

**Study Title**

**Bioinformatics Evaluation of the DMO+27 Protein in MON 87708 Utilizing the  
AD\_2010, TOX\_2010, and PRT\_2010 Databases**

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**Study Completed On**

**March 22, 2010**

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**Laboratory Project ID**

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**Study Number: REG-10-104**

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This project does not meet the U.S. EPA Good Laboratory Practice requirements as specified in 40 CFR Part 160.

\_\_\_\_\_  
Submitter

Date: \_\_\_\_\_



Melinda C. McCann  
Sponsor Representative

Date: 22 Mar 2010



Haidi Tu  
Author

Date: 3-22-10

### Quality Assurance Statement

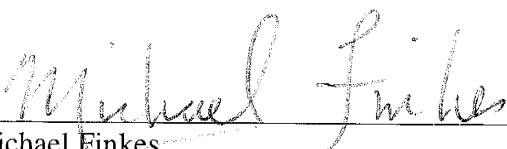
**Study Title:** Bioinformatics Evaluation of the DMO+27 Protein in MON 87708  
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**Study Number:** REG-10-104

Reviews conducted by the Quality Assurance Unit confirm that the final report accurately describes the methods and standard operating procedures followed and accurately reflects the raw data of the study.

Following is a list of reviews conducted by the Monsanto Regulatory Quality Assurance Unit on the study reported herein.

Dates of Inspection/Audit	Phase	Date Reported to Study Director	Date Reported to Management
03/19/2010	Draft Report and Data Audit	03/19/2010	03/19/2010

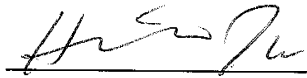
  
\_\_\_\_\_  
Michael Finkes  
Quality Assurance Specialist  
Monsanto Regulatory, Monsanto Company

  
\_\_\_\_\_  
Date

**Study Certification Page**

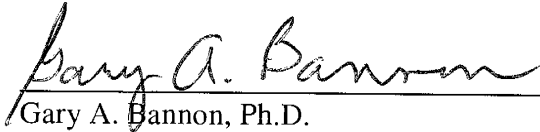
This report is an accurate and complete representation of the study/project activities.

**Signatures of Final Report Approval:**



Haidi Tu, M.S.  
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Date: 3-22-10



Gary A. Bannon, Ph.D.  
Lead, Regulatory Product Characterization Center

Date: 03-22-2010

### **Study Information**

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**Records Retention:** All study-specific raw data and the final report will be retained at Monsanto-St. Louis.

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### Abbreviations and Definitions

AA	Amino acid
AD_2010	Allergen and gliadin protein sequence database (Release date January 22, 2010)
BLOCKS	A database of amino acid motifs found in protein families
BLOSUM50	BLOcks SUBstitution Matrix, used to score similarities between pairs of distantly related of protein or nucleotide sequences
CP4 EPSPS	5-enolpyruvylshikimate-3-phosphate synthase from <i>Agrobacterium tumefaciens</i> sp. strain CP4
DMO	Dicamba Mono-Oxygenase
E-Score	Expectation Score
FASTA	Algorithm used to find local high scoring alignments between a pair of protein or nucleotide sequences
GenBank	A public genetic database maintained by the National Center for Biotechnology Information at the National Institutes of Health, Bethesda, MD
GI	Gene Identification number
NCBI	National Center of Biotechnology Information at the National Institutes of Health, Bethesda, MD, USA
ORF	Open Reading Frame
PRT_2010	GenBank protein database, 175.0 (Release date January 22, 2010)
TOX_2010	Toxin protein sequence database (Release date January 22, 2010)



## 1.0 Summary

Monsanto Company has developed herbicide-tolerant soybean MON 87708, which is tolerant to dicamba (3,6-dichloro-2-methoxybenzoic acid) herbicide. MON 87708 contains a demethylase gene from *Stenotrophomonas maltophilia* that expresses the dicamba mono-oxygenase (DMO) protein to confer tolerance to dicamba herbicide.

Structurally, the MON 87708-produced DMO enzyme functions as a trimer and consists of two forms of the DMO protein, namely DMO and DMO+27. The DMO protein is the mature form of the protein while the DMO+27 protein contains an additional 27 amino acids on its amino terminus, originating from the pea Rubisco small subunit.

As part of a comprehensive safety assessment, bioinformatic analyses were performed to assess the potential of allergenicity, toxicity, or biological activity of the DMO+27 protein contained in MON 87708. DMO+27 was chosen as the query sequence as it fully contains the DMO sequence. As such, any conclusions that are drawn regarding the bioinformatic evaluation of DMO+27 are also applicable to DMO. The DMO+27 protein sequence was compared to allergen (AD\_2010), toxin (TOX\_2010) and public domain (PRT\_2010) sequence databases using the FASTA sequence comparison algorithm.

The FASTA sequence alignment tool was used to assess structural relatedness between the query sequences and any protein sequences in the AD\_2010, TOX\_2010, and PRT\_2010 databases. Structural similarities shared between the DMO+27 sequence with each sequence in the database were examined. The extent of structural relatedness was evaluated by detailed visual inspection of the alignment, the calculated percent identity, and the *E*-score. Alignments having *E*-score less than or equal to  $1e-5$  ( $1 \times 10^{-5}$ ) are deemed significant because they may reflect shared structure and function among sequences. In addition to structural similarity, the DMO+27 sequence was screened for short polypeptide matches using a pair-wise comparison algorithm. In these analyses, eight contiguous and identical amino acids were defined as immunologically relevant, where eight represents the typical minimum sequence length likely to represent an immunological epitope (Silvanovich et al., 2006).

Results indicate there were no biologically relevant sequence similarities to allergens or toxins when the DMO+27 protein sequence was used as a query for a FASTA search of the AD\_2010 or TOX\_2010 database. Furthermore, no short (eight amino acid) polypeptide matches were shared between the DMO+27 protein sequence and proteins in the allergen database. When searching the PRT\_2010 database, results confirm that no biologically relevant structural similarity to proteins of concern was observed for DMO+27 sequence. Taken together, these bioinformatic search data indicate the lack of

structurally relevant sequence similarity of DMO+27, as well as DMO, to allergens, toxins or biologically active proteins that could be harmful to human or animal health.

## 2.0 Introduction

Monsanto Company has developed herbicide-tolerant soybean MON 87708, which is tolerant to dicamba (3,6-dichloro-2-methoxybenzoic acid) herbicide. MON 87708 contains a demethylase gene from *Stenotrophomonas maltophilia* that expresses the dicamba mono-oxygenase (DMO) protein to confer tolerance to dicamba herbicide.

Structurally, the MON 87708-produced DMO enzyme functions as a trimer and consists of two forms of the DMO protein, namely DMO and DMO+27. The DMO protein is the mature form of the protein while the DMO+27 protein contains an additional 27 amino acids on its amino terminus, originating from the pea Rubisco small subunit.

As part of a comprehensive safety assessment, bioinformatic analyses were performed to assess the potential of allergenicity, toxicity, or biological activity of the DMO+27 protein contained in MON 87708. DMO+27 was chosen as the query sequence as it fully contains the DMO sequence. As such, any conclusions that are drawn regarding the bioinformatic evaluation of DMO+27 are also applicable to DMO. The DMO+27 protein sequence was compared to allergen (AD\_2010), toxin (TOX\_2010) and public domain (PRT\_2010) sequence databases using the FASTA sequence comparison algorithm.

The FASTA sequence alignment tool was used to assess structural relatedness between the query sequences and any protein sequences in the AD\_2010, TOX\_2010, and PRT\_2010 databases. Structural similarities shared between the DMO+27 sequence with each sequence in the database were examined. The extent of structural relatedness was evaluated by detailed visual inspection of the alignment, the calculated percent identity, and the *E*-score. Alignments having *E*-score less than or equal to  $1e-5$  ( $1 \times 10^{-5}$ ) are deemed significant because they may reflect shared structure and function among sequences. In addition to structural similarity, the DMO+27 sequence was screened for short polypeptide matches using a pair-wise comparison algorithm. In these analyses, eight contiguous and identical amino acids were defined as immunologically relevant, where eight represents the typical minimum sequence length likely to represent an immunological epitope (Silvanovich et al., 2006).

This report describes the bioinformatic evaluation of the DMO+27 protein sequence contained in MON 87708. The bioinformatics analysis results indicate that no structurally relevant sequence similarity of DMO+27, as well as DMO, to allergens, toxins, or other biologically active proteins that could be harmful to human or animal health.

### **3.0 Purpose**

The purpose of this study was to evaluate, using bioinformatic techniques, the DMO+27 protein sequence contained in MON 87708 for its allergenicity, toxicity, and potential adverse biological activity. Sequence similarities towards allergens was assessed using the FASTA sequence alignment and a sliding window search of the AD\_2010 allergen database. Sequence similarities towards toxins and biologically active proteins was assessed using the FASTA sequence alignment search of the TOX\_2010 and PRT\_2010 databases, respectively.

### **4.0 Methods**

#### **4.1 Database assembly**

The allergen, gliadin, and glutenin sequence database (AD\_2010) was obtained from FARRP (2010)<sup>1</sup> and was used as provided. The AD\_2010 database contains 1,471 sequences. A complete description of the AD\_2010 database can be found in Tu and Silvanovich (2010).

GenBank protein database, release 175.0, was downloaded from NCBI and formatted for use in these bioinformatic analyses. It is referred to herein as the PRT\_2010 database and contains 17,815,538 sequences. A complete description of the PRT\_2010 database can be found in Tu and Silvanovich (2010).

The toxin database is a subset of sequences derived from the PRT\_2010 database that was selected using a keyword search and filtered to remove likely non-toxin proteins. It is referred to herein as the TOX\_2010 database and contains 8,448 sequences. A complete description of the TOX\_2010 database can be found in Tu and Silvanovich (2010).

#### **4.2 Sequence Database Searches**

The DMO+27 protein sequence described in Wang et al. (2010) was used as query sequence in this analysis (Figure 1). FASTA analyses using the AD\_2010, TOX\_2010, and PRT\_2010 databases were performed on a virtual machine loaded with a SUSE LINUX version 10 operating system and FASTA version 3.4t26 (July 7, 2006). The structural similarity of the protein sequence to sequences in each database (AD\_2010, TOX\_2010, and PRT\_2010) was assessed using the FASTA

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<sup>1</sup> located at <http://www.allergenonline.com>

algorithm (Lipman and Pearson, 1985; Pearson and Lipman, 1988). In the case of FASTA searches of the PRT\_2010 database performed using the DMO+27 sequence, alignment descriptions contained in Appendix 1 were truncated to display only the top 50 alignments with DMO and eight additional alignments with Rubisco small subunit (the +27 portion of DMO+27).

FASTA comparisons are initiated by aligning the first match of a specific wordsize. The alignment is then extended based on the chosen scoring matrix. With the exception of expectation threshold (*E*-score) of one, default FASTA search parameters were used. The *E*-score is a statistical measure of the likelihood that the observed similarity score could have occurred by chance in a search. A larger *E*-score indicates a lower degree of similarity between the query sequence and the sequence from the database. Typically, alignments between two sequences will need to have an *E*-score of 1e-5 or smaller to be considered to have significant homology. FASTA comparisons were performed using the BLOSUM50 scoring matrix (Henikoff and Henikoff, 1992). Multiple alignments are made between the query sequence and each sequence in the database with a score calculated for each alignment. Only the top scoring alignments are extensively analyzed for each database sequence. The BLOSUM50 matrix series was derived from a set of aligned, ungapped regions from protein families, called the BLOCKS database. Sequences from each block were clustered based on the percent of identical residues in the alignments (Henikoff and Henikoff, 1996). The BLOSUM50 matrix will identify blocks of conserved residues that are at least 50% identical. BLOSUM50 works well for identifying sequence similarities that include gaps, and thus recognizes distant evolutionary relationships (Pearson, 2000).

If two proteins share sufficient linear sequence similarity and identity, they will also share three-dimensional structure and, therefore, functional homology. By definition, homologous proteins share secondary structure and common three-dimensional folds (Pearson, 2000). Because the degree of relatedness between homologs varies widely, the data need to be carefully evaluated in order to maximize their potential predictive value. The allergenicity assessment is used to identify known allergens or potentially cross-reactive proteins. While related (homologous) proteins may share 25% amino acid identity in a 200 amino acid overlap (Pearson, 2000), this is not generally sufficient to indicate IgE-mediated cross-reactivity (Aalberse et al., 2001). Indeed, allergenic cross-reactivity caused by proteins is rare at 50% identity and typically requires >70% amino acid identity across the full length of the protein sequences (Aalberse, 2000). A conservative approach is currently applied by which related protein sequences are identified as potentially cross-reactive if linear identity is 35% or greater in an 80 amino acid overlap (Thomas et al., 2005). Such levels of identity are readily detected using

FASTA. Additionally, proteins closely related to gliadins or glutenins, the proteins that trigger celiac disease, can be easily identified using FASTA.

#### **4.3**    *Significance of the Alignment*

An *E*-score of  $1e-5$  was set as an initial high cut-off value for alignment significance. Although all alignments were inspected visually, any aligned sequence that yielded an *E*-score less than or equal to  $1e-5$  was analyzed further to determine if such an alignment represented significant sequence homology.

### **5.0**    **Results and Discussion**

Potential structural similarities shared between the DMO+27 protein and proteins in the allergen, toxin, or protein databases were evaluated using the FASTA sequence alignment tool. Identified proteins were ranked according to their degree of similarity (Appendix 1).

#### **5.1**    *Assessment of Potential Allergenicity*

Using DMO+27 as the query sequence to search the AD\_2010 database, no alignment met or exceeded the threshold of 35% identity over 80 amino acids recommended by Codex Alimentarius (2003). Furthermore, no FASTA alignment displayed an *E*-score of less than or equal to  $1e-5$  and no eight contiguous amino acid identities were identified (Appendix 1).

#### **5.2**    *Assessment of Potential Toxicity*

Using DMO+27 as the query sequence to search the TOX\_2010 database, no FASTA alignment displayed an *E*-score of less than or equal to  $1e-5$  (Appendix 1).

#### **5.3**    *Assessment of Potential Adverse Biological Activity*

Using DMO+27 as the query sequence to search the PRT\_2010 database, the top alignments positively identified DMO protein with 99.704% identity over 339 amino acids with an *E*-score of  $2.9e-148$  (Appendix 1). The DMO+27 sequence also yielded a secondary group of alignments that positively identified ribulose 1,5-bisphosphate carboxylase small subunit propeptide from *Pisum sativum* (GI-169156; Appendix 1). Through the observation of alignments displaying 100% identity over the first 24 amino acids of DMO+27, this secondary group of alignments is consistent with the known structure of DMO+27 which contains the first 24 amino acids of the mature protein of the *RbcS* gene (Rubisco small subunit )

from *Pisum sativum* (pea) that directs transport of the DMO protein to the chloroplast and 3' amino acids of intervening sequence (Song et al., 2009). The positive identification of DMO and the Rubisco small subunit does not indicate potential adverse biological activity of the DMO, DMO+27 protein or the +27 portion of DMO+27.

## **6.0 Conclusions**

The results of these data indicate that no biologically relevant sequence similarities were observed between the DMO+27, as well as DMO, protein and allergens, toxins, or biologically active proteins. These results demonstrated the lack of both structurally and immunologically relevant similarities between the DMO+27 or DMO protein and known allergens, toxins, or other biologically active proteins that could be harmful to human or animal health.

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novel proteins: international bioinformatics workshop meeting report, 23-24  
February 2005. *Toxicol Sci* **88**:307-310.

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001 MQVWPPIGKK KFETLSYLPP LTRDSRAMAT FVRNAWYVAA LPEELSEKPL  
051 GRTILDTPLA LYRQPDGVVA ALLDICPHRF APLSDGILVN GHLQCPYHGL  
101 EFDGGGQCVH NPHGNGARPA SLNVRSFPVV ERDALIWICP GDPALADPGA  
151 IPDFGCRVDP AYRTVGGYGH VDCNYKLLVD NLMDLGHAQY VHRANAQTDA  
201 FDRLEREVIV GDGEIQALMK IPGGTPSVLM AKFLRGANTP VDAWNDIRWN  
251 KVSAMLNFIA VAPEGTPKEQ SIHSRGTHIL TPETEASCHY FFGSSRNFGI  
301 DDPEDMGVLR SWQAQALVKE DKVVVEAIER RRAYVEANGI RPAMLSDEA  
351 AVRVSREIEK LEQLEAA

**Figure 1: The DMO+27 Protein Sequence**

## Appendix 1. Bioinformatic analysis of DMO+27 protein

```
>DMO+27
MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPALYRQPDGVVAALLDIC
PHRFAPLSDGILVNGHLQCPYHGLEFDGGQCVDHNPNGARFASLNVRSPVVERDALIWICPGDPALADPGAIP
DFGCRVDPAYRTVGGYGHVDCNYKLLVDNMDLGHQAQYVHRANAQTDAFDRLEREVIVGDGEIQALMKIPGGTPSV
LMAKFLRGANTPVDWDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTHILTPETEASCHYFFGSSRNFGIDDPE
MDGVLRSWQAQALVKEDKVVVEAIERRRAYVEANGIRPAMLSCEAAVRVSREIEKLEQLEAA
```

Sliding 8 amino acid window search  
Database searched = AD\_2010  
Query = DMO+27

Start time: Tue Feb 16 16:23:48 GMT 2010 Finish time: Tue Feb 16 16:23:49 GMT 2010

No 8 amino acid matches exist between DMO+27 and the AD\_2010 database

```
# fasta34 DMO+27.pep /genedata/1/db/AD_2010 -Q -E 1 -O DMO+27.pep_ad.fasta
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7, 2006
```

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

DMO+27, 367 aa  
vs /genedata/1/db/AD\_2010 library

```
opt      E()
< 20      2      0:=
22         0      0:          one = represents 3 library sequences
24         0      0:
26         2      0:=
28         9      0:===
30         7      2:*==
32        14      8:==*==
34        32     21:=====*=====
36        45     44:=====*=====
38        74     72:=====*=====
40       107    101:=====*=====
42        98    123:=====
44       162    136:=====*=====
46       126    138:=====
48       141    132:=====*=====
50        99    121:=====
52        96    106:=====
54        75     91:=====
56        41     76:=====
58        61     62:=====
60        69     50:=====
```

```
62      61      40:=====*=====
64      51      32:=====*=====
66      33      25:=====*=====
68      17      20:=====*=====
70      16      16:=====*=====
72       7      12:=====
74       6      10:== *
76       4       7:==*
78       4       6:==*
80       0       4: *
82       1       3:*
84       0       3:*
86       5       2:*
88       5       2:*          inset = represents 1 library sequences
90       0       1:*
92       0       1:*          :*
94       0       1:*          :*
96       1       1:*          :*
98       0       0:          *
100      0       0:          *
102      0       0:          *
104      0       0:          *
106      0       0:          *
108      0       0:          *
110      0       0:          *
112      0       0:          *
114      0       0:          *
116      0       0:          *
118      0       0:          *
>120     0       0:          *
331323 residues in 1471 sequences
Expectation_n fit: rho(ln(x))= 6.7611+/-0.00387; mu= 3.3641+/- 0.199
mean_var=60.9242+/-16.237, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda= 0.164316
Kolmogorov-Smirnov statistic: 0.0296 (N=27) at 44

FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 37, opt: 25, open/ext: -10/-2, width: 16
!! No sequences with E() < 1.000000
```

367 residues in 1 query sequences  
331323 residues in 1471 library sequences  
Scomplib [34t26]  
start: Tue Feb 16 16:23:48 2010 done: Tue Feb 16 16:23:48 2010  
Total Scan time: 0.050 Total Display time: 0.000

Function used was FASTA [version 3.4t26 July 7, 2006]

```
# fasta34 DMO+27.pep /genedata/1/db/TOX_2010 -Q -E 1 -O DMO+27.pep_tx.fasta
```

FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7,  
2006  
Please cite:  
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

DMO+27, 367 aa  
vs /genedata/1/db/TOX\_2010 library

```

      opt      E()
< 20  61      0:=====
 22   1      0:=          one = represents 15 library sequences
 24   2      0:=
 26   0      0:
 28   8      2:*
 30  13     12:*
 32  90     45:=====
 34 150    122:=====*=
 36 272    250:=====*=
 38 527    414:=====*=
 40 423    577:=====          *
 42 776    706:=====*=
 44 687    779:=====          *
 46 583    793:=====          *
 48 900
759:=====*=
 50 516    693:=====          *
 52 659    609:=====*=
 54 482    520:=====          *
 56 606    435:=====*=
 58 295    357:=====          *
 60 383    289:=====*=
 62 268    232:=====*=
 64 161    184:=====          *
 66 141    146:=====*=
 68 89     115:=====          *
 70 62     90:=====*=
 72 83     70:=====*=
 74 34     55:=====*=
 76 21     43:=====*=
 78 40     33:=====*=
 80 9       26:=====*=
 82 20     20:=====*=
 84 11     16:=====*=
 86 13     12:=====*=
 88 6       9:*          inset = represents 1 library sequences
 90 22     7:*
 92 6       6:*          :=====
 94 4       4:*          :=====
 96 3       3:*          :=====
 98 6       3:*          :=====
100 6       2:*          :=====
```

```

102   1      2:*          :*=
104   1      1:*          :*
106   1      1:*          :*
108   1      1:*          :*
110   0      1:*          :*
112   0      0:          :*
114   0      0:          :*
116   0      0:          :*
118   0      0:          :*
>120  0      0:          *
```

2069351 residues in 8448 sequences  
Expectation\_n fit: rho(ln(x))= 5.3676+/-0.000627; mu= 9.5218+/- 0.031  
mean\_var=58.1590+/-12.019, 0's: 60 Z-trim: 60 B-trim: 56 in 2/60  
Lambda= 0.168177  
Kolmogorov-Smirnov statistic: 0.0260 (N=29) at 38

FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15;-5)] ktup: 2  
join: 37, opt: 25, open/ext: -10/-2, width: 16  
!! No sequences with E() < 1.000000

367 residues in 1 query sequences  
2069351 residues in 8448 library sequences  
Scomplib [34t26]  
start: Tue Feb 16 16:23:49 2010 done: Tue Feb 16 16:23:49 2010  
Total Scan time: 0.280 Total Display time: 0.010

Function used was FASTA [version 3.4t26 July 7, 2006]

# fasta34 DMO+27.pep /genedata/1/db/PRT\_2010 -Q -E 1 -O DMO+27.pep\_prt.fasta  
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7,  
2006  
Please cite:  
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

DMO+27, 367 aa  
vs /genedata/1/db/PRT\_2010 library

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 28 4535  4037:*
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 38 760974 872864:=====          *
 40 1103869 1217569:=====          *
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50 1484735 1460845:=====
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4761287459 residues in 17815538 sequences
statistics sampled from 60000 to 17801687 sequences
Expectation_n fit: rho(ln(x))= 5.3994+/-0.000185; mu= 9.1670+/- 0.010
mean_var=66.6660+/-13.569, 0's: 949 Z-trim: 976 B-trim: 3304 in 1/64
Lambda= 0.157080
Kolmogorov-Smirnov statistic: 0.0246 (N=29) at 44
FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2
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join: 37, opt: 25, open/ext: -10/-2, width: 16
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gi|91175995|gb|ABE26579.1| Sequence 4 from patent ( 339) 2306 531.1 2.9e-148
gi|115833518|gb|ABJ40820.1| Sequence 3 from patent ( 339) 2306 531.1 2.9e-148
gi|148502355|gb|ABQ70609.1| Vanillate monooxygenas ( 351) 912 215.2 3.7e-53
gi|148500390|gb|ABQ68644.1| Vanillate monooxygenas ( 367) 832 197.1 1.1e-47
gi|148499658|gb|ABQ67912.1| Vanillate monooxygenas ( 359) 816 193.5 1.3e-46
gi|148499796|gb|ABQ68050.1| Vanillate monooxygenas ( 338) 813 192.8 2e-46
gi|148502359|gb|ABQ70613.1| Vanillate monooxygenas ( 350) 799 189.6 1.9e-45
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gi|148499650|gb|ABQ67904.1| Vanillate monooxygenas ( 423) 761 181.1 8.7e-43
gi|87135570|gb|ABD26312.1| Rieske (2Fe-2S) protein ( 356) 757 180.1 1.4e-42
gi|115284366|gb|ABJ89882.1| Vanillate monooxygenas ( 366) 756 179.9 1.7e-42
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gi|148501505|gb|ABQ69759.1| Vanillate monooxygenas ( 345) 721 171.9 3.9e-40
gi|17430690|emb|CAD17373.1| probable vanillate o-d ( 342) 719 171.5 5.3e-40
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gi|121552984|gb|ABM57133.1| Vanillate monooxygenas ( 352) 683 163.3 1.6e-37
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gi|87134412|gb|ABD25154.1| Rieske (2Fe-2S) protein ( 341) 678 162.2 3.3e-37
gi|160343813|gb|ABX16898.1| Rieske (2Fe-2S) domain ( 347) 678 162.2 3.4e-37
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gi|39650537|emb|CAE29060.1| putative vanillate O-d ( 347) 670 160.4 1.2e-36
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gi|124258972|gb|ABM93966.1| putative vanillate O-d ( 353) 662 158.6 4.2e-36
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gi 72121507 gb AAZ63693.1	Rieske (2Fe-2S) region	(350)	661	158.4	4.9e-36	gi 2271500 gb AAC27107.1	vanillate demethylase [A	(358)	613	147.5	9.4e-33
gi 219951453 gb ACL61845.1	Rieske (2Fe-2S) domain	(361)	661	158.4	5e-36	gi 28853329 gb AAO56397.1	vanillate O-demethylase	(354)	611	147.0	1.3e-32
gi 219676989 gb EED33354.1	vanillate demethylase	(346)	660	158.1	5.7e-36	gi 21111340 gb AAM39682.1	vanillate O-demethylase	(358)	610	146.8	1.5e-32
gi 120594588 gb ABM38027.1	Rieske (2Fe-2S) domain	(354)	659	157.9	6.8e-36	gi 66572050 gb AAY47460.1	vanillate O-demethylase	(358)	610	146.8	1.5e-32
gi 169759229 gb ACA72545.1	Rieske (2Fe-2S) domain	(355)	655	157.0	1.3e-35	gi 148501358 gb ABQ69612.1	Rieske (2Fe-2S) domain	(353)	607	146.1	2.4e-32
gi 237879482 gb ACR31814.1	Vanillate monooxygenas	(359)	655	157.0	1.3e-35	gi 160362386 gb ABX33999.1	Rieske (2Fe-2S) domain	(358)	607	146.1	2.4e-32
gi 87135187 gb ABD25929.1	Rieske (2Fe-2S) protein	(356)	654	156.8	1.5e-35	gi 78034363 emb CAJ22008.1	putative vanillate O-d	(358)	606	145.9	2.8e-32
gi 239805217 gb ACS22283.1	Rieske (2Fe-2S) domain	(352)	652	156.3	2e-35	gi 140896069 gb ECO23181.1	hypothetical protein G	(307)	605	145.6	2.9e-32
gi 223518190 gb EEF25490.1	oxidoreductase, putati	(293)	651	156.0	2e-35	gi 151280005 gb ABR88415.1	vanillate monooxygenas	(358)	605	145.7	3.3e-32
gi 124258969 gb ABM93963.1	putative vanillate O-d	(349)	651	156.1	2.4e-35	gi 21106440 gb AAM35255.1	vanillate O-demethylase	(358)	605	145.7	3.3e-32
gi 262260078 gb EEY78811.1	vanillate O-demethylas	(358)	651	156.1	2.4e-35	gi 167731545 emb CAP49720.1	oxygenase subunit [Xa	(358)	605	145.7	3.3e-32
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gi 33705318 gb AAQ29793.1	Sequence 6765 from pate	(392)	649	155.7	3.6e-35	gi 148501488 gb ABQ69742.1	Vanillate monooxygenas	(348)	603	145.2	4.4e-32
gi 68345132 gb AAY92738.1	vanillate O-demethylase	(352)	648	155.4	3.8e-35	gi 144012446 gb EDI23829.1	hypothetical protein G	(377)	600	144.5	7.6e-32
gi 91696118 gb ABE42947.1	Rieske (2Fe-2S) region	(350)	645	154.7	6.1e-35	gi 1790867 gb AAC44804.1	toluenesulfonate methyl-	(347)	599	144.3	8.3e-32
gi 171996654 gb ACB67572.1	Vanillate monooxygenas	(352)	642	154.0	9.7e-35	gi 239800225 gb ACS17292.1	Rieske (2Fe-2S) domain	(353)	599	144.3	8.4e-32
gi 213987796 gb ACS58095.1	Vanillate O-demethylas	(358)	642	154.1	9.9e-35	gi 57116474 gb AAW33716.1	IvaA [Comamonas testost	(359)	596	143.6	1.4e-31
gi 142041989 gb ECV10558.1	hypothetical protein G	(372)	641	153.8	1.2e-34	gi 256586463 gb ACU97596.1	vanillate demethylase	(377)	594	143.2	1.9e-31
gi 260409080 gb EEQ02383.1	vanillate O-demethylas	(358)	640	153.6	1.4e-34	gi 262208485 gb ACY32583.1	Rieske iron-sulfur pro	(354)	592	142.7	2.5e-31
gi 142223040 gb ECW51489.1	hypothetical protein G	(344)	638	153.1	1.8e-34	gi 143912782 gb EDH52778.1	hypothetical protein G	(284)	589	142.0	3.4e-31
gi 169149568 emb CAM87457.1	vanillate O-demethyla	(358)	638	153.1	1.9e-34	gi 91686245 gb ABE29445.1	Vanillate O-demethylase	(345)	590	142.3	3.4e-31
gi 213055323 gb ACJ40223.1	vanillate O-demethylas	(358)	638	153.1	1.9e-34	gi 142829789 gb EDA89889.1	hypothetical protein G	(329)	584	140.9	8.3e-31
gi 136477056 gb EBQ41570.1	hypothetical protein G	(367)	638	153.2	1.9e-34	gi 136134706 gb EBI14431.1	hypothetical protein G	(347)	582	140.4	1.2e-30
gi 150960710 gb ABR82735.1	vanillate O-demethylas	(351)	634	152.2	3.4e-34	gi 260645582 emb CBG68673.1	oxidoreductase alpha	(351)	579	139.8	1.9e-30
gi 77969155 gb ABB10534.1	Rieske (2Fe-2S) protein	(353)	634	152.2	3.4e-34	gi 3334811 emb CAA19959.1	oxidoreductase alpha su	(359)	578	139.5	2.3e-30
gi 260406928 gb EEX00406.1	vanillate O-demethylas	(358)	633	152.0	4.1e-34	gi 115391876 dbj BAF33363.1	alpha-subunit oxygena	(356)	577	139.3	2.7e-30
gi 136072874 gb EBL72690.1	hypothetical protein G	(360)	631	151.6	5.6e-34	gi 2765429 emb CAA75050.1	vanillate demethylase A	(353)	572	138.2	5.8e-30
gi 1946284 emb CAA72287.1	a-subunit oxygenase [Ps	(354)	630	151.3	6.4e-34	gi 88865992 gb ABD56869.1	Rieske (2Fe-2S) protein	(340)	568	137.3	1.1e-29
gi 6740889 emb CAB69476.1	VANILLINSAEURE-O-DEMETH	(354)	630	151.3	6.4e-34	gi 143981224 gb EDH01351.1	hypothetical protein G	(346)	567	137.0	1.3e-29
gi 262313627 gb EEY94677.1	vanillate O-demethylas	(358)	630	151.3	6.5e-34	gi 114050057 emb CAK51082.1	putative vanillate O-	(362)	565	136.6	1.8e-29
gi 229362611 emb CAY49519.1	oxidoreductase alpha	(353)	629	151.1	7.5e-34	gi 141537905 gb ECS21723.1	hypothetical protein G	(276)	557	137.4	5e-29
gi 63256651 gb AAY37747.1	Rieske [2Fe-2S] region	(354)	628	150.9	8.8e-34	gi 12543780 emb CAC26273.1	unnamed protein produc	(376)	558	135.0	5.5e-29
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gi 115284627 gb ABI90143.1	Rieske (2Fe-2S) domain	(353)	627	150.7	1e-33	gi 56674602 gb AAW21013.1	Sequence 412 from paten	(376)	558	135.0	5.5e-29
gi 227015885 gb ACP17982.1	putative vanillate-O-d	(354)	627	150.7	1e-33	gi 111921114 emb CAL31770.1	unnamed protein produ	(376)	558	135.0	5.5e-29
gi 262210840 gb ACY34938.1	vanillate monooxygenase	(358)	627	150.7	1e-33	gi 41326566 emb CAF21048.1	PROBABLE VANILLATE O-D	(376)	558	135.0	5.5e-29
gi 218774227 emb CAW30044.1	vanillate O-demethyla	(351)	626	150.4	1.2e-33	gi 140846270 dbj BAF55269.1	hypothetical protein	(376)	558	135.0	5.5e-29
gi 126170309 gb EAZ55820.1	vanillate O-demethylas	(351)	626	150.4	1.2e-33	gi 21325154 dbj BAB99776.1	Ferredoxin subunits of	(376)	558	135.0	5.5e-29
gi 115588274 gb ABJ14289.1	vanillate O-demethylas	(351)	626	150.4	1.2e-33	gi 256360258 gb ACU73755.1	Vanillate monooxygenas	(336)	557	134.8	5.9e-29
gi 9951180 gb AAG08289.1	AE004903_7 vanillate O-de	(351)	626	150.4	1.2e-33	gi 260422114 gb EEX15365.1	rieske domain protein	(356)	553	133.9	1.2e-28
gi 49086646 gb AAT51369.1	PA4904 [synthetic const	(352)	626	150.4	1.2e-33	gi 121552986 gb ABM57135.1	Vanillate monooxygenas	(363)	552	133.7	1.4e-28
gi 228390633 gb ACQ34586.1	Sequence 27100 from pa	(629)	626	150.6	2e-33	gi 134597525 gb EBC29366.1	hypothetical protein G	(290)	547	132.5	2.5e-28
gi 71556083 gb AAZ35294.1	vanillate monooxygenase	(354)	622	149.5	2.3e-33	gi 139017488 gb ECC83481.1	hypothetical protein G	(290)	546	132.3	2.9e-28
gi 57116471 gb AAW33713.1	VanA [Comamonas testost	(358)	622	149.5	2.3e-33	gi 143971374 gb EDH94724.1	hypothetical protein G	(368)	547	132.5	3.1e-28
gi 169760293 gb ACA73609.1	Vanillate monooxygenas	(358)	622	149.5	2.3e-33	gi 134135872 gb ABO56986.1	Rieske (2Fe-2S) domain	(334)	546	132.3	3.3e-28
gi 136769130 gb EBQ28347.1	hypothetical protein G	(381)	620	149.1	3.3e-33	gi 197711787 gb EDY55821.1	alpha-subunit oxygenas	(357)	544	131.8	4.8e-28
gi 166859664 gb ABY98071.1	Rieske (2Fe-2S) domain	(355)	619	148.8	3.6e-33	gi 138376444 gb EB224416.1	hypothetical protein G	(215)	541	131.1	5e-28
gi 13661652 gb AAK37996.1	monooxygenase Tsam2 [Co	(346)	616	148.2	5.7e-33	gi 148499651 gb ABQ67905.1	Rieske (2Fe-2S) domain	(366)	543	131.6	5.7e-28
gi 24985413 gb AAN69332.1	AE016570_9 vanillate dem	(355)	616	148.2	5.8e-33	gi 139762040 gb ECH28305.1	hypothetical protein G	(159)	538	130.3	6.2e-28
gi 148511307 gb ABQ78167.1	Rieske (2Fe-2S) domain	(355)	616	148.2	5.8e-33	gi 134434097 gb EBB32597.1	hypothetical protein G	(282)	538	130.4	1e-27
gi 109699452 gb ABG39372.1	Rieske (2Fe-2S) region	(349)	613	147.5	9.2e-33	gi 137774856 gb EBV92612.1	hypothetical protein G	(271)	537	130.2	1.1e-27

