



**AvHPPD-03: Assessment of Amino Acid Sequence Similarity to
Known or Putative Toxins**

Data Requirement(s): Not applicable

Author:



Study Completion Date: July 30, 2010

Performing Laboratory: Syngenta Biotechnology, Inc.
Product Safety
3054 East Cornwallis Road
PO Box 12257
Research Triangle Park, NC 27709-2257, USA

Syngenta Study No.: Not applicable

Report No.: SSB-210-10

STATEMENTS OF DATA CONFIDENTIALITY CLAIMS

The following statement applies to submissions to the United States Environmental Protection Agency (US EPA).

Statement of No Data Confidentiality Claim

No claim of confidentiality is made for any information contained in this report on the basis of its falling within the scope of Federal Insecticide, Fungicide, and Rodenticide Act (FIFRA) Section 10 (d) (1) (A), (B), or (C).

Company: *Syngenta Seeds, Inc.*

Company Representative:

[Redacted Signature]

30 July 2010
Date

Regulatory Affairs Manager

These data are the property of Syngenta Seeds Inc. and, as such, are considered to be confidential for all purposes other than compliance with the regulations implementing FIFRA Section 10. Submission of these data in compliance with FIFRA does not constitute a waiver of any right to confidentiality that may exist under any other provision of common law or statute or in any other country.

The following statement applies to submissions to regulatory agencies and other competent authorities other than the US EPA and all other viewers.

This Document Contains Confidential Business Information

This document contains information that is proprietary to Syngenta and, as such, is considered to be confidential for all purposes other than compliance with the relevant registration procedures.

Without the prior written consent of Syngenta, this information may (i) not be used by any third party including, but not limited to, any other regulatory authority for the support of regulatory approval of this product or any other product, and (ii) not be published or disclosed to any third party including, but not limited to, any authority for the support of regulatory approval of any products.

Its submission does not constitute a waiver of any right to confidentiality that may exist in any other country.

© 2010. Syngenta. All Rights Reserved

STATEMENT CONCERNING GOOD LABORATORY PRACTICES STANDARDS

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

Study Director:

[Redacted Signature]

July 30, 2010
Date

*Regulatory Scientist, Toxicology and Health Science
Product Safety
Syngenta Biotechnology, Inc.*

Submitted by:

[Redacted Signature]

30 July 2010
Date

*Regulatory Affairs Manager
Syngenta Seeds, Inc.
3054 East Cornwallis Road
PO Box 12257
Research Triangle Park, NC 27709-2257, USA*

Sponsor:

[Redacted Signature]

July 29, 2010
Date

*Team Leader, Molecular Characterization Team
Product Safety
Syngenta Biotechnology, Inc.*

TABLE OF CONTENTS

STATEMENT CONCERNING GOOD LABORATORY PRACTICES STANDARDS	3
LIST OF FIGURES.....	5
LIST OF ACRONYMS AND ABBREVIATIONS	6
SUMMARY.....	7
INTRODUCTION	8
MATERIALS AND METHODS	8
Sequence Similarity Search.....	8
Assessment of the Significance of Sequence Similarity	9
Analysis of Sequences Showing Significant Similarity to the AvHPPD-03 Amino Acid Sequence .	9
RESULTS AND DISCUSSION.....	10
CONCLUSIONS.....	11
RECORDS RETENTION.....	12
CONTRIBUTING SCIENTISTS	12
REFERENCES.....	13
APPENDICES	15
Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database.....	15
Appendix B. Sources of the 773 HPPD or similar proteins including glyoxylases and members of the dioxygenase superfamily showing significant sequence similarity to the AvHPPD-03 amino acid sequence in BLASTP analysis	111
Appendix C. Proteins of various function showing significant sequence similarity to the AvHPPD-03 amino acid sequence in BLASTP analysis	122
Appendix D. Sources of the 85 proteins identified as hypothetical, unknown, or with unknown function showing significant sequence similarity to the AvHPPD-03 amino acid sequence in BLASTP analysis	124

LIST OF FIGURES

Figure 1. Amino acid sequence of AvHPPD-03	8
--	---

LIST OF ACRONYMS AND ABBREVIATIONS

aa	amino acid
<i>avhppd-03</i>	oat derived p-hydroxyphenylpyruvate dioxygenase gene
AvHPPD-03	oat derived p-hydroxyphenylpyruvate dioxygenase protein
BLASTP	Basic Local Alignment Search Tool for Proteins
BLOSUM62	Blocks Substitution Matrix62
<i>E</i> -value	Expectation value
FIFRA	Federal Insecticide, Fungicide, and Rodenticide Act
GLPS	Good Laboratory Practice Standards
HGA	homogentisic acid
HPP	4-hydroxyphenylpyruvate
<i>hppd</i>	p-hydroxyphenylpyruvate dioxygenase gene
NCBI	National Center for Biotechnology Information
US EPA	United States Environmental Protection Agency
®	registered trademark

SUMMARY

AvHPPD-03 is a *p*-hydroxyphenylpyruvate dioxygenase enzyme that catalyzes the formation of homogentisic acid, the aromatic precursor in plastoquinone and vitamin E biosynthesis. Transgenic soybean plants expressing *avhppd-03* derived from the *hppd* gene from oat (*Avena sativa*) exhibit a mesotrione-tolerance phenotype. The Basic Local Alignment Search Tool for Proteins program was used to search the National Center for Biotechnology Information Entrez® Protein Database to determine if the oat-derived AvHPPD-03 amino acid sequence showed biologically relevant similarity to known and putative toxins. The threshold value from the Basic Local Alignment Search Tool for determining potential significance of matches was based on searches conducted with randomly shuffled sequences of the amino acids comprising AvHPPD-03. Of 916 protein sequences identified as having potential significance to AvHPPD-03, inspection of these alignments showed that there were no biologically relevant sequence homologies with any proteins known to be toxins. AvHPPD-03 is unlikely to share toxicity or other biological activity with known toxins that are harmful to human or animal health.

INTRODUCTION

The purpose of this study is to determine whether the oat derived *p*-hydroxyphenylpyruvate dioxygenase protein (AvHPPD-03) amino acid sequence has significant similarity with proteins that are known or putative toxins.

The AvHPPD-03 protein is a *p*-hydroxyphenylpyruvate dioxygenase enzyme that catalyzes the formation of homogentisic acid, the aromatic precursor in plastoquinone and vitamin E biosynthesis. Transgenic soybean plants expressing *avhppd-03* derived from the *hppd* gene from oat (*Avena sativa*) exhibit a mesotrione-tolerance phenotype.

The AvHPPD-03 amino acid sequence was systematically compared with the latest posting of the National Center for Biotechnology Information (NCBI) Entrez® Protein Database (NCBI 2010). This procedure identified (1) whether any proteins in the database showed significant similarity to the AvHPPD-03 amino acid sequence (*i.e.*, alignments with Basic Local Alignment Search Tool for Proteins [BLASTP] Expectation values [*E* -values] below an established threshold), indicating that the amino acid sequence might be closely related to the AvHPPD-03 amino acid sequence, and (2) whether any proteins showing sequence similarity to the AvHPPD-03 amino acid sequence were known or putative toxins.

MATERIALS AND METHODS

Sequence Similarity Search

The BLASTP program (Altschul *et al.* 1997) was used to search the NCBI Entrez® Protein Database with the AvHPPD-03 amino acid sequence as the query sequence (439 amino acids [Figure 1]).

Figure 1. Amino acid sequence of AvHPPD-03

```

1  MPPTPATATG  AAAA AVTPEH  AARSFPRVVR  VNPRSDRFPV  LSFHHVELWC  ADAASAAGR
61  SFALGAPLAA  RSDLSTGNSA  HASLLLLRSGA  LAFLFTAPYA  PPPQEAATAA  TASIPSFSAD
121 AARTFAAAHG  LAVRSVGVRV  ADAAEAFRVS  VAGGARPAFA  PADLGHGFGL  AEVELYGDVV
181 LRFVSYPDET  DLPFLPGFER  VSSPGAVDYG  LTRFDHVVG  VPEMAPVIDY  MKGFLGFHEF
241 AEFTAEDVGT  TESGLNSVVL  ANNSEAVLLP  LNEPVHGTR  RSQIQTYLEY  HGGPGVQHIA
301 LASNDVLR  TL  REMRARTPMG  GFEFMAPPQA  KYEGVRRIA  GDVLSEEQIK  ECQELGVLVD
361 RDDQGVLLQI  FTKPVGDRPT  FFLEMIQRIG  CMEKDEVGQE  YQKGGCGGFG  KGNFSELFKS
421 IEDYEKSLEV  KQSVVAQKS

```

The NCBI Entrez® Protein Database was used to identify the potential similarity between the query protein amino acid sequence and known and putative toxins. For this analysis, the NCBI Entrez® Protein Database (containing over 10 million protein sequences) was accessed on May 5, 2010. The BLASTP is a program used to search protein sequences for sequence similarities. Most proteins are modular in nature and contain repeating functional domains within the protein. Similarly, functional domains are conserved across different proteins from different species. The BLASTP algorithm is optimized to identify these domains or shorter sequence similarities present within the full length query sequence; as a result, this approach detects more similarities than would a search started by aligning two sequences over their entire length. The BLASTP

program, version 2.2.8, was used to perform the similarity searches with the following default parameters:

No complexity filter

E -value = 10

Word size = 3

Gap costs: existence = 11 and extension = 1

Similarity matrix: Blocks Substitution Matrix62 (BLOSUM62)

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

Assessment of the Significance of Sequence Similarity

A threshold below which similarity to the query sequence is considered significant, and not the result of random similarity in amino acid composition, is required for meaningful analysis of database alignments. To assess the significance of sequence similarity to the AvHPPD-03 amino acid sequence, additional searches were conducted with shuffled versions of the AvHPPD-03 amino acid sequence. Five shuffled sequences were created through random shuffling of the AvHPPD-03 amino acid sequence using the modern version of the Fisher-Yates shuffle (Knuth 1998).

The resulting shuffled sequences all had the same amino acid composition as AvHPPD-03 (*i.e.*, the same number of residues of each specific amino acid), but were unlikely to have amino acid sequences similar to those of either AvHPPD-03 or other proteins found in the NCBI Entrez® Protein Database. Searches using these shuffled sequences provided an estimate of the background incidence of alignments that would be expected for any sequence with the same amino acid composition as AvHPPD-03. Searches with the five shuffled versions of the AvHPPD-03 amino acid sequence identified sequences with search results yielding E -values that ranged from 0.15 to 1.6; therefore, the threshold E -value for significant amino acid sequence similarity to AvHPPD-03 was considered to be 0.15. Sequences with significant similarity to the AvHPPD-03 amino acid sequence (*i.e.*, E -values less than 0.15) were evaluated for source and biological function.

Analysis of Sequences Showing Significant Similarity to the AvHPPD-03 Amino Acid Sequence

The identity and biological function, if known, were determined for each protein identified in the BLASTP search as having significant similarity to the AvHPPD-03 amino acid sequence (*i.e.*, E -value less than 0.15). The NCBI Entrez® Protein Database records were accessed, if needed, using the Entrez® Accession Numbers. If an entry in the NCBI Entrez® Protein Database record was vague (*e.g.*, “hypothetical protein”), the individual record and supporting literature were examined in an attempt to clarify the identity and/or function of the protein associated with that record.

RESULTS AND DISCUSSION

The NCBI Entrez® Protein Database search identified 916 sequences that exceeded the BLAST similarity threshold to the AvHPPD-03 amino acid sequence (*i.e.*, *E*-values less than 0.15) (Appendix A). Of these, 775 were identified as HPPD or similar proteins including glyoxylases and members of the dioxygenase superfamily, from 409 species. The *E*-values for alignments between these sequences and the AvHPPD-03 amino acid sequence ranged from 0 to 0.039. Appendix B shows the source organisms for these proteins.

An additional 14 sequences are also referred to as putative, related to hemolysins or “hemolysin-like”. HPPD catalyzes the conversion of 4-hydroxyphenylpyruvate (HPP) to homogentisic acid (HGA) in aerobic metabolism. HGA, not HPPD, can undergo a further nonenzymatic oxidation and polymerization that protect some bacterial species from light. A similar non-enzymatic process can occur with high concentrations of HGA that then can induce hemolysis to occur spontaneously in certain mammalian diseases, including bacterial infections. For this reason, HPPD from bacteria is sometimes identified as a putative hemolysin (Lee *et al.* 2008). Therefore, the distinction should be made that HPPD protein itself does not cause hemolysis, HGA, a metabolite of HPPD, is the metabolic product of HPPD that can lead to hemolysis. Fourteen sequences in the database are described as hemolysins, however this HPPD-hemolysin association does not itself indicate a cause for concern regarding exposure to HPPD protein. In each of these 14 alignments, it is not the protein that is the hemolysin but rather HGA that is a putative hemolytic precursor. The association with hemolysis that some of these aligned proteins have is limited to bacterial species for which there are very specific metabolic pathways. There is no evidence that the aerobic HPPD metabolic pathway in plants leads to metabolites associated with hemolysis.

The alignments between AvHPPD-03 and these 14 sequences have an *E*-value range of 3×10^{-50} to 0.087 and are from 12 bacterial species including *Bacillus* sp., *Bordetella avium*, *Bordetella parapertussis*, *Bordetella pertussis*, *Deinococcus geothermalis*, *Pantoeas anantis*, *Vibrio alginolyticus*, *Vibrio harveyi*, *Vibrio mimicus*, *Vibrio splendidus*, *Vibrio vulnificus*. These are specifically Hit Ranks 82, 373, 448, 487, 492, 509, 540, 545, 549, 564, 596, 754, 782, and 914 (Appendix A).

HPPD is a ubiquitous protein throughout the plant and animal taxonomic kingdoms and is not itself a hemolysin. HPPD is found in aerobic forms of life with the exception of some Gram positive bacteria (Gunsior *et al.* 2004); this includes human (Lindstedt and Odelhog 1987, Ruetschi *et al.* 1993), pig (Roche *et al.* 1982), chicken (Wada *et al.* 1975), plants (Garcia *et al.* 1999), and prokaryotes (Denoya *et al.* 1994) and is essential to all aerobic forms of life (Lee *et al.* 2008)). In some Gram-negative bacteria such as *Shewanella*, *Legionella*, and *Vibrio*, HGA is converted into melanin or melanin-like pigments, fluorescent substances and hemolysin substances (Kakidani and Hirai 2003).

An additional 43 protein sequences of various function were identified and are described in Appendix C.

An additional 85 sequences were identified as hypothetical or unnamed proteins or proteins with unknown function from 63 species, with *E*-values that ranged from 6×10^{-43} to 0.11; the source organisms for these proteins are shown in Appendix D.

CONCLUSIONS

In a comprehensive amino acid similarity search and analysis of bioinformatic alignments between the NCBI Entrez Protein database and the AvHPPD-03 query sequence there were no biologically relevant sequence homologies with any proteins known to be toxins. AvHPPD-03 is unlikely to share toxicity or other biological activity with known toxins that are harmful to human or animal health.

RECORDS RETENTION

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

CONTRIBUTING SCIENTISTS

The analytical work reported herein was conducted by [REDACTED] This work was conducted at Syngenta Biotechnology, Inc.

Reported by:

[REDACTED]

July 30, 2010
Date

*Regulatory Scientist, Toxicology and Health Science
Product Safety
Syngenta Biotechnology, Inc.*

Approved by:

[REDACTED]

July 24, 2010
Date

*Team Leader, Molecular Characterization Team
Product Safety
Syngenta Biotechnology, Inc.*

REFERENCES

- Altschul SF, Madden TL, Schäffer AA, Zhang J, Zhang Z, Miller W, Lipman DJ. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res* 25:3389–3402.
- Denoya CD, Skinner DD, Morgenstern MR. 1994. A *Streptomyces avermitilis* gene encoding a 4-hydroxyphenylpyruvic acid dioxygenase-like protein that directs the production of homogentisic acid and an ochronotic pigment in *Escherichia coli*. *J Bacteriol* 176:5312–5319.
- Ferris H, Minamino T. 2006. Flipping the switch: bringing order to flagellar assembly. *Trends in Microbiology* 14:519–526.
- Fuqua W, Coyne V, Stein D, Lin C, Weiner R. 1991. Characterization of *melaA*: a gene encoding melanin biosynthesis from the marine bacterium *Shewanella colwelliana*. *Gene* 109:131–136.
- Garcia I, Rodgers M, Pepin R, Hsieh TF, Matringe M. 1999. Characterization and subcellular compartmentation of recombinant 4-hydroxyphenylpyruvate dioxygenase from *Arabidopsis* in transgenic tobacco. *Plant Physiol* 119:1507–1516.
- Gunsior M, Ravel J, Challis G, Townsend C. 2004. Engineering *p*-hydroxyphenylpyruvate dioxygenase to a *p*-hydroxymandelate Synthase and evidence for the proposed benzene oxide intermediate in homogentisate formation. *Biochemistry-US* 43:663–674.
- Kakidani H, Hirai K. 2003. Three-dimensional modeling of plant 4-hydroxyphenylpyruvate dioxygenase, a molecular target of triketone-type herbicides. *J Pestic Sci* 28:409–415.
- Knuth DE. 1998. *The Art of Computer Programming, Vol. 2*, 3rd ed. Reading, MA: Harlow: Addison-Wesley. pp. 145–146.
- Lee CM, Yeo YS, Lee JH, Kim SJ, Kim JB, Han NS, Koo BS, Yoon SH. 2008. Identification of a novel 4-hydroxyphenylpyruvate dioxygenase from the soil megatome. *Biochem Biophys Res Commun* 370:322–326.
- Lindstedt S, Odelhog B. 1987. 4-Hydroxyphenylpyruvate dioxygenase from human liver. *Methods Enzymol* 142:139–142.
- Liu SY, Yu XD, Song CJ, Lu W, Zhang JD, Shi XR, Duan Y, Zhang J. 2007. Cloning and expression of special F protein from human liver. *World J Gastro* 13:1799–1804.
- Mendel D, Crabtree G. 1991. HNF-1, a member of a novel class of dimerizing homeodomain proteins. *J Biol Chem* 266:677–680.

- NCBI. 2010. Entrez® Protein database. Bethesda, MD: National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health. <http://www.ncbi.nlm.nih.gov/sites/entrez?db=Protein> (accessed May 5, 2010).
- Ponting C. 2001. Issues in predicting protein function from sequence. *Brief Bioinform* 2:19–29.
- Roche PA, Moorhead TJ, Hamilton GA. 1982. Purification and properties of hog liver 4-hydroxyphenylpyruvate dioxygenase. *Arch Biochem Biophys* 216:62–73.
- Ruetschi U, Dellsen A, Sahlin P, Stenman G, Rymo L, Lindstedt S. 1993. Human 4-hydroxyphenylpyruvate dioxygenase. Primary structure and chromosomal location of the gene. *Eur J Biochem* 213:1081–1089.
- Steinert M, Flugel M, Schuppler M, Helbig J, Supriyono A, Proksch P, Luck P. 2001. The Lly protein is essential for p-hydroxyphenylpyruvate dioxygenase activity in *Legionella pneumophila*. *FEMS Microbiol Lett* 203:41–47.
- US EPA. 1989. Good Laboratory Practice Standards. 40 CFR Part 160.3.
- Venketesh S, Dayananda C. 2008. Properties, potentials, and prospects of antifreeze proteins. *CRC Cr Rev Biotechn* 28:57–82.
- Wada GH, Fellman JH, Fujita TS, Roth ES. 1975. Purification and properties of avian liver p-hydroxyphenylpyruvate hydrolase. *J Biol Chem* 250:6720–6726.

