMGFGKGNFKALEAIEREQEKRGNL-----

f Q9S2F4 (325) DRD----EDGYLLQIFTKPVQDRPTVFFEFIERH-----GSMGFGKGNFKALEAIEREQEKRGNL-----

f Q76NV5 (311) DYD----DKGYLLQIFTNNVEDKPTVFFEFIORN-----NHDGFGAGNFKSLFEAIEREQEETRGNL-----

f Q4WPV8 (350) DFD----EKGYLLQIFSKHVLDRPTVFLFLEVIORN-----NFDGFGAGNFKSLFEAFEREQARRGNL-----

f Q872T7 (356) DYD----EGGYLLQLFTKPIMDRPTVFIETIORN-----NFGGFGAGNFKSLFEAIEREQAERGNL-----

f Q96X22 (363) DYD----EGGYLLQLFTTRPIMDRPTVFIETIORN-----EFDGFGAGNFKSLFEAIEREQAERGNL-----

f O42764 (363) DFD----EGGYLLQLFTKPIMDRPTVFIETIORN-----NFDGFGAGNFKSLFEAIEREQDLRGNL-----

f Q00415 (342) DFD----ENGYYLLQLFTKHLMDRPTVFIETIORN-----NFSGFGAGNFRALFEAIEREQALRGTLI-----

f Q1E803 (342) DFD----E GYLLQLFTK L DRPTVFIETIOR-----NFSGFGAGNFRALFEAIEREQALRGTLI-----

f Q4WHU1 (346) DFD----EGGYLLQLFTKHLMDRPTVFIETIORH-----NFSGFGAGNFKSLFEAIEREQALRGNLV-----

f Q6CDR5 (338) DFD----EGGYLLQLFTKPIMDRPTVFIETIORR-----NFGGFGAGNFKSLFEAIEREQAKRGNL-----

HPPDconsens. (401) DYD E GYLLQIFTKPV DRPTVFIETIOR N GFGAGNFKSLFEAIE EQ RGNL

LLY_LEGPC (287) DGEADPKD-GILLQIFTENIFG-P-VFFEFIORK-----GNQGFGGEGNFQALFEAIERDQVRRGTLKELT-----

HPPD W336 Protein
Amino acid sequence homology search with known toxins

Legend

The first three rows reproduce the results of the BLAST analysis presented in [Figure 1](#), showing a homology between the query sequence HPPD-W336 and the sequence VLLY annotated as a bacterial toxin. On the second row (Blast identities), the following information is represented:

The grey background recalls the consensus positions of the HPPD multiple alignment.

The bold letters indicate the amino acids that are identical to or of same physico-chemical properties as at least 4 of the 27 HPPD entries.

The underscored letters indicate the amino acids that are identical to or of same physico-chemical properties as at least 8 of the 27 HPPD entries.

The double-underscored letters indicate the amino acids that are strictly conserved in all HPPD sequences.

These sequences were manually aligned with a multiple alignment of 27 HPPD sequences. The 27 subsequent rows show this multiple alignment. The letter at the beginning of each row indicates the origin of each sequence:

b: bacterial

p: plant

v: vertebrate

i: invertebrate

f: fungi

At the bottom of the multiple alignment, the row in bold letters gives the consensus sequence obtained from the multiple alignment of the 27 HPPD sequences.

The black background *Indicates* amino acids conserved in 100% of the sequences, the dark grey background *Indicate* amino acids conserved in 80% of the sequences, and the light grey background, the amino acids conserved in 60% of the sequences.

The last row (LLY_LEGPC) shows the legiolysin sequence.

Out of the 192 identical residues between HPPD-W336 and VLLY, only 53 line up with less than 4 HPPD entries on the multiple alignment. These 53 residues are distributed in short stretches (1 to 3) of amino acids. The 139 other identical residues line up with 4 or more HPPD entries, and are mainly distributed in long stretches (5 to 21) of consecutive amino acids. The 41 residues that are strictly conserved amongst HPPDs are part of the identical residues between HPPD-W336, VLLY and legiolysin.

7.3. Figure 3 – Alignment of the HPPD W336 sequence with the Legiolysin sequence

Uniprot_Swissprot:LLY_LEGPC |P69053|LLY_LEGPC|4-hydroxyphenylpyruvate dioxygenase;
Short=HPPDase; Short=4HPPD; Short=HPD; EC=1.13.11.27;
Legiolysin; |*Legionella pneumophila* (strain Corby).
|AA|348
Length = 348