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gi 134642825 gb EBC56556.1	hypothetical protein G ( 365)	538	130.5	1.2e-27	gi 150836249 gb ABR70225.1	Rieske (2Fe-2S) domain ( 367)	497	121.2	7.9e-25
gi 237881549 gb EEP70377.1	oxygenase alpha subunit ( 347)	537	130.3	1.4e-27	gi 139085017 gb ECD30759.1	hypothetical protein G ( 238)	494	120.4	8.7e-25
gi 142848438 gb EDB03791.1	hypothetical protein G ( 389)	536	130.0	1.8e-27	gi 226241993 dbj BAH52341.1	putative vanillate de ( 355)	496	121.0	8.9e-25
gi 141169706 gb ECQ11356.1	hypothetical protein G ( 271)	531	128.8	2.9e-27	gi 136702430 gb EBP84318.1	hypothetical protein G ( 342)	493	120.3	1.4e-24
gi 239805806 gb ACS22872.1	Rieske (2Fe-2S) domain ( 341)	532	129.1	3e-27	gi 109455731 gb ABG31936.1	vanillate O-demethylas ( 356)	490	119.6	2.3e-24
gi 160362383 gb ABX33996.1	Vanillate monooxygenas ( 363)	532	129.1	3.2e-27	gi 148501502 gb ABQ69756.1	Rieske (2Fe-2S) domain ( 357)	490	119.6	2.3e-24
gi 139156205 gb ECD78682.1	hypothetical protein G ( 248)	529	128.4	3.7e-27	gi 139612925 gb ECG27281.1	hypothetical protein G ( 275)	488	119.1	2.5e-24
gi 136440917 gb EBO18192.1	hypothetical protein G ( 340)	529	128.4	4.8e-27	gi 124258931 gb ABM93925.1	vanillate O-demethylas ( 350)	488	119.1	3.1e-24
gi 144184117 gb EDJ48105.1	hypothetical protein G ( 345)	529	128.4	4.9e-27	gi 134567415 gb EBC11421.1	hypothetical protein G ( 275)	486	118.6	3.5e-24
gi 143059498 gb EDC51756.1	hypothetical protein G ( 367)	529	128.5	5.2e-27	gi 143951043 gb EDH80509.1	hypothetical protein G ( 341)	487	118.9	3.6e-24
gi 142657805 gb EC264376.1	hypothetical protein G ( 307)	527	128.0	6.1e-27	gi 148499179 gb ABQ67433.1	Vanillate monooxygenas ( 359)	487	118.9	3.7e-24
gi 23492471 dbj BAC17444.1	putative vanillate O-d ( 433)	528	128.3	6.9e-27	gi 93358317 gb ABF12405.1	Rieske (2Fe-2S) region ( 347)	486	118.7	4.2e-24
gi 91795559 gb ABE57698.1	Rieske (2Fe-2S) protein ( 370)	527	128.0	7.1e-27	gi 144058413 gb EDI56617.1	hypothetical protein G ( 346)	485	118.5	4.9e-24
gi 148499795 gb ABG68049.1	Rieske (2Fe-2S) domain ( 357)	526	127.8	8.1e-27	gi 134775120 gb EBD36480.1	hypothetical protein G ( 310)	484	118.2	5.3e-24
gi 86570282 gb ABD04839.1	Rieske (2Fe-2S) protein ( 355)	523	127.1	1.3e-26	gi 134869853 gb EBD97034.1	hypothetical protein G ( 250)	482	117.7	6e-24
gi 137103212 gb EBS22007.1	hypothetical protein G ( 266)	521	126.6	1.4e-26	gi 137095831 gb EBS17871.1	hypothetical protein G ( 264)	482	117.7	6.3e-24
gi 139880606 gb ECI09781.1	hypothetical protein G ( 234)	517	125.6	2.3e-26	gi 135004498 gb EBE87082.1	hypothetical protein G ( 280)	482	117.7	6.6e-24
gi 221532626 gb EEE35621.1	vanillate O-demethylas ( 349)	519	126.2	2.4e-26	gi 142987376 gb EDC00006.1	hypothetical protein G ( 341)	483	118.0	6.7e-24
gi 13423928 gb AAK24364.1	vanillate O-demethylase ( 353)	519	126.2	2.4e-26	gi 142840171 gb EDA97704.1	hypothetical protein G ( 256)	480	117.3	8.4e-24
gi 220964585 gb ACL95941.1	vanillate demethylase ( 358)	519	126.2	2.4e-26	gi 142992295 gb EDC03519.1	hypothetical protein G ( 346)	479	117.1	1.3e-23
gi 137343374 gb EBT56608.1	hypothetical protein G ( 259)	517	125.7	2.5e-26	gi 136282891 gb EBN11601.1	hypothetical protein G ( 352)	477	116.7	1.8e-23
gi 144200813 gb EDJ60354.1	hypothetical protein G ( 330)	516	125.5	3.6e-26	gi 140229246 gb ECK40344.1	hypothetical protein G ( 193)	473	115.6	2e-23
gi 72123638 gb AAZ65781.1	Rieske (2Fe-2S) region ( 358)	515	125.3	4.6e-26	gi 142800088 gb EBD67526.1	hypothetical protein G ( 341)	476	116.4	2e-23
gi 39777480 gb AAR31055.1	putative vanillate O-de ( 358)	515	125.3	4.6e-26	gi 135529038 gb EBI23049.1	hypothetical protein G ( 294)	474	115.9	2.4e-23
gi 148499652 gb ABQ67906.1	Vanillate monooxygenas ( 366)	514	125.1	5.4e-26	gi 137717616 gb EBV62362.1	hypothetical protein G ( 247)	473	115.7	2.4e-23
gi 143859144 gb EDH14233.1	hypothetical protein G ( 326)	513	124.8	5.8e-26	gi 214042208 gb EEB82847.1	vanillate O-demethylas ( 355)	469	114.8	6.2e-23
gi 136139601 gb EBM16475.1	hypothetical protein G ( 291)	512	124.5	6.1e-26	gi 139900290 gb ECI23331.1	hypothetical protein G ( 184)	463	113.3	9.1e-23
gi 141751505 gb ECT10418.1	hypothetical protein G ( 225)	509	123.8	7.9e-26	gi 137760795 gb EBV85123.1	hypothetical protein G ( 220)	463	113.4	1.1e-22
gi 115587352 gb ABJ13367.1	possible ferridoxin ox ( 370)	511	124.4	8.8e-26	gi 148502944 gb ABQ71198.1	Rieske (2Fe-2S) domain ( 365)	463	113.5	1.6e-22
gi 126196154 gb EAB260217.1	conserved hypothetical ( 370)	511	124.4	8.8e-26	gi 135815235 gb EBK01786.1	hypothetical protein G ( 284)	461	113.0	1.8e-22
gi 218769848 emb CAW25608.1	possible ferridoxin o ( 370)	511	124.4	8.8e-26	gi 198253612 gb EDY77926.1	Rieske (2Fe-2S) domain ( 346)	462	113.3	1.8e-22
gi 141300981 gb ECQ94038.1	hypothetical protein G ( 187)	507	123.3	9.2e-26	gi 139594311 gb ECG14416.1	hypothetical protein G ( 254)	460	112.7	1.9e-22
gi 228391904 gb ACQ35857.1	Sequence 28371 from pa ( 395)	511	124.4	9.3e-26	gi 255103564 gb EET46238.1	rieske domain protein ( 346)	461	113.0	2.1e-22
gi 142798150 gb EDA66094.1	hypothetical protein G ( 235)	508	123.6	9.6e-26	gi 139723903 gb ECH03449.1	hypothetical protein G ( 312)	460	112.8	2.3e-22
gi 148499659 gb ABQ67913.1	Rieske (2Fe-2S) domain ( 353)	509	123.9	1.2e-25	gi 227015857 gb ACP17954.1	putative Rieske (2Fe-2 ( 353)	458	112.4	3.5e-22
gi 109699475 gb ABG39395.1	Rieske (2Fe-2S) region ( 357)	508	123.7	1.4e-25	gi 88863615 gb ABD54492.1	vanillate O-demethylase ( 346)	456	111.9	4.7e-22
gi 86611381 gb ABD14374.1	vanillate monooxygenase ( 356)	506	123.2	1.9e-25	gi 138221046 gb EBY50770.1	hypothetical protein G ( 219)	453	111.1	5.1e-22
gi 148502364 gb ABQ70618.1	Rieske (2Fe-2S) domain ( 362)	506	123.2	1.9e-25	gi 142594318 gb ECZ19702.1	hypothetical protein G ( 345)	453	111.2	7.5e-22
gi 141448267 gb ECR89773.1	hypothetical protein G ( 287)	504	122.7	2.1e-25	gi 136702366 gb EBP84278.1	hypothetical protein G ( 140)	446	109.4	1e-21
gi 87135188 gb ABD25930.1	Rieske (2Fe-2S) protein ( 351)	505	123.0	2.2e-25	gi 137749005 gb EBV79093.1	hypothetical protein G ( 213)	447	109.7	1.3e-21
gi 110820674 gb ABG95958.1	possible vanillate mon ( 356)	505	123.0	2.2e-25	gi 151636 gb AAA26019.1	monooxygenase [Pseudomonas ( 329)	447	109.8	1.8e-21
gi 109456951 gb ABG33156.1	vanillate O-demethylas ( 346)	504	122.8	2.5e-25	gi 148499661 gb ABQ67915.1	Rieske (2Fe-2S) domain ( 367)	447	109.9	2e-21
gi 143007076 gb EDC13528.1	hypothetical protein G ( 349)	504	122.8	2.5e-25	gi 262081290 gb ACY17259.1	Rieske (2Fe-2S) iron-s ( 367)	443	109.0	3.8e-21
gi 91698468 gb ABE45297.1	Rieske (2Fe-2S) region ( 369)	503	122.6	3.1e-25	gi 141775929 gb ECT22978.1	hypothetical protein G ( 232)	439	108.0	4.8e-21
gi 137188961 gb EBS70004.1	hypothetical protein G ( 182)	499	121.5	3.2e-25	gi 134931314 gb EBE37840.1	hypothetical protein G ( 177)	437	107.4	5.3e-21
gi 143053217 gb EDC47173.1	hypothetical protein G ( 349)	502	122.3	3.4e-25	gi 138871099 gb ECC23345.1	hypothetical protein G ( 246)	433	106.6	1.3e-20
gi 8346964 emb CAB93956.1	a-subunit oxygenase [Ps ( 353)	501	122.1	4.1e-25	gi 139772531 gb ECH35548.1	hypothetical protein G ( 191)	430	105.9	1.7e-20
gi 198265864 gb EDY90134.1	vanillate O-demethylas ( 346)	499	121.6	5.5e-25	gi 140269621 gb ECK68336.1	hypothetical protein G ( 235)	428	105.5	2.7e-20
gi 133911987 emb CAM02100.1	oxidoreductase alpha ( 354)	499	121.6	5.6e-25	gi 141191184 gb ECQ25996.1	hypothetical protein G ( 279)	427	105.3	3.7e-20
gi 206677616 gb ED242103.1	vanillate O-demethylas ( 355)	499	121.6	5.6e-25	gi 169886511 gb ACB00225.1	Rieske [2Fe-2S] domain ( 367)	425	104.9	6.4e-20
gi 260221223 emb CBA29571.1	Vanillate O-demethyla ( 351)	497	121.2	7.6e-25	gi 139335678 gb ECE54697.1	hypothetical protein G ( 318)	423	104.4	7.8e-20

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gi 143576423 gb EDF71945.1	hypothetical protein G ( 240)	421	103.9	8.4e-20	gi 17133000 dbj BAB75565.1	all13866 [Nostoc sp. PC ( 351)	373	93.1	2.2e-16
gi 141046149 gb ECP26191.1	hypothetical protein G ( 297)	421	103.9	1e-19	gi 75701773 gb ABA21449.1	Rieske (2Fe-2S) region ( 347)	372	92.9	2.5e-16
gi 137076394 gb EBS07368.1	hypothetical protein G ( 279)	420	103.7	1.1e-19	gi 218173894 gb ACK72627.1	Rieske (2Fe-2S) domain ( 349)	371	92.6	3e-16
gi 109699460 gb ABG39380.1	Rieske (2Fe-2S) region ( 355)	417	103.1	2.2e-19	gi 38488613 dbj BAD02269.1	chlorophyllide a oxyge ( 366)	371	92.6	3.1e-16
gi 196179900 gb EDX74893.1	Pheophorbide a oxygena ( 449)	415	102.7	3.7e-19	gi 256640098 dbj BAI06060.1	ring-hydroxylating di ( 372)	371	92.6	3.1e-16
gi 138743966 gb ECB70949.1	hypothetical protein G ( 181)	410	101.3	3.7e-19	gi 256646210 dbj BAI12158.1	ring-hydroxylating di ( 372)	371	92.6	3.1e-16
gi 352124888 dbj BAC89863.1	gll1922 [Gloeobacter v ( 346)	411	101.7	5.5e-19	gi 256633986 dbj BAH99961.1	ring-hydroxylating di ( 372)	371	92.6	3.1e-16
gi 141513976 gb ECS12034.1	hypothetical protein G ( 127)	405	100.1	6e-19	gi 256643155 dbj BAI09110.1	ring-hydroxylating di ( 372)	371	92.6	3.1e-16
gi 143304066 gb EDE21627.1	hypothetical protein G ( 321)	408	101.0	8.3e-19	gi 256652249 dbj BAI18183.1	ring-hydroxylating di ( 372)	371	92.6	3.1e-16
gi 140942968 gb ECO55752.1	hypothetical protein G ( 126)	401	99.2	1.1e-18	gi 256637046 dbj BAI03015.1	ring-hydroxylating di ( 372)	371	92.6	3.1e-16
gi 139414646 gb ECE95275.1	hypothetical protein G ( 317)	404	100.1	1.5e-18	gi 256655306 dbj BAI21233.1	ring-hydroxylating di ( 372)	371	92.6	3.1e-16
gi 140437554 gb ECL74771.1	hypothetical protein G ( 200)	401	99.3	1.7e-18	gi 256649262 dbj BAI15203.1	ring-hydroxylating di ( 372)	371	92.6	3.1e-16
gi 143730143 gb EDG48919.1	hypothetical protein G ( 372)	404	100.1	1.8e-18	gi 256646317 dbj BAI12265.1	ring-hydroxylating di ( 375)	371	92.6	3.2e-16
gi 134415727 gb EBB21941.1	hypothetical protein G ( 298)	402	99.6	2e-18	gi 256649370 dbj BAI15311.1	ring-hydroxylating di ( 375)	371	92.6	3.2e-16
gi 187720150 gb ACD21373.1	Rieske (2Fe-2S) domain ( 406)	403	99.9	2.2e-18	gi 256643262 dbj BAI09217.1	ring-hydroxylating di ( 375)	371	92.6	3.2e-16
gi 148501356 gb ABQ69610.1	Vanillate monooxygenas ( 350)	397	98.5	5e-18	gi 256634093 dbj BAI00069.1	ring-hydroxylating di ( 375)	371	92.6	3.2e-16
gi 124261630 gb ABM96624.1	oxidoreductase alpha s ( 407)	397	98.6	5.7e-18	gi 256652356 dbj BAI18290.1	ring-hydroxylating di ( 375)	371	92.6	3.2e-16
gi 161786538 emb CAP56120.1	Vanillate O-demethyla ( 360)	396	98.3	6e-18	gi 256640205 dbj BAI06167.1	ring-hydroxylating di ( 375)	371	92.6	3.2e-16
gi 209530255 gb ACI50192.1	Rieske (2Fe-2S) domain ( 360)	396	98.3	6e-18	gi 256655414 dbj BAI21341.1	ring-hydroxylating di ( 375)	371	92.6	3.2e-16
gi 137915540 gb EBW73197.1	hypothetical protein G ( 127)	387	96.0	1e-17	gi 256637153 dbj BAI03122.1	ring-hydroxylating di ( 375)	371	92.6	3.2e-16
gi 209531301 gb ACI51238.1	Rieske (2Fe-2S) domain ( 357)	391	97.2	1.3e-17	gi 110168118 gb ABG52658.1	Rieske (2Fe-2S) region ( 349)	370	92.4	3.5e-16
gi 161784949 emb CAP54492.1	putative Ubiquinol-cy ( 369)	391	97.2	1.3e-17	gi 17134145 dbj BAB76706.1	alr5007 [Nostoc sp. PC ( 450)	371	92.7	3.7e-16
gi 39576876 emb CAE78105.1	oxidase-related protei ( 346)	390	96.9	1.5e-17	gi 58002640 gb AAW61534.1	Bacterial ring hydroxyl ( 390)	370	92.4	3.8e-16
gi 135783997 gb EBJ82099.1	hypothetical protein G ( 296)	389	96.7	1.5e-17	gi 142041602 gb ECV10171.1	hypothetical protein G ( 384)	368	92.0	5.2e-16
gi 138342750 gb EBZ08470.1	hypothetical protein G ( 229)	386	95.3	2e-17	gi 219863226 gb ACL43565.1	Rieske (2Fe-2S) domain ( 364)	366	91.5	6.8e-16
gi 81169725 gb ABBS8065.1	hypothetical protein Sy ( 345)	387	96.9	2.4e-17	gi 237878437 gb ACR30769.1	Rieske (2Fe-2S) domain ( 374)	366	91.5	6.9e-16
gi 139178314 gb ECD94316.1	hypothetical protein G ( 178)	383	95.2	2.5e-17	gi 196179242 gb EDX74238.1	Rieske (2Fe-2S) domain ( 357)	365	91.3	7.8e-16
gi 56687027 dbj BAD80249.1	unknown protein [Synec ( 233)	384	95.5	2.7e-17	gi 21106382 gb AAM35203.1	vanillate O-demethylase ( 350)	363	90.8	1e-15
gi 91692542 gb ABE35740.1	putative rieske (2Fe-2S ( 406)	385	95.8	3.7e-17	gi 77969476 gb ABB10855.1	Rieske (2Fe-2S) protein ( 382)	363	90.8	1.1e-15
gi 137465924 gb EBU25543.1	hypothetical protein G ( 153)	379	94.3	4.2e-17	gi 262210326 gb ACY34424.1	Rieske iron-sulfur pro ( 324)	362	90.6	1.1e-15
gi 142774561 gb EDA48526.1	hypothetical protein G ( 421)	383	95.4	5.3e-17	gi 138394402 gb EBZ36629.1	hypothetical protein G ( 164)	358	89.5	1.2e-15
gi 1653312 dbj BAA18227.1	3-chlorobenzoate-3,4-di ( 357)	382	95.1	5.4e-17	gi 270511044 gb ACZ89322.1	vanillate demethylase ( 380)	362	90.6	1.3e-15
gi 78034306 emb CAJ21951.1	putative vanillate O-d ( 350)	380	94.7	7.2e-17	gi 5478801 dbj BAA82481.1	chlorophyll b synthase ( 463)	363	90.9	1.3e-15
gi 219864921 gb ACL45260.1	Rieske (2Fe-2S) domain ( 338)	379	94.4	8.2e-17	gi 139466796 gb ECF29942.1	hypothetical protein G ( 249)	359	89.8	1.5e-15
gi 140496623 gb ECM01910.1	hypothetical protein G ( 261)	377	93.9	9e-17	gi 142154230 gb ECV99038.1	hypothetical protein G ( 467)	362	90.7	1.6e-15
gi 58002934 gb AAW61828.1	Bacterial ring hydroxyl ( 223)	376	93.7	9.3e-17	gi 218166439 gb ACK65176.1	Rieske (2Fe-2S) domain ( 362)	360	90.1	1.7e-15
gi 72122946 gb AAZ65132.1	Rieske (2Fe-2S) region ( 349)	378	94.2	9.9e-17	gi 136671391 gb EBP64062.1	hypothetical protein G ( 289)	356	89.2	2.7e-15
gi 158279835 gb EDP05594.1	predicted protein [Chl ( 349)	378	94.2	9.9e-17	gi 148501120 gb ABQ69374.1	Vanillate monooxygenas ( 361)	357	89.5	2.8e-15
gi 144118207 gb EDI99530.1	hypothetical protein G ( 146)	373	92.9	1e-16	gi 139910097 gb ECI30359.1	hypothetical protein G ( 123)	351	87.9	2.8e-15
gi 140536305 gb ECM14579.1	hypothetical protein G ( 172)	373	92.9	1.2e-16	gi 114315327 gb ABI61387.1	rieske [2Fe-2S] domain ( 350)	356	89.2	3.1e-15
gi 138041240 gb EBX42137.1	hypothetical protein G ( 316)	376	93.7	1.2e-16	gi 108461668 gb ABF86853.1	iron-sulfur cluster-bi ( 363)	354	88.8	4.4e-15
gi 141317276 gb ECR00474.1	hypothetical protein G ( 113)	370	92.2	1.3e-16	gi 53758618 gb AAU92909.1	putative dioxygenase, i ( 369)	354	88.8	4.5e-15
gi 197624747 gb EDY37306.1	rieske (2Fe-2S) domain ( 330)	375	93.5	1.5e-16	gi 169819074 gb ACA93656.1	Rieske (2Fe-2S) domain ( 373)	354	88.8	4.5e-15
gi 256634372 dbj BAI00348.1	vanillate O-demethyla ( 351)	375	93.5	1.6e-16	gi 124876018 gb EAY66008.1	Phenylpropionate dioxy ( 375)	354	88.8	4.6e-15
gi 256652635 dbj BAI18569.1	vanillate O-demethyla ( 351)	375	93.5	1.6e-16	gi 141884918 gb ECT92777.1	hypothetical protein G ( 216)	350	87.8	5.4e-15
gi 256640482 dbj BAI06444.1	vanillate O-demethyla ( 351)	375	93.5	1.6e-16	gi 93354602 gb ABF08691.1	Rieske (2Fe-2S) region ( 383)	353	88.6	5.4e-15
gi 256649647 dbj BAI15588.1	vanillate O-demethyla ( 351)	375	93.5	1.6e-16	gi 119694430 gb ABL91503.1	Rieske (2Fe-2S) domain ( 352)	352	88.3	5.9e-15
gi 256643539 dbj BAI09494.1	vanillate O-demethyla ( 351)	375	93.5	1.6e-16	gi 126234683 gb ABN98083.1	Rieske (2Fe-2S) domain ( 352)	352	88.3	5.9e-15
gi 256646594 dbj BAI12542.1	vanillate O-demethyla ( 351)	375	93.5	1.6e-16	gi 108769644 gb ABG08366.1	Rieske (2Fe-2S) region ( 352)	352	88.3	5.9e-15
gi 256655691 dbj BAI21618.1	vanillate O-demethyla ( 351)	375	93.5	1.6e-16	gi 167731479 emb CAP49654.1	oxygenase subunit [Xa ( 350)	350	87.9	8.1e-15
gi 256637430 dbj BAI03399.1	vanillate O-demethyla ( 351)	375	93.5	1.6e-16	gi 66571984 gb AAY47394.1	vanillate O-demethylase ( 350)	350	87.9	8.1e-15

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gi 21111267 gb AAM39616.1	vanillate O-demethylase ( 350)	350	87.9	8.1e-15	gi 196179229 gb EDX74225.1	Rieske (2Fe-2S) domain ( 371)	333	84.0	1.2e-13
gi 136314050 gb EBN32798.1	hypothetical protein G ( 131)	344	86.3	9e-15	gi 219864920 gb ACL45259.1	Rieske (2Fe-2S) domain ( 337)	332	83.8	1.3e-13
gi 162676019 gb EDQ62507.1	predicted protein [Phy ( 487)	351	88.2	9.1e-15	gi 169820134 gb ACA94716.1	Rieske (2Fe-2S) domain ( 356)	332	83.8	1.4e-13
gi 86557245 gb ABD02202.1	iron-sulfur cluster-bin ( 281)	348	87.4	9.2e-15	gi 77964331 gb ABB05712.1	Dioxygenase, iron-sulfu ( 371)	332	83.8	1.4e-13
gi 238767622 dbj BAH66650.1	chlorophyllide a oxyg ( 322)	347	87.2	1.2e-14	gi 3786324 dbj BAA33964.1	chlorophyll a oxygenase ( 463)	333	84.1	1.5e-13
gi 108460916 gb ABF86101.1	iron-sulfur cluster-bi ( 349)	347	87.2	1.3e-14	gi 142551094 gb ECY89541.1	hypothetical protein G ( 153)	327	82.5	1.5e-13
gi 59739317 gb AAW93227.1	Sequence 10790 from pat ( 349)	347	87.2	1.3e-14	gi 260223404 emb CBA33939.1	hypothetical protein ( 346)	331	83.6	1.6e-13
gi 196177991 gb EDX72993.1	Rieske (2Fe-2S) domain ( 353)	347	87.2	1.3e-14	gi 116650803 gb ABK11443.1	Rieske (2Fe-2S) domain ( 356)	331	83.6	1.6e-13
gi 162694938 gb EDQ81284.1	predicted protein [Phy ( 481)	348	87.5	1.4e-14	gi 105895386 gb ABF78550.1	Rieske (2Fe-2S) region ( 356)	331	83.6	1.6e-13
gi 219863225 gb ACL43564.1	Rieske (2Fe-2S) domain ( 358)	346	87.0	1.5e-14	gi 77969840 gb ABB11219.1	Rieske (2Fe-2S) protein ( 358)	331	83.6	1.6e-13
gi 270231846 emb CBI21171.1	unnamed protein produ ( 544)	348	87.5	1.6e-14	gi 61742126 gb AAX54904.1	chloroplast chlorophyll ( 645)	334	84.4	1.7e-13
gi 142043101 gb ECV11669.1	hypothetical protein G ( 389)	346	87.0	1.7e-14	gi 158284163 gb EDP09913.1	chlorophyll a oxygenas ( 645)	334	84.4	1.7e-13
gi 5478803 dbj BAA82482.1	chlorophyll b synthase ( 276)	344	86.5	1.7e-14	gi 256589581 gb ACV00468.1	Rieske (2Fe-2S) domain ( 450)	332	83.9	1.7e-13
gi 81169726 gb ABB58066.1	conserved hypothetical ( 334)	345	86.7	1.7e-14	gi 218160232 gb ACK60214.1	vanillate O-demethylas ( 315)	330	83.3	1.7e-13
gi 56687026 dbj BAD80248.1	hypothetical protein [ ( 340)	345	86.7	1.7e-14	gi 142156967 gb ECW01125.1	hypothetical protein G ( 338)	330	83.3	1.8e-13
gi 5478799 dbj BAA82480.1	chlorophyll b synthase ( 282)	343	86.2	2e-14	gi 198039740 emb CAR55710.1	[2Fe-2S]-binding prot ( 356)	330	83.3	1.9e-13
gi 68347720 gb AAY95326.1	Rieske 2Fe-2S domain pr ( 338)	343	86.3	2.4e-14	gi 115284140 gb ABT89656.1	Rieske (2Fe-2S) domain ( 356)	330	83.3	1.9e-13
gi 222855669 gb EEE93216.1	predicted protein [Pop ( 556)	344	86.6	3.1e-14	gi 171996106 gb ACB67024.1	Rieske (2Fe-2S) domain ( 356)	330	83.3	1.9e-13
gi 125541435 gb EAY87830.1	hypothetical protein O ( 539)	343	86.4	3.5e-14	gi 91692570 gb ABE35768.1	iron-sulfur cluster-bin ( 363)	330	83.4	1.9e-13
gi 125583977 gb EAE224908.1	hypothetical protein O ( 539)	343	86.4	3.5e-14	gi 218166847 gb ACK65584.1	Rieske (2Fe-2S) domain ( 450)	331	83.6	2e-13
gi 113537894 dbj BAF10277.1	Os02g0792800 [Oryza s ( 539)	343	86.4	3.5e-14	gi 256591555 gb ACV02442.1	Rieske (2Fe-2S) domain ( 362)	329	83.1	2.2e-13
gi 47497583 dbj BAD19653.1	putative Rieske iron-s ( 539)	343	86.4	3.5e-14	gi 218172648 gb ACK71381.1	Rieske (2Fe-2S) domain ( 367)	329	83.1	2.3e-13
gi 215767906 dbj BAH00135.1	unnamed protein produ ( 539)	343	86.4	3.5e-14	gi 140390532 gb ECL45063.1	hypothetical protein G ( 122)	323	81.5	2.3e-13
gi 215740658 dbj BAG97314.1	unnamed protein produ ( 539)	343	86.4	3.5e-14	gi 114462367 gb ABI75109.1	phenylpropionate dioxy ( 334)	328	82.9	2.5e-13
gi 47497136 dbj BAD19185.1	putative Rieske iron-s ( 539)	343	86.4	3.5e-14	gi 254215056 gb EET04441.1	iron-sulfur cluster-bi ( 355)	328	82.9	2.6e-13
gi 256589173 gb ACV00060.1	Rieske (2Fe-2S) domain ( 362)	340	85.6	4e-14	gi 126221945 gb ABN85450.1	iron-sulfur cluster-bi ( 355)	328	82.9	2.6e-13
gi 160363170 gb ABX34783.1	Rieske (2Fe-2S) domain ( 372)	339	85.4	4.8e-14	gi 169649758 gb EDS82451.1	iron-sulfur cluster-bi ( 355)	328	82.9	2.6e-13
gi 58001180 gb AAW60074.1	Putative ferredoxin sub ( 374)	339	85.4	4.8e-14	gi 126229834 gb ABN93247.1	iron-sulfur cluster-bi ( 355)	328	82.9	2.6e-13
gi 178463310 dbj BAG17830.1	putative oxygenase Ri ( 407)	339	85.4	5.2e-14	gi 147754352 gb EDR61416.1	iron-sulfur cluster-bi ( 355)	328	82.9	2.6e-13
gi 118172964 gb ABK73860.1	capreomycinidine hydroxy ( 364)	338	85.2	5.5e-14	gi 76584082 gb ABA53556.1	iron-sulfur cluster-bin ( 355)	328	82.9	2.6e-13
gi 169821251 gb ACA95832.1	Rieske (2Fe-2S) domain ( 371)	338	85.2	5.6e-14	gi 157937661 gb EDO93331.1	iron-sulfur cluster-bi ( 355)	328	82.9	2.6e-13
gi 223947409 gb ACN27788.1	unknown [Zea mays] ( 538)	340	85.7	5.6e-14	gi 121225811 gb ABM49342.1	iron-sulfur cluster-bi ( 355)	328	82.9	2.6e-13
gi 134134133 gb ABO58458.1	Rieske (2Fe-2S) domain ( 373)	338	85.2	5.6e-14	gi 160695365 gb EDP85335.1	iron-sulfur cluster-bi ( 355)	328	82.9	2.6e-13
gi 58003211 gb AAW62105.1	Ring-hydroxylating diox ( 363)	337	84.9	6.4e-14	gi 157809865 gb EDO87035.1	iron-sulfur cluster-bi ( 355)	328	82.9	2.6e-13
gi 189338875 dbj BAG47943.1	putative ring-hydroxy ( 370)	337	84.9	6.5e-14	gi 242134799 gb EES21202.1	iron-sulfur cluster-bi ( 355)	328	82.9	2.6e-13
gi 160345940 gb ABX19024.1	Rieske (2Fe-2S) domain ( 370)	337	84.9	6.5e-14	gi 52212334 emb CAH38358.1	Rieske [2Fe-2S] domain ( 355)	328	82.9	2.6e-13
gi 141223238 gb ECQ47191.1	hypothetical protein G ( 145)	331	83.4	7.6e-14	gi 147748407 gb EDK55482.1	iron-sulfur cluster-bi ( 355)	328	82.9	2.6e-13
gi 114462356 gb ABI75098.1	phenylpropionate dioxy ( 334)	335	84.5	8.2e-14	gi 52423115 gb AAU46685.1	iron-sulfur cluster-bin ( 355)	328	82.9	2.6e-13
gi 194740221 gb ACF94648.1	dioxygenase [Cylindros ( 334)	335	84.5	8.2e-14	gi 4559369 gb AAD23030.1	putative Rieske iron-sul ( 539)	330	83.4	2.7e-13
gi 140665805 gb ECM67079.1	hypothetical protein G ( 241)	333	83.9	8.5e-14	gi 223545335 gb EEF46840.1	chlorophyll a oxygenas ( 552)	330	83.4	2.7e-13
gi 158112838 gb ABW15035.1	Rieske (2Fe-2S) domain ( 353)	335	84.5	8.6e-14	gi 155273552 gb ABT29156.1	Sequence 116626 from p ( 558)	330	83.4	2.8e-13
gi 116652335 gb ABK12974.1	Rieske (2Fe-2S) domain ( 371)	335	84.5	8.9e-14	gi 138154685 gb EBY06010.1	hypothetical protein G ( 277)	326	82.4	2.9e-13
gi 105893329 gb ABF76494.1	Rieske (2Fe-2S) region ( 371)	335	84.5	8.9e-14	gi 187717400 gb ACD18623.1	Rieske (2Fe-2S) domain ( 352)	327	82.7	3e-13
gi 115286031 gb ABT191506.1	Rieske (2Fe-2S) domain ( 373)	335	84.5	9e-14	gi 151282074 gb ABR90484.1	Uncharacterized conser ( 354)	327	82.7	3e-13
gi 171997243 gb ACB68160.1	Rieske (2Fe-2S) domain ( 373)	335	84.5	9e-14	gi 124874609 gb EAY64599.1	Phenylpropionate dioxy ( 356)	327	82.7	3e-13
gi 184195262 gb ACC73226.1	Rieske (2Fe-2S) domain ( 374)	335	84.5	9e-14	gi 142023376 gb ECU93026.1	hypothetical protein G ( 386)	327	82.7	3.2e-13
gi 124879961 gb EAY67317.1	Phenylpropionate dioxy ( 386)	335	84.5	9.2e-14	gi 140289552 gb ECK76877.1	hypothetical protein G ( 285)	325	82.2	3.4e-13
gi 116223956 gb ABJ82665.1	Rieske (2Fe-2S) domain ( 363)	334	84.3	1e-13	gi 136043837 gb EBL53131.1	hypothetical protein G ( 328)	325	82.2	3.9e-13
gi 241932797 gb EES05942.1	hypothetical protein S ( 538)	336	84.8	1e-13	gi 224965794 emb CAX57326.1	vanillate O-demethyla ( 344)	325	82.2	4e-13
gi 136650361 gb EBP51022.1	hypothetical protein G ( 127)	328	82.7	1.1e-13	gi 124898885 gb EBP70728.1	Phenylpropionate dioxy ( 356)	324	82.0	4.9e-13
gi 83650472 gb ABC34536.1	iron-sulfur cluster-bin ( 355)	333	84.0	1.2e-13	gi 187720124 gb ACD21347.1	Rieske (2Fe-2S) domain ( 364)	324	82.0	5e-13



gi 28853256 gb AAO56324.1  iron-sulfur cluster-bin ( 358)	323	81.8	5.7e-13	gi 9949646 gb AAG06888.1 AE004770_13 conserved hyp ( 339)	313	79.5	2.6e-12
gi 166085962 dbj BAG00670.1  probable dioxygenase ( 446)	324	82.0	5.9e-13	gi 49087536 gb AAT51469.1  PA3500 [synthetic const ( 340)	313	79.5	2.6e-12
gi 195945036 emb CAR57661.1  putative oxidoreductas ( 371)	323	81.8	5.9e-13	gi 139895010 gb ECI19722.1  hypothetical protein G ( 258)	311	79.0	2.8e-12
gi 142407469 gb ECX84665.1  hypothetical protein G ( 371)	323	81.8	5.9e-13	gi 143755010 gb EDG61867.1  hypothetical protein G ( 393)	313	79.5	3e-12
gi 111148441 emb CAJ60112.1  putative oxidoreducta ( 383)	323	81.8	6e-13	gi 162667637 gb EDQ54262.1  predicted protein [Phy ( 507)	314	79.8	3.2e-12
gi 140334697 gb ECL05956.1  hypothetical protein G ( 224)	320	81.0	6.1e-13	gi 134439298 gb EBB35597.1  hypothetical protein G ( 300)	311	79.0	3.2e-12
gi 139083288 gb ECD29598.1  hypothetical protein G ( 225)	320	81.0	6.2e-13	gi 136689230 gb EBP75700.1  hypothetical protein G ( 374)	312	79.3	3.3e-12
gi 124258775 gb ABM93769.1  vanillate O-demethylas ( 331)	322	81.5	6.3e-13	gi 83636220 gb ABC32187.1  Phenylpropionate dioxyg ( 335)	311	79.0	3.6e-12
gi 140012252 gb ECI99833.1  hypothetical protein G ( 191)	319	80.7	6.3e-13	gi 186467244 gb ACC83045.1  Rieske (2Fe-2S) domain ( 340)	311	79.0	3.6e-12
gi 184213885 gb EDU10928.1  iron-sulfur cluster-bi ( 355)	322	81.5	6.6e-13	gi 226488393 emb CAX69282.1  unnamed protein produ ( 530)	313	79.6	3.8e-12
gi 142025673 gb ECU95155.1  hypothetical protein G ( 371)	322	81.5	6.9e-13	gi 137038624 gb EBR86001.1  hypothetical protein G ( 219)	308	78.3	4e-12
gi 195984486 gb ACG63831.1  SxtH [Lyngbya wollei] ( 342)	321	81.3	7.5e-13	gi 195984490 gb ACG63835.1  SxtDIOX [Lyngbya wolle ( 334)	310	78.8	4.1e-12
gi 194740217 gb ACF94646.1  dioxygenase [Lyngbya w ( 342)	321	81.3	7.5e-13	gi 137266085 gb EBT13443.1  hypothetical protein G ( 239)	308	78.3	4.3e-12
gi 91694040 gb ABE37237.1  putative oxygenase [Bur ( 359)	321	81.3	7.8e-13	gi 77969522 gb ABB10901.1  Rieske (2Fe-2S) protein ( 351)	310	78.8	4.3e-12
gi 218167754 gb ACK66491.1  Rieske (2Fe-2S) domain ( 362)	321	81.3	7.9e-13	gi 146404632 gb ABQ33138.1  putative dioxygenase [ ( 452)	311	79.1	4.6e-12
gi 226488387 emb CAX69279.1  unnamed protein produ ( 534)	323	81.8	8e-13	gi 222843959 gb EEE81506.1  predicted protein [Pop ( 472)	311	79.1	4.8e-12
gi 142211399 gb ECW42706.1  hypothetical protein G ( 444)	322	81.6	8e-13	gi 141761632 gb ECT15290.1  hypothetical protein G ( 156)	305	77.5	4.8e-12
gi 226488389 emb CAX69280.1  unnamed protein produ ( 535)	323	81.8	8e-13	gi 142552651 gb ECY90640.1  hypothetical protein G ( 290)	308	78.3	5e-12
gi 146196234 emb CAL80261.1  putative dioxygenase; ( 452)	322	81.6	8.1e-13	gi 238767600 dbj BAH66639.1  chlorophyllide a oxyg ( 297)	308	78.3	5.1e-12
gi 222866362 gb EEF03493.1  predicted protein [Pop ( 549)	323	81.9	8.2e-13	gi 137123744 gb EBB33561.1  hypothetical protein G ( 81)	300	76.2	6e-12
gi 140777051 gb ECN43462.1  hypothetical protein G ( 252)	318	80.6	9.3e-13	gi 270252402 emb CBI19013.1  unnamed protein produ ( 537)	310	78.9	6.2e-12
gi 135119834 gb EBF61882.1  hypothetical protein G ( 235)	317	80.3	1e-12	gi 13876511 gb AAK43487.1  AC084807_12 chlorophyll ( 536)	309	78.7	7.3e-12
gi 136362862 gb EBN65827.1  hypothetical protein G ( 341)	319	80.8	1e-12	gi 5853117 gb AAD54323.1  chlorophyll a oxygenase ( 536)	309	78.7	7.3e-12
gi 171696797 gb ACB49778.1  probable oxygenase [Cy ( 344)	319	80.8	1e-12	gi 22135956 gb AAM91560.1  chlorophyll a oxygenase ( 536)	309	78.7	7.3e-12
gi 141340995 gb ECR15369.1  hypothetical protein G ( 292)	318	80.6	1.1e-12	gi 25083487 gb AAN72086.1  chlorophyll a oxygenase ( 536)	309	78.7	7.3e-12
gi 160344582 gb ABX17667.1  Rieske (2Fe-2S) domain ( 356)	319	80.9	1.1e-12	gi 110737210 dbj BAF00553.1  chlorophyll a oxygena ( 536)	309	78.7	7.3e-12
gi 189337300 dbj BAG46369.1  vanillate monooxygena ( 356)	319	80.9	1.1e-12	gi 5478807 dbj BAA82484.1  chlorophyll b synthase ( 536)	309	78.7	7.3e-12
gi 140655229 gb ECM59732.1  hypothetical protein G ( 246)	317	80.3	1.1e-12	gi 6855279 dbj BAA90462.1  chlorophyll a oxygenase ( 536)	309	78.7	7.3e-12
gi 142169865 gb ECW11012.1  hypothetical protein G ( 252)	317	80.3	1.1e-12	gi 86572416 gb ABD06973.1  Rieske (2Fe-2S) protein ( 452)	308	78.4	7.3e-12
gi 142774526 gb EDA48491.1  hypothetical protein G ( 351)	318	80.6	1.2e-12	gi 24984845 gb AAN68820.1 AE016514_9 Rieske 2Fe-2S ( 341)	306	77.9	7.9e-12
gi 192283334 gb ACE99714.1  Phthalate 4,5-dioxygen ( 452)	319	80.9	1.3e-12	gi 238858999 dbj BAH70269.1  oxygenase component o ( 424)	307	78.2	8.1e-12
gi 39647906 emb CAE26426.1  possible phthalate dio ( 452)	319	80.9	1.3e-12	gi 60326839 gb AAX18934.1  isophthalate dioxygenas ( 424)	307	78.2	8.1e-12
gi 27349320 dbj BAC46335.1  bll1070 [Bradyrhizobiu ( 452)	319	80.9	1.3e-12	gi 88863485 gb ABD54362.1  putative dioxygenase [J ( 437)	307	78.2	8.3e-12
gi 162670942 gb EDQ57502.1  predicted protein [Phy ( 562)	320	81.2	1.3e-12	gi 71534968 gb AAZ32888.1  putative chlorophyll sy ( 219)	303	77.1	8.7e-12
gi 135150340 gb EBF81486.1  hypothetical protein G ( 232)	315	79.9	1.4e-12	gi 137322302 gb EBT44838.1  hypothetical protein G ( 272)	304	77.4	8.9e-12
gi 143280817 gb EDE09877.1  hypothetical protein G ( 284)	316	80.1	1.4e-12	gi 195984495 gb ACG63840.1  SxtT [Lyngbya wollei] ( 334)	305	77.7	9.1e-12
gi 140644004 gb ECM52005.1  hypothetical protein G ( 99)	310	78.5	1.5e-12	gi 113529180 emb CAJ95527.1  Ring-hydroxylating di ( 353)	305	77.7	9.5e-12
gi 135414375 gb EBH47833.1  hypothetical protein G ( 174)	313	79.3	1.5e-12	gi 196480021 gb ACG79549.1  putative phenylpropion ( 362)	305	77.7	9.7e-12
gi 114315506 gb ABI61566.1  vanillate demethylase ( 383)	317	80.4	1.6e-12	gi 238767608 dbj BAH66643.1  chlorophyllide a oxyg ( 304)	304	77.4	9.8e-12
gi 124291242 gb ABN00512.1  iron-sulfur cluster-bi ( 355)	316	80.2	1.7e-12	gi 223546843 gb EEF48340.1  chlorophyll synthase, ( 535)	307	78.2	9.9e-12
gi 148026042 gb EDK84165.1  iron-sulfur cluster-bi ( 355)	316	80.2	1.7e-12	gi 4981900 gb AAD36412.1 AE001788_7 oxidase-relate ( 321)	304	77.4	1e-11
gi 126239544 gb ABO02656.1  iron-sulfur cluster-bi ( 355)	316	80.2	1.7e-12	gi 143196631 gb EDD51367.1  hypothetical protein G ( 471)	305	77.7	1.2e-11
gi 35210587 dbj BAC87968.1  gl10027 [Gloeobacter v ( 360)	316	80.2	1.7e-12	gi 194740219 gb ACF94647.1  dioxygenase [Aphanizom ( 339)	303	77.2	1.3e-11
gi 194740223 gb ACF94649.1  dioxygenase [Anabaena ( 339)	315	79.9	1.9e-12	gi 195984468 gb ACG63814.1  SxtH [Aphanizomenon sp ( 339)	303	77.2	1.3e-11
gi 114462401 gb ABI75137.1  phenylpropionate dioxy ( 339)	315	79.9	1.9e-12	gi 238767620 dbj BAH66649.1  chlorophyllide a oxyg ( 299)	302	77.0	1.3e-11
gi 169759768 gb ACA73084.1  Rieske (2Fe-2S) domain ( 341)	315	79.9	1.9e-12	gi 110169366 gb ABG53906.1  Rieske (2Fe-2S) region ( 366)	303	77.2	1.3e-11
gi 226488391 emb CAX69281.1  unnamed protein produ ( 532)	317	80.5	2.1e-12	gi 2764524 emb CAA04157.1  Rieske iron-sulfur prot ( 553)	305	77.8	1.4e-11
gi 142743502 gb EDA25835.1  hypothetical protein G ( 158)	310	78.6	2.2e-12	gi 195984464 gb ACG63810.1  SxtT [Aphanizomenon sp ( 339)	302	77.0	1.5e-11
gi 143343923 gb EDE45798.1  hypothetical protein G ( 196)	311	78.9	2.3e-12	gi 247539755 gb ACT08376.1  Rieske (2Fe-2S) domain ( 344)	302	77.0	1.5e-11
gi 186464719 gb ACC80520.1  Rieske (2Fe-2S) domain ( 451)	315	80.0	2.4e-12	gi 239802711 gb ACS19778.1  Rieske (2Fe-2S) domain ( 347)	302	77.0	1.5e-11
gi 1652273 dbj BAA17196.1  phenoxybenzoate dioxyge ( 338)	313	79.5	2.6e-12	gi 143170231 gb EDD32240.1  hypothetical protein G ( 434)	303	77.3	1.6e-11