APPENDICES

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
1	NR gi 3334222 sp O48604.1 HPPD_HORVU RecName: Full=4-hydroxyphenylpyruvate dioxygenase; AltName: Full=4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD 4-hydroxyphenylpyruvate dioxygenase [Hordeum vulgare subsp. vulgare]	434	0	1 - 439 (82%)
2	NR gi 72256523 gb AAZ67144.1 4-hydroxyphenylpyruvate dioxygenase [Triticum aestivum]	436	0	1 - 439 (82%)
3	NR gi 49387760 dbj BAD26248.1 putative 4-hydroxyphenylpyruvate dioxygenase [Oryza sativa Japonica Group] putative 4-hydroxyphenylpyruvate dioxygenase [Oryza sativa Japonica Group]	446	0	1 - 439 (80%)
4	NR gi 242064140 ref XP_002453359.1 hypothetical protein SORBIDRAFT_04g004560 [Sorghum bicolor] hypothetical protein SORBIDRAFT_04g004560 [Sorghum bicolor]	440	0	1 - 439 (79%)
5	NR gi 162459274 ref NP_001105782.1 4-hydroxyphenylpyruvate dioxygenase 1 [Zea mays] putative p-hydroxyphenylpyruvate dioxygenase [Zea mays]	444	0	1 - 436 (78%)
6	NR gi 55669753 pdb 1SP8 A Chain A, 4-Hydroxyphenylpyruvate Dioxygenase Chain B, 4-Hydroxyphenylpyruvate Dioxygenase Chain C, 4-Hydroxyphenylpyruvate Dioxygenase Chain D, 4-Hydroxyphenylpyruvate Dioxygenase	418	0	29 - 432 (82%)
7	NR gi 224034593 gb ACN36372.1 unknown [Zea mays]	426	0	1 - 436 (76%)
8	NR gi 125580949 gb EAZ21880.1 hypothetical protein OsJ_05532 [Oryza sativa Japonica Group]	447	1×10^{-179}	1 - 439 (73%)
9	NR gi 157040846 emb CAJ29893.1 4-hydroxyphenylpyruvate dioxygenase [Triticum aestivum]	381	1×10^{-172}	1 - 380 (81%)
10	NR gi 218190140 gb EEC72567.1 hypothetical protein Osl_06005 [Oryza sativa Indica Group]	601	1×10^{-172}	55 - 439 (80%)
11	NR gi 3334219 sp O23920.1 HPPD_DAUCA RecName: Full=4-hydroxyphenylpyruvate dioxygenase; AltName: Full=4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD 4-hydroxyphenylpyruvate dioxygenase [Daucus carota]	442	1×10^{-154}	25 - 432 (66%)
12	NR gi 255558690 ref XP_002520369.1 4-hydroxyphenylpyruvate dioxygenase, putative [Ricinus communis] 4-hydroxyphenylpyruvate dioxygenase, putative [Ricinus communis]	441	1×10^{-151}	17 - 432 (63%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
13	NR gi 242048166 ref XP_002461829.1 hypothetical protein SORBIDRAFT_02g008850 [Sorghum bicolor] hypothetical protein SORBIDRAFT_02g008850 [Sorghum bicolor]	496	1×10^{-149}	36 - 436 (66%)
14	NR gi 62003087 gb AAX59006.1 4-hydroxyphenylpyruvate dioxygenase [Medicago truncatula]	437	1×10^{-149}	25 - 433 (63%)
15	NR gi 224062651 ref XP_002300867.1 predicted protein [Populus trichocarpa] predicted protein [Populus trichocarpa]	444	1×10^{-148}	25 - 431 (63%)
16	NR gi 154240639 dbj BAF74636.1 hydroxyphenylpyruvate dioxygenase [Coptis japonica var. dissecta]	430	1×10^{-148}	29 - 436 (63%)
17	NR gi 3334223 sp P93836.2 HPPD_ARATH RecName: Full=4-hydroxyphenylpyruvate dioxygenase; AltName: Full=4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD Chain A, 4-Hydroxyphenylpyruvate Dioxygenase Chain B, 4-Hydroxyphenylpyruvate Dioxygenase At1g06570/F12K11_12 [Arabidopsis thaliana] p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] 4-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] 4-hydroxyphenylpyruvate dioxygenase (HPD) [Arabidopsis thaliana] 4-hydroxyphenylpyruvate dioxygenase (HPD) [Arabidopsis thaliana]	445	1×10^{-148}	14 - 434 (61%)
18	NR gi 30679736 ref NP_172144.2 PDS1 (PHYTOENE DESATURATION 1); 4-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] F12K11.9 [Arabidopsis thaliana]	473	1×10^{-148}	14 - 434 (61%)
19	NR gi 22530912 gb AAM96960.1 4-hydroxyphenylpyruvate dioxygenase HPD [Arabidopsis thaliana]	473	1×10^{-147}	14 - 434 (61%)
20	NR gi 219842162 dbj BAH10638.1 4-hydroxyphenylpyruvate dioxygenase [Hevea brasiliensis]	445	1×10^{-147}	25 - 437 (61%)
21	NR gi 148616206 gb ABQ96868.1 4-hydroxyphenylpyruvate dioxygenase [Glycine max]	443	1×10^{-147}	12 - 433 (61%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
22	NR gi 52695552 pdb 1SQD A Chain A, Structural Basis For Inhibitor Selectivity Revealed By Crystal Structures Of Plant And Mammalian 4-Hydroxyphenylpyruvate Dioxygenases Chain A, Structural Basis For Herbicidal Inhibitor Selectivity Revealed By Comparison Of Crystal Structures Of Plant And Mammalian 4-Hydroxyphenylpyruvate Dioxygenases Chain A, Crystal Structures Of Plant 4-Hydroxyphenylpyruvate Dioxygenases Complexed With Das645	424	1×10^{-147}	25 - 434 (62%)
23	NR gi 17366672 sp Q9ARF9.1 HPPD_SOLSC RecName: Full=4-hydroxyphenylpyruvate dioxygenase; AltName: Full=4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD 4-hydroxyphenylpyruvate dioxygenase [Solenostemon scutellarioides]	436	1×10^{-146}	11 - 431 (62%)
24	NR gi 225446801 ref XP_002283275.1 PREDICTED: hypothetical protein [Vitis vinifera]	448	1×10^{-146}	6 - 434 (61%)
25	NR gi 225001452 gb ACN78586.1 4-hydroxyphenylpyruvate dioxygenase [Lactuca sativa]	446	1×10^{-146}	25 - 431 (62%)
26	NR gi 134284741 gb ABO69440.1 hydroxyphenylpyruvate dioxygenase [Salvia miltiorrhiza]	481	1×10^{-145}	11 - 436 (62%)
27	NR gi 147787057 emb CAN71143.1 hypothetical protein [Vitis vinifera]	445	1×10^{-145}	25 - 434 (62%)
28	NR gi 114324487 gb ABI63586.1 4-hydroxyphenylpyruvate dioxygenase [Brassica rapa subsp. pekinensis]	443	1×10^{-145}	11 - 434 (61%)
29	NR gi 242048184 ref XP_002461838.1 hypothetical protein SORBIDRAFT_02g008990 [Sorghum bicolor] hypothetical protein SORBIDRAFT_02g008990 [Sorghum bicolor]	480	1×10^{-135}	16 - 436 (61%)
30	NR gi 3694811 gb AAC62457.1 p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]	419	1×10^{-134}	14 - 408 (59%)
31	NR gi 168010496 ref XP_001757940.1 predicted protein [Physcomitrella patens subsp. patens] predicted protein [Physcomitrella patens subsp. patens]	432	1×10^{-126}	27 - 429 (57%)
32	NR gi 168006779 ref XP_001756086.1 predicted protein [Physcomitrella patens subsp. patens] predicted protein [Physcomitrella patens subsp. patens]	433	1×10^{-125}	27 - 429 (57%)
33	NR gi 238478369 ref NP_001154311.1 PDS1 (PHYTOENE DESATURATION 1); 4-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]	418	1×10^{-119}	14 - 378 (58%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
34	NR gi 223717664 emb CAR47957.1 p-hydroxyphenylpyruvate dioxygenase [Chlamydomonas reinhardtii]	432	1×10^{-118}	25 - 430 (53%)
35	NR gi 23505684 gb AAN28922.1 4-hydroxyphenylpyruvate dioxygenase [Abutilon theophrasti]	363	1×10^{-118}	50 - 407 (59%)
36	NR gi 159473192 ref XP_001694723.1 4-hydroxyphenylpyruvate dioxygenase [Chlamydomonas reinhardtii] p-hydroxyphenylpyruvate dioxygenase [Chlamydomonas reinhardtii] 4-hydroxyphenylpyruvate dioxygenase [Chlamydomonas reinhardtii]	432	1×10^{-118}	25 - 430 (53%)
37	NR gi 115444461 ref NP_001046010.1 Os02g0168100 [Oryza sativa (japonica cultivar-group)] Os02g0168100 [Oryza sativa Japonica Group]	239	1×10^{-116}	201 - 439 (86%)
38	NR gi 262101174 gb EEY59226.1 4-hydroxyphenylpyruvate dioxygenase [Phytophthora infestans T30-4]	418	1×10^{-116}	29 - 430 (53%)
39	NR gi 116056732 emb CAL53021.1 p-hydroxyphenylpyruvate dioxygenase (ISS) [Ostreococcus tauri]	432	1×10^{-114}	29 - 430 (52%)
40	NR gi 145344381 ref XP_001416712.1 predicted protein [Ostreococcus lucimarinus CCE9901] predicted protein [Ostreococcus lucimarinus CCE9901]	427	1×10^{-114}	29 - 430 (52%)
41	NR gi 255071413 ref XP_002499380.1 predicted protein [Micromonas sp. RCC299] predicted protein [Micromonas sp. RCC299]	441	1×10^{-113}	30 - 430 (54%)
42	NR gi 226463796 gb EEH61074.1 predicted protein [Micromonas pusilla CCMP1545]	447	1×10^{-112}	11 - 430 (51%)
43	NR gi 159473190 ref XP_001694722.1 4-hydroxyphenylpyruvate dioxygenase [Chlamydomonas reinhardtii] 4-hydroxyphenylpyruvate dioxygenase [Chlamydomonas reinhardtii]	372	1×10^{-102}	67 - 430 (53%)
44	NR gi 224085389 ref XP_002307562.1 predicted protein [Populus trichocarpa] predicted protein [Populus trichocarpa]	343	3×10^{-97}	25 - 432 (50%)
45	NR gi 116793541 gb ABK26783.1 unknown [Picea sitchensis]	263	4×10^{-95}	170 - 429 (65%)
46	NR gi 223995177 ref XP_002287272.1 4-hydroxyphenylpyruvate dioxygenase [Thalassiosira pseudonana CCMP1335] 4-hydroxyphenylpyruvate dioxygenase [Thalassiosira pseudonana CCMP1335]	418	8×10^{-90}	43 - 430 (46%)
47	NR gi 262098253 gb EEY56305.1 4-hydroxyphenylpyruvate dioxygenase [Phytophthora infestans T30-4]	335	8×10^{-83}	35 - 361 (49%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
48	NR gi 94969031 ref YP_591079.1 4-hydroxyphenylpyruvate dioxygenase [Candidatus Koribacter versatilis Ellin345] 4-hydroxyphenylpyruvate dioxygenase [Candidatus Koribacter versatilis Ellin345]	361	2×10^{-55}	44 - 422 (38%)
49	NR gi 145314566 gb ABI53728.2 4-hydroxyphenylpyruvate dioxygenase [uncultured bacterium]	375	1×10^{-54}	44 - 426 (36%)
50	NR gi 226313929 ref YP_002773825.1 probable 4-hydroxyphenylpyruvate dioxygenase [Brevibacillus brevis NBRC 100599] probable 4-hydroxyphenylpyruvate dioxygenase [Brevibacillus brevis NBRC 100599]	363	3×10^{-54}	35 - 422 (33%)
51	NR gi 254379706 ref ZP_04995120.1 4-hydroxyphenylpyruvate dioxygenase [Streptomyces sp. SPB74] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces sp. SPB74]	401	4×10^{-54}	28 - 422 (38%)
52	NR gi 256677662 ref ZP_05487973.1 4-hydroxyphenylpyruvate dioxygenase [Streptomyces sp. SPB78]	401	6×10^{-54}	23 - 422 (37%)
53	NR gi 205372789 ref ZP_03225599.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus coahuilensis m4-4]	374	2×10^{-53}	36 - 422 (36%)
54	NR gi 116623260 ref YP_825416.1 4-hydroxyphenylpyruvate dioxygenase [Solibacter usitatus Ellin6076] 4-hydroxyphenylpyruvate dioxygenase [Candidatus Solibacter usitatus Ellin6076]	375	4×10^{-53}	36 - 422 (36%)
55	NR gi 163846389 ref YP_001634433.1 4-hydroxyphenylpyruvate dioxygenase [Chloroflexus aurantiacus J-10-fl] 4-hydroxyphenylpyruvate dioxygenase [Chloroflexus sp. Y-400-fl] 4-hydroxyphenylpyruvate dioxygenase [Chloroflexus aurantiacus J-10-fl] 4-hydroxyphenylpyruvate dioxygenase [Chloroflexus sp. Y-400-fl]	365	5×10^{-53}	35 - 422 (35%)
56	NR gi 219849610 ref YP_002464043.1 4-hydroxyphenylpyruvate dioxygenase [Chloroflexus aggregans DSM 9485] 4-hydroxyphenylpyruvate dioxygenase [Chloroflexus aggregans DSM 9485]	365	2×10^{-52}	36 - 422 (35%)
57	NR gi 152974072 ref YP_001373589.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus subsp. cytotoxis NVH 391-98] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cytotoxicus NVH 391-98]	372	3×10^{-52}	36 - 422 (35%)
58	NR gi 225874851 ref YP_002756310.1 4-hydroxyphenylpyruvate dioxygenase [Acidobacterium capsulatum ATCC 51196] 4-hydroxyphenylpyruvate dioxygenase [Acidobacterium capsulatum ATCC 51196]	374	4×10^{-52}	31 - 422 (36%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
59	NR gi 83816571 ref YP_445494.1 4-hydroxyphenylpyruvate dioxygenase [Salinibacter ruber DSM 13855] 4-hydroxyphenylpyruvate dioxygenase [Salinibacter ruber DSM 13855]	384	4×10^{-52}	31 - 422 (36%)
60	NR gi 149181237 ref ZP_01859736.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus sp. SG-1] 4-hydroxyphenylpyruvate dioxygenase [Bacillus sp. SG-1]	378	5×10^{-52}	36 - 422 (35%)
61	NR gi 284990446 ref YP_003409000.1 4-hydroxyphenylpyruvate dioxygenase [Geodermatophilus obscurus DSM 43160] 4-hydroxyphenylpyruvate dioxygenase [Geodermatophilus obscurus DSM 43160]	401	7×10^{-52}	28 - 422 (38%)
62	NR gi 159031819 dbj BAF91881.1 4-hydroxyphenylpyruvate dioxygenase homolog [Blepharisma japonicum]	382	7×10^{-52}	34 - 426 (34%)
63	NR gi 256778918 ref ZP_05517381.1 putative 4-hydroxyphenylpyruvate dioxygenase [Streptomyces hygroscopicus ATCC 53653]	381	2×10^{-51}	34 - 422 (38%)
64	NR gi 168701840 ref ZP_02734117.1 4-hydroxyphenylpyruvate dioxygenase [Gemmata obscuriglobus UQM 2246]	366	3×10^{-51}	39 - 422 (35%)
65	NR gi 226227529 ref YP_002761635.1 4-hydroxyphenylpyruvate dioxygenase [Gemmatisimonas aurantiaca T-27] 4-hydroxyphenylpyruvate dioxygenase [Gemmatisimonas aurantiaca T-27]	374	6×10^{-51}	31 - 422 (35%)
66	NR gi 229083517 ref ZP_04215856.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus Rock3-44] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus Rock3-44]	372	8×10^{-51}	36 - 422 (35%)
67	NR gi 228989407 ref ZP_04149396.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus pseudomycoideus DSM 12442] 4-hydroxyphenylpyruvate dioxygenase [Bacillus mycoideus Rock3-17] 4-hydroxyphenylpyruvate dioxygenase [Bacillus mycoideus Rock3-17] 4-hydroxyphenylpyruvate dioxygenase [Bacillus pseudomycoideus DSM 12442]	372	1×10^{-50}	36 - 422 (35%)
68	NR gi 228983486 ref ZP_04143696.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar tochiensis BGSC 4Y1] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 4342] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 4342] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar tochiensis BGSC 4Y1]	389	1×10^{-50}	36 - 422 (35%)
69	NR gi 256767667 ref ZP_05506841.1 4-hydroxyphenylpyruvate dioxygenase [Streptomyces sp. C]	381	1×10^{-50}	35 - 422 (37%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
70	NR gi 255035874 ref YP_003086495.1 4-hydroxyphenylpyruvate dioxygenase [Dyadobacter fermentans DSM 18053] 4-hydroxyphenylpyruvate dioxygenase [Dyadobacter fermentans DSM 18053]	374	1×10^{-50}	35 - 422 (36%)
71	NR gi 229159393 ref ZP_04287413.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus R309803] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus R309803]	385	2×10^{-50}	36 - 422 (35%)
72	NR gi 228906011 ref ZP_04069903.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis IBL 200] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis IBL 200]	385	2×10^{-50}	36 - 422 (35%)
73	NR gi 47567476 ref ZP_00238188.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus G9241] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus G9241]	372	2×10^{-50}	36 - 422 (35%)
74	NR gi 228919165 ref ZP_04082539.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar huazhongensis BGSC 4BD1] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar huazhongensis BGSC 4BD1]	385	3×10^{-50}	36 - 422 (35%)
75	NR gi 228898969 ref ZP_04063247.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis IBL 4222] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar berliner ATCC 10792] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar sotto str. T04001] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar thuringiensis str. T01001] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis Bt407] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis Bt407] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar thuringiensis str. T01001] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar sotto str. T04001] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar berliner ATCC 10792] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis IBL 4222]	385	3×10^{-50}	36 - 422 (35%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
76	NR gi 228912971 ref ZP_04076615.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar pulsiensis BGSC 4CC1] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar pondicheriensis BGSC 4BA1] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar andalousiensis BGSC 4AW1] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus Rock3-42] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus BDRD-ST26] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus BGSC 6E1] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus m1293] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus m1293] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus BGSC 6E1] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus BDRD-ST26] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus Rock3-42] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar andalousiensis BGSC 4AW1] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar pondicheriensis BGSC 4BA1] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar pulsiensis BGSC 4CC1]	385	3×10^{-50}	36 - 422 (35%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
77	NR gi 228950761 ref ZP_04112890.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar kurstaki str. T03a001] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus AH676] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus F65185] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus Rock1-15] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus BDRD-Cer4] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus BDRD-ST24] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus m1550] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus 172560W] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 10876] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 10876] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus 172560W] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus m1550] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus BDRD-ST24] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus BDRD-Cer4] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus Rock1-15] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus F65185] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus AH676] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar kurstaki str. T03a001]	385	3×10^{-50}	36 - 422 (35%)
78	NR gi 218895352 ref YP_002443763.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus G9842] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus G9842]	372	3×10^{-50}	36 - 422 (35%)
79	NR gi 118475988 ref YP_893139.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis str. Al Hakam] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis str. Al Hakam]	389	3×10^{-50}	36 - 422 (35%)
80	NR gi 30018489 ref NP_830120.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 14579] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus AH1134] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus B4264] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 14579] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus AH1134] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus B4264]	372	3×10^{-50}	36 - 422 (35%)
81	NR gi 75760149 ref ZP_00740208.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar israelensis ATCC 35646] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar israelensis ATCC 35646]	389	3×10^{-50}	36 - 422 (35%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
82	NR gil30260417 ref NP_842794.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. Ames] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 10987] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. 'Ames Ancestor'] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. Sterne] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar konkukian str. 97-27] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus E33L] COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Bacillus anthracis str. A2012] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. A0488] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. A0442] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. A0193] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. A0465] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. A0389] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. A0174] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis Tsiankovskii-I] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus W] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus NVH0597-99] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus 03BB108] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus H3081.97] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus AH187] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus AH820] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus Q1] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus 03BB102] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. CDC 684] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. A0248] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. CNEVA-9066] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. A1055] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. Western North America USA6153] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. Kruger B] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. Vollum] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. Australia 94] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. Ames] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 10987] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. 'Ames Ancestor'] 4-hydroxyphenylpyruvate dioxygenase [Bacillus anthracis str. Sterne] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar konkukian str. 97-27] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus E33L] 4-hydroxyphenylpyruvate dioxygenase [Bacillus	372	3 x 10 ⁻⁵⁰	36 - 422 (35%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
83	NR gi 228956663 ref ZP_04118454.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar pakistani str. T13001] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar pakistani str. T13001]	385	4×10^{-50}	36 - 422 (35%)
84	NR gi 229165211 ref ZP_04293003.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus AH621] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus AH621]	385	4×10^{-50}	36 - 422 (36%)
85	NR gi 91215525 ref ZP_01252496.1 4-hydroxyphenylpyruvate dioxygenase [Psychroflexus torquis ATCC 700755] 4-hydroxyphenylpyruvate dioxygenase [Psychroflexus torquis ATCC 700755]	379	4×10^{-50}	27 - 422 (33%)
86	NR gi 239941600 ref ZP_04693537.1 putative 4-hydroxyphenylpyruvate dioxygenase [Streptomyces roseosporus NRRL 15998] putative 4-hydroxyphenylpyruvate dioxygenase [Streptomyces roseosporus NRRL 11379] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces roseosporus NRRL 15998] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces roseosporus NRRL 15998]	381	5×10^{-50}	34 - 422 (37%)
87	NR gi 229074278 ref ZP_04207322.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus Rock4-18] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus Rock3-28] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus Rock3-28] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus Rock4-18]	385	5×10^{-50}	36 - 422 (35%)
88	NR gi 229094939 ref ZP_04225942.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus Rock3-29] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus Rock1-3] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus Rock1-3] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus Rock3-29]	385	5×10^{-50}	36 - 422 (35%)
89	NR gi 228944039 ref ZP_04106423.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar monterrey BGSC 4AJ1] 4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar monterrey BGSC 4AJ1]	385	7×10^{-50}	36 - 422 (35%)
90	NR gi 260061495 ref YP_003194575.1 4-hydroxyphenylpyruvate dioxygenase [Robiginitalea biformata HTCC2501] 4-hydroxyphenylpyruvate dioxygenase [Robiginitalea biformata HTCC2501]	380	7×10^{-50}	32 - 427 (34%)
91	NR gi 229119897 ref ZP_04249156.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus 95/8201] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus 95/8201]	385	9×10^{-50}	36 - 422 (35%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
92	NR gi 86143740 ref ZP_01062116.1 4-hydroxyphenylpyruvate dioxygenase [Leeuwenhoekiella blandensis MED217] 4-hydroxyphenylpyruvate dioxygenase [Leeuwenhoekiella blandensis MED217]	386	9×10^{-50}	36 - 422 (34%)
93	NR gi 256424397 ref YP_003125050.1 4-hydroxyphenylpyruvate dioxygenase [Chitinophaga pinensis DSM 2588] 4-hydroxyphenylpyruvate dioxygenase [Chitinophaga pinensis DSM 2588]	378	1×10^{-49}	7 - 422 (34%)
94	NR gi 229009730 ref ZP_04166953.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus mycoides DSM 2048] 4-hydroxyphenylpyruvate dioxygenase [Bacillus mycoides DSM 2048]	385	1×10^{-49}	36 - 422 (35%)
95	NR gi 120437495 ref YP_863181.1 4-hydroxyphenylpyruvate dioxygenase [Gramella forsetii KT0803] 4-hydroxyphenylpyruvate dioxygenase [Gramella forsetii KT0803]	380	1×10^{-49}	30 - 422 (33%)
96	NR gi 239930984 ref ZP_04687937.1 4-hydroxyphenylpyruvate dioxygenase [Streptomyces ghanaensis ATCC 14672] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces ghanaensis ATCC 14672] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces ghanaensis ATCC 14672]	382	1×10^{-49}	34 - 422 (37%)
97	NR gi 270500552 ref ZP_06217482.1 4-hydroxyphenylpyruvate dioxygenase [Micromonospora aurantiaca ATCC 27029] 4-hydroxyphenylpyruvate dioxygenase [Micromonospora aurantiaca ATCC 27029]	401	2×10^{-49}	36 - 422 (37%)
98	NR gi 229015631 ref ZP_04172621.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus AH1273] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus AH1272] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus AH1272] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus AH1273]	385	2×10^{-49}	36 - 422 (35%)
99	NR gi 229055070 ref ZP_04195501.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus AH603] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus BDRD-ST196] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus BDRD-ST196] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus AH603]	385	2×10^{-49}	36 - 422 (35%)
100	NR gi 163938231 ref YP_001643115.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus weihenstephanensis KBAB4] 4-hydroxyphenylpyruvate dioxygenase [Bacillus weihenstephanensis KBAB4]	372	2×10^{-49}	36 - 422 (35%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
101	NR gi 288793867 ref ZP_06399586.1 4-hydroxyphenylpyruvate dioxygenase [Micromonospora sp. L5] 4-hydroxyphenylpyruvate dioxygenase [Micromonospora sp. L5]	401	3×10^{-49}	36 - 422 (37%)
102	NR gi 159899283 ref YP_001545530.1 4-hydroxyphenylpyruvate dioxygenase [Herpetosiphon aurantiacus ATCC 23779] 4-hydroxyphenylpyruvate dioxygenase [Herpetosiphon aurantiacus ATCC 23779]	373	3×10^{-49}	36 - 422 (33%)
103	NR gi 82187435 sp Q6TGZ5.1 HPPD_DANRE RecName: Full=4-hydroxyphenylpyruvate dioxygenase; AltName: Full=4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD 4-hydroxyphenylpyruvate dioxygenase [Danio rerio]	397	3×10^{-49}	34 - 422 (34%)
104	NR gi 229028077 ref ZP_04184228.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus AH1271] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus MM3] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus MM3] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus AH1271]	385	6×10^{-49}	36 - 422 (34%)
105	NR gi 169627992 ref YP_001701641.1 putative 4-hydroxyphenylpyruvate dioxygenase [Mycobacterium abscessus ATCC 19977] Putative 4-hydroxyphenylpyruvate dioxygenase [Mycobacterium abscessus]	401	6×10^{-49}	23 - 422 (36%)
106	NR gi 89098389 ref ZP_01171273.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus sp. NRRL B-14911] 4-hydroxyphenylpyruvate dioxygenase [Bacillus sp. NRRL B-14911]	371	6×10^{-49}	38 - 422 (34%)
107	NR gi 126645219 ref ZP_01717763.1 4-hydroxyphenylpyruvate dioxygenase [Algoriphagus sp. PR1] 4-hydroxyphenylpyruvate dioxygenase [Algoriphagus sp. PR1]	364	9×10^{-49}	36 - 422 (33%)
108	NR gi 269125316 ref YP_003298686.1 4-hydroxyphenylpyruvate dioxygenase [Thermomonospora curvata DSM 43183] 4-hydroxyphenylpyruvate dioxygenase [Thermomonospora curvata DSM 43183]	364	1×10^{-48}	35 - 422 (36%)
109	NR gi 226361126 ref YP_002778904.1 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus opacus B4] 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus opacus B4]	402	1×10^{-48}	9 - 422 (35%)
110	NR gi 145545087 ref XP_001458228.1 hypothetical protein [Paramecium tetraurelia strain d4-2] unnamed protein product [Paramecium tetraurelia]	390	1×10^{-48}	30 - 422 (35%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
111	NR gil124003065 ref ZP_01687916.1 4-hydroxyphenylpyruvate dioxygenase [Microscilla marina ATCC 23134] 4-hydroxyphenylpyruvate dioxygenase [Microscilla marina ATCC 23134]	365	1 x 10 ⁻⁴⁸	36 - 422 (33%)
112	NR gil146298492 ref YP_001193083.1 4-hydroxyphenylpyruvate dioxygenase [Flavobacterium johnsoniae UW101] 4-hydroxyphenylpyruvate dioxygenase [Flavobacterium johnsoniae UW101]	386	1 x 10 ⁻⁴⁸	36 - 422 (33%)
113	NR gil124088111 ref XP_001346967.1 4-hydroxyphenylpyruvate dioxygenase [Paramecium tetraurelia strain d4-2] hypothetical protein [Paramecium tetraurelia strain d4-2] 4-hydroxyphenylpyruvate dioxygenase, putative [Paramecium tetraurelia] unnamed protein product [Paramecium tetraurelia]	390	1 x 10 ⁻⁴⁸	30 - 422 (35%)
114	NR gil256815986 ref ZP_05541001.1 4-hydroxyphenylpyruvate dioxygenase [Streptomyces griseoflavus Tu4000]	382	2 x 10 ⁻⁴⁸	34 - 422 (36%)
115	NR gil160420207 ref NP_001104220.1 hypothetical protein LOC100126650 [Xenopus laevis] LOC100126650 protein [Xenopus laevis]	383	2 x 10 ⁻⁴⁸	33 - 422 (34%)
116	NR gil3334221 sp O42764.1 HPPD_MYCGR RecName: Full=4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD 4-hydroxyphenylpyruvate dioxygenase [Mycosphaerella graminicola]	419	2 x 10 ⁻⁴⁸	43 - 422 (33%)
117	NR gil111019033 ref YP_702005.1 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus jostii RHA1] 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus jostii RHA1]	402	3 x 10 ⁻⁴⁸	23 - 422 (36%)
118	NR gil41054723 ref NP_957461.1 4-hydroxyphenylpyruvate dioxygenase [Danio rerio] Zgc:56326 [Danio rerio]	387	3 x 10 ⁻⁴⁸	34 - 422 (34%)
119	NR gil226308548 ref YP_002768508.1 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus erythropolis PR4] probable 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus erythropolis PR4]	401	4 x 10 ⁻⁴⁸	23 - 422 (35%)
120	NR gil284041148 ref YP_003391078.1 4-hydroxyphenylpyruvate dioxygenase [Spirosoma linguale DSM 74] 4-hydroxyphenylpyruvate dioxygenase [Spirosoma linguale DSM 74]	377	6 x 10 ⁻⁴⁸	36 - 422 (34%)
121	NR gil148231342 ref NP_001088204.1 4-hydroxyphenylpyruvate dioxygenase [Xenopus laevis] LOC495029 protein [Xenopus laevis]	393	6 x 10 ⁻⁴⁸	41 - 422 (36%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
122	NR gi 226364545 ref YP_002782327.1 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus opacus B4] 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus opacus B4]	401	1×10^{-47}	28 - 422 (36%)
123	NR gi 169597549 ref XP_001792198.1 hypothetical protein SNOG_01560 [Phaeosphaeria nodorum SN15] hypothetical protein SNOG_01560 [Phaeosphaeria nodorum SN15]	406	1×10^{-47}	12 - 422 (33%)
124	NR gi 126324268 ref XP_001373762.1 PREDICTED: similar to 4-hydroxyphenylpyruvate dioxygenase [Monodelphis domestica]	395	1×10^{-47}	33 - 427 (35%)
125	NR gi 288921486 ref ZP_06415762.1 4-hydroxyphenylpyruvate dioxygenase [Frankia sp. EUN1f] 4-hydroxyphenylpyruvate dioxygenase [Frankia sp. EUN1f]	401	1×10^{-47}	28 - 422 (35%)
126	NR gi 111022041 ref YP_705013.1 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus jostii RHA1] 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus jostii RHA1]	401	1×10^{-47}	28 - 422 (36%)
127	NR gi 158315577 ref YP_001508085.1 4-hydroxyphenylpyruvate dioxygenase [Frankia sp. EAN1pec] 4-hydroxyphenylpyruvate dioxygenase [Frankia sp. EAN1pec]	401	1×10^{-47}	4 - 422 (35%)
128	NR gi 229489250 ref ZP_04383116.1 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus erythropolis SK121] 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus erythropolis SK121]	401	2×10^{-47}	23 - 422 (35%)
129	NR gi 182438405 ref YP_001826124.1 putative 4-hydroxyphenylpyruvate dioxygenase [Streptomyces griseus subsp. griseus NBRC 13350] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces sp. ACT-1] putative 4-hydroxyphenylpyruvate dioxygenase [Streptomyces griseus subsp. griseus NBRC 13350] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces sp. ACT-1]	381	2×10^{-47}	34 - 422 (35%)
130	NR gi 159040171 ref YP_001539424.1 4-hydroxyphenylpyruvate dioxygenase [Salinispora arenicola CNS-205] 4-hydroxyphenylpyruvate dioxygenase [Salinispora arenicola CNS-205]	401	2×10^{-47}	36 - 422 (36%)
131	NR gi 213512690 ref NP_001133898.1 4-hydroxyphenylpyruvate dioxygenase [Salmo salar] 4-hydroxyphenylpyruvate dioxygenase [Salmo salar]	386	2×10^{-47}	33 - 422 (33%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
132	NR gi 196256715 ref ZP_03155252.1 4-hydroxyphenylpyruvate dioxygenase [Cyanotheca sp. PCC 7822] 4-hydroxyphenylpyruvate dioxygenase [Cyanotheca sp. PCC 7822]	362	2×10^{-47}	36 - 422 (33%)
133	NR gi 111020030 ref YP_703002.1 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus jostii RHA1] 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus jostii RHA1]	401	2×10^{-47}	28 - 422 (36%)
134	NR gi 254389788 ref ZP_05005012.1 4-hydroxyphenylpyruvate dioxygenase [Streptomyces clavuligerus ATCC 27064] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces clavuligerus ATCC 27064]	381	3×10^{-47}	36 - 422 (36%)
135	NR gi 126662632 ref ZP_01733631.1 4-hydroxyphenylpyruvate dioxygenase [Flavobacterium bacterium BAL38] 4-hydroxyphenylpyruvate dioxygenase [Flavobacterium bacterium BAL38]	387	3×10^{-47}	36 - 422 (34%)
136	NR gi 71896159 ref NP_001025588.1 4-hydroxyphenylpyruvate dioxygenase [Xenopus (Silurana) tropicalis] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; AltName: Full=4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD hpd protein [Xenopus (Silurana) tropicalis]	394	3×10^{-47}	41 - 422 (33%)
137	NR gi 239981983 ref ZP_04704507.1 putative 4-hydroxyphenylpyruvate dioxygenase [Streptomyces albus J1074] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces albus J1074] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces albus J1074]	387	4×10^{-47}	13 - 422 (35%)
138	NR gi 258650779 ref YP_003199935.1 4-hydroxyphenylpyruvate dioxygenase [Nakamurella multipartita DSM 44233] 4-hydroxyphenylpyruvate dioxygenase [Nakamurella multipartita DSM 44233]	401	4×10^{-47}	9 - 422 (35%)
139	NR gi 54027055 ref YP_121297.1 putative 4-hydroxyphenylpyruvate dioxygenase [Nocardia farcinica IFM 10152] putative 4-hydroxyphenylpyruvate dioxygenase [Nocardia farcinica IFM 10152]	392	4×10^{-47}	36 - 422 (36%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
140	NR gi 21221374 ref NP_627153.1 4-hydroxyphenylpyruvate dioxygenase [Streptomyces coelicolor A3(2)] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces lividans TK24] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces lividans TK24] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD putative 4-hydroxyphenylpyruvate dioxygenase [Streptomyces coelicolor A3(2)] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces lividans TK24]	381	4×10^{-47}	34 - 422 (36%)
141	NR gi 254385771 ref ZP_05001092.1 4-hydroxyphenylpyruvate dioxygenase [Streptomyces sp. Mg1] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces sp. Mg1]	380	5×10^{-47}	35 - 422 (36%)
142	NR gi 260454691 ref ZP_05803088.1 4-hydroxyphenylpyruvate dioxygenase [Streptomyces flavogriseus ATCC 33331] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces flavogriseus ATCC 33331]	381	7×10^{-47}	34 - 422 (35%)
143	NR gi 256824904 ref YP_003148864.1 4-hydroxyphenylpyruvate dioxygenase [Kytococcus sedentarius DSM 20547] 4-hydroxyphenylpyruvate dioxygenase [Kytococcus sedentarius DSM 20547]	407	7×10^{-47}	28 - 422 (34%)
144	NR gi 291297820 ref YP_003509098.1 4-hydroxyphenylpyruvate dioxygenase [Stackebrandtia nassauensis DSM 44728] 4-hydroxyphenylpyruvate dioxygenase [Stackebrandtia nassauensis DSM 44728]	392	7×10^{-47}	35 - 422 (34%)
145	NR gi 290960022 ref YP_003491204.1 putative 4-hydroxyphenylpyruvate dioxygenase [Streptomyces scabiei 87.22] putative 4-hydroxyphenylpyruvate dioxygenase [Streptomyces scabiei 87.22]	384	9×10^{-47}	15 - 422 (35%)
146	NR gi 238061408 ref ZP_04606117.1 4-hydroxyphenylpyruvate dioxygenase [Micromonospora sp. ATCC 39149] 4-hydroxyphenylpyruvate dioxygenase [Micromonospora sp. ATCC 39149]	401	9×10^{-47}	36 - 422 (35%)
147	NR gi 281343778 gb EFB19362.1 hypothetical protein PANDA_000905 [Ailuropoda melanoleuca]	384	1×10^{-46}	33 - 423 (34%)
148	NR gi 256374854 ref YP_003098514.1 4-hydroxyphenylpyruvate dioxygenase [Actinosynnema mirum DSM 43827] 4-hydroxyphenylpyruvate dioxygenase [Actinosynnema mirum DSM 43827]	393	2×10^{-46}	36 - 422 (36%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
149	NR gi 149275943 ref ZP_01882088.1 4-hydroxyphenylpyruvate dioxygenase [Pedobacter sp. BAL39] 4-hydroxyphenylpyruvate dioxygenase [Pedobacter sp. BAL39]	403	2×10^{-46}	30 - 422 (33%)
150	NR gi 229366896 gb ACQ58428.1 4-hydroxyphenylpyruvate dioxygenase [Anoplopoma fimbria]	395	2×10^{-46}	43 - 422 (33%)
151	NR gi 226362180 ref YP_002779958.1 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus opacus B4] 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus opacus B4]	401	2×10^{-46}	28 - 422 (35%)
152	NR gi 195442575 ref XP_002069028.1 GK12342 [Drosophila willistoni] GK12342 [Drosophila willistoni]	380	2×10^{-46}	33 - 422 (34%)
153	NR gi 149370106 ref ZP_01889957.1 4-hydroxyphenylpyruvate dioxygenase [unidentified eubacterium SCB49] 4-hydroxyphenylpyruvate dioxygenase [unidentified eubacterium SCB49]	387	2×10^{-46}	36 - 422 (33%)
154	NR gi 124006550 ref ZP_01691383.1 4-hydroxyphenylpyruvate dioxygenase [Microscilla marina ATCC 23134] 4-hydroxyphenylpyruvate dioxygenase [Microscilla marina ATCC 23134]	375	2×10^{-46}	39 - 422 (33%)
155	NR gi 86134911 ref ZP_01053493.1 4-hydroxyphenylpyruvate dioxygenase [Polaribacter sp. MED152] 4-hydroxyphenylpyruvate dioxygenase [Polaribacter sp. MED152]	386	2×10^{-46}	36 - 422 (33%)
156	NR gi 290972745 ref XP_002669111.1 predicted protein [Naegleria gruberi] predicted protein [Naegleria gruberi]	393	3×10^{-46}	41 - 426 (34%)
157	NR gi 254401014 ref ZP_05015971.1 4-hydroxyphenylpyruvate dioxygenase [Streptomyces svaceus ATCC 29083] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces svaceus ATCC 29083]	381	3×10^{-46}	34 - 422 (35%)
158	NR gi 229003228 ref ZP_04161067.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus mycoides Rock1-4] 4-hydroxyphenylpyruvate dioxygenase [Bacillus mycoides Rock1-4]	303	4×10^{-46}	125 - 422 (39%)
159	NR gi 111020159 ref YP_703131.1 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus jostii RHA1] 4-hydroxyphenylpyruvate dioxygenase [Rhodococcus jostii RHA1]	404	4×10^{-46}	28 - 422 (33%)
160	NR gi 239882267 gb EER07716.1 4-hydroxyphenylpyruvate dioxygenase, putative [Perkinsus marinus ATCC 50983]	441	6×10^{-46}	22 - 426 (33%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
161	NR gi 88801956 ref ZP_01117484.1 4-hydroxyphenylpyruvate dioxygenase [Polaribacter irgensii 23-P] 4-hydroxyphenylpyruvate dioxygenase [Polaribacter irgensii 23-P]	387	6×10^{-46}	36 - 422 (32%)
162	NR gi 282865147 ref ZP_06274200.1 4-hydroxyphenylpyruvate dioxygenase [Streptomyces sp. ACTE] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces sp. ACTE]	381	8×10^{-46}	34 - 422 (35%)
163	NR gi 227538614 ref ZP_03968663.1 4-hydroxyphenylpyruvate dioxygenase [Sphingobacterium spiritivorum ATCC 33300] 4-hydroxyphenylpyruvate dioxygenase [Sphingobacterium spiritivorum ATCC 33300]	375	8×10^{-46}	36 - 422 (33%)
164	NR gi 163787194 ref ZP_02181641.1 4-hydroxyphenylpyruvate dioxygenase [Flavobacteriales bacterium ALC-1] 4-hydroxyphenylpyruvate dioxygenase [Flavobacteriales bacterium ALC-1]	386	8×10^{-46}	36 - 422 (33%)
165	NR gi 156553875 ref XP_001600932.1 PREDICTED: similar to 4-hydroxyphenylpyruvate dioxygenase [Nasonia vitripennis]	412	8×10^{-46}	41 - 422 (34%)
166	NR gi 148223387 ref NP_001091344.1 hypothetical protein LOC100037181 [Xenopus laevis] LOC100037181 protein [Xenopus laevis]	383	8×10^{-46}	33 - 422 (33%)
167	NR gi 89891109 ref ZP_01202617.1 4-hydroxyphenylpyruvate dioxygenase [Flavobacteria bacterium BBFL7] 4-hydroxyphenylpyruvate dioxygenase [Flavobacteria bacterium BBFL7]	387	8×10^{-46}	36 - 422 (33%)
168	NR gi 84494414 ref ZP_00993533.1 putative 4-hydroxyphenylpyruvate dioxygenase [Janibacter sp. HTCC2649] putative 4-hydroxyphenylpyruvate dioxygenase [Janibacter sp. HTCC2649]	420	8×10^{-46}	3 - 422 (32%)
169	NR gi 118404104 ref NP_001072376.1 4-hydroxyphenylpyruvate dioxygenase [Xenopus (Silurana) tropicalis] 4-hydroxyphenylpyruvate dioxygenase [Xenopus (Silurana) tropicalis]	393	1×10^{-45}	41 - 422 (36%)
170	NR gi 73995174 ref XP_853422.1 PREDICTED: similar to 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Canis familiaris]	393	1×10^{-45}	33 - 423 (34%)
171	NR gi 86130810 ref ZP_01049409.1 4-hydroxyphenylpyruvate dioxygenase [Dokdonia donghaensis MED134] 4-hydroxyphenylpyruvate dioxygenase [Dokdonia donghaensis MED134]	386	1×10^{-45}	36 - 422 (33%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
172	NR gi 227369863 ref ZP_03853367.1 4-hydroxyphenylpyruvate dioxygenase [Chryseobacterium gleum ATCC 35910] 4-hydroxyphenylpyruvate dioxygenase [Chryseobacterium gleum ATCC 35910]	376	1×10^{-45}	39 - 422 (32%)
173	NR gi 256802189 ref ZP_05531813.1 4-hydroxyphenylpyruvate dioxygenase [Streptomyces viridochromogenes DSM 40736]	381	2×10^{-45}	34 - 422 (35%)
174	NR gi 289742529 gb ADD20012.1 4-hydroxyphenylpyruvate dioxygenase [Glossina morsitans morsitans]	380	2×10^{-45}	33 - 422 (33%)
175	NR gi 198463883 ref XP_001352980.2 GA11203 [Drosophila pseudoobscura pseudoobscura] GA11203 [Drosophila pseudoobscura pseudoobscura]	381	2×10^{-45}	33 - 422 (34%)
176	NR gi 195378695 ref XP_002048117.1 GJ13785 [Drosophila virilis] GJ13785 [Drosophila virilis]	380	3×10^{-45}	33 - 422 (34%)
177	NR gi 255533165 ref YP_003093537.1 4-hydroxyphenylpyruvate dioxygenase [Pedobacter heparinus DSM 2366] 4-hydroxyphenylpyruvate dioxygenase [Pedobacter heparinus DSM 2366]	376	4×10^{-45}	36 - 422 (33%)
178	NR gi 256390686 ref YP_003112250.1 4-hydroxyphenylpyruvate dioxygenase [Catenulispora acidiphila DSM 44928] 4-hydroxyphenylpyruvate dioxygenase [Catenulispora acidiphila DSM 44928]	379	5×10^{-45}	7 - 422 (34%)
179	NR gi 195021255 ref XP_001985359.1 GH17018 [Drosophila grimshawi] GH17018 [Drosophila grimshawi]	387	5×10^{-45}	33 - 422 (34%)
180	NR gi 163754368 ref ZP_02161490.1 4-hydroxyphenylpyruvate dioxygenase [Kordia algicida OT-1] 4-hydroxyphenylpyruvate dioxygenase [Kordia algicida OT-1]	387	5×10^{-45}	36 - 422 (32%)
181	NR gi 115644360 ref XP_798672.2 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus] PREDICTED: hypothetical protein [Strongylocentrotus purpuratus]	558	5×10^{-45}	33 - 422 (32%)
182	NR gi 83855941 ref ZP_00949470.1 4-hydroxyphenylpyruvate dioxygenase [Croceibacter atlanticus HTCC2559] 4-hydroxyphenylpyruvate dioxygenase [Croceibacter atlanticus HTCC2559]	390	5×10^{-45}	36 - 422 (33%)
183	NR gi 194749703 ref XP_001957278.1 GF24132 [Drosophila ananassae] GF24132 [Drosophila ananassae]	402	6×10^{-45}	33 - 422 (34%)
184	NR gi 51230599 ref NP_001003742.1 4-hydroxyphenylpyruvate dioxygenase [Danio rerio] 4-hydroxyphenylpyruvate dioxygenase [Danio rerio] Hpd protein [Danio rerio]	393	6×10^{-45}	41 - 422 (34%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
185	NR gi 29831692 ref NP_826326.1 4-hydroxyphenylpyruvate dioxygenase [Streptomyces avermitilis MA-4680] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD Chain A, Structure Of Fe2-Hppd Bound To Ntbc Chain B, Structure Of Fe2-Hppd Bound To Ntbc 4-hydroxyphenylpyruvate dioxygenase [Streptomyces avermitilis] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces avermitilis MA-4680]	381	6×10^{-45}	34 - 422 (35%)
186	NR gi 289620409 emb CBI53267.1 unnamed protein product [Sordaria macrospora]	413	8×10^{-45}	43 - 422 (34%)
187	NR gi 195480027 ref XP_002086629.1 GE22742 [Drosophila yakuba] GE22742 [Drosophila yakuba]	380	8×10^{-45}	33 - 422 (34%)
188	NR gi 281202907 gb EFA77109.1 4-hydroxyphenylpyruvate dioxygenase [Polysphondylium pallidum PN500]	925	1×10^{-44}	43 - 422 (32%)
189	NR gi 118389434 ref XP_001027802.1 4-hydroxyphenylpyruvate dioxygenase family protein [Tetrahymena thermophila] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; AltName: Full=4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD; AltName: Full=F-antigen homolog; AltName: Full=TF-AG F-antigen [Tetrahymena thermophila] 4-hydroxyphenylpyruvate dioxygenase family protein [Tetrahymena thermophila SB210]	404	1×10^{-44}	41 - 422 (32%)
190	NR gi 88711872 ref ZP_01105960.1 4-hydroxyphenylpyruvate dioxygenase [Flavobacteriales bacterium HTCC2170] 4-hydroxyphenylpyruvate dioxygenase [Flavobacteriales bacterium HTCC2170]	380	1×10^{-44}	32 - 427 (32%)
191	NR gi 24667510 ref NP_730536.1 CG11796, isoform A [Drosophila melanogaster] CG11796, isoform A [Drosophila melanogaster] GH11957p [Drosophila melanogaster] CG11796-PA [synthetic construct] CG11796-PA [synthetic construct]	380	1×10^{-44}	33 - 422 (34%)
192	NR gi 241890972 ref ZP_04778268.1 4-hydroxyphenylpyruvate dioxygenase [Sphingobacterium spiritivorum ATCC 33861] 4-hydroxyphenylpyruvate dioxygenase [Sphingobacterium spiritivorum ATCC 33861]	375	2×10^{-44}	36 - 422 (33%)
193	NR gi 257057151 ref YP_003134983.1 4-hydroxyphenylpyruvate dioxygenase [Saccharomonospora viridis DSM 43017] 4-hydroxyphenylpyruvate dioxygenase [Saccharomonospora viridis DSM 43017]	394	2×10^{-44}	23 - 422 (34%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
194	NR gi 260784978 ref XP_002587540.1 hypothetical protein BRAFLDRAFT_282735 [Branchiostoma floridae] hypothetical protein BRAFLDRAFT_282735 [Branchiostoma floridae]	382	2×10^{-44}	33 - 422 (33%)
195	NR gi 195591863 ref XP_002085658.1 GD12185 [Drosophila simulans] GD12185 [Drosophila simulans]	380	2×10^{-44}	33 - 422 (34%)
196	NR gi 202924 gb AAA40740.1 F alloantigen [Rattus norvegicus]	376	2×10^{-44}	33 - 423 (33%)
197	NR gi 62751490 ref NP_001015611.1 4-hydroxyphenylpyruvate dioxygenase [Bos taurus] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; AltName: Full=4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD 4-hydroxyphenylpyruvate dioxygenase [Bos taurus] 4-hydroxyphenylpyruvate dioxygenase [Bos taurus]	393	2×10^{-44}	33 - 423 (34%)
198	NR gi 8393557 ref NP_058929.1 4-hydroxyphenylpyruvate dioxygenase [Rattus norvegicus] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; AltName: Full=4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD; AltName: Full=F Alloantigen; Short=F protein Chain A, Structural Basis For Inhibitor Selectivity Revealed By Crystal Structures Of Plant And Mammalian 4-Hydroxyphenylpyruvate Dioxygenases Chain B, Structural Basis For Inhibitor Selectivity Revealed By Crystal Structures Of Plant And Mammalian 4-Hydroxyphenylpyruvate Dioxygenases 4-hydroxyphenylpyruvate dioxygenase [Rattus norvegicus] 4-hydroxyphenylpyruvate dioxygenase [Rattus norvegicus]	393	2×10^{-44}	33 - 423 (33%)
199	NR gi 291413050 ref XP_002722789.1 PREDICTED: 4-hydroxyphenylpyruvate dioxygenase [Oryctolagus cuniculus]	395	2×10^{-44}	33 - 423 (34%)