Score = 335 bits (860), Expect = 2e-91, Method: Compositional matrix adjust.
Identities = 175/349 (50%), Positives = 231/349 (66%), Gaps = 9/349 (2%)

```
Query: 7   NPMGLMGFEFIEFASPTPGTLEPIFEIMGFTKVATHRSKNVHLYRQGEINLILNNEPNSI 66
          NP GL GF F+EF+ P   L   F MGF VA H+++++ L++QGEI I+N   +
Sbjct: 5   NPCGLDGFAFLEFSGPDRNKLHQQFSEMGEQAVAHKKNQDITLFKQGEIQFIVNAASHCQ 64

Query: 67  ASYFAAEHGPSVCGMAFRVKDSQKAYNRALELGAQPIHIDTGPMEINLPAIKGIGGAPLY 126
          A   A+ HGP C M F+VKD++ A+ A+ G       D       LPAI+ IGG+ +Y
Sbjct: 65  AEAHASTHGPACAMGFKVKDAKAAFQHAIAHGGAIFQ-DAPHANHGLPAIQAIGGSVIY 123

Query: 127  LIDRFEGEGSSIYDIDFVYLEGVERNVPVAGLKVIDLHNLHNVYRGRMVYWANFYEKLFNFR 186
          +D   + S ++ +   E V   VG GL IDHLTHNVYRG M WA+FY +FNF+
Sbjct: 124  FVDEEHQPFS-HEWNITSSEPV----VGNGLTAIDLHNLHNVYRGNMDKWASFYASIFNFQ 178

Query: 187  EARYFDIKGEYTGLTSKAMSAPDGMIRIPLNEESSKGAGQIEEFLMQFNAGEGIQHVAFLT 246
          E R+F+IKG+ TGL S+A+ +P G I+IPLN ES   QIEEFL +++GEGIQH+A T
Sbjct: 179  EIRFFNIKGKMTGLVSRALGSPCGKIKIPLN-ESKDDLSQIEEFLHEYHGEGIQHIALNT 237

Query: 247  DDLVKTWDALKKIGMRFMTAPPDTYYEMLEGRLPDHGEPVDQLQARGILLDGSSVEGDKR 306
          +D+ KT + L+K G++F+   PDTYYEM+ RLP H EP++QL A IL+DG +   D
Sbjct: 238  NDIYKTVNGLRKQGVKFLDV-PDTYYEMINDRLPWHKEPLNQLHAEKILIDGEADPKDG- 295

Query: 307  LLLQIFSETLMGPVFFFEFIQRKGDDGFGEWNFKALFESIERDQVRRGVL 355
          LLLQIF+E + GPVFFE IQRKG+ GFGE NF+ALFE+IERDQVRRG L
Sbjct: 296  LLLQIFTENIFGPVFFFEIIQRKGNQGFEGGNFQALFEAIEDQVRRGTL 344
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8. Annex 1 – Description of the sequences included in the HPPD dataset

Accession	ID	Description	Organism	Sequence Length
Q4WHU1	HPPD1_ASPFU	Probable 4-hydroxyphenylpyruvate dioxygenase 1 (EC 1.13.11.27) (4HPPD 1) (HPD 1) (HPPDase 1).	<i>Aspergillus fumigatus</i> (<i>Sartorya fumigata</i>)	403
Q4WPV8	HPPD2_ASPFU	Probable 4-hydroxyphenylpyruvate dioxygenase 2 (EC 1.13.11.27) (4HPPD 2) (HPD 2) (HPPDase 2).	<i>Aspergillus fumigatus</i> (<i>Sartorya fumigata</i>)	406
P93836	HPPD_ARATH	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase).	<i>Arabidopsis thaliana</i> (Mouse-ear cress)	445
Q5EA20	HPPD_BOVIN	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase).	<i>Bos taurus</i> (Bovine)	393
Q60Y65	HPPD_CAEBR	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase).	<i>Caenorhabditis briggsae</i>	393
Q22633	HPPD_CAEEL	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase).	<i>Caenorhabditis elegans</i>	393
Q1E803	HPPD_COCIM	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (T-cell reactive protein).	<i>Coccidioides immitis</i>	399
Q00415	HPPD_COCPO	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (T-cell reactive protein).	<i>Coccidioides posadasii</i>	399
Q6TGZ5	HPPD_DANRE	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase).	<i>Danio rerio</i> (Zebrafish) (<i>BrachyDanio rerio</i>)	397
O23920	HPPD_DAUCA	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase).	<i>Daucus carota</i> (Carrot)	442
Q76NV5	HPPD_DICDI	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase).	<i>Dictyostelium discoideum</i> (Slime mold)	367
O48604	HPPD_HORVU	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase).	<i>Hordeum vulgare</i> (Barley)	434
P32754	HPPD_HUMAN	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase).	<i>Homo sapiens</i> (Human)	393
Q96X22	HPPD_MAGGR	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase).	<i>Magnaporthe grisea</i> (Rice blast fungus) (<i>Pyricularia grisea</i>)	419
P49429	HPPD_MOUSE	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (4-hydroxyphenylpyruvic acid oxidase) (HPPDase) (F protein) (F Alloantigen).	<i>Mus musculus</i> (Mouse)	393
O42764	HPPD_MYCGR	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase).	<i>Mycosphaerella graminicola</i> (<i>Septoria tritici</i>)	419
Q872T7	HPPD_NEUCR	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase).	<i>Neurospora crassa</i>	412
Q02110	HPPD_PIG	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase).	<i>Sus scrofa</i> (Pig)	393

HPPD W336 Protein
Amino acid sequence homology search with known toxins

Accession	ID	Description	Organism	Sequence Length
Q9I576	HPPD_PSEAE	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase).	<i>Pseudomonas aeruginosa</i>	357
P80064	HPPD_PSEUJ	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase).	<i>Pseudomonas</i> sp (strain PJ 874)	357
P32755	HPPD_RAT	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (4-hydroxyphenylpyruvic acid oxidase) (HPPDase) (F protein) (F Alloantigen).	<i>Rattus norvegicus</i> (Rat)	393
Q9ARF9	HPPD_SOLSC	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase).	<i>Solenostemon scutellarioides</i> (Coleus) (<i>Coleus blumei</i>)	436
Q53586	HPPD_STRAW	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase).	<i>Streptomyces avermitilis</i>	381
Q9S2F4	HPPD_STRCO	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase).	<i>Streptomyces coelicolor</i>	381
Q27203	HPPD_TETTH	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase) (F-antigen homolog) (TF-AG).	<i>Tetrahymena thermophila</i>	404
Q5BKL0	HPPD_XENTR	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase).	<i>Xenopus tropicalis</i> (Western clawed frog) (<i>Silurana tropicalis</i>)	394
Q6CDR5	HPPD_YARLI	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) (HPPDase).	<i>Yarrowia lipolytica</i> (Candida lipolytica)	394