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gi 184195389 gb ACC73353.1	Rieske (2Fe-2S) domain ( 362)	302	77.0	1.6e-11	gi 86557316 gb ABD02273.1	iron-sulfur cluster-bin ( 339)	291	74.5	8.3e-11
gi 170176780 gb ACB09832.1	Rieske (2Fe-2S) domain ( 321)	301	76.8	1.6e-11	gi 138225709 gb EBY54127.1	hypothetical protein G ( 162)	287	73.4	8.3e-11
gi 214041652 gb EEB82299.1	oxidase-related protei ( 321)	301	76.8	1.6e-11	gi 254266513 emb CAX22277.1	putative rieske 2Fe-2 ( 361)	291	74.5	8.8e-11
gi 221572614 gb ACM23426.1	Rieske (2Fe-2S) domain ( 324)	301	76.8	1.7e-11	gi 218520996 gb ACK81581.1	Rieske (2Fe-2S) domain ( 361)	291	74.5	8.8e-11
gi 147736115 gb ABQ47455.1	Rieske (2Fe-2S) domain ( 324)	301	76.8	1.7e-11	gi 184198025 gb ACC75988.1	Phthalate 4,5-dioxygen ( 438)	292	74.8	8.8e-11
gi 40105970 gb AAR49909.1	Sequence 9626 from pate ( 350)	301	76.8	1.8e-11	gi 197625129 gb EDY37688.1	pheophorbide A oxygena ( 464)	292	74.8	9.3e-11
gi 254842208 gb EET20622.1	Rieske domain-containi ( 299)	300	76.5	1.8e-11	gi 136381519 gb EBN78606.1	hypothetical protein G ( 275)	289	74.0	9.5e-11
gi 91700848 gb ABE47021.1	Rieske (2Fe-2S) region ( 440)	302	77.0	1.8e-11	gi 140036246 gb ECJ16030.1	hypothetical protein G ( 103)	283	72.4	1.1e-10
gi 136770490 gb EBQ29255.1	hypothetical protein G ( 176)	297	75.7	1.9e-11	gi 195973390 gb ACG63333.1	(hypo)xanthine hydroxy ( 345)	289	74.0	1.2e-10
gi 142610362 gb EC230947.1	hypothetical protein G ( 448)	302	77.1	1.9e-11	gi 72122938 gb AAZ65124.1	Rieske (2Fe-2S) region ( 417)	290	74.3	1.2e-10
gi 237875904 gb ACR28237.1	Iron-sulfur cluster-bi ( 345)	300	76.5	2.1e-11	gi 262310695 gb EEY91784.1	conserved hypothetical ( 351)	289	74.1	1.2e-10
gi 141138302 gb ECP89253.1	hypothetical protein G ( 284)	298	76.0	2.4e-11	gi 162439504 gb ABX90772.1	Sequence 38 from paten ( 356)	289	74.1	1.2e-10
gi 15451611 gb AAK98735.1	AC090485_14 Putative cel ( 515)	301	76.9	2.5e-11	gi 117168631 gb ABK32295.1	JerL [Polyangium cellu ( 356)	289	74.1	1.2e-10
gi 5478797 dbj BAA82479.1	chlorophyll b synthase ( 356)	299	76.3	2.5e-11	gi 139764363 gb EBQ12672.1	hypothetical protein G ( 210)	286	73.3	1.2e-10
gi 219952182 gb ACL62573.1	Rieske (2Fe-2S) domain ( 448)	300	76.6	2.6e-11	gi 166088173 dbj BAG02881.1	pheophorbide a oxygen ( 460)	290	74.3	1.3e-10
gi 136901257 gb EBR13154.1	hypothetical protein G ( 190)	295	75.3	2.7e-11	gi 257478743 gb ACV59062.1	Rieske (2Fe-2S) iron-s ( 327)	288	73.8	1.3e-10
gi 167341526 gb AB268926.1	Sequence 19 from paten ( 343)	298	76.1	2.8e-11	gi 136745674 gb EBQ12672.1	hypothetical protein G ( 278)	287	73.5	1.3e-10
gi 32967993 gb AAP92508.1	capreomycinidine hydroxyl ( 343)	298	76.1	2.8e-11	gi 198268651 gb EDY92921.1	vanillate O-demethylas ( 356)	288	73.8	1.4e-10
gi 187728436 gb ACD29600.1	Rieske (2Fe-2S) domain ( 355)	298	76.1	2.9e-11	gi 238767604 dbj BAH66641.1	chlorophyllide a oxyg ( 264)	286	73.3	1.5e-10
gi 240868221 gb ACS65881.1	Rieske (2Fe-2S) domain ( 355)	298	76.1	2.9e-11	gi 214037983 gb EEB78647.1	Rieske (2Fe-2S) domain ( 388)	288	73.8	1.5e-10
gi 136402265 gb EBN92943.1	hypothetical protein G ( 120)	292	74.5	2.9e-11	gi 209958894 gb ACI99530.1	Rieske [2Fe-2S] domain ( 344)	287	73.6	1.6e-10
gi 72120742 gb AAZ62928.1	Rieske (2Fe-2S) region ( 355)	297	75.9	3.4e-11	gi 151569707 gb EDN35361.1	hypothetical protein F ( 298)	285	73.1	1.9e-10
gi 110289597 gb ABB48003.2	chlorophyll a oxygenas ( 526)	299	76.4	3.4e-11	gi 33632562 emb CAH07374.1	cell death suppressor ( 455)	287	73.7	2e-10
gi 110289598 gb AAP55073.2	chlorophyll a oxygenas ( 527)	299	76.4	3.4e-11	gi 91687753 gb ABE30953.1	Putative Rieske (2Fe-2S ( 348)	285	73.1	2.2e-10
gi 9944967 gb AAG03051.1	AF284781_1 LLS1 protein [ ( 540)	299	76.4	3.5e-11	gi 157121398 gb EDO65599.1	hypothetical protein F ( 298)	284	72.9	2.2e-10
gi 113639965 dbj BAF27270.1	Os10g0567400 [Oryza s ( 541)	299	76.4	3.5e-11	gi 240007189 gb ACG38415.1	putative rieske 2Fe-2S ( 361)	285	73.2	2.2e-10
gi 18855011 gb AAL79703.1	AC087599_22 putative chl ( 541)	299	76.4	3.5e-11	gi 260412376 gb EEX05672.1	rieske-type iron-sulfu ( 465)	286	73.4	2.4e-10
gi 110289596 gb ABB48002.2	chlorophyll a oxygenas ( 541)	299	76.4	3.5e-11	gi 136224491 gb EBM71849.1	hypothetical protein G ( 282)	283	72.6	2.5e-10
gi 215694378 dbj BAG89371.1	unnamed protein produ ( 541)	299	76.4	3.5e-11	gi 142810906 gb EDA75577.1	hypothetical protein G ( 236)	282	72.4	2.5e-10
gi 222613297 gb EEE51429.1	hypothetical protein O ( 541)	299	76.4	3.5e-11	gi 151572836 gb EDN38490.1	rieske domain protein ( 298)	283	72.7	2.6e-10
gi 218185043 gb EEC67470.1	hypothetical protein O ( 541)	299	76.4	3.5e-11	gi 13421968 gb AAK22722.1	Rieske 2Fe-2S family pr ( 367)	284	72.9	2.7e-10
gi 262078446 gb ACY14415.1	Rieske (2Fe-2S) iron-s ( 388)	297	75.9	3.6e-11	gi 220962883 gb ACL94239.1	ring hydroxylating dio ( 369)	284	72.9	2.7e-10
gi 158139847 gb ABW18159.1	Rieske (2Fe-2S) domain ( 324)	296	75.6	3.6e-11	gi 213385128 dbj BAG84256.1	putative oxygenase [S ( 381)	284	72.9	2.8e-10
gi 206565021 gb ACI06797.1	Rieske 2Fe-2S domain p ( 345)	296	75.6	3.8e-11	gi 142067585 gb ECV32064.1	hypothetical protein G ( 127)	278	71.3	2.8e-10
gi 238547017 dbj BAH63368.1	vanillate O-demethyla ( 345)	295	75.4	4.5e-11	gi 144581432 gb ABO99488.1	predicted protein [Ost ( 492)	285	73.2	2.9e-10
gi 141497980 gb ECS07057.1	hypothetical protein G ( 115)	289	73.8	4.5e-11	gi 137508742 gb EBU47530.1	hypothetical protein G ( 137)	278	71.4	3e-10
gi 163661695 gb ABY29062.1	Rieske (2Fe-2S) domain ( 361)	295	75.4	4.7e-11	gi 135049449 gb EBF16922.1	hypothetical protein G ( 137)	278	71.4	3e-10
gi 195645962 gb ACG42449.1	chlorophyllide a oxyge ( 542)	297	76.0	4.8e-11	gi 142148241 gb ECV94521.1	hypothetical protein G ( 137)	278	71.4	3e-10
gi 223948119 gb ACN28143.1	unknown [Zea mays] ( 542)	297	76.0	4.8e-11	gi 142177783 gb ECW17068.1	hypothetical protein G ( 137)	278	71.4	3e-10
gi 193225244 emb CAQ71186.1	putative oxidoreducta ( 353)	294	75.2	5.4e-11	gi 49529682 emb CAG67394.1	putative vanillate O-d ( 351)	283	72.7	3e-10
gi 18643160 gb AAL76235.1	AF441246_1 LppA [Pseudoa ( 370)	294	75.2	5.6e-11	gi 118424214 gb ABK90604.1	Rieske (2Fe-2S) domain ( 298)	282	72.4	3.1e-10
gi 241931118 gb EES04263.1	hypothetical protein S ( 542)	295	75.5	6.6e-11	gi 114738624 gb AB176749.1	Rieske 2Fe-2S family p ( 365)	283	72.7	3.1e-10
gi 108462453 gb ABF87638.1	iron-sulfur cluster-bi ( 330)	292	74.7	6.9e-11	gi 238767602 dbj BAH66640.1	chlorophyllide a oxyg ( 305)	282	72.4	3.1e-10
gi 114462397 gb AB175133.1	phenylpropionate dioxy ( 339)	292	74.7	7.1e-11	gi 111147441 emb CAJ59091.1	Vanillate O-demethyla ( 370)	283	72.7	3.1e-10
gi 136637539 gb EBP43441.1	hypothetical protein G ( 282)	291	74.5	7.1e-11	gi 262308558 gb EEY89692.1	vanillate demethylase ( 349)	282	72.5	3.5e-10
gi 194399727 gb ACF60811.1	Hpxd [Klebsiella pneum ( 345)	292	74.7	7.2e-11	gi 135060585 gb EBF24018.1	hypothetical protein G ( 351)	282	72.5	3.5e-10
gi 114341367 gb AB166647.1	Rieske (2Fe-2S) domain ( 349)	292	74.7	7.3e-11	gi 134048967 gb ABO46038.1	Rieske (2Fe-2S) domain ( 298)	281	72.2	3.6e-10
gi 262308548 gb EEY89682.1	phenylpropionate dioxy ( 351)	292	74.7	7.3e-11	gi 140540055 gb ECM15688.1	hypothetical protein G ( 248)	280	71.9	3.6e-10
gi 136485815 gb EBO47227.1	hypothetical protein G ( 245)	290	74.2	7.4e-11	gi 187717401 gb ACD18624.1	Rieske (2Fe-2S) domain ( 371)	282	72.5	3.7e-10
gi 194706992 gb ACF87580.1	unknown [Zea mays] ( 440)	293	75.0	7.6e-11	gi 78197761 gb ABB35526.1	cell death suppressor p ( 456)	283	72.7	3.8e-10
gi 145282453 gb ABP50035.1	Rieske (2Fe-2S) domain ( 326)	291	74.5	8e-11	gi 1652868 dbj BAA17786.1	slr1747 [Synechocystis ( 469)	283	72.8	3.8e-10

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gi 160361997 gb ABX33610.1	Rieske (2Fe-2S) domain ( 341)	281	72.2	4e-10	gi 261826768 gb ABM99526.2	Rieske [2Fe-2S] domain ( 330)	274	70.6	1.2e-09
gi 262211251 gb ACY35349.1	Rieske iron-sulfur pro ( 347)	281	72.2	4.1e-10	gi 148028210 gb EDK86170.1	rieske (2Fe-2S) domain ( 330)	274	70.6	1.2e-09
gi 187711880 gb ACD30177.1	rieske protein [Franci ( 298)	280	72.0	4.2e-10	gi 226514886 gb ACO60882.1	chlorophyllide a oxyge ( 436)	275	70.9	1.3e-09
gi 196190206 gb EDX85170.1	Rieske (2Fe-2S) domain ( 363)	281	72.2	4.2e-10	gi 183207931 gb ACC55329.1	Phenylpropionate dioxy ( 351)	273	70.4	1.4e-09
gi 142013456 gb ECU83474.1	hypothetical protein G ( 383)	281	72.3	4.4e-10	gi 147847687 emb CAK23238.1	Rieske-type iron-sulf ( 440)	274	70.7	1.5e-09
gi 142016742 gb ECU86644.1	hypothetical protein G ( 389)	281	72.3	4.5e-10	gi 167597081 gb ABZ87079.1	Rieske (2Fe-2S) domain ( 148)	268	69.1	1.5e-09
gi 247544636 gb ACT01655.1	Rieske (2Fe-2S) domain ( 325)	280	72.0	4.5e-10	gi 169886870 gb ACB00584.1	probable Rieske iron-s ( 452)	274	70.7	1.5e-09
gi 2815311 emb CAA16434.1	putative oxidase [Strep ( 395)	281	72.3	4.6e-10	gi 170656542 gb ACB25597.1	Rieske (2Fe-2S) domain ( 377)	273	70.4	1.5e-09
gi 142707050 gb ECZ99569.1	hypothetical protein G ( 137)	275	70.7	4.8e-10	gi 139625607 gb ECG34646.1	hypothetical protein G ( 217)	270	69.6	1.5e-09
gi 218170950 gb ACK69683.1	Rieske (2Fe-2S) domain ( 349)	280	72.0	4.8e-10	gi 194740227 gb ACF94651.1	dioxygenase [Anabaena ( 280)	271	69.9	1.6e-09
gi 18854993 gb AAL76685.1	AC087599_4 putative chlo ( 519)	282	72.6	4.9e-10	gi 238767606 dbj BAH66642.1	chlorophyllide a oxyg ( 338)	272	70.2	1.6e-09
gi 179343393 gb ACB78805.1	Rieske (2Fe-2S) domain ( 361)	280	72.0	4.9e-10	gi 194740229 gb ACF94652.1	dioxygenase [Anabaena ( 287)	271	69.9	1.7e-09
gi 222856087 gb EEE93634.1	predicted protein [Pop ( 531)	282	72.6	5e-10	gi 141754963 gb ECT12024.1	hypothetical protein G ( 249)	270	69.7	1.7e-09
gi 138997027 gb ECZ72348.1	hypothetical protein G ( 146)	275	70.7	5e-10	gi 83317156 gb ABC02752.1	chlorophyll synthase [P ( 541)	274	70.7	1.8e-09
gi 27349188 dbj BAC46203.1	blr0938 [Bradyrhizobiu ( 445)	281	72.3	5e-10	gi 137743221 gb EBV76113.1	hypothetical protein G ( 165)	267	68.9	2e-09
gi 215693283 dbj BAG88665.1	unnamed protein produ ( 542)	282	72.6	5.1e-10	gi 262257008 gb EEY75747.1	conserved hypothetical ( 351)	271	70.0	2e-09
gi 222613295 gb EEE51427.1	hypothetical protein O ( 542)	282	72.6	5.1e-10	gi 119537029 gb ABE1646.1	Rieske (2Fe-2S) domain ( 450)	272	70.3	2.1e-09
gi 113639962 dbj BAF27267.1	Osl0g0567100 [Oryza s ( 542)	282	72.6	5.1e-10	gi 4981841 gb AAD36358.1	AE001783_9 oxidase-relate ( 331)	270	69.7	2.2e-09
gi 78709025 gb ABB48000.1	chlorophyll a oxygenase ( 542)	282	72.6	5.1e-10	gi 260422803 gb EEEX16054.1	rieske domain protein ( 209)	267	69.0	2.4e-09
gi 218185041 gb EEC67468.1	hypothetical protein O ( 542)	282	72.6	5.1e-10	gi 120588290 gb ABM31730.1	Rieske (2Fe-2S) domain ( 373)	270	69.8	2.4e-09
gi 52211728 emb CAH37726.1	putative rieske iron-s ( 315)	279	71.8	5.1e-10	gi 136423865 gb EBO07155.1	hypothetical protein G ( 222)	267	69.0	2.5e-09
gi 86568240 gb ABD12049.1	Rieske (2Fe-2S) protein ( 352)	279	71.8	5.7e-10	gi 91795357 gb ABE57496.1	Rieske (2Fe-2S) protein ( 343)	269	69.5	2.7e-09
gi 136584258 gb EBF12311.1	hypothetical protein G ( 425)	280	72.1	5.7e-10	gi 213054564 gb ACQ39466.1	rieske protein [Acinet ( 351)	269	69.5	2.7e-09
gi 219864932 gb ACL45271.1	Pheophorbide a oxygena ( 477)	280	72.1	6.2e-10	gi 213985884 gb ACJ56183.1	Vanillate O-demethylas ( 351)	269	69.5	2.7e-09
gi 114227900 gb ABI57699.1	Rieske (2Fe-2S) domain ( 410)	279	71.8	6.4e-10	gi 260408434 gb EEEX01741.1	vanillate O-demethylas ( 351)	269	69.5	2.7e-09
gi 161165832 emb CAN97137.1	oxidase-related prote ( 341)	278	71.6	6.4e-10	gi 169150725 emb CAM88635.1	putative vanillate O- ( 351)	269	69.5	2.7e-09
gi 148906570 gb ABR16437.1	unknown [Picea sitchen ( 303)	277	71.3	6.8e-10	gi 253787589 dbj BAH84854.1	putative chlorophylli ( 235)	266	68.8	3.1e-09
gi 134331028 gb EBA69069.1	hypothetical protein G ( 400)	278	71.6	7.4e-10	gi 262312082 gb EEY93167.1	Rieske 2Fe-2S domain-c ( 350)	268	69.3	3.2e-09
gi 146404995 gb ABQ33501.1	hypothetical protein B ( 340)	277	71.3	7.5e-10	gi 5669516 gb AAD46364.1	AF161183_4 PrnD [Burkhold ( 373)	268	69.3	3.3e-09
gi 144105145 gb EDI90137.1	hypothetical protein G ( 456)	278	71.6	8.2e-10	gi 135216455 gb EBG22767.1	hypothetical protein G ( 376)	268	69.3	3.4e-09
gi 5478805 dbj BAA82483.1	chlorophyll b synthase ( 276)	275	70.8	8.6e-10	gi 91698753 gb ABE45582.1	Rieske (2Fe-2S) region ( 346)	267	69.1	3.7e-09
gi 140981200 gb ECO82358.1	hypothetical protein G ( 161)	272	70.0	8.7e-10	gi 139831559 gb ECH76917.1	hypothetical protein G ( 244)	265	68.5	3.7e-09
gi 138451861 gb EBZ76902.1	hypothetical protein G ( 134)	271	69.8	8.8e-10	gi 124879891 gb EAY67247.1	Phenylpropionate dioxy ( 362)	267	69.1	3.8e-09
gi 135277218 gb EBG58500.1	hypothetical protein G ( 241)	274	70.6	9e-10	gi 158514367 gb ABW69177.1	PrnD [Pseudomonas chlo ( 363)	267	69.1	3.8e-09
gi 242135271 gb EES21674.1	iron-sulfur cluster-bi ( 330)	275	70.9	1e-09	gi 141243793 gb ECQ61830.1	hypothetical protein G ( 122)	261	67.5	3.9e-09
gi 76582428 gb ABA51902.1	putative rieske iron-su ( 330)	275	70.9	1e-09	gi 138721812 gb ECB55276.1	hypothetical protein G ( 215)	264	68.3	3.9e-09
gi 83652080 gb ABC36144.1	Rieske [2Fe-2S] domain ( 330)	275	70.9	1e-09	gi 217036657 gb ACJ75179.1	oxidase-related protei ( 326)	266	68.8	4.1e-09
gi 254214188 gb EET03573.1	Rieske (2Fe-2S) domain ( 330)	275	70.9	1e-09	gi 142023156 gb ECU92806.1	hypothetical protein G ( 495)	268	69.4	4.2e-09
gi 126229373 gb ABN92786.1	iron-sulfur cluster-bi ( 330)	275	70.9	1e-09	gi 113524870 emb CAJ91215.1	conserved hypotherica ( 346)	266	68.8	4.3e-09
gi 157809462 gb EDO86632.1	iron-sulfur cluster-bi ( 330)	275	70.9	1e-09	gi 137031069 gb EBR81758.1	hypothetical protein G ( 291)	265	68.6	4.3e-09
gi 126221901 gb ABN85406.1	iron-sulfur cluster-bi ( 330)	275	70.9	1e-09	gi 193078401 gb ABO13374.2	putative vanillate O-d ( 351)	266	68.8	4.3e-09
gi 157937095 gb EDO92765.1	iron-sulfur cluster-bi ( 330)	275	70.9	1e-09	gi 155283394 gb ABT38998.1	Sequence 126468 from p ( 430)	267	69.1	4.4e-09
gi 169652293 gb EDS84986.1	iron-sulfur cluster-bi ( 330)	275	70.9	1e-09	gi 194295400 gb ACF40773.1	dioxygenase [Anabaena ( 270)	264	68.3	4.8e-09
gi 262312865 gb EEY93950.1	phenylpropionate dioxy ( 351)	275	70.9	1.1e-09	gi 170176820 gb ACB09872.1	Rieske (2Fe-2S) domain ( 331)	265	68.6	4.8e-09
gi 134395240 gb EBB10733.1	hypothetical protein G ( 305)	274	70.6	1.1e-09	gi 138115772 gb EBX83089.1	hypothetical protein G ( 96)	258	66.7	5.1e-09
gi 213385123 dbj BAG84251.1	putative oxygenase [S ( 442)	276	71.2	1.1e-09	gi 14597390 emb CAC43617.1	unnamed protein produc ( 363)	265	68.6	5.2e-09
gi 86568238 gb ABD12047.1	Rieske (2Fe-2S) protein ( 376)	275	70.9	1.1e-09	gi 1710901 gb AAB97507.1	aminopyrrolnitrin oxidas ( 363)	265	68.6	5.2e-09
gi 160697331 gb EDP87301.1	rieske (2Fe-2S) domain ( 330)	274	70.6	1.2e-09	gi 2487867 gb AAB76003.1	I51331 Sequence 5 from pa ( 363)	265	68.6	5.2e-09
gi 147748554 gb EDK55629.1	conserved hypothetical ( 330)	274	70.6	1.2e-09	gi 2490906 gb AAB79042.1	I63756 Sequence 5 from pa ( 363)	265	68.6	5.2e-09
gi 147754490 gb EDK61554.1	conserved hypothetical ( 330)	274	70.6	1.2e-09	gi 5969556 gb AAE10894.1	Sequence 5 from patent U ( 363)	265	68.6	5.2e-09
gi 126239639 gb ABO02751.1	Rieske [2Fe-2S] domain ( 330)	274	70.6	1.2e-09	gi 3205656 gb AAC19509.1	I85938 Sequence 5 from pa ( 363)	265	68.6	5.2e-09

gi 14597395 emb CAC43621.1  unnamed protein produc ( 363)	265	68.6	5.2e-09	gi 141645989 gb ECS644496.1  hypothetical protein G ( 193)	252	65.5	2.4e-08
gi 2487158 gb AAB75294.1 I48912 Sequence 5 from pa ( 363)	265	68.6	5.2e-09	gi 110820498 gb ABG95782.1  conserved hypothetical ( 348)	255	66.3	2.4e-08
gi 3006910 gb AAC09752.1 I70775 Sequence 5 from pa ( 363)	265	68.6	5.2e-09	gi 1935912 gb AAC49678.1  lethal leaf-spot 1 [Zea ( 505)	257	66.9	2.4e-08
gi 3410676 gb AAC31098.1 I90736 Sequence 5 from pa ( 363)	265	68.6	5.2e-09	gi 166089818 dbj BAG04526.1  rieske 2Fe-2S family ( 349)	255	66.3	2.4e-08
gi 142243980 gb ECW67021.1  hypothetical protein G ( 366)	265	68.6	5.3e-09	gi 15108632 gb AAE67668.1  Sequence 2 from patent ( 520)	257	66.9	2.5e-08
gi 238767610 dbj BAH66644.1  chlorophyllide a oxyg ( 318)	264	68.4	5.5e-09	gi 223624752 gb ACN06434.1  Sequence 38 from paten ( 520)	257	66.9	2.5e-08
gi 139522297 gb ECF64976.1  hypothetical protein G ( 277)	263	68.1	5.7e-09	gi 33769191 gb AAQ53822.1  Sequence 2 from patent ( 520)	257	66.9	2.5e-08
gi 169153723 emb CAP02924.1  putative vanillate O- ( 351)	264	68.4	5.9e-09	gi 68345267 gb AAY92873.1  aminopyrrolnitritin oxida ( 363)	255	66.4	2.5e-08
gi 260405089 gb EEW98589.1  phenylpropionate dioxy ( 351)	264	68.4	5.9e-09	gi 125542400 gb EAY88539.1  hypothetical protein O ( 526)	257	66.9	2.5e-08
gi 33703509 gb AAQ27984.1  Sequence 4956 from pate ( 364)	264	68.4	6.1e-09	gi 222624188 gb EEE58320.1  hypothetical protein O ( 526)	257	66.9	2.5e-08
gi 77964377 gb ABB5758.1  Rieske (2Fe-2S) protein ( 373)	264	68.4	6.3e-09	gi 113547429 dbj BAF10872.1  Os03g0146400 [Oryza s ( 529)	257	66.9	2.5e-08
gi 262310710 gb EEY91799.1  Rieske protein [Acinet ( 351)	263	68.2	7e-09	gi 113880945 gb ABI45903.1  cell death suppressor ( 440)	256	66.6	2.5e-08
gi 86568239 gb ABD12048.1  Rieske (2Fe-2S) protein ( 356)	263	68.2	7e-09	gi 112821583 dbj BAF03454.1  putative phthalate di ( 442)	256	66.6	2.5e-08
gi 75700483 gb ABA20159.1  Rieske (2Fe-2S) region ( 460)	264	68.4	7.5e-09	gi 239801270 gb ECS18337.1  Rieske (2Fe-2S) domain ( 449)	256	66.6	2.6e-08
gi 144578929 gb ABO96992.1  predicted protein [Ost ( 386)	263	68.2	7.5e-09	gi 136541802 gb EBO83181.1  hypothetical protein G ( 263)	253	65.8	2.6e-08
gi 83653728 gb ABC37791.1  Rieske [2Fe-2S] domain ( 326)	262	67.9	7.6e-09	gi 33566917 emb CAE39133.1  putative dioxygenase [ ( 478)	256	66.6	2.7e-08
gi 194740231 gb ACF94653.1  dioxygenase [Anabaena ( 235)	260	67.4	7.9e-09	gi 33577416 emb CAE37468.1  putative dioxygenase [ ( 478)	256	66.6	2.7e-08
gi 218166963 gb ACK65700.1  Rieske (2Fe-2S) domain ( 370)	262	67.9	8.5e-09	gi 142718743 gb EDA07950.1  hypothetical protein G ( 134)	249	64.8	2.8e-08
gi 254041194 gb ACT57989.1  Rieske (2Fe-2S) domain ( 374)	262	67.9	8.6e-09	gi 142042824 gb ECV11392.1  hypothetical protein G ( 411)	255	66.4	2.8e-08
gi 134433529 gb EBB32271.1  hypothetical protein G ( 90)	254	65.8	9e-09	gi 159029863 emb CAO90917.1  unnamed protein produ ( 349)	254	66.1	2.8e-08
gi 140288270 gb ECK76154.1  hypothetical protein G ( 84)	253	65.6	1e-08	gi 91686258 gb ABE29458.1  Putative rieske (2Fe-2S ( 433)	255	66.4	2.9e-08
gi 108465455 gb ABF90640.1  iron-sulfur cluster-bi ( 332)	260	67.5	1.1e-08	gi 260054816 gb ACX24433.1  Sequence 55397 from pa ( 535)	256	66.7	3e-08
gi 148500626 gb ABQ68880.1  Rieske (2Fe-2S) domain ( 343)	260	67.5	1.1e-08	gi 242137337 gb EES23740.1  PrnD [Burkholderia pse ( 370)	254	66.1	3e-08
gi 37962890 gb AAR05799.1  lethal leaf-spot 1 [Zea ( 197)	257	66.7	1.1e-08	gi 254216289 gb EET05674.1  PrnD [Burkholderia pse ( 370)	254	66.1	3e-08
gi 189186647 gb ACD83832.1  Ring-hydroxylating dio ( 359)	260	67.5	1.1e-08	gi 169650796 gb EDS83489.1  PrnD [Burkholderia pse ( 370)	254	66.1	3e-08
gi 158274708 gb EDP00489.1  pheophorbide a oxygena ( 542)	262	68.0	1.2e-08	gi 157810694 gb EDO87646.1  PrnD [Burkholderia pse ( 370)	254	66.1	3e-08
gi 138602569 gb ECA73585.1  hypothetical protein G ( 103)	253	65.6	1.2e-08	gi 126231459 gb ABN94872.1  PrnD [Burkholderia pse ( 370)	254	66.1	3e-08
gi 157323965 gb ABV43062.1  Rieske (2Fe-2S) domain ( 347)	259	67.3	1.3e-08	gi 108706168 gb ABF93963.1  Pheophorbide a oxygena ( 654)	257	66.9	3e-08
gi 226460859 gb EEH58153.1  chloroplast envelope p ( 289)	258	67.0	1.3e-08	gi 140763235 gb ECH34381.1  hypothetical protein G ( 107)	247	64.3	3.1e-08
gi 142477637 gb ECY36942.1  hypothetical protein G ( 358)	259	67.3	1.3e-08	gi 143754072 gb EDG61439.1  hypothetical protein G ( 327)	253	65.9	3.2e-08
gi 186463547 gb ACC79348.1  Rieske (2Fe-2S) domain ( 358)	259	67.3	1.3e-08	gi 223624750 gb ACN06432.1  Sequence 36 from paten ( 487)	255	66.4	3.2e-08
gi 140853574 gb ECN94651.1  hypothetical protein G ( 175)	255	66.2	1.4e-08	gi 115284763 gb ABI90279.1  Rieske (2Fe-2S) domain ( 370)	253	65.9	3.5e-08
gi 141810187 gb ECT40477.1  hypothetical protein G ( 217)	256	66.5	1.4e-08	gi 171996793 gb ACB67711.1  Rieske (2Fe-2S) domain ( 370)	253	65.9	3.5e-08
gi 158306287 gb ABW27904.1  pheophorbide A oxygena ( 458)	260	67.5	1.4e-08	gi 95007733 dbj BAE94192.1  Rieske-domain protein ( 453)	254	66.2	3.6e-08
gi 139775893 gb ECH37933.1  hypothetical protein G ( 151)	254	65.9	1.4e-08	gi 221737653 gb ACM30490.1  oxidoreductase protein ( 230)	250	65.1	3.7e-08
gi 154153178 gb ABS60410.1  Rieske (2Fe-2S) domain ( 324)	258	67.0	1.4e-08	gi 148498785 gb ABQ67039.1  Rieske (2Fe-2S) domain ( 344)	252	65.7	3.9e-08
gi 139868847 gb ECI02979.1  hypothetical protein G ( 195)	255	66.2	1.5e-08	gi 148500344 gb ABQ68598.1  Rieske (2Fe-2S) domain ( 350)	252	65.7	3.9e-08
gi 142673847 gb ECZ75755.1  hypothetical protein G ( 302)	257	66.8	1.6e-08	gi 78168733 gb ABB25830.1  cell death suppressor p ( 438)	253	65.9	4e-08
gi 116780249 gb ABK21605.1  unknown [Picea sitchen ( 180)	254	66.0	1.6e-08	gi 140935171 gb ECO50352.1  hypothetical protein G ( 266)	250	65.2	4.2e-08
gi 5969564 gb AAE10902.1  Sequence 27 from patent ( 370)	257	66.8	1.9e-08	gi 135141393 gb EBF75740.1  hypothetical protein G ( 287)	250	65.2	4.5e-08
gi 5669528 gb AAD46373.1 AF161186_4 PrnD [Burkhold ( 370)	257	66.8	1.9e-08	gi 158274709 gb EDP00490.1  pheophorbide a oxygena ( 526)	253	66.0	4.7e-08
gi 135987300 gb EBL16729.1  hypothetical protein G ( 278)	255	66.3	2e-08	gi 184215208 gb EDU12189.1  PrnD [Burkholderia pse ( 370)	251	65.5	4.8e-08
gi 158311119 gb ABW32732.1  conserved hypothetical ( 234)	254	66.0	2e-08	gi 196182990 gb EDX77974.1  Pheophorbide a oxygena ( 446)	252	65.7	4.8e-08
gi 226241763 dbj BAH52111.1  putative iron-sulfur ( 342)	256	66.6	2e-08	gi 111971101 gb ABH80052.1  Sequence 9895 from pat ( 371)	251	65.5	4.8e-08
gi 196192520 gb EDX87484.1  Pheophorbide a oxygena ( 503)	258	67.1	2.1e-08	gi 218522336 gb ACK82921.1  Rieske (2Fe-2S) domain ( 217)	248	64.7	4.9e-08
gi 256589694 gb ACV00581.1  Rieske (2Fe-2S) domain ( 349)	256	66.6	2.1e-08	gi 157807918 gb EDO85088.1  iron-sulfur cluster-bi ( 332)	250	65.2	5.1e-08
gi 171700762 gb ACB53743.1  putative rieske 2Fe-2S ( 349)	256	66.6	2.1e-08	gi 142564551 gb ECY98969.1  hypothetical protein G ( 402)	251	65.5	5.1e-08
gi 139853278 gb ECH92335.1  hypothetical protein G ( 263)	254	66.1	2.2e-08	gi 157915075 gb ABV96502.1  Phthalate 4,5-dioxygen ( 406)	251	65.5	5.2e-08
gi 1935909 gb AAC49676.1  lethal leaf-spot 1 [Zea ( 467)	257	66.9	2.3e-08	gi 184196023 gb ACC73987.1  Phthalate 4,5-dioxygen ( 422)	251	65.5	5.4e-08
gi 137271444 gb EBT16410.1  hypothetical protein G ( 230)	253	65.8	2.3e-08	gi 77970183 gb ABB11562.1  Rieske (2Fe-2S) protein ( 359)	250	65.2	5.5e-08
gi 223624747 gb ACN06429.1  Sequence 30 from paten ( 485)	257	66.9	2.3e-08	gi 239803515 gb ACS20582.1  Rieske (2Fe-2S) domain ( 360)	250	65.2	5.5e-08

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gi 143358220 gb EDE53858.1	hypothetical protein G ( 301)	249	65.0	5.5e-08	gi 198039509 emb CAR55476.1	Rieske iron-sulphur d ( 359)	245	64.1	1.2e-07
gi 93358319 gb ABF12407.1	Rieske (2Fe-2S) region ( 439)	251	65.5	5.5e-08	gi 136841640 gb EBQ76572.1	hypothetical protein G ( 307)	244	63.8	1.2e-07
gi 126223999 gb ABN87504.1	PrnD [Burkholderia pse ( 370)	250	65.2	5.6e-08	gi 142364634 gb ECX54854.1	hypothetical protein G ( 462)	246	64.4	1.3e-07
gi 142136843 gb ECV86003.1	hypothetical protein G ( 384)	250	65.2	5.8e-08	gi 124262336 gb ABM97325.1	Phthalate 4,5-dioxygen ( 470)	246	64.4	1.3e-07
gi 142387769 gb ECX70172.1	hypothetical protein G ( 465)	251	65.5	5.8e-08	gi 219950456 gb ACL60848.1	Rieske (2Fe-2S) domain ( 344)	244	63.8	1.4e-07
gi 141687272 gb ECS81341.1	hypothetical protein G ( 222)	247	64.4	5.8e-08	gi 49530168 emb CAG67880.1	putative vanillate O-d ( 353)	244	63.9	1.4e-07
gi 115421703 emb CAJ48214.1	putative iron-sulphur ( 408)	250	65.2	6.1e-08	gi 142821320 gb EDA83448.1	hypothetical protein G ( 316)	243	63.6	1.5e-07
gi 40063004 gb AAR37860.1	iron-sulfur cluster-bin ( 346)	249	65.0	6.2e-08	gi 136862647 gb EBQ90668.1	hypothetical protein G ( 331)	243	63.6	1.5e-07
gi 158306233 gb ABW27850.1	rieske 2Fe-2S domain p ( 507)	251	65.5	6.3e-08	gi 1612341 gb AAB15321.1	Sequence 2 from patent U ( 351)	243	63.6	1.6e-07
gi 31441772 emb CAA98235.2	C. elegans protein C12 ( 428)	250	65.3	6.3e-08	gi 140627675 gb ECM42069.1	hypothetical protein G ( 117)	237	62.0	1.6e-07
gi 9798391 emb CAC03538.1	lethal leaf-spot 1 homo ( 537)	251	65.5	6.6e-08	gi 179343859 gb ACB79271.1	Rieske (2Fe-2S) domain ( 357)	243	63.6	1.6e-07
gi 20260386 gb AAM13091.1	lethal leaf-spot 1 homo ( 537)	251	65.5	6.6e-08	gi 142754048 gb EDA33463.1	hypothetical protein G ( 359)	243	63.6	1.6e-07
gi 222839785 gb EEE78108.1	predicted protein [Pop ( 179)	245	63.9	6.6e-08	gi 241922363 gb EER95507.1	hypothetical protein S ( 524)	245	64.2	1.7e-07
gi 196185016 gb EDX79992.1	Rieske (2Fe-2S) domain ( 376)	249	65.0	6.7e-08	gi 41469408 gb AAS07231.1	putative iron-sulfur cl ( 527)	245	64.2	1.7e-07
gi 76582362 gb ABA51836.1	PrnD [Burkholderia pseu ( 346)	248	64.8	7.3e-08	gi 91686255 gb ABE29455.1	Putative rieske (2Fe-2S ( 446)	244	63.9	1.7e-07
gi 117168600 gb ABK32265.1	AmbP [Polyangium cellu ( 356)	248	64.8	7.4e-08	gi 136585751 gb EBP11254.1	hypothetical protein G ( 213)	240	62.8	1.7e-07
gi 182912733 gb ACC07798.1	Sequence 16 from paten ( 356)	248	64.8	7.4e-08	gi 125546115 gb EAY92254.1	hypothetical protein O ( 543)	245	64.2	1.7e-07
gi 136588915 gb EBP13266.1	hypothetical protein G ( 251)	246	64.2	7.6e-08	gi 113550102 dbj BAF13545.1	Os03g0805700 [Oryza s ( 543)	245	64.2	1.7e-07
gi 89077585 gb ABD60316.1	chloroplast pheophorbid ( 535)	250	65.3	7.7e-08	gi 108711641 gb ABF99436.1	Rieske domain containi ( 543)	245	64.2	1.7e-07
gi 141913542 gb ECU12779.1	hypothetical protein G ( 213)	245	64.0	7.7e-08	gi 222626003 gb EEE60135.1	hypothetical protein O ( 548)	245	64.2	1.7e-07
gi 89077587 gb ABD60317.1	chloroplast pheophorbid ( 538)	250	65.3	7.7e-08	gi 171698332 gb ACB51313.1	putative Rieske [2Fe-2 ( 465)	244	63.9	1.7e-07
gi 91693323 gb ABE36520.1	Putative Rieske (2Fe-2S ( 314)	247	64.5	7.8e-08	gi 151282076 gb ABR90486.1	Uncharacterized conser ( 231)	240	62.9	1.8e-07
gi 148500139 gb ABQ68393.1	Rieske (2Fe-2S) domain ( 400)	248	64.8	8.2e-08	gi 138492487 gb EBZ98854.1	hypothetical protein G ( 199)	239	62.6	1.9e-07
gi 37962886 gb AAR05797.1	accelerated cell death ( 537)	249	65.1	9e-08	gi 147849140 emb CAK24691.1	Putative dioxygenase ( 349)	242	63.4	1.9e-07
gi 1935914 gb AAC49679.1	lethal leaf-spot 1 homol ( 539)	249	65.1	9e-08	gi 137496591 gb EBU41334.1	hypothetical protein G ( 96)	235	61.5	1.9e-07
gi 15622052 dbj BAB66045.1	312aa long hypothetica ( 312)	246	64.3	9.1e-08	gi 158282066 gb EDP07819.1	pheophorbide A oxygena ( 365)	242	63.4	1.9e-07
gi 179344000 gb ACB79412.1	Rieske (2Fe-2S) domain ( 217)	244	63.7	9.2e-08	gi 262207954 gb ACY32052.1	Phenylpropionate dioxy ( 369)	242	63.4	2e-07
gi 139607548 gb ECG23461.1	hypothetical protein G ( 127)	241	63.0	9.3e-08	gi 169821506 gb ACA96087.1	Rieske (2Fe-2S) domain ( 374)	242	63.4	2e-07
gi 137759080 gb EBV84219.1	hypothetical protein G ( 138)	241	63.0	1e-07	gi 142416870 gb ECX91735.1	hypothetical protein G ( 452)	243	63.7	2e-07
gi 168198140 gb ACA20087.1	Rieske (2Fe-2S) domain ( 354)	246	64.3	1e-07	gi 268311703 gb ACY98077.1	Rieske (2Fe-2S) domain ( 326)	241	63.2	2.1e-07
gi 136470031 gb EBO37026.1	hypothetical protein G ( 255)	244	63.8	1e-07	gi 183177269 gb ACC42379.1	oxidoreductase [Mycoba ( 375)	241	63.2	2.3e-07
gi 27271989 gb AAN90915.1	Sequence 57 from patent ( 256)	244	63.8	1.1e-07	gi 229294832 gb EEN65486.1	hypothetical protein B ( 452)	242	63.5	2.3e-07
gi 52209659 emb CAH35615.1	putative iron-sulphur ( 321)	245	64.1	1.1e-07	gi 136973013 gb EBR48974.1	hypothetical protein G ( 89)	233	61.1	2.4e-07
gi 158273779 gb EDO99565.1	rieske iron-sulfur clu ( 563)	248	64.9	1.1e-07	gi 143469979 gb EDF15519.1	hypothetical protein G ( 489)	242	63.5	2.5e-07
gi 184210204 gb EDU07247.1	iron-sulfur cluster-bi ( 332)	245	64.1	1.1e-07	gi 226242296 dbj BAH52644.1	putative iron-sulfur ( 341)	240	62.9	2.5e-07
gi 169654256 gb EDS86949.1	iron-sulfur cluster-bi ( 332)	245	64.1	1.1e-07	gi 143964900 gb EDH90258.1	hypothetical protein G ( 359)	240	63.0	2.6e-07
gi 148027747 gb EDK85768.1	conserved domain prote ( 332)	245	64.1	1.1e-07	gi 223537039 gb EEF38675.1	pheophorbide A oxygena ( 531)	242	63.5	2.7e-07
gi 242140392 gb EES26794.1	iron-sulfur cluster-bi ( 332)	245	64.1	1.1e-07	gi 5669522 gb AAD46368.1	AF161185_3 PrnD [Myxococc ( 379)	240	63.0	2.8e-07
gi 147749259 gb EDK56333.1	conserved domain prote ( 332)	245	64.1	1.1e-07	gi 169239152 emb CAM60180.1	Putative oxygenase [M ( 385)	240	63.0	2.8e-07
gi 126226951 gb ABN90491.1	iron-sulfur cluster-bi ( 332)	245	64.1	1.1e-07	gi 110168798 gb ABG53338.1	Pheophorbide a oxygena ( 465)	241	63.2	2.8e-07
gi 157936627 gb EDO92297.1	iron-sulfur cluster-bi ( 332)	245	64.1	1.1e-07	gi 158303502 gb ABW25119.1	pheophorbide A oxygena ( 467)	241	63.2	2.8e-07
gi 160699661 gb EDP89631.1	conserved domain prote ( 332)	245	64.1	1.1e-07	gi 144018232 gb EDT27796.1	hypothetical protein G ( 290)	238	62.5	3e-07
gi 126218251 gb ABN81757.1	iron-sulfur cluster-bi ( 332)	245	64.1	1.1e-07	gi 225794057 gb ACO34147.1	Rieske 2Fe-2S domain p ( 367)	239	62.7	3.1e-07
gi 254218128 gb EDT07512.1	iron-sulfur cluster-bi ( 332)	245	64.1	1.1e-07	gi 209532947 gb ACI52884.1	Rieske (2Fe-2S) domain ( 221)	236	61.9	3.3e-07
gi 147753424 gb EDK60489.1	conserved domain prote ( 332)	245	64.1	1.1e-07	gi 161787554 emb CAP57150.1	putative oxidoreducta ( 223)	236	61.9	3.3e-07
gi 237505159 gb ACQ97477.1	Rieske (2Fe-2S) domain ( 332)	245	64.1	1.1e-07	gi 218171878 gb ACK70611.1	Pheophorbide a oxygena ( 474)	240	63.0	3.3e-07
gi 76578772 gb ABA48247.1	Rieske (2Fe-2S) domain ( 332)	245	64.1	1.1e-07	gi 162679590 gb EDQ66036.1	predicted protein [Phy ( 484)	240	63.0	3.4e-07
gi 260648326 emb CBG71437.1	putative oxidoreducta ( 406)	246	64.3	1.1e-07	gi 150956737 gb ABR78767.1	3-phenylpropionate dio ( 340)	238	62.5	3.4e-07
gi 148498950 gb ABQ67204.1	Rieske (2Fe-2S) domain ( 346)	245	64.1	1.2e-07	gi 195612454 gb ACG28057.1	pheophorbide a oxygena ( 525)	240	63.0	3.6e-07
gi 137979721 gb EBX09481.1	hypothetical protein G ( 244)	243	63.5	1.2e-07	gi 136513425 gb EBO65087.1	hypothetical protein G ( 289)	236	62.0	4.1e-07
gi 187720318 gb ACD21540.1	Rieske (2Fe-2S) domain ( 430)	246	64.4	1.2e-07	gi 136488516 gb EBO48965.1	hypothetical protein G ( 242)	235	61.7	4.1e-07