200	NR gi 271969733 ref YP_003343929.1 4-hydroxyphenylpyruvate dioxygenase [Streptosporangium roseum DSM 43021] 4-hydroxyphenylpyruvate dioxygenase [Streptosporangium roseum DSM 43021]	381	2×10^{-44}	35 - 422 (34%)
201	NR gi 221116511 ref XP_002159059.1 PREDICTED: similar to 4-hydroxyphenylpyruvate dioxygenase [Hydra magnipapillata]	386	2×10^{-44}	41 - 422 (32%)
202	NR gi 194874924 ref XP_001973493.1 GG13309 [Drosophila erecta] GG13309 [Drosophila erecta]	380	2×10^{-44}	33 - 422 (34%)
203	NR gi 195348265 ref XP_002040671.1 GM22213 [Drosophila sechellia] GM22213 [Drosophila sechellia]	380	3×10^{-44}	33 - 422 (34%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
204	NR gi 149720751 ref XP_001492351.1 PREDICTED: similar to 4-hydroxyphenylpyruvate dioxygenase [Equus caballus]	406	3×10^{-44}	24 - 423 (33%)
205	NR gi 145596759 ref YP_001161056.1 4-hydroxyphenylpyruvate dioxygenase [Salinispora tropica CNB-440] 4-hydroxyphenylpyruvate dioxygenase [Salinispora tropica CNB-440]	401	5×10^{-44}	36 - 422 (35%)
206	NR gi 555806 gb AAA50231.1 4-hydroxyphenylpyruvate acid dioxygenase [Streptomyces avermitilis]	380	5×10^{-44}	34 - 422 (35%)
207	NR gi 85080847 ref XP_956614.1 4-hydroxyphenylpyruvate dioxygenase [Neurospora crassa OR74A] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD probable 4-hydroxyphenylpyruvate dioxygenase [Neurospora crassa] 4-hydroxyphenylpyruvate dioxygenase [Neurospora crassa OR74A]	412	5×10^{-44}	43 - 422 (33%)
208	NR gi 154274526 ref XP_001538114.1 4-hydroxyphenylpyruvate dioxygenase [Ajellomyces capsulatus NAM1] 4-hydroxyphenylpyruvate dioxygenase [Ajellomyces capsulatus NAM1]	402	7×10^{-44}	21 - 422 (32%)
209	NR gi 289641866 ref ZP_06474022.1 4-hydroxyphenylpyruvate dioxygenase [Frankia symbiont of Datisca glomerata] 4-hydroxyphenylpyruvate dioxygenase [Frankia symbiont of Datisca glomerata]	416	1×10^{-43}	7 - 422 (33%)
210	NR gi 255534597 ref YP_003094968.1 4-hydroxyphenylpyruvate dioxygenase [Flavobacteriaceae bacterium 3519-10] 4-hydroxyphenylpyruvate dioxygenase [Flavobacteriaceae bacterium 3519-10]	313	1×10^{-43}	129 - 422 (36%)
211	NR gi 150024336 ref YP_001295162.1 4-hydroxyphenylpyruvate dioxygenase [Flavobacterium psychrophilum JIP02/86] 4-hydroxyphenylpyruvate dioxygenase [Flavobacterium psychrophilum JIP02/86]	386	1×10^{-43}	36 - 422 (32%)
212	NR gi 134097503 ref YP_001103164.1 4-hydroxyphenylpyruvate dioxygenase [Saccharopolyspora erythraea NRRL 2338] 4-hydroxyphenylpyruvate dioxygenase [Saccharopolyspora erythraea NRRL 2338] 4-hydroxyphenylpyruvate dioxygenase [Saccharopolyspora erythraea NRRL 2338]	401	2×10^{-43}	36 - 422 (35%)
213	NR gi 114647465 ref XP_528667.2 PREDICTED: 4-hydroxyphenylpyruvate dioxygenase isoform 3 [Pan troglodytes]	393	2×10^{-43}	33 - 423 (33%)
214	NR gi 258588704 pdb 3ISQ A Chain A, Crystal Structure Of Human 4-Hydroxyphenylpyruvate Dioxygenase	393	2×10^{-43}	33 - 423 (33%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
215	NR gi 74418655 gb ABA03141.1 liver F protein [Homo sapiens]	377	2×10^{-43}	33 - 423 (33%)
216	NR gi 189196054 ref XP_001934365.1 4-hydroxyphenylpyruvate dioxygenase [Pyrenophora tritici-repentis Pt-1C-BFP] 4-hydroxyphenylpyruvate dioxygenase [Pyrenophora tritici-repentis Pt-1C-BFP]	405	2×10^{-43}	43 - 422 (32%)
217	NR gi 109099057 ref XP_001096175.1 PREDICTED: 4-hydroxyphenylpyruvate dioxygenase isoform 2 [Macaca mulatta]	393	2×10^{-43}	33 - 423 (33%)
218	NR gi 4504477 ref NP_002141.1 4-hydroxyphenylpyruvate dioxygenase isoform 1 [Homo sapiens] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; AltName: Full=4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD 4-hydroxyphenylpyruvate dioxygenase [Homo sapiens] 4-hydroxyphenylpyruvic acid dioxygenase [Homo sapiens] 4-hydroxyphenylpyruvate dioxygenase [Homo sapiens] 4-hydroxyphenylpyruvate dioxygenase, isoform CRA_b [Homo sapiens] 4-hydroxyphenylpyruvate dioxygenase [synthetic construct] 4-hydroxyphenylpyruvate dioxygenase [synthetic construct] unnamed protein product [Homo sapiens]	393	2×10^{-43}	33 - 423 (33%)
219	NR gi 284029753 ref YP_003379684.1 4-hydroxyphenylpyruvate dioxygenase [Kribbella flavida DSM 17836] 4-hydroxyphenylpyruvate dioxygenase [Kribbella flavida DSM 17836]	400	3×10^{-43}	28 - 422 (34%)
220	NR gi 242007588 ref XP_002424619.1 4-hydroxyphenylpyruvate dioxygenase, putative [Pediculus humanus corporis] 4-hydroxyphenylpyruvate dioxygenase, putative [Pediculus humanus corporis]	406	3×10^{-43}	18 - 420 (33%)
221	NR gi 159898412 ref YP_001544659.1 4-hydroxyphenylpyruvate dioxygenase [Herpetosiphon aurantiacus ATCC 23779] 4-hydroxyphenylpyruvate dioxygenase [Herpetosiphon aurantiacus ATCC 23779]	366	3×10^{-43}	43 - 422 (32%)
222	NR gi 3860238 gb AAC73008.1 4-hydroxyphenylpyruvate-dioxygenase [Homo sapiens]	393	3×10^{-43}	33 - 423 (33%)
223	NR gi 240277944 gb EER41451.1 T-cell reactive protein [Ajellomyces capsulatus H143]	402	3×10^{-43}	21 - 422 (31%)
224	NR gi 225561209 gb EEH09490.1 T-cell reactive protein [Ajellomyces capsulatus G186AR]	402	3×10^{-43}	21 - 422 (31%)
225	NR gi 1841443 emb CAA42111.1 F1 protein [Mus musculus]	379	3×10^{-43}	33 - 423 (33%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
226	NR gi 33859486 ref NP_032303.1 4-hydroxyphenylpyruvic acid dioxygenase [Mus musculus] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; AltName: Full=4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD; AltName: Full=F Alloantigen; Short=F protein 4-hydroxyphenylpyruvic acid dioxygenase [Mus musculus] 4-hydroxyphenylpyruvic acid dioxygenase [Mus musculus]	393	5×10^{-43}	33 - 423 (33%)
227	NR gi 158297828 ref XP_318007.3 AGAP004802-PA [Anopheles gambiae str. PEST] AGAP004802-PA [Anopheles gambiae str. PEST]	381	6×10^{-43}	33 - 422 (32%)
228	NR gi 157126195 ref XP_001660843.1 4-hydroxyphenylpyruvate dioxygenase [Aedes aegypti] 4-hydroxyphenylpyruvate dioxygenase [Aedes aegypti]	378	6×10^{-43}	33 - 422 (32%)
229	NR gi 849053 dbj BAA06267.1 4-hydroxyphenylpyruvate dioxygenase [Mus musculus]	393	6×10^{-43}	33 - 423 (33%)
230	NR gi 195127619 ref XP_002008266.1 G111911 [Drosophila mojavensis] G111911 [Drosophila mojavensis]	402	8×10^{-43}	33 - 422 (33%)
231	NR gi 110755389 ref XP_001121254.1 PREDICTED: similar to CG11796-PA, isoform A [Apis mellifera]	388	8×10^{-43}	41 - 422 (32%)
232	NR gi 50547455 ref XP_501197.1 YALI0B21846p [Yarrowia lipolytica] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD YALI0B21846p [Yarrowia lipolytica]	394	8×10^{-43}	16 - 422 (33%)
233	NR gi 39977613 ref XP_370194.1 hypothetical protein MGG_06691 [Magnaporthe grisea 70-15] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD 4-hydroxyphenylpyruvate dioxygenase [Magnaporthe grisea] hypothetical protein MGG_06691 [Magnaporthe grisea 70-15]	419	8×10^{-43}	12 - 422 (32%)
234	NR gi 258575077 ref XP_002541720.1 4-hydroxyphenylpyruvate dioxygenase [Uncinocarpus reesii 1704] 4-hydroxyphenylpyruvate dioxygenase [Uncinocarpus reesii 1704]	397	1×10^{-42}	31 - 422 (31%)
235	NR gi 116199507 ref XP_001225565.1 hypothetical protein CHGG_07909 [Chaetomium globosum CBS 148.51] hypothetical protein CHGG_07909 [Chaetomium globosum CBS 148.51]	413	1×10^{-42}	43 - 422 (32%)
236	NR gi 195172126 ref XP_002026852.1 GL12777 [Drosophila persimilis] GL12777 [Drosophila persimilis]	350	2×10^{-42}	56 - 422 (34%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
237	NR gi 224071202 ref XP_002190392.1 PREDICTED: hypothetical protein [Taeniopygia guttata]	396	2×10^{-42}	33 - 422 (33%)
238	NR gi 157105932 ref XP_001649088.1 4-hydroxyphenylpyruvate dioxygenase [Aedes aegypti] 4-hydroxyphenylpyruvate dioxygenase [Aedes aegypti]	381	2×10^{-42}	33 - 422 (32%)
239	NR gi 196014870 ref XP_002117293.1 expressed hypothetical protein [Trichoplax adhaerens] expressed hypothetical protein [Trichoplax adhaerens]	403	4×10^{-42}	41 - 422 (33%)
240	NR gi 171689424 ref XP_001909652.1 unnamed protein product [Podospira anserina] unnamed protein product [Podospira anserina]	418	4×10^{-42}	43 - 422 (31%)
241	NR gi 170036301 ref XP_001846003.1 4-hydroxyphenylpyruvate dioxygenase [Culex quinquefasciatus] 4-hydroxyphenylpyruvate dioxygenase [Culex quinquefasciatus]	388	4×10^{-42}	33 - 426 (32%)
242	NR gi 167522589 ref XP_001745632.1 hypothetical protein [Monosiga brevicollis MX1] predicted protein [Monosiga brevicollis MX1]	385	4×10^{-42}	41 - 422 (31%)
243	NR gi 118098511 ref XP_415144.2 PREDICTED: similar to LOC495029 protein [Gallus gallus]	393	4×10^{-42}	41 - 422 (33%)
244	NR gi 74143620 dbj BAE28861.1 unnamed protein product [Mus musculus]	393	4×10^{-42}	33 - 423 (33%)
245	NR gi 238487766 ref XP_002375121.1 4-hydroxyphenylpyruvate dioxygenase, putative [Aspergillus flavus NRRL3357] 4-hydroxyphenylpyruvate dioxygenase, putative [Aspergillus flavus NRRL3357]	398	5×10^{-42}	33 - 422 (32%)
246	NR gi 242763023 ref XP_002340495.1 4-hydroxyphenylpyruvate dioxygenase, putative [Talaromyces stipitatus ATCC 10500] 4-hydroxyphenylpyruvate dioxygenase, putative [Talaromyces stipitatus ATCC 10500]	415	5×10^{-42}	43 - 422 (31%)
247	NR gi 256732546 gb EEU45894.1 predicted protein [Nectria haematococca mpVI 77-13-4]	423	9×10^{-42}	43 - 422 (32%)
248	NR gi 169769905 ref XP_001819422.1 hypothetical protein [Aspergillus oryzae RIB40] unnamed protein product [Aspergillus oryzae]	398	9×10^{-42}	33 - 422 (32%)
249	NR gi 226282873 gb EEH38439.1 4-hydroxyphenylpyruvate dioxygenase [Paracoccidioides brasiliensis Pb01]	403	1×10^{-41}	12 - 422 (30%)
250	NR gi 226288135 gb EEH43648.1 4-hydroxyphenylpyruvate dioxygenase [Paracoccidioides brasiliensis Pb18]	404	1×10^{-41}	43 - 422 (31%)
251	NR gi 238837974 gb EEQ27636.1 4-hydroxyphenylpyruvate dioxygenase [Microsporium canis CBS 113480]	400	2×10^{-41}	43 - 422 (32%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
252	NR gi 256672096 ref ZP_05483049.1 4-hydroxyphenylpyruvate dioxygenase [Streptomyces sp. AA4]	395	3×10^{-41}	35 - 422 (34%)
253	NR gi 115399020 ref XP_001215099.1 4-hydroxyphenylpyruvate dioxygenase [Aspergillus terreus NIH2624] 4-hydroxyphenylpyruvate dioxygenase [Aspergillus terreus NIH2624]	403	3×10^{-41}	43 - 422 (32%)
254	NR gi 46123247 ref XP_386177.1 hypothetical protein FG06001.1 [Gibberella zeae PH-1]	424	3×10^{-41}	43 - 422 (31%)
255	NR gi 291232232 ref XP_002736061.1 PREDICTED: 4-hydroxyphenylpyruvate dioxygenase-like [Saccoglossus kowalevskii]	395	7×10^{-41}	33 - 422 (31%)
256	NR gi 154317978 ref XP_001558308.1 hypothetical protein BC1G_02972 [Botryotinia fuckeliana B05.10] hypothetical protein BC1G_02972 [Botryotinia fuckeliana B05.10]	422	7×10^{-41}	12 - 422 (32%)
257	NR gi 239615652 gb EEQ92639.1 4-hydroxyphenylpyruvate dioxygenase [Ajellomyces dermatitidis ER-3]	402	1×10^{-40}	21 - 422 (31%)
258	NR gi 91090908 ref XP_973835.1 PREDICTED: similar to 4-hydroxyphenylpyruvate dioxygenase [Tribolium castaneum] hypothetical protein TcasGA2 TC012702 [Tribolium castaneum]	380	1×10^{-40}	33 - 422 (32%)
259	NR gi 145243382 ref XP_001394222.1 hypothetical protein An11g02200 [Aspergillus niger] unnamed protein product [Aspergillus niger]	403	2×10^{-40}	35 - 422 (31%)
260	NR gi 119715531 ref YP_922496.1 4-hydroxyphenylpyruvate dioxygenase [Nocardioides sp. JS614] 4-hydroxyphenylpyruvate dioxygenase [Nocardioides sp. JS614]	397	2×10^{-40}	28 - 422 (33%)
261	NR gi 3334224 sp Q00415.1 HPPD_COCP7 RecName: Full=4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD; AltName: Full=T-cell reactive protein T-cell reactive protein [Coccidioides posadasii] 4-hydroxyphenylpyruvate dioxygenase/T-cell reactive protein [Coccidioides posadasii C735 delta SOWgp]	399	2×10^{-40}	35 - 422 (31%)
262	NR gi 119480047 ref XP_001260052.1 4-hydroxyphenylpyruvate dioxygenase, putative [Neosartorya fischeri NRRL 181] 4-hydroxyphenylpyruvate dioxygenase, putative [Neosartorya fischeri NRRL 181]	403	2×10^{-40}	43 - 422 (32%)
263	NR gi 119193871 ref XP_001247539.1 4-hydroxyphenylpyruvate dioxygenase [Coccidioides immitis RS] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD; AltName: Full=T-cell reactive protein	399	2×10^{-40}	35 - 422 (31%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
264	NR gi 156050089 ref XP_001591006.1 4-hydroxyphenylpyruvate dioxygenase [Sclerotinia sclerotiorum 1980] 4-hydroxyphenylpyruvate dioxygenase [Sclerotinia sclerotiorum 1980]	422	4×10^{-40}	43 - 422 (32%)
265	NR gi 121710300 ref XP_001272766.1 4-hydroxyphenylpyruvate dioxygenase, putative [Aspergillus clavatus NRRL 1] 4-hydroxyphenylpyruvate dioxygenase, putative [Aspergillus clavatus NRRL 1]	401	5×10^{-40}	43 - 422 (32%)
266	NR gi 147902599 ref NP_001083378.1 hypothetical protein LOC398893 [Xenopus laevis] MGC68535 protein [Xenopus laevis]	313	5×10^{-40}	129 - 422 (35%)
267	NR gi 47523532 ref NP_999389.1 4-hydroxyphenylpyruvate dioxygenase [Sus scrofa] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; AltName: Full=4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD 4-hydroxyphenylpyruvic acid dioxygenase [Sus scrofa]	393	5×10^{-40}	33 - 426 (32%)
268	NR gi 226290002 gb EEH45486.1 4-hydroxyphenylpyruvate dioxygenase [Paracoccidioides brasiliensis Pb18]	427	8×10^{-40}	43 - 422 (31%)
269	NR gi 198424770 ref XP_002128262.1 PREDICTED: similar to 4-hydroxyphenylpyruvate dioxygenase [Ciona intestinalis]	381	8×10^{-40}	43 - 422 (32%)
270	NR gi 241250750 ref XP_002403366.1 4-hydroxyphenylpyruvate dioxygenase, putative [Ixodes scapularis] 4-hydroxyphenylpyruvate dioxygenase, putative [Ixodes scapularis]	381	1×10^{-39}	33 - 422 (31%)
271	NR gi 212529478 ref XP_002144896.1 4-hydroxyphenylpyruvate dioxygenase, putative [Penicillium marneffei ATCC 18224] 4-hydroxyphenylpyruvate dioxygenase, putative [Penicillium marneffei ATCC 18224]	415	1×10^{-39}	43 - 422 (31%)
272	NR gi 111226747 ref XP_001134587.1 4-hydroxyphenylpyruvate dioxygenase [Dictyostelium discoideum AX4] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; AltName: Full=4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD 4-hydroxyphenylpyruvate dioxygenase [Dictyostelium discoideum AX4]	367	1×10^{-39}	43 - 427 (30%)
273	NR gi 66817524 ref XP_642615.1 4-hydroxyphenylpyruvate dioxygenase [Dictyostelium discoideum AX4] 4-hydroxyphenylpyruvate dioxygenase [Dictyostelium discoideum AX4]	369	1×10^{-39}	43 - 427 (30%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
274	NR gi 114647467 ref XP_001166423.1 PREDICTED: 4-hydroxyphenylpyruvate dioxygenase isoform 1 [Pan troglodytes] PREDICTED: 4-hydroxyphenylpyruvate dioxygenase isoform 2 [Pan troglodytes]	354	2×10^{-39}	67 - 423 (34%)
275	NR gi 285002264 ref NP_001165464.1 4-hydroxyphenylpyruvate dioxygenase isoform 2 [Homo sapiens] unnamed protein product [Homo sapiens]	354	2×10^{-39}	67 - 423 (34%)
276	NR gi 149063328 gb EDM13651.1 4-hydroxyphenylpyruvic acid dioxygenase [Rattus norvegicus]	354	2×10^{-39}	67 - 423 (34%)
277	NR gi 109099059 ref XP_001096061.1 PREDICTED: 4-hydroxyphenylpyruvate dioxygenase isoform 1 [Macaca mulatta]	354	2×10^{-39}	67 - 423 (34%)
278	NR gi 70989405 ref XP_749552.1 4-hydroxyphenylpyruvate dioxygenase [Aspergillus fumigatus Af293] RecName: Full=Probable 4-hydroxyphenylpyruvate dioxygenase 1; Short=HPPDase 1; Short=4HPPD 1; Short=HPD 1 4-hydroxyphenylpyruvate dioxygenase, putative [Aspergillus fumigatus Af293] 4-hydroxyphenylpyruvate dioxygenase, putative [Aspergillus fumigatus A1163]	403	2×10^{-39}	43 - 422 (31%)
279	NR gi 226285073 gb EEH40639.1 4-hydroxyphenylpyruvate dioxygenase [Paracoccidioides brasiliensis Pb01]	427	3×10^{-39}	43 - 422 (31%)
280	NR gi 70993834 ref XP_751764.1 4-hydroxyphenylpyruvate dioxygenase [Aspergillus fumigatus Af293] RecName: Full=Probable 4-hydroxyphenylpyruvate dioxygenase 2; Short=HPPDase 2; Short=4HPPD 2; Short=HPD 2 4-hydroxyphenylpyruvate dioxygenase, putative [Aspergillus fumigatus Af293] 4-hydroxyphenylpyruvate dioxygenase, putative [Aspergillus fumigatus A1163]	406	3×10^{-39}	41 - 422 (31%)
281	NR gi 268574768 ref XP_002642363.1 C. briggsae CBR-HPD-1 protein [Caenorhabditis briggsae] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; AltName: Full=4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD C. briggsae CBR-HPD-1 protein [Caenorhabditis briggsae]	393	4×10^{-39}	40 - 422 (32%)
282	NR gi 1362503 pir JC4215 T-cell reactive protein - Coccidioides immitis	399	5×10^{-39}	35 - 422 (31%)
283	NR gi 291184790 gb EFE40302.1 hypothetical protein TRV_04996 [Trichophyton verrucosum HKI 0517]	402	7×10^{-39}	41 - 422 (30%)
284	NR gi 270232765 emb CBI22086.1 unnamed protein product [Vitis vinifera]	115	7×10^{-39}	325 - 434 (69%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
285	NR gi 291225288 ref XP_002732632.1 PREDICTED: 4-hydroxyphenylpyruvate dioxygenase-like [Saccoglossus kowalevskii]	381	9×10^{-39}	35 - 427 (29%)
286	NR gi 259487254 tpe CBF85783.1 TPA: 4-hydroxyphenylpyruvate dioxygenase (Eurofung) [Aspergillus nidulans FGSC A4]	401	9×10^{-39}	43 - 422 (31%)
287	NR gi 48478441 ref YP_024147.1 4-hydroxyphenylpyruvate dioxygenase [Picrophilus torridus DSM 9790] 4-hydroxyphenylpyruvate dioxygenase [Picrophilus torridus DSM 9790]	368	9×10^{-39}	44 - 422 (32%)
288	NR gi 261199924 ref XP_002626363.1 4-hydroxyphenylpyruvate dioxygenase [Ajellomyces dermatitidis SLH14081] 4-hydroxyphenylpyruvate dioxygenase [Ajellomyces dermatitidis SLH14081]	424	1×10^{-38}	43 - 422 (31%)
289	NR gi 257075555 ref ZP_05569916.1 4-hydroxyphenylpyruvate dioxygenase [Ferroplasma acidarmanus fer1]	359	1×10^{-38}	44 - 422 (32%)
290	NR gi 239607961 gb EEQ84948.1 4-hydroxyphenylpyruvate dioxygenase [Ajellomyces dermatitidis ER-3]	424	2×10^{-38}	43 - 422 (31%)
291	NR gi 255947942 ref XP_002564738.1 Pc22g07130 [Penicillium chrysogenum Wisconsin 54-1255] Pc22g07130 [Penicillium chrysogenum Wisconsin 54-1255]	407	2×10^{-38}	41 - 422 (30%)
292	NR gi 21356105 ref NP_649225.1 CG11796, isoform B [Drosophila melanogaster] CG11796, isoform B [Drosophila melanogaster] GH03058p [Drosophila melanogaster] CG11796-PB [synthetic construct] CG11796-PB [synthetic construct]	294	2×10^{-38}	129 - 422 (38%)
293	NR gi 291174958 gb EFE30767.1 hypothetical protein ARB_02257 [Arthroderma benhamiae CBS 112371]	474	2×10^{-38}	41 - 422 (30%)
294	NR gi 119500396 ref XP_001266955.1 4-hydroxyphenylpyruvate dioxygenase, putative [Neosartorya fischeri NRRL 181] 4-hydroxyphenylpyruvate dioxygenase, putative [Neosartorya fischeri NRRL 181]	406	2×10^{-38}	41 - 422 (30%)
295	NR gi 254573294 ref XP_002493756.1 hypothetical protein [Pichia pastoris GS115] Hypothetical protein [Pichia pastoris GS115]	435	1×10^{-37}	41 - 422 (30%)
296	NR gi 17555220 ref NP_499324.1 4-HydroxyPhenylpyruvate Dioxygenase (HPD) family member (hpd-1) [Caenorhabditis elegans] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; AltName: Full=4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=4HPPD; Short=HPD C. elegans protein T21C12.2, confirmed by transcript evidence [Caenorhabditis elegans]	393	1×10^{-37}	41 - 422 (31%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
297	NR gi 261199756 ref XP_002626279.1 4-hydroxyphenylpyruvate dioxygenase [Ajellomyces dermatitidis SLH14081] 4-hydroxyphenylpyruvate dioxygenase [Ajellomyces dermatitidis SLH14081]	356	1×10^{-37}	64 - 422 (31%)
298	NR gi 238843961 gb EEQ33623.1 4-hydroxyphenylpyruvate dioxygenase [Microsporum canis CBS 113480]	402	1×10^{-37}	41 - 422 (30%)
299	NR gi 255932355 ref XP_002557734.1 Pc12g09060 [Penicillium chrysogenum Wisconsin 54-1255] Pc12g09060 [Penicillium chrysogenum Wisconsin 54-1255]	403	1×10^{-37}	43 - 422 (30%)
300	NR gi 225559907 gb EEH08189.1 4-hydroxyphenylpyruvate dioxygenase [Ajellomyces capsulatus G186AR] 4-hydroxyphenylpyruvate dioxygenase [Ajellomyces capsulatus G186AR]	428	2×10^{-37}	43 - 422 (31%)
301	NR gi 225679114 gb EEH17398.1 4-hydroxyphenylpyruvate dioxygenase [Paracoccidioides brasiliensis Pb03]	385	2×10^{-37}	43 - 422 (31%)
302	NR gi 291185021 gb EFE40521.1 hypothetical protein TRV_04754 [Trichophyton verrucosum HKI 0517]	422	4×10^{-37}	22 - 422 (29%)
303	NR gi 291175264 gb EFE31071.1 hypothetical protein ARB_01938 [Arthroderma benhamiae CBS 112371]	422	4×10^{-37}	22 - 422 (29%)
304	NR gi 154287682 ref XP_001544636.1 4-hydroxyphenylpyruvate dioxygenase [Ajellomyces capsulatus NAM1] 4-hydroxyphenylpyruvate dioxygenase [Ajellomyces capsulatus NAM1]	428	4×10^{-37}	43 - 422 (31%)
305	NR gi 240276187 gb EER39699.1 4-hydroxyphenylpyruvate dioxygenase [Ajellomyces capsulatus H143]	428	5×10^{-37}	43 - 422 (31%)
306	NR gi 145237260 ref XP_001391277.1 hypothetical protein An07g01900 [Aspergillus niger] unnamed protein product [Aspergillus niger]	409	8×10^{-37}	7 - 422 (28%)
307	NR gi 145256717 ref XP_001401493.1 hypothetical protein An04g01280 [Aspergillus niger] unnamed protein product [Aspergillus niger]	511	1×10^{-36}	43 - 422 (29%)
308	NR gi 83318921 emb CAJ38798.1 4-hydroxyphenylpyruvate dioxygenase protein [Platynereis dumerilii]	287	1×10^{-36}	171 - 422 (39%)
309	NR gi 258567394 ref XP_002584441.1 4-hydroxyphenylpyruvate dioxygenase [Uncinocarpus reesii 1704] 4-hydroxyphenylpyruvate dioxygenase [Uncinocarpus reesii 1704]	398	2×10^{-36}	43 - 422 (29%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
310	NR gi 240105413 gb EER23606.1 4-hydroxyphenylpyruvate dioxygenase , putative [Coccidioides posadasii C735 delta SOWgp]	400	4×10^{-36}	41 - 422 (29%)
311	NR gi 47223760 emb CAF98530.1 unnamed protein product [Tetraodon nigroviridis]	255	1×10^{-35}	194 - 422 (39%)
312	NR gi 212536602 ref XP_002148457.1 4-hydroxyphenylpyruvate dioxygenase, putative [Penicillium marneffei ATCC 18224] 4-hydroxyphenylpyruvate dioxygenase, putative [Penicillium marneffei ATCC 18224]	407	2×10^{-35}	32 - 422 (28%)
313	NR gi 261354473 gb EEY16901.1 4-hydroxyphenylpyruvate dioxygenase [Verticillium albo-atrum VaMs.102]	478	3×10^{-34}	50 - 422 (32%)
314	NR gi 50423723 ref XP_460446.1 hypothetical protein DEHA0F02156g [Debaryomyces hansenii CBS767] DEHA2F01892p [Debaryomyces hansenii]	473	4×10^{-34}	108 - 426 (32%)
315	NR gi 119618697 gb EAW98291.1 4-hydroxyphenylpyruvate dioxygenase, isoform CRA_a [Homo sapiens]	375	1×10^{-33}	33 - 423 (30%)
316	NR gi 45580880 emb CAG15040.1 HmaS protein [Actinoplanes teichomyceticus]	353	1×10^{-32}	38 - 422 (32%)
317	NR gi 40713178 emb CAE53378.1 HmaS protein [Actinoplanes teichomyceticus]	351	1×10^{-32}	38 - 422 (32%)
318	NR gi 93209319 gb ABB86496.1 HNF-HNF class homeobox protein [Nematostella vectensis]	873	2×10^{-32}	201 - 422 (39%)
319	NR gi 284033937 ref YP_003383868.1 4-hydroxyphenylpyruvate dioxygenase [Kribbella flavida DSM 17836] 4-hydroxyphenylpyruvate dioxygenase [Kribbella flavida DSM 17836]	357	2×10^{-31}	40 - 430 (30%)
320	NR gi 260941121 ref XP_002614727.1 hypothetical protein CLUG_05505 [Clavispora lusitaniae ATCC 42720] hypothetical protein CLUG_05505 [Clavispora lusitaniae ATCC 42720]	469	7×10^{-31}	37 - 422 (28%)
321	NR gi 225682587 gb EEH20871.1 4-hydroxyphenylpyruvate dioxygenase [Paracoccidioides brasiliensis Pb03]	366	1×10^{-30}	43 - 422 (29%)
322	NR gi 226358517 gb ACO51111.1 4-hydroxyphenylpyruvate dioxygenase [Hypophthalmichthys nobilis]	175	2×10^{-30}	253 - 422 (45%)
323	NR gi 288794506 ref ZP_06400213.1 4-hydroxyphenylpyruvate dioxygenase [Micromonospora sp. L5] 4-hydroxyphenylpyruvate dioxygenase [Micromonospora sp. L5]	366	6×10^{-30}	45 - 422 (30%)
324	NR gi 270498475 ref ZP_06215419.1 4-hydroxyphenylpyruvate dioxygenase [Micromonospora aurantiaca ATCC 27029] 4-hydroxyphenylpyruvate dioxygenase [Micromonospora aurantiaca ATCC 27029]	366	6×10^{-30}	45 - 422 (30%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
325	NR gi 159038248 ref YP_001537501.1 4-hydroxyphenylpyruvate dioxygenase [Salinispora arenicola CNS-205] 4-hydroxyphenylpyruvate dioxygenase [Salinispora arenicola CNS-205]	369	6×10^{-30}	45 - 422 (31%)
326	NR gi 86741150 ref YP_481550.1 4-hydroxyphenylpyruvate dioxygenase [Frankia sp. Ccl3] 4-hydroxyphenylpyruvate dioxygenase [Frankia sp. Ccl3]	355	4×10^{-29}	42 - 422 (31%)
327	NR gi 54302859 ref YP_132852.1 putative 4-hydroxyphenylpyruvate dioxygenase [Photobacterium profundum SS9] putative 4-hydroxyphenylpyruvate dioxygenase [Photobacterium profundum SS9]	365	1×10^{-28}	122 - 422 (35%)
328	NR gi 90414163 ref ZP_01222145.1 putative 4-hydroxyphenylpyruvate dioxygenase [Photobacterium profundum 3TCK] putative 4-hydroxyphenylpyruvate dioxygenase [Photobacterium profundum 3TCK]	356	4×10^{-28}	122 - 422 (35%)
329	NR gi 281205211 gb EFA79404.1 hypothetical protein PPL_07822 [Polysphondylium pallidum PN500]	376	5×10^{-28}	42 - 422 (26%)
330	NR gi 271968218 ref YP_003342414.1 4-hydroxyphenylpyruvate dioxygenase [Streptosporangium roseum DSM 43021] 4-hydroxyphenylpyruvate dioxygenase [Streptosporangium roseum DSM 43021]	362	5×10^{-28}	38 - 422 (29%)
331	NR gi 89274982 gb ABD65945.1 4-hydroxyphenylpyruvate dioxygenase [Streptomyces fungicidicus]	356	7×10^{-28}	40 - 422 (30%)
332	NR gi 150865616 ref XP_001384908.2 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Pichia stipitis CBS 6054] 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Pichia stipitis CBS 6054]	530	9×10^{-28}	125 - 426 (31%)
333	NR gi 190346165 gb EDK38185.2 hypothetical protein PGUG_02283 [Pichia guilliermondii ATCC 6260]	309	1×10^{-27}	147 - 426 (32%)
334	NR gi 262199705 ref YP_003270914.1 4-hydroxyphenylpyruvate dioxygenase [Haliangium ochraceum DSM 14365] 4-hydroxyphenylpyruvate dioxygenase [Haliangium ochraceum DSM 14365]	382	3×10^{-27}	113 - 422 (32%)
335	NR gi 162454256 ref YP_001616623.1 4-hydroxyphenylpyruvate dioxygenase [Sorangium cellulosum 'So ce 56'] 4-hydroxyphenylpyruvate dioxygenase [Sorangium cellulosum 'So ce 56']	382	3×10^{-27}	104 - 427 (34%)
336	NR gi 145595017 ref YP_001159314.1 4-hydroxyphenylpyruvate dioxygenase [Salinispora tropica CNB-440] 4-hydroxyphenylpyruvate dioxygenase [Salinispora tropica CNB-440]	389	4×10^{-27}	45 - 422 (30%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
337	NR gi 146421325 ref XP_001486612.1 hypothetical protein PGUG_02283 [Pichia guilliermondii ATCC 6260]	309	5×10^{-27}	147 - 426 (32%)
338	NR gi 162453169 ref YP_001615536.1 4-hydroxyphenylpyruvate dioxygenase [Sorangium cellulosum 'So ce 56'] 4-hydroxyphenylpyruvate dioxygenase [Sorangium cellulosum 'So ce 56']	383	1×10^{-26}	104 - 427 (33%)
339	NR gi 170586320 ref XP_001897927.1 4-hydroxyphenylpyruvate dioxygenase family protein [Brugia malayi] 4-hydroxyphenylpyruvate dioxygenase family protein [Brugia malayi]	403	1×10^{-26}	41 - 422 (28%)
340	NR gi 239944911 ref ZP_04696848.1 4-hydroxyphenylpyruvate dioxygenase [Streptomyces roseosporus NRRL 15998] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces roseosporus NRRL 11379] NocF [Streptomyces roseosporus NRRL 15998] NocF [Streptomyces roseosporus NRRL 15998]	354	3×10^{-26}	33 - 422 (29%)
341	NR gi 254433327 ref ZP_05046835.1 4-hydroxyphenylpyruvate dioxygenase [Nitrosococcus oceanus AFC27] 4-hydroxyphenylpyruvate dioxygenase [Nitrosococcus oceanus AFC27]	363	4×10^{-26}	122 - 422 (33%)
342	NR gi 77164931 ref YP_343456.1 4-hydroxyphenylpyruvate dioxygenase [Nitrosococcus oceanus ATCC 19707] 4-hydroxyphenylpyruvate dioxygenase [Nitrosococcus oceanus ATCC 19707]	351	4×10^{-26}	122 - 422 (33%)
343	NR gi 163795164 ref ZP_02189132.1 4-hydroxyphenylpyruvate dioxygenase [alpha proteobacterium BAL199] 4-hydroxyphenylpyruvate dioxygenase [alpha proteobacterium BAL199]	363	9×10^{-26}	122 - 422 (35%)
344	NR gi 256392440 ref YP_003114004.1 4-hydroxyphenylpyruvate dioxygenase [Catenulispora acidiphila DSM 44928] 4-hydroxyphenylpyruvate dioxygenase [Catenulispora acidiphila DSM 44928]	367	1×10^{-25}	40 - 390 (31%)
345	NR gi 256378609 ref YP_003102269.1 4-hydroxyphenylpyruvate dioxygenase [Actinosynnema mirum DSM 43827] NocF [Nocardia uniformis subsp. tsuyamanensis] 4-hydroxyphenylpyruvate dioxygenase [Actinosynnema mirum DSM 43827]	345	1×10^{-25}	38 - 422 (29%)
346	NR gi 42524895 ref NP_970275.1 4-hydroxyphenylpyruvate dioxygenase [Bdellovibrio bacteriovorus HD100] 4-hydroxyphenylpyruvate dioxygenase [Bdellovibrio bacteriovorus HD100]	352	3×10^{-25}	122 - 422 (32%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
347	NR gi 89076762 ref ZP_01163038.1 putative 4-hydroxyphenylpyruvate dioxygenase [Photobacterium sp. SKA34] putative 4-hydroxyphenylpyruvate dioxygenase [Photobacterium sp. SKA34]	356	4×10^{-25}	118 - 439 (31%)
348	NR gi 291579922 gb ADE14379.1 4-hydroxyphenylpyruvate dioxygenase [Nitrosococcus halophilus Nc4]	351	7×10^{-25}	122 - 422 (34%)
349	NR gi 158667951 gb ABW76439.1 4-hydroxyphenylpyruvate dioxygenase [uncultured bacterium]	354	7×10^{-25}	122 - 423 (35%)
350	NR gi 17550752 ref NP_508875.1 hypothetical protein C31H2.4 [Caenorhabditis elegans] RecName: Full=Putative protein C31H2.4 Hypothetical protein C31H2.4 [Caenorhabditis elegans]	364	7×10^{-25}	215 - 422 (36%)
351	NR gi 83643833 ref YP_432268.1 4-hydroxyphenylpyruvate dioxygenase [Hahella chejuensis KCTC 2396] 4-hydroxyphenylpyruvate dioxygenase [Hahella chejuensis KCTC 2396]	365	2×10^{-24}	125 - 423 (32%)
352	NR gi 67522885 ref XP_659503.1 hypothetical protein AN1899.2 [Aspergillus nidulans FGSC A4] hypothetical protein AN1899.2 [Aspergillus nidulans FGSC A4]	169	2×10^{-24}	253 - 422 (39%)
353	NR gi 288962318 ref YP_003452613.1 4-hydroxyphenylpyruvate dioxygenase [Azospirillum sp. B510] 4-hydroxyphenylpyruvate dioxygenase [Azospirillum sp. B510]	357	3×10^{-24}	123 - 422 (36%)
354	NR gi 90578056 ref ZP_01233867.1 putative 4-hydroxyphenylpyruvate dioxygenase [Vibrio angustum S14] putative 4-hydroxyphenylpyruvate dioxygenase [Vibrio angustum S14]	356	3×10^{-24}	118 - 439 (31%)
355	NR gi 170292354 pdb 2R5V A Chain A, Hydroxymandelate Synthase Crystal Structure Chain B, Hydroxymandelate Synthase Crystal Structure PCZA361.1 [Amycolatopsis orientalis]	357	4×10^{-24}	76 - 422 (29%)
356	NR gi 262275272 ref ZP_06053082.1 4-hydroxyphenylpyruvate dioxygenase [Grimontia hollisae CIP 101886] 4-hydroxyphenylpyruvate dioxygenase [Grimontia hollisae CIP 101886]	357	6×10^{-24}	122 - 422 (34%)
357	NR gi 255725086 ref XP_002547472.1 hypothetical protein CTRG_01779 [Candida tropicalis MYA-3404] hypothetical protein CTRG_01779 [Candida tropicalis MYA-3404]	638	6×10^{-24}	166 - 426 (30%)
358	NR gi 238882397 gb EEQ46035.1 4-hydroxyphenylpyruvate dioxygenase [Candida albicans WO-1]	476	6×10^{-24}	125 - 426 (27%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
359	NR gi 117621161 ref YP_857172.1 4-hydroxyphenylpyruvate dioxygenase [Aeromonas hydrophila subsp. hydrophila ATCC 7966] 4-hydroxyphenylpyruvate dioxygenase [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	365	6×10^{-24}	122 - 422 (32%)
360	NR gi 113477599 ref YP_723660.1 4-hydroxyphenylpyruvate dioxygenase [Trichodesmium erythraeum IMS101] 4-hydroxyphenylpyruvate dioxygenase [Trichodesmium erythraeum IMS101]	353	6×10^{-24}	119 - 422 (30%)
361	NR gi 21911428 gb AAM80551.1 HmaS [Streptomyces toyocaensis]	369	8×10^{-24}	35 - 422 (28%)
362	NR gi 145299456 ref YP_001142297.1 4-hydroxyphenylpyruvate dioxygenase [Aeromonas salmonicida subsp. salmonicida A449] 4-hydroxyphenylpyruvate dioxygenase [Aeromonas salmonicida subsp. salmonicida A449]	370	1×10^{-23}	122 - 422 (32%)
363	NR gi 34496424 ref NP_900639.1 4-hydroxyphenylpyruvate dioxygenase [Chromobacterium violaceum ATCC 12472] 4-hydroxyphenylpyruvate dioxygenase [Chromobacterium violaceum ATCC 12472]	358	1×10^{-23}	85 - 423 (30%)
364	NR gi 241951662 ref XP_002418553.1 4-hydroxyphenylpyruvate dioxygenase, putative [Candida dubliniensis CD36] 4-hydroxyphenylpyruvate dioxygenase, putative [Candida dubliniensis CD36]	570	1×10^{-23}	125 - 426 (27%)
365	NR gi 153006326 ref YP_001380651.1 4-hydroxyphenylpyruvate dioxygenase [Anaeromyxobacter sp. Fw109-5] 4-hydroxyphenylpyruvate dioxygenase [Anaeromyxobacter sp. Fw109-5]	391	1×10^{-23}	113 - 422 (33%)
366	NR gi 268579327 ref XP_002644646.1 Hypothetical protein CBG14622 [Caenorhabditis briggsae] Hypothetical protein CBG14622 [Caenorhabditis briggsae]	364	2×10^{-23}	215 - 422 (35%)
367	NR gi 68489346 ref XP_711514.1 hypothetical protein CaO19.12954 [Candida albicans SC5314] hypothetical protein CaO19.5499 [Candida albicans SC5314] hypothetical protein CaO19.5499 [Candida albicans SC5314] hypothetical protein CaO19.12954 [Candida albicans SC5314]	572	2×10^{-23}	125 - 426 (27%)
368	NR gi 209966600 ref YP_002299515.1 4-hydroxyphenylpyruvate dioxygenase [Rhodospirillum centenum SW] 4-hydroxyphenylpyruvate dioxygenase [Rhodospirillum centenum SW]	377	2×10^{-23}	122 - 422 (33%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
369	NR gi 148652847 ref YP_001279940.1 4-hydroxyphenylpyruvate dioxygenase [Psychrobacter sp. PRwf-1] 4-hydroxyphenylpyruvate dioxygenase [Psychrobacter sp. PRwf-1]	372	3×10^{-23}	122 - 422 (30%)
370	NR gi 262171624 ref ZP_06039302.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio mimicus MB-451] 4-hydroxyphenylpyruvate dioxygenase [Vibrio mimicus MB-451]	357	4×10^{-23}	122 - 423 (32%)
371	NR gi 220918663 ref YP_002493967.1 4-hydroxyphenylpyruvate dioxygenase [Anaeromyxobacter dehalogenans 2CP-1] 4-hydroxyphenylpyruvate dioxygenase [Anaeromyxobacter dehalogenans 2CP-1]	395	4×10^{-23}	129 - 422 (33%)
372	NR gi 262165586 ref ZP_06033323.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio mimicus VM223] 4-hydroxyphenylpyruvate dioxygenase [Vibrio mimicus VM223]	342	5×10^{-23}	122 - 423 (32%)
373	NR gi 258621558 ref ZP_05716591.1 Hemolysin vIY [Vibrio mimicus VM573] Hemolysin vIY [Vibrio mimicus VM573]	358	5×10^{-23}	122 - 423 (32%)
374	NR gi 119513418 ref ZP_01632449.1 4-hydroxyphenylpyruvate dioxygenase [Nodularia spumigena CCY9414] 4-hydroxyphenylpyruvate dioxygenase [Nodularia spumigena CCY9414]	343	5×10^{-23}	203 - 422 (35%)
375	NR gi 218248164 ref YP_002373535.1 4-hydroxyphenylpyruvate dioxygenase [Cyanotheca sp. PCC 8801] 4-hydroxyphenylpyruvate dioxygenase [Cyanotheca sp. PCC 8801]	363	9×10^{-23}	201 - 438 (31%)
376	NR gi 257060512 ref YP_003138400.1 4-hydroxyphenylpyruvate dioxygenase [Cyanotheca sp. PCC 8802] 4-hydroxyphenylpyruvate dioxygenase [Cyanotheca sp. PCC 8802]	388	9×10^{-23}	201 - 438 (31%)
377	NR gi 37522660 ref NP_926037.1 4-hydroxyphenylpyruvate dioxygenase [Gloeobacter violaceus PCC 7421] 4-hydroxyphenylpyruvate dioxygenase [Gloeobacter violaceus PCC 7421]	344	9×10^{-23}	187 - 427 (36%)
378	NR gi 113970627 ref YP_734420.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. MR-4] 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. MR-7] 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. ANA-3] 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. MR-4] 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. MR-7] 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. ANA-3]	346	9×10^{-23}	117 - 422 (31%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
379	NR gi 87118546 ref ZP_01074445.1 4-hydroxyphenylpyruvate dioxygenase [Marinomonas sp. MED121] 4-hydroxyphenylpyruvate dioxygenase [Marinomonas sp. MED121]	363	2×10^{-22}	122 - 423 (31%)
380	NR gi 114563498 ref YP_751011.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella frigidimarina NCIMB 400] 4-hydroxyphenylpyruvate dioxygenase [Shewanella frigidimarina NCIMB 400]	346	2×10^{-22}	117 - 422 (31%)
381	NR gi 226947009 ref YP_002802082.1 4-hydroxyphenylpyruvate dioxygenase [Azotobacter vinelandii DJ] 4-hydroxyphenylpyruvate dioxygenase [Azotobacter vinelandii DJ]	345	2×10^{-22}	125 - 422 (33%)
382	NR gi 229521453 ref ZP_04410872.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae TM 11079-80] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae TM 11079-80]	369	2×10^{-22}	122 - 423 (32%)
383	NR gi 262199452 ref YP_003270661.1 4-hydroxyphenylpyruvate dioxygenase [Haliangium ochraceum DSM 14365] 4-hydroxyphenylpyruvate dioxygenase [Haliangium ochraceum DSM 14365]	384	2×10^{-22}	40 - 423 (29%)
384	NR gi 197106294 ref YP_002131671.1 4-hydroxyphenylpyruvate dioxygenase [Phenylobacterium zucineum HLK1] 4-hydroxyphenylpyruvate dioxygenase [Phenylobacterium zucineum HLK1]	374	2×10^{-22}	122 - 422 (32%)
385	NR gi 217972908 ref YP_002357659.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella baltica OS223] 4-hydroxyphenylpyruvate dioxygenase [Shewanella baltica OS223]	346	2×10^{-22}	125 - 422 (31%)
386	NR gi 124547188 ref ZP_01706141.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella putrefaciens 200] 4-hydroxyphenylpyruvate dioxygenase [Shewanella putrefaciens 200]	346	2×10^{-22}	125 - 422 (31%)
387	NR gi 86605196 ref YP_473959.1 putative 4-hydroxyphenylpyruvate dioxygenase [Synechococcus sp. JA-3-3Ab] putative 4-hydroxyphenylpyruvate dioxygenase [Synechococcus sp. JA-3-3Ab]	350	2×10^{-22}	212 - 426 (34%)
388	NR gi 167624333 ref YP_001674627.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella halifaxensis HAW-EB4] 4-hydroxyphenylpyruvate dioxygenase [Shewanella halifaxensis HAW-EB4]	346	3×10^{-22}	117 - 422 (32%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
389	NR gi 197123894 ref YP_002135845.1 4-hydroxyphenylpyruvate dioxygenase [Anaeromyxobacter sp. K] 4-hydroxyphenylpyruvate dioxygenase [Anaeromyxobacter sp. K]	393	3×10^{-22}	129 - 422 (32%)
390	NR gi 116048789 ref YP_792411.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa UCBPP-PA14] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa UCBPP-PA14]	357	3×10^{-22}	125 - 423 (32%)
391	NR gi 262404028 ref ZP_06080583.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio sp. RC586] 4-hydroxyphenylpyruvate dioxygenase [Vibrio sp. RC586]	357	3×10^{-22}	122 - 423 (31%)
392	NR gi 261210928 ref ZP_05925218.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio sp. RC341] 4-hydroxyphenylpyruvate dioxygenase [Vibrio sp. RC341]	357	3×10^{-22}	122 - 423 (31%)
393	NR gi 260772776 ref ZP_05881692.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio metschnikovii CIP 69.14] 4-hydroxyphenylpyruvate dioxygenase [Vibrio metschnikovii CIP 69.14]	357	3×10^{-22}	122 - 423 (32%)
394	NR gi 258627572 ref ZP_05722349.1 Hemolysin vIY [Vibrio mimicus VM603] Hemolysin vIY [Vibrio mimicus VM603]	358	3×10^{-22}	122 - 423 (31%)
395	NR gi 220910562 ref YP_002485873.1 4-hydroxyphenylpyruvate dioxygenase [Cyanosphaera sp. PCC 7425] 4-hydroxyphenylpyruvate dioxygenase [Cyanosphaera sp. PCC 7425]	358	3×10^{-22}	80 - 422 (29%)
396	NR gi 115377234 ref ZP_01464445.1 glyoxalase family protein [Stigmatella aurantiaca DW4/3-1] glyoxalase family protein [Stigmatella aurantiaca DW4/3-1]	386	3×10^{-22}	113 - 427 (31%)
397	NR gi 91793517 ref YP_563168.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella denitrificans OS217] 4-hydroxyphenylpyruvate dioxygenase [Shewanella denitrificans OS217]	346	3×10^{-22}	117 - 422 (30%)
398	NR gi 85712096 ref ZP_01043149.1 4-hydroxyphenylpyruvate dioxygenase [Idiomarina baltica OS145] 4-hydroxyphenylpyruvate dioxygenase [Idiomarina baltica OS145]	357	3×10^{-22}	122 - 423 (34%)
399	NR gi 157961697 ref YP_001501731.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella pealeana ATCC 700345] 4-hydroxyphenylpyruvate dioxygenase [Shewanella pealeana ATCC 700345]	346	4×10^{-22}	117 - 426 (31%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
400	NR gi 146292770 ref YP_001183194.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella putrefaciens CN-32] 4-hydroxyphenylpyruvate dioxygenase [Shewanella putrefaciens CN-32]	346	4×10^{-22}	125 - 422 (31%)
401	NR gi 282899867 ref ZP_06307828.1 4-hydroxyphenylpyruvate dioxygenase [Cylindrospermopsis raciborskii CS-505] 4-hydroxyphenylpyruvate dioxygenase [Cylindrospermopsis raciborskii CS-505]	347	6×10^{-22}	215 - 423 (34%)
402	NR gi 271502712 ref YP_003335738.1 4-hydroxyphenylpyruvate dioxygenase [Dickeya dadantii Ech586] 4-hydroxyphenylpyruvate dioxygenase [Dickeya dadantii Ech586]	362	6×10^{-22}	123 - 422 (31%)
403	NR gi 153213481 ref ZP_01948792.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae 1587] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae MZO-2] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae 623-39] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae 1587] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae 623-39] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae MZO-2]	369	6×10^{-22}	122 - 423 (31%)
404	NR gi 120599159 ref YP_963733.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. W3-18-1] 4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. W3-18-1]	346	6×10^{-22}	125 - 422 (31%)
405	NR gi 153001171 ref YP_001366852.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella baltica OS185] 4-hydroxyphenylpyruvate dioxygenase [Shewanella baltica OS195] 4-hydroxyphenylpyruvate dioxygenase [Shewanella baltica OS185] 4-hydroxyphenylpyruvate dioxygenase [Shewanella baltica OS195]	346	8×10^{-22}	125 - 422 (31%)
406	NR gi 126174829 ref YP_001050978.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella baltica OS155] 4-hydroxyphenylpyruvate dioxygenase [Shewanella baltica OS155]	346	8×10^{-22}	125 - 422 (31%)
407	NR gi 262192401 ref ZP_06050554.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae CT 5369-93] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae CT 5369-93]	357	1×10^{-21}	122 - 423 (31%)
408	NR gi 119484929 ref ZP_01619411.1 4-hydroxyphenylpyruvate dioxygenase [Lyngbya sp. PCC 8106] 4-hydroxyphenylpyruvate dioxygenase [Lyngbya sp. PCC 8106]	363	1×10^{-21}	215 - 422 (33%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
409	NR gi 86159841 ref YP_466626.1 4-hydroxyphenylpyruvate dioxygenase [Anaeromyxobacter dehalogenans 2CP-C] 4-hydroxyphenylpyruvate dioxygenase [Anaeromyxobacter dehalogenans 2CP-C]	393	1×10^{-21}	129 - 422 (33%)
410	NR gi 88858042 ref ZP_01132684.1 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Pseudoalteromonas tunicata D2] 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Pseudoalteromonas tunicata D2]	348	1×10^{-21}	117 - 422 (32%)
411	NR gi 282897063 ref ZP_06305065.1 4-hydroxyphenylpyruvate dioxygenase [Raphidiopsis brookii D9] 4-hydroxyphenylpyruvate dioxygenase [Raphidiopsis brookii D9]	357	1×10^{-21}	85 - 423 (27%)
412	NR gi 56459831 ref YP_155112.1 4-hydroxyphenylpyruvate dioxygenase [Idiomarina loihiensis L2TR] 4-hydroxyphenylpyruvate dioxygenase [Idiomarina loihiensis L2TR]	357	1×10^{-21}	122 - 423 (33%)
413	NR gi 126951 sp P23996.1 MELA_SHECO RecName: Full=Protein melA melA [Shewanella colwelliana]	346	1×10^{-21}	125 - 422 (31%)
414	NR gi 15596062 ref NP_249556.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa PAO1] hypothetical protein PaerPA_01001348 [Pseudomonas aeruginosa PACS2] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa C3719] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa 2192] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa PAO1] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa C3719] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa 2192]	357	1×10^{-21}	125 - 423 (31%)
415	NR gi 238059402 ref ZP_04604111.1 4-hydroxyphenylpyruvate dioxygenase [Micromonospora sp. ATCC 39149] 4-hydroxyphenylpyruvate dioxygenase [Micromonospora sp. ATCC 39149]	266	2×10^{-21}	171 - 436 (34%)
416	NR gi 163752337 ref ZP_02159534.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella benthica KT99] 4-hydroxyphenylpyruvate dioxygenase [Shewanella benthica KT99]	346	2×10^{-21}	117 - 422 (31%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
417	NR gi 153802276 ref ZP_01956862.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae MZO-3] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholera CIRS 101] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae INDRE 91/1] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae RC27] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae MZO-3] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholera CIRS 101] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae RC27] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae INDRE 91/1]	357	2×10^{-21}	122 - 423 (31%)
418	NR gi 24373526 ref NP_717569.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella oneidensis MR-1] 4-hydroxyphenylpyruvate dioxygenase [Shewanella oneidensis MR-1]	346	2×10^{-21}	125 - 422 (31%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
419	NR gi 15641356 ref NP_230988.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae O1 biovar El Tor str. N16961] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae 2740-80] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae V52] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae O395] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae MAK 757] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae NCTC 8457] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae B33] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae MZO-3] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae M66-2] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae BX 330286] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae B33] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae RC9] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae bv. albensis VL426] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae 12129(1)] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae MJ-1236] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae RC385] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae V51] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae AM-19226] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae MO10] p-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae O1 biovar El Tor str. N16961] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae 2740-80] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae V52] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae MAK 757] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae V51] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae NCTC 8457] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae B33] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae O395] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae RC385] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae AM-19226] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae MZO-3] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae M66-2] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae O395] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae 12129(1)] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae bv. albensis VL426] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae RC9] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae B33] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae BX 330286] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae M-1236] 4-	369	2 x 10 ⁻²¹	122 - 423 (31%)