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gi 163662750 gb ABY30117.1	Rieske (2Fe-2S) domain ( 357)	237	62.3	4.2e-07	gi 155266717 gb ABT22321.1	Sequence 109791 from p ( 278)	229	60.4	1.2e-06
gi 148501158 gb ABQ69412.1	Phthalate 4,5-dioxygen ( 431)	238	62.5	4.2e-07	gi 255292310 dbj BAH89431.1	aromatic acid dioxyge ( 421)	231	60.9	1.2e-06
gi 225214839 gb ACN83573.1	Rieske (2Fe-2S) domain ( 327)	236	62.0	4.6e-07	gi 135381117 gb EBH25441.1	hypothetical protein G ( 264)	228	60.2	1.3e-06
gi 142625906 gb ECZ41886.1	hypothetical protein G ( 130)	231	60.7	4.6e-07	gi 124874885 gb EAY64875.1	Phenylpropionate dioxy ( 399)	230	60.7	1.4e-06
gi 240008267 gb ACS39493.1	rieske 2Fe-2S family p ( 357)	236	62.0	4.9e-07	gi 143496810 gb EDF31178.1	hypothetical protein G ( 490)	231	61.0	1.4e-06
gi 91690421 gb ABE33619.1	Putative phthalate 4,5- ( 440)	237	62.3	5e-07	gi 141354604 gb ECR24388.1	hypothetical protein G ( 298)	228	60.2	1.5e-06
gi 144038577 gb EDI42033.1	hypothetical protein G ( 383)	236	62.1	5.2e-07	gi 142228205 gb ECW55300.1	hypothetical protein G ( 451)	230	60.7	1.5e-06
gi 144580242 gb ABO98302.1	predicted protein [Ost ( 668)	239	62.9	5.2e-07	gi 143940190 gb EDH72838.1	hypothetical protein G ( 312)	228	60.2	1.5e-06
gi 156222436 gb EDO43280.1	predicted protein [Nem ( 324)	235	61.8	5.3e-07	gi 212515049 gb EEB17256.1	conserved hypothetical ( 452)	230	60.7	1.5e-06
gi 140817731 gb ECN72048.1	hypothetical protein G ( 225)	233	61.3	5.3e-07	gi 135155385 gb EBF84722.1	hypothetical protein G ( 86)	221	58.3	1.5e-06
gi 142444312 gb ECY12318.1	hypothetical protein G ( 165)	231	60.7	5.6e-07	gi 135567679 gb EBI47808.1	hypothetical protein G ( 157)	224	59.1	1.6e-06
gi 142270698 gb ECW86698.1	hypothetical protein G ( 115)	229	60.2	5.6e-07	gi 136397059 gb EBN89359.1	hypothetical protein G ( 274)	227	59.9	1.6e-06
gi 218522299 gb ACK82884.1	Rieske (2Fe-2S) domain ( 357)	235	61.8	5.7e-07	gi 142094314 gb ECV54168.1	hypothetical protein G ( 335)	228	60.2	1.6e-06
gi 254268118 emb CAX23994.1	rieske 2Fe-2S family ( 357)	235	61.8	5.7e-07	gi 75701004 gb ABA20680.1	Rieske (2Fe-2S) region ( 499)	230	60.8	1.7e-06
gi 136546517 gb EBO86181.1	hypothetical protein G ( 248)	233	61.3	5.8e-07	gi 135362450 gb EBH12902.1	hypothetical protein G ( 415)	229	60.5	1.7e-06
gi 240866389 gb ACS64050.1	Rieske (2Fe-2S) domain ( 443)	236	62.1	5.9e-07	gi 186464561 gb ACC80362.1	Rieske (2Fe-2S) domain ( 362)	228	60.2	1.7e-06
gi 240868533 gb ABX19384.1	Rieske (2Fe-2S) domain ( 443)	236	62.1	5.9e-07	gi 118169695 gb ABK70591.1	oxygenase KshA [Mycoba ( 386)	228	60.2	1.8e-06
gi 222873560 gb EEF10691.1	predicted protein [Pop ( 535)	237	62.4	5.9e-07	gi 226243772 dbj BAH54120.1	3-ketosteroid 9alpha- ( 387)	228	60.2	1.8e-06
gi 33577388 emb CAE34653.1	iron-sulphur protein [ ( 453)	236	62.1	6e-07	gi 139523114 gb ECF65372.1	hypothetical protein G ( 268)	226	59.7	1.9e-06
gi 135367246 gb EBH16123.1	hypothetical protein G ( 390)	235	61.8	6.2e-07	gi 142946240 gb EDB71089.1	hypothetical protein G ( 334)	227	60.0	1.9e-06
gi 137757369 gb EBV83338.1	hypothetical protein G ( 225)	232	61.0	6.2e-07	gi 91697231 gb ABE44060.1	Twin-arginine transloca ( 484)	229	60.5	1.9e-06
gi 142135610 gb ECV85086.1	hypothetical protein G ( 304)	233	61.3	6.9e-07	gi 139444422 gb ECF14208.1	hypothetical protein G ( 253)	225	59.5	2.1e-06
gi 162568916 gb ABY19384.1	pheophorbide A oxygena ( 531)	236	62.1	6.9e-07	gi 72001908 gb ABZ57710.1	rieske 2Fe-2S family pr ( 444)	228	60.3	2.1e-06
gi 138758991 gb ECB77564.1	hypothetical protein G ( 309)	233	61.3	7e-07	gi 123960625 gb ABM75408.1	Rieske iron-sulfur pro ( 444)	228	60.3	2.1e-06
gi 33564657 emb CAE43979.1	iron-sulphur protein [ ( 453)	235	61.9	7e-07	gi 142522838 gb ECY69151.1	hypothetical protein G ( 177)	223	58.9	2.1e-06
gi 186468971 gb ACC84772.1	Pheophorbide a oxygena ( 482)	235	61.9	7.4e-07	gi 238767612 dbj BAH66645.1	chlorophyllide a oxyg ( 151)	222	58.7	2.1e-06
gi 134743614 gb EBD15151.1	hypothetical protein G ( 192)	230	60.5	7.4e-07	gi 143930787 gb EDH65938.1	hypothetical protein G ( 328)	226	59.8	2.2e-06
gi 136060772 gb EBL64476.1	hypothetical protein G ( 340)	233	61.4	7.5e-07	gi 223505736 gb EEF22903.1	conserved hypothetical ( 197)	223	59.0	2.3e-06
gi 162568918 gb ABY19385.1	pheophorbide A oxygena ( 531)	235	61.9	8e-07	gi 17131188 dbj BAB73796.1	cell death suppressor ( 499)	228	60.3	2.3e-06
gi 4128221 gb AAD03558.1	phthalate dioxygenase [B ( 443)	234	61.6	8.1e-07	gi 140310383 gb ECK89066.1	hypothetical protein G ( 141)	221	58.4	2.4e-06
gi 160345391 gb ABX18476.1	Rieske (2Fe-2S) domain ( 443)	234	61.6	8.1e-07	gi 91686250 gb ABE29450.1	aromatic acid dioxygena ( 440)	227	60.1	2.4e-06
gi 189336514 dbj BAG45583.1	phthalate dioxygenase ( 443)	234	61.6	8.1e-07	gi 218172785 gb ACK71518.1	Pheophorbide a oxygena ( 442)	227	60.1	2.4e-06
gi 134136139 gb ABO57253.1	Rieske (2Fe-2S) domain ( 443)	234	61.6	8.1e-07	gi 54016833 dbj BAD58203.1	putative oxygenase [No ( 382)	226	59.8	2.5e-06
gi 140608503 gb ECM36643.1	hypothetical protein G ( 101)	226	59.5	8.1e-07	gi 110824764 gb ABH00047.1	terminal oxygenase Ksh ( 387)	226	59.8	2.5e-06
gi 118571171 gb ABL05922.1	oxidoreductase [Mycoba ( 375)	233	61.4	8.2e-07	gi 54016851 dbj BAD58221.1	putative oxygenase [No ( 391)	226	59.8	2.5e-06
gi 116787254 gb ABK24432.1	unknown [Picea sitchen ( 544)	235	61.9	8.2e-07	gi 148498618 gb ABQ66872.1	Rieske (2Fe-2S) domain ( 337)	225	59.5	2.6e-06
gi 224286860 gb ACN41133.1	unknown [Picea sitchen ( 544)	235	61.9	8.2e-07	gi 141889558 gb ECT95926.1	hypothetical protein G ( 283)	224	59.3	2.7e-06
gi 119954834 gb ABM11839.1	Rieske (2Fe-2S) domain ( 380)	233	61.4	8.3e-07	gi 142057758 gb ECV23464.1	hypothetical protein G ( 419)	226	59.8	2.7e-06
gi 226187717 dbj BAH35821.1	probable 3-ketosteroi ( 387)	233	61.4	8.4e-07	gi 51243146 gb AAT99362.1	unknown [Sphingomonas s ( 425)	226	59.8	2.7e-06
gi 110165481 gb ABG50021.1	Rieske (2Fe-2S) region ( 323)	232	61.1	8.4e-07	gi 145048130 gb ABP34757.1	Rieske (2Fe-2S) domain ( 519)	227	60.1	2.8e-06
gi 116058796 emb CAL54503.1	chloroplast chlorophy ( 327)	232	61.1	8.5e-07	gi 194740225 gb AC94650.1	dioxygenase [Anabaena ( 250)	223	59.0	2.8e-06
gi 22295419 dbj BAC09246.1	Rieske 2Fe-2S family p ( 357)	232	61.1	9.2e-07	gi 17133490 dbj BAB76053.1	alr4354 [Nostoc sp. PC ( 443)	226	59.8	2.8e-06
gi 141136066 gb ECP87946.1	hypothetical protein G ( 297)	231	60.9	9.2e-07	gi 262208136 gb ACY32234.1	Rieske iron-sulfur pro ( 443)	226	59.8	2.8e-06
gi 184194397 gb ACC72361.1	Phthalate 4,5-dioxygen ( 436)	233	61.4	9.3e-07	gi 86284239 gb ABC93299.1	probable oxidoreductase ( 213)	222	58.8	2.9e-06
gi 213385125 dbj BAG84253.1	putative oxygenase [S ( 366)	232	61.1	9.4e-07	gi 108461216 gb ABF86401.1	iron-sulfur cluster-bi ( 376)	225	59.6	2.9e-06
gi 112821359 dbj BAF03230.1	terminal oxygenase co ( 383)	232	61.2	9.8e-07	gi 30088964 gb AAP13565.1	lethal leaf spot 1-like ( 545)	227	60.1	2.9e-06
gi 84871618 dbj BAE75864.1	terminal oxygenase com ( 383)	232	61.2	9.8e-07	gi 91693683 gb ABE36880.1	Putative Rieske-type ri ( 387)	225	59.6	3e-06
gi 143258846 gb EDD95717.1	hypothetical protein G ( 331)	231	60.9	1e-06	gi 76162840 gb ABA40832.1	lethal leaf spot 1-like ( 563)	227	60.1	3e-06
gi 140898852 gb ECO24943.1	hypothetical protein G ( 168)	227	59.8	1.1e-06	gi 162695870 gb EDQ82212.1	predicted protein [Phy ( 475)	226	59.8	3e-06
gi 140706286 gb ECM95791.1	hypothetical protein G ( 204)	228	60.1	1.1e-06	gi 141042250 gb ECP23509.1	hypothetical protein G ( 275)	223	59.0	3e-06
gi 135410418 gb EBH45163.1	hypothetical protein G ( 447)	232	61.2	1.1e-06	gi 140245769 gb ECK51996.1	hypothetical protein G ( 282)	223	59.0	3.1e-06

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gi 134886969 gb EBE08404.1	hypothetical protein G ( 238)	222	58.8	3.1e-06	gi 161160737 emb CAN92042.1	hypothetical protein ( 307)	219	58.2	6.2e-06
gi 140216761 gb ECK32010.1	hypothetical protein G ( 243)	222	58.8	3.2e-06	gi 240863557 gb ACS61219.1	Rieske (2Fe-2S) domain ( 217)	217	57.6	6.4e-06
gi 223533590 gb EEF35329.1	pheophorbide A oxygena ( 248)	222	58.8	3.2e-06	gi 2271506 gb AAC27113.1	unknown [Acinetobacter s ( 316)	219	58.2	6.4e-06
gi 17133694 dbj BAB76257.1	all4558 [Nostoc sp. PC ( 363)	224	59.3	3.3e-06	gi 145217630 gb ABP47034.1	Rieske (2Fe-2S) domain ( 386)	220	58.4	6.5e-06
gi 140653723 gb ECM58685.1	hypothetical protein G ( 100)	217	57.5	3.3e-06	gi 136835681 gb EBQ72611.1	hypothetical protein G ( 466)	221	58.7	6.5e-06
gi 136066179 gb EBL68164.1	hypothetical protein G ( 210)	221	58.5	3.3e-06	gi 162666703 gb EDQ53350.1	predicted protein [Phy ( 474)	221	58.7	6.6e-06
gi 16973465 gb AAL32300.1	AF321984_1 lethal leaf s ( 537)	226	59.9	3.3e-06	gi 136267227 gb EBN00889.1	hypothetical protein G ( 193)	216	57.4	6.7e-06
gi 169242673 emb CAM63701.1	Possible oxidoreducta ( 379)	224	59.3	3.4e-06	gi 262299136 gb EEY87049.1	phenylpropionate dioxy ( 355)	219	58.2	7.1e-06
gi 54015725 dbj BAD57095.1	putative terminal oxyg ( 395)	224	59.3	3.5e-06	gi 136010304 gb EBL30470.1	hypothetical protein G ( 297)	218	57.9	7.1e-06
gi 143248957 gb EDD88629.1	hypothetical protein G ( 277)	222	58.8	3.6e-06	gi 72118679 gb AAZ60942.1	Rieske (2Fe-2S) region ( 358)	219	58.2	7.1e-06
gi 260410790 gb EEX04088.1	phenylpropionate dioxy ( 355)	223	59.1	3.8e-06	gi 72123473 gb AAZ65627.1	Phthalate 4,5-dioxygena ( 437)	220	58.5	7.2e-06
gi 193076681 gb ABO11379.2	putative vanillate O-d ( 355)	223	59.1	3.8e-06	gi 140772195 gb ECN40093.1	hypothetical protein G ( 251)	217	57.7	7.2e-06
gi 169149783 emb CAM87674.1	putative vanillate O- ( 355)	223	59.1	3.8e-06	gi 154159079 gb ABS66295.1	Phthalate 4,5-dioxygen ( 454)	220	58.5	7.4e-06
gi 213055913 gb ACJ40815.1	rieske (2Fe-2S) protei ( 355)	223	59.1	3.8e-06	gi 226240116 dbj BAH13547.1	3-ketosteroid 9alpha- ( 397)	219	58.2	7.8e-06
gi 183208823 gb ACC56221.1	Phenylpropionate dioxy ( 355)	223	59.1	3.8e-06	gi 110819011 gb ABG94295.1	probable dioxygenase R ( 397)	219	58.2	7.8e-06
gi 260405780 gb EEW99269.1	phenylpropionate dioxy ( 355)	223	59.1	3.8e-06	gi 143239232 gb EDD81927.1	hypothetical protein G ( 275)	217	57.7	7.8e-06
gi 213987162 gb ACJ57461.1	Vanillate O-demethylas ( 355)	223	59.1	3.8e-06	gi 166915668 gb ABZ02687.1	accelerated cell death ( 92)	211	56.1	7.9e-06
gi 33704514 gb AAQ28989.1	Sequence 5961 from pate ( 363)	223	59.1	3.8e-06	gi 166915564 gb ABZ02635.1	accelerated cell death ( 80)	210	55.8	8.2e-06
gi 226434019 gb ACO56118.1	pheide a oxygenase [Vi ( 539)	225	59.6	3.9e-06	gi 197718889 gb EDY62797.1	Rieske domain-containi ( 355)	218	58.0	8.3e-06
gi 270228317 emb CBI17127.1	unnamed protein produ ( 539)	225	59.6	3.9e-06	gi 166915524 gb ABZ02615.1	accelerated cell death ( 81)	210	55.8	8.3e-06
gi 155289343 gb ABT44947.1	Sequence 132417 from p ( 541)	225	59.6	3.9e-06	gi 166915534 gb ABZ02620.1	accelerated cell death ( 81)	210	55.8	8.3e-06
gi 139175118 gb ECD92207.1	hypothetical protein G ( 258)	221	58.6	3.9e-06	gi 170938721 emb CAP63708.1	putative oxydoreducta ( 358)	218	58.0	8.3e-06
gi 141157440 gb ECQ02595.1	hypothetical protein G ( 180)	219	58.0	4e-06	gi 113550104 dbj BAH13547.1	Os03g0805900 [Oryza s ( 525)	220	58.5	8.4e-06
gi 119956670 gb ABM13675.1	Rieske (2Fe-2S) domain ( 385)	223	59.1	4e-06	gi 222629206 gb EEE61338.1	hypothetical protein O ( 525)	220	58.5	8.4e-06
gi 143107220 gb EDC86592.1	hypothetical protein G ( 331)	222	58.9	4.1e-06	gi 125546117 gb EAY92256.1	hypothetical protein O ( 525)	220	58.5	8.4e-06
gi 140364930 gb ECL27102.1	hypothetical protein G ( 276)	221	58.6	4.2e-06	gi 108711643 gb ABF99438.1	Rieske domain containi ( 525)	220	58.5	8.4e-06
gi 110822304 gb ABG97588.1	probable dioxygenase R ( 401)	223	59.1	4.2e-06	gi 30102995 gb AAP21408.1	putative cell death sup ( 525)	220	58.5	8.4e-06
gi 141198162 gb ECQ29793.1	hypothetical protein G ( 282)	221	58.6	4.2e-06	gi 136552145 gb EBO89810.1	hypothetical protein G ( 376)	218	58.0	8.7e-06
gi 141099034 gb ECP61797.1	hypothetical protein G ( 284)	221	58.6	4.3e-06	gi 223624748 gb ACN06430.1	Sequence 32 from paten ( 563)	220	58.5	8.9e-06
gi 121554515 gb ABM58664.1	phthalate 4,5-dioxygen ( 445)	223	59.1	4.6e-06	gi 166915682 gb ABZ02694.1	accelerated cell death ( 89)	210	55.8	9e-06
gi 81169854 gb ABB58194.1	cell death suppressor p ( 461)	223	59.2	4.7e-06	gi 166915652 gb ABZ02679.1	accelerated cell death ( 90)	210	55.9	9.1e-06
gi 56686899 dbj BAD80121.1	cell death suppressor ( 461)	223	59.2	4.7e-06	gi 134846781 gb EBD81759.1	hypothetical protein G ( 397)	218	58.0	9.1e-06
gi 41469411 gb AAS07234.1	putative iron-sulfur cl ( 521)	223	59.2	5.2e-06	gi 119537405 gb ABL82022.1	Rieske (2Fe-2S) domain ( 398)	218	58.0	9.1e-06
gi 196180400 gb EDX75391.1	Pheophorbide a oxygena ( 443)	222	58.9	5.3e-06	gi 166915520 gb ABZ02613.1	accelerated cell death ( 91)	210	55.9	9.1e-06
gi 189187201 gb ACD84386.1	Ring-hydroxylating dio ( 309)	220	58.4	5.4e-06	gi 166915592 gb ABZ02649.1	accelerated cell death ( 92)	210	55.9	9.2e-06
gi 139123289 gb ECD57475.1	hypothetical protein G ( 179)	217	57.6	5.4e-06	gi 166915566 gb ABZ02636.1	accelerated cell death ( 92)	210	55.9	9.2e-06
gi 136378675 gb EBN76637.1	hypothetical protein G ( 216)	218	57.9	5.4e-06	gi 166915680 gb ABZ02693.1	accelerated cell death ( 92)	210	55.9	9.2e-06
gi 209537783 gb ACI57717.1	Rieske (2Fe-2S) domain ( 216)	218	57.9	5.4e-06	gi 166915552 gb ABZ02629.1	accelerated cell death ( 92)	210	55.9	9.2e-06
gi 139862696 gb ECH98703.1	hypothetical protein G ( 104)	214	56.8	5.5e-06	gi 166915658 gb ABZ02682.1	accelerated cell death ( 92)	210	55.9	9.2e-06
gi 134663165 gb EBC68413.1	hypothetical protein G ( 274)	219	58.1	5.7e-06	gi 166915616 gb ABZ02661.1	accelerated cell death ( 92)	210	55.9	9.2e-06
gi 143205868 gb EDD58113.1	hypothetical protein G ( 330)	220	58.4	5.7e-06	gi 166915708 gb ABZ02707.1	accelerated cell death ( 92)	210	55.9	9.2e-06
gi 134440420 gb EBB36264.1	hypothetical protein G ( 334)	220	58.4	5.7e-06	gi 166915562 gb ABZ02634.1	accelerated cell death ( 92)	210	55.9	9.2e-06
gi 138112303 gb EBX81114.1	hypothetical protein G ( 282)	219	58.1	5.8e-06	gi 166915610 gb ABZ02658.1	accelerated cell death ( 92)	210	55.9	9.2e-06
gi 138961436 gb ECC60084.1	hypothetical protein G ( 235)	218	57.9	5.8e-06	gi 166915678 gb ABZ02692.1	accelerated cell death ( 92)	210	55.9	9.2e-06
gi 141220464 gb ECQ45253.1	hypothetical protein G ( 238)	218	57.9	5.9e-06	gi 166915644 gb ABZ02675.1	accelerated cell death ( 92)	210	55.9	9.2e-06
gi 117168629 gb ABK32293.1	JerP [Polyangium cellu ( 352)	220	58.4	6e-06	gi 166915648 gb ABZ02677.1	accelerated cell death ( 92)	210	55.9	9.2e-06
gi 162439502 gb ABX90770.1	Sequence 36 from paten ( 352)	220	58.4	6e-06	gi 166915654 gb ABZ02680.1	accelerated cell death ( 92)	210	55.9	9.2e-06
gi 196191245 gb EDX86209.1	Rieske (2Fe-2S) domain ( 355)	220	58.4	6e-06	gi 166915660 gb ABZ02683.1	accelerated cell death ( 92)	210	55.9	9.2e-06
gi 215503223 gb EEC12717.1	conserved hypothetical ( 428)	221	58.7	6e-06	gi 166915634 gb ABZ02670.1	accelerated cell death ( 92)	210	55.9	9.2e-06
gi 75702439 gb ABA22115.1	Rieske (2Fe-2S) region ( 359)	220	58.4	6.1e-06	gi 166915544 gb ABZ02625.1	accelerated cell death ( 92)	210	55.9	9.2e-06
gi 138677132 gb ECB24263.1	hypothetical protein G ( 248)	218	57.9	6.1e-06	gi 166915650 gb ABZ02678.1	accelerated cell death ( 92)	210	55.9	9.2e-06

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gi 166915640 gb ABZ02673.1	accelerated cell death (	92)	210	55.9	9.2e-06	gi 166915614 gb ABZ02660.1	accelerated cell death (	92)	209	55.6	1.1e-05
gi 166915554 gb ABZ02630.1	accelerated cell death (	92)	210	55.9	9.2e-06	gi 166915590 gb ABZ02648.1	accelerated cell death (	92)	209	55.6	1.1e-05
gi 166915620 gb ABZ02663.1	accelerated cell death (	92)	210	55.9	9.2e-06	gi 166915694 gb ABZ02700.1	accelerated cell death (	92)	209	55.6	1.1e-05
gi 166915624 gb ABZ02665.1	accelerated cell death (	92)	210	55.9	9.2e-06	gi 166915546 gb ABZ02626.1	accelerated cell death (	92)	209	55.6	1.1e-05
gi 166915576 gb ABZ02641.1	accelerated cell death (	92)	210	55.9	9.2e-06	gi 166915588 gb ABZ02647.1	accelerated cell death (	92)	209	55.6	1.1e-05
gi 166915630 gb ABZ02668.1	accelerated cell death (	92)	210	55.9	9.2e-06	gi 166915612 gb ABZ02659.1	accelerated cell death (	92)	209	55.6	1.1e-05
gi 166915522 gb ABZ02614.1	accelerated cell death (	92)	210	55.9	9.2e-06	gi 166915698 gb ABZ02702.1	accelerated cell death (	92)	209	55.6	1.1e-05
gi 166915704 gb ABZ02705.1	accelerated cell death (	92)	210	55.9	9.2e-06	gi 166915578 gb ABZ02642.1	accelerated cell death (	92)	209	55.6	1.1e-05
gi 166915662 gb ABZ02684.1	accelerated cell death (	92)	210	55.9	9.2e-06	gi 166915700 gb ABZ02703.1	accelerated cell death (	92)	209	55.6	1.1e-05
gi 166915604 gb ABZ02655.1	accelerated cell death (	92)	210	55.9	9.2e-06	gi 166915664 gb ABZ02685.1	accelerated cell death (	92)	209	55.6	1.1e-05
gi 166915584 gb ABZ02645.1	accelerated cell death (	92)	210	55.9	9.2e-06	gi 166915632 gb ABZ02669.1	accelerated cell death (	92)	209	55.6	1.1e-05
gi 166915710 gb ABZ02708.1	accelerated cell death (	92)	210	55.9	9.2e-06	gi 166915560 gb ABZ02633.1	accelerated cell death (	92)	209	55.6	1.1e-05
gi 166915618 gb ABZ02662.1	accelerated cell death (	92)	210	55.9	9.2e-06	gi 166915706 gb ABZ02706.1	accelerated cell death (	92)	209	55.6	1.1e-05
gi 166915558 gb ABZ02632.1	accelerated cell death (	80)	209	55.6	9.6e-06	gi 166915642 gb ABZ02674.1	accelerated cell death (	92)	209	55.6	1.1e-05
gi 141562643 gb ECS39221.1	hypothetical protein G (	251)	215	57.2	9.9e-06	gi 134827291 gb EBD69254.1	hypothetical protein G (	280)	215	57.2	1.1e-05
gi 110168299 gb ABG52839.1	Pheophorbide a oxygena (	443)	218	58.0	1e-05	gi 137109813 gb EBS25724.1	hypothetical protein G (	240)	214	57.0	1.1e-05
gi 108767695 gb ABG06417.1	Rieske (2Fe-2S) region (	378)	217	57.8	1e-05	gi 142706403 gb ECZ99123.1	hypothetical protein G (	349)	216	57.5	1.1e-05
gi 119692450 gb ABL89523.1	Rieske (2Fe-2S) domain (	378)	217	57.8	1e-05	gi 144099349 gb EDI86017.1	hypothetical protein G (	293)	215	57.2	1.1e-05
gi 126232700 gb ABN96100.1	Rieske (2Fe-2S) domain (	378)	217	57.8	1e-05	gi 75701251 gb ABA20927.1	Rieske (2Fe-2S) region (	443)	217	57.8	1.2e-05
gi 229295834 gb EEN66478.1	hypothetical protein B (	455)	218	58.0	1e-05	gi 139426626 gb ECF03619.1	hypothetical protein G (	258)	214	57.0	1.2e-05
gi 137705256 gb EBV55735.1	hypothetical protein G (	268)	215	57.2	1e-05	gi 166915580 gb ABZ02643.1	accelerated cell death (	92)	208	55.4	1.3e-05
gi 138584340 gb ECA60783.1	hypothetical protein G (	270)	215	57.2	1e-05	gi 166915622 gb ABZ02664.1	accelerated cell death (	92)	208	55.4	1.3e-05
gi 141360517 gb ECR28432.1	hypothetical protein G (	273)	215	57.2	1.1e-05	gi 113529122 emb CAJ95469.1	Ring-hydroxylating di (	366)	215	57.3	1.4e-05
gi 166915594 gb ABZ02650.1	accelerated cell death (	90)	209	55.6	1.1e-05	gi 207083487 gb EDZ60913.1	iron-sulphur protein [ (	451)	216	57.6	1.4e-05
gi 166915540 gb ABZ02623.1	accelerated cell death (	91)	209	55.6	1.1e-05	gi 226463072 gb EEH60350.1	chloroplast envelope p (	662)	218	58.1	1.4e-05
gi 166915536 gb ABZ02621.1	accelerated cell death (	91)	209	55.6	1.1e-05	gi 138625546 gb ECA89504.1	hypothetical protein G (	323)	214	57.0	1.4e-05
gi 166915542 gb ABZ02624.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 140852576 gb ECN93978.1	hypothetical protein G (	116)	208	55.5	1.5e-05
gi 166915548 gb ABZ02627.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 260054725 gb ACX24342.1	Sequence 55215 from pa (	531)	216	57.6	1.6e-05
gi 166915602 gb ABZ02654.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 119951057 gb ABM09968.1	putative iron-sulfur c (	367)	214	57.1	1.6e-05
gi 166915530 gb ABZ02618.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 144070032 gb EDI65212.1	hypothetical protein G (	212)	211	56.3	1.6e-05
gi 166915638 gb ABZ02672.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 140363381 gb ECL26019.1	hypothetical protein G (	124)	208	55.5	1.6e-05
gi 166915570 gb ABZ02638.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 137508576 gb EBU47448.1	hypothetical protein G (	183)	210	56.0	1.7e-05
gi 166915572 gb ABZ02639.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 166915690 gb ABZ02698.1	accelerated cell death (	89)	206	54.9	1.7e-05
gi 166915656 gb ABZ02681.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 140436354 gb ECL73955.1	hypothetical protein G (	272)	212	56.5	1.7e-05
gi 166915596 gb ABZ02651.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 115259421 emb CAK10559.1	conserved hypothetica (	193)	210	56.0	1.7e-05
gi 166915684 gb ABZ02695.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 135924921 gb EBK74603.1	hypothetical protein G (	193)	210	56.0	1.7e-05
gi 166915598 gb ABZ02652.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 115285971 gb ABI91446.1	Rieske (2Fe-2S) domain (	408)	214	57.1	1.7e-05
gi 166915628 gb ABZ02667.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 171997204 gb ACB68121.1	Rieske (2Fe-2S) domain (	408)	214	57.1	1.7e-05
gi 166915586 gb ABZ02646.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 143522676 gb EDF44616.1	hypothetical protein G (	282)	212	56.6	1.7e-05
gi 166915670 gb ABZ02688.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 141589969 gb ECS48974.1	hypothetical protein G (	164)	209	55.8	1.8e-05
gi 166915702 gb ABZ02704.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 262260300 gb EY79033.1	Rieske protein [Acinet (	355)	213	56.8	1.8e-05
gi 166915600 gb ABZ02653.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 134724711 gb EBD04350.1	hypothetical protein G (	314)	212	56.6	1.9e-05
gi 166915672 gb ABZ02689.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 137941665 gb EBW87877.1	hypothetical protein G (	181)	209	55.8	1.9e-05
gi 166915626 gb ABZ02666.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 226935179 gb ACQ92627.1	DpaAa [Burkholderia sp (	382)	213	56.8	1.9e-05
gi 166915692 gb ABZ02699.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 142767951 gb EDA43590.1	hypothetical protein G (	473)	214	57.1	2e-05
gi 166915526 gb ABZ02616.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 142165538 gb ECW07697.1	hypothetical protein G (	226)	210	56.1	2e-05
gi 166915676 gb ABZ02691.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 158283094 gb EDP08845.1	predicted protein [Chl (	108)	206	55.0	2e-05
gi 166915666 gb ABZ02686.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 87134899 gb ABD25641.1	Rieske (2Fe-2S) protein (	401)	213	56.9	2e-05
gi 166915574 gb ABZ02640.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 160346522 gb ABX19606.1	Rieske (2Fe-2S) domain (	341)	212	56.6	2e-05
gi 166915582 gb ABZ02644.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 135580671 gb EBT56105.1	hypothetical protein G (	346)	212	56.6	2.1e-05
gi 166915696 gb ABZ02701.1	accelerated cell death (	92)	209	55.6	1.1e-05	gi 222842294 gb EEE79841.1	predicted protein [Pop (	256)	210	56.1	2.2e-05



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gi 143729952 gb EDG48831.1	hypothetical protein G ( 311)	211	56.3	2.2e-05	gi 116652599 gb ABK13238.1	Rieske (2Fe-2S) domain ( 351)	207	55.5	4.6e-05
gi 138314700 gb EBY93141.1	hypothetical protein G ( 215)	209	55.8	2.2e-05	gi 137881326 gb EBW53615.1	hypothetical protein G ( 245)	205	54.9	4.6e-05
gi 141441920 gb ECR85545.1	hypothetical protein G ( 183)	208	55.6	2.3e-05	gi 136559276 gb EBO94378.1	hypothetical protein G ( 358)	207	55.5	4.7e-05
gi 1653587 dbj BAA18500.1	sll0264 [Synechocystis ( 396)	212	56.6	2.3e-05	gi 33769192 gb AAQ53823.1	Sequence 5 from patent ( 520)	209	56.0	4.7e-05
gi 166915556 gb ABZ02631.1	accelerated cell death ( 92)	204	54.5	2.4e-05	gi 15108633 gb AAE67669.1	Sequence 5 from patent ( 520)	209	56.0	4.7e-05
gi 139203715 gb ECE12009.1	hypothetical protein G ( 199)	208	55.6	2.4e-05	gi 151282075 gb ABR90485.1	Uncharacterized conser ( 365)	207	55.5	4.8e-05
gi 2073550 gb AAC45716.1	3-chlorobenzoate-3,4/4,5 ( 432)	212	56.6	2.5e-05	gi 134715339 gb EBC99021.1	hypothetical protein G ( 259)	205	54.9	4.9e-05
gi 144027290 gb EDI34144.1	hypothetical protein G ( 435)	212	56.6	2.5e-05	gi 136559735 gb EBO94671.1	hypothetical protein G ( 380)	207	55.5	4.9e-05
gi 134682811 gb EBC79924.1	hypothetical protein G ( 251)	209	55.8	2.5e-05	gi 135414980 gb EBH48239.1	hypothetical protein G ( 317)	206	55.2	4.9e-05
gi 163258284 emb CAP40583.1	putative dioxygenase ( 439)	212	56.7	2.5e-05	gi 140439323 gb ECL76009.1	hypothetical protein G ( 264)	205	55.0	4.9e-05
gi 142602832 gb EC225636.1	hypothetical protein G ( 258)	209	55.9	2.6e-05	gi 141536199 gb ECS20643.1	hypothetical protein G ( 272)	205	55.0	5.1e-05
gi 148500607 gb ABQ68861.1	Rieske (2Fe-2S) domain ( 332)	210	56.1	2.7e-05	gi 141831776 gb ECT55464.1	hypothetical protein G ( 232)	204	54.7	5.2e-05
gi 166915688 gb ABZ02697.1	accelerated cell death ( 92)	203	54.3	2.8e-05	gi 215503221 gb EEC12715.1	conserved hypothetical ( 409)	207	55.5	5.2e-05
gi 158111460 gb ABW13657.1	Rieske (2Fe-2S) domain ( 356)	210	56.2	2.9e-05	gi 137907185 gb EBW68439.1	hypothetical protein G ( 284)	205	55.0	5.3e-05
gi 136197816 gb EBM53855.1	hypothetical protein G ( 358)	210	56.2	2.9e-05	gi 256588847 gb ACU99733.1	Rieske (2Fe-2S) domain ( 497)	208	55.8	5.3e-05
gi 136229108 gb EBM74981.1	hypothetical protein G ( 206)	207	55.4	2.9e-05	gi 218166114 gb ACK64851.1	Rieske (2Fe-2S) domain ( 497)	208	55.8	5.3e-05
gi 138814499 gb ECB98083.1	hypothetical protein G ( 300)	209	55.9	2.9e-05	gi 166915608 gb ABZ02657.1	accelerated cell death ( 78)	198	53.1	5.3e-05
gi 295710 dbj BAA02511.1	PHT3 [Pseudomonas putida ( 439)	211	56.4	3e-05	gi 134784110 gb EBD40910.1	hypothetical protein G ( 170)	202	54.2	5.5e-05
gi 139620579 gb ECG31205.1	hypothetical protein G ( 182)	206	55.1	3.1e-05	gi 143180672 gb EDD39676.1	hypothetical protein G ( 440)	207	55.5	5.6e-05
gi 124879777 gb EAY67133.1	2,4-D oxygenase large ( 382)	210	56.2	3.1e-05	gi 136256626 gb EBM63486.1	hypothetical protein G ( 304)	205	55.0	5.6e-05
gi 144055918 gb EDI54788.1	hypothetical protein G ( 462)	211	56.4	3.1e-05	gi 167041467 gb ABZ06218.1	putative Rieske [2Fe-2 ( 443)	207	55.5	5.6e-05
gi 148500158 gb ABQ68412.1	Rieske (2Fe-2S) domain ( 398)	210	56.2	3.2e-05	gi 33237867 gb AAP99934.1	Rieske 2Fe-2S family pr ( 445)	207	55.5	5.6e-05
gi 140350439 gb ECL17207.1	hypothetical protein G ( 279)	208	55.6	3.2e-05	gi 159888665 gb ABX08879.1	Rieske iron-sulfur pro ( 448)	207	55.5	5.7e-05
gi 142272187 gb ECW87802.1	hypothetical protein G ( 200)	206	55.1	3.3e-05	gi 140797737 gb ECN57994.1	hypothetical protein G ( 263)	204	54.7	5.8e-05
gi 143613852 gb EDF86928.1	hypothetical protein G ( 175)	205	54.9	3.5e-05	gi 116060175 emb CAL56234.1	cell death suppressor ( 664)	209	56.1	5.8e-05
gi 118166929 gb ABK67826.1	oxygenase KshA [Mycoba ( 368)	209	55.9	3.5e-05	gi 206676815 gb EDZ41302.1	choline monooxygenase, ( 384)	206	55.3	5.8e-05
gi 135014824 gb EBE94064.1	hypothetical protein G ( 260)	207	55.4	3.6e-05	gi 126223180 gb ABN86685.1	iron-sulfur cluster-bi ( 326)	205	55.0	5.9e-05
gi 158279358 gb EDP05119.1	predicted protein [Chl ( 103)	202	54.1	3.6e-05	gi 242135201 gb EES21604.1	iron-sulfur cluster-bi ( 326)	205	55.0	5.9e-05
gi 142392242 gb ECX73395.1	hypothetical protein G ( 217)	206	55.1	3.6e-05	gi 142949436 gb EDB73363.1	hypothetical protein G ( 474)	207	55.5	5.9e-05
gi 139938283 gb ECI50196.1	hypothetical protein G ( 219)	206	55.1	3.6e-05	gi 151281954 gb ABR90364.1	Uncharacterized conser ( 580)	208	55.8	6e-05
gi 49900452 gb AAH75979.1	Zgc:92275 [Danio rerio] ( 460)	210	56.2	3.6e-05	gi 157937784 gb EDO93454.1	iron-sulfur cluster-bi ( 334)	205	55.0	6e-05
gi 143597617 gb EDF79045.1	hypothetical protein G ( 185)	205	54.9	3.7e-05	gi 126239431 gb ABO02543.1	iron-sulfur cluster-bi ( 334)	205	55.0	6e-05
gi 237686912 gb ACR14176.1	carbazole dioxygenase- ( 390)	209	55.9	3.7e-05	gi 52423049 gb AAU46619.1	iron-sulfur cluster-bin ( 334)	205	55.0	6e-05
gi 111152241 emb CAJ63970.1	Putative ring hydroxy ( 399)	209	56.0	3.7e-05	gi 121225312 gb ABM48843.1	iron-sulfur cluster-bi ( 334)	205	55.0	6e-05
gi 135587205 gb EBI60169.1	hypothetical protein G ( 231)	206	55.2	3.8e-05	gi 76583343 gb ABA52817.1	iron-sulfur cluster-bin ( 334)	205	55.0	6e-05
gi 166915606 gb ABZ02656.1	accelerated cell death ( 92)	201	53.8	3.8e-05	gi 169649675 gb EDS82368.1	iron-sulfur cluster-bi ( 334)	205	55.0	6e-05
gi 142369979 gb ECX58297.1	hypothetical protein G ( 197)	205	54.9	3.9e-05	gi 160695130 gb EDP85100.1	iron-sulfur cluster-bi ( 334)	205	55.0	6e-05
gi 139834025 gb ECH78618.1	hypothetical protein G ( 204)	205	54.9	4e-05	gi 126229487 gb ABN92900.1	iron-sulfur cluster-bi ( 334)	205	55.0	6e-05
gi 143749359 gb EDG59256.1	hypothetical protein G ( 440)	209	56.0	4.1e-05	gi 148025919 gb EDK84042.1	iron-sulfur cluster-bi ( 334)	205	55.0	6e-05
gi 135227729 gb EBG29358.1	hypothetical protein G ( 146)	203	54.4	4.1e-05	gi 147748289 gb EDK55364.1	iron-sulfur cluster-bi ( 334)	205	55.0	6e-05
gi 154156350 gb ABS63567.1	Rieske (2Fe-2S) domain ( 376)	208	55.7	4.2e-05	gi 124289227 gb ABM98496.1	iron-sulfur cluster-bi ( 334)	205	55.0	6e-05
gi 141873183 gb ECT84813.1	hypothetical protein G ( 221)	205	54.9	4.3e-05	gi 254213937 gb EET03322.1	iron-sulfur cluster-bi ( 334)	205	55.0	6e-05
gi 143485515 gb EDF24263.1	hypothetical protein G ( 128)	202	54.1	4.3e-05	gi 52212431 emb CAH38457.1	Rieske iron-sulphur do ( 334)	205	55.0	6e-05
gi 141874518 gb ECT85600.1	hypothetical protein G ( 224)	205	54.9	4.3e-05	gi 141110883 gb ECP70206.1	hypothetical protein G ( 278)	204	54.7	6e-05
gi 144066584 gb EDI62696.1	hypothetical protein G ( 279)	206	55.2	4.4e-05	gi 140378682 gb ECL36733.1	hypothetical protein G ( 279)	204	54.7	6.1e-05
gi 136890393 gb EBR07550.1	hypothetical protein G ( 193)	204	54.7	4.4e-05	gi 137150681 gb EBS48630.1	hypothetical protein G ( 234)	203	54.5	6.1e-05
gi 125546118 gb EAY92257.1	hypothetical protein O ( 134)	202	54.1	4.5e-05	gi 120325981 gb ABM20296.1	Rieske (2Fe-2S) domain ( 412)	206	55.3	6.2e-05
gi 125588317 gb EAA228981.1	hypothetical protein O ( 134)	202	54.1	4.5e-05	gi 110646643 emb CAL16119.1	oxidoreductase [Alcan ( 412)	206	55.3	6.2e-05
gi 136960475 gb EBR41869.1	hypothetical protein G ( 234)	205	54.9	4.5e-05	gi 120596613 gb ABM40048.1	phthalate 4,5-dioxygen ( 417)	206	55.3	6.2e-05
gi 137907979 gb EBW68890.1	hypothetical protein G ( 197)	204	54.7	4.5e-05	gi 166915550 gb ABZ02628.1	accelerated cell death ( 79)	197	52.9	6.2e-05
gi 105893062 gb ABF76227.1	Rieske (2Fe-2S) region ( 351)	207	55.5	4.6e-05	gi 143030782 gb EDC30718.1	hypothetical protein G ( 241)	203	54.5	6.3e-05

gi 166915568 gb ABZ02637.1	accelerated cell death ( 80)	197	52.9	6.3e-05	gi 137171426 gb EBS60284.1	hypothetical protein G ( 214)	200	53.8	9.1e-05
gi 136373969 gb EBN73413.1	hypothetical protein G ( 429)	206	55.3	6.4e-05	gi 137985279 gb EBX12685.1	hypothetical protein G ( 185)	199	53.5	9.4e-05
gi 226518590 gb ACO64582.1	chloroplast envelope p ( 903)	210	56.4	6.4e-05	gi 222841433 gb EEE78980.1	predicted protein [Pop ( 475)	204	54.9	9.5e-05
gi 143461828 gb EDF10601.1	hypothetical protein G ( 440)	206	55.3	6.5e-05	gi 144213951 gb EDJ69541.1	hypothetical protein G ( 328)	202	54.3	9.5e-05
gi 123198515 gb ABM70156.1	Rieske iron-sulfur pro ( 440)	206	55.3	6.5e-05	gi 118569824 gb ABL04575.1	oxidoreductase [Mycoba ( 341)	202	54.3	9.8e-05
gi 135346394 gb EBH02144.1	hypothetical protein G ( 255)	203	54.5	6.6e-05	gi 183175274 gb ACC40384.1	oxidoreductase [Mycoba ( 341)	202	54.3	9.8e-05
gi 142295194 gb ECX04622.1	hypothetical protein G ( 447)	206	55.3	6.6e-05	gi 145322582 gb ABP64525.1	Rieske (2Fe-2S) domain ( 359)	202	54.3	0.0001
gi 143010457 gb EDC16014.1	hypothetical protein G ( 451)	206	55.3	6.7e-05	gi 126543250 gb ABO17492.1	Rieske iron-sulfur pro ( 440)	203	54.6	0.0001
gi 189338340 dbj BAG47408.1	putative ring-hydroxy ( 314)	204	54.8	6.7e-05	gi 41395885 gb AAS03751.1	hypothetical protein MA ( 372)	202	54.3	0.00011
gi 209573265 gb ACI62780.1	terminal oxygenase [Rh ( 378)	205	55.0	6.7e-05	gi 135446148 gb EBH69132.1	hypothetical protein G ( 103)	195	52.5	0.00011
gi 226183519 dbj BAH31623.1	3-ketosteroid 9alpha- ( 383)	205	55.0	6.8e-05	gi 142576906 gb ECZ07580.1	hypothetical protein G ( 261)	200	53.8	0.00011
gi 226519116 gb ACO65107.1	chloroplast envelope p ( 668)	208	55.8	6.8e-05	gi 135153913 gb EBF83768.1	hypothetical protein G ( 264)	200	53.8	0.00011
gi 139229251 gb ECE29615.1	hypothetical protein G ( 185)	201	54.0	6.9e-05	gi 91693115 gb ABE36312.1	Putative Rieske-type ri ( 387)	202	54.4	0.00011
gi 143417886 gb EDS84881.1	hypothetical protein G ( 391)	205	55.0	6.9e-05	gi 218170687 gb ACK69420.1	Rieske (2Fe-2S) domain ( 468)	203	54.6	0.00011
gi 136231041 gb EBM76275.1	hypothetical protein G ( 392)	205	55.0	6.9e-05	gi 226463719 gb EEH60997.1	chloroplast envelope p ( 582)	204	54.9	0.00011
gi 140037718 gb ECJ17071.1	hypothetical protein G ( 277)	203	54.5	7.1e-05	gi 209528461 emb CAR802238.1	pheophorbide a oxygen ( 282)	200	53.8	0.00011
gi 166915528 gb ABZ02617.1	accelerated cell death ( 65)	195	52.4	7.3e-05	gi 142694208 gb ECZ90394.1	hypothetical protein G ( 341)	201	54.1	0.00012
gi 141797578 gb ECT33875.1	hypothetical protein G ( 198)	201	54.0	7.3e-05	gi 166915636 gb ABZ02671.1	accelerated cell death ( 54)	191	51.4	0.00012
gi 137128767 gb EBS36405.1	hypothetical protein G ( 241)	202	54.3	7.3e-05	gi 141656914 gb ECS67534.1	hypothetical protein G ( 204)	198	53.3	0.00012
gi 41397339 gb AAS05199.1	hypothetical protein MA ( 353)	204	54.8	7.4e-05	gi 136683528 gb EBP71953.1	hypothetical protein G ( 130)	195	52.5	0.00013
gi 137663260 gb EBV32070.1	hypothetical protein G ( 244)	202	54.3	7.4e-05	gi 143706812 gb EDG37911.1	hypothetical protein G ( 417)	201	54.1	0.00014
gi 143608639 gb EDF84425.1	hypothetical protein G ( 355)	204	54.8	7.4e-05	gi 139420075 gb ECE99166.1	hypothetical protein G ( 206)	197	53.1	0.00014
gi 141678600 gb ECS77269.1	hypothetical protein G ( 246)	202	54.3	7.5e-05	gi 142512946 gb ECY61964.1	hypothetical protein G ( 447)	201	54.2	0.00014
gi 178462743 dbj BAG17263.1	hypothetical protein ( 362)	204	54.8	7.6e-05	gi 136708328 gb EBP88163.1	hypothetical protein G ( 216)	197	53.1	0.00015
gi 143426390 gb EDE89068.1	hypothetical protein G ( 436)	205	55.1	7.6e-05	gi 226242352 dbj BAH52700.1	3-ketosteroid 9alpha- ( 387)	200	53.9	0.00015
gi 91697014 gb ABE43843.1	phthalate 4,5-dioxygena ( 438)	205	55.1	7.6e-05	gi 135154936 gb EBF84427.1	hypothetical protein G ( 106)	193	52.0	0.00015
gi 134361552 gb EBA89271.1	hypothetical protein G ( 440)	205	55.1	7.6e-05	gi 118167252 gb ABK68149.1	iron-sulfur cluster-bi ( 337)	199	53.6	0.00016
gi 142058759 gb ECV24314.1	hypothetical protein G ( 440)	205	55.1	7.6e-05	gi 158303628 gb ABW25245.1	rieske 2Fe-2S domain p ( 496)	201	54.2	0.00016
gi 118166259 gb ABK67156.1	Rieske [2Fe-2S] domain ( 375)	204	54.8	7.8e-05	gi 217402990 gb EEC42947.1	Tic55 component of chl ( 498)	201	54.2	0.00016
gi 139709670 gb ECG93311.1	hypothetical protein G ( 259)	202	54.3	7.8e-05	gi 134962952 gb EBE58924.1	hypothetical protein G ( 358)	199	53.7	0.00016
gi 41396797 gb AAS04660.1	hypothetical protein MA ( 384)	204	54.8	8e-05	gi 167354039 gb ABZ76652.1	Rieske (2Fe-2S) domain ( 364)	199	53.7	0.00017
gi 187472112 gb ACD11366.1	KshA2 [Rhodococcus ery ( 388)	204	54.8	8e-05	gi 137697572 gb EBV51535.1	hypothetical protein G ( 303)	198	53.4	0.00017
gi 141946910 gb ECU36152.1	hypothetical protein G ( 269)	202	54.3	8.1e-05	gi 136152613 gb EBM24167.1	hypothetical protein G ( 308)	198	53.4	0.00017
gi 142606729 gb ECZ28389.1	hypothetical protein G ( 326)	203	54.5	8.1e-05	gi 140381749 gb ECL38936.1	hypothetical protein G ( 314)	198	53.4	0.00017
gi 256360333 gb ACU73830.1	Rieske (2Fe-2S) domain ( 328)	203	54.5	8.1e-05	gi 136231009 gb EBM76256.1	hypothetical protein G ( 184)	195	52.6	0.00018
gi 186467252 gb ACC83053.1	Rieske (2Fe-2S) domain ( 334)	203	54.6	8.3e-05	gi 226183358 dbj BAH31462.1	probable 3-ketosteroid ( 386)	199	53.7	0.00018
gi 184214011 gb EDU11054.1	iron-sulfur cluster-bi ( 334)	203	54.6	8.3e-05	gi 268312671 gb ACY99045.1	Rieske (2Fe-2S) domain ( 386)	199	53.7	0.00018
gi 157810114 gb EDG87284.1	iron-sulfur cluster-bi ( 334)	203	54.6	8.3e-05	gi 222842292 gb EEE79839.1	predicted protein [Pop ( 267)	197	53.1	0.00018
gi 166915532 gb ABZ02619.1	accelerated cell death ( 64)	194	52.2	8.4e-05	gi 238550035 dbj BAH60859.1	terminal oxygenase co ( 387)	199	53.7	0.00018
gi 110646644 emb CAL16120.1	oxidoreductase [Alcan ( 411)	204	54.8	8.4e-05	gi 135089828 gb EBF42676.1	hypothetical protein G ( 223)	196	52.9	0.00018
gi 120325980 gb ABM20295.1	Rieske (2Fe-2S) domain ( 411)	204	54.8	8.4e-05	gi 215502533 gb EEC12027.1	conserved hypothetical ( 273)	197	53.1	0.00018
gi 136298351 gb EBN22116.1	hypothetical protein G ( 236)	201	54.0	8.4e-05	gi 140013140 gb ECJ00444.1	hypothetical protein G ( 138)	193	52.1	0.00019
gi 144209737 gb EDJ66483.1	hypothetical protein G ( 422)	204	54.8	8.6e-05	gi 256653167 dbj BAI19100.1	ring-hydroxylating di ( 296)	197	53.2	0.00019
gi 136942120 gb EBR31531.1	hypothetical protein G ( 244)	201	54.0	8.7e-05	gi 256634904 dbj BAI00879.1	ring-hydroxylating di ( 296)	197	53.2	0.00019
gi 144130940 gb EDJ08863.1	hypothetical protein G ( 428)	204	54.8	8.7e-05	gi 256656220 dbj BAI22146.1	ring-hydroxylating di ( 296)	197	53.2	0.00019
gi 221538165 gb EEE40618.1	rieske iron-sulfur pro ( 440)	204	54.8	8.9e-05	gi 256641013 dbj BAI06974.1	ring-hydroxylating di ( 296)	197	53.2	0.00019
gi 157387813 gb ABV50518.1	Rieske iron-sulfur pro ( 440)	204	54.8	8.9e-05	gi 256647123 dbj BAI13070.1	ring-hydroxylating di ( 296)	197	53.2	0.00019
gi 143367431 gb EDE59377.1	hypothetical protein G ( 100)	196	52.7	8.9e-05	gi 256644068 dbj BAI10022.1	ring-hydroxylating di ( 296)	197	53.2	0.00019
gi 134587715 gb EBC23641.1	hypothetical protein G ( 146)	198	53.2	9e-05	gi 256650176 dbj BAI16116.1	ring-hydroxylating di ( 296)	197	53.2	0.00019
gi 118166243 gb ABK67140.1	oxygenase KshA [Mycoba ( 370)	203	54.6	9e-05	gi 256637959 dbj BAI03927.1	ring-hydroxylating di ( 296)	197	53.2	0.00019
gi 143788482 gb EDG78744.1	hypothetical protein G ( 447)	204	54.8	9e-05	gi 138392124 gb EBZ35223.1	hypothetical protein G ( 302)	197	53.2	0.00019

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gi 1653688 dbj BAA18600.1	sll1849 [Synechocystis ( 211)	195	52.6	0.0002	gi 17134547 dbj BAB77106.1	all17348 [Nostoc sp. PC ( 460)	196	53.0	0.00033
gi 189496109 gb ACE04657.1	Rieske (2Fe-2S) domain ( 101)	191	51.6	0.0002	gi 137272729 gb EBT17146.1	hypothetical protein G ( 126)	189	51.2	0.00033
gi 142497331 gb ECY50863.1	hypothetical protein G ( 315)	197	53.2	0.0002	gi 139315341 gb ECE51349.1	hypothetical protein G ( 226)	192	52.0	0.00033
gi 40062902 gb AAR37773.1	iron-sulfur cluster-bin ( 321)	197	53.2	0.00021	gi 21309823 gb AAL96829.1	terminal oxygenase KshA ( 398)	195	52.8	0.00034
gi 197624788 gb EDY37347.1	iron-sulfur cluster-bi ( 325)	197	53.2	0.00021	gi 226183984 dbj BAH32088.1	3-ketosteroid 9alpha- ( 398)	195	52.8	0.00034
gi 76583435 gb ABA52909.1	iron-sulfur cluster-bin ( 109)	191	51.6	0.00021	gi 262084263 gb ACY20231.1	Rieske (2Fe-2S) iron-s ( 413)	195	52.8	0.00035
gi 184215368 gb EDU12349.1	aromatic-ring-hydroxyl ( 109)	191	51.6	0.00021	gi 143118372 gb EDC94804.1	hypothetical protein G ( 286)	193	52.3	0.00035
gi 52213321 emb CAH39364.1	putative aromatic hydr ( 109)	191	51.6	0.00021	gi 142859036 gb EDB08375.1	hypothetical protein G ( 362)	194	52.5	0.00036
gi 126230352 gb ABN93765.1	aromatic-ring-hydroxyl ( 109)	191	51.6	0.00021	gi 33577871 emb CAE35136.1	putative 3-chlorobenzo ( 436)	195	52.8	0.00036
gi 121225248 gb ABM48779.1	aromatic-ring-hydroxyl ( 109)	191	51.6	0.00021	gi 41469406 gb AAS07229.1	putative iron-sulfur cl ( 538)	196	53.1	0.00037
gi 261826856 gb ABM95562.2	aromatic-ring-hydroxyl ( 109)	191	51.6	0.00021	gi 125546114 gb EAY92253.1	hypothetical protein O ( 556)	196	53.1	0.00038
gi 126238856 gb ABO01968.1	aromatic-ring-hydroxyl ( 109)	191	51.6	0.00021	gi 139263842 gb ECE39976.1	hypothetical protein G ( 185)	190	51.5	0.00039
gi 242134575 gb EES20978.1	aromatic-ring-hydroxyl ( 109)	191	51.6	0.00021	gi 115286305 gb ABI91780.1	Rieske (2Fe-2S) domain ( 392)	194	52.5	0.00039
gi 52422480 gb AAU46050.1	iron-sulfur cluster-bin ( 109)	191	51.6	0.00021	gi 239801289 gb ABS18356.1	Rieske (2Fe-2S) domain ( 225)	191	51.7	0.00039
gi 126224192 gb ABN87697.1	aromatic-ring-hydroxyl ( 109)	191	51.6	0.00021	gi 138784267 gb ECB84772.1	hypothetical protein G ( 63)	184	49.9	0.0004
gi 157811074 gb EDO88244.1	aromatic-ring-hydroxyl ( 109)	191	51.6	0.00021	gi 141894057 gb ECT99155.1	hypothetical protein G ( 160)	189	51.2	0.0004
gi 157933681 gb EDO89351.1	aromatic-ring-hydroxyl ( 109)	191	51.6	0.00021	gi 136483652 gb EB045826.1	hypothetical protein G ( 351)	193	52.3	0.00041
gi 147746009 gb EDK53087.1	aromatic-ring-hydroxyl ( 109)	191	51.6	0.00021	gi 186467250 gb ACC83051.1	Rieske (2Fe-2S) domain ( 353)	193	52.3	0.00042
gi 160698239 gb EDP88209.1	aromatic-ring-hydroxyl ( 109)	191	51.6	0.00021	gi 135293560 gb EBG68064.1	hypothetical protein G ( 255)	191	51.8	0.00043
gi 254215629 gb EET05014.1	aromatic-ring-hydroxyl ( 109)	191	51.6	0.00021	gi 137026636 gb EBR79251.1	hypothetical protein G ( 307)	192	52.0	0.00043
gi 169650861 gb EDS83554.1	aromatic-ring-hydroxyl ( 109)	191	51.6	0.00021	gi 138039762 gb EBX41307.1	hypothetical protein G ( 263)	191	51.8	0.00044
gi 147750985 gb EDK58053.1	aromatic-ring-hydroxyl ( 109)	191	51.6	0.00021	gi 118163941 gb ABK64838.1	Rieske [2Fe-2S] domain ( 385)	193	52.3	0.00045
gi 136725760 gb EBP99625.1	hypothetical protein G ( 400)	198	53.5	0.00021	gi 150956738 gb ABR78768.1	putative ferredoxin [K ( 107)	186	50.4	0.00045
gi 136003118 gb EBL26045.1	hypothetical protein G ( 413)	198	53.5	0.00022	gi 119957561 gb ABM14566.1	Rieske (2Fe-2S) domain ( 342)	192	52.1	0.00047
gi 138046161 gb EBX44873.1	hypothetical protein G ( 296)	196	52.9	0.00022	gi 135494999 gb EBI01250.1	hypothetical protein G ( 136)	187	50.7	0.00048
gi 139112541 gb ECD49865.1	hypothetical protein G ( 60)	187	50.5	0.00024	gi 133633942 emb CABL9267.1	Rieske iron-sulfur pro ( 440)	193	52.3	0.0005
gi 143957050 gb EDH84743.1	hypothetical protein G ( 463)	198	53.5	0.00024	gi 113529248 emb CAJ95595.1	ferredoxin of a ring- ( 101)	185	50.2	0.00051
gi 134151604 gb EBA43649.1	hypothetical protein T ( 386)	197	53.2	0.00024	gi 134513611 gb EBB79187.1	hypothetical protein G ( 321)	191	51.8	0.00053
gi 121495093 emb CAL73579.1	Possible oxidoreducta ( 386)	197	53.2	0.00024	gi 255922180 gb ACU37691.1	Rieske (2Fe-2S) domain ( 325)	191	51.8	0.00053
gi 1666134 emb CAB05051.1	POSSIBLE OXIDOREDUCTASE ( 386)	197	53.2	0.00024	gi 169156 gb AAA33686.1	ribulose 1,5-bisphosphate ( 156)	187	50.8	0.00054
gi 148507541 gb ABQ75350.1	putative oxidoreductas ( 386)	197	53.2	0.00024	gi 76580933 gb ABA50408.1	nitrite reductase [NAD( ( 131)	186	50.5	0.00054
gi 224775057 dbj BAH27863.1	putative oxidoreducta ( 386)	197	53.2	0.00024	gi 169653608 gb EDS86301.1	nitrite reductase [NAD ( 131)	186	50.5	0.00054
gi 124603771 gb EAY61734.1	hypothetical protein T ( 386)	197	53.2	0.00024	gi 157935491 gb EDO91161.1	nitrite reductase [NAD ( 131)	186	50.5	0.00054
gi 31620299 emb CAD95742.1	POSSIBLE OXIDOREDUCTAS ( 386)	197	53.2	0.00024	gi 118164295 gb ABK65192.1	iron-sulfur cluster-bi ( 332)	191	51.8	0.00054
gi 253322070 gb ACT26673.1	oxidoreductase [Mycoba ( 386)	197	53.2	0.00024	gi 126235951 gb ABN99351.1	Rieske (2Fe-2S) domain ( 341)	191	51.8	0.00055
gi 148723259 gb ABR07884.1	hypothetical oxidoredu ( 386)	197	53.2	0.00024	gi 119695763 gb ABL92836.1	Rieske (2Fe-2S) domain ( 341)	191	51.8	0.00055
gi 83652761 gb ABC36824.1	nitrite reductase [NAD( ( 131)	191	51.6	0.00025	gi 108770954 gb ABG09676.1	Rieske (2Fe-2S) region ( 341)	191	51.8	0.00055
gi 135760683 gb EBJ67516.1	hypothetical protein G ( 239)	194	52.4	0.00026	gi 72121957 gb AAZ64143.1	Phthalate 4,5-dioxygena ( 412)	192	52.1	0.00056
gi 134386199 gb EBB05821.1	hypothetical protein G ( 201)	193	52.2	0.00026	gi 139636944 gb ECG42452.1	hypothetical protein G ( 78)	183	49.7	0.00056
gi 169820639 gb ACA95220.1	Rieske (2Fe-2S) domain ( 351)	196	53.0	0.00026	gi 78712700 gb ABB49877.1	rieske iron-sulfur prot ( 440)	192	52.1	0.00059
gi 135938307 gb EBK83676.1	hypothetical protein G ( 172)	192	51.9	0.00027	gi 119957285 gb ABM14290.1	Rieske (2Fe-2S) domain ( 100)	184	50.0	0.00059
gi 141165729 gb ECQ08542.1	hypothetical protein G ( 121)	190	51.4	0.00027	gi 157846942 gb ABV87441.1	Rieske (2Fe-2S) domain ( 377)	191	51.9	0.0006
gi 134919809 gb EBE30181.1	hypothetical protein G ( 121)	190	51.4	0.00027	gi 217075090 gb ACJ85905.1	unknown [Medicago trun ( 181)	187	50.8	0.00061
gi 135855670 gb EBK27255.1	hypothetical protein G ( 315)	195	52.7	0.00028	gi 136203701 gb EBM57792.1	hypothetical protein G ( 219)	188	51.1	0.00061
gi 214037577 gb EEB78243.1	Rieske (2Fe-2S) domain ( 324)	195	52.7	0.00028	gi 184197139 gb ACC75102.1	Rieske (2Fe-2S) domain ( 382)	191	51.9	0.00061
gi 118165730 gb ABK66627.1	Rieske [2Fe-2S] domain ( 331)	195	52.7	0.00029	gi 242137956 gb EES24358.1	nitrite reductase [NAD ( 152)	186	50.5	0.00061
gi 110821040 gb ABG96324.1	ketosteroid-9-alpha-hy ( 409)	196	53.0	0.00029	gi 126226655 gb ABN90195.1	nitrite reductase [NAD ( 152)	186	50.5	0.00061
gi 138908222 gb ECC37669.1	hypothetical protein G ( 139)	190	51.4	0.0003	gi 126219857 gb ABN83363.1	nitrite reductase [NAD ( 152)	186	50.5	0.00061
gi 143921377 gb EDH58991.1	hypothetical protein G ( 171)	191	51.7	0.00031	gi 184212415 gb EDU09458.1	nitrite reductase [NAD ( 152)	186	50.5	0.00061
gi 141063710 gb ECP38022.1	hypothetical protein G ( 122)	189	51.2	0.00032	gi 254218919 gb EET08303.1	nitrite reductase [NAD ( 152)	186	50.5	0.00061
gi 139573508 gb ECF99922.1	hypothetical protein G ( 259)	193	52.2	0.00032	gi 237503674 gb ACQ95992.1	nitrite reductase [Bur ( 152)	186	50.5	0.00061

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gi 238550028 dbj BAH60853.1  terminal oxygenase co ( 387)	191	51.9	0.00062	gi 54014654 dbj BAD56024.1  hypothetical protein [ ( 331)	186	50.7	0.0012
gi 91175993 gb ABE26577.1  Sequence 1 from patent ( 29)	177	48.1	0.00062	gi 145322518 gb ABP64461.1  Rieske (2Fe-2S) domain ( 335)	186	50.7	0.0012
gi 115833517 gb ABJ40819.1  Sequence 1 from patent ( 29)	177	48.1	0.00062	gi 139861632 gb ECH97960.1  hypothetical protein G ( 161)	182	49.6	0.0012
gi 258677109 gb ACV87349.1  3-ketosteroid 9-alpha- ( 395)	191	51.9	0.00063	gi 136728365 gb EBQ01332.1  hypothetical protein G ( 416)	187	51.0	0.0012
gi 188030493 emb CAO98387.1  Vanillate O-demethyla ( 91)	183	49.7	0.00064	gi 136069154 gb EBL70188.1  hypothetical protein G ( 66)	177	48.3	0.0012
gi 140757682 gb ECN31388.1  hypothetical protein G ( 159)	186	50.5	0.00064	gi 137044382 gb EBR89250.1  hypothetical protein G ( 294)	185	50.4	0.0013
gi 169148 gb AAA33684.1  ribulose-1,5-bisphosphate ( 136)	185	50.3	0.00065	gi 138700255 gb ECB40483.1  hypothetical protein G ( 205)	183	49.9	0.0013
gi 134734843 gb EBD10155.1  hypothetical protein G ( 287)	189	51.3	0.00066	gi 167733462 emb CAP51663.1  Nitrite reductase [NA ( 119)	180	49.1	0.0013
gi 138298823 gb EBY86608.1  hypothetical protein G ( 291)	189	51.3	0.00066	gi 143956396 gb EDH84266.1  hypothetical protein G ( 146)	181	49.4	0.0013
gi 12019640 gb AAA33685.2  ribulose 1,5 bisphospha ( 139)	185	50.3	0.00066	gi 143968933 gb EDH93023.1  hypothetical protein G ( 374)	186	50.7	0.0013
gi 140470881 gb ECL93467.1  hypothetical protein G ( 204)	187	50.8	0.00067	gi 134450521 gb EBB42048.1  hypothetical protein G ( 179)	182	49.7	0.0013
gi 21113128 gb AAM41297.1  Nitrite assimilation sm ( 119)	184	50.0	0.00068	gi 139893113 gb ECI18404.1  hypothetical protein G ( 268)	184	50.2	0.0014
gi 66573822 gb AAY49232.1  Nitrite assimilation sm ( 119)	184	50.0	0.00068	gi 143583031 gb EDF75073.1  hypothetical protein G ( 390)	186	50.7	0.0014
gi 156235047 gb ABU59830.1  Rieske (2Fe-2S) domain ( 362)	190	51.6	0.00068	gi 135302143 gb EBG73086.1  hypothetical protein G ( 130)	180	49.1	0.0014
gi 20859 emb CAA25390.1  ribulose bisphosphate car ( 180)	186	50.6	0.00071	gi 52427518 gb AAU48111.1  nitrite reductase [NAD( ( 131)	180	49.1	0.0014
gi 20855 emb CAA27864.1  ribulose bisphosphate car ( 180)	186	50.6	0.00071	gi 136403717 gb EBN93945.1  hypothetical protein G ( 229)	183	49.9	0.0014
gi 20857 emb CAA27865.1  ribulose 1,5-bisphosphate ( 180)	186	50.6	0.00071	gi 189232097 emb CAP53718.1  aminopyrrolnitrin oxy ( 232)	183	49.9	0.0014
gi 27353187 dbj BAC50187.1  blr4922 [Bradyrhizobiu ( 396)	190	51.6	0.00074	gi 142868904 gb EDB15554.1  hypothetical protein G ( 288)	184	50.2	0.0014
gi 72118580 gb AAZ60843.1  Rieske (2Fe-2S) region ( 398)	190	51.6	0.00074	gi 110816972 gb ABG92256.1  ring hydroxylating dio ( 420)	186	50.7	0.0015
gi 140598465 gb ECM34037.1  hypothetical protein G ( 277)	188	51.1	0.00074	gi 111153043 emb CAJ64790.1  Hypothetical protein; ( 427)	186	50.8	0.0015
gi 137446843 gb EBU15071.1  hypothetical protein G ( 133)	184	50.0	0.00075	gi 141149512 gb ECP97043.1  hypothetical protein G ( 248)	183	50.0	0.0015
gi 5748650 emb CAB53155.1  putative methylesterase ( 336)	189	51.4	0.00075	gi 138984069 gb ECC68769.1  hypothetical protein G ( 173)	181	49.4	0.0015
gi 114339162 gb ABU64442.1  Rieske (2Fe-2S) domain ( 358)	189	51.4	0.00079	gi 56680234 gb AAV96900.1  Rieske 2Fe-2S domain pr ( 369)	185	50.5	0.0015
gi 86565772 gb ABD09581.1  Rieske (2Fe-2S) protein ( 365)	189	51.4	0.0008	gi 126235621 gb ABN99021.1  Rieske (2Fe-2S) domain ( 102)	178	48.6	0.0015
gi 142446217 gb ECY13735.1  hypothetical protein G ( 374)	189	51.4	0.00082	gi 142482656 gb ECY40712.1  hypothetical protein G ( 385)	185	50.5	0.0016
gi 148502236 gb ABQ70490.1  Rieske (2Fe-2S) domain ( 384)	189	51.4	0.00084	gi 143148689 gb EDD17050.1  hypothetical protein G ( 386)	185	50.5	0.0016
gi 218174072 gb ACK72805.1  Rieske (2Fe-2S) domain ( 321)	188	51.1	0.00084	gi 136733278 gb EBQ04531.1  hypothetical protein G ( 323)	184	50.2	0.0016
gi 197697208 gb EDY44141.1  rieske (2Fe-2S) domain ( 340)	188	51.2	0.00089	gi 124293505 gb ABN02774.1  nitrite reductase [NAD ( 154)	180	49.2	0.0016
gi 142137867 gb ECV86775.1  hypothetical protein G ( 411)	189	51.4	0.00089	gi 126244259 gb ABO07352.1  nitrite reductase [NAD ( 154)	180	49.2	0.0016
gi 148501399 gb ABQ69653.1  Rieske (2Fe-2S) domain ( 357)	188	51.2	0.00092	gi 148026580 gb EDK84665.1  nitrite reductase [NAD ( 154)	180	49.2	0.0016
gi 116055637 emb CAL58305.1  unnamed protein produ ( 523)	190	51.7	0.00093	gi 147752578 gb EDK59644.1  nitrite reductase [NAD ( 154)	180	49.2	0.0016
gi 222836377 gb EEE74784.1  predicted protein [Pop ( 144)	183	49.8	0.00094	gi 160696166 gb EDP86136.1  nitrite reductase [NAD ( 154)	180	49.2	0.0016
gi 260644813 emb CBG67898.1  putative 2Fe-2S riesk ( 120)	182	49.6	0.00094	gi 121228206 gb ABM50724.1  nitrite reductase [NAD ( 154)	180	49.2	0.0016
gi 138740764 gb ECB68790.1  hypothetical protein G ( 254)	186	50.6	0.00095	gi 147747596 gb EDK54672.1  nitrite reductase [NAD ( 154)	180	49.2	0.0016
gi 116487684 gb AAI26023.1  MGC154819 protein [Xen ( 454)	189	51.4	0.00097	gi 136683464 gb EBP71912.1  hypothetical protein G ( 224)	182	49.7	0.0016
gi 87130821 gb ABD24045.1  carbazole 1,9a-dioxygen ( 378)	188	51.2	0.00097	gi 141982650 gb ECU61121.1  hypothetical protein G ( 274)	183	50.0	0.0016
gi 28201225 dbj BAC56759.1  terminal oxygenase com ( 378)	188	51.2	0.00097	gi 83650007 gb ABC34071.1  iron-sulfur cluster-bin ( 109)	178	48.6	0.0016
gi 112821398 dbj BAF03269.1  terminal oxygenase co ( 378)	188	51.2	0.00097	gi 137305608 gb EBT35483.1  hypothetical protein G ( 277)	183	50.0	0.0016
gi 17227031 gb AAL37976.1 AF442494_1 carbazole dio ( 378)	188	51.2	0.00097	gi 137998347 gb EBX19615.1  hypothetical protein G ( 196)	181	49.4	0.0017
gi 154156175 gb ABS63392.1  Rieske (2Fe-2S) domain ( 383)	188	51.2	0.00098	gi 139644872 gb ECG47897.1  hypothetical protein G ( 285)	183	50.0	0.0017
gi 136898538 gb EBR12134.1  hypothetical protein G ( 220)	185	50.4	0.00098	gi 4062861 dbj BAA36168.1  LigX [Sphingomonas pauc ( 422)	185	50.5	0.0017
gi 238550020 dbj BAH60846.1  terminal oxygenase co ( 387)	188	51.2	0.00099	gi 142606089 gb EC227933.1  hypothetical protein G ( 351)	184	50.3	0.0017
gi 139914811 gb ECI33724.1  hypothetical protein G ( 223)	185	50.4	0.00099	gi 226245070 dbj BAH55418.1  putative aromatic hyd ( 431)	185	50.5	0.0017
gi 148502383 gb ABQ70637.1  Phthalate 4,5-dioxygen ( 392)	188	51.2	0.001	gi 76875971 emb CAT87193.1  putative protein with ( 364)	184	50.3	0.0018
gi 139407547 gb ECE90280.1  hypothetical protein G ( 195)	184	50.1	0.001	gi 111971100 gb ABH80051.1  Sequence 9894 from pat ( 145)	179	48.9	0.0018
gi 145215826 gb ABP45230.1  Rieske (2Fe-2S) region ( 342)	187	50.9	0.001	gi 141433766 gb ECR79692.1  hypothetical protein G ( 311)	183	50.0	0.0018
gi 142091089 gb ECV51501.1  hypothetical protein G ( 351)	187	50.9	0.0011	gi 140635295 gb ECM46562.1  hypothetical protein G ( 312)	183	50.0	0.0018
gi 136145182 gb EBM19333.1  hypothetical protein G ( 307)	186	50.7	0.0011	gi 217071562 gb ACU84141.1  unknown [Medicago trun ( 180)	180	49.2	0.0018
gi 140943414 gb ECO56049.1  hypothetical protein G ( 178)	183	49.9	0.0011	gi 186464778 gb ACC80579.1  Rieske (2Fe-2S) domain ( 461)	185	50.5	0.0018
gi 203366799 gb ACH98389.1  terminal oxygenase [Sp ( 379)	187	51.0	0.0011	gi 229002443 dbj BAH57734.1  terminal oxygenase co ( 386)	184	50.3	0.0018
gi 138711840 gb ECB48343.1  hypothetical protein G ( 224)	184	50.2	0.0012	gi 144143890 gb EDJ18358.1  hypothetical protein G ( 392)	184	50.3	0.0019