Page 57 of 125

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
420	NR gi 172036226 ref YP_001802727.1 4-hydroxyphenylpyruvate dioxygenase [Cyanotheca sp. ATCC 51142] 4-hydroxyphenylpyruvate dioxygenase [Cyanotheca sp. ATCC 51142]	386	2×10^{-21}	215 - 422 (32%)
421	NR gi 126727508 ref ZP_01743342.1 probable 4-hydroxyphenylpyruvate dioxygenase protein [Rhodobacterales bacterium HTCC2150] probable 4-hydroxyphenylpyruvate dioxygenase protein [Rhodobacterales bacterium HTCC2150]	373	2×10^{-21}	125 - 422 (31%)
422	NR gi 260768363 ref ZP_05877297.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio furnissii CIP 102972] 4-hydroxyphenylpyruvate dioxygenase [Vibrio furnissii CIP 102972]	357	3×10^{-21}	122 - 423 (30%)
423	NR gi 229515718 ref ZP_04405177.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae TMA 21] 4-hydroxyphenylpyruvate dioxygenase [Vibrio cholerae TMA 21]	369	4×10^{-21}	122 - 423 (31%)
424	NR gi 218893166 ref YP_002442035.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa LESB58] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa LESB58]	357	4×10^{-21}	125 - 423 (31%)
425	NR gi 212635659 ref YP_002312184.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella piezotolerans WP3] 4-hydroxyphenylpyruvate dioxygenase [Shewanella piezotolerans WP3]	346	4×10^{-21}	117 - 422 (31%)
426	NR gi 114177171 gb ABI53729.1 4-hydroxyphenylpyruvate dioxygenase [uncultured bacterium] 4-hydroxyphenylpyruvate dioxygenase [uncultured soil bacterium]	367	4×10^{-21}	116 - 422 (32%)
427	NR gi 119194183 ref XP_001247695.1 hypothetical protein CIMG_01466 [Coccidioides immitis RS]	345	4×10^{-21}	41 - 422 (24%)
428	NR gi 15131503 emb CAC48371.1 putative hydroxyphenyl pyruvate dioxygenase [Amycolatopsis balhimycina]	356	4×10^{-21}	81 - 422 (27%)
429	NR gi 256822447 ref YP_003146410.1 4-hydroxyphenylpyruvate dioxygenase [Kangiella koreensis DSM 16069] 4-hydroxyphenylpyruvate dioxygenase [Kangiella koreensis DSM 16069]	356	5×10^{-21}	122 - 422 (31%)
430	NR gi 289608645 emb CBI60555.1 unnamed protein product [Sordaria macrospora]	352	6×10^{-21}	122 - 422 (32%)
431	NR gi 152987711 ref YP_001349996.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa PA7] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa PA7]	357	6×10^{-21}	125 - 423 (32%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
432	NR gi 127513083 ref YP_001094280.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella loihica PV-4] 4-hydroxyphenylpyruvate dioxygenase [Shewanella loihica PV-4]	346	6×10^{-21}	117 - 422 (31%)
433	NR gi 254506248 ref ZP_05118391.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio parahaemolyticus 16] 4-hydroxyphenylpyruvate dioxygenase [Vibrio parahaemolyticus 16]	357	8×10^{-21}	122 - 423 (31%)
434	NR gi 254411060 ref ZP_05024838.1 4-hydroxyphenylpyruvate dioxygenase [Microcoleus chthonoplastes PCC 7420] 4-hydroxyphenylpyruvate dioxygenase [Microcoleus chthonoplastes PCC 7420]	431	8×10^{-21}	204 - 422 (33%)
435	NR gi 146306727 ref YP_001187192.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas mendocina ymp] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas mendocina ymp]	360	8×10^{-21}	123 - 423 (32%)
436	NR gi 87198621 ref YP_495878.1 4-hydroxyphenylpyruvate dioxygenase [Novosphingobium aromaticivorans DSM 12444] 4-hydroxyphenylpyruvate dioxygenase [Novosphingobium aromaticivorans DSM 12444]	370	8×10^{-21}	122 - 422 (32%)
437	NR gi 262097095 gb EEY55147.1 4-hydroxyphenylpyruvate dioxygenase, putative [Phytophthora infestans T30-4] 4-hydroxyphenylpyruvate dioxygenase, putative [Phytophthora infestans T30-4]	175	1×10^{-20}	35 - 164 (43%)
438	NR gi 256787144 ref ZP_05525575.1 4-hydroxyphenylpyruvic acid dioxygenase [Streptomyces lividans TK24] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces lividans TK24] 4-hydroxyphenylpyruvate dioxygenase [Streptomyces lividans TK24]	358	1×10^{-20}	39 - 422 (26%)
439	NR gi 157375822 ref YP_001474422.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella sediminis HAW-EB3] 4-hydroxyphenylpyruvate dioxygenase [Shewanella sediminis HAW-EB3]	346	1×10^{-20}	114 - 422 (30%)
440	NR gi 146281255 ref YP_001171408.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas stutzeri A1501] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas stutzeri A1501]	361	1×10^{-20}	123 - 423 (32%)
441	NR gi 170726285 ref YP_001760311.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella woodyi ATCC 51908] 4-hydroxyphenylpyruvate dioxygenase [Shewanella woodyi ATCC 51908]	346	1×10^{-20}	125 - 422 (30%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
442	NR gi 145595252 ref YP_001159549.1 4-hydroxyphenylpyruvate dioxygenase [Salinispora tropica CNB-440] 4-hydroxyphenylpyruvate dioxygenase [Salinispora tropica CNB-440]	358	1×10^{-20}	38 - 422 (27%)
443	NR gi 21221663 ref NP_627442.1 4-hydroxyphenylpyruvic acid dioxygenase [Streptomyces coelicolor A3(2)] putative 4-hydroxyphenylpyruvic acid dioxygenase [Streptomyces coelicolor A3(2)]	371	1×10^{-20}	39 - 422 (26%)
444	NR gi 241773670 ref ZP_04771017.1 4-hydroxyphenylpyruvate dioxygenase [Asticcacaulis excentricus CB 48] 4-hydroxyphenylpyruvate dioxygenase [Asticcacaulis excentricus CB 48]	353	2×10^{-20}	119 - 422 (32%)
445	NR gi 149188318 ref ZP_01866612.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio shilonii AK1] 4-hydroxyphenylpyruvate dioxygenase [Vibrio shilonii AK1]	357	2×10^{-20}	122 - 423 (31%)
446	NR gi 31324014 gb AAP47152.1 4-hydroxyphenylpyruvate dioxygenase [uncultured soil bacterium]	353	2×10^{-20}	122 - 433 (30%)
447	NR gi 86607745 ref YP_476507.1 4-hydroxyphenylpyruvate dioxygenase, putative [Synechococcus sp. JA-2-3B'a(2-13)] 4-hydroxyphenylpyruvate dioxygenase, putative [Synechococcus sp. JA-2-3B'a(2-13)]	359	2×10^{-20}	195 - 426 (32%)
448	NR gi 27366056 ref NP_761584.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio vulnificus CMCP6] putative hemolysin [Vibrio vulnificus YJ016] RecName: Full=Hemolysin vIIY 4-hydroxyphenylpyruvate dioxygenase [Vibrio vulnificus CMCP6] putative hemolysin [Vibrio vulnificus YJ016]	357	2×10^{-20}	122 - 423 (31%)
449	NR gi 109899304 ref YP_662559.1 4-hydroxyphenylpyruvate dioxygenase [Pseudoalteromonas atlantica T6c] 4-hydroxyphenylpyruvate dioxygenase [Pseudoalteromonas atlantica T6c]	360	2×10^{-20}	119 - 422 (32%)
450	NR gi 186684229 ref YP_001867425.1 4-hydroxyphenylpyruvate dioxygenase [Nostoc punctiforme PCC 73102] 4-hydroxyphenylpyruvate dioxygenase [Nostoc punctiforme PCC 73102]	361	2×10^{-20}	208 - 422 (31%)
451	NR gi 289636572 ref ZP_06468853.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1003] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1003]	365	2×10^{-20}	122 - 422 (30%)
452	NR gi 282884078 ref ZP_06292666.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1001] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1001]	365	2×10^{-20}	122 - 422 (30%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
453	NR gi 148556766 ref YP_001264348.1 4-hydroxyphenylpyruvate dioxygenase [Sphingomonas wittichii RW1] 4-hydroxyphenylpyruvate dioxygenase [Sphingomonas wittichii RW1]	367	3×10^{-20}	122 - 422 (32%)
454	NR gi 15029330 gb AAK81835.1 hydroxyphenyl pyruvate dioxygenase [Streptomyces lavendulae]	338	3×10^{-20}	81 - 422 (28%)
455	NR gi 261252816 ref ZP_05945389.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio orientalis CIP 102891] 4-hydroxyphenylpyruvate dioxygenase [Vibrio orientalis CIP 102891]	357	4×10^{-20}	122 - 423 (31%)
456	NR gi 18104608 gb AAL59614.1 AF457645_1 4-hydroxyphenylpyruvate dioxygenase [Listonella anguillarum]	357	4×10^{-20}	122 - 423 (30%)
457	NR gi 75910862 ref YP_325158.1 4-hydroxyphenylpyruvate dioxygenase [Anabaena variabilis ATCC 29413] 4-hydroxyphenylpyruvate dioxygenase [Anabaena variabilis ATCC 29413]	344	4×10^{-20}	41 - 422 (26%)
458	NR gi 17228266 ref NP_484814.1 4-hydroxyphenylpyruvate dioxygenase [Nostoc sp. PCC 7120] 4-hydroxyphenylpyruvate dioxygenase [Nostoc sp. PCC 7120]	344	4×10^{-20}	211 - 422 (33%)
459	NR gi 284050157 ref ZP_06380367.1 4-hydroxyphenylpyruvate dioxygenase [Arthrospira platensis str. Paraca]	351	5×10^{-20}	41 - 422 (23%)
460	NR gi 198412646 ref XP_002125704.1 PREDICTED: similar to 4-hydroxyphenylpyruvate dioxygenase, partial [Ciona intestinalis]	278	5×10^{-20}	43 - 307 (29%)
461	NR gi 171058725 ref YP_001791074.1 4-hydroxyphenylpyruvate dioxygenase [Leptothrix cholodnii SP-6] 4-hydroxyphenylpyruvate dioxygenase [Leptothrix cholodnii SP-6]	358	5×10^{-20}	121 - 422 (32%)
462	NR gi 93006379 ref YP_580816.1 4-hydroxyphenylpyruvate dioxygenase [Psychrobacter cryohalolentis K5] 4-hydroxyphenylpyruvate dioxygenase [Psychrobacter cryohalolentis K5]	368	5×10^{-20}	125 - 422 (30%)
463	NR gi 256822736 ref YP_003146699.1 4-hydroxyphenylpyruvate dioxygenase [Kangiella koreensis DSM 16069] 4-hydroxyphenylpyruvate dioxygenase [Kangiella koreensis DSM 16069]	353	7×10^{-20}	125 - 422 (29%)
464	NR gi 214003852 gb ACJ60972.1 VEG30 [uncultured soil bacterium]	357	7×10^{-20}	76 - 422 (28%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
465	NR gi 148359822 ref YP_001251029.1 4-hydroxyphenylpyruvate dioxygenase [Legionella pneumophila str. Corby] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD; AltName: Full=Legiolysin 4-hydroxyphenylpyruvate dioxygenase [Legionella pneumophila str. Corby]	348	7×10^{-20}	122 - 422 (32%)
466	NR gi 148975373 ref ZP_01812297.1 4-hydroxyphenylpyruvate dioxygenase [Vibrionales bacterium SWAT-3] 4-hydroxyphenylpyruvate dioxygenase [Vibrionales bacterium SWAT-3]	357	7×10^{-20}	122 - 423 (31%)
467	NR gi 126657122 ref ZP_01728293.1 4-hydroxyphenylpyruvate dioxygenase [Cyanotheca sp. CCY0110] 4-hydroxyphenylpyruvate dioxygenase [Cyanotheca sp. CCY0110]	379	7×10^{-20}	215 - 422 (31%)
468	NR gi 32487230 emb CAD91197.1 putative hydroxymandelate synthase [Nonomuraea sp. ATCC 39727]	356	7×10^{-20}	36 - 422 (28%)
469	NR gi 77361091 ref YP_340666.1 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Pseudoalteromonas haloplanktis TAC125] 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Pseudoalteromonas haloplanktis TAC125]	348	7×10^{-20}	125 - 422 (31%)
470	NR gi 226945526 ref YP_002800599.1 4-hydroxyphenylpyruvate dioxygenase [Azotobacter vinelandii DJ] 4-hydroxyphenylpyruvate dioxygenase [Azotobacter vinelandii DJ]	359	7×10^{-20}	123 - 423 (31%)
471	NR gi 291572007 dbj BAI94279.1 4-hydroxyphenylpyruvate dioxygenase [Arthrospira platensis NIES-39]	351	9×10^{-20}	41 - 422 (23%)
472	NR gi 289635582 ref ZP_06467867.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1003] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1003]	357	9×10^{-20}	122 - 422 (30%)
473	NR gi 71281576 ref YP_270158.1 4-hydroxyphenylpyruvate dioxygenase [Colwellia psychrerythraea 34H] 4-hydroxyphenylpyruvate dioxygenase [Colwellia psychrerythraea 34H]	351	9×10^{-20}	119 - 422 (32%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
474	NR gi 28898123 ref NP_797728.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio parahaemolyticus RIMD 2210633] 4-hydroxyphenylpyruvate dioxygenase [Vibrio parahaemolyticus AQ3810] 4-hydroxyphenylpyruvate dioxygenase [Vibrio parahaemolyticus K5030] 4-hydroxyphenylpyruvate dioxygenase [Vibrio parahaemolyticus AN-5034] 4-hydroxyphenylpyruvate dioxygenase [Vibrio parahaemolyticus Peru-466] 4-hydroxyphenylpyruvate dioxygenase [Vibrio parahaemolyticus AQ4037] 4-hydroxyphenylpyruvate dioxygenase [Vibrio parahaemolyticus RIMD 2210633] 4-hydroxyphenylpyruvate dioxygenase [Vibrio parahaemolyticus AQ3810]	357	9×10^{-20}	122 - 423 (30%)
475	NR gi 119774705 ref YP_927445.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella amazonensis SB2B] 4-hydroxyphenylpyruvate dioxygenase [Shewanella amazonensis SB2B]	345	9×10^{-20}	125 - 422 (31%)
476	NR gi 224824800 ref ZP_03697907.1 4-hydroxyphenylpyruvate dioxygenase [Lutiella nitroferum 2002] 4-hydroxyphenylpyruvate dioxygenase [Lutiella nitroferum 2002]	360	1×10^{-19}	122 - 423 (31%)
477	NR gi 170696548 ref ZP_02887671.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia graminis C4D1M] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia graminis C4D1M]	365	1×10^{-19}	122 - 422 (30%)
478	NR gi 89055751 ref YP_511202.1 4-hydroxyphenylpyruvate dioxygenase [Jannaschia sp. CCS1] 4-hydroxyphenylpyruvate dioxygenase [Jannaschia sp. CCS1]	363	1×10^{-19}	122 - 423 (32%)
479	NR gi 91785493 ref YP_560699.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia xenovorans LB400] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia xenovorans LB400]	365	1×10^{-19}	122 - 422 (29%)
480	NR gi 254295012 ref YP_003061035.1 4-hydroxyphenylpyruvate dioxygenase [Hirschia baltica ATCC 49814] 4-hydroxyphenylpyruvate dioxygenase [Hirschia baltica ATCC 49814]	366	2×10^{-19}	121 - 422 (31%)
481	NR gi 218438778 ref YP_002377107.1 4-hydroxyphenylpyruvate dioxygenase [Cyanotheca sp. PCC 7424] 4-hydroxyphenylpyruvate dioxygenase [Cyanotheca sp. PCC 7424]	363	2×10^{-19}	194 - 422 (33%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
482	NR gij119468369 ref ZP_01611460.1 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Alteromonadales bacterium TW-7] 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Alteromonadales bacterium TW-7]	348	2×10^{-19}	117 - 422 (31%)
483	NR gij91223907 ref ZP_01259171.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio alginolyticus 12G01] 4-hydroxyphenylpyruvate dioxygenase [Vibrio sp. Ex25] 4-hydroxyphenylpyruvate dioxygenase [Vibrio sp. Ex25] 4-hydroxyphenylpyruvate dioxygenase [Vibrio alginolyticus 12G01] 4-hydroxyphenylpyruvate dioxygenase [Vibrio sp. Ex25] 4-hydroxyphenylpyruvate dioxygenase [Vibrio sp. Ex25]	357	2×10^{-19}	122 - 423 (30%)
484	NR gij209527909 ref ZP_03276397.1 4-hydroxyphenylpyruvate dioxygenase [Arthrospira maxima CS-328] 4-hydroxyphenylpyruvate dioxygenase [Arthrospira maxima CS-328]	351	2×10^{-19}	41 - 422 (23%)
485	NR gij163801003 ref ZP_02194903.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio sp. AND4] 4-hydroxyphenylpyruvate dioxygenase [Vibrio sp. AND4]	357	2×10^{-19}	122 - 423 (30%)
486	NR gij17547822 ref NP_521224.1 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein [Ralstonia solanacearum GMI1000] probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein [Ralstonia solanacearum GMI1000]	367	2×10^{-19}	122 - 422 (30%)
487	NR gij269968294 ref ZP_06182318.1 Hemolysin vIY [Vibrio alginolyticus 40B] Hemolysin vIY [Vibrio alginolyticus 40B]	357	3×10^{-19}	122 - 423 (30%)
488	NR gij126741219 ref ZP_01756899.1 4-hydroxyphenylpyruvate dioxygenase [Roseobacter sp. SK209-2-6] 4-hydroxyphenylpyruvate dioxygenase [Roseobacter sp. SK209-2-6]	366	3×10^{-19}	122 - 422 (30%)
489	NR gij119384401 ref YP_915457.1 4-hydroxyphenylpyruvate dioxygenase [Paracoccus denitrificans PD1222] 4-hydroxyphenylpyruvate dioxygenase [Paracoccus denitrificans PD1222]	370	3×10^{-19}	122 - 423 (31%)
490	NR gij52842491 ref YP_096290.1 4-hydroxyphenylpyruvate dioxygenase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] 4-hydroxyphenylpyruvate dioxygenase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	361	3×10^{-19}	122 - 422 (31%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
491	NR gi 54295124 ref YP_127539.1 4-hydroxyphenylpyruvate dioxygenase (legiolysin) [Legionella pneumophila str. Lens] RecName: Full=4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD; AltName: Full=Legiolysin legiolysin [Legionella pneumophila] 4-hydroxyphenylpyruvate dioxygenase (legiolysin) [Legionella pneumophila str. Lens]	348	3×10^{-19}	122 - 422 (31%)
492	NR gi 269962247 ref ZP_06176600.1 Hemolysin vIY [Vibrio harveyi 1DA3] Hemolysin vIY [Vibrio harveyi 1DA3]	357	4×10^{-19}	122 - 423 (30%)
493	NR gi 242241416 ref YP_002989597.1 4-hydroxyphenylpyruvate dioxygenase [Dickeya dadantii Ech703] 4-hydroxyphenylpyruvate dioxygenase [Dickeya dadantii Ech703]	362	4×10^{-19}	123 - 422 (30%)
494	NR gi 254475606 ref ZP_05088992.1 4-hydroxyphenylpyruvate dioxygenase [Ruegeria sp. R11] 4-hydroxyphenylpyruvate dioxygenase [Ruegeria sp. R11]	366	4×10^{-19}	122 - 422 (30%)
495	NR gi 254421250 ref ZP_05034968.1 glyoxalase family protein [Synechococcus sp. PCC 7335] glyoxalase family protein [Synechococcus sp. PCC 7335]	387	4×10^{-19}	211 - 422 (34%)
496	NR gi 187925643 ref YP_001897285.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia phytofirmans PsJN] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia phytofirmans PsJN]	365	4×10^{-19}	122 - 422 (30%)
497	NR gi 83746408 ref ZP_00943460.1 4-hydroxyphenylpyruvate dioxygenase [Ralstonia solanacearum UW551] 4-hydroxyphenylpyruvate dioxygenase protein [Ralstonia solanacearum IPO1609] 4-hydroxyphenylpyruvate dioxygenase [Ralstonia solanacearum UW551] 4-hydroxyphenylpyruvate dioxygenase protein [Ralstonia solanacearum IPO1609]	367	4×10^{-19}	122 - 422 (30%)
498	NR gi 163738521 ref ZP_02145936.1 4-hydroxyphenylpyruvate dioxygenase [Phaeobacter gallaeciensis BS107] 4-hydroxyphenylpyruvate dioxygenase [Phaeobacter gallaeciensis BS107]	366	5×10^{-19}	122 - 422 (32%)
499	NR gi 163743567 ref ZP_02150944.1 4-hydroxyphenylpyruvate dioxygenase [Phaeobacter gallaeciensis 2.10] 4-hydroxyphenylpyruvate dioxygenase [Phaeobacter gallaeciensis 2.10]	366	5×10^{-19}	122 - 422 (32%)
500	NR gi 149908593 ref ZP_01897255.1 4-hydroxyphenylpyruvate dioxygenase [Moritella sp. PE36] 4-hydroxyphenylpyruvate dioxygenase [Moritella sp. PE36]	362	5×10^{-19}	122 - 422 (31%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
501	NR gi 13508831 emb CAC35138.1 human T-cell reactive protein [Uncinocarpus reesii]	130	5×10^{-19}	247 - 380 (40%)
502	NR gi 270157783 ref ZP_06186440.1 4-hydroxyphenylpyruvate dioxygenase [Legionella longbeachae D-4968] 4-hydroxyphenylpyruvate dioxygenase (legiolysin) [Legionella longbeachae NSW150] 4-hydroxyphenylpyruvate dioxygenase [Legionella longbeachae D-4968] 4-hydroxyphenylpyruvate dioxygenase (legiolysin) [Legionella longbeachae NSW150]	350	6×10^{-19}	122 - 422 (31%)
503	NR gi 260778443 ref ZP_05887335.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio coralliilyticus ATCC BAA-450] 4-hydroxyphenylpyruvate dioxygenase [Vibrio coralliilyticus ATCC BAA-450]	357	6×10^{-19}	122 - 423 (29%)
504	NR gi 241766856 ref ZP_04764672.1 4-hydroxyphenylpyruvate dioxygenase [Acidovorax delafieldii 2AN] 4-hydroxyphenylpyruvate dioxygenase [Acidovorax delafieldii 2AN]	377	6×10^{-19}	122 - 422 (28%)
505	NR gi 207722800 ref YP_002253235.1 4-hydroxyphenylpyruvate dioxygenase protein [Ralstonia solanacearum MolK2] 4-hydroxyphenylpyruvate dioxygenase protein [Ralstonia solanacearum]	358	6×10^{-19}	122 - 422 (30%)
506	NR gi 153833408 ref ZP_01986075.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio harveyi HY01] 4-hydroxyphenylpyruvate dioxygenase [Vibrio harveyi ATCC BAA-1116] 4-hydroxyphenylpyruvate dioxygenase [Vibrio harveyi HY01] hypothetical protein VIBHAR_02177 [Vibrio harveyi ATCC BAA-1116]	357	6×10^{-19}	122 - 423 (30%)
507	NR gi 91790051 ref YP_551003.1 4-hydroxyphenylpyruvate dioxygenase [Polaromonas sp. JS666] 4-hydroxyphenylpyruvate dioxygenase [Polaromonas sp. JS666]	376	6×10^{-19}	122 - 422 (29%)
508	NR gi 84386189 ref ZP_00989218.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio splendidus 12B01] 4-hydroxyphenylpyruvate dioxygenase [Vibrio splendidus 12B01]	357	6×10^{-19}	122 - 423 (29%)
509	NR gi 218677260 ref YP_002396079.1 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (hemolysin) [Vibrio splendidus LGP32] 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (hemolysin) [Vibrio splendidus LGP32]	357	8×10^{-19}	122 - 423 (30%)
510	NR gi 272539732 ref ZP_06229359.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1002] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1002]	365	1×10^{-18}	122 - 422 (29%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
511	NR gi 163854986 ref YP_001629284.1 putative 4-hydroxyphenylpyruvate dioxygenase [Bordetella petrii DSM 12804] putative 4-hydroxyphenylpyruvate dioxygenase [Bordetella petrii]	370	1×10^{-18}	122 - 422 (30%)
512	NR gi 13508825 emb CAC35135.1 human T-cell reactive protein [Uncinocarpus reesii] human T-cell reactive protein [Uncinocarpus reesii] human T-cell reactive protein [Uncinocarpus reesii]	130	1×10^{-18}	247 - 380 (39%)
513	NR gi 2632111 emb CAA04693.1 legiolysin [Legionella pneumophila str. Corby]	348	1×10^{-18}	122 - 422 (31%)
514	NR gi 86144791 ref ZP_01063123.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio sp. MED222] 4-hydroxyphenylpyruvate dioxygenase [Vibrio sp. MED222]	357	1×10^{-18}	122 - 423 (29%)
515	NR gi 255262963 ref ZP_05342305.1 4-hydroxyphenylpyruvate dioxygenase [Thalassiosira sp. R2A62] 4-hydroxyphenylpyruvate dioxygenase [Thalassiosira sp. R2A62]	364	1×10^{-18}	122 - 422 (30%)
516	NR gi 167587796 ref ZP_02380184.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ubonensis Bu]	365	2×10^{-18}	122 - 422 (29%)
517	NR gi 160900227 ref YP_001565809.1 4-hydroxyphenylpyruvate dioxygenase [Delftia acidovorans SPH-1] 4-hydroxyphenylpyruvate dioxygenase [Delftia acidovorans SPH-1]	364	2×10^{-18}	122 - 437 (28%)
518	NR gi 13508693 emb CAC35132.1 human T-cell reactive protein [Coccidioides immitis] human T-cell reactive protein [Coccidioides immitis]	130	2×10^{-18}	247 - 380 (38%)
519	NR gi 54298175 ref YP_124544.1 4-hydroxyphenylpyruvate dioxygenase (legiolysin) [Legionella pneumophila str. Paris] 4-hydroxyphenylpyruvate dioxygenase (legiolysin) [Legionella pneumophila str. Paris]	348	2×10^{-18}	122 - 422 (31%)
520	NR gi 134294416 ref YP_001118151.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia vietnamiensis G4] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia vietnamiensis G4]	365	2×10^{-18}	122 - 422 (29%)
521	NR gi 269921779 ref ZP_06170688.1 4-hydroxyphenylpyruvate dioxygenase [Brevundimonas subvibrioides ATCC 15264] 4-hydroxyphenylpyruvate dioxygenase [Brevundimonas subvibrioides ATCC 15264]	370	2×10^{-18}	122 - 422 (31%)
522	NR gi 260429855 ref ZP_05783831.1 4-hydroxyphenylpyruvate dioxygenase [Citricella sp. SE45] 4-hydroxyphenylpyruvate dioxygenase [Citricella sp. SE45]	370	2×10^{-18}	122 - 423 (31%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
523	NR gi 259418868 ref ZP_05742785.1 4-hydroxyphenylpyruvate dioxygenase [Silicibacter sp. TrichCH4B] 4-hydroxyphenylpyruvate dioxygenase [Silicibacter sp. TrichCH4B]	366	2×10^{-18}	122 - 422 (31%)
524	NR gi 251791785 ref YP_003006506.1 4-hydroxyphenylpyruvate dioxygenase [Dickeya zeae Ech1591] 4-hydroxyphenylpyruvate dioxygenase [Dickeya zeae Ech1591]	362	2×10^{-18}	123 - 422 (29%)
525	NR gi 209517367 ref ZP_03266210.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. H160] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. H160]	365	2×10^{-18}	122 - 439 (29%)
526	NR gi 13508701 emb CAC35129.1 human T-cell reactive protein [Auxarthron zuffianum]	130	2×10^{-18}	247 - 380 (40%)
527	NR gi 13508697 emb CAC35127.1 human T-cell reactive protein [Auxarthron zuffianum] human T-cell reactive protein [Auxarthron zuffianum] human T-cell reactive protein [Auxarthron zuffianum] human T-cell reactive protein [Auxarthron zuffianum]	130	2×10^{-18}	247 - 380 (40%)
528	NR gi 77459142 ref YP_348648.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens Pf0-1] putative hemolysin [Pseudomonas fluorescens Pf0-1]	358	2×10^{-18}	122 - 422 (30%)
529	NR gi 148252169 ref YP_001236754.1 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium sp. BTAi1] 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium sp. BTAi1]	372	2×10^{-18}	125 - 423 (32%)
530	NR gi 103488594 ref YP_618155.1 4-hydroxyphenylpyruvate dioxygenase [Sphingopyxis alaskensis RB2256] 4-hydroxyphenylpyruvate dioxygenase [Sphingopyxis alaskensis RB2256]	363	2×10^{-18}	122 - 422 (31%)
531	NR gi 256758053 ref ZP_05498725.1 4-hydroxyphenylpyruvate dioxygenase [Thiomonas intermedia K12] 4-hydroxyphenylpyruvate dioxygenase [Thiomonas intermedia K12]	371	3×10^{-18}	122 - 422 (29%)
532	NR gi 158337667 ref YP_001518843.1 4-hydroxyphenylpyruvate dioxygenase [Acaryochloris marina MBIC11017] 4-hydroxyphenylpyruvate dioxygenase [Acaryochloris marina MBIC11017]	355	3×10^{-18}	212 - 422 (31%)
533	NR gi 170721621 ref YP_001749309.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida W619] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida W619]	358	3×10^{-18}	122 - 422 (31%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
534	NR gi 104782117 ref YP_608615.1 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Pseudomonas entomophila L48] 4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Pseudomonas entomophila L48]	357	3×10^{-18}	122 - 422 (30%)
535	NR gi 37727200 gb AAO12525.1 p-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida]	358	3×10^{-18}	122 - 422 (30%)
536	NR gi 254250853 ref ZP_04944171.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia dolosa AUO158] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia dolosa AUO158]	365	3×10^{-18}	122 - 422 (29%)
537	NR gi 260219629 emb CBA26474.1 4-hydroxyphenylpyruvate dioxygenase [Curvibacter putative symbiont of Hydra magnipapillata]	362	4×10^{-18}	125 - 422 (31%)
538	NR gi 221202330 ref ZP_03575363.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans CGD2M] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans CGD2] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans CGD1] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans CGD1] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans CGD2] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans CGD2M]	365	4×10^{-18}	122 - 422 (29%)
539	NR gi 146343715 ref YP_001208763.1 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium sp. ORS278] 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium sp. ORS278]	372	4×10^{-18}	125 - 423 (31%)
540	NR gi 33598277 ref NP_885920.1 putative hemolysin [Bordetella parapertussis 12822] putative hemolysin [Bordetella bronchiseptica RB50] putative hemolysin [Bordetella parapertussis] putative hemolysin [Bordetella bronchiseptica RB50]	370	4×10^{-18}	122 - 422 (29%)
541	NR gi 86137851 ref ZP_01056427.1 4-hydroxyphenylpyruvate dioxygenase [Roseobacter sp. MED193] 4-hydroxyphenylpyruvate dioxygenase [Roseobacter sp. MED193]	391	4×10^{-18}	122 - 422 (30%)
542	NR gi 99080423 ref YP_612577.1 4-hydroxyphenylpyruvate dioxygenase [Ruegeria sp. TM1040] 4-hydroxyphenylpyruvate dioxygenase [Ruegeria sp. TM1040]	366	4×10^{-18}	122 - 422 (30%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
543	NR gi 262372711 ref ZP_06065990.1 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter junii SH205] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter junii SH205]	308	5×10^{-18}	122 - 422 (31%)
544	NR gi 237799406 ref ZP_04587867.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. oryzae str. 1 6]	358	5×10^{-18}	122 - 422 (30%)
545	NR gi 33593969 ref NP_881613.1 putative hemolysin [Bordetella pertussis Tohama I] putative hemolysin [Bordetella pertussis Tohama I]	370	5×10^{-18}	122 - 422 (29%)
546	NR gi 123491 sp P80064.1 HPPD_PSEUJ RecName: Full=4-hydroxyphenylpyruvate dioxygenase; Short=HPPDase; Short=4HPPD; Short=HPD 4-hydroxyphenylpyruvate dioxygenase {EC 1.13.11.27} [Pseudomonas, P.J. 874, Peptide, 357 aa]	357	5×10^{-18}	122 - 422 (30%)
547	NR gi 254466641 ref ZP_05080052.1 4-hydroxyphenylpyruvate dioxygenase [Rhodobacterales bacterium Y4I] 4-hydroxyphenylpyruvate dioxygenase [Rhodobacterales bacterium Y4I]	366	7×10^{-18}	122 - 422 (30%)
548	NR gi 149184587 ref ZP_01862905.1 4-hydroxyphenylpyruvate dioxygenase [Erythrobacter sp. SD-21] 4-hydroxyphenylpyruvate dioxygenase [Erythrobacter sp. SD-21]	373	7×10^{-18}	121 - 422 (31%)
549	NR gi 187479365 ref YP_787390.1 4-hydroxyphenylpyruvate dioxygenase (hemolysin) [Bordetella avium 197N] 4-hydroxyphenylpyruvate dioxygenase (putative hemolysin) [Bordetella avium 197N]	370	7×10^{-18}	122 - 422 (29%)
550	NR gi 120612827 ref YP_972505.1 4-hydroxyphenylpyruvate dioxygenase [Acidovorax avenae subsp. citrulli AAC00-1] 4-hydroxyphenylpyruvate dioxygenase [Acidovorax citrulli AAC00-1]	378	7×10^{-18}	122 - 422 (27%)
551	NR gi 270493488 ref ZP_06210543.1 4-hydroxyphenylpyruvate dioxygenase [Acidovorax avenae subsp. avenae ATCC 19860] 4-hydroxyphenylpyruvate dioxygenase [Acidovorax avenae subsp. avenae ATCC 19860]	378	9×10^{-18}	122 - 422 (27%)
552	NR gi 270250655 emb CBI33833.1 unnamed protein product [Vitis vinifera]	67	9×10^{-18}	336 - 399 (64%)
553	NR gi 213968989 ref ZP_03397129.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. tomato T1] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. tomato T1]	329	9×10^{-18}	122 - 422 (30%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
554	NR gi 116251628 ref YP_767466.1 putative 4-hydroxyphenylpyruvate dioxygenase [Rhizobium leguminosarum bv. viciae 3841] putative 4-hydroxyphenylpyruvate dioxygenase [Rhizobium leguminosarum bv. viciae 3841]	369	9×10^{-18}	122 - 422 (32%)
555	NR gi 28870714 ref NP_793333.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. tomato str. DC3000] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. tomato str. DC3000]	363	9×10^{-18}	122 - 422 (30%)
556	NR gi 27375450 ref NP_766979.1 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium japonicum USDA 110] 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium japonicum USDA 110]	372	9×10^{-18}	125 - 423 (31%)
557	NR gi 148547550 ref YP_001267652.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida F1] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida F1]	358	9×10^{-18}	122 - 422 (30%)
558	NR gi 67922247 ref ZP_00515761.1 4-hydroxyphenylpyruvate dioxygenase [Crocospaera watsonii WH 8501] 4-hydroxyphenylpyruvate dioxygenase [Crocospaera watsonii WH 8501]	386	9×10^{-18}	215 - 422 (32%)
559	NR gi 239817727 ref YP_002946637.1 4-hydroxyphenylpyruvate dioxygenase [Variovorax paradoxus S110] 4-hydroxyphenylpyruvate dioxygenase [Variovorax paradoxus S110]	375	1×10^{-17}	122 - 422 (28%)
560	NR gi 170079303 ref YP_001735941.1 glyoxalase family protein [Synechococcus sp. PCC 7002] glyoxalase family protein [Synechococcus sp. PCC 7002]	337	1×10^{-17}	212 - 426 (33%)
561	NR gi 241664622 ref YP_002982982.1 4-hydroxyphenylpyruvate dioxygenase [Ralstonia pickettii 12D] 4-hydroxyphenylpyruvate dioxygenase [Ralstonia pickettii 12D]	368	1×10^{-17}	122 - 422 (29%)
562	NR gi 86357375 ref YP_469267.1 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium etli CFN 42] probable 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium etli CFN 42]	369	1×10^{-17}	122 - 422 (32%)
563	NR gi 39933085 ref NP_945361.1 4-hydroxyphenylpyruvate dioxygenase [Rhodopseudomonas palustris CGA009] 4-hydroxyphenylpyruvate dioxygenase [Rhodopseudomonas palustris CGA009]	372	1×10^{-17}	125 - 423 (31%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
564	NR gi 53720847 ref YP_109833.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei K96243] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei ATCC 23344] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei GB8 horse 4] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 1710b] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei SAVP1] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei SAVP1] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei NCTC 10229] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 668] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei NCTC 10247] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 1106a] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 305] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei PRL-20] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei DM98] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 14] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 91] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 9] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei B7210] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 7894] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei NCTC 13177] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 112] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei BCC215] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 576] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei Pakistan 9] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei MSHR346] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 1106b] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei ATCC 10399] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 1655] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei Pasteur 52237] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei S13] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei FMH14-	365	1×10^{-17}	122 - 422 (29%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
565	NR gi 264679969 ref YP_003279878.1 4-hydroxyphenylpyruvate dioxygenase [Comamonas testosteroni CNB-2] 4-hydroxyphenylpyruvate dioxygenase [Comamonas testosteroni CNB-2]	362	1×10^{-17}	122 - 422 (29%)
566	NR gi 194291669 ref YP_002007576.1 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE PROTEIN [Cupriavidus taiwanensis] 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE PROTEIN [Cupriavidus taiwanensis]	359	1×10^{-17}	122 - 422 (31%)
567	NR gi 187930454 ref YP_001900941.1 4-hydroxyphenylpyruvate dioxygenase [Ralstonia pickettii 12J] 4-hydroxyphenylpyruvate dioxygenase [Ralstonia pickettii 12J]	368	1×10^{-17}	122 - 422 (29%)
568	NR gi 161523403 ref YP_001578415.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans ATCC 17616] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans ATCC 17616] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans ATCC 17616] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans ATCC 17616]	365	1×10^{-17}	122 - 422 (29%)
569	NR gi 186477614 ref YP_001859084.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia phymatum STM815] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia phymatum STM815]	365	1×10^{-17}	122 - 422 (29%)
570	NR gi 115350295 ref YP_772134.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria AMMD] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria AMMD]	365	1×10^{-17}	122 - 422 (29%)
571	NR gi 260831031 ref XP_002610463.1 hypothetical protein BRAFLDRAFT_59543 [Branchiostoma floridae] hypothetical protein BRAFLDRAFT_59543 [Branchiostoma floridae]	429	2×10^{-17}	194 - 424 (29%)
572	NR gi 206558614 ref YP_002229374.1 4-hydroxyphenylpyruvic acid dioxygenase [Burkholderia cenocepacia J2315] 4-hydroxyphenylpyruvic acid dioxygenase [Burkholderia cenocepacia J2315]	365	2×10^{-17}	122 - 422 (28%)
573	NR gi 124265539 ref YP_001019543.1 4-hydroxyphenylpyruvate dioxygenase [Methylobium petroleiphilum PM1] 4-hydroxyphenylpyruvate dioxygenase [Methylobium petroleiphilum PM1]	370	2×10^{-17}	122 - 422 (30%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
574	NR gi 121604028 ref YP_981357.1 4-hydroxyphenylpyruvate dioxygenase [Polaromonas naphthalenivorans CJ2] 4-hydroxyphenylpyruvate dioxygenase [Polaromonas naphthalenivorans CJ2]	360	2×10^{-17}	125 - 422 (32%)
575	NR gi 66046559 ref YP_236400.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. syringae B728a] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. syringae B728a]	358	2×10^{-17}	122 - 422 (31%)
576	NR gi 26990146 ref NP_745571.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida KT2440] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida KT2440]	358	2×10^{-17}	122 - 422 (30%)
577	NR gi 266628596 ref ZP_06121517.1 4-hydroxyphenylpyruvate dioxygenase [Caulobacter segnis ATCC 21756] 4-hydroxyphenylpyruvate dioxygenase [Caulobacter segnis ATCC 21756]	357	3×10^{-17}	125 - 422 (29%)
578	NR gi 171057125 ref YP_001789474.1 4-hydroxyphenylpyruvate dioxygenase [Leptothrix cholodnii SP-6] 4-hydroxyphenylpyruvate dioxygenase [Leptothrix cholodnii SP-6]	358	3×10^{-17}	122 - 422 (31%)
579	NR gi 167033506 ref YP_001668737.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida GB-1] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida GB-1]	358	3×10^{-17}	122 - 422 (30%)
580	NR gi 126305802 ref XP_001375958.1 PREDICTED: similar to Glyoxalase domain containing 1 [Monodelphis domestica]	392	3×10^{-17}	193 - 424 (30%)
581	NR gi 289678769 ref ZP_06499659.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. syringae FF5]	358	3×10^{-17}	122 - 422 (31%)
582	NR gi 159030261 emb CAO91156.1 unnamed protein product [Microcystis aeruginosa PCC 7806]	361	3×10^{-17}	196 - 422 (30%)
583	NR gi 116695028 ref YP_840604.1 4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha H16] 4-Hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha H16]	359	3×10^{-17}	122 - 422 (30%)
584	NR gi 85374110 ref YP_458172.1 4-hydroxyphenylpyruvate dioxygenase [Erythrobacter litoralis HTCC2594] 4-hydroxyphenylpyruvate dioxygenase [Erythrobacter litoralis HTCC2594]	373	3×10^{-17}	121 - 422 (32%)
585	NR gi 73538328 ref YP_298695.1 4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha JMP134] 4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha JMP134]	359	3×10^{-17}	122 - 422 (29%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
586	NR gi 238025906 ref YP_002910137.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia glumae BGR1] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia glumae BGR1]	365	4×10^{-17}	122 - 422 (29%)
587	NR gi 192288438 ref YP_001989043.1 4-hydroxyphenylpyruvate dioxygenase [Rhodopseudomonas palustris TIE-1] 4-hydroxyphenylpyruvate dioxygenase [Rhodopseudomonas palustris TIE-1]	372	4×10^{-17}	125 - 423 (32%)
588	NR gi 70730751 ref YP_260492.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens Pf-5] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens Pf-5]	358	4×10^{-17}	122 - 422 (31%)
589	NR gi 196157342 ref YP_002126831.1 4-hydroxyphenylpyruvate dioxygenase [Alteromonas macleodii 'Deep ecotype'] 4-hydroxyphenylpyruvate dioxygenase [Alteromonas macleodii 'Deep ecotype']	357	4×10^{-17}	122 - 422 (30%)
590	NR gi 289623523 ref ZP_06456477.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. aesculi str. NCPPB3681] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. aesculi str. 2250]	358	6×10^{-17}	122 - 422 (31%)
591	NR gi 285019498 ref YP_003377209.1 probable 4-hydroxyphenylpyruvate dioxygenase protein [Xanthomonas albilineans] probable 4-hydroxyphenylpyruvate dioxygenase protein [Xanthomonas albilineans]	370	6×10^{-17}	116 - 422 (31%)
592	NR gi 239995092 ref ZP_04715616.1 4-hydroxyphenylpyruvate dioxygenase [Alteromonas macleodii ATCC 27126]	357	6×10^{-17}	122 - 422 (30%)
593	NR gi 229590458 ref YP_002872577.1 putative 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens SBW25] putative 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens SBW25]	358	6×10^{-17}	122 - 422 (31%)
594	NR gi 224058040 ref XP_002191187.1 PREDICTED: hypothetical protein [Taeniopygia guttata]	494	6×10^{-17}	194 - 424 (29%)
595	NR gi 221065010 ref ZP_03541115.1 4-hydroxyphenylpyruvate dioxygenase [Comamonas testosteroni KF-1] 4-hydroxyphenylpyruvate dioxygenase [Comamonas testosteroni KF-1]	373	6×10^{-17}	122 - 422 (28%)
596	NR gi 2108220 gb AAC45755.1 hemolysin [Vibrio vulnificus]	357	6×10^{-17}	122 - 423 (29%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
597	NR gi 83720009 ref YP_443601.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis E264] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis TXDOH] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis Bt4] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis E264] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis E264]	365	6×10^{-17}	122 - 422 (29%)
598	NR gi 13476861 ref NP_108430.1 4-hydroxyphenylpyruvate dioxygenase [Mesorhizobium loti MAFF303099] 4-hydroxyphenylpyruvate dioxygenase [Mesorhizobium loti MAFF303099]	371	6×10^{-17}	122 - 422 (31%)
599	NR gi 282887321 ref ZP_06295902.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1001] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1001]	359	7×10^{-17}	122 - 422 (29%)
600	NR gi 262368905 ref ZP_06062234.1 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter johnsonii SH046] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter johnsonii SH046]	353	7×10^{-17}	122 - 422 (30%)
601	NR gi 264680378 ref YP_003280288.1 4-hydroxyphenylpyruvate dioxygenase [Comamonas testosteroni CNB-2] 4-hydroxyphenylpyruvate dioxygenase [Comamonas testosteroni CNB-2]	373	7×10^{-17}	122 - 422 (28%)
602	NR gi 94982482 gb ABF50055.1 4-hydroxyphenylpyruvate dioxygenase [Plastid transformation vector pCLT111] 4-hydroxyphenylpyruvate dioxygenase [Plastid transformation vector pCLT323]	358	7×10^{-17}	122 - 422 (30%)
603	NR gi 167838237 ref ZP_02465096.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis MSMB43]	365	7×10^{-17}	122 - 422 (29%)
604	NR gi 167564442 ref ZP_02357358.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia oklahomensis EO147] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia oklahomensis C6786]	365	7×10^{-17}	122 - 422 (29%)
605	NR gi 172059313 ref YP_001806965.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria MC40-6] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria MC40-6]	365	7×10^{-17}	122 - 422 (29%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
606	NR gi 94313847 ref YP_587056.1 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein [Cupriavidus metallidurans CH34] 4-hydroxyphenylpyruvate dioxygenase, oxidoreductase protein [Cupriavidus metallidurans CH34]	357	7×10^{-17}	122 - 422 (29%)
607	NR gi 7766898 pdb 1CJX A Chain A, Crystal Structure Of Pseudomonas Fluorescens Hppd Chain B, Crystal Structure Of Pseudomonas Fluorescens Hppd Chain C, Crystal Structure Of Pseudomonas Fluorescens Hppd Chain D, Crystal Structure Of Pseudomonas Fluorescens Hppd	357	7×10^{-17}	122 - 422 (30%)
608	NR gi 88798032 ref ZP_01113619.1 4-hydroxyphenylpyruvate dioxygenase [Reinekea sp. MED297] 4-hydroxyphenylpyruvate dioxygenase [Reinekea sp. MED297]	365	7×10^{-17}	122 - 439 (30%)
609	NR gi 272540131 ref ZP_06229545.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1002] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1002]	357	1×10^{-16}	122 - 422 (30%)
610	NR gi 218681320 ref ZP_03529217.1 probable 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium etli CIAT 894]	369	1×10^{-16}	122 - 422 (32%)
611	NR gi 110679125 ref YP_682132.1 4-hydroxyphenylpyruvate dioxygenase [Roseobacter denitrificans OCh 114] 4-hydroxyphenylpyruvate dioxygenase [Roseobacter denitrificans OCh 114]	364	1×10^{-16}	122 - 422 (30%)
612	NR gi 71737014 ref YP_275410.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. phaseolicola 1448A] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. phaseolicola 1448A]	358	1×10^{-16}	122 - 422 (31%)
613	NR gi 110635218 ref YP_675426.1 4-hydroxyphenylpyruvate dioxygenase [Mesorhizobium sp. BNC1] 4-hydroxyphenylpyruvate dioxygenase [Chelativorans sp. BNC1]	369	1×10^{-16}	122 - 423 (32%)
614	NR gi 291231184 ref XP_002735549.1 PREDICTED: glyoxalase domain containing 1-like [Saccoglossus kowalevskii]	420	1×10^{-16}	44 - 439 (25%)
615	NR gi 241204244 ref YP_002975340.1 4-hydroxyphenylpyruvate dioxygenase [Rhizobium leguminosarum bv. trifolii WSM1325] 4-hydroxyphenylpyruvate dioxygenase [Rhizobium leguminosarum bv. trifolii WSM1325]	369	1×10^{-16}	122 - 422 (31%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
616	NR gi 108760279 ref YP_631003.1 4-hydroxyphenylpyruvate dioxygenase [Myxococcus xanthus DK 1622] 4-hydroxyphenylpyruvate dioxygenase [Myxococcus xanthus DK 1622]	354	1×10^{-16}	122 - 422 (29%)
617	NR gi 16126772 ref NP_421336.1 4-hydroxyphenylpyruvate dioxygenase [Caulobacter crescentus CB15] 4-hydroxyphenylpyruvate dioxygenase [Caulobacter crescentus NA1000] 4-hydroxyphenylpyruvate dioxygenase [Caulobacter crescentus CB15] 4-hydroxyphenylpyruvate dioxygenase [Caulobacter crescentus NA1000]	357	1×10^{-16}	125 - 422 (30%)
618	NR gi 85710284 ref ZP_01041349.1 4-hydroxyphenylpyruvate dioxygenase [Erythrobacter sp. NAP1] 4-hydroxyphenylpyruvate dioxygenase [Erythrobacter sp. NAP1]	372	1×10^{-16}	121 - 422 (31%)
619	NR gi 107024329 ref YP_622656.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia AU 1054] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia HI2424] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia MC0-3] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia PC184] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia AU 1054] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia HI2424] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia PC184] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia MC0-3]	365	1×10^{-16}	122 - 422 (28%)
620	NR gi 257484753 ref ZP_05638794.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. tabaci ATCC 11528]	358	2×10^{-16}	122 - 422 (31%)
621	NR gi 254514730 ref ZP_05126791.1 4-hydroxyphenylpyruvate dioxygenase [gamma proteobacterium NOR5-3] 4-hydroxyphenylpyruvate dioxygenase [gamma proteobacterium NOR5-3]	361	2×10^{-16}	125 - 422 (30%)
622	NR gi 188575036 ref YP_001911965.1 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas oryzae pv. oryzae PXO99A] 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas oryzae pv. oryzae PXO99A]	371	2×10^{-16}	116 - 422 (30%)
623	NR gi 166710354 ref ZP_02241561.1 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas oryzae pv. oryzae BLS256]	356	2×10^{-16}	116 - 422 (30%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
624	NR gi 58583694 ref YP_202710.1 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas oryzae pv. oryzae KACC10331] 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas oryzae pv. oryzae KACC10331]	403	2×10^{-16}	116 - 422 (30%)
625	NR gi 56696310 ref YP_166667.1 4-hydroxyphenylpyruvate dioxygenase [Ruegeria pomeroyi DSS-3] 4-hydroxyphenylpyruvate dioxygenase [Ruegeria pomeroyi DSS-3]	366	2×10^{-16}	122 - 422 (29%)
626	NR gi 78064897 ref YP_367666.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. 383] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. 383]	365	2×10^{-16}	122 - 422 (28%)
627	NR gi 84625503 ref YP_452875.1 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas oryzae pv. oryzae MAFF 311018] 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas oryzae pv. oryzae MAFF 311018]	356	2×10^{-16}	116 - 422 (30%)
628	NR gi 88706514 ref ZP_01104218.1 4-hydroxyphenylpyruvate dioxygenase [Congregibacter litoralis KT71] 4-hydroxyphenylpyruvate dioxygenase [Congregibacter litoralis KT71]	361	2×10^{-16}	125 - 422 (30%)
629	NR gi 83858849 ref ZP_00952371.1 4-hydroxyphenylpyruvate dioxygenase [Oceanicaulis alexandrii HTCC2633] 4-hydroxyphenylpyruvate dioxygenase [Oceanicaulis alexandrii HTCC2633]	354	2×10^{-16}	122 - 422 (31%)
630	NR gi 289663817 ref ZP_06485398.1 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. vasculorum NCPPB702] 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. musacearum NCPPB4381]	356	2×10^{-16}	116 - 422 (30%)
631	NR gi 260434057 ref ZP_05788028.1 4-hydroxyphenylpyruvate dioxygenase [Silicibacter lacuscaerulensis ITI-1157] 4-hydroxyphenylpyruvate dioxygenase [Silicibacter lacuscaerulensis ITI-1157]	365	2×10^{-16}	122 - 422 (29%)
632	NR gi 152996750 ref YP_001341585.1 4-hydroxyphenylpyruvate dioxygenase [Marinomonas sp. MWYL1] 4-hydroxyphenylpyruvate dioxygenase [Marinomonas sp. MWYL1]	358	2×10^{-16}	125 - 422 (29%)
633	NR gi 115956651 ref XP_001182551.1 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus]	270	2×10^{-16}	282 - 429 (36%)
634	NR gi 115749101 ref XP_781821.2 PREDICTED: hypothetical protein, partial [Strongylocentrotus purpuratus]	212	2×10^{-16}	282 - 429 (36%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
635	NR gi 262280574 ref ZP_06058358.1 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter calcoaceticus RUH2202] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter calcoaceticus RUH2202]	351	3×10^{-16}	122 - 422 (30%)
636	NR gi 254503272 ref ZP_05115423.1 4-hydroxyphenylpyruvate dioxygenase [Labrenzia alexandrii DFL-11] 4-hydroxyphenylpyruvate dioxygenase [Labrenzia alexandrii DFL-11]	378	3×10^{-16}	122 - 423 (30%)
637	NR gi 170700202 ref ZP_02891219.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria IOP40-10] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria MEX-5] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria IOP40-10] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria MEX-5]	365	3×10^{-16}	122 - 422 (28%)
638	NR gi 169794266 ref YP_001712059.1 4-hydroxyphenylpyruvate dioxygenase (4HPPD)(HPPDase) [Acinetobacter baumannii AYE] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter baumannii ACICU] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter baumannii AB0057] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter baumannii AB307-0294] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter baumannii AB900] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter baumannii ATCC 19606] 4-hydroxyphenylpyruvate dioxygenase (4HPPD)(HPPDase) [Acinetobacter baumannii] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter baumannii ACICU] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter baumannii ATCC 17978] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter baumannii AB0057] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter baumannii AB307-0294] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter baumannii ATCC 19606]	351	3×10^{-16}	122 - 422 (30%)
639	NR gi 167647615 ref YP_001685278.1 4-hydroxyphenylpyruvate dioxygenase [Caulobacter sp. K31] 4-hydroxyphenylpyruvate dioxygenase [Caulobacter sp. K31]	353	3×10^{-16}	125 - 422 (30%)
640	NR gi 16331765 ref NP_442493.1 4-hydroxyphenylpyruvic acid dioxgenase [Synechocystis sp. PCC 6803] RecName: Full=Uncharacterized protein slr0090 4-hydroxyphenylpyruvic acid dioxgenase [Synechocystis sp. PCC 6803]	339	3×10^{-16}	210 - 430 (32%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
641	NR gi 260464375 ref ZP_05812566.1 4-hydroxyphenylpyruvate dioxygenase [Mesorhizobium opportunistum WSM2075] 4-hydroxyphenylpyruvate dioxygenase [Mesorhizobium opportunistum WSM2075]	370	4×10^{-16}	122 - 422 (30%)
642	NR gi 225520054 ref ZP_03766964.1 4-hydroxyphenylpyruvate dioxygenase [Nostoc azollae' 0708] 4-hydroxyphenylpyruvate dioxygenase [Nostoc azollae' 0708]	381	4×10^{-16}	212 - 438 (30%)
643	NR gi 118591507 ref ZP_01548904.1 probable 4-hydroxyphenylpyruvate dioxygenase protein [Stappia aggregata IAM 12614] probable 4-hydroxyphenylpyruvate dioxygenase protein [Stappia aggregata IAM 12614]	370	4×10^{-16}	125 - 423 (31%)
644	NR gi 114798568 ref YP_761578.1 4-hydroxyphenylpyruvate dioxygenase [Hyphomonas neptunium ATCC 15444] 4-hydroxyphenylpyruvate dioxygenase [Hyphomonas neptunium ATCC 15444]	366	4×10^{-16}	121 - 422 (30%)
645	NR gi 21241225 ref NP_640807.1 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas axonopodis pv. citri str. 306] 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas axonopodis pv. citri str. 306]	356	4×10^{-16}	116 - 422 (30%)
646	NR gi 188989866 ref YP_001901876.1 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. campestris str. B100] 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. campestris]	371	5×10^{-16}	116 - 422 (30%)
647	NR gi 166364482 ref YP_001656755.1 4-hydroxyphenylpyruvate dioxygenase [Microcystis aeruginosa NIES-843] 4-hydroxyphenylpyruvate dioxygenase [Microcystis aeruginosa NIES-843]	361	5×10^{-16}	196 - 422 (28%)
648	NR gi 14249394 ref NP_116145.1 4-hydroxyphenylpyruvate dioxygenase-like protein [Homo sapiens] RecName: Full=4-hydroxyphenylpyruvate dioxygenase-like protein; AltName: Full=Glyoxalase domain-containing protein 1 4-hydroxyphenylpyruvate dioxygenase-like [Homo sapiens] 4-hydroxyphenylpyruvate dioxygenase-like [Homo sapiens] glyoxalase domain containing 1 [Homo sapiens] unnamed protein product [Homo sapiens]	371	5×10^{-16}	60 - 423 (29%)
649	NR gi 57097061 ref XP_539633.1 PREDICTED: similar to CG11796-PA, isoform A isoform 1 [Canis familiaris] PREDICTED: similar to CG11796-PA, isoform A isoform 2 [Canis familiaris]	399	5×10^{-16}	84 - 423 (26%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
650	NR gi 21229913 ref NP_635830.1 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. campestris str. ATCC 33913] 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. campestris str. 8004] 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. campestris str. ATCC 33913] 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris str. 8004]	356	5×10^{-16}	116 - 422 (30%)
651	NR gi 55586263 ref XP_524567.1 PREDICTED: glyoxalase domain containing 1 [Pan troglodytes]	371	6×10^{-16}	84 - 423 (29%)
652	NR gi 73912476 dbj BAE20318.1 dioxygenase [Coccidioides posadasii]	147	6×10^{-16}	253 - 375 (38%)
653	NR gi 163732458 ref ZP_02139904.1 4-hydroxyphenylpyruvate dioxygenase [Roseobacter litoralis Och 149] 4-hydroxyphenylpyruvate dioxygenase [Roseobacter litoralis Och 149]	364	8×10^{-16}	122 - 422 (29%)
654	NR gi 227823524 ref YP_002827497.1 4-hydroxyphenylpyruvate dioxygenase [Rhizobium sp. NGR234] 4-hydroxyphenylpyruvate dioxygenase [Rhizobium sp. NGR234]	372	1E-15	122 - 422 (31%)
655	NR gi 225707312 gb ACO09502.1 4-hydroxyphenylpyruvate dioxygenase [Osmerus mordax]	451	1E-15	194 - 424 (28%)
656	NR gi 126728952 ref ZP_01744767.1 4-hydroxyphenylpyruvate dioxygenase [Sagittula stellata E-37] 4-hydroxyphenylpyruvate dioxygenase [Sagittula stellata E-37]	364	1E-15	122 - 422 (29%)
657	NR gi 78046038 ref YP_362213.1 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. vesicatoria str. 85-10] 4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campestris pv. vesicatoria str. 85-10]	356	1E-15	116 - 422 (29%)
658	NR gi 254482041 ref ZP_05095283.1 4-hydroxyphenylpyruvate dioxygenase [marine gamma proteobacterium HTCC2148] 4-hydroxyphenylpyruvate dioxygenase [marine gamma proteobacterium HTCC2148]	362	1E-15	125 - 422 (28%)
659	NR gi 254418829 ref ZP_05032553.1 4-hydroxyphenylpyruvate dioxygenase [Brevundimonas sp. BAL3] 4-hydroxyphenylpyruvate dioxygenase [Brevundimonas sp. BAL3]	373	1E-15	122 - 422 (29%)
660	NR gi 190891432 ref YP_001977974.1 probable 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium etli CIAT 652] probable 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium etli CIAT 652]	369	1E-15	122 - 422 (31%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
661	NR gi 73912458 dbj BAE20309.1 dioxygenase [Coccidioides posadasii] dioxygenase [Coccidioides posadasii] dioxygenase [Coccidioides posadasii] dioxygenase [Coccidioides posadasii] dioxygenase [Coccidioides posadasii] dioxygenase [Coccidioides posadasii] dioxygenase [Coccidioides immitis] dioxygenase [Coccidioides immitis] dioxygenase [Coccidioides immitis] dioxygenase [Coccidioides immitis] dioxygenase [Coccidioides posadasii] dioxygenase [Coccidioides posadasii] dioxygenase [Coccidioides immitis] dioxygenase [Coccidioides posadasii] dioxygenase [Coccidioides posadasii] dioxygenase [Coccidioides posadasii] dioxygenase	147	1E-15	253 - 375 (37%)
662	NR gi 254473024 ref ZP_05086422.1 4-hydroxyphenylpyruvate dioxygenase [Pseudovibrio sp. JE062] 4-hydroxyphenylpyruvate dioxygenase [Pseudovibrio sp. JE062]	370	2E-15	122 - 423 (31%)
663	NR gi 163746979 ref ZP_02154336.1 4-hydroxyphenylpyruvate dioxygenase [Oceanibulbus indolifex HEL-45] 4-hydroxyphenylpyruvate dioxygenase [Oceanibulbus indolifex HEL-45]	364	2E-15	122 - 422 (28%)
664	NR gi 149694497 ref XP_001496335.1 PREDICTED: similar to glyoxalase domain containing 1 [Equus caballus]	371	2E-15	67 - 423 (29%)
665	NR gi 94495996 ref ZP_01302575.1 4-hydroxyphenylpyruvate dioxygenase [Sphingomonas sp. SKA58] 4-hydroxyphenylpyruvate dioxygenase [Sphingomonas sp. SKA58]	355	2E-15	120 - 422 (28%)
666	NR gi 254521476 ref ZP_05133531.1 4-hydroxyphenylpyruvate dioxygenase [Stenotrophomonas sp. SKA14] 4-hydroxyphenylpyruvate dioxygenase [Stenotrophomonas sp. SKA14]	370	2E-15	116 - 422 (28%)
667	NR gi 118094554 ref XP_426651.2 PREDICTED: hypothetical protein [Gallus gallus]	387	2E-15	193 - 424 (26%)
668	NR gi 218462924 ref ZP_03503015.1 4-hydroxyphenylpyruvate dioxygenase [Rhizobium etli Kim 5]	369	3E-15	122 - 422 (30%)
669	NR gi 169634870 ref YP_001708606.1 4-hydroxyphenylpyruvate dioxygenase (4HPPD)(HPPDase) [Acinetobacter baumannii SDF] 4-hydroxyphenylpyruvate dioxygenase (4HPPD)(HPPDase) [Acinetobacter baumannii]	351	3E-15	122 - 422 (30%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
670	NR gi 209549009 ref YP_002280926.1 4-hydroxyphenylpyruvate dioxygenase [Rhizobium leguminosarum bv. trifolii WSM2304] 4-hydroxyphenylpyruvate dioxygenase [Rhizobium leguminosarum bv. trifolii WSM2304]	369	3E-15	122 - 422 (31%)
671	NR gi 163761579 ref ZP_02168650.1 probable 4-hydroxyphenylpyruvate dioxygenase protein [Hoeflea phototrophica DFL-43] probable 4-hydroxyphenylpyruvate dioxygenase protein [Hoeflea phototrophica DFL-43]	369	3E-15	122 - 423 (30%)
672	NR gi 150398034 ref YP_001328501.1 4-hydroxyphenylpyruvate dioxygenase [Sinorhizobium medicae WSM419] 4-hydroxyphenylpyruvate dioxygenase [Sinorhizobium medicae WSM419]	370	3E-15	122 - 422 (30%)
673	NR gi 94449351 gb ABC88387.2 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens]	358	3E-15	122 - 422 (29%)
674	NR gi 62078869 ref NP_001014090.1 4-hydroxyphenylpyruvate dioxygenase-like [Rattus norvegicus] RecName: Full=4-hydroxyphenylpyruvate dioxygenase-like protein; AltName: Full=Glyoxalase domain-containing protein 1 4-hydroxyphenylpyruvate dioxygenase-like [Rattus norvegicus] glyoxalase domain containing 1 [Rattus norvegicus]	371	3E-15	84 - 423 (27%)
675	NR gi 114568887 ref YP_755567.1 4-hydroxyphenylpyruvate dioxygenase [Maricaulis maris MCS10] 4-hydroxyphenylpyruvate dioxygenase [Maricaulis maris MCS10]	359	4E-15	122 - 422 (30%)
676	NR gi 83942846 ref ZP_00955307.1 4-hydroxyphenylpyruvate dioxygenase [Sulfitobacter sp. EE-36] 4-hydroxyphenylpyruvate dioxygenase [Sulfitobacter sp. EE-36]	364	4E-15	122 - 422 (28%)
677	NR gi 157841205 ref NP_001103178.1 glyoxalase domain containing 1 [Danio rerio] Zgc:171978 protein [Danio rerio]	420	5E-15	193 - 429 (29%)
678	NR gi 126643425 ref YP_001086409.1 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter baumannii ATCC 17978]	273	7E-15	136 - 422 (30%)
679	NR gi 109003851 ref XP_001100445.1 PREDICTED: similar to glyoxalase domain containing 1 [Macaca mulatta]	381	7E-15	84 - 423 (28%)
680	NR gi 83955679 ref ZP_00964259.1 4-hydroxyphenylpyruvate dioxygenase [Sulfitobacter sp. NAS-14.1] 4-hydroxyphenylpyruvate dioxygenase [Sulfitobacter sp. NAS-14.1]	364	7E-15	122 - 422 (27%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
681	NR gi 91777364 ref YP_552572.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia xenovorans LB400] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia xenovorans LB400]	377	9E-15	122 - 422 (30%)
682	NR gi 190576153 ref YP_001973998.1 putative 4-hydroxyphenylpyruvate dioxygenase [Stenotrophomonas maltophilia K279a] putative 4-hydroxyphenylpyruvate dioxygenase [Stenotrophomonas maltophilia K279a]	356	1E-14	116 - 422 (28%)
683	NR gi 119897484 ref YP_932697.1 4-hydroxyphenylpyruvate dioxygenase [Azoarcus sp. BH72] probable 4-hydroxyphenylpyruvate dioxygenase [Azoarcus sp. BH72]	373	2E-14	125 - 422 (28%)
684	NR gi 222081772 ref YP_002541137.1 4-hydroxyphenylpyruvate dioxygenase [Agrobacterium radiobacter K84] 4-hydroxyphenylpyruvate dioxygenase [Agrobacterium radiobacter K84]	333	2E-14	122 - 422 (31%)
685	NR gi 84500900 ref ZP_00999135.1 4-hydroxyphenylpyruvate dioxygenase [Oceanicola batsensis HTCC2597] 4-hydroxyphenylpyruvate dioxygenase [Oceanicola batsensis HTCC2597]	364	2E-14	122 - 422 (28%)
686	NR gi 222109752 ref YP_002552016.1 4-hydroxyphenylpyruvate dioxygenase [Acidovorax ebreus TPSY] 4-hydroxyphenylpyruvate dioxygenase [Acidovorax ebreus TPSY]	372	3E-14	119 - 422 (28%)
687	NR gi 121609096 ref YP_996903.1 4-hydroxyphenylpyruvate dioxygenase [Verminephrobacter eiseniae EF01-2] 4-hydroxyphenylpyruvate dioxygenase [Verminephrobacter eiseniae EF01-2]	377	3E-14	122 - 422 (27%)
688	NR gi 121592950 ref YP_984846.1 4-hydroxyphenylpyruvate dioxygenase [Acidovorax sp. JS42] 4-hydroxyphenylpyruvate dioxygenase [Acidovorax sp. JS42]	372	3E-14	119 - 422 (28%)
689	NR gi 47217705 emb CAG13336.1 unnamed protein product [Tetraodon nigroviridis]	418	3E-14	194 - 422 (28%)
690	NR gi 17549535 ref NP_522875.1 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein [Ralstonia solanacearum GMI1000] 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein [Ralstonia solanacearum GMI1000] probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein [Ralstonia solanacearum GMI1000] probable 4-hydroxyphenylpyruvate dioxygenase oxidoreductase protein [Ralstonia solanacearum GMI1000]	361	3E-14	121 - 422 (28%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
691	NR gil15966695 ref NP_387048.1 putative 4-hydroxyphenylpyruvate dioxygenase protein [Sinorhizobium meliloti 1021] Putative 4-hydroxyphenylpyruvate dioxygenase [Sinorhizobium meliloti 1021]	370	3E-14	122 - 422 (30%)
692	NR gil255319075 ref ZP_05360296.1 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter radioresistens SK82] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter radioresistens SH164] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter radioresistens SK82] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter radioresistens SH164]	352	3E-14	122 - 422 (28%)
693	NR gil170691178 ref ZP_02882344.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia graminis C4D1M] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia graminis C4D1M]	377	3E-14	122 - 417 (29%)
694	NR gil272538050 ref ZP_06228650.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1002] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1002]	375	6E-14	122 - 417 (29%)
695	NR gil254487017 ref ZP_05100222.1 4-hydroxyphenylpyruvate dioxygenase [Roseobacter sp. GAI101] 4-hydroxyphenylpyruvate dioxygenase [Roseobacter sp. GAI101]	364	8E-14	122 - 422 (27%)
696	NR gil194367511 ref YP_002030121.1 4-hydroxyphenylpyruvate dioxygenase [Stenotrophomonas maltophilia R551-3] 4-hydroxyphenylpyruvate dioxygenase [Stenotrophomonas maltophilia R551-3]	356	8E-14	116 - 422 (27%)
697	NR gil156367361 ref XP_001627386.1 predicted protein [Nematostella vectensis] predicted protein [Nematostella vectensis]	330	8E-14	194 - 421 (27%)
698	NR gil187921391 ref YP_001890423.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia phytotirmans PsJN] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia phytotirmans PsJN]	377	8E-14	122 - 422 (29%)
699	NR gil31324016 gb AAP47153.1 4-hydroxyphenylpyruvate dioxygenase [uncultured soil bacterium]	301	8E-14	122 - 373 (29%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
700	NR gi 221196424 ref ZP_03569471.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans CGD2M] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans CGD2] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans CGD2] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans CGD2M]	375	1E-13	122 - 420 (28%)
701	NR gi 187926478 ref YP_001892823.1 4-hydroxyphenylpyruvate dioxygenase [Ralstonia pickettii 12J] 4-hydroxyphenylpyruvate dioxygenase [Ralstonia pickettii 12D] 4-hydroxyphenylpyruvate dioxygenase [Ralstonia pickettii 12J] 4-hydroxyphenylpyruvate dioxygenase [Ralstonia pickettii 12D]	357	1E-13	122 - 417 (28%)
702	NR gi 221210050 ref ZP_03583031.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans CGD1] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans CGD1]	375	1E-13	122 - 420 (28%)
703	NR gi 209517810 ref ZP_03266645.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. H160] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. H160]	375	1E-13	122 - 417 (29%)
704	NR gi 189353046 ref YP_001948673.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans ATCC 17616] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans ATCC 17616]	351	1E-13	122 - 420 (28%)
705	NR gi 161520772 ref YP_001584199.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans ATCC 17616] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans ATCC 17616]	375	1E-13	122 - 420 (28%)
706	NR gi 186472720 ref YP_001860062.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia phymatum STM815] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia phymatum STM815]	375	1E-13	122 - 417 (29%)
707	NR gi 73538853 ref YP_299220.1 4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha JMP134] 4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha JMP134]	357	2E-13	122 - 417 (29%)
708	NR gi 207722366 ref YP_002252802.1 4-hydroxyphenylpyruvate dioxygenase protein [Ralstonia solanacearum MolK2] 4-hydroxyphenylpyruvate dioxygenase protein [Ralstonia solanacearum]	322	2E-13	121 - 422 (26%)
709	NR gi 158187231 gb ABW22850.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. NCIMB 10467]	377	2E-13	122 - 422 (30%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
710	NR gi 229077582 ref ZP_04210224.1 hypothetical protein bcere0023_2910 [Bacillus cereus Rock4-2] hypothetical protein bcere0023_2910 [Bacillus cereus Rock4-2]	92	4E-13	323 - 422 (47%)
711	NR gi 78062475 ref YP_372383.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. 383] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. 383]	375	4E-13	122 - 420 (29%)
712	NR gi 281351925 gb EFB27509.1 hypothetical protein PANDA_008125 [Ailuropoda melanoleuca]	371	5E-13	140 - 423 (26%)
713	NR gi 290991733 ref XP_002678489.1 4-hydroxyphenylpyruvate dioxygenase [Naegleria gruberi] 4-hydroxyphenylpyruvate dioxygenase [Naegleria gruberi]	486	6E-13	227 - 422 (26%)
714	NR gi 167584232 ref ZP_02376620.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ubonensis Bu]	351	6E-13	122 - 390 (30%)
715	NR gi 22122847 ref NP_666368.1 4-hydroxyphenylpyruvate dioxygenase-like [Mus musculus] RecName: Full=4-hydroxyphenylpyruvate dioxygenase-like protein; AltName: Full=Glyoxalase domain-containing protein 1 4-hydroxyphenylpyruvate dioxygenase-like [Mus musculus] unnamed protein product [Mus musculus] unnamed protein product [Mus musculus] unnamed protein product [Mus musculus] 4-hydroxyphenylpyruvate dioxygenase-like [Mus musculus] glyoxalase domain containing 1 [Mus musculus]	371	6E-13	84 - 423 (26%)
716	NR gi 134293607 ref YP_001117343.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia vietnamiensis G4] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia vietnamiensis G4]	375	6E-13	122 - 420 (29%)
717	NR gi 289637194 ref ZP_06469471.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1003] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1003]	373	8E-13	122 - 417 (29%)
718	NR gi 170698644 ref ZP_02889711.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria IOP40-10] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria IOP40-10]	375	8E-13	122 - 420 (29%)
719	NR gi 172063303 ref YP_001810954.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria MC40-6] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria MC40-6]	375	8E-13	122 - 420 (29%)
720	NR gi 150247134 ref NP_001092841.1 glyoxalase domain containing 1 [Bos taurus] HPDL protein [Bos taurus]	390	8E-13	84 - 423 (27%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
721	NR gi 115358556 ref YP_775694.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria AMMD] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria AMMD]	375	8E-13	122 - 420 (29%)
722	NR gi 171319677 ref ZP_02908769.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria MEX-5] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria MEX-5]	374	1E-12	122 - 420 (29%)
723	NR gi 109897450 ref YP_660705.1 4-hydroxyphenylpyruvate dioxygenase [Pseudoalteromonas atlantica T6c] 4-hydroxyphenylpyruvate dioxygenase [Pseudoalteromonas atlantica T6c]	358	1E-12	125 - 422 (29%)
724	NR gi 238024554 ref YP_002908786.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia glumae BGR1] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia glumae BGR1]	375	2E-12	122 - 422 (28%)
725	NR gi 220920171 ref YP_002495472.1 Xylose isomerase domain protein TIM barrel [Methylobacterium nodulans ORS 2060] Xylose isomerase domain protein TIM barrel [Methylobacterium nodulans ORS 2060]	627	2E-12	122 - 388 (27%)
726	NR gi 282888880 ref ZP_06297453.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1001] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1001]	373	2E-12	122 - 417 (28%)
727	NR gi 260553369 ref ZP_05825983.1 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter sp. RUH2624] 4-hydroxyphenylpyruvate dioxygenase [Acinetobacter sp. RUH2624]	220	2E-12	210 - 422 (33%)
728	NR gi 206563370 ref YP_002234133.1 putative dioxygenase [Burkholderia cenocepacia J2315] putative dioxygenase [Burkholderia cenocepacia J2315]	375	4E-12	122 - 420 (28%)
729	NR gi 172355342 ref NP_001116495.1 4-hydroxyphenylpyruvate dioxygenase-like [Xenopus (Silurana) tropicalis] hpdI protein [Xenopus (Silurana) tropicalis]	386	4E-12	67 - 432 (24%)
730	NR gi 254254040 ref ZP_04947357.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia dolosa AUO158] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia dolosa AUO158]	415	4E-12	122 - 420 (28%)
731	NR gi 254248402 ref ZP_04941722.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia PC184] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia PC184]	381	4E-12	122 - 420 (28%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
732	NR gi 170738311 ref YP_001779571.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia MC0-3] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia MC0-3]	375	4E-12	122 - 420 (28%)
733	NR gi 107026323 ref YP_623834.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia AU 1054] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia HI2424] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia AU 1054] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia HI2424]	375	4E-12	122 - 420 (28%)
734	NR gi 254497939 ref ZP_05110703.1 4-hydroxyphenylpyruvate dioxygenase [Legionella drancourtii LLAP12] 4-hydroxyphenylpyruvate dioxygenase [Legionella drancourtii LLAP12]	344	2E-11	122 - 375 (28%)
735	NR gi 167615983 ref ZP_02384618.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis Bt4] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis E264]	357	2E-11	122 - 417 (29%)
736	NR gi 167577860 ref ZP_02370734.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis TXDOH]	357	2E-11	122 - 417 (29%)
737	NR gi 83716682 ref YP_439418.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis E264] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis E264]	381	2E-11	122 - 417 (29%)
738	NR gi 241774181 ref ZP_04771517.1 4-hydroxyphenylpyruvate dioxygenase [Asticcacaulis excentricus CB 48] 4-hydroxyphenylpyruvate dioxygenase [Asticcacaulis excentricus CB 48]	353	5E-11	122 - 420 (29%)
739	NR gi 153011743 ref YP_001372957.1 4-hydroxyphenylpyruvate dioxygenase [Ochrobactrum anthropi ATCC 49188] 4-hydroxyphenylpyruvate dioxygenase [Ochrobactrum anthropi ATCC 49188]	633	5E-11	127 - 390 (26%)
740	NR gi 167624338 ref YP_001674632.1 4-hydroxyphenylpyruvate dioxygenase [Shewanella halifaxensis HAW-EB4] 4-hydroxyphenylpyruvate dioxygenase [Shewanella halifaxensis HAW-EB4]	173	8E-11	247 - 422 (31%)
741	NR gi 118591013 ref ZP_01548413.1 putative 4-hydroxyphenylpyruvate dioxygenase protein [Stappia aggregata IAM 12614] putative 4-hydroxyphenylpyruvate dioxygenase protein [Stappia aggregata IAM 12614]	630	2E-10	128 - 413 (24%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
742	NR gi 84683598 ref ZP_01011501.1 hypothetical protein RB2654_19533 [Rhodobacterales bacterium HTCC2654] hypothetical protein RB2654_19533 [Rhodobacterales bacterium HTCC2654]	627	2E-10	122 - 388 (27%)
743	NR gi 114769014 ref ZP_01446640.1 putative 4-hydroxyphenylpyruvate dioxygenase protein [alpha proteobacterium HTCC2255] putative 4-hydroxyphenylpyruvate dioxygenase protein [alpha proteobacterium HTCC2255]	580	4E-10	122 - 415 (24%)
744	NR gi 281211380 gb EFA85545.1 4-hydroxyphenylpyruvate dioxygenase-like protein [Polysphondylium pallidum PN500]	720	5E-10	129 - 426 (23%)
745	NR gi 239834584 ref ZP_04682912.1 4-hydroxyphenylpyruvate dioxygenase [Ochrobactrum intermedium LMG 3301] 4-hydroxyphenylpyruvate dioxygenase [Ochrobactrum intermedium LMG 3301]	657	5E-10	127 - 388 (27%)
746	NR gi 66822517 ref XP_644613.1 4-hydroxyphenylpyruvate dioxygenase-like protein [Dictyostelium discoideum AX4] 4-hydroxyphenylpyruvate dioxygenase-like protein [Dictyostelium discoideum AX4] RecName: Full=Uncharacterized 4-hydroxyphenylpyruvate dioxygenase-like protein 4-hydroxyphenylpyruvate dioxygenase-like protein [Dictyostelium discoideum AX4] 4-hydroxyphenylpyruvate dioxygenase-like protein [Dictyostelium discoideum AX4]	494	7E-10	254 - 431 (26%)
747	NR gi 221104961 ref XP_002161869.1 PREDICTED: similar to AGAP004802-PA, partial [Hydra magnipapillata]	115	9E-10	176 - 285 (37%)
748	NR gi 121707768 ref XP_001271935.1 hypothetical protein ACLA_049810 [Aspergillus clavatus NRRL 1] hypothetical protein ACLA_049810 [Aspergillus clavatus NRRL 1]	132	9E-10	311 - 422 (38%)
749	NR gi 31324018 gb AAP47154.1 4-hydroxyphenylpyruvate dioxygenase [uncultured soil bacterium]	308	1E-09	122 - 360 (28%)
750	NR gi 159186203 ref NP_356129.2 hypothetical protein Atu4529 [Agrobacterium tumefaciens str. C58] conserved hypothetical protein [Agrobacterium tumefaciens str. C58]	633	1E-09	73 - 413 (25%)