gi 138047462 gb EBX45613.1	hypothetical protein G ( 156)	179	48.9	0.0019	gi 78036080 emb CAJ23771.1	nitrite reductase [NAD ( 122)	173	47.5	0.0039
gi 157805619 gb EDO82789.1	nitrite reductase [NAD ( 131)	178	48.7	0.0019	gi 134512621 gb EBB78596.1	hypothetical protein G ( 124)	173	47.5	0.004
gi 52208565 emb CAH34501.1	putative nitrite reduc ( 131)	178	48.7	0.0019	gi 195539851 gb AAI68106.1	Unknown (protein for M ( 455)	180	49.4	0.004
gi 139365935 gb ECE63725.1	hypothetical protein G ( 233)	181	49.5	0.0019	gi 118164783 gb ABK65680.1	Rieske [2Fe-2S] domain ( 381)	179	49.1	0.004
gi 136685322 gb EBP73138.1	hypothetical protein G ( 339)	183	50.0	0.0019	gi 142550852 gb ECY89370.1	hypothetical protein G ( 382)	179	49.1	0.004
gi 119698399 gb ABL95962.1	PrnD [Pseudomonas fluo ( 173)	179	49.0	0.0021	gi 91686317 gb ABE29517.1	Putative iron-sulphur r ( 387)	179	49.1	0.0041
gi 141985746 gb ECU63338.1	hypothetical protein G ( 148)	178	48.7	0.0021	gi 217503017 gb ACK50426.1	Rieske (2Fe-2S) domain ( 107)	172	47.3	0.0041
gi 119698401 gb ABL95963.1	PrnD [Pseudomonas fluo ( 180)	179	49.0	0.0021	gi 167864110 gb EDS27493.1	rieske-domain protein ( 481)	180	49.4	0.0042
gi 135482219 gb EBH93026.1	hypothetical protein G ( 314)	182	49.8	0.0021	gi 138007177 gb EBX24232.1	hypothetical protein G ( 234)	176	48.4	0.0042
gi 221532933 gb EEE35928.1	iron-sulphur protein [ ( 461)	184	50.3	0.0021	gi 136702514 gb EBP84374.1	hypothetical protein G ( 343)	178	48.9	0.0043
gi 270227787 emb CBI16520.1	unnamed protein produ ( 571)	185	50.6	0.0022	gi 137309142 gb EBT37467.1	hypothetical protein G ( 136)	173	47.6	0.0043
gi 141288072 gb ECQ88837.1	hypothetical protein G ( 115)	176	48.2	0.0023	gi 137880540 gb EBW53169.1	hypothetical protein G ( 294)	177	48.6	0.0044
gi 145216085 gb ABP45489.1	Rieske (2Fe-2S) domain ( 96)	175	47.9	0.0023	gi 144218286 gb EDJ72663.1	hypothetical protein G ( 360)	178	48.9	0.0045
gi 143440679 gb EDB97114.1	hypothetical protein G ( 424)	183	50.1	0.0023	gi 135053364 gb EBF19412.1	hypothetical protein G ( 443)	179	49.2	0.0046
gi 139775668 gb ECH37767.1	hypothetical protein G ( 117)	176	48.2	0.0024	gi 136400751 gb EBN91909.1	hypothetical protein G ( 147)	173	47.6	0.0046
gi 138808304 gb ECB95309.1	hypothetical protein G ( 119)	176	48.2	0.0024	gi 108770617 gb ABG09339.1	Rieske (2Fe-2S) region ( 102)	171	47.0	0.0046
gi 123200373 gb ABM71981.1	Rieske iron-sulfur pro ( 439)	183	50.1	0.0024	gi 119695415 gb ABJ92488.1	Rieske (2Fe-2S) domain ( 102)	171	47.0	0.0046
gi 135132152 gb EBF69811.1	hypothetical protein G ( 458)	183	50.1	0.0025	gi 2665670 gb AAC18406.1	ribulose-1,5-bisphosphat ( 178)	174	47.8	0.0046
gi 214037440 gb EEB78107.1	Rieske (2Fe-2S) domain ( 386)	182	49.8	0.0025	gi 138001687 gb EBX21373.1	hypothetical protein G ( 149)	173	47.6	0.0046
gi 183178309 gb ACC43419.1	conserved hypothetical ( 394)	182	49.8	0.0026	gi 41396790 gb AAS04653.1	hypothetical protein MA ( 381)	178	48.9	0.0047
gi 138519339 gb ECA15495.1	hypothetical protein G ( 165)	177	48.5	0.0027	gi 143947606 gb EDH78057.1	hypothetical protein G ( 381)	178	48.9	0.0047
gi 141081761 gb ECP49674.1	hypothetical protein G ( 119)	175	48.0	0.0028	gi 135005121 gb EBE87509.1	hypothetical protein G ( 384)	178	48.9	0.0047
gi 189232095 emb CAQ53717.1	aminopyrrolnitrin oxy ( 210)	178	48.8	0.0028	gi 109701219 gb ABG41139.1	Rieske (2Fe-2S) region ( 384)	178	48.9	0.0047
gi 72120950 gb AAZ63136.1	Rieske (2Fe-2S) region ( 101)	174	47.7	0.0029	gi 189338337 dbj BAG47405.1	putative ring-hydroxy ( 324)	177	48.7	0.0048
gi 138828729 gb ECC05132.1	hypothetical protein G ( 258)	179	49.1	0.0029	gi 138936693 gb ECC49587.1	hypothetical protein G ( 270)	176	48.4	0.0048
gi 135201849 gb EBG14152.1	hypothetical protein G ( 381)	181	49.6	0.0029	gi 137912906 gb EBW71725.1	hypothetical protein G ( 273)	176	48.4	0.0048
gi 214044399 gb EEB85037.1	rieske (2Fe-2S) protei ( 382)	181	49.6	0.0029	gi 141586608 gb ECS47746.1	hypothetical protein G ( 228)	175	48.1	0.0049
gi 33567688 emb CAE31602.1	[2Fe-2S] protein [Bord ( 383)	181	49.6	0.0029	gi 473250 emb CAA55400.1	phenoxybenzoate dioxygen ( 409)	178	48.9	0.005
gi 118169069 gb ABK69965.1	Rieske [2Fe-2S] domain ( 383)	181	49.6	0.0029	gi 160346525 gb ABX19609.1	Rieske (2Fe-2S) domain ( 342)	177	48.7	0.005
gi 89243566 gb ABC86866.1	terminal oxygenase of 3 ( 383)	181	49.6	0.0029	gi 139401370 gb ECE86074.1	hypothetical protein G ( 113)	171	47.1	0.005
gi 87239943 dbj BAE79498.1	terminal oxygenase com ( 388)	181	49.6	0.003	gi 95111173 emb CAK15893.1	putative ferredoxin re ( 513)	179	49.2	0.0052
gi 135829037 gb EBK10496.1	hypothetical protein G ( 330)	180	49.3	0.003	gi 209530476 gb ACI50413.1	Rieske (2Fe-2S) domain ( 118)	171	47.1	0.0052
gi 237883917 gb EEP72745.1	2Fe-2S domain-containi ( 283)	179	49.1	0.0031	gi 140402192 gb ECL53007.1	hypothetical protein G ( 171)	173	47.6	0.0052
gi 258380645 emb CAQ48268.1	AerC protein [Planko ( 736)	184	50.4	0.0032	gi 136353176 gb EBN59213.1	hypothetical protein G ( 253)	175	48.1	0.0053
gi 135041343 gb EBF11739.1	hypothetical protein G ( 248)	178	48.8	0.0033	gi 145214919 gb ABP44323.1	Rieske (2Fe-2S) domain ( 367)	177	48.7	0.0053
gi 137103446 gb EBS22137.1	hypothetical protein G ( 307)	179	49.1	0.0033	gi 35213254 dbj BAC90626.1	glr2685 [Gloeobacter v ( 179)	173	47.6	0.0054
gi 119698397 gb ABL95961.1	PrnD [Pseudomonas fluo ( 177)	176	48.3	0.0034	gi 270383724 dbj BAI53120.1	ribulose-1,5-bisphosp ( 179)	173	47.6	0.0054
gi 3044116 gb AAC13293.1	ribulose-1,5-bisphosphat ( 180)	176	48.3	0.0034	gi 49529457 emb CAG67169.1	hypothetical protein; ( 216)	174	47.9	0.0054
gi 7269415 emb CAB81375.1	putative protein [Arabi ( 548)	182	49.9	0.0034	gi 260644656 emb CBG67741.1	putative iron-sulfur ( 316)	176	48.4	0.0055
gi 4914457 emb CAB43696.1	putative protein [Arabi ( 548)	182	49.9	0.0034	gi 15108657 gb AAE67693.1	Sequence 29 from patent ( 35)	164	45.2	0.0056
gi 3928152 emb CAA10290.1	ribulose 1,5-bisphospha ( 181)	176	48.3	0.0034	gi 33769216 gb AAQ53847.1	Sequence 29 from patent ( 35)	164	45.2	0.0056
gi 270383722 dbj BAI53119.1	ribulose-1,5-bisphosp ( 181)	176	48.3	0.0034	gi 126236489 gb ABN99889.1	Rieske (2Fe-2S) domain ( 335)	176	48.4	0.0058
gi 144177642 gb EDJ43277.1	hypothetical protein G ( 387)	180	49.4	0.0035	gi 143568120 gb EDF67864.1	hypothetical protein G ( 357)	176	48.4	0.0061
gi 118571384 gb ABL06135.1	conserved hypothetical ( 394)	180	49.4	0.0035	gi 136618851 gb EBP32371.1	hypothetical protein G ( 171)	172	47.4	0.0061
gi 169239794 emb CAM60822.1	Conserved hypotherica ( 332)	179	49.1	0.0036	gi 194312239 gb ACP46634.1	Rieske (2Fe-2S) domain ( 101)	169	46.6	0.0063
gi 135380198 gb EBH24824.1	hypothetical protein G ( 404)	180	49.4	0.0036	gi 143113461 gb EDC91191.1	hypothetical protein G ( 311)	175	48.2	0.0063
gi 166915538 gb ABZ02622.1	accelerated cell death ( 53)	169	46.4	0.0036	gi 135322083 gb EBG85811.1	hypothetical protein G ( 186)	172	47.4	0.0066
gi 137911754 gb EBW71055.1	hypothetical protein G ( 284)	178	48.9	0.0037	gi 143884135 gb EDH32544.1	hypothetical protein G ( 403)	176	48.5	0.0067
gi 135150962 gb EBF81893.1	hypothetical protein G ( 415)	180	49.4	0.0037	gi 137956235 gb EBW96097.1	hypothetical protein G ( 112)	169	46.6	0.0068
gi 88863929 gb ABD54806.1	Rieske (2Fe-2S) protein ( 420)	180	49.4	0.0037	gi 147754491 gb EDR61555.1	putative oxygenase [Bu ( 342)	175	48.2	0.0069
gi 141230622 gb ECQ52556.1	hypothetical protein G ( 115)	173	47.5	0.0037	gi 157937096 gb EDO92766.1	conserved hypothetical ( 342)	175	48.2	0.0069

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gi 147748555 gb EDK55630.1	putative oxygenase [Bu ( 342)	175	48.2	0.0069	gi 119696846 gb ABL93919.1	Rieske (2Fe-2S) domain ( 385)	173	47.8	0.01
gi 126240331 gb ABO03443.1	oxygenase [Burkholderi ( 342)	175	48.2	0.0069	gi 108772022 gb ABG10744.1	Rieske (2Fe-2S) region ( 385)	173	47.8	0.01
gi 148028211 gb EDK86171.1	conserved hypothetical ( 342)	175	48.2	0.0069	gi 126237386 gb ABO00787.1	Rieske (2Fe-2S) domain ( 385)	173	47.8	0.01
gi 126224669 gb ABN88174.1	putative oxygenase [Bu ( 345)	175	48.2	0.0069	gi 142502234 gb ECY54200.1	hypothetical protein G ( 395)	173	47.8	0.011
gi 261826334 gb ABN00007.2	conserved hypothetical ( 345)	175	48.2	0.0069	gi 112821376 dbj BAF03247.1	anthranilate dioxygen ( 90)	165	45.7	0.011
gi 126230029 gb ABN93442.1	conserved hypothetical ( 345)	175	48.2	0.0069	gi 226239702 dbj BAH50050.1	putative iron-sulfur ( 399)	173	47.8	0.011
gi 254213495 gb EET02880.1	oxygenase [Burkholderi ( 345)	175	48.2	0.0069	gi 169243218 emb CAM64246.1	Possible oxidoreducta ( 400)	173	47.8	0.011
gi 52211727 emb CAH37725.1	putative oxygenase [Bu ( 346)	175	48.2	0.0069	gi 158308995 gb ABW30612.1	rieske 2Fe-2S domain p ( 334)	172	47.5	0.011
gi 160697007 gb EDP86977.1	putative oxygenase [Bu ( 346)	175	48.2	0.0069	gi 115253852 emb CAK12247.1	putative Rieske 2Fe2S ( 417)	173	47.8	0.011
gi 157809602 gb EDO86772.1	conserved hypothetical ( 346)	175	48.2	0.0069	gi 199595097 gb ACH91010.1	KshA3 [Rhodococcus ery ( 199)	169	46.7	0.011
gi 242134407 gb EES20810.1	conserved hypothetical ( 346)	175	48.2	0.0069	gi 126220361 gb ABN83867.1	conserved domain prote ( 347)	172	47.5	0.011
gi 169652133 gb EDS84826.1	putative oxygenase [Bu ( 346)	175	48.2	0.0069	gi 126227034 gb ABN90574.1	conserved domain prote ( 349)	172	47.5	0.011
gi 226514723 gb ACO60719.1	chloroplast envelope p ( 609)	178	49.0	0.007	gi 242137417 gb EES23819.1	conserved domain prote ( 349)	172	47.5	0.011
gi 133917247 emb CAJ21199.2	hypothetical protein ( 736)	179	49.3	0.007	gi 167349347 gb ABZ72082.1	nitrite reductase (NAD ( 115)	166	45.9	0.011
gi 111150446 emb CAJ62145.1	hypothetical protein; ( 354)	175	48.2	0.0071	gi 169654920 gb EDS87613.1	conserved domain prote ( 350)	172	47.5	0.011
gi 138722921 gb ECB56043.1	hypothetical protein G ( 295)	174	48.0	0.0071	gi 137764827 gb EBV87188.1	hypothetical protein G ( 292)	171	47.3	0.011
gi 142059703 gb ECV25110.1	hypothetical protein G ( 437)	176	48.5	0.0072	gi 223526763 gb EEF28989.1	pheophorbide A oxygena ( 509)	174	48.1	0.011
gi 295846 emb CAA36542.1	ribulose bisphosphate ca ( 178)	171	47.2	0.0074	gi 144582041 gb ABP00097.1	predicted protein [Ost ( 510)	174	48.1	0.011
gi 139544655 gb ECF79826.1	hypothetical protein G ( 178)	171	47.2	0.0074	gi 140912122 gb ECO34081.1	hypothetical protein G ( 203)	169	46.7	0.011
gi 223528742 gb EEF30752.1	Ribulose bisphosphate ( 180)	171	47.2	0.0075	gi 126236445 gb ABN99845.1	Rieske (2Fe-2S) domain ( 429)	173	47.8	0.011
gi 158107344 gb ABW09541.1	Rieske (2Fe-2S) domain ( 396)	175	48.2	0.0078	gi 118168209 gb ABK69106.1	dioxygenase large subu ( 431)	173	47.8	0.011
gi 240861408 gb ACS59074.1	Rieske (2Fe-2S) domain ( 417)	175	48.3	0.0081	gi 90658396 gb ABD93563.2	chloroplast chlorophyll ( 99)	165	45.7	0.012
gi 142524365 gb ECY70250.1	hypothetical protein G ( 371)	174	48.0	0.0086	gi 90658395 gb ABD93562.2	chloroplast chlorophyll ( 99)	165	45.7	0.012
gi 140772063 gb ECN40006.1	hypothetical protein G ( 102)	167	46.1	0.0086	gi 148567243 gb ABQ89388.1	Rieske (2Fe-2S) domain ( 362)	172	47.5	0.012
gi 118170567 gb ABK71463.1	pyruvate dehydrogenase ( 651)	177	48.8	0.0086	gi 253987171 gb ACT52028.1	Rieske (2Fe-2S) domain ( 371)	172	47.5	0.012
gi 134596467 gb EBC28761.1	hypothetical protein G ( 258)	172	47.5	0.0087	gi 189232085 emb CAQ53712.1	aminopyrrolnitrin oxy ( 221)	169	46.8	0.012
gi 161786737 emb CAP56320.1	putative Ubiquinol-cy ( 124)	168	46.4	0.0087	gi 211959387 gb EEA94585.1	dioxygenase, putative ( 386)	172	47.6	0.012
gi 167270 gb AAA33036.1	ribulose 1,5-bisphosphate ( 180)	170	46.9	0.0087	gi 50978421 emb CAH10355.1	ribulose 1,5 bisphosph ( 153)	167	46.2	0.012
gi 304444 gb AAA03694.1	ribulose-1,5-bisphosphate ( 180)	170	46.9	0.0087	gi 223528159 gb EEF30223.1	Ribulose bisphosphate ( 185)	168	46.5	0.012
gi 304442 gb AAA03693.1	ribulose-1,5-bisphosphate ( 182)	170	46.9	0.0088	gi 50978423 emb CAH10356.1	ribulose 1,5 bisphosph ( 154)	167	46.2	0.012
gi 167268 gb AAA33035.1	ribulose-1-5-bisphosphate ( 182)	170	46.9	0.0088	gi 76582534 gb ABA52008.1	conserved domain protei ( 679)	175	48.4	0.012
gi 167272 gb AAA33037.1	ribulose 1,5-bisphosphate ( 183)	170	46.9	0.0089	gi 142407878 gb ECX84972.1	hypothetical protein G ( 394)	172	47.6	0.012
gi 436487 gb AAA03695.1	ribulose-1,5-bisphosphate ( 183)	170	46.9	0.0089	gi 142589878 gb ECZ16620.1	hypothetical protein G ( 399)	172	47.6	0.013
gi 196112072 gb ACG65788.1	dioxygenase, ferredoxi ( 559)	176	48.5	0.0089	gi 142926962 gb EDB57336.1	hypothetical protein G ( 191)	168	46.5	0.013
gi 304447 gb AAA03698.1	ribulose-1,5-bisphosphate ( 186)	170	46.9	0.009	gi 189232071 emb CAQ53705.1	aminopyrrolnitrin oxy ( 230)	169	46.8	0.013
gi 145322407 gb ABP64350.1	Rieske (2Fe-2S) domain ( 392)	174	48.0	0.009	gi 136190361 gb EBM48907.1	hypothetical protein G ( 403)	172	47.6	0.013
gi 142383146 gb ECX67115.1	hypothetical protein G ( 393)	174	48.0	0.009	gi 189232081 emb CAQ53710.1	aminopyrrolnitrin oxy ( 232)	169	46.8	0.013
gi 260644351 emb CBG67436.1	ferredoxin subunit of ( 111)	167	46.2	0.0093	gi 163261680 emb CAP43982.1	nitrite reductase (NA ( 111)	165	45.7	0.013
gi 142445251 gb ECY13016.1	hypothetical protein G ( 233)	171	47.2	0.0093	gi 54310848 gb AAV33660.1	MnbA [Comamonas sp. JS4 ( 414)	172	47.6	0.013
gi 139554297 gb ECF86657.1	hypothetical protein G ( 196)	170	47.0	0.0094	gi 196477856 gb ACG77384.1	nitrite reductase [NAD ( 137)	166	46.0	0.013
gi 142732527 gb EDA17825.1	hypothetical protein G ( 114)	167	46.2	0.0095	gi 135665462 gb EBJ08630.1	hypothetical protein G ( 353)	171	47.3	0.013
gi 142779744 gb EDA52396.1	hypothetical protein G ( 417)	174	48.0	0.0095	gi 121554190 gb ABM58339.1	assimilatory nitrite r ( 140)	166	46.0	0.013
gi 145047590 gb ABP34217.1	assimilatory nitrite r ( 116)	167	46.2	0.0096	gi 206677910 gb EDZ42397.1	rieske 2Fe-2S domain p ( 363)	171	47.3	0.014
gi 170776805 gb ACB34944.1	nitrite reductase (NAD ( 118)	167	46.2	0.0098	gi 144047439 gb EDT48512.1	hypothetical protein G ( 146)	166	46.0	0.014
gi 118174153 gb ABK75049.1	Rieske [2Fe-2S] domain ( 359)	173	47.8	0.0098	gi 134365514 gb EBA91950.1	hypothetical protein G ( 372)	171	47.3	0.014
gi 29604666 dbj BAC68735.1	putative methylesteras ( 359)	173	47.8	0.0098	gi 5002365 gb AAD37440.1	AF150667_1 ribulose 1,5 b ( 180)	167	46.3	0.014
gi 15823923 dbj BAB69146.1	methyltransferase [Str ( 359)	173	47.8	0.0098	gi 138469856 gb EBZ89581.1	hypothetical protein G ( 181)	167	46.3	0.014
gi 262087500 gb ACY23468.1	Rieske (2Fe-2S) iron-s ( 369)	173	47.8	0.01	gi 142012923 gb ECU82956.1	hypothetical protein G ( 382)	171	47.3	0.014
gi 136735511 gb EBQ06013.1	hypothetical protein G ( 215)	170	47.0	0.01	gi 91795355 gb ABE57494.1	Rieske (2Fe-2S) protein ( 106)	164	45.5	0.014
gi 221155472 gb ECM04599.1	rieske 2Fe-2S domain p ( 378)	173	47.8	0.01	gi 140708546 gb ECM97045.1	hypothetical protein G ( 186)	167	46.3	0.014
gi 135309038 gb EBG77134.1	hypothetical protein G ( 261)	171	47.2	0.01	gi 143283066 gb EDE11032.1	hypothetical protein G ( 399)	171	47.3	0.015

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gi 136009721 gb EBL30064.1	hypothetical protein G ( 279)	169	46.8	0.015	gi 134967502 gb EBE61995.1	hypothetical protein G ( 242)	166	46.1	0.021
gi 14524315 gb AAK65812.1	oxidoreductase [Sinorhi ( 588)	173	47.9	0.015	gi 260024743 gb ACX04274.1	Sequence 27038 from pa ( 170)	164	45.6	0.021
gi 142803989 gb EDA70435.1	hypothetical protein G ( 112)	164	45.5	0.015	gi 260024742 gb ACX04273.1	Sequence 27037 from pa ( 176)	164	45.6	0.022
gi 140687833 gb ECM82619.1	hypothetical protein G ( 291)	169	46.8	0.015	gi 141129088 gb ECP82976.1	hypothetical protein G ( 260)	166	46.1	0.022
gi 142750478 gb EDA30890.1	hypothetical protein G ( 351)	170	47.1	0.015	gi 33575314 emb CAE30777.1	ferredoxin [Bordetella ( 103)	161	44.8	0.022
gi 144223809 gb EDJ76622.1	hypothetical protein G ( 431)	171	47.4	0.016	gi 33571431 emb CAE44914.1	ferredoxin [Bordetella ( 103)	161	44.8	0.022
gi 135578054 gb EBI54438.1	hypothetical protein G ( 431)	171	47.4	0.016	gi 33565067 emb CAE40017.1	ferredoxin [Bordetella ( 103)	161	44.8	0.022
gi 142820679 gb EDA82927.1	hypothetical protein G ( 120)	164	45.5	0.016	gi 25083492 gb AAN72087.1	ribulose bisphosphate c ( 180)	164	45.6	0.022
gi 143125213 gb EDC99819.1	hypothetical protein G ( 444)	171	47.4	0.016	gi 260024741 gb ACX04272.1	Sequence 27036 from pa ( 180)	164	45.6	0.022
gi 136330004 gb EBN43441.1	hypothetical protein G ( 258)	168	46.6	0.016	gi 23198308 gb AAN15681.1	ribulose bisphosphate c ( 180)	164	45.6	0.022
gi 215491344 gb EEC00985.1	conserved hypothetical ( 376)	170	47.1	0.016	gi 110741446 dbj BAE98685.1	ribulose bisphosphate ( 180)	164	45.6	0.022
gi 13926229 gb AAK49590.1	AF372874_1 F1019.10/F101 ( 125)	164	45.5	0.016	gi 110741032 dbj BAE98610.1	ribulose bisphosphate ( 180)	164	45.6	0.022
gi 161162154 emb CAN93459.1	hypothetical protein ( 380)	170	47.1	0.016	gi 17473628 gb AAL38277.1	ribulose bisphosphate c ( 180)	164	45.6	0.022
gi 83651848 gb ABC35912.1	naphthalene 1,2-dioxyge ( 105)	163	45.2	0.017	gi 17065270 gb AAL32789.1	ribulose bisphosphate c ( 180)	164	45.6	0.022
gi 141792533 gb ECT31778.1	hypothetical protein G ( 184)	166	46.0	0.017	gi 11762170 gb AAG40363.1	AF325011_1 000C10C11 [Ar ( 180)	164	45.6	0.022
gi 33769217 gb AAQ53848.1	Sequence 30 from patent ( 35)	157	43.6	0.017	gi 16604426 gb AAL24219.1	Atl67090/F1019.10 [Ara ( 180)	164	45.6	0.022
gi 15108658 gb AAE67694.1	Sequence 30 from patent ( 35)	157	43.6	0.017	gi 15294200 gb AAK95277.1	AF140291_1 F1019.10/F101 ( 180)	164	45.6	0.022
gi 136688642 gb EBP75311.1	hypothetical protein G ( 228)	167	46.3	0.017	gi 15809842 gb AAL06849.1	Atl67090/F1019.10 [Ara ( 180)	164	45.6	0.022
gi 150027647 gb ABR59764.1	Rieske (2Fe-2S) domain ( 109)	163	45.2	0.017	gi 4204274 gb AAD10655.1	ribulose bisphosphate ca ( 180)	164	45.6	0.022
gi 145570956 gb ABP80062.1	assimilatory nitrite r ( 109)	163	45.2	0.017	gi 20260064 gb AAM13379.1	ribulose bisphosphate c ( 180)	164	45.6	0.022
gi 144053764 gb EDI53213.1	hypothetical protein G ( 334)	169	46.8	0.017	gi 15451002 gb AAK96772.1	ribulose bisphosphate c ( 180)	164	45.6	0.022
gi 136598578 gb EBP19445.1	hypothetical protein G ( 341)	169	46.9	0.018	gi 20453287 gb AAM19882.1	Atl67090/F1019.10 [Ara ( 180)	164	45.6	0.022
gi 142217525 gb ECW47425.1	hypothetical protein G ( 138)	164	45.5	0.018	gi 16649141 gb AAL24422.1	ribulose bisphosphate c ( 180)	164	45.6	0.022
gi 139530619 gb ECF70162.1	hypothetical protein G ( 169)	165	45.8	0.018	gi 20260080 gb AAM13387.1	ribulose bisphosphate c ( 180)	164	45.6	0.022
gi 53758879 gb AAU93170.1	nitrite reductase [NAD( ( 118)	163	45.3	0.018	gi 110741475 dbj BAE98695.1	ribulose bisphosphate ( 180)	164	45.6	0.022
gi 144099438 gb EDI86079.1	hypothetical protein G ( 171)	165	45.8	0.018	gi 17065072 gb AAL32690.1	ribulose bisphosphate c ( 180)	164	45.6	0.022
gi 197714994 gb EDY59028.1	3-phenylpropionate dio ( 119)	163	45.3	0.018	gi 110741865 dbj BAE98874.1	ribulose bisphosphate ( 180)	164	45.6	0.022
gi 189232091 emb CAQ53715.1	aminopyrrolnitritr oxy ( 208)	166	46.1	0.018	gi 6635351 gb AAF19793.1	AF162210_1 ribulose-1,5-b ( 181)	164	45.6	0.023
gi 30698449 dbj BAC76562.1	putative methyltransfer ( 305)	168	46.6	0.019	gi 295792 emb CAA31948.1	ribulose bisphosphate ca ( 182)	164	45.6	0.023
gi 149938960 gb ABR45725.1	RBCS1 [Actinidia delic ( 176)	165	45.8	0.019	gi 226934608 gb ACO92379.1	salicylate 5-hydroxyla ( 105)	161	44.8	0.023
gi 136235976 gb EBM79611.1	hypothetical protein G ( 372)	169	46.9	0.019	gi 52423116 gb AAU46686.1	naphthalene 1,2-dioxyge ( 105)	161	44.8	0.023
gi 189232087 emb CAQ53713.1	aminopyrrolnitritr oxy ( 214)	166	46.1	0.019	gi 157323967 gb ABV43064.1	Rieske (2Fe-2S) domain ( 105)	161	44.8	0.023
gi 141502271 gb ECS08228.1	hypothetical protein G ( 258)	167	46.3	0.019	gi 126239302 gb ABO02414.1	naphthalene 1,2-dioxyg ( 105)	161	44.8	0.023
gi 11762156 gb AAG40356.1	AF325004_1 Atl67090 [Ar ( 180)	165	45.8	0.019	gi 52212332 emb CAH38356.1	Rieske [2Fe-2S] domain ( 105)	161	44.8	0.023
gi 5002361 gb AAD37438.1	AF150665_1 ribulose 1,5 b ( 183)	165	45.8	0.019	gi 157810415 gb EDO87585.1	iron-sulfur cluster-bi ( 105)	161	44.8	0.023
gi 809533 emb CAA60636.1	ribulose 1,5-bisphosphat ( 183)	165	45.8	0.019	gi 147748409 gb EDK55484.1	iron-sulfur cluster-bi ( 105)	161	44.8	0.023
gi 143283823 gb EDE11401.1	hypothetical protein G ( 385)	169	46.9	0.019	gi 184213883 gb EDU10926.1	iron-sulfur cluster-bi ( 105)	161	44.8	0.023
gi 5002363 gb AAD37439.1	AF150666_1 ribulose 1,5 b ( 184)	165	45.8	0.02	gi 124290700 gb ABM99969.1	naphthalene 1,2-dioxyg ( 105)	161	44.8	0.023
gi 32446983 emb CAD78889.1	probable dioxygenase R ( 386)	169	46.9	0.02	gi 126232250 gb ABN95663.1	iron-sulfur cluster-bi ( 105)	161	44.8	0.023
gi 28201189 dbj BAC56726.1	partial terminal oxyge ( 268)	167	46.3	0.02	gi 126224763 gb ABN88268.1	iron-sulfur cluster-bi ( 105)	161	44.8	0.023
gi 121552602 gb ABM56751.1	putative vanillate O-d ( 107)	162	45.0	0.02	gi 147754354 gb EDK61418.1	iron-sulfur cluster-bi ( 105)	161	44.8	0.023
gi 136468506 gb EB036027.1	hypothetical protein G ( 393)	169	46.9	0.02	gi 254215229 gb EET04614.1	iron-sulfur cluster-bi ( 105)	161	44.8	0.023
gi 140260854 gb ECK62196.1	hypothetical protein G ( 273)	167	46.3	0.02	gi 242135695 gb EES22098.1	iron-sulfur cluster-bi ( 105)	161	44.8	0.023
gi 136375233 gb EBN74267.1	hypothetical protein G ( 398)	169	46.9	0.02	gi 169649783 gb EDS8247.1	iron-sulfur cluster-bi ( 105)	161	44.8	0.023
gi 143364384 gb EDE57484.1	hypothetical protein G ( 482)	170	47.2	0.02	gi 76582904 gb ABA52378.1	Rieske (2Fe-2S) domain ( 105)	161	44.8	0.023
gi 140643128 gb ECM51397.1	hypothetical protein G ( 111)	162	45.0	0.02	gi 121225562 gb ABM49093.1	naphthalene 1,2-dioxyg ( 105)	161	44.8	0.023
gi 237902872 gb EEP77273.1	conserved hypothetical ( 407)	169	46.9	0.02	gi 160695198 gb EDP85168.1	naphthalene 1,2-dioxyg ( 105)	161	44.8	0.023
gi 198268818 gb EDY93088.1	rieske (2Fe-2S) protei ( 411)	169	46.9	0.021	gi 28201207 dbj BAC56742.1	terminal oxygenase com ( 384)	168	46.7	0.023
gi 135977540 gb EBL10094.1	hypothetical protein G ( 237)	166	46.1	0.021	gi 144200955 gb EDJ60444.1	hypothetical protein G ( 388)	168	46.7	0.023
gi 170655416 gb ACB24471.1	Rieske (2Fe-2S) domain ( 419)	169	46.9	0.021	gi 138498429 gb ECA02378.1	hypothetical protein G ( 323)	167	46.4	0.023
gi 141495284 gb ECS06252.1	hypothetical protein G ( 290)	167	46.4	0.021	gi 8574396 emb CAB94799.1	methylesterase [Mycobac ( 325)	167	46.4	0.023

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gi 124899763 gb EAY71606.1	Rieske (2Fe-2S) protei	( 108)	161	44.8	0.023	gi 138131164 gb EBX91732.1	hypothetical protein G	( 279)	165	45.9	0.028
gi 135455815 gb EBH75583.1	hypothetical protein G	( 398)	168	46.7	0.023	gi 139862918 gb ECH98860.1	hypothetical protein G	( 238)	164	45.6	0.028
gi 136026041 gb EBL41208.1	hypothetical protein G	( 191)	164	45.6	0.024	gi 89346072 gb ABD70275.1	assimilatory nitrite re	( 115)	160	44.6	0.029
gi 33415332 gb AAQ18185.1	NirD [Rhodobacter capsu	( 110)	161	44.8	0.024	gi 118163681 gb ABK64578.1	dioxygenase large subu	( 422)	167	46.4	0.029
gi 13421823 gb AAK22601.1	nitrite reductase [NAD(	( 110)	161	44.8	0.024	gi 184210203 gb EDU07246.1	conserved domain prote	( 353)	166	46.2	0.029
gi 119955406 gb ABM12411.1	Rieske (2Fe-2S) domain	( 335)	167	46.4	0.024	gi 139172482 gb ECD90427.1	hypothetical protein G	( 248)	164	45.6	0.029
gi 148026044 gb EDK84167.1	iron-sulfur cluster-bi	( 111)	161	44.8	0.024	gi 241865463 gb ACS68764.1	ribulose-1,5-bisphosph	( 173)	162	45.1	0.03
gi 157937659 gb ED093329.1	iron-sulfur cluster-bi	( 111)	161	44.8	0.024	gi 241865230 gb ACS68693.1	ribulose-1,5-bisphosph	( 173)	162	45.1	0.03
gi 158309960 gb ABW31576.1	rieske 2Fe-2S domain p	( 492)	169	46.9	0.024	gi 143772463 gb EDG70859.1	hypothetical protein G	( 367)	166	46.2	0.03
gi 254218503 gb EET07887.1	conserved domain prote	( 346)	167	46.4	0.024	gi 134380450 gb EBB02085.1	hypothetical protein G	( 368)	166	46.2	0.03
gi 52209658 emb CAH35614.1	hypothetical protein [	( 346)	167	46.4	0.024	gi 149938962 gb ABR45726.1	RBCS1 [Actinidia chine	( 176)	162	45.1	0.03
gi 76581091 gb ABA50566.1	conserved domain protei	( 346)	167	46.4	0.024	gi 146454996 gb ABQ42164.1	ribulose bisphosphate	( 178)	162	45.1	0.03
gi 157936628 gb ED092298.1	conserved domain prote	( 346)	167	46.4	0.024	gi 146454846 gb ABQ42089.1	ribulose bisphosphate	( 178)	162	45.1	0.03
gi 237505599 gb ACQ97917.1	oxygenase [Burkholderi	( 346)	167	46.4	0.024	gi 134770011 gb EBD31115.1	hypothetical protein G	( 258)	164	45.7	0.03
gi 220962761 gb ACL94117.1	nitrite reductase (NAD	( 114)	161	44.8	0.024	gi 135022682 gb EBE99344.1	hypothetical protein G	( 377)	166	46.2	0.031
gi 157807100 gb EDO84270.1	conserved domain prote	( 347)	167	46.4	0.024	gi 155362255 gb ABU17860.1	Sequence 205329 from p	( 125)	160	44.6	0.031
gi 135928606 gb EBK77105.1	hypothetical protein G	( 240)	165	45.9	0.024	gi 134393617 gb EBB10090.1	hypothetical protein G	( 182)	162	45.1	0.031
gi 137140982 gb EBS43205.1	hypothetical protein G	( 289)	166	46.1	0.024	gi 436488 gb AAA03696.1	ribulose-1,5-bisphosphate	( 183)	162	45.1	0.031
gi 52428736 gb AAU49329.1	conserved domain protei	( 349)	167	46.4	0.025	gi 167274 gb AAA33038.1	ribulose 1,5-bisphosphate	( 183)	162	45.1	0.031
gi 83655380 gb ABC39443.1	conserved hypothetical	( 349)	167	46.4	0.025	gi 108461247 gb ABF86432.1	iron-sulfur cluster-bi	( 319)	165	45.9	0.031
gi 184195071 gb ACC73035.1	Rieske (2Fe-2S) domain	( 115)	161	44.8	0.025	gi 184185951 dbj BAG30826.1	terminal oxygenase co	( 385)	166	46.2	0.031
gi 169820638 gb ACA95219.1	Rieske (2Fe-2S) domain	( 350)	167	46.4	0.025	gi 142021623 gb ECU91316.1	hypothetical protein G	( 108)	159	44.3	0.032
gi 147753423 gb EDK60488.1	conserved domain prote	( 350)	167	46.4	0.025	gi 142507168 gb ECY57735.1	hypothetical protein G	( 228)	163	45.4	0.032
gi 147749258 gb EDK56332.1	conserved domain prote	( 350)	167	46.4	0.025	gi 13241113 gb AAK16233.1	AF044401_1 ribulose-1,5-	( 131)	160	44.6	0.032
gi 148027748 gb EDK85769.1	conserved domain prote	( 350)	167	46.4	0.025	gi 13241109 gb AAK16231.1	AF044399_1 ribulose-1,5-	( 131)	160	44.6	0.032
gi 160699220 gb EDP89190.1	conserved domain prote	( 350)	167	46.4	0.025	gi 13241107 gb AAK16230.1	AF044398_1 ribulose-1,5-	( 131)	160	44.6	0.032
gi 141043536 gb ECP24394.1	hypothetical protein G	( 202)	164	45.6	0.025	gi 3243169 gb AAC38618.1	initial dioxygenase ferr	( 109)	159	44.3	0.032
gi 140936215 gb ECO51102.1	hypothetical protein G	( 244)	165	45.9	0.025	gi 144048516 gb EDI49311.1	hypothetical protein G	( 406)	166	46.2	0.033
gi 137007529 gb EBR68564.1	hypothetical protein G	( 118)	161	44.8	0.025	gi 86285220 gb ABC94278.1	putative dyoxygenase (a	( 417)	166	46.2	0.033
gi 261836182 gb ACX95949.1	nitrite reductase (NAD	( 120)	161	44.8	0.025	gi 166860165 gb ABY98572.1	FAD-dependent pyridine	( 506)	167	46.5	0.034
gi 144169803 gb EDJ37491.1	hypothetical protein G	( 260)	165	45.9	0.026	gi 118165717 gb ABK66614.1	dioxygenase large subu	( 431)	166	46.2	0.034
gi 217946 dbj BAA03103.1	ribulose-1,5-bisphosphat	( 181)	163	45.4	0.026	gi 12240092 gb AAG49562.1	ribulose-1,5-bisphospha	( 118)	159	44.4	0.034
gi 215491346 gb EEC00987.1	conserved hypothetical	( 664)	170	47.2	0.026	gi 141542167 gb ECS24774.1	hypothetical protein G	( 208)	162	45.2	0.035
gi 168217 gb AAA33361.1	ribulose-1,5-bisphosphate	( 183)	163	45.4	0.027	gi 140361516 gb ECL24700.1	hypothetical protein G	( 173)	161	44.9	0.035
gi 3293058 dbj BAA31266.1	carbazole dioxygenase s	( 384)	167	46.4	0.027	gi 141754144 gb ECT11650.1	hypothetical protein G	( 303)	164	45.7	0.035
gi 2317679 dbj BAA21729.1	terminal dioxygenase co	( 384)	167	46.4	0.027	gi 138531149 gb ECA23543.1	hypothetical protein G	( 147)	160	44.6	0.035
gi 2317678 dbj BAA21728.1	terminal dioxygenase co	( 384)	167	46.4	0.027	gi 143138836 gb EDD09832.1	hypothetical protein G	( 378)	165	46.0	0.036
gi 3293059 dbj BAA31267.1	carbazole dioxygenase s	( 384)	167	46.4	0.027	gi 137294565 gb EBT29356.1	hypothetical protein G	( 263)	163	45.4	0.036
gi 119376772 gb ABL71536.1	Rieske (2Fe-2S) domain	( 384)	167	46.4	0.027	gi 450505 emb CAA38026.1	ribulose bisphosphate ca	( 182)	161	44.9	0.036
gi 219688866 dbj BAH09957.1	terminal oxygenase co	( 384)	167	46.4	0.027	gi 142394307 gb ECX74896.1	hypothetical protein G	( 264)	163	45.4	0.036
gi 66775533 gb AAY56339.1	CarAa [Pseudomonas sp.	( 384)	167	46.4	0.027	gi 206677230 gb ED241717.1	hypothetical protein R	( 388)	165	46.0	0.037
gi 219688865 dbj BAH09956.1	terminal oxygenase co	( 384)	167	46.4	0.027	gi 140868658 gb ECO05404.1	hypothetical protein G	( 185)	161	44.9	0.037
gi 26106105 dbj BAC41545.1	terminal oxygenase com	( 384)	167	46.4	0.027	gi 137952755 gb EBW94138.1	hypothetical protein G	( 268)	163	45.4	0.037
gi 13094176 dbj BAB32765.1	terminal oxygenase com	( 384)	167	46.4	0.027	gi 15108685 gb AAE67721.1	Sequence 57 from patent	( 35)	152	42.5	0.037
gi 13094177 dbj BAB32766.1	terminal oxygenase com	( 384)	167	46.4	0.027	gi 33769244 gb AAQ53875.1	Sequence 57 from patent	( 35)	152	42.5	0.037
gi 26106104 dbj BAC41544.1	terminal oxygenase com	( 384)	167	46.4	0.027	gi 135457171 gb EBH76487.1	hypothetical protein G	( 132)	159	44.4	0.038
gi 143259857 gb EDD96452.1	hypothetical protein G	( 390)	167	46.4	0.027	gi 11066679 gb AAG28702.1	AF272737_5 CrtV [Strepto	( 338)	164	45.7	0.038
gi 143865155 gb EDH18673.1	hypothetical protein G	( 227)	164	45.6	0.027	gi 138501640 gb ECA04687.1	hypothetical protein G	( 199)	161	44.9	0.039
gi 136861088 gb EBQ89620.1	hypothetical protein G	( 329)	166	46.2	0.027	gi 77380412 gb ABA71925.1	putative ferredoxin red	( 509)	166	46.3	0.04
gi 137028913 gb EBR80538.1	hypothetical protein G	( 277)	165	45.9	0.028	gi 140760657 gb ECN33189.1	hypothetical protein G	( 97)	157	43.9	0.04
gi 133912434 emb CAM02547.1	methylesterase [Sacch	( 335)	166	46.2	0.028	gi 142500477 gb ECY53016.1	hypothetical protein G	( 295)	163	45.5	0.04