751	NR gi 83744141 gb ABC42332.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas chlororaphis]	636	1E-09	122 - 413 (29%)
752	NR gi 254511680 ref ZP_05123747.1 4-hydroxyphenylpyruvate dioxygenase [Rhodobacteraceae bacterium KLH11] 4-hydroxyphenylpyruvate dioxygenase [Rhodobacteraceae bacterium KLH11]	629	3E-09	129 - 388 (26%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
753	NR gi 18201639 gb AAL65390.1 4-hydroxyphenylpyruvate dioxygenase [Oryza sativa Japonica Group]	38	3E-09	402 - 439 (81%)
754	NR gi 262410278 gb ACY66660.1 hemolysin [Vibrio splendidus]	240	7E-09	122 - 316 (29%)
755	NR gi 147900566 ref NP_001085702.1 4-hydroxyphenylpyruvate dioxygenase-like [Xenopus laevis] MGC80543 protein [Xenopus laevis]	391	7E-09	135 - 432 (25%)
756	NR gi 17549619 ref NP_522959.1 hypothetical protein RS02058 [Ralstonia solanacearum GMI1000] probable 4-hydroxyphenylpyruvate dioxygenase-related protein [Ralstonia solanacearum GMI1000]	626	7E-09	121 - 390 (26%)
757	NR gi 255263825 ref ZP_05343167.1 4-hydroxyphenylpyruvate dioxygenase [Thalassiosira sp. R2A62] 4-hydroxyphenylpyruvate dioxygenase [Thalassiosira sp. R2A62]	579	0.00000001	121 - 390 (26%)
758	NR gi 116252593 ref YP_768431.1 putative glyoxalase/dioxygenase [Rhizobium leguminosarum bv. viciae 3841] putative glyoxalase/dioxygenase [Rhizobium leguminosarum bv. viciae 3841]	630	0.00000001	129 - 390 (25%)
759	NR gi 7705186 gb AAC60567.2 fusion protein T-cell stimulating antigen [Coccidioides immitis]	73	0.00000001	253 - 327 (41%)
760	NR gi 227818275 ref YP_002822246.1 putative 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium sp. NGR234] putative 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium sp. NGR234]	629	0.00000002	129 - 390 (25%)
761	NR gi 167839796 ref ZP_02466480.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis MSMB43]	349	0.00000002	122 - 420 (26%)
762	NR gi 126729601 ref ZP_01745414.1 hypothetical protein SSE37_03985 [Sagittula stellata E-37] hypothetical protein SSE37_03985 [Sagittula stellata E-37]	629	0.00000002	119 - 393 (26%)
763	NR gi 260767383 ref ZP_05876321.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio furnissii CIP 102972] 4-hydroxyphenylpyruvate dioxygenase [Vibrio furnissii CIP 102972]	613	0.00000003	122 - 389 (24%)
764	NR gi 218513460 ref ZP_03510300.1 probable 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium etli 8C-3]	145	0.00000004	282 - 422 (36%)
765	NR gi 260791777 ref XP_002590904.1 hypothetical protein BRAFLDRAFT_84450 [Branchiostoma floridae] hypothetical protein BRAFLDRAFT_84450 [Branchiostoma floridae]	145	0.00000006	208 - 285 (45%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
766	NR gi 196009153 ref XP_002114442.1 hypothetical protein TRIADDRAFT_58263 [Trichoplax adhaerens] hypothetical protein TRIADDRAFT_58263 [Trichoplax adhaerens]	388	0.00000006	132 - 423 (25%)
767	NR gi 237805506 ref ZP_04592210.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. oryzae str. 1_6]	137	0.00000008	283 - 422 (34%)
768	NR gi 85704035 ref ZP_01035138.1 hypothetical protein ROS217_13591 [Roseovarius sp. 217] hypothetical protein ROS217_13591 [Roseovarius sp. 217]	628	0.00000008	129 - 388 (25%)
769	NR gi 207725008 ref YP_002255405.1 4-hydroxyphenylpyruvate dioxygenase-related protein [Ralstonia solanacearum MolK2] 4-hydroxyphenylpyruvate dioxygenase-related protein [Ralstonia solanacearum]	626	0.00000001	121 - 390 (27%)
770	NR gi 170742864 ref YP_001771519.1 4-hydroxyphenylpyruvate dioxygenase [Methylobacterium sp. 4-46] 4-hydroxyphenylpyruvate dioxygenase [Methylobacterium sp. 4-46]	637	0.00000001	122 - 390 (24%)
771	NR gi 104781153 ref YP_607651.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas entomophila L48] putative 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas entomophila L48]	634	0.00000001	122 - 413 (28%)
772	NR gi 387590 gb AAA33047.1 T-cell reactive fusion protein [Coccidioides posadasii]	69	0.00000001	253 - 316 (42%)
773	NR gi 280493 pir A43602 T-cell-stimulating antigen - Coccidioides immitis (fragment) T-cell reactive fusion protein [Coccidioides posadasii]	66	0.00000001	253 - 316 (42%)
774	NR gi 83749409 ref ZP_00946403.1 3-dehydroshikimate dehydratase / 4-hydroxyphenylpyruvate dioxygenase [Ralstonia solanacearum UW551] 4-hydroxyphenylpyruvate dioxygenase-related protein [Ralstonia solanacearum IPO1609] 3-dehydroshikimate dehydratase / 4-hydroxyphenylpyruvate dioxygenase [Ralstonia solanacearum UW551] 4-hydroxyphenylpyruvate dioxygenase-related protein [Ralstonia solanacearum IPO1609]	626	0.00000001	121 - 390 (27%)
775	NR gi 84516831 ref ZP_01004189.1 hypothetical protein SKA53_06627 [Loktanella vestfoldensis SKA53] hypothetical protein SKA53_06627 [Loktanella vestfoldensis SKA53]	628	0.00000001	129 - 388 (25%)
776	NR gi 241666979 ref YP_002985063.1 4-hydroxyphenylpyruvate dioxygenase [Rhizobium leguminosarum bv. trifolii WSM1325] 4-hydroxyphenylpyruvate dioxygenase [Rhizobium leguminosarum bv. trifolii WSM1325]	631	0.00000002	119 - 390 (24%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
777	NR gi 148257361 ref YP_001241946.1 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium sp. BTAi1] 4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium sp. BTAi1]	623	0.0000002	198 - 388 (26%)
778	NR gi 291294995 ref YP_003506393.1 4-hydroxyphenylpyruvate dioxygenase [Meiothermus ruber DSM 1279] 4-hydroxyphenylpyruvate dioxygenase [Meiothermus ruber DSM 1279]	624	0.0000002	122 - 393 (25%)
779	NR gi 256071900 ref XP_002572276.1 4-hydroxyphenylpyruvate dioxygenase [Schistosoma mansoni] 4-hydroxyphenylpyruvate dioxygenase, putative [Schistosoma mansoni]	345	0.0000002	282 - 422 (27%)
780	NR gi 146342433 ref YP_001207481.1 putative 4-hydroxyphenylpyruvate dioxygenase containing a TIM-barrel fold (N-ter) [Bradyrhizobium sp. ORS278] putative 4-hydroxyphenylpyruvate dioxygenase containing a TIM-barrel fold (N-ter) [Bradyrhizobium sp. ORS278]	623	0.0000002	198 - 388 (27%)
781	NR gi 229592746 ref YP_002874865.1 hypothetical protein PFLU5367 [Pseudomonas fluorescens SBW25] conserved hypothetical protein [Pseudomonas fluorescens SBW25]	633	0.0000003	122 - 413 (28%)
782	NR gi 291618895 ref YP_003521637.1 VIIY [Pantoea ananatis LMG 20103] VIIY [Pantoea ananatis LMG 20103]	638	0.0000004	255 - 413 (30%)
783	NR gi 209546332 ref YP_002278222.1 4-hydroxyphenylpyruvate dioxygenase [Rhizobium leguminosarum bv. trifolii WSM2304] 4-hydroxyphenylpyruvate dioxygenase [Rhizobium leguminosarum bv. trifolii WSM2304]	631	0.0000004	119 - 390 (24%)
784	NR gi 27376164 ref NP_767693.1 putative 4-hydroxyphenylpyruvate dioxygenase protein [Bradyrhizobium japonicum USDA 110] bll1053 [Bradyrhizobium japonicum USDA 110]	623	0.0000005	122 - 388 (22%)
785	NR gi 186475846 ref YP_001857316.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia phymatum STM815] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia phymatum STM815]	628	0.0000007	105 - 413 (26%)
786	NR gi 70732690 ref YP_262453.1 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas fluorescens Pf-5] 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas fluorescens Pf-5]	636	0.0000007	122 - 413 (28%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
787	NR gi 77461126 ref YP_350633.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens Pf0-1] conserved hypothetical protein [Pseudomonas fluorescens Pf0-1]	633	0.0000007	124 - 413 (27%)
788	NR gi 73538860 ref YP_299227.1 4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha JMP134] 4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha JMP134]	632	0.0000009	208 - 390 (27%)
789	NR gi 152997910 ref YP_001342745.1 xylose isomerase domain-containing protein [Marinomonas sp. MWYL1] Xylose isomerase domain protein TIM barrel [Marinomonas sp. MWYL1]	617	0.000001	161 - 390 (26%)
790	NR gi 163796008 ref ZP_02189971.1 putative glyoxalase/dioxygenase [alpha proteobacterium BAL199] putative glyoxalase/dioxygenase [alpha proteobacterium BAL199]	630	0.000002	122 - 388 (26%)
791	NR gi 116255274 ref YP_771107.1 putative dioxygenase [Rhizobium leguminosarum bv. viciae 3841] putative dioxygenase [Rhizobium leguminosarum bv. viciae 3841]	631	0.000002	119 - 390 (24%)
792	NR gi 110633139 ref YP_673347.1 4-hydroxyphenylpyruvate dioxygenase [Mesorhizobium sp. BNC1] 4-hydroxyphenylpyruvate dioxygenase [Chelativorans sp. BNC1]	630	0.000002	129 - 413 (22%)
793	NR gi 289632178 ref ZP_06464469.1 xylose isomerase domain protein TIM barrel [Burkholderia sp. CCGE1003] xylose isomerase domain protein TIM barrel [Burkholderia sp. CCGE1003]	627	0.000003	122 - 413 (24%)
794	NR gi 226357596 ref YP_002787336.1 putative bifunctional protein : Xylose isomerase-like TIM barrel; 4-hydroxyphenylpyruvate dioxygenase [Deinococcus deserti VCD115] putative bifunctional protein : Xylose isomerase-like TIM barrel; 4-hydroxyphenylpyruvate dioxygenase [Deinococcus deserti VCD115]	618	0.000003	122 - 390 (25%)
795	NR gi 222082224 ref YP_002541589.1 4-hydroxyphenylpyruvate dioxygenase [Agrobacterium radiobacter K84] 4-hydroxyphenylpyruvate dioxygenase [Agrobacterium radiobacter K84]	629	0.000003	118 - 388 (23%)
796	NR gi 150376346 ref YP_001312942.1 xylose isomerase domain-containing protein [Sinorhizobium medicae WSM419] Xylose isomerase domain protein TIM barrel [Sinorhizobium medicae WSM419]	629	0.000003	129 - 388 (25%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
797	NR gi 282883628 ref ZP_06292217.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1001] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. CCGE1001]	627	0.000003	122 - 413 (25%)
798	NR gi 221113264 ref XP_002168852.1 PREDICTED: similar to predicted protein [Hydra magnipapillata]	552	0.000003	194 - 424 (22%)
799	NR gi 167034359 ref YP_001669590.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida GB-1] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida GB-1]	635	0.000003	210 - 413 (30%)
800	NR gi 198437899 ref XP_002119608.1 PREDICTED: similar to 4-hydroxyphenylpyruvate dioxygenase-like [Ciona intestinalis]	414	0.000004	194 - 422 (24%)
801	NR gi 209520129 ref ZP_03268903.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. H160] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. H160]	630	0.000006	122 - 413 (24%)
802	NR gi 272528128 ref ZP_06224270.1 xylose isomerase domain protein TIM barrel [Burkholderia sp. CCGE1002] xylose isomerase domain protein TIM barrel [Burkholderia sp. CCGE1002]	629	0.000008	122 - 413 (24%)
803	NR gi 92112426 ref YP_572354.1 4-hydroxyphenylpyruvate dioxygenase [Chromohalobacter salexigens DSM 3043] 4-hydroxyphenylpyruvate dioxygenase [Chromohalobacter salexigens DSM 3043]	615	0.000008	116 - 390 (24%)
804	NR gi 16265241 ref NP_438033.1 putative 4-hydroxyphenylpyruvate dioxygenase protein [Sinorhizobium meliloti 1021] putative 4-hydroxyphenylpyruvate dioxygenase protein [Sinorhizobium meliloti 1021]	629	0.000008	129 - 388 (25%)
805	NR gi 170696212 ref ZP_02887345.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia graminis C4D1M] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia graminis C4D1M]	627	0.00001	122 - 413 (24%)
806	NR gi 227820501 ref YP_002824472.1 putative 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium sp. NGR234] putative 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium sp. NGR234]	630	0.00002	127 - 390 (25%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
807	NR gi 187926483 ref YP_001892828.1 4-hydroxyphenylpyruvate dioxygenase [Ralstonia pickettii 12J] 4-hydroxyphenylpyruvate dioxygenase [Ralstonia pickettii 12D] 4-hydroxyphenylpyruvate dioxygenase [Ralstonia pickettii 12J] 4-hydroxyphenylpyruvate dioxygenase [Ralstonia pickettii 12D]	628	0.00002	121 - 390 (24%)
808	NR gi 26989274 ref NP_744699.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida KT2440] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida F1] 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas putida KT2440] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida F1]	635	0.00002	210 - 413 (30%)
809	NR gi 187919279 ref YP_001888310.1 Xylose isomerase domain protein TIM barrel [Burkholderia phytofirmans PsJN] Xylose isomerase domain protein TIM barrel [Burkholderia phytofirmans PsJN]	627	0.00002	122 - 413 (24%)
810	NR gi 90419886 ref ZP_01227795.1 4-hydroxyphenylpyruvate dioxygenase [Aurantimonas manganoxydans SI85-9A1] 4-hydroxyphenylpyruvate dioxygenase [Aurantimonas manganoxydans SI85-9A1]	628	0.00002	129 - 390 (22%)
811	NR gi 170737323 ref YP_001778583.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia MC0-3] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia MC0-3]	630	0.00003	122 - 413 (25%)
812	NR gi 152987263 ref YP_001345723.1 hypothetical protein PSPA7_0327 [Pseudomonas aeruginosa PA7] hypothetical protein PSPA7_0327 [Pseudomonas aeruginosa PA7]	634	0.00003	122 - 388 (28%)
813	NR gi 107025420 ref YP_622931.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia AU 1054] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia HI2424] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia AU 1054] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia cenocepacia HI2424]	630	0.00003	122 - 413 (25%)
814	NR gi 206564343 ref YP_002235106.1 putative amino acid dioxygenase [Burkholderia cenocepacia J2315] putative amino acid dioxygenase [Burkholderia cenocepacia J2315]	630	0.00004	122 - 413 (25%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
815	NR gi 29828318 ref NP_822952.1 sugar phosphate isomerase/epimerase [Streptomyces avermitilis MA-4680] putative sugar phosphate isomerase/epimerase [Streptomyces avermitilis MA-4680]	601	0.00004	70 - 388 (27%)
816	NR gi 222106497 ref YP_002547288.1 4-hydroxyphenylpyruvate dioxygenase [Agrobacterium vitis S4] 4-hydroxyphenylpyruvate dioxygenase [Agrobacterium vitis S4]	615	0.00005	127 - 413 (25%)
817	NR gi 146280596 ref YP_001170749.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas stutzeri A1501] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas stutzeri A1501]	641	0.00005	122 - 388 (25%)
818	NR gi 91779214 ref YP_554422.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia xenovorans LB400] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia xenovorans LB400]	627	0.00005	122 - 413 (23%)
819	NR gi 288961687 ref YP_003451997.1 4-hydroxyphenylpyruvate dioxygenase [Azospirillum sp. B510] 4-hydroxyphenylpyruvate dioxygenase [Azospirillum sp. B510]	645	0.00006	264 - 390 (31%)
820	NR gi 218680933 ref ZP_03528830.1 4-hydroxyphenylpyruvate dioxygenase [Rhizobium etli CIAT 894]	230	0.00006	205 - 390 (24%)
821	NR gi 167584809 ref ZP_02377197.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ubonensis Bu]	630	0.00006	122 - 413 (25%)
822	NR gi 86360259 ref YP_472148.1 putative 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium etli CFN 42] putative 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium etli CFN 42]	629	0.00006	127 - 390 (22%)
823	NR gi 170721406 ref YP_001749094.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida W619] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida W619]	635	0.0001	210 - 413 (30%)
824	NR gi 78061195 ref YP_371103.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. 383] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia sp. 383]	630	0.0001	122 - 413 (25%)
825	NR gi 239927688 ref ZP_04684641.1 sugar phosphate isomerase/epimerase [Streptomyces ghanaensis ATCC 14672] sugar phosphate isomerase/epimerase [Streptomyces ghanaensis ATCC 14672] sugar phosphate isomerase/epimerase [Streptomyces ghanaensis ATCC 14672]	595	0.0002	70 - 390 (26%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
826	NR gi 224824323 ref ZP_03697431.1 4-hydroxyphenylpyruvate dioxygenase [Lutiella nitroferum 2002] 4-hydroxyphenylpyruvate dioxygenase [Lutiella nitroferum 2002]	645	0.0002	189 - 390 (28%)
827	NR gi 153831985 ref ZP_01984652.1 4-hydroxyphenylpyruvate dioxygenase [Vibrio harveyi HY01] 4-hydroxyphenylpyruvate dioxygenase [Vibrio harveyi HY01]	607	0.0002	122 - 394 (20%)
828	NR gi 913553 gb AAB33021.1 p-hydroxyphenylpyruvate dioxygenase=melA product [Shewanella colwelliana, Peptide Partial, 88 aa, segment 2 of 3]	88	0.0002	281 - 373 (36%)
829	NR gi 256781601 ref ZP_05520064.1 sugar phosphate isomerase/epimerase [Streptomyces hygroscopicus ATCC 53653]	418	0.0002	91 - 390 (24%)
830	NR gi 221210184 ref ZP_03583164.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans CGD1] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans CGD1]	630	0.0002	122 - 413 (25%)
831	NR gi 47217704 emb CAG13335.1 unnamed protein product [Tetraodon nigroviridis]	199	0.0002	281 - 362 (36%)
832	NR gi 115359412 ref YP_776550.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria AMMD] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria AMMD]	630	0.0002	122 - 413 (25%)
833	NR gi 221200954 ref ZP_03573995.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans CGD2M] AP endonuclease, family 2 [Burkholderia multivorans CGD2] AP endonuclease, family 2 [Burkholderia multivorans CGD2] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans CGD2M]	630	0.0003	122 - 413 (25%)
834	NR gi 161519967 ref YP_001583394.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans ATCC 17616] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans ATCC 17616] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans ATCC 17616] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia multivorans ATCC 17616]	630	0.0003	122 - 413 (25%)
835	NR gi 170700051 ref ZP_02891074.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria IOP40-10] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria IOP40-10]	312	0.0004	122 - 413 (25%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
836	NR gij172064204 ref YP_001811855.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria MC40-6] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria MC40-6]	630	0.0004	122 - 413 (25%)
837	NR gij270261957 ref ZP_06190229.1 hypothetical protein SOD_b01640 [Serratia odorifera 4Rx13] hypothetical protein SOD_b01640 [Serratia odorifera 4Rx13]	624	0.0005	211 - 390 (27%)
838	NR gij256805837 ref ZP_05535461.1 sugar phosphate isomerase/epimerase [Streptomyces viridochromogenes DSM 40736]	598	0.0005	70 - 388 (25%)
839	NR gij158423078 ref YP_001524370.1 putative 4-hydroxyphenylpyruvate dioxygenase protein [Azorhizobium caulinodans ORS 571] putative 4-hydroxyphenylpyruvate dioxygenase protein [Azorhizobium caulinodans ORS 571]	639	0.0005	122 - 390 (25%)
840	NR gij107099231 ref ZP_01363149.1 hypothetical protein PaerPA_01000242 [Pseudomonas aeruginosa PACS2]	634	0.0005	122 - 388 (27%)
841	NR gij254237521 ref ZP_04930844.1 hypothetical protein PACG_03600 [Pseudomonas aeruginosa C3719] hypothetical protein PACG_03600 [Pseudomonas aeruginosa C3719]	634	0.0005	122 - 388 (27%)
842	NR gij238023846 ref YP_002908078.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia glumae BGR1] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia glumae BGR1]	630	0.0007	106 - 413 (25%)
843	NR gij116053955 ref YP_788393.1 hypothetical protein PA14_03000 [Pseudomonas aeruginosa UCBPP-PA14] putative 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa UCBPP-PA14]	634	0.0007	122 - 388 (27%)
844	NR gij254488914 ref ZP_05102119.1 4-hydroxyphenylpyruvate dioxygenase [Roseobacter sp. GAI101] 4-hydroxyphenylpyruvate dioxygenase [Roseobacter sp. GAI101]	628	0.001	129 - 390 (22%)
845	NR gij66045370 ref YP_235211.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. syringae B728a] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. syringae B728a]	635	0.001	210 - 413 (29%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
846	NR gi 19551667 ref NP_599669.1 sugar phosphate isomerase/epimerase [Corynebacterium glutamicum ATCC 13032] phosphate isomerase/epimerase [Corynebacterium glutamicum ATCC 13032] Sugar phosphate isomerases/epimerases [Corynebacterium glutamicum ATCC 13032] phosphate isomerase/epimerase [Corynebacterium glutamicum ATCC 13032]	618	0.001	297 - 428 (27%)
847	NR gi 290956102 ref YP_003487284.1 putative amino acid dioxygenase [Streptomyces scabiei 87.22] putative amino acid dioxygenase [Streptomyces scabiei 87.22]	637	0.001	292 - 388 (34%)
848	NR gi 218508960 ref ZP_03506838.1 putative 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium etli Brasil 5]	502	0.001	127 - 390 (21%)
849	NR gi 171315708 ref ZP_02904941.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria MEX-5] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia ambifaria MEX-5]	630	0.001	122 - 413 (24%)
850	NR gi 167838858 ref ZP_02465635.1 4-hydroxyphenylpyruvate dioxygenase, putative [Burkholderia thailandensis MSMB43]	362	0.001	122 - 413 (26%)
851	NR gi 237801047 ref ZP_04589508.1 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas syringae pv. oryzae str. 1_6]	635	0.002	210 - 413 (29%)
852.1	NR gi 224001134 ref XP_002290239.1 predicted protein [Thalassiosira pseudonana CCMP1335] predicted protein [Thalassiosira pseudonana CCMP1335]	699	0.002	333 - 433 (35%)
852.2	NR gi 224001134 ref XP_002290239.1 predicted protein [Thalassiosira pseudonana CCMP1335] predicted protein [Thalassiosira pseudonana CCMP1335]	699	0.002	180 - 332 (28%)
853	NR gi 213970527 ref ZP_03398654.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. tomato T1] 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. tomato T1]	635	0.002	210 - 413 (29%)
854	NR gi 91790328 ref YP_551280.1 4-hydroxyphenylpyruvate dioxygenase [Polaromonas sp. JS666] 4-hydroxyphenylpyruvate dioxygenase [Polaromonas sp. JS666]	638	0.002	122 - 390 (23%)
855	NR gi 289675114 ref ZP_06496004.1 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringae pv. syringae FF5]	635	0.002	210 - 413 (29%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
856	NR gi 289623668 ref ZP_06456622.1 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas syringae pv. aesculi str. NCPPB3681] 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas syringae pv. aesculi str. 2250]	635	0.002	210 - 413 (29%)
857.1	NR gi 219115405 ref XP_002178498.1 predicted protein [Phaeodactylum tricornutum CCAP 1055/1] predicted protein [Phaeodactylum tricornutum CCAP 1055/1]	730	0.002	344 - 434 (36%)
857.2	NR gi 219115405 ref XP_002178498.1 predicted protein [Phaeodactylum tricornutum CCAP 1055/1] predicted protein [Phaeodactylum tricornutum CCAP 1055/1]	730	0.01	180 - 332 (28%)
858	NR gi 198422279 ref XP_002120769.1 PREDICTED: similar to 4-hydroxyphenylpyruvate dioxygenase-like [Ciona intestinalis]	414	0.002	280 - 422 (23%)
859	NR gi 28869544 ref NP_792163.1 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas syringae pv. tomato str. DC3000] 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas syringae pv. tomato str. DC3000]	635	0.002	210 - 413 (29%)
860	NR gi 71737084 ref YP_274324.1 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas syringae pv. phaseolicola 1448A] 4-hydroxyphenylpyruvate dioxygenase, putative [Pseudomonas syringae pv. phaseolicola 1448A]	635	0.002	210 - 413 (29%)
861	NR gi 254243341 ref ZP_04936663.1 hypothetical protein PA2G_04153 [Pseudomonas aeruginosa 2192] hypothetical protein PA2G_04153 [Pseudomonas aeruginosa 2192]	634	0.002	122 - 388 (27%)
862	NR gi 195124401 ref XP_002006681.1 G118454 [Drosophila mojavensis] G118454 [Drosophila mojavensis]	1008	0.003	5 - 141 (31%)
863	NR gi 217423154 ref ZP_03454656.1 AP endonuclease, family 2/putative 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 576] AP endonuclease, family 2/putative 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 576]	683	0.004	122 - 413 (25%)
864	NR gi 167913696 ref ZP_02500787.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 112]	687	0.004	122 - 413 (25%)
865	NR gi 167905401 ref ZP_02492606.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei NCTC 13177]	687	0.004	122 - 413 (25%)
866	NR gi 167741391 ref ZP_02414165.1 putative amino acid dioxygenase [Burkholderia pseudomallei 14]	388	0.004	122 - 413 (25%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
867	NR gil167722407 ref ZP_02405643.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei DM98]	687	0.004	122 - 413 (25%)
868	NR gil167616949 ref ZP_02385580.1 4-hydroxyphenylpyruvate dioxygenase, putative [Burkholderia thailandensis Bt4]	679	0.004	122 - 413 (25%)
869	NR gil167578857 ref ZP_02371731.1 4-hydroxyphenylpyruvate dioxygenase, putative [Burkholderia thailandensis TXDOH]	693	0.004	122 - 413 (25%)
870	NR gil134284226 ref ZP_01770918.1 AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 305] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 305]	684	0.004	122 - 413 (25%)
871	NR gil254254621 ref ZP_04947938.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia dolosa AUO158] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia dolosa AUO158]	658	0.004	122 - 413 (24%)
872	NR gil254179145 ref ZP_04885797.1 AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei ATCC 10399] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei ATCC 10399]	684	0.004	122 - 413 (25%)
873	NR gil254299397 ref ZP_04966846.1 AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 406e] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 406e]	684	0.004	122 - 413 (25%)
874.1	NR gil5001993 gb AAD37247.1 AF134321_1 chimeric AFGP/trypsinogen-like serine protease precursor [Dissostichus mawsoni]	675	0.004	2 - 169 (30%)
874.2	NR gil5001993 gb AAD37247.1 AF134321_1 chimeric AFGP/trypsinogen-like serine protease precursor [Dissostichus mawsoni]	675	0.067	2 - 168 (27%)
874.3	NR gil5001993 gb AAD37247.1 AF134321_1 chimeric AFGP/trypsinogen-like serine protease precursor [Dissostichus mawsoni]	675	0.11	8 - 162 (30%)
875	NR gil83718326 ref YP_440247.1 4-hydroxyphenylpyruvate dioxygenase, putative [Burkholderia thailandensis E264] 4-hydroxyphenylpyruvate dioxygenase, putative [Burkholderia thailandensis E264] 4-hydroxyphenylpyruvate dioxygenase, putative [Burkholderia thailandensis E264]	687	0.004	122 - 413 (25%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
876	NR gij126442980 ref YP_001061582.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 668] putative 4-hydroxyphenylpyruvate dioxygenase HppD [Burkholderia pseudomallei 668]	687	0.004	122 - 413 (25%)
877	NR gij76818027 ref YP_337051.1 putative amino acid dioxygenase [Burkholderia pseudomallei 1710b] putative amino acid dioxygenase [Burkholderia pseudomallei 7894] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei Pasteur 52237] putative 4-hydroxyphenylpyruvate dioxygenase HppD [Burkholderia pseudomallei 1710a] putative amino acid dioxygenase [Burkholderia pseudomallei 1710b] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei Pasteur 52237] putative 4-hydroxyphenylpyruvate dioxygenase HppD [Burkholderia pseudomallei 1710a]	684	0.004	122 - 413 (25%)
878	NR gij254182671 ref ZP_04889264.1 AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 1655] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 1655]	684	0.004	122 - 413 (25%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
879	NR gi 53717571 ref YP_105549.1 putative 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei ATCC 23344] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei GB8 horse 4] putative 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei SAVP1] putative 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei NCTC 10229] AP endonuclease [Burkholderia mallei NCTC 10247] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei PRL-20] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei FMH] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei JHU] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei 2002721280] putative 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei ATCC 23344] putative 4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei SAVP1] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei NCTC 10247] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei FMH] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei JHU] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei 2002721280] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei GB8 horse 4] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei PRL-20] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia mallei NCTC 10229]	684	0.004	122 - 413 (25%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
880	NR gi 53721374 ref YP_110359.1 amino acid dioxygenase [Burkholderia pseudomallei K96243] AP endonuclease [Burkholderia pseudomallei 1106a] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 91] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 9] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei B7210] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei BCC215] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei Pakistan 9] putative 4-hydroxyphenylpyruvate dioxygenase HppD [Burkholderia pseudomallei 1106b] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei S13] putative amino acid dioxygenase [Burkholderia pseudomallei K96243] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei 1106a] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei S13] AP endonuclease, family 2/4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei Pakistan 9] putative 4-hydroxyphenylpyruvate dioxygenase HppD [Burkholderia pseudomallei 1106b]	684	0.004	122 - 413 (25%)
881	NR gi 239816294 ref YP_002945204.1 4-hydroxyphenylpyruvate dioxygenase [Variovorax paradoxus S110] 4-hydroxyphenylpyruvate dioxygenase [Variovorax paradoxus S110]	630	0.005	122 - 388 (25%)
882.1	NR gi 90102218 gb ABD85297.1 antifreeze glycoprotein [Boreogadus saida]	683	0.005	2 - 158 (30%)
882.2	NR gi 90102218 gb ABD85297.1 antifreeze glycoprotein [Boreogadus saida]	683	0.006	2 - 162 (31%)
882.3	NR gi 90102218 gb ABD85297.1 antifreeze glycoprotein [Boreogadus saida]	683	0.018	4 - 162 (32%)
882.4	NR gi 90102218 gb ABD85297.1 antifreeze glycoprotein [Boreogadus saida]	683	0.051	2 - 162 (29%)
882.5	NR gi 90102218 gb ABD85297.1 antifreeze glycoprotein [Boreogadus saida]	683	0.087	4 - 160 (30%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
883	NR gi 15595439 ref NP_248933.1 hypothetical protein PA0242 [Pseudomonas aeruginosa PAO1] putative 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa LESB58] hypothetical protein PA0242 [Pseudomonas aeruginosa PAO1] putative 4-hydroxyphenylpyruvate dioxygenase [Pseudomonas aeruginosa LESB58]	634	0.005	210 - 388 (31%)
884	NR gi 256670620 ref ZP_05481573.1 sugar phosphate isomerase/epimerase [Streptomyces sp. AA4]	374	0.008	294 - 390 (36%)
885	NR gi 218674917 ref ZP_03524586.1 putative dioxygenase [Rhizobium etli GR56]	637	0.008	127 - 390 (21%)
886	NR gi 145294541 ref YP_001137362.1 hypothetical protein cgR_0493 [Corynebacterium glutamicum R] hypothetical protein [Corynebacterium glutamicum R]	618	0.008	297 - 428 (26%)
887	NR gi 134292269 ref YP_001116005.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia vietnamiensis G4] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia vietnamiensis G4]	630	0.008	122 - 413 (23%)
888	NR gi 237510384 ref ZP_04523099.1 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei MSHR346] 4-hydroxyphenylpyruvate dioxygenase [Burkholderia pseudomallei MSHR346]	687	0.01	122 - 413 (25%)
889	NR gi 60692862 gb AAX30651.1 SJCHGC06518 protein [Schistosoma japonicum]	98	0.01	323 - 422 (32%)
890	NR gi 242796210 ref XP_002482751.1 4-hydroxyphenylpyruvate dioxygenase, putative [Talaromyces stipitatus ATCC 10500] 4-hydroxyphenylpyruvate dioxygenase, putative [Talaromyces stipitatus ATCC 10500]	116	0.013	346 - 388 (46%)
891	NR gi 195129219 ref XP_002009056.1 G11474 [Drosophila mojavensis] G11474 [Drosophila mojavensis]	730	0.013	8 - 132 (31%)
892	NR gi 88319761 emb CAH10097.1 putative 4-hydroxyphenyl pyruvate dioxygenase [Streptomyces sp. SCC 2136]	626	0.013	293 - 388 (32%)
893.1	NR gi 8488962 sp P24856.2 ANP_NOTCO RecName: Full=Ice-structuring glycoprotein; Short=ISGP; AltName: Full=Antifreeze glycopeptide polyprotein; Short=AFGP polyprotein; Contains: RecName: Full=AFGP7; AltName: Full=AFGP 7; Contains: RecName: Full=AFGP8; AltName: Full=AFGP 8; Contains: RecName: Full=AFGP8-like; Flags: Precursor antifreeze glycoprotein precursor [Notothernia coriiceps]	790	0.013	4 - 158 (31%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
893.2	NR gi 8488962 sp P24856.2 ANP_NOTCO RecName: Full=Ice-structuring glycoprotein; Short=ISGP; AltName: Full=Antifreeze glycopeptide polyprotein; Short=AFGP polyprotein; Contains: RecName: Full=AFGP7; AltName: Full=AFGP 7; Contains: RecName: Full=AFGP8; AltName: Full=AFGP 8; Contains: RecName: Full=AFGP8-like; Flags: Precursor antifreeze glycoprotein precursor [Notothenia coriiceps]	790	0.039	4 - 158 (32%)
893.3	NR gi 8488962 sp P24856.2 ANP_NOTCO RecName: Full=Ice-structuring glycoprotein; Short=ISGP; AltName: Full=Antifreeze glycopeptide polyprotein; Short=AFGP polyprotein; Contains: RecName: Full=AFGP7; AltName: Full=AFGP 7; Contains: RecName: Full=AFGP8; AltName: Full=AFGP 8; Contains: RecName: Full=AFGP8-like; Flags: Precursor antifreeze glycoprotein precursor [Notothenia coriiceps]	790	0.051	4 - 160 (31%)
893.4	NR gi 8488962 sp P24856.2 ANP_NOTCO RecName: Full=Ice-structuring glycoprotein; Short=ISGP; AltName: Full=Antifreeze glycopeptide polyprotein; Short=AFGP polyprotein; Contains: RecName: Full=AFGP7; AltName: Full=AFGP 7; Contains: RecName: Full=AFGP8; AltName: Full=AFGP 8; Contains: RecName: Full=AFGP8-like; Flags: Precursor antifreeze glycoprotein precursor [Notothenia coriiceps]	790	0.051	4 - 158 (30%)
894.1	NR gi 2078483 gb AAC60129.1 antifreeze glycopeptide AFGP polyprotein precursor [Boreogadus saida]	507	0.018	4 - 162 (32%)
894.2	NR gi 2078483 gb AAC60129.1 antifreeze glycopeptide AFGP polyprotein precursor [Boreogadus saida]	507	0.11	2 - 160 (28%)
895	NR gi 159482392 ref XP_001699255.1 hypothetical protein CHLREDRAFT_177931 [Chlamydomonas reinhardtii] predicted protein [Chlamydomonas reinhardtii]	969	0.023	51 - 187 (29%)
896	NR gi 76262383 gb ABA41360.1 antifreeze glycoprotein [Harpagifer antarcticus]	156	0.023	2 - 144 (32%)
897.1	NR gi 2102688 gb AAB57731.1 AFGP polyprotein precursor [Dissostichus mawsoni]	722	0.023	4 - 160 (32%)
897.2	NR gi 2102688 gb AAB57731.1 AFGP polyprotein precursor [Dissostichus mawsoni]	722	0.11	4 - 158 (32%)
898	NR gi 260427452 ref ZP_05781431.1 AP endonuclease, family 2 [Citricella sp. SE45] AP endonuclease, family 2 [Citricella sp. SE45]	629	0.03	130 - 388 (22%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
899	NR gi 254406875 ref ZP_05021780.1 sugar phosphate isomerase/epimerase [Streptomyces svaceus ATCC 29083] sugar phosphate isomerase/epimerase [Streptomyces svaceus ATCC 29083]	592	0.03	70 - 413 (25%)
900	NR gi 167574945 ref ZP_02367819.1 4-hydroxyphenylpyruvate dioxygenase, putative [Burkholderia oklahomensis C6786]	654	0.03	122 - 413 (24%)
901	NR gi 289634694 ref ZP_06466981.1 membrane protein-like protein [Burkholderia sp. CCGE1003] membrane protein-like protein [Burkholderia sp. CCGE1003]	988	0.039	66 - 172 (36%)
902	NR gi 167567140 ref ZP_02360056.1 4-hydroxyphenylpyruvate dioxygenase, putative [Burkholderia oklahomensis EO147]	654	0.039	122 - 413 (24%)
903	NR gi 226945854 ref YP_002800927.1 4-hydroxyphenylpyruvate dioxygenase [Azotobacter vinelandii DJ] 4-hydroxyphenylpyruvate dioxygenase [Azotobacter vinelandii DJ]	632	0.039	122 - 388 (24%)
904	NR gi 291302545 ref YP_003513823.1 Xylose isomerase domain-containing protein TIM barrel [Stackebrandtia nassauensis DSM 44728] Xylose isomerase domain protein TIM barrel [Stackebrandtia nassauensis DSM 44728]	604	0.051	178 - 390 (25%)
905	NR gi 254514291 ref ZP_05126352.1 methylmalonyl-CoA epimerase [gamma proteobacterium NOR5-3] methylmalonyl-CoA epimerase [gamma proteobacterium NOR5-3]	136	0.051	211 - 330 (31%)
906.1	NR gi 226455108 gb EEH52412.1 predicted protein [Micromonas pusilla CCMP1545]	1593	0.067	6 - 155 (31%)
906.2	NR gi 226455108 gb EEH52412.1 predicted protein [Micromonas pusilla CCMP1545]	1593	0.11	6 - 152 (28%)
906.3	NR gi 226455108 gb EEH52412.1 predicted protein [Micromonas pusilla CCMP1545]	1593	0.11	8 - 176 (27%)
907	NR gi 195419564 ref XP_002060706.1 GK16094 [Drosophila willistoni] GK16094 [Drosophila willistoni]	316	0.067	1 - 161 (31%)
908	NR gi 194751001 ref XP_001957815.1 GF10597 [Drosophila ananassae] GF10597 [Drosophila ananassae]	823	0.067	6 - 146 (29%)
909	NR gi 159468536 ref XP_001692430.1 predicted protein [Chlamydomonas reinhardtii] predicted protein [Chlamydomonas reinhardtii]	1063	0.067	2 - 169 (28%)
910	NR gi 229205039 ref ZP_04331499.1 methylmalonyl-CoA epimerase [Nocardiopsis dassonvillei subsp. dassonvillei DSM 43111] methylmalonyl-CoA epimerase [Nocardiopsis dassonvillei subsp. dassonvillei DSM 43111]	192	0.087	187 - 309 (30%)

Appendix A. All sequences showing significant similarity to AvHPPD-03 amino acid sequence in BLASTP analysis of the NCBI Entrez® Protein Database
(Continued)

Alignment Rank	Alignment name	Amino acid length	E-value	Query range and identity
911	NR gi 195457618 ref XP_002075642.1 GK18624 [Drosophila willistoni] GK18624 [Drosophila willistoni]	720	0.087	1 - 162 (28%)
912	NR gi 90102220 gb ABD85298.1 antifreeze glycoprotein [Boreogadus saida]	257	0.087	2 - 161 (31%)
913	NR gi 126462461 ref YP_001043575.1 flagellar hook-length control protein [Rhodobacter sphaeroides ATCC 17029] flagellar hook-length control protein [Rhodobacter sphaeroides ATCC 17029]	703	0.087	2 - 163 (29%)
914	NR gi 94971847 ref YP_593887.1 4-hydroxyphenylpyruvate dioxygenase [Deinococcus geothermalis DSM 11300] Hemolysin-like protein, 4-hydroxyphenylpyruvate dioxygenase related [Deinococcus geothermalis DSM 11300]	149	0.087	255 - 403 (27%)
915	NR gi 195032808 ref XP_001988565.1 GH10507 [Drosophila grimshawi] GH10507 [Drosophila grimshawi]	1112	0.11	3 - 162 (30%)
916	NR gi 170782653 ref YP_001710987.1 2-methylcitrate dehydratase [Clavibacter michiganensis subsp. sepedonicus] 2-methylcitrate dehydratase [Clavibacter michiganensis subsp. sepedonicus]	516	0.11	107 - 319 (23%)

Appendix B. Sources of the 773 HPPD or similar proteins including glyoxylases and members of the dioxygenase superfamily showing significant sequence similarity to the AvHPPD-03 amino acid sequence in BLASTP analysis

Organism	No. of proteins	E-value
<i>Abutilon theophrasti</i>	1	1×10^{-118}
<i>Acaryochloris marina</i>	1	3×10^{-18}
<i>Acidobacterium capsulatum</i>	1	4×10^{-52}
<i>Acidovorax avenae</i>	2	7×10^{-18} and 9×10^{-18}
<i>Acidovorax delafieldii</i>	1	6×10^{-19}
<i>Acidovorax ebreus</i>	1	3×10^{-14}
<i>Acidovorax</i> sp.	1	3×10^{-14}
<i>Acinetobacter baumannii</i>	3	3×10^{-16} - 7×10^{-15}
<i>Acinetobacter calcoaceticus</i>	1	3×10^{-16}
<i>Acinetobacter johnsonii</i>	1	7×10^{-17}
<i>Acinetobacter junii</i>	1	5×10^{-18}
<i>Acinetobacter radioresistens</i>	1	3×10^{-14}
<i>Acinetobacter</i> sp.	1	2×10^{-12}
<i>Actinoplanes teichomyceticus</i>	2	1×10^{-32} and 1×10^{-32}
<i>Actinosynnema mirum</i>	2	2×10^{-46} and 1×10^{-25}
<i>Aedes aegypti</i>	2	6×10^{-43} and 2×10^{-42}
<i>Aeromonas hydrophila</i>	1	6×10^{-24}
<i>Aeromonas salmonicida</i>	1	1×10^{-23}
<i>Agrobacterium radiobacter</i>	2	2×10^{-14} and 3×10^{-5}
<i>Agrobacterium vitis</i>	1	0.00005
<i>Ailuropoda melanoleuca</i>	1	1×10^{-46}
<i>Ajellomyces capsulatus</i>	4	7×10^{-44} - 5×10^{-37}
<i>Ajellomyces dermatitidis</i>	4	1×10^{-40} - 1×10^{-37}
<i>Algoriphagus</i> sp.	1	9×10^{-49}
<i>alpha proteobacterium</i>	3	9×10^{-26} - 2×10^{-6}
<i>Alteromonadales bacterium</i>	1	2×10^{-19}
<i>Alteromonas macleodii</i>	2	4×10^{-17} and 6×10^{-17}
<i>Amycolatopsis balhimycina</i>	1	4×10^{-21}
<i>Amycolatopsis orientalis</i>	1	4×10^{-24}
<i>Anabaena variabilis</i>	1	4×10^{-20}
<i>Anaeromyxobacter dehalogenans</i>	2	4×10^{-23} and 1×10^{-21}
<i>Anaeromyxobacter</i> sp.	2	1×10^{-23} and 3×10^{-22}
<i>Anoplopoma fimbria</i>	1	2×10^{-46}
<i>Arabidopsis thaliana</i>	6	1×10^{-148} - 1×10^{-119}
<i>Arthrospira maxima</i>	1	2×10^{-19}
<i>Arthrospira platensis</i>	2	5×10^{-20} and 9×10^{-20}
<i>Aspergillus clavatus</i>	1	5×10^{-40}
<i>Aspergillus flavus</i>	1	5×10^{-42}
<i>Aspergillus fumigatus</i>	2	2×10^{-39} and 3×10^{-39}

Appendix B. Sources of the HPPD or similar proteins including glyoxylases and members of the dioxygenase superfamily showing significant sequence similarity to the AvHPPD (Continued)

Organism	No. of proteins	E-value
<i>Aspergillus nidulans</i>	2	9×10^{-39} and 2×10^{-24}
<i>Aspergillus terreus</i>	1	3×10^{-41}
<i>Asticcacaulis excentricus</i>	2	2×10^{-20} and 5×10^{-10}
<i>Aurantimonas manganoxydans</i>	1	0.00002
<i>Azoarcus</i> sp.	1	2×10^{-14} and 3×10^{-5}
<i>Azorhizobium caulinodans</i>	1	0.0005
<i>Azospirillum</i> sp.	2	3×10^{-24} and 0.00006
<i>Azotobacter vinelandii</i>	3	2×10^{-22} - 0.039
<i>Bacillus cereus</i>	13	3×10^{-52} - 6×10^{-49}
<i>Bacillus coahuilensis</i>	1	2×10^{-53}
<i>Bacillus mycoides</i>	2	1×10^{-49} and 4×10^{-46}
<i>Bacillus pseudomycoides</i>	1	1×10^{-50}
<i>Bacillus</i> sp.	2	5×10^{-52} and 6×10^{-49}
<i>Bacillus thuringiensis</i>	10	1×10^{-50} - 7×10^{-50}
<i>Bacillus weihenstephanensis</i>	1	2×10^{-49}
<i>Bdellovibrio bacteriovorus</i>	1	3×10^{-25}
<i>Blepharisma japonicum</i>	1	7×10^{-52}
<i>Bordetella petrii</i>	1	1×10^{-18}
<i>Bos taurus</i>	2	2×10^{-44} and 8×10^{-13}
<i>Bradyrhizobium japonicum</i>	2	9×10^{-18} and 5×10^{-7}
<i>Bradyrhizobium</i> sp.	4	2×10^{-18} - 2×10^{-7}
<i>Branchiostoma floridae</i>	1	2×10^{-44}
<i>Brassica rapa</i>	1	1×10^{-145}
<i>Brevibacillus brevis</i>	1	3×10^{-54}
<i>Brevundimonas</i> sp.	1	1E-15
<i>Brevundimonas subvibrioides</i>	1	2×10^{-18}
<i>Brugia malayi</i>	1	1×10^{-26}
<i>Burkholderia ambifaria</i>	11	1×10^{-17} - 0.001
<i>Burkholderia cenocepacia</i>	9	2×10^{-17} - 0.00004
<i>Burkholderia dolosa</i>	3	3×10^{-18} - 0.004
<i>Burkholderia glumae</i>	3	4×10^{-17} - 0.0007
<i>Burkholderia graminis</i>	3	1×10^{-19} - 0.00001
<i>Burkholderia mallei</i>	2	0.004 and 0.004
<i>Burkholderia multivorans</i>	9	4×10^{-18} - 0.0003
<i>Burkholderia oklahomensis</i>	3	7×10^{-17} - 0.039
<i>Burkholderia phymatum</i>	3	1×10^{-17} - 7×10^{-7}
<i>Burkholderia phytofirmans</i>	2	4×10^{-19} and 8×10^{-13}