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gi 133737607 emb CAL60650.1	nitrite reductase [NA	( 117)	158	44.1	0.04	gi 144197668 gb EDJ58159.1	hypothetical protein G	( 111)	156	43.7	0.052
gi 184196022 gb ACC73986.1	Rieske (2Fe-2S) domain	( 434)	165	46.0	0.04	gi 108772463 gb ABG11185.1	Rieske (2Fe-2S) region	( 338)	162	45.3	0.052
gi 30421144 gb AAP31054.1	ribulose-1,5-bisphospha	( 173)	160	44.7	0.041	gi 119697285 gb ABL94358.1	Rieske (2Fe-2S) domain	( 338)	162	45.3	0.052
gi 148499936 gb ABQ68190.1	Rieske (2Fe-2S) domain	( 365)	164	45.7	0.041	gi 256559448 gb ACU85295.1	ferredoxin subunit of	( 112)	156	43.7	0.053
gi 143413504 gb EDE82380.1	hypothetical protein G	( 257)	162	45.2	0.041	gi 262209537 gb ACY33635.1	Rieske iron-sulfur pro	( 114)	156	43.7	0.053
gi 118489530 gb ABK96567.1	unknown [Populus trich	( 181)	160	44.7	0.042	gi 137027143 gb EBR79542.1	hypothetical protein G	( 95)	155	43.4	0.054
gi 4689388 gb AAD27881.1	AF139469_1 ribulose-1,5-b	( 181)	160	44.7	0.042	gi 105893063 gb ABF76228.1	Rieske (2Fe-2S) region	( 350)	162	45.3	0.054
gi 19581 emb CAA46475.1	ribulose bisphosphate car	( 183)	160	44.7	0.043	gi 116652598 gb ABK13237.1	Rieske (2Fe-2S) domain	( 350)	162	45.3	0.054
gi 141817307 gb ECT45375.1	hypothetical protein G	( 106)	157	43.9	0.043	gi 33633122 emb CAE07933.1	Putative Rieske [2Fe-2	( 351)	162	45.3	0.054
gi 135370213 gb EBH18108.1	hypothetical protein G	( 186)	160	44.7	0.043	gi 147851881 emb CAK29375.1	Putative dioxygenase	( 351)	162	45.3	0.054
gi 18033077 gb AAL56980.1	ribulose 1,5-bisphospha	( 107)	157	43.9	0.043	gi 143704024 gb EDG36638.1	hypothetical protein G	( 353)	162	45.3	0.054
gi 226238500 dbj BAH48848.1	nitrite reductase sma	( 108)	157	43.9	0.044	gi 143048128 gb EDC43469.1	hypothetical protein G	( 355)	162	45.3	0.055
gi 110817412 gb ABG92696.1	nitrite reductase [NAD	( 108)	157	43.9	0.044	gi 137395657 gb EBT86122.1	hypothetical protein G	( 205)	159	44.5	0.055
gi 118489576 gb ABK96590.1	unknown [Populus trich	( 189)	160	44.7	0.044	gi 135370925 gb EBH18581.1	hypothetical protein G	( 121)	156	43.7	0.056
gi 15075551 emb CAC47106.1	Dioxygenase ferredoxin	( 109)	157	43.9	0.044	gi 141805229 gb ECT37081.1	hypothetical protein G	( 311)	161	45.0	0.057
gi 178462366 dbj BAG16886.1	putative methylestera	( 334)	163	45.5	0.044	gi 137263621 gb EBT12025.1	hypothetical protein G	( 215)	159	44.5	0.057
gi 178469389 dbj BAG23909.1	putative methylestera	( 334)	163	45.5	0.044	gi 17855 emb CAA30290.1	rubisco ssu precursor [Br	( 181)	158	44.2	0.058
gi 198256000 gb EDY80314.1	Rieske (2Fe-2S) domain	( 402)	164	45.8	0.044	gi 134461041 gb EBB48265.1	hypothetical protein G	( 218)	159	44.5	0.058
gi 142451917 gb ECY17845.1	hypothetical protein G	( 134)	158	44.2	0.045	gi 77969838 gb ABB11217.1	Rieske (2Fe-2S) protein	( 105)	155	43.4	0.058
gi 91801353 gb ABE63728.1	assimilatory nitrite re	( 112)	157	43.9	0.045	gi 198039742 emb CAR55712.1	[2Fe-2S]-binding prot	( 105)	155	43.4	0.058
gi 142948037 gb EDB72364.1	hypothetical protein G	( 412)	164	45.8	0.045	gi 260417233 gb EEX10492.1	rieske domain protein	( 385)	162	45.3	0.058
gi 59747069 gb AAW97360.1	Sequence 14923 from pat	( 113)	157	43.9	0.045	gi 262080644 gb ACY16613.1	Rieske (2Fe-2S) iron-s	( 127)	156	43.7	0.059
gi 108461331 gb ABK86516.1	iron-sulfur cluster-bi	( 113)	157	43.9	0.045	gi 41397190 gb AAS05050.1	hypothetical protein MA	( 323)	161	45.0	0.059
gi 137274683 gb EBT18273.1	hypothetical protein G	( 200)	160	44.7	0.046	gi 118166570 gb ABK67467.1	Rieske [2Fe-2S] domain	( 323)	161	45.0	0.059
gi 139636207 gb ECG41937.1	hypothetical protein G	( 116)	157	43.9	0.046	gi 139207881 gb ECE15017.1	hypothetical protein G	( 269)	160	44.8	0.059
gi 218520183 gb ACK80769.1	iron-sulfur cluster-bi	( 296)	162	45.2	0.047	gi 158113982 gb ABW16179.1	Rieske (2Fe-2S) domain	( 398)	162	45.3	0.06
gi 141345060 gb ECR17790.1	hypothetical protein G	( 98)	156	43.6	0.047	gi 136549923 gb EBO88379.1	hypothetical protein G	( 111)	155	43.4	0.061
gi 198247515 gb ACH83108.1	Rieske (2Fe-2S) domain	( 301)	162	45.2	0.047	gi 138189377 gb EBV30339.1	hypothetical protein G	( 111)	155	43.4	0.061
gi 30421141 gb AAP31053.1	ribulose-1,5-bisphospha	( 173)	159	44.4	0.048	gi 150032449 gb ABR64564.1	ferredoxin [Sinorhizob	( 588)	164	45.8	0.061
gi 136683718 gb EBP72076.1	hypothetical protein G	( 302)	162	45.2	0.048	gi 809069 emb CAA42617.1	ribulose bisphosphate ca	( 135)	156	43.7	0.062
gi 143208157 gb EDD59774.1	hypothetical protein G	( 253)	161	45.0	0.048	gi 137031727 gb EBR82132.1	hypothetical protein G	( 136)	156	43.7	0.062
gi 139704833 gb ECG89883.1	hypothetical protein G	( 253)	161	45.0	0.048	gi 142023063 gb ECC92713.1	hypothetical protein G	( 114)	155	43.4	0.063
gi 146454848 gb ABQ42090.1	ribulose bisphosphate	( 178)	159	44.4	0.049	gi 134765560 gb EBD28040.1	hypothetical protein G	( 351)	161	45.0	0.063
gi 403160 gb AAA33866.1	ribulose 1,5-bisphosphate	( 179)	159	44.4	0.049	gi 18466 emb CAA28711.1	unnamed protein product	( 173)	157	44.0	0.065
gi 170936751 emb CAP61409.1	unnamed protein produ	( 545)	165	46.0	0.049	gi 140109650 gb ECJ60212.1	hypothetical protein G	( 251)	159	44.5	0.065
gi 142577250 gb EC207825.1	hypothetical protein G	( 103)	156	43.6	0.049	gi 224463960 gb EEF80226.1	nitrite reductase (NAD	( 101)	154	43.2	0.066
gi 217506891 gb ACK53902.1	nitrite reductase (NAD	( 103)	156	43.6	0.049	gi 32562912 dbj BAC79226.1	large subunit of biphe	( 446)	162	45.3	0.066
gi 142041743 gb ECV10312.1	hypothetical protein G	( 124)	157	43.9	0.049	gi 137699324 gb EBV52546.1	hypothetical protein G	( 261)	159	44.5	0.067
gi 142749784 gb EDA30387.1	hypothetical protein G	( 150)	158	44.2	0.049	gi 16193 emb CAA32700.1	ribulose bisphosphate car	( 181)	157	44.0	0.068
gi 71915031 gb AAZ54933.1	conserved hypothetical	( 315)	162	45.2	0.049	gi 15294184 gb AAK95269.1	AF410283_1 F1019.10/F101	( 181)	157	44.0	0.068
gi 183177262 gb ACC42372.1	ring-hydroxylating dio	( 380)	163	45.5	0.049	gi 23505787 gb AAN28753.1	At5g38430/F1019.10 [Ara	( 181)	157	44.0	0.068
gi 142938452 gb EDB65514.1	hypothetical protein G	( 104)	156	43.6	0.049	gi 9758821 dbj BAB09355.1	ribulose bisphosphate c	( 181)	157	44.0	0.068
gi 196184923 gb EDX79899.1	nitrite reductase (NAD	( 104)	156	43.6	0.049	gi 142281000 gb ECW94246.1	hypothetical protein G	( 263)	159	44.5	0.068
gi 218021 dbj BAA00450.1	RuBisCO small subunit [P	( 183)	159	44.4	0.05	gi 171700990 gb ACB53971.1	putative Rieske [2Fe-2	( 461)	162	45.3	0.068
gi 15108656 gb AAE67692.1	Sequence 28 from patent	( 35)	150	42.0	0.05	gi 259348379 gb EEW60156.1	rieske domain protein	( 384)	161	45.1	0.068
gi 33769215 gb AAQ53846.1	Sequence 28 from patent	( 35)	150	42.0	0.05	gi 187715544 gb ACD16768.1	Rieske (2Fe-2S) domain	( 387)	161	45.1	0.069
gi 142336992 gb ECX35692.1	hypothetical protein G	( 389)	163	45.5	0.05	gi 142043103 gb ECV11671.1	hypothetical protein G	( 128)	155	43.5	0.069
gi 140766633 gb ECN36280.1	hypothetical protein G	( 107)	156	43.7	0.051	gi 221730946 gb ACM33766.1	nitrite reductase (NAD	( 129)	155	43.5	0.069
gi 142691225 gb ECZ88242.1	hypothetical protein G	( 227)	160	44.7	0.051	gi 160345541 gb ABX18626.1	Rieske (2Fe-2S) domain	( 108)	154	43.2	0.07
gi 136664426 gb BEP59540.1	hypothetical protein G	( 337)	162	45.3	0.052	gi 189336362 dbj BAG45431.1	ferredoxin subunit of	( 108)	154	43.2	0.07
gi 135167961 gb EBF92858.1	hypothetical protein G	( 111)	156	43.7	0.052	gi 144177929 gb EDJ43481.1	hypothetical protein G	( 229)	158	44.3	0.071

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gi 35210927 dbj BAC88307.1  gl10366 [Gloeobacter v ( 110) 154 43.2 0.071	gi 240862526 gb ACS60191.1  Rieske (2Fe-2S) domain ( 104) 152 42.7 0.093
gi 14523944 gb AAK65474.1  oxidoreductase [Sinorhi ( 588) 163 45.6 0.072	gi 137429143 gb EUB05109.1  hypothetical protein G ( 182) 155 43.5 0.093
gi 136725177 gb EBP99237.1  hypothetical protein G ( 112) 154 43.2 0.072	gi 116650805 gb ABK11445.1  Rieske (2Fe-2S) domain ( 105) 152 42.7 0.093
gi 134344483 gb EBA78166.1  hypothetical protein G ( 421) 161 45.1 0.074	gi 189337302 dbj BAG46371.1  ferredoxin subunit of ( 105) 152 42.7 0.093
gi 137369068 gb EBT71117.1  hypothetical protein G ( 292) 159 44.6 0.074	gi 124874607 gb EAY64597.1  Rieske [Burkholderia c ( 105) 152 42.7 0.093
gi 136612572 gb EBP28666.1  hypothetical protein G ( 244) 158 44.3 0.074	gi 160344580 gb ABX17665.1  Rieske (2Fe-2S) domain ( 105) 152 42.7 0.093
gi 137892023 gb EBW59723.1  hypothetical protein G ( 140) 155 43.5 0.074	gi 169820132 gb ACA94714.1  Rieske (2Fe-2S) domain ( 105) 152 42.7 0.093
gi 142217043 gb ECW47051.1  hypothetical protein G ( 118) 154 43.2 0.075	gi 105895384 gb ABF78548.1  Rieske (2Fe-2S) region ( 105) 152 42.7 0.093
gi 4104752 gb AAD02135.1  naphthalene dioxygenase ( 118) 154 43.2 0.075	gi 148728554 gb ABR08705.1  PrnD [Burkholderia cen ( 221) 156 43.8 0.094
gi 226243262 dbj BAH53610.1  putative iron-sulfur ( 298) 159 44.6 0.075	gi 219885421 gb ACL53085.1  unknown [Zea mays] ( 153) 154 43.3 0.094
gi 239802401 gb ACS19468.1  nitrite reductase (NAD ( 143) 155 43.5 0.076	gi 226245948 dbj BAH47212.1  naphthalene dioxygena ( 468) 160 44.9 0.094
gi 143966205 gb EDH91153.1  hypothetical protein G ( 300) 159 44.6 0.076	gi 259157446 gb ACV96857.1  putative naphthalene d ( 468) 160 44.9 0.094
gi 2781431 gb AAB97165.1  ribulose 1,5-bisphosphat ( 101) 153 43.0 0.077	gi 38524454 dbj BAD02377.1  terminal dioxygenase 1 ( 468) 160 44.9 0.094
gi 138044239 gb EBX43792.1  hypothetical protein G ( 122) 154 43.2 0.077	gi 37912029 gb AAR05114.1  naphthalene dioxygenase ( 468) 160 44.9 0.094
gi 21050 emb CAA42618.1  ribulose bisphosphate car ( 180) 156 43.8 0.079	gi 37912015 gb AAR05106.1  naphthalene dioxygenase ( 468) 160 44.9 0.094
gi 21053 emb CAA40339.1  small subunit of ribulose ( 180) 156 43.8 0.079	gi 120607241 gb ABM42981.1  assimilatory nitrite r ( 129) 153 43.0 0.095
gi 223539597 gb EEF41184.1  Ribulose bisphosphate ( 181) 156 43.8 0.079	gi 144212247 gb EDJ68318.1  hypothetical protein G ( 130) 153 43.0 0.096
gi 406727 emb CAA53083.1  ribulose-1,5-bisphosphat ( 181) 156 43.8 0.079	gi 13241103 gb AAK16228.1 AF044396_1 ribulose-1,5- ( 131) 153 43.0 0.096
gi 270383720 dbj BAI53118.1  ribulose-1,5-bisphosp ( 181) 156 43.8 0.079	gi 49079954 gb AAT49953.1  PA1780 [synthetic const ( 109) 152 42.7 0.096
gi 239803079 gb ACS20146.1  nitrite reductase (NAD ( 152) 155 43.5 0.08	gi 74057821 gb AAZ98261.1  nitrite reductase (NAD( ( 110) 152 42.8 0.097
gi 171996108 gb ACB67026.1  Rieske (2Fe-2S) domain ( 105) 153 43.0 0.08	gi 126237823 gb ABO01224.1  Rieske (2Fe-2S) domain ( 338) 158 44.4 0.098
gi 124898887 gb EAY70730.1  Rieske (2Fe-2S) protei ( 105) 153 43.0 0.08	gi 260037942 gb ACX07559.1  Sequence 31503 from pa ( 162) 154 43.3 0.099
gi 77382010 gb ABA73523.1  putative dioxygenase sy ( 105) 153 43.0 0.08	gi 134995420 gb EBE80948.1  hypothetical protein G ( 196) 155 43.6 0.099
gi 115284142 gb ABI89658.1  Rieske (2Fe-2S) domain ( 105) 153 43.0 0.08	gi 169243412 emb CAM64440.1  Putative ferredoxin s ( 114) 152 42.8 0.1
gi 143956658 gb EDH84455.1  hypothetical protein G ( 384) 160 44.8 0.08	gi 148499045 gb ABQ67299.1  Rieske (2Fe-2S) domain ( 418) 159 44.6 0.1
gi 6272551 gb AAF06101.1  ribulose 1,5-bisphosphat ( 184) 156 43.8 0.08	gi 197719107 gb EDY63015.1  Rieske Fe-S membrane p ( 289) 157 44.1 0.1
gi 6272548 gb AAF06098.1  ribulose 1,5-bisphosphat ( 184) 156 43.8 0.08	gi 142994603 gb EDC04665.1  hypothetical protein G ( 97) 151 42.5 0.1
gi 6272550 gb AAF06100.1  ribulose 1,5-bisphosphat ( 184) 156 43.8 0.08	gi 135899302 gb EBK56932.1  hypothetical protein G ( 97) 151 42.5 0.1
gi 4585359 gb AAD25395.1 AF121905_1 NidA dioxygena ( 468) 161 45.1 0.081	gi 136030313 gb EBL44060.1  hypothetical protein G ( 355) 158 44.4 0.1
gi 82949296 dbj BAE53376.1  naphthalene-inducible ( 468) 161 45.1 0.081	gi 262084708 gb ACY20676.1  Rieske (2Fe-2S) iron-s ( 117) 152 42.8 0.1
gi 91698363 gb ABE45192.1  assimilatory nitrite re ( 128) 154 43.2 0.081	gi 135479940 gb EBH91571.1  hypothetical protein G ( 204) 155 43.6 0.1
gi 183173589 gb ACC38699.1  dioxygenase [Mycobacte ( 394) 160 44.8 0.082	gi 194702782 gb ACF85475.1  unknown [Zea mays] ( 170) 154 43.3 0.1
gi 169818316 gb ACA92898.1  Rieske (2Fe-2S) domain ( 108) 153 43.0 0.082	gi 195636562 gb ACG37749.1  ribulose bisphosphate ( 170) 154 43.3 0.1
gi 105896303 gb ABF79467.1  Rieske (2Fe-2S) region ( 108) 153 43.0 0.082	gi 217964 dbj BAA00120.1  ribulose 1,5-bisphosphat ( 170) 154 43.3 0.1
gi 124875375 gb EAY65365.1  Rieske [Burkholderia c ( 108) 153 43.0 0.082	gi 194702004 gb ACF85086.1  unknown [Zea mays] ( 170) 154 43.3 0.1
gi 116649874 gb ABK10514.1  Rieske (2Fe-2S) domain ( 108) 153 43.0 0.082	gi 194703936 gb ACF86052.1  unknown [Zea mays] ( 170) 154 43.3 0.1
gi 142784293 gb EDA55742.1  hypothetical protein G ( 157) 155 43.5 0.082	gi 22474 emb CAA29784.1  ribulose-1,5-bisphosphate ( 170) 154 43.3 0.1
gi 142471781 gb ECY32545.1  hypothetical protein G ( 398) 160 44.8 0.082	gi 116224829 gb ABJ83538.1  Rieske (2Fe-2S) domain ( 365) 158 44.4 0.1
gi 143550176 gb EDF58330.1  hypothetical protein G ( 230) 157 44.0 0.083	gi 1673456 emb CAA70416.1  rubisco small subunit [ ( 170) 154 43.3 0.1
gi 211907943 gb ACJ12463.1  CinA3 [Rhodococcus sp. ( 111) 153 43.0 0.084	gi 140099283 gb ECJ52989.1  hypothetical protein G ( 205) 155 43.6 0.1
gi 219678279 gb EED34628.1  rieske (2Fe-2S) domain ( 413) 160 44.9 0.085	gi 140981610 gb ECO82628.1  hypothetical protein G ( 171) 154 43.3 0.1
gi 141690463 gb ECS82830.1  hypothetical protein G ( 289) 158 44.3 0.086	gi 139050637 gb ECD06743.1  hypothetical protein G ( 250) 156 43.8 0.1
gi 135557085 gb EBI40983.1  hypothetical protein G ( 351) 159 44.6 0.087	gi 6063022 gb AAF03096.1 AF162195_1 ribulose-1,5-b ( 174) 154 43.3 0.1
gi 22465 emb CAA68419.1  ribulose 1,5-bisphosphate ( 169) 155 43.5 0.087	gi 116224829 gb ABJ83538.1  Rieske (2Fe-2S) domain ( 365) 158 44.4 0.1
gi 35211520 dbj BAC88898.1  gl10957 [Gloeobacter v ( 357) 159 44.6 0.088	gi 141976377 gb ECU56604.1  hypothetical protein G ( 256) 156 43.8 0.11
gi 56900734 gb AAW31667.1  ribulose-1,5-bisphospha ( 174) 155 43.5 0.089	gi 260037941 gb ACX07558.1  Sequence 31502 from pa ( 177) 154 43.3 0.11
gi 28139169 gb AAO25119.1  ribulose-1,5-bisphospha ( 179) 155 43.5 0.092	gi 17978793 gb AAL47390.1  ribulose bisphosphate c ( 181) 154 43.3 0.11
gi 118488741 gb ABK96181.1  unknown [Populus trich ( 181) 155 43.5 0.093	gi 25083689 gb AAN72105.1  ribulose bisphosphate c ( 181) 154 43.3 0.11
gi 222870738 gb EEF07869.1  predicted protein [Pop ( 181) 155 43.5 0.093	gi 27311897 gb AAO00914.1  ribulose bisphosphate c ( 181) 154 43.3 0.11
gi 118488169 gb ABK95904.1  unknown [Populus trich ( 181) 155 43.5 0.093	gi 17064722 gb AAL32515.1  ribulose bisphosphate c ( 181) 154 43.3 0.11
gi 115260471 emb CAK03575.1  putative rieske-type ( 104) 152 42.7 0.093	gi 20259880 gb AAM13287.1  ribulose bisphosphate c ( 181) 154 43.3 0.11

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gi 16195 emb CAA32702.1  ribulose bisphosphate car ( 181) 154 43.3 0.11	gi 17852 emb CAA39402.1  ribulose bisphosphate car ( 181) 153 43.1 0.13
gi 15293183 gb AAK93702.1  putative RuBisCO small ( 181) 154 43.3 0.11	gi 30407679 gb AAP30019.1  assimilatory nitrite re ( 105) 150 42.3 0.13
gi 13430424 gb AAK25834.1 AF360124_1 putative ribu ( 181) 154 43.3 0.11	gi 5823007 gb AAD53004.1 AF076471_2 MocE [Sinorhiz ( 105) 150 42.3 0.13
gi 20466117 gb AAM19980.1  At5g38410/F1019.10 [Ara ( 181) 154 43.3 0.11	gi 206684505 gb EDZ44988.1  rieske (2Fe-2S) domain ( 384) 157 44.2 0.13
gi 16194 emb CAA32701.1  ribulose bisphosphate car ( 181) 154 43.3 0.11	gi 115285535 gb ABI91051.1  Rieske (2Fe-2S) domain ( 108) 150 42.3 0.13
gi 15294246 gb AAK95300.1 AF410314_1 F1019.10/F101 ( 181) 154 43.3 0.11	gi 134136030 gb ABO57144.1  Rieske (2Fe-2S) domain ( 108) 150 42.3 0.13
gi 23397160 gb AAN31863.1  putative ribulose bisph ( 181) 154 43.3 0.11	gi 1513105 gb AAB06726.1  naphthalenesulfonate dio ( 108) 150 42.3 0.13
gi 16649139 gb AAL24421.1  ribulose bisphosphate c ( 181) 154 43.3 0.11	gi 29568952 gb AAO83641.1  anthranilate dioxygenas ( 108) 150 42.3 0.13
gi 18087561 gb AAL58912.1 AF462822_1 At5g38410/F10 ( 181) 154 43.3 0.11	gi 142756629 gb EDA35338.1  hypothetical protein G ( 109) 150 42.3 0.13
gi 9758819 dbj BAB09353.1  ribulose bisphosphate c ( 181) 154 43.3 0.11	gi 134346212 gb EBA79333.1  hypothetical protein G ( 402) 157 44.2 0.13
gi 17064934 gb AAL32621.1  ribulose bisphosphate c ( 181) 154 43.3 0.11	gi 143958422 gb EDH85742.1  hypothetical protein G ( 335) 156 43.9 0.13
gi 9758820 dbj BAB09354.1  ribulose bisphosphate c ( 181) 154 43.3 0.11	gi 137963387 gb EBX00095.1  hypothetical protein G ( 161) 152 42.8 0.13
gi 28058980 gb AAO29974.1  ribulose bisphosphate c ( 181) 154 43.3 0.11	gi 142294368 gb ECX04024.1  hypothetical protein G ( 134) 151 42.6 0.13
gi 260037940 gb ACX07557.1  Sequence 31501 from pa ( 181) 154 43.3 0.11	gi 139004275 gb ECC75016.1  hypothetical protein G ( 234) 154 43.4 0.13
gi 17064764 gb AAL32536.1  ribulose bisphosphate c ( 181) 154 43.3 0.11	gi 141631774 gb ECS60536.1  hypothetical protein G ( 201) 153 43.1 0.14
gi 15450944 gb AAK96743.1  ribulose bisphosphate c ( 181) 154 43.3 0.11	gi 169842 gb AAA33922.1  ribulose 1,5-bisphosphate ( 168) 152 42.8 0.14
gi 154269258 gb ABS72189.1  ribulose-1,5-bisphosph ( 183) 154 43.3 0.11	gi 136244771 gb EBM85557.1  hypothetical protein G ( 354) 156 43.9 0.14
gi 136981316 gb EBR53678.1  hypothetical protein G ( 183) 154 43.3 0.11	gi 228393828 gb ACQ37781.1  Sequence 30295 from pa ( 141) 151 42.6 0.14
gi 142185510 gb ECW22959.1  hypothetical protein G ( 465) 159 44.7 0.11	gi 187718421 gb ACD19644.1  FAD-dependent pyridine ( 521) 158 44.5 0.14
gi 167347459 gb ABZ70194.1  Rieske (2Fe-2S) domain ( 387) 158 44.4 0.11	gi 30523254 gb AAP31674.1  ribulose-1,5-bisphospha ( 119) 150 42.3 0.14
gi 91696110 gb ABE42939.1  Rieske (2Fe-2S) region ( 106) 151 42.5 0.11	gi 145322565 gb ABP64508.1  Rieske (2Fe-2S) domain ( 362) 156 43.9 0.14
gi 140136528 gb ECJ78377.1  hypothetical protein G ( 106) 151 42.5 0.11	gi 967219 gb AAB67845.1  ribulose-1,5-bisphosphate ( 173) 152 42.9 0.14
gi 15108686 gb AAE67722.1  Sequence 58 from patent ( 35) 145 40.9 0.11	gi 967225 gb AAB67848.1  ribulose-1,5-bisphosphate ( 178) 152 42.9 0.15
gi 33769245 gb AAQ53876.1  Sequence 58 from patent ( 35) 145 40.9 0.11	gi 142019135 gb ECU88932.1  hypothetical protein G ( 374) 156 43.9 0.15
gi 139892805 gb ECI18182.1  hypothetical protein G ( 89) 150 42.3 0.11	gi 143939341 gb EDH72222.1  hypothetical protein G ( 179) 152 42.9 0.15
gi 126193500 gb EAA257563.1  assimilatory nitrite r ( 108) 151 42.5 0.11	gi 755803 emb CAA29801.1  carboxylase [Raphanus sa ( 181) 152 42.9 0.15
gi 150961234 gb ABR83259.1  assimilatory nitrite r ( 108) 151 42.5 0.11	gi 142774525 gb EDA48490.1  hypothetical protein G ( 104) 149 42.1 0.15
gi 218772494 emb CAW28276.1  assimilatory nitrite ( 108) 151 42.5 0.11	gi 6272549 gb AAF06099.1  ribulose 1,5-bisphosphat ( 182) 152 42.9 0.15
gi 115584949 gb ABJ10964.1  assimilatory nitrite r ( 108) 151 42.5 0.11	gi 168363 gb AAA99429.1  ribulose 1,5-bisphosphate ( 182) 152 42.9 0.15
gi 126166805 gb EAA252316.1  assimilatory nitrite r ( 108) 151 42.5 0.11	gi 189232077 emb CAQ53708.1  aminopyrrolnitritin oxy ( 220) 153 43.1 0.15
gi 99477760 gb AAG05169.1 AE004603_9 assimilatory n ( 108) 151 42.5 0.11	gi 139466307 gb ECF29623.1  hypothetical protein G ( 265) 154 43.4 0.15
gi 139908240 gb ECI29016.1  hypothetical protein G ( 130) 152 42.8 0.11	gi 140869759 gb ECO06181.1  hypothetical protein G ( 221) 153 43.1 0.15
gi 141173178 gb ECQ13788.1  hypothetical protein G ( 227) 155 43.6 0.11	gi 138731942 gb ECB62522.1  hypothetical protein G ( 266) 154 43.4 0.15
gi 13241111 gb AAK16232.1 AF044400_1 ribulose-1,5- ( 131) 152 42.8 0.11	gi 142024291 gb ECU93900.1  hypothetical protein G ( 127) 150 42.3 0.15
gi 13241101 gb AAK16227.1 AF044395_1 ribulose-1,5- ( 131) 152 42.8 0.11	gi 77971055 gb ABB12434.1  Rieske (2Fe-2S) protein ( 108) 149 42.1 0.15
gi 119720808 gb ABL97974.1  ribulose bisphosphate ( 162) 153 43.1 0.12	gi 171995218 gb ACB66136.1  Rieske (2Fe-2S) domain ( 108) 149 42.1 0.15
gi 142043815 gb ECV12383.1  hypothetical protein G ( 284) 156 43.9 0.12	gi 143834019 gb EDG96082.1  hypothetical protein G ( 396) 156 43.9 0.15
gi 222450107 gb ACM54373.1  Rieske (2Fe-2S) domain ( 285) 156 43.9 0.12	gi 142663501 gb ECZ68370.1  hypothetical protein G ( 396) 156 43.9 0.15
gi 135440202 gb EBH65171.1  hypothetical protein G ( 345) 157 44.1 0.12	gi 111147727 emb CAJ59385.1  hypothetical protein; ( 276) 154 43.4 0.15
gi 136645961 gb EBP48417.1  hypothetical protein G ( 289) 156 43.9 0.12	gi 138517740 gb ECA14392.1  hypothetical protein G ( 133) 150 42.3 0.16
gi 137225718 gb EBS90785.1  hypothetical protein G ( 168) 153 43.1 0.12	gi 142905289 gb EDB41632.1  hypothetical protein G ( 409) 156 43.9 0.16
gi 163669602 gb ABY35968.1  Rieske (2Fe-2S) domain ( 293) 156 43.9 0.12	gi 141710276 gb ECS87143.1  hypothetical protein G ( 290) 154 43.4 0.16
gi 136637933 gb EBP43677.1  hypothetical protein G ( 296) 156 43.9 0.12	gi 137355026 gb EBT63153.1  hypothetical protein G ( 290) 154 43.4 0.16
gi 139243021 gb ECE34511.1  hypothetical protein G ( 170) 153 43.1 0.12	gi 139654227 gb ECG54604.1  hypothetical protein G ( 203) 152 42.9 0.16
gi 261358545 gb EEY20973.1  monodehydroascorbate r ( 521) 159 44.7 0.12	gi 241936147 gb EE809292.1  hypothetical protein S ( 169) 151 42.6 0.16
gi 137597674 gb EBU96563.1  hypothetical protein G ( 254) 155 43.6 0.12	gi 139879072 gb ECI08745.1  hypothetical protein G ( 169) 151 42.6 0.16
gi 158110525 gb ABW12722.1  Rieske (2Fe-2S) domain ( 447) 158 44.4 0.12	gi 164698713 gb ABY66909.1  chloroplast ribulose-1 ( 169) 151 42.6 0.16
gi 143504122 gb EDF34766.1  hypothetical protein G ( 215) 154 43.4 0.13	gi 164698711 gb ABY66908.1  chloroplast ribulose-1 ( 169) 151 42.6 0.16
gi 119720784 gb ABL97962.1  ribulose-1,5-bisphosph ( 181) 153 43.1 0.13	gi 136814236 gb EBQ58315.1  hypothetical protein G ( 355) 155 43.7 0.16
gi 17850 emb CAA43410.1  ribulose bisphosphate car ( 181) 153 43.1 0.13	gi 135525513 gb EBT20824.1  hypothetical protein G ( 297) 154 43.4 0.16
gi 79013990 gb ABB51649.1  chloroplast ribulose-1, ( 181) 153 43.1 0.13	gi 134770938 gb EBD31766.1  hypothetical protein G ( 143) 150 42.4 0.17

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gi 214037559 gb EEB78225.1  Rieske (2Fe-2S) domain ( 362) 155 43.7 0.17	gi 154000871 gb ABS57004.1  ribulose-1,5-bisphosph ( 129) 149 42.1 0.18
gi 142045620 gb ECV13862.1  hypothetical protein G ( 208) 152 42.9 0.17	gi 137079117 gb EBS08891.1  hypothetical protein G ( 225) 152 42.9 0.18
gi 967223 gb AAB67847.1  ribulose-1,5-bisphosphate ( 173) 151 42.6 0.17	gi 136327069 gb EBN41484.1  hypothetical protein G ( 399) 155 43.7 0.18
gi 142786651 gb EDA57487.1  hypothetical protein G ( 251) 153 43.2 0.17	gi 143407937 gb EDE79159.1  hypothetical protein G ( 399) 155 43.7 0.18
gi 124428843 emb CAK93614.1  unnamed protein produ ( 438) 156 44.0 0.17	gi 137089779 gb EBS14676.1  hypothetical protein G ( 276) 153 43.2 0.18
gi 139972103 gb ECI73349.1  hypothetical protein G ( 209) 152 42.9 0.17	gi 134444235 gb EBB38426.1  hypothetical protein G ( 230) 152 42.9 0.18
gi 256359699 gb ACU73196.1  Rieske (2Fe-2S) domain ( 121) 149 42.1 0.17	gi 189232083 emb CAQ53711.1  aminopyrrolnitrin oxy ( 231) 152 42.9 0.18
gi 119670681 emb CAL94594.1  putative 2-oxo-1,2-di ( 446) 156 44.0 0.17	gi 140712860 gb ECN00049.1  hypothetical protein G ( 336) 154 43.4 0.18
gi 119670665 emb CAL94578.1  putative 2-oxo-1,2-di ( 446) 156 44.0 0.17	gi 280990468 gb ADA02444.1  Sequence 32 from paten ( 92) 147 41.6 0.18
gi 135376502 gb EBH22337.1  hypothetical protein G ( 371) 155 43.7 0.17	gi 259208198 gb ACW17486.1  Sequence 32 from paten ( 92) 147 41.6 0.18
gi 53748417 emb CAH59401.1  Rubisco SSU [Plantago ( 177) 151 42.6 0.17	gi 155717958 gb ABU37509.1  Sequence 32 from paten ( 92) 147 41.6 0.18
gi 255630492 gb ACU15604.1  unknown [Glycine max] ( 178) 151 42.6 0.17	gi 281023167 gb ADA14293.1  Sequence 32 from paten ( 92) 147 41.6 0.18
gi 18742 emb CAA23736.1  rubpcase [Glycine max] ( 178) 151 42.6 0.17	gi 209536644 gb ACI56579.1  Rieske (2Fe-2S) domain ( 408) 155 43.7 0.18
gi 260421507 gb EEEX14758.1  rieske 2Fe-2S domain p ( 374) 155 43.7 0.17	gi 141761682 gb ECT15318.1  hypothetical protein G ( 195) 151 42.6 0.18
gi 135962917 gb EBL00241.1  hypothetical protein G ( 215) 152 42.9 0.17	gi 134918171 gb EBE29085.1  hypothetical protein G ( 195) 151 42.6 0.18
gi 189232079 emb CAQ53709.1  aminopyrrolnitrin oxy ( 216) 152 42.9 0.17	gi 139554296 gb ECF86656.1  hypothetical protein G ( 112) 148 41.8 0.18
gi 142014430 gb ECU84416.1  hypothetical protein G ( 380) 155 43.7 0.17	gi 142736358 gb EDA20615.1  hypothetical protein G ( 341) 154 43.5 0.19
gi 56680237 gb AAV96903.1  Rieske 2Fe-2S domain pr ( 380) 155 43.7 0.17	gi 135287607 gb EBG64579.1  hypothetical protein G ( 342) 154 43.5 0.19
gi 116235037 dbj BAF34965.1  naphthalene 1,2-dioxy ( 104) 148 41.8 0.17	gi 138009861 gb EBX25663.1  hypothetical protein G ( 237) 152 42.9 0.19
gi 294350 gb AAA16124.1  DoxA [Pseudomonas sp.] ( 104) 148 41.8 0.17	gi 140367739 gb ECL29019.1  hypothetical protein G ( 164) 150 42.4 0.19
gi 151391 gb AAA25905.1  naphthalene 1,2-dioxygena ( 104) 148 41.8 0.17	gi 136397561 gb EBN89704.1  hypothetical protein G ( 239) 152 42.9 0.19
gi 229424266 gb ACQ63490.1  naphthalene 1,2-dioxyg ( 104) 148 41.8 0.17	gi 140767020 gb ECN36545.1  hypothetical protein G ( 239) 152 42.9 0.19
gi 116235026 dbj BAF34955.1  naphthalene 1,2-dioxy ( 104) 148 41.8 0.17	gi 190700564 gb ACE94646.1  putative Rieske [2Fe-2 ( 417) 155 43.7 0.19
gi 34335389 gb AAP44287.1  naphthalene dioxygenase ( 104) 148 41.8 0.17	gi 136092287 gb EBL85891.1  hypothetical protein G ( 347) 154 43.5 0.19
gi 151393 gb AAB47590.1  naphthalene dioxygenase A ( 104) 148 41.8 0.17	gi 143884379 gb EDH32719.1  hypothetical protein G ( 420) 155 43.7 0.19
gi 2246753 gb AAB62706.1  naphthalene-1,2-dioxygen ( 104) 148 41.8 0.17	gi 148511816 gb ABQ78676.1  FAD-dependent pyridine ( 506) 156 44.0 0.19
gi 22252962 gb AAM94034.1  ferredoxin [Pseudomonas ( 104) 148 41.8 0.17	gi 135401008 gb EBH38831.1  hypothetical protein G ( 291) 153 43.2 0.19
gi 114050449 dbj BAF30935.1  naphthalene 1,2-dioxy ( 104) 148 41.8 0.17	gi 133912311 emb CAM02424.1  hypothetical protein ( 116) 148 41.9 0.19
gi 3059179 dbj BAA25601.1  orf12 [Rhodococcus eryt ( 316) 154 43.4 0.17	gi 137339844 gb EBT54610.1  hypothetical protein G ( 116) 148 41.9 0.19
gi 223526766 gb EEF28992.1  pheophorbide A oxygena ( 552) 157 44.2 0.17	gi 139764074 gb ECH29717.1  hypothetical protein G ( 300) 153 43.2 0.19
gi 141931191 gb ECU25280.1  hypothetical protein G ( 317) 154 43.4 0.17	gi 19408 emb CAA35104.1  unnamed protein product [ ( 173) 150 42.4 0.2
gi 118489251 gb ABK96431.1  unknown [Populus trich ( 182) 151 42.6 0.17	gi 124429019 emb CAK93813.1  unnamed protein produ ( 438) 155 43.7 0.2
gi 77157637 dbj BAE46384.1  ribulose-1,5-bisphosph ( 183) 151 42.6 0.18	gi 53748423 emb CAH59404.1  Rubisco SSU [Plantago ( 174) 150 42.4 0.2
gi 143030926 gb EDC30822.1  hypothetical protein G ( 319) 154 43.4 0.18	gi 148498441 gb ABQ66695.1  Rieske (2Fe-2S) domain ( 442) 155 43.7 0.2
gi 142140098 gb ECV88400.1  hypothetical protein G ( 105) 148 41.8 0.18	gi 141900484 gb ECU03769.1  hypothetical protein G ( 213) 151 42.7 0.2
gi 255105193 gb EET47867.1  rieske domain protein ( 384) 155 43.7 0.18	gi 295819 emb CAA35103.1  ribulose bisphosphate ca ( 177) 150 42.4 0.2
gi 142811965 gb EDA76409.1  hypothetical protein G ( 184) 151 42.6 0.18	gi 295820 emb CAA35099.1  ribulose bisphosphate ca ( 177) 150 42.4 0.2
gi 226888915 emb CAX87032.1  unnamed protein produ ( 88) 147 41.6 0.18	gi 295818 emb CAA35102.1  ribulose bisphosphate ca ( 177) 150 42.4 0.2
gi 27269176 gb AAN89735.1  Sequence 10 from patent ( 88) 147 41.6 0.18	gi 295817 emb CAA35101.1  ribulose bisphosphate ca ( 177) 150 42.4 0.2
gi 155108040 gb ABT05660.1  Sequence 72 from paten ( 88) 147 41.6 0.18	gi 295821 emb CAA35100.1  ribulose bisphosphate ca ( 177) 150 42.4 0.2
gi 259216836 gb APC17728.1  Sequence 10 from paten ( 88) 147 41.6 0.18	gi 158306686 gb ABW28303.1  thiamine pyrophosphate ( 650) 157 44.3 0.2
gi 2632615 emb CAB12123.1  assimilatory nitrite re ( 106) 148 41.8 0.18	gi 10946377 gb AAG24883.1 AF303940_1 ribulose-1,5- ( 178) 150 42.4 0.2
gi 710021 dbj BAA06355.1  subunit of nitrite reduc ( 106) 148 41.8 0.18	gi 1055368 gb AAA81328.1  ribulose-1,5-bisphosphat ( 178) 150 42.4 0.2
gi 1805401 dbj BAA08963.1  subunit of nitrite redu ( 106) 148 41.8 0.18	gi 10946375 gb AAG24882.1 AF303939_1 ribulose-1,5- ( 178) 150 42.4 0.2
gi 58299 emb CAA48415.1  unnamed protein product [ ( 89) 147 41.6 0.18	gi 10946379 gb AAG24884.1 AF303941_1 ribulose-1,5- ( 178) 150 42.4 0.2
gi 27311147 gb AAO00675.1  Sequence 6 from patent ( 89) 147 41.6 0.18	gi 170058 gb AAA34008.1  ribulose 1,5-bisphosphate ( 178) 150 42.4 0.2
gi 31689669 gb AAP61110.1  Sequence 6 from patent ( 89) 147 41.6 0.18	gi 1079736 gb AAA82069.1  ribulose 1,5-bisphosphat ( 178) 150 42.4 0.2
gi 2488687 gb AAB76823.1 I56241 Sequence 6 from pa ( 89) 147 41.6 0.18	gi 270508491 gb AC286769.1  Rieske (2Fe-2S) protei ( 374) 154 43.5 0.2
gi 2097179 gb AAB56011.1  Sequence 6 from patent U ( 89) 147 41.6 0.18	gi 295823 emb CAA37516.1  NySS41 [Nicotiana sylv ( 181) 150 42.4 0.2
gi 31689720 gb AAP61115.1  Sequence 6 from patent ( 89) 147 41.6 0.18	gi 118571164 gb ABU05915.1  ring-hydroxylating dio ( 380) 154 43.5 0.2
gi 1607715 gb AAB10670.1  Sequence 6 from patent U ( 89) 147 41.6 0.18	gi 118486831 gb ABK95250.1  unknown [Populus trich ( 182) 150 42.4 0.2

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gi 118486788 gb ABK95229.1	unknown [Populus trich ( 182)	150	42.4	0.2	gi 219541679 gb ACL23417.1	nitrogen-fixing NifU d ( 286)	151	42.7	0.26
gi 118487084 gb ABK95372.1	unknown [Populus trich ( 182)	150	42.4	0.2	gi 268311418 gb ACY97792.1	Rieske (2Fe-2S) domain ( 114)	146	41.4	0.26
gi 118488041 gb ABK95841.1	unknown [Populus trich ( 182)	150	42.4	0.2	gi 114227995 gb ABI57794.1	Rieske (2Fe-2S) domain ( 421)	153	43.3	0.26
gi 222848126 gb EEE85673.1	predicted protein [Pop ( 182)	150	42.4	0.2	gi 120593280 gb ABM36719.1	assimilatory nitrite r ( 140)	147	41.7	0.26
gi 142295069 gb ECX04529.1	hypothetical protein G ( 105)	147	41.6	0.2	gi 155277376 gb ABT32980.1	Sequence 120450 from p ( 169)	148	41.9	0.26
gi 138737211 gb ECB66271.1	hypothetical protein G ( 266)	152	42.9	0.21	gi 144197153 gb EDJ57775.1	hypothetical protein G ( 171)	148	41.9	0.26
gi 141319761 gb ECR02205.1	hypothetical protein G ( 226)	151	42.7	0.21	gi 184196528 gb ACC74492.1	Rieske (2Fe-2S) domain ( 521)	154	43.5	0.27
gi 198038709 emb CAR54670.1	putative aromatic hyd ( 108)	147	41.6	0.21	gi 33634963 emb CAE20949.1	Rieske iron-sulfur pro ( 436)	153	43.3	0.27
gi 226459512 gb EEH56807.1	chloroplast envelope p ( 573)	156	44.0	0.21	gi 135645360 gb EBI96181.1	hypothetical protein G ( 208)	149	42.2	0.27
gi 142284485 gb ECW96798.1	hypothetical protein G ( 109)	147	41.6	0.21	gi 967227 gb AAB67849.1	ribulose-1,5-bisphosphate ( 173)	148	41.9	0.27
gi 137517533 gb EBU51988.1	hypothetical protein G ( 109)	147	41.6	0.21	gi 967231 gb AAB67851.1	ribulose-1,5-bisphosphate ( 173)	148	41.9	0.27
gi 178469136 dbj BAG23656.1	putative methylestera ( 338)	153	43.2	0.22	gi 141811468 gb ECT41353.1	hypothetical protein G ( 302)	151	42.7	0.27
gi 140195250 gb ECK17132.1	hypothetical protein G ( 134)	148	41.9	0.22	gi 135787122 gb EBJ84074.1	hypothetical protein G ( 304)	151	42.7	0.27
gi 139856284 gb ECH94325.1	hypothetical protein G ( 162)	149	42.2	0.22	gi 134569197 gb EBC12510.1	hypothetical protein G ( 308)	151	42.7	0.27
gi 140792642 gb ECN54293.1	hypothetical protein G ( 164)	149	42.2	0.22	gi 189187331 gb ACD84516.1	Ferredoxin [Methylacid ( 103)	145	41.2	0.28
gi 219677875 gb EED34224.1	rieske (2Fe-2S) domain ( 416)	154	43.5	0.22	gi 114196898 gb EAU38598.1	conserved hypothetical ( 547)	154	43.6	0.28
gi 139729494 gb ECH07177.1	hypothetical protein G ( 117)	147	41.6	0.22	gi 51949879 gb AAU14862.1	chloroplast ribulose-1, ( 181)	148	42.0	0.28
gi 155359497 gb ABU15102.1	Sequence 202571 from p ( 141)	148	41.9	0.22	gi 1255668 dbj BAA12239.1	ferredoxin [Pseudomonas ( 104)	145	41.2	0.28
gi 137624166 gb EBV11680.1	hypothetical protein G ( 171)	149	42.2	0.23	gi 155342759 gb ABT98363.1	Sequence 185833 from p ( 151)	147	41.7	0.28
gi 20958 emb CAA31774.1	ribulose bisphosphate car ( 171)	149	42.2	0.23	gi 436489 gb AAB03697.1	ribulose-1,5-bisphosphate ( 182)	148	42.0	0.28
gi 91691435 gb ABE34633.1	Putative dioxygenase, f ( 521)	155	43.8	0.23	gi 139748294 gb ECH18900.1	hypothetical protein G ( 126)	146	41.4	0.28
gi 138340692 gb EBZ07101.1	hypothetical protein G ( 249)	151	42.7	0.23	gi 135501009 gb EBI05121.1	hypothetical protein G ( 152)	147	41.7	0.28
gi 136933772 gb EBR26779.1	hypothetical protein G ( 143)	148	41.9	0.23	gi 142733629 gb EBC18629.1	hypothetical protein G ( 269)	150	42.5	0.28
gi 136609805 gb EBP26817.1	hypothetical protein G ( 120)	147	41.6	0.23	gi 139540510 gb ECF76856.1	hypothetical protein G ( 129)	146	41.4	0.29
gi 40062920 gb AAR37791.1	iron-sulfur cluster-bin ( 366)	153	43.2	0.23	gi 143013960 gb EDC18573.1	hypothetical protein G ( 392)	152	43.0	0.29
gi 136256100 gb EBM93148.1	hypothetical protein G ( 306)	152	43.0	0.23	gi 138532368 gb ECA24375.1	hypothetical protein G ( 272)	150	42.5	0.29
gi 134534272 gb EBB91496.1	hypothetical protein G ( 146)	148	41.9	0.23	gi 215503222 gb EEC12716.1	conserved hypothetical ( 274)	150	42.5	0.29
gi 147847924 emb CAK23475.1	Predicted membrane pr ( 369)	153	43.2	0.23	gi 28056681 gb AAO28560.1	benzene 1,2-dioxygenase ( 109)	145	41.2	0.29
gi 158111889 gb ABW14086.1	Rieske (2Fe-2S) domain ( 447)	154	43.5	0.23	gi 182631390 gb ACB92166.1	Rieske (2Fe-2S) domain ( 109)	145	41.2	0.29
gi 967221 gb AAB67846.1	ribulose-1,5-bisphosphate ( 178)	149	42.2	0.23	gi 71917208 gb AAZ57110.1	putative methylesterase ( 334)	151	42.8	0.29
gi 755735 emb CAA28737.1	RuBisCO (SSU) [Helianthu ( 178)	149	42.2	0.23	gi 1204056 emb CAA63441.1	Rubisco; ribulose-1,5-b ( 110)	145	41.2	0.29
gi 18808 emb CAA68490.1	ribulose bisphosphate car ( 178)	149	42.2	0.23	gi 134641419 gb EBC55700.1	hypothetical protein G ( 133)	146	41.4	0.29
gi 143759252 gb EDG64008.1	hypothetical protein G ( 149)	148	41.9	0.24	gi 140213545 gb ECK30203.1	hypothetical protein G ( 279)	150	42.5	0.29
gi 141913689 gb ECU12870.1	hypothetical protein G ( 124)	147	41.6	0.24	gi 124400216 emb CAK65703.1	unnamed protein produ ( 406)	152	43.0	0.29
gi 136873905 gb EBQ98078.1	hypothetical protein G ( 181)	149	42.2	0.24	gi 142025772 gb ECU95242.1	hypothetical protein G ( 344)	151	42.8	0.3
gi 91692572 gb ABE35770.1	Rieske (2Fe-2S) region ( 104)	146	41.4	0.24	gi 28853484 gb AAO56551.1	iron-sulfur cluster-bin ( 416)	152	43.0	0.3
gi 190699628 gb ACE93712.1	ferredoxin of the Ries ( 104)	146	41.4	0.24	gi 139253200 gb ECE37074.1	hypothetical protein G ( 95)	144	40.9	0.3
gi 142562016 gb ECY97213.1	hypothetical protein G ( 320)	152	43.0	0.24	gi 269789963 gb ACZ42104.1	Rieske (2Fe-2S) domain ( 289)	150	42.5	0.3
gi 120589247 gb ABM32687.1	assimilatory nitrite r ( 127)	147	41.6	0.24	gi 133913642 emb CAM03755.1	hypothetical protein ( 115)	145	41.2	0.3
gi 239609769 gb EEQ86756.1	apoptosis-inducing fac ( 560)	155	43.8	0.24	gi 140295347 gb ECK79941.1	hypothetical protein G ( 293)	150	42.5	0.31
gi 239595139 gb EEQ77720.1	apoptosis-inducing fac ( 560)	155	43.8	0.24	gi 124401476 emb CAK66954.1	unnamed protein produ ( 425)	152	43.0	0.31
gi 142548585 gb ECY87788.1	hypothetical protein G ( 270)	151	42.7	0.24	gi 3243167 gb AAC38616.1	initial dioxygenase larg ( 431)	152	43.1	0.31
gi 56909630 dbj BAD64157.1	assimilatory nitrite r ( 107)	146	41.4	0.24	gi 143914502 gb EDH53954.1	hypothetical protein G ( 118)	145	41.2	0.31
gi 220967978 gb EED86341.1	hypothetical protein T ( 187)	149	42.2	0.24	gi 140774809 gb ECN41888.1	hypothetical protein G ( 248)	149	42.2	0.31
gi 143965387 gb EDH90586.1	hypothetical protein G ( 393)	153	43.3	0.24	gi 219680597 gb EED36946.1	rieske (2Fe-2S) domain ( 362)	151	42.8	0.31
gi 142526549 gb ECY71831.1	hypothetical protein G ( 396)	153	43.3	0.25	gi 134884939 gb EBE07042.1	hypothetical protein G ( 362)	151	42.8	0.31
gi 143245134 gb EDD85960.1	hypothetical protein G ( 396)	153	43.3	0.25	gi 141955226 gb ECU42163.1	hypothetical protein G ( 144)	146	41.5	0.31
gi 143196668 gb EDD51395.1	hypothetical protein G ( 109)	146	41.4	0.25	gi 124400223 emb CAK65710.1	unnamed protein produ ( 438)	152	43.1	0.31
gi 137226686 gb EBS91318.1	hypothetical protein G ( 111)	146	41.4	0.25	gi 87134243 gb ABD24985.1	Rieske (2Fe-2S) protein ( 444)	152	43.1	0.32
gi 110284789 gb ABG62848.1	nitrite reductase (NAD ( 112)	146	41.4	0.25	gi 116672873 gb ABK15574.1	ribulose-1,5-bisphosph ( 176)	147	41.7	0.32
gi 134669376 gb EBC71968.1	hypothetical protein G ( 344)	152	43.0	0.26	gi 72123472 gb AAZ65626.1	Rieske (2Fe-2S) region ( 101)	144	40.9	0.32

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gi 141990470 gb ECU66694.1	hypothetical protein G ( 255)	149	42.3	0.32	gi 2072732 emb CAA73203.1	2-oxo-1,2-dihydroquinol ( 446)	151	42.8	0.37
gi 141607848 gb ECS54391.1	hypothetical protein G ( 256)	149	42.3	0.32	gi 170776293 gb ACB34432.1	Rieske (2Fe-2S) domain ( 123)	144	41.0	0.38
gi 155356211 gb ABU11816.1	Sequence 199285 from p ( 147)	146	41.5	0.32	gi 138876229 gb ECC25715.1	hypothetical protein G ( 180)	146	41.5	0.38
gi 142479872 gb ECY38605.1	hypothetical protein G ( 213)	148	42.0	0.32	gi 143991226 gb EDI08457.1	hypothetical protein G ( 314)	149	42.3	0.38
gi 136804748 gb EBQ52024.1	hypothetical protein G ( 372)	151	42.8	0.32	gi 134447582 gb EBB40332.1	hypothetical protein G ( 217)	147	41.8	0.38
gi 133913670 emb CAM03783.1	ferredoxin subunits o ( 372)	151	42.8	0.32	gi 2199562 gb AAB61372.1	naphthalene dioxygenase ( 104)	143	40.7	0.38
gi 219677344 gb EED333709.1	rieske (2Fe-2S) domain ( 372)	151	42.8	0.32	gi 187720122 gb ACD21345.1	Rieske (2Fe-2S) domain ( 104)	143	40.7	0.38
gi 143920280 gb EDH58171.1	hypothetical protein G ( 450)	152	43.1	0.32	gi 247547501 gb ACT04520.1	nitrite reductase (NAD ( 104)	143	40.7	0.38
gi 257477710 gb ACV58029.1	Rieske (2Fe-2S) iron-s ( 103)	144	40.9	0.32	gi 139096375 gb ECD38735.1	hypothetical protein G ( 263)	148	42.0	0.38
gi 143643055 gb EDG02770.1	hypothetical protein G ( 377)	151	42.8	0.32	gi 119671218 emb CAL95131.1	putative ferredoxin [ ( 105)	143	40.7	0.38
gi 133912315 emb CAM02428.1	ferredoxin subunits o ( 378)	151	42.8	0.32	gi 145701427 gb ABP94569.1	Rieske (2Fe-2S) domain ( 105)	143	40.7	0.38
gi 4756150 emb CAB42154.1	unnamed protein product ( 104)	144	40.9	0.33	gi 150031671 gb ABR63787.1	Rieske (2Fe-2S) domain ( 105)	143	40.7	0.38
gi 4433640 gb AAD20826.1	NirD [Staphylococcus car ( 104)	144	40.9	0.33	gi 137544498 gb EBU66583.1	hypothetical protein G ( 266)	148	42.0	0.39
gi 222427844 emb CAL28802.1	NirD protein [Staphyl ( 104)	144	40.9	0.33	gi 159123033 gb EDP48153.1	AIF-like mitochondrial ( 558)	152	43.1	0.39
gi 2588890 dbj BAA23214.1	small subunit of ribulo ( 182)	147	41.7	0.33	gi 119411002 gb EAW20947.1	AIF-like mitochondrial ( 558)	152	43.1	0.39
gi 139885435 gb ECI13080.1	hypothetical protein G ( 182)	147	41.7	0.33	gi 136767901 gb EBQ27532.1	hypothetical protein G ( 153)	145	41.2	0.39
gi 163663831 gb ABY31198.1	Rieske (2Fe-2S) domain ( 382)	151	42.8	0.33	gi 138337132 gb EBZ04626.1	hypothetical protein G ( 222)	147	41.8	0.39
gi 134404257 gb EBB15429.1	hypothetical protein G ( 220)	148	42.0	0.33	gi 143255285 gb EDD93125.1	hypothetical protein G ( 323)	149	42.3	0.39
gi 134654313 gb EBC63298.1	hypothetical protein G ( 183)	147	41.7	0.33	gi 143924016 gb EDH60944.1	hypothetical protein G ( 389)	150	42.6	0.39
gi 15140444 emb CAC48959.1	MocE [Sinorhizobium me ( 105)	144	40.9	0.33	gi 143130168 gb EDD03478.1	hypothetical protein G ( 390)	150	42.6	0.39
gi 32447078 emb CAD76887.1	putative dioxygenase a ( 387)	151	42.8	0.33	gi 94551750 gb ABF41674.1	Rieske (2Fe-2S) oxidore ( 270)	148	42.0	0.39
gi 154350670 gb ABS72749.1	NasE [Bacillus amyloli ( 106)	144	40.9	0.33	gi 91691647 gb ABE34845.1	Anthranyl dioxygenas ( 107)	143	40.7	0.39
gi 142227844 gb ECW91946.1	hypothetical protein G ( 388)	151	42.8	0.33	gi 142621223 gb ECZ32854.1	hypothetical protein G ( 394)	150	42.6	0.39
gi 33769243 gb AAQ53874.1	Sequence 56 from patent ( 35)	138	39.3	0.33	gi 159884040 emb CAB55362.3	apoptosis-inducing fa ( 575)	152	43.1	0.4
gi 15108684 gb AAE67720.1	Sequence 56 from patent ( 35)	138	39.3	0.33	gi 182635566 gb ACB96340.1	Rieske (2Fe-2S) domain ( 109)	143	40.7	0.4
gi 137957693 gb EBW96895.1	hypothetical protein G ( 269)	149	42.3	0.33	gi 142302710 gb ECX10150.1	hypothetical protein G ( 335)	149	42.3	0.4
gi 135410947 gb EBH45519.1	hypothetical protein G ( 269)	149	42.3	0.33	gi 259216837 gb ACW17729.1	Sequence 12 from paten ( 232)	147	41.8	0.4
gi 166860302 gb ABY98709.1	Rieske (2Fe-2S) domain ( 107)	144	40.9	0.33	gi 226888917 emb CAX87033.1	unnamed protein produ ( 232)	147	41.8	0.4
gi 143103990 gb EDC84227.1	hypothetical protein G ( 396)	151	42.8	0.34	gi 27269177 gb AAN89736.1	Sequence 12 from patent ( 232)	147	41.8	0.4
gi 9106496 gb AAF84281.1	AE003977_4 benzene 1,2-di ( 109)	144	40.9	0.34	gi 119377751 gb ABL72515.1	assimilatory nitrite r ( 111)	143	40.7	0.4
gi 142261585 gb ECW80001.1	hypothetical protein G ( 109)	144	40.9	0.34	gi 138209202 gb EBY42583.1	hypothetical protein G ( 236)	147	41.8	0.41
gi 137418297 gb EBT98929.1	hypothetical protein G ( 111)	144	40.9	0.34	gi 135347385 gb EBH02805.1	hypothetical protein G ( 136)	144	41.0	0.41
gi 134775523 gb EBD34962.1	hypothetical protein G ( 409)	151	42.8	0.35	gi 219947962 gb ACL58354.1	Rieske (2Fe-2S) domain ( 599)	152	43.1	0.41
gi 135881384 gb EBK44361.1	hypothetical protein G ( 409)	151	42.8	0.35	gi 169759869 gb ACA73185.1	FAD-dependent pyridine ( 506)	151	42.9	0.41
gi 143678247 gb EDG22540.1	hypothetical protein G ( 409)	151	42.8	0.35	gi 135592711 gb EBI63577.1	hypothetical protein G ( 292)	148	42.1	0.42
gi 146402742 gb ABQ31269.1	Rieske (2Fe-2S) domain ( 413)	151	42.8	0.35	gi 221727019 gb ACM30108.1	oxidoreductase protein ( 168)	145	41.3	0.42
gi 256357686 gb ACU71183.1	Rieske (2Fe-2S) domain ( 113)	144	40.9	0.35	gi 256359899 gb ACU73396.1	Rieske (2Fe-2S) domain ( 294)	148	42.1	0.42
gi 141018231 gb ECP08345.1	hypothetical protein G ( 238)	148	42.0	0.35	gi 135510420 gb EBI11155.1	hypothetical protein G ( 141)	144	41.0	0.42
gi 143829629 gb EDG92908.1	hypothetical protein G ( 345)	150	42.5	0.35	gi 215491345 gb EEC00986.1	conserved hypothetical ( 358)	149	42.3	0.42
gi 136459828 gb EBO30435.1	hypothetical protein G ( 288)	149	42.3	0.35	gi 3644000 gb AAC69486.1	2-hydroxybenzoate 5-hydr ( 99)	142	40.5	0.43
gi 135302578 gb EBG73349.1	hypothetical protein G ( 199)	147	41.7	0.35	gi 967229 gb AAB67850.1	ribulose-1,5-bisphosphate ( 173)	145	41.3	0.43
gi 137177414 gb EBS63599.1	hypothetical protein G ( 240)	148	42.0	0.35	gi 143387425 gb EDE68774.1	hypothetical protein G ( 175)	145	41.3	0.43
gi 133913668 emb CAM03781.1	hypothetical protein ( 115)	144	40.9	0.35	gi 134877660 gb EBE02192.1	hypothetical protein G ( 443)	150	42.6	0.43
gi 156235055 gb ABU59838.1	nitrogen-fixing NifU d ( 291)	149	42.3	0.36	gi 140299293 gb ECC81794.1	hypothetical protein G ( 146)	144	41.0	0.43
gi 148502705 gb ABQ70959.1	Rieske (2Fe-2S) domain ( 423)	151	42.8	0.36	gi 51856866 dbj BAD41024.1	biphenyl dioxygenase [ ( 101)	142	40.5	0.43
gi 82408426 gb ABB73052.1	putative ferredoxin [Ar ( 116)	144	40.9	0.36	gi 155354343 gb ABU09948.1	Sequence 197417 from p ( 147)	144	41.0	0.44
gi 86565911 gb ABD09720.1	Rieske (2Fe-2S) protein ( 298)	149	42.3	0.36	gi 155362243 gb ABU17848.1	Sequence 205317 from p ( 102)	142	40.5	0.44
gi 143199028 gb EDD53111.1	hypothetical protein G ( 362)	150	42.6	0.37	gi 108862471 gb ABG21958.1	Ribulose bisphosphate ( 148)	144	41.0	0.44
gi 186468967 gb ACC84768.1	Rieske (2Fe-2S) domain ( 367)	150	42.6	0.37	gi 141011667 gb ECP03671.1	hypothetical protein G ( 149)	144	41.0	0.44
gi 170328 gb AAA34116.1	ribulose-1,5-bisphosphate ( 101)	143	40.7	0.37	gi 39982715 gb AAR34175.1	Rieske 2Fe-2S family pr ( 103)	142	40.5	0.44
gi 134390544 gb EBB08649.1	hypothetical protein G ( 307)	149	42.3	0.37	gi 30013663 gb AAP03874.1	putative ribulose bisph ( 180)	145	41.3	0.44

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gi 125119921 gb ABN25683.1	Sequence 3 from patent ( 181)	145	41.3	0.45	gi 135166437 gb EBF91874.1	hypothetical protein G ( 368)	148	42.1	0.51
gi 24940140 emb CAD11991.1	rubisco small subunit ( 181)	145	41.3	0.45	gi 68051305 gb AAY84916.1	IP11809p [Drosophila me ( 534)	150	42.6	0.51
gi 24940138 emb CAD11990.1	rubisco small subunit ( 181)	145	41.3	0.45	gi 111150977 emb CAJ62683.1	putative Rieske Fe-S ( 309)	147	41.8	0.51
gi 58416251 emb CAI47845.1	ferredoxin component o ( 104)	142	40.5	0.45	gi 225905973 gb ACO35888.1	ribulose-1,5-bisphosph ( 178)	144	41.0	0.51
gi 109454490 gb ABG30695.1	Rieske 2Fe-2S domain p ( 381)	149	42.3	0.45	gi 139753864 gb ECH22719.1	hypothetical protein G ( 215)	145	41.3	0.52
gi 1536889 emb CAA69102.1	ribulose-bisphosphate c ( 182)	145	41.3	0.45	gi 71846077 gb AAZ45573.1	assimilatory nitrite re ( 103)	141	40.2	0.52
gi 240009530 gb ACS40756.1	putative Naphthalene 1 ( 382)	149	42.3	0.45	gi 142969579 gb EDB87404.1	hypothetical protein G ( 377)	148	42.1	0.52
gi 218523288 gb ACK83873.1	Rieske (2Fe-2S) domain ( 382)	149	42.3	0.45	gi 206679720 gb EDZ44207.1	rieske 2Fe-2S domain p ( 379)	148	42.1	0.52
gi 136549801 gb EBO88302.1	hypothetical protein G ( 183)	145	41.3	0.45	gi 137682847 gb EBV43254.1	hypothetical protein G ( 262)	146	41.6	0.52
gi 135146246 gb EBF78858.1	hypothetical protein G ( 266)	147	41.8	0.45	gi 256585766 gb ACU96899.1	ring-hydroxylating dio ( 380)	148	42.1	0.52
gi 124260280 gb ABM95274.1	assimilatory nitrite r ( 127)	143	40.7	0.45	gi 134648546 gb EBC59947.1	hypothetical protein G ( 105)	141	40.2	0.53
gi 137690769 gb EBV47638.1	hypothetical protein G ( 321)	148	42.1	0.45	gi 140384064 gb ECL40595.1	hypothetical protein G ( 153)	143	40.8	0.53
gi 144099439 gb EDI86080.1	hypothetical protein G ( 387)	149	42.3	0.45	gi 136331604 gb EBN44515.1	hypothetical protein G ( 321)	147	41.9	0.53
gi 144221507 gb EDJ74966.1	hypothetical protein G ( 387)	149	42.3	0.45	gi 122090573 emb CAL13442.1	putative Rieske prote ( 106)	141	40.3	0.53
gi 140900901 gb ECO26354.1	hypothetical protein G ( 268)	147	41.8	0.45	gi 143530106 gb EDF48219.1	hypothetical protein G ( 61)	138	39.4	0.53
gi 155351267 gb ABU06872.1	Sequence 194341 from p ( 154)	144	41.0	0.45	gi 4704462 gb AAD28100.1	AF082663_1 naphthalene di ( 470)	149	42.4	0.53
gi 91693788 gb ABE36985.1	Anthranilate dioxygenas ( 107)	142	40.5	0.46	gi 110825901 gb ABH01029.1	naphthalene dioxygenas ( 470)	149	42.4	0.53
gi 155353432 gb ABU09037.1	Sequence 196506 from p ( 156)	144	41.0	0.46	gi 141014028 gb ECP05334.1	hypothetical protein G ( 270)	146	41.6	0.53
gi 116789830 gb ABK25403.1	unknown [Picea sitchen ( 188)	145	41.3	0.46	gi 135472210 gb EBH86569.1	hypothetical protein G ( 187)	144	41.1	0.54
gi 89952129 gb ABD82144.1	Rieske (2Fe-2S) region ( 475)	150	42.6	0.46	gi 33333869 gb AAQ12033.1	putative ring-hydroxyla ( 393)	148	42.1	0.54
gi 142911971 gb EDB46550.1	hypothetical protein G ( 157)	144	41.0	0.46	gi 28971825 dbj BAC65428.1	ferredoxin component o ( 108)	141	40.3	0.54
gi 155342828 gb ABT98432.1	Sequence 185902 from p ( 157)	144	41.0	0.46	gi 256858063 gb ACV31385.1	dioxygenase ferredoxin ( 108)	141	40.3	0.54
gi 155351375 gb ABU06980.1	Sequence 194449 from p ( 157)	144	41.0	0.46	gi 123967434 gb ABM79783.1	ferredoxin component o ( 108)	141	40.3	0.54
gi 139236337 gb ECE32253.1	hypothetical protein G ( 274)	147	41.8	0.46	gi 86557285 gb ABD02242.1	iron-sulfur cluster-bin ( 395)	148	42.1	0.54
gi 139591662 gb ECG12543.1	hypothetical protein G ( 109)	142	40.5	0.46	gi 143655131 gb EDG09975.1	hypothetical protein G ( 109)	141	40.3	0.54
gi 142532054 gb ECY75855.1	hypothetical protein G ( 109)	142	40.5	0.46	gi 138218911 gb EBY49294.1	hypothetical protein G ( 230)	145	41.3	0.55
gi 143833574 gb EDG95751.1	hypothetical protein G ( 399)	149	42.4	0.46	gi 135459252 gb EBH77878.1	hypothetical protein G ( 401)	148	42.1	0.55
gi 143053351 gb EDC47271.1	hypothetical protein G ( 399)	149	42.4	0.46	gi 134509660 gb EBB76849.1	hypothetical protein G ( 277)	146	41.6	0.55
gi 143227482 gb EDD73788.1	hypothetical protein G ( 76)	140	40.0	0.47	gi 139026287 gb ECC89537.1	hypothetical protein G ( 192)	144	41.1	0.55
gi 140219556 gb ECK33668.1	hypothetical protein G ( 232)	146	41.6	0.47	gi 140314099 gb ECK91718.1	hypothetical protein G ( 135)	142	40.5	0.56
gi 140634904 gb ECM46405.1	hypothetical protein G ( 282)	147	41.8	0.47	gi 137949988 gb EBW92577.1	hypothetical protein G ( 285)	146	41.6	0.56
gi 143964017 gb EDH89659.1	hypothetical protein G ( 112)	142	40.5	0.47	gi 143263811 gb EDD99288.1	hypothetical protein G ( 345)	147	41.9	0.56
gi 135710406 gb EBJ36369.1	hypothetical protein G ( 237)	146	41.6	0.48	gi 134625856 gb EBC46481.1	hypothetical protein G ( 239)	145	41.3	0.56
gi 143731343 gb EDG49496.1	hypothetical protein G ( 114)	142	40.5	0.48	gi 143995385 gb EDI11506.1	hypothetical protein G ( 166)	143	40.8	0.57
gi 209538537 gb ACI58471.1	Rieske (2Fe-2S) domain ( 417)	149	42.4	0.48	gi 137134460 gb EBS39565.1	hypothetical protein G ( 202)	144	41.1	0.57
gi 143057106 gb EDC50021.1	hypothetical protein G ( 349)	148	42.1	0.48	gi 137715871 gb EBV61389.1	hypothetical protein G ( 202)	144	41.1	0.57
gi 74419160 gb ABA03359.1	leucyl-tRNA synthetase ( 883)	153	43.4	0.49	gi 135421176 gb EBH52390.1	hypothetical protein G ( 246)	145	41.3	0.58
gi 136224039 gb EBM71544.1	hypothetical protein G ( 350)	148	42.1	0.49	gi 140680655 gb ECM77750.1	hypothetical protein G ( 118)	141	40.3	0.58
gi 146401693 gb ABQ30220.1	Rieske (2Fe-2S) domain ( 423)	149	42.4	0.49	gi 139910095 gb ECI30357.1	hypothetical protein G ( 208)	144	41.1	0.59
gi 139386661 gb ECE76605.1	hypothetical protein G ( 243)	146	41.6	0.49	gi 143570703 gb EDF69233.1	hypothetical protein G ( 368)	147	41.9	0.59
gi 138731491 gb ECB62204.1	hypothetical protein G ( 202)	145	41.3	0.49	gi 142943973 gb EDB69473.1	hypothetical protein G ( 306)	146	41.6	0.59
gi 142143398 gb ECV90877.1	hypothetical protein G ( 117)	142	40.5	0.49	gi 135346393 gb EBH02143.1	hypothetical protein G ( 176)	143	40.8	0.6
gi 136373571 gb EBN73138.1	hypothetical protein G ( 356)	148	42.1	0.49	gi 136362512 gb EBN65584.1	hypothetical protein G ( 122)	141	40.3	0.6
gi 134406531 gb EBB16682.1	hypothetical protein G ( 297)	147	41.8	0.49	gi 257046871 gb ACC336059.1	nitrite reductase (NAD ( 102)	140	40.0	0.6
gi 143644555 gb EDG03654.1	hypothetical protein G ( 359)	148	42.1	0.5	gi 142434595 gb ECY05155.1	hypothetical protein G ( 310)	146	41.6	0.6
gi 197627017 gb EDY39576.1	putative Rieske (2Fe-2 ( 362)	148	42.1	0.5	gi 137327751 gb EBT47846.1	hypothetical protein G ( 178)	143	40.8	0.6
gi 134456596 gb EBB45637.1	hypothetical protein G ( 301)	147	41.8	0.5	gi 143082788 gb EDC68829.1	hypothetical protein G ( 374)	147	41.9	0.6
gi 140776608 gb ECN42730.1	hypothetical protein G ( 252)	146	41.6	0.5	gi 135510419 gb EBI11154.1	hypothetical protein G ( 259)	145	41.4	0.6
gi 135527622 gb EBI22151.1	hypothetical protein G ( 210)	145	41.3	0.5	gi 142937236 gb EDB64642.1	hypothetical protein G ( 377)	147	41.9	0.61
gi 136726838 gb EBQ00331.1	hypothetical protein G ( 253)	146	41.6	0.51	gi 197601 emb CAA25862.1	unnamed protein product [ ( 180)	143	40.8	0.61
gi 228267187 gb ACP97860.1	Sequence 30078 from pa ( 175)	144	41.0	0.51	gi 20024 emb CAA26208.1	small subunit ribulose 1, ( 180)	143	40.8	0.61

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gi 136151978 gb EBM23753.1	hypothetical protein G ( 261)	145	41.4	0.61	gi 137204980 gb EBS78942.1	hypothetical protein G ( 212)	143	40.9	0.7
gi 145020099 gb EDK04327.1	hypothetical protein M ( 548)	149	42.4	0.61	gi 142553842 gb ECY91479.1	hypothetical protein G ( 370)	146	41.7	0.7
gi 143972451 gb EDH95489.1	hypothetical protein G ( 456)	148	42.2	0.61	gi 137913950 gb EBW72314.1	hypothetical protein G ( 311)	145	41.4	0.7
gi 141455921 gb ECR94709.1	hypothetical protein G ( 262)	145	41.4	0.61	gi 194176764 gb EDW90375.1	GE12673 [Drosophila ya ( 543)	148	42.2	0.71
gi 137719162 gb EBV63230.1	hypothetical protein G ( 181)	143	40.8	0.61	gi 124396265 emb CAK61776.1	unnamed protein produ ( 545)	148	42.2	0.71
gi 142047148 gb ECV14993.1	hypothetical protein G ( 125)	141	40.3	0.61	gi 20491 emb CAA27444.1	ribulose 1,5-bisphosphate ( 180)	142	40.6	0.71
gi 136576272 gb EBP05208.1	hypothetical protein G ( 104)	140	40.0	0.61	gi 20493 emb CAA27445.1	ribulose 1,5-bisphosphate ( 180)	142	40.6	0.71
gi 144207262 gb EDJ64678.1	hypothetical protein G ( 184)	143	40.8	0.62	gi 15108654 gb AAE67690.1	Sequence 26 from patent ( 34)	133	38.2	0.71
gi 206676911 gb EDZ41398.1	rieske (2Fe-2S) protei ( 386)	147	41.9	0.62	gi 33769213 gb AAQ53844.1	Sequence 26 from patent ( 34)	133	38.2	0.71
gi 90787419 gb ABD97973.1	putative ring-hydroxyla ( 387)	147	41.9	0.62	gi 139925902 gb ECI41385.1	hypothetical protein G ( 315)	145	41.4	0.71
gi 49072904 gb AAT51755.1	aromatic oxygenase larg ( 387)	147	41.9	0.62	gi 18413570 emb CAD21856.1	putative ribulose 1,5 ( 181)	142	40.6	0.71
gi 134345613 gb EBA78930.1	hypothetical protein G ( 322)	146	41.6	0.62	gi 117661825 gb EBK55670.1	chloroplast ribulose-1 ( 125)	140	40.1	0.71
gi 139476756 gb ECF34993.1	hypothetical protein G ( 185)	143	40.8	0.62	gi 197721534 gb EDY65442.1	ferredoxin subunit of ( 104)	139	39.8	0.71
gi 143826513 gb EDG90683.1	hypothetical protein G ( 268)	145	41.4	0.62	gi 86284821 gb ABC93880.1	ferredoxin of the Riese ( 104)	139	39.8	0.71
gi 142705544 gb ECZ98496.1	hypothetical protein G ( 224)	144	41.1	0.62	gi 113526418 emb CAJ92763.1	ferredoxin subunits o ( 104)	139	39.8	0.71
gi 143142807 gb EDD12750.1	hypothetical protein G ( 391)	147	41.9	0.62	gi 108743909 gb ABG02223.1	dioxygenase large alph ( 458)	147	41.9	0.71
gi 139182447 gb ECD97254.1	hypothetical protein G ( 187)	143	40.8	0.63	gi 144040443 gb EDI43315.1	hypothetical protein G ( 382)	146	41.7	0.72
gi 144224693 gb EDJ77274.1	hypothetical protein G ( 326)	146	41.6	0.63	gi 168997361 gb ACA42439.1	ribulose-1,5-bisphosph ( 183)	142	40.6	0.72
gi 126234014 gb ABN97414.1	Rieske (2Fe-2S) domain ( 393)	147	41.9	0.63	gi 99038179 gb ABF64791.1	Rieske (2Fe-2S) region ( 384)	146	41.7	0.72
gi 119954332 gb ABM11337.1	Rieske (2Fe-2S) domain ( 393)	147	41.9	0.63	gi 226292818 gb EEH48238.1	rhodocoxin reductase [ ( 561)	148	42.2	0.73
gi 145213651 gb ABP43055.1	Rieske (2Fe-2S) domain ( 393)	147	41.9	0.63	gi 144142847 gb EDJ17599.1	hypothetical protein G ( 106)	139	39.8	0.73
gi 119697740 gb ABL94812.1	Rieske (2Fe-2S) domain ( 393)	147	41.9	0.63	gi 261282912 gb ACX64883.1	nitrite reductase (NAD) ( 106)	139	39.8	0.73
gi 126234619 gb ABN98019.1	Rieske (2Fe-2S) domain ( 393)	147	41.9	0.63	gi 136779708 gb EBQ35364.1	hypothetical protein G ( 388)	146	41.7	0.73
gi 108769034 gb ABG07756.1	Rieske (2Fe-2S) region ( 393)	147	41.9	0.63	gi 155348854 gb ABU04459.1	Sequence 191928 from p ( 154)	141	40.3	0.73
gi 145213743 gb ABP43147.1	Rieske (2Fe-2S) domain ( 393)	147	41.9	0.63	gi 136580815 gb EBP08115.1	hypothetical protein G ( 108)	139	39.8	0.74
gi 119693802 gb ABL90875.1	Rieske (2Fe-2S) domain ( 393)	147	41.9	0.63	gi 142784330 gb EDA55766.1	hypothetical protein G ( 227)	143	40.9	0.74
gi 158308661 gb ABW30278.1	Ferredoxin subunits of ( 572)	149	42.4	0.63	gi 136031560 gb EBL44904.1	hypothetical protein G ( 397)	146	41.7	0.74
gi 143992223 gb EDI09189.1	hypothetical protein G ( 398)	147	41.9	0.63	gi 238843481 gb EEQ33143.1	flavoprotein [Microspo ( 576)	148	42.2	0.74
gi 209874149 gb ACI93945.1	nitrite reductase [NAD ( 109)	140	40.0	0.64	gi 155314463 gb ABT70067.1	Sequence 157537 from p ( 131)	140	40.1	0.74
gi 141246970 gb ECQ64015.1	hypothetical protein G ( 231)	144	41.1	0.64	gi 136511607 gb EBO63936.1	hypothetical protein G ( 398)	146	41.7	0.74
gi 118166677 gb ABK67574.1	Rieske [2Fe-2S] domain ( 337)	146	41.6	0.64	gi 194340215 gb EDX21181.1	methylesterase [Strept ( 331)	145	41.4	0.74
gi 41396831 gb AAS04694.1	hypothetical protein MA ( 337)	146	41.6	0.64	gi 167964792 gb ACA11802.1	benzene 1,2-dioxygenas ( 109)	139	39.8	0.74
gi 155356492 gb ABU12097.1	Sequence 199566 from p ( 134)	141	40.3	0.65	gi 139222090 gb ECE24