Appendix B. Sources of the HPPD or similar proteins including glyoxylases and members of the dioxygenase superfamily showing significant sequence similarity to the AvHPPD (Continued)

Organism	No. of proteins	E-value
<i>Burkholderia pseudomallei</i>	13	1×10^{-17} - 0.01
<i>Burkholderia</i> sp.	17	2×10^{-20} - 0.0001
<i>Burkholderia thailandensis</i>	10	6×10^{-17} - 0.004
<i>Burkholderia ubonensis</i>	3	2×10^{-18} - 0.00006
<i>Burkholderia vietnamiensis</i>	3	2×10^{-18} - 0.008
<i>Burkholderia xenovorans</i>	3	1×10^{-19} - 0.00005
<i>Caenorhabditis briggsae</i>	1	4×10^{-39}
<i>Caenorhabditis elegans</i>	1	1×10^{-37}
<i>Candida albicans</i>	1	6×10^{-24}
<i>Candida dubliniensis</i>	1	1×10^{-23}
<i>Candidatus Koribacter</i>	1	2×10^{-55}
<i>Canis familiaris</i>	1	1×10^{-45}
<i>Catenulispora acidiphila</i>	2	5×10^{-45} and 1×10^{-25}
<i>Caulobacter crescentus</i>	1	1×10^{-16}
<i>Caulobacter segnis</i>	1	3×10^{-17}
<i>Caulobacter</i> sp.	1	3×10^{-16}
<i>Chitinophaga pinensis</i>	1	1×10^{-49}
<i>Chlamydomonas reinhardtii</i>	3	1×10^{-118} - 1×10^{-102}
<i>Chloroflexus aggregans</i>	1	2×10^{-52}
<i>Chloroflexus aurantiacus</i>	1	5×10^{-53}
<i>Chromobacterium violaceum</i>	1	1×10^{-23}
<i>Chromohalobacter salexigens</i>	1	8×10^{-6}
<i>Chryseobacterium gleum</i>	1	1×10^{-45}
<i>Ciona intestinalis</i>	4	8×10^{-40} - 0.002
<i>Citreicella</i> sp.	1	2×10^{-18}
<i>Coccidioides immitis</i>	2	2×10^{-40} and 5×10^{-39}
<i>Coccidioides posadasii</i>	4	2×10^{-40} - 1×10^{-15}
<i>Colwellia psychrerythraea</i>	1	9×10^{-20}
<i>Comamonas testosteroni</i>	3	1×10^{-17} - 7×10^{-17}
<i>Congregibacter litoralis</i>	1	2×10^{-16}
<i>Coptis japonica</i>	1	1×10^{-148}
<i>Croceibacter atlanticus</i>	1	5×10^{-45}
<i>Crocospaera watsonii</i>	1	9×10^{-18}
<i>Culex quinquefasciatus</i>	1	4×10^{-42}
<i>Cupriavidus metallidurans</i>	1	7×10^{-17}
<i>Cupriavidus taiwanensis</i>	1	1×10^{-17}
<i>Curvibacter putative</i>	1	4×10^{-18}
<i>Cyanotheca</i> sp.	7	2×10^{-47} - 2×10^{-19}
<i>Cylindrospermopsis raciborskii</i>	1	6×10^{-22}

Appendix B. Sources of the HPPD or similar proteins including glyoxylases and members of the dioxygenase superfamily showing significant sequence similarity to the AvHPPD (Continued)

Organism	No. of proteins	E-value
<i>Danio rerio</i>	4	3×10^{-49} - 5×10^{-14}
<i>Daucus carota</i>	1	1×10^{-154}
<i>Deinococcus deserti</i>	1	0.000003
<i>Delftia acidovorans</i>	1	2×10^{-18}
<i>Dickeya dadantii</i>	2	6×10^{-22} and 4×10^{-19}
<i>Dickeya zeae</i>	1	2×10^{-18}
<i>Dictyostelium discoideum</i>	3	1×10^{-39} - 7×10^{-10}
<i>Dokdonia donghaensis</i>	1	1×10^{-45}
<i>Drosophila ananassae</i>	1	6×10^{-45}
<i>Drosophila erecta</i>	1	2×10^{-44}
<i>Drosophila grimshawi</i>	1	5×10^{-45}
<i>Drosophila pseudoobscura</i>	1	2×10^{-45}
<i>Drosophila sechellia</i>	1	3×10^{-44}
<i>Drosophila simulans</i>	1	2×10^{-44}
<i>Drosophila virilis</i>	1	3×10^{-45}
<i>Drosophila willistoni</i>	1	2×10^{-46}
<i>Drosophila yakuba</i>	1	8×10^{-45}
<i>Dyadobacter fermentans</i>	1	1×10^{-50}
<i>Equus caballus</i>	2	3×10^{-44} and 2×10^{-15}
<i>Erythrobacter litoralis</i>	1	3×10^{-17}
<i>Erythrobacter sp.</i>	2	7×10^{-18} and 1×10^{-16}
<i>Ferroplasma acidarmanus</i>	1	1×10^{-38}
<i>Flavobacteria bacterium</i>	2	3×10^{-47} and 8×10^{-46}
<i>Flavobacteriaceae bacterium</i>	1	1×10^{-43}
<i>Flavobacteriales bacterium</i>	2	8×10^{-46} and 1×10^{-44}
<i>Flavobacterium johnsoniae</i>	1	1×10^{-48}
<i>Flavobacterium psychrophilum</i>	1	1×10^{-43}
<i>Frankia sp.</i>	3	1×10^{-47} - 4×10^{-29}
<i>Frankia symbiont</i>	1	1×10^{-43}
<i>gamma proteobacterium</i>	1	2×10^{-16}
<i>Gemmata obscuriglobus</i>	1	3×10^{-51}
<i>Gemmatimonas aurantiaca</i>	1	6×10^{-51}
<i>Geodermatophilus obscurus</i>	1	7×10^{-52}
<i>Gloeobacter violaceus</i>	1	9×10^{-23}
<i>Glossina morsitans</i>	1	2×10^{-45}
<i>Glycine max</i>	1	1×10^{-147}
<i>Gramella forsetii</i>	1	1×10^{-49}
<i>Grimontia hollisae</i>	1	6×10^{-24}
<i>Hahella chejuensis</i>	1	2×10^{-24}

Appendix B. Sources of the HPPD or similar proteins including glyoxylases and members of the dioxygenase superfamily showing significant sequence similarity to the AvHPPD (Continued)

Organism	No. of proteins	E-value
<i>Haliangium ochraceum</i>	2	3×10^{-27} and 2×10^{-22}
<i>Herpetosiphon aurantiacus</i>	2	3×10^{-49} and 3×10^{-43}
<i>Hevea brasiliensis</i>	1	1×10^{-147}
<i>Hirschia baltica</i>	1	2×10^{-19}
<i>Hoeflea phototrophica</i>	1	3E-15
<i>Homo sapiens</i>	6	2×10^{-43} - 5×10^{-16}
<i>Hordeum vulgare</i>	1	0
<i>Hydra magnipapillata</i>	1	2×10^{-44}
<i>Hyphomonas neptunium</i>	1	4×10^{-16}
<i>Hypophthalmichthys nobilis</i>	1	2×10^{-30}
<i>Idiomarina baltica</i>	1	3×10^{-22}
<i>Idiomarina loihiensis</i>	1	1×10^{-21}
<i>Ixodes scapularis</i>	1	1×10^{-39}
<i>Janibacter</i> sp.	1	8×10^{-46}
<i>Jannaschia</i> sp.	1	1×10^{-19}
<i>Kangiella koreensis</i>	2	5×10^{-21} and 7×10^{-20}
<i>Kordia algicida</i>	1	5×10^{-45}
<i>Kribbella flavida</i>	2	3×10^{-43} and 2×10^{-31}
<i>Kytococcus sedentarius</i>	1	7×10^{-47}
<i>Labrenzia alexandrii</i>	1	3×10^{-16}
<i>Lactuca sativa</i>	1	1×10^{-146}
<i>Leeuwenhoekiella blandensis</i>	1	9×10^{-50}
<i>Legionella drancourtii</i>	1	2×10^{-11}
<i>Legionella longbeachae</i>	1	6×10^{-19}
<i>Legionella pneumophila</i>	4	7×10^{-20} - 2×10^{-18}
<i>Leptothrix cholodnii</i>	2	5×10^{-20} and 3×10^{-17}
<i>Listonella anguillarum</i>	1	4×10^{-20}
<i>Lutiella nitroferrum</i>	2	1×10^{-19} and 0.0002
<i>Lyngbya</i> sp.	1	1×10^{-21}
<i>Macaca mulatta</i>	3	2×10^{-43} - 7×10^{-15}
<i>Magnaporthe grisea</i>	1	8×10^{-43}
<i>Maricaulis maris</i>	1	4×10^{-15}
<i>marine gamma probacterium</i>	1	1×10^{-15}
<i>Marinomonas</i> sp.	2	2×10^{-22} and 2×10^{-16}
<i>Medicago truncatula</i>	1	1×10^{-149}
<i>Meiothermus ruber</i>	1	2×10^{-7}
<i>Mesorhizobium loti</i>	1	6×10^{-17}
<i>Mesorhizobium opportunistum</i>	1	4×10^{-16}
<i>Mesorhizobium</i> sp.	2	1×10^{-16} and 2×10^{-5}

Appendix B. Sources of the HPPD or similar proteins including glyoxylases and members of the dioxygenase superfamily showing significant sequence similarity to the AvHPPD (Continued)

Organism	No. of proteins	E-value
<i>Methylibium petroleiphilum</i>	1	2×10^{-17}
<i>Methylobacterium</i> sp.	1	1×10^{-7}
<i>Microcoleus chthonoplastes</i>	1	8×10^{-21}
<i>Microcystis aeruginosa</i>	1	5×10^{-16}
<i>Micromonas pusilla</i>	1	1×10^{-112}
<i>Micromonas</i> sp.	1	1×10^{-113}
<i>Micromonospora aurantiaca</i>	2	2×10^{-49} and 6×10^{-30}
<i>Micromonospora</i> sp.	4	3×10^{-49} - 2×10^{-21}
<i>Microscilla marina</i>	2	1×10^{-48} and 2×10^{-46}
<i>Microsporum canis</i>	2	2×10^{-41} and 1×10^{-37}
<i>Monodelphis domestica</i>	1	1×10^{-47}
<i>Moritella</i> sp.	1	5×10^{-19}
<i>Mus musculus</i>	3	5×10^{-43} - 6×10^{-13}
<i>Mycobacterium abscessus</i>	1	6×10^{-49}
<i>Mycosphaerella graminicola</i>	1	2×10^{-48}
<i>Myxococcus xanthus</i>	1	1×10^{-16}
<i>Naegleria gruberi</i>	2	3×10^{-46} and 6×10^{-13}
<i>Nakamurella multipartita</i>	1	4×10^{-47}
<i>Nasonia vitripennis</i>	1	8×10^{-46}
<i>Neosartorya fischeri</i>	2	2×10^{-40} and 2×10^{-38}
<i>Neurospora crassa</i>	1	5×10^{-44}
<i>Nitrosococcus halophilus</i>	1	7×10^{-25}
<i>Nitrosococcus oceani</i>	2	4×10^{-26} and 4×10^{-26}
<i>Nocardia farcinica</i>	1	4×10^{-47}
<i>Nocardioides</i> sp.	1	2×10^{-40}
<i>Nodularia spumigena</i>	1	5×10^{-23}
<i>Nonomuraea</i> sp.	1	7×10^{-20}
<i>Nostoc azollae</i>	1	4×10^{-16}
<i>Nostoc punctiforme</i>	1	2×10^{-20}
<i>Nostoc</i> sp.	1	4×10^{-20}
<i>Novosphingobium aromaticivorans</i>	1	8×10^{-21}
<i>Oceanibulbus indolifex</i>	1	2×10^{-14}
<i>Oceanicaulis alexandrii</i>	1	2×10^{-16}
<i>Oceanicola batsensis</i>	1	2×10^{-16}
<i>Ochrobactrum anthropi</i>	1	5×10^{-11}
<i>Ochrobactrum intermedium</i>	1	5×10^{-10}
<i>Oryctolagus cuniculus</i>	1	2×10^{-44}
<i>Oryza sativa</i>	5	$0 - 3 \times 10^{-9}$

Appendix B. Sources of the HPPD or similar proteins including glyoxylases and members of the dioxygenase superfamily showing significant sequence similarity to the AvHPPD (Continued)

Organism	No. of proteins	E-value
<i>Osmerus mordax</i>	1	1×10^{-15}
<i>Ostreococcus lucimarinus</i>	1	1×10^{-114}
<i>Ostreococcus tauri</i>	1	1×10^{-114}
<i>Pan troglodytes</i>	3	2×10^{-43} - 6×10^{-16}
<i>Paracoccidioides brasiliensis</i>	6	1×10^{-41} - 1×10^{-30}
<i>Paracoccus denitrificans</i>	1	3×10^{-19}
<i>Paramecium tetraurelia</i>	2	1×10^{-48} and 1×10^{-48}
<i>Pediculus humanus</i>	1	3×10^{-43}
<i>Pedobacter heparinus</i>	1	4×10^{-45}
<i>Pedobacter</i> sp.	1	2×10^{-46}
<i>Penicillium marneffeii</i>	2	1×10^{-39} and 2×10^{-35}
<i>Perkinsus marinus</i>	1	6×10^{-46}
<i>Phaeobacter gallaeciensis</i>	2	5×10^{-19} and 5×10^{-19}
<i>Phaeosphaeria nodorum</i>	1	1×10^{-47}
<i>Phenylobacterium zucineum</i>	1	2×10^{-22}
<i>Photobacterium profundum</i>	2	1×10^{-28} and 4×10^{-28}
<i>Photobacterium</i> sp.	1	4×10^{-25}
<i>Physcomitrella patens</i>	2	1×10^{-126} and 1×10^{-125}
<i>Phytophthora infestans</i>	3	1×10^{-116} - 1×10^{-20}
<i>Picea sitchensis</i>	1	4×10^{-95}
<i>Pichia stipitis</i>	1	9×10^{-28}
<i>Picrophilus torridus</i>	1	9×10^{-39}
<i>Plastid transformation</i>	1	7×10^{-17}
<i>Platynereis dumerilii</i>	1	1×10^{-36}
<i>Polaribacter irgensii</i>	1	6×10^{-46}
<i>Polaribacter</i> sp.	1	2×10^{-46}
<i>Polaromonas naphthalenivorans</i>	1	2×10^{-17}
<i>Polaromonas</i> sp.	2	6×10^{-19} and 0.002
<i>Polysphondylium pallidum</i>	2	1×10^{-44} and 5×10^{-11}
<i>Populus trichocarpa</i>	2	1×10^{-148} and 3×10^{-97}
<i>Pseudoalteromonas atlantica</i>	2	2×10^{-20} and 1×10^{-12}
<i>Pseudoalteromonas haloplanktis</i>	1	7×10^{-20}
<i>Pseudoalteromonas tunicata</i>	1	1×10^{-21}
<i>Pseudomonas aeruginosa</i>	6	3×10^{-22} - 0.005
<i>Pseudomonas chlororaphis</i>	1	1×10^{-10}
<i>Pseudomonas entomophila</i>	2	3×10^{-18} and 1×10^{-8}
<i>Pseudomonas fluorescens</i>	7	2×10^{-18} - 7×10^{-7}
<i>Pseudomonas mendocina</i>	1	8×10^{-21}

Appendix B. Sources of the HPPD or similar proteins including glyoxylases and members of the dioxygenase superfamily showing significant sequence similarity to the AvHPPD (Continued)

Organism	No. of proteins	E-value
<i>Pseudomonas putida</i>	8	3×10^{-18} - 0.0001
<i>Pseudomonas stutzeri</i>	2	1×10^{-20} and 0.00005
<i>Pseudomonas</i> sp.	1	5×10^{-18}
<i>Pseudomonas syringae</i>	16	5×10^{-18} - 0.002
<i>Pseudovibrio</i> sp.	1	2×10^{-15}
<i>Psychrobacter cryohalolentis</i>	1	5×10^{-20}
<i>Psychrobacter</i> sp.	1	3×10^{-23}
<i>Psychroflexus torquis</i>	1	4×10^{-50}
<i>Pyrenophora tritici-repentis</i>	1	2×10^{-43}
<i>Ralstonia eutropha</i>	4	3×10^{-17} - 9×10^{-7}
<i>Ralstonia pickettii</i>	4	1×10^{-17} - 0.00002
<i>Ralstonia solanacearum</i>	7	2×10^{-19} - 1×10^{-8}
<i>Raphidiopsis brookii</i>	1	1×10^{-21}
<i>Rattus norvegicus</i>	4	2×10^{-44} - 3×10^{-15}
<i>Reinekea</i> sp.	1	7×10^{-17}
<i>Rhizobium etli</i>	9	1×10^{-17} - 0.008
<i>Rhizobium leguminosarum</i>	7	9×10^{-18} - 2×10^{-6}
<i>Rhizobium</i> sp.	3	1×10^{-15} - 0.00002
<i>Rhodobacteraceae</i> bacterium	1	3×10^{-9}
<i>Rhodobacterales</i> bacterium	2	2×10^{-21} and 7×10^{-18}
<i>Rhodococcus erythropolis</i>	2	4×10^{-48} and 2×10^{-47}
<i>Rhodococcus jostii</i>	4	3×10^{-48} - 4×10^{-46}
<i>Rhodococcus opacus</i>	3	1×10^{-48} - 2×10^{-46}
<i>Rhodopseudomonas palustris</i>	2	1×10^{-17} and 4×10^{-17}
<i>Rhodospirillum centenum</i>	1	2×10^{-23}
<i>Ricinus communis</i>	1	1×10^{-151}
<i>Robiginitalea biformata</i>	1	7×10^{-50}
<i>Roseobacter denitrificans</i>	1	1×10^{-16}
<i>Roseobacter litoralis</i>	1	8×10^{-16}
<i>Roseobacter</i> sp.	4	3×10^{-19} - 0.001
<i>Ruegeria pomeroyi</i>	1	2×10^{-16}
<i>Ruegeria</i> sp.	2	4×10^{-19} and 4×10^{-18}
<i>Saccharomonospora viridis</i>	1	2×10^{-44}
<i>Saccharopolyspora erythraea</i>	1	2×10^{-43}
<i>Saccoglossus kowalevskii</i>	3	7×10^{-41} - 1×10^{-16}
<i>Sagittula stellata</i>	1	1×10^{-15}
<i>Salinibacter ruber</i>	1	4×10^{-52}
<i>Salinispora arenicola</i>	2	2×10^{-47} and 6×10^{-30}

Appendix B. Sources of the HPPD or similar proteins including glyoxylases and members of the dioxygenase superfamily showing significant sequence similarity to the AvHPPD (Continued)

Organism	No. of proteins	E-value
<i>Salinispora tropica</i>	3	5×10^{-44} - 1×10^{-20}
<i>Salmo salar</i>	1	2×10^{-47}
<i>Salvia miltiorrhiza</i>	1	1×10^{-145}
<i>Schistosoma mansoni</i>	1	2×10^{-7}
<i>Sclerotinia sclerotiorum</i>	1	4×10^{-40}
<i>Shewanella amazonensis</i>	1	9×10^{-20}
<i>Shewanella baltica</i>	3	2×10^{-22} - 8×10^{-22}
<i>Shewanella benthica</i>	1	2×10^{-21}
<i>Shewanella colwelliana</i> ,	1	0.0002
<i>Shewanella denitrificans</i>	1	3×10^{-22}
<i>Shewanella frigidimarina</i>	1	2×10^{-22}
<i>Shewanella halifaxensis</i>	2	3×10^{-22} and 8×10^{-11}
<i>Shewanella loihica</i>	1	6×10^{-21}
<i>Shewanella oneidensis</i>	1	2×10^{-21}
<i>Shewanella pealeana</i>	1	4×10^{-22}
<i>Shewanella piezotolerans</i>	1	4×10^{-21}
<i>Shewanella putrefaciens</i>	2	2×10^{-22} and 4×10^{-22}
<i>Shewanella sediminis</i>	1	1×10^{-20}
<i>Shewanella</i> sp.	2	9×10^{-23} and 6×10^{-22}
<i>Shewanella woodyi</i>	1	1×10^{-20}
<i>Silicibacter lacuscaerulensis</i>	1	2×10^{-16}
<i>Silicibacter</i> sp.	1	2×10^{-18}
<i>Sinorhizobium medicae</i>	1	3×10^{-15}
<i>Sinorhizobium meliloti</i>	2	3×10^{-14} and 8×10^{-6}
<i>Solenostemon scutellarioides</i>	1	1×10^{-146}
<i>Solibacter usitatus</i>	1	4×10^{-53}
<i>Sorangium cellulosum</i>	2	3×10^{-27} and 1×10^{-26}
<i>Sordaria macrospora</i>	1	8×10^{-45}
<i>Sorghum bicolor</i>	3	$0 - 1 \times 10^{-135}$
<i>Sphingobacterium spiritivorum</i>	2	8×10^{-46} and 2×10^{-44}
<i>Sphingomonas</i> sp.	1	2×10^{-15}
<i>Sphingomonas wittichii</i>	1	3×10^{-20}
<i>Sphingopyxis alaskensis</i>	1	2×10^{-18}
<i>Spirosoma linguale</i>	1	6×10^{-48}
<i>Stackebrandtia nassauensis</i>	1	7×10^{-47}
<i>Stappia aggregata</i>	2	4×10^{-16} and 2×10^{-10}
<i>Stenotrophomonas maltophilia</i>	2	1×10^{-14} and 8×10^{-14}
<i>Stenotrophomonas</i> sp.	1	2×10^{-15}
<i>Stigmatella aurantiaca</i>	1	3×10^{-22}

Appendix B. Sources of the HPPD or similar proteins including glyoxylases and members of the dioxygenase superfamily showing significant sequence similarity to the AvHPPD (Continued)

Organism	No. of proteins	E-value
<i>Streptomyces albus</i>	1	4×10^{-47}
<i>Streptomyces avermitilis</i>	2	6×10^{-45} and 5×10^{-44}
<i>Streptomyces clavuligerus</i>	1	3×10^{-47}
<i>Streptomyces coelicolor</i>	2	4×10^{-47} and 1×10^{-20}
<i>Streptomyces flavogriseus</i>	1	7×10^{-47}
<i>Streptomyces fungicidicus</i>	1	7×10^{-28}
<i>Streptomyces ghanaensis</i>	1	1×10^{-49}
<i>Streptomyces griseoflavus</i>	1	2×10^{-48}
<i>Streptomyces griseus</i>	1	2×10^{-47}
<i>Streptomyces hygroscopicus</i>	1	2×10^{-51}
<i>Streptomyces lavendulae</i>	1	3×10^{-20}
<i>Streptomyces lividans</i>	1	1×10^{-20}
<i>Streptomyces roseosporus</i>	2	5×10^{-50} and 3×10^{-26}
<i>Streptomyces scabiei</i>	2	9×10^{-47} and 0.001
<i>Streptomyces</i> sp.	7	4×10^{-54} - 0.013
<i>Streptomyces sviveus</i>	1	3×10^{-46}
<i>Streptomyces toyocaensis</i>	1	8×10^{-24}
<i>Streptomyces viridochromogenes</i>	1	2×10^{-45}
<i>Streptosporangium roseum</i>	2	2×10^{-44} and 5×10^{-28}
<i>Strongylocentrotus purpuratus</i>	1	5×10^{-45}
<i>Sulfitobacter</i> sp.	2	4×10^{-15} and 7×10^{-15}
<i>Sus scrofa</i>	1	5×10^{-40}
<i>Synechococcus</i> sp.	4	2×10^{-22} - 1×10^{-17}
<i>Synechocystis</i> sp.	1	3×10^{-16}
<i>Talaromyces stipitatus</i>	2	5×10^{-42} and 0.013
<i>Tetrahymena thermophila</i>	1	1×10^{-44}
<i>Thalassiosira pseudonana</i>	1	8×10^{-90}
<i>Thermomonospora curvata</i>	1	1×10^{-48}
<i>Thiomonas intermedia</i>	1	3×10^{-18}
<i>Tribolium castaneum</i>	1	1×10^{-40}
<i>Trichodesmium erythraeum</i>	1	6×10^{-24}
<i>Triticum aestivum</i>	2	0 and 1×10^{-172}
<i>Uncinocarpus reesii</i>	2	1×10^{-42} and 2×10^{-36}
uncultured bacterium	3	1×10^{-54} - 4×10^{-21}
uncultured soil	4	2×10^{-20} - 1×10^{-9}
unidentified eubacterium	1	2×10^{-46}
<i>Variovorax paradoxus</i>	2	1×10^{-17} and 0.005

Appendix B. Sources of the HPPD or similar proteins including glyoxylases and members of the dioxygenase superfamily showing significant sequence similarity to the AvHPPD (Continued)

Organism	No. of proteins	E-value
<i>Verminephrobacter eiseniae</i>	1	3×10^{-14}
<i>Verticillium albo-atrum</i>	1	3×10^{-34}
<i>Vibrio alginolyticus</i>	1	2×10^{-19}
<i>Vibrio angustum</i>	1	3×10^{-24}
<i>Vibrio cholerae</i>	6	2×10^{-22} - 4×10^{-21}
<i>Vibrio coralliilyticus</i>	1	6×10^{-19}
<i>Vibrio furnissii</i>	2	3×10^{-21} and 3×10^{-8}
<i>Vibrio harveyi</i>	2	6×10^{-19} and 0.0002
<i>Vibrio metschnikovii</i>	1	3×10^{-22}
<i>Vibrio mimicus</i>	2	4×10^{-23} and 5×10^{-23}
<i>Vibrio orientalis</i>	1	4×10^{-20}
<i>Vibrio parahaemolyticus</i>	2	8×10^{-21} and 9×10^{-20}
<i>Vibrio shilonii</i>	1	2×10^{-20}
<i>Vibrio</i> sp.	4	3×10^{-22} - 1×10^{-18}
<i>Vibrio splendidus</i>	1	6×10^{-19}
<i>Vibrionales bacterium</i>	1	7×10^{-20}
<i>Vitis vinifera</i>	2	1×10^{-146} and 1×10^{-145}
<i>Xanthomonas albilineans</i>	1	6×10^{-17}
<i>Xanthomonas axonopodis</i>	1	4×10^{-16}
<i>Xanthomonas campestris</i>	4	2×10^{-16} - 1×10^{-15}
<i>Xanthomonas oryzae</i>	4	2×10^{-16} - 2×10^{-16}
<i>Xenopus silurana</i>	3	3×10^{-47} - 4×10^{-12}
<i>Xenopus laevis</i>	4	2×10^{-48} - 7×10^{-10}
<i>Yarrowia lipolytica</i>	1	8×10^{-43}
<i>Zea mays</i>	3	0

Appendix C. Proteins of various function showing significant sequence similarity to the AvHPPD-03 amino acid sequence in BLASTP analysis

Description	Species	Number of Entries	E-value
Legiolysin (HPPD-like)- This is similar to other HPPD proteins, hemolytic activity sometimes associated with legiolysin may actually be due to the oxidation and polymerization process of HGA (Steinert <i>et al.</i> 2001).	<i>Legionella pneumophila</i>	1	1×10^{-18}
T-cell reactive proteins. All have glyoxalase or dioxygenase domains.	<i>Ajellomyces capsulatus</i>	2	3×10^{-43} and 3×10^{-43}
	<i>Auxarthron zuffianum</i>	2	2×10^{-18} and 2×10^{-18}
	<i>Coccidioides immitis</i>	2	2×10^{-18} and 1×10^{-8}
	<i>Coccidioides posadasii</i>	2	1×10^{-7}
	<i>Uncinocarpus reesii</i>	2	5×10^{-19} and 1×10^{-18}
Sugar phosphate epimerases and isomerases	<i>Streptomyces</i> sp.	1	0.008
	<i>Streptomyces hygroscopicus</i>	1	0.0002
	<i>Streptomyces ghanaensis</i>	1	0.0002
	<i>Stackebrandtia nassauensis</i>	1	0.051
	<i>Streptomyces sviveus</i>	1	0.03
	<i>Streptomyces viridochromogenes</i>	1	0.0005
	<i>Streptomyces avermitilis</i>	1	0.00004
	<i>Burkholderia</i> sp.	2	3×10^{-6} and 8×10^{-6}
	<i>Burkholderia phytofirmans</i>	1	0.00002
	<i>Sinorhizobium medicae</i>	1	0.000003
	<i>Methylobacterium nodulans</i>	1	2×10^{-12}
	<i>Corynebacterium glutamicum</i>	1	0.001
Anti-freeze glycoproteins - a group of proteins that protect organisms from deep freezing temperatures and are expressed in vertebrates, invertebrates, plants, bacteria, and fungi (Venketesh and Dayananda 2008).	<i>Dissostichus mawsoni</i>	7	0.003, 0.018
	<i>Boreogadus saida</i>		0.004, 0.15, 0.068
	<i>Notothernia coriiceps</i>		0.01
	<i>Harpagifer antarcticus</i>		0.018

Appendix C. Proteins of various function showing significant sequence similarity to the AvHPPD-03 amino acid sequence in BLASTP analysis (Continued)

Description	Species	Number of Entries	E-value
Liver F proteins - although the biological function of this protein is unclear, it is possibly responsible for immune tolerance and immune response observed in rats following transplantation (Liu <i>et al.</i> 2007).	<i>Homo sapiens</i> <i>Mus musculus</i>	2	2×10^{-43} 3×10^{-43}
HNF-HNF class homeobox protein - a transcription factor (Mendel and Crabtree 1991).	<i>Nematostella vectensis</i>	1	2×10^{-32}
Flagellar hook-length control protein which is involved in developing the flagellar structure (Ferris and Minamino 2006)	<i>Rhodobacter sphaeroides</i>	1	0.087
MelA - a protein involved in melanin biosynthesis (Fuqua <i>et al.</i> 1991).	<i>Drosophila melanogaster</i> <i>Shewanella colwelliana</i>	1 1	1×10^{-44} 1×10^{-21}
membrane protein-like protein	<i>Burkholderia</i> sp.	1	0.039
2-methylcitrate dehydratase belonging to a family of hydro-lyases	<i>Clavibacter michiganensis</i>	1	0.11
methylmalonyl-CoA epimerase - an enzyme involved in propionyl-CoA metabolism	<i>gamma proteobacterium</i> <i>Nocardiopsis dassonvillei</i>	1 1	0.051 0.087
AP endonuclease, family 2 - apurinic/aprimidinic (AP) endonucleases are generally expressed by all organisms as dedicated repair enzymes for damaged DNA	<i>Citricella</i> sp.	1	0.03

Appendix D. Sources of the 85 proteins identified as hypothetical, unknown, or with unknown function showing significant sequence similarity to the AvHPPD-03 amino acid sequence in BLASTP analysis

Organism	No. of proteins	E-value
<i>Abutilon theophrasti</i>	1	1×10^{-118}
<i>Acaryochloris marina</i>	1	3×10^{-18}
<i>Acidobacterium capsulatum</i>	1	4×10^{-52}
<i>Acidovorax avenae</i>	2	7×10^{-18} and 9×10^{-18}
<i>Acidovorax delafieldii</i>	1	6×10^{-19}
<i>Acidovorax ebreus</i>	1	3×10^{-14}
<i>Acidovorax</i> sp.	1	3×10^{-14}
<i>Acinetobacter baumannii</i>	3	3×10^{-16} - 7×10^{-15}
<i>Acinetobacter calcoaceticus</i>	1	3×10^{-16}
<i>Acinetobacter johnsonii</i>	1	7×10^{-17}
<i>Acinetobacter junii</i>	1	5×10^{-18}
<i>Acinetobacter radioresistens</i>	1	3×10^{-14}
<i>Acinetobacter</i> sp.	1	2×10^{-12}
<i>Actinoplanes teichomyceticus</i>	2	1×10^{-32} and 1×10^{-32}
<i>Actinosynnema mirum</i>	2	2×10^{-46} and 1×10^{-25}
<i>Aedes aegypti</i>	2	6×10^{-43} and 2×10^{-42}
<i>Aeromonas hydrophila</i>	1	6×10^{-24}
<i>Aeromonas salmonicida</i>	1	1×10^{-23}
<i>Agrobacterium radiobacter</i>	2	2×10^{-14} and 3×10^{-5}
<i>Agrobacterium vitis</i>	1	0.00005
<i>Ailuropoda melanoleuca</i>	1	1×10^{-46}
<i>Ajellomyces capsulatus</i>	4	7×10^{-44} - 5×10^{-37}
<i>Ajellomyces dermatitidis</i>	4	1×10^{-40} - 1×10^{-37}
<i>Algoriphagus</i> sp.	1	9×10^{-49}
<i>alpha proteobacterium</i>	3	9×10^{-26} - 2×10^{-6}
<i>Alteromonadales bacterium</i>	1	2×10^{-19}
<i>Alteromonas macleodii</i>	2	4×10^{-17} and 6×10^{-17}
<i>Amycolatopsis balhimycina</i>	1	4×10^{-21}
<i>Amycolatopsis orientalis</i>	1	4×10^{-24}
<i>Anabaena variabilis</i>	1	4×10^{-20}
<i>Anaeromyxobacter dehalogenans</i>	2	4×10^{-23} and 1×10^{-21}
<i>Anaeromyxobacter</i> sp.	2	1×10^{-23} and 3×10^{-22}
<i>Anoplopoma fimbria</i>	1	2×10^{-46}
<i>Arabidopsis thaliana</i>	6	1×10^{-148} - 1×10^{-119}
<i>Arthrospira maxima</i>	1	2×10^{-19}
<i>Arthrospira platensis</i>	2	5×10^{-20} and 9×10^{-20}
<i>Aspergillus clavatus</i>	1	5×10^{-40}
<i>Aspergillus flavus</i>	1	5×10^{-42}
<i>Aspergillus fumigatus</i>	2	2×10^{-39} and 3×10^{-39}

Appendix D. Sources of the 85 proteins identified as hypothetical, unknown, or with unknown function showing significant sequence similarity to the AvHPPD-03 amino acid sequence in BLASTP analysis (Continued)

Organism	No. of proteins	E-value
<i>Nematostella vectensis</i>	1	8×10^{-14}
<i>Penicillium chrysogenum</i>	2	2×10^{-38} and 1×10^{-37}
<i>Phaeodactylum tricornutum</i>	1	0.002
<i>Pichia guilliermondii</i>	2	1×10^{-27} and 5×10^{-27}
<i>Pichia pastoris</i>	1	1×10^{-37}
<i>Podospora anserina</i>	1	4×10^{-42}
<i>Polysphondylium pallidum</i>	1	5×10^{-28}
<i>Pseudomonas aeruginosa</i>	4	0.00003 - 0.002
<i>Pseudomonas fluorescens</i>	1	3×10^{-7}
<i>Ralstonia solanacearum</i>	1	7×10^{-9}
<i>Rhodobacterales bacterium</i>	1	2×10^{-10}
<i>Roseovarius sp.</i>	1	8×10^{-8}
<i>Sagittula stellata</i>	1	2×10^{-8}
<i>Schistosoma japonicum</i>	1	0.01
<i>Serratia odorifera</i>	1	0.0005
<i>Sordaria macrospora</i>	1	6×10^{-21}
<i>Strongylocentrotus purpuratus</i>	2	2×10^{-16} and 2×10^{-16}
<i>Taeniopygia guttata</i>	2	2×10^{-42} and 6×10^{-17}
<i>Tetraodon nigroviridis</i>	3	1×10^{-35} - 0.0002
<i>Thalassiosira pseudonana</i>	1	0.002
<i>Trichophyton verrucosum</i>	2	7×10^{-39} and 4×10^{-37}
<i>Trichoplax adhaerens</i>	2	4×10^{-42} and 6×10^{-8}
<i>Vitis vinifera</i>	2	7×10^{-39} and 9×10^{-18}
<i>Xenopus laevis</i>	1	5×10^{-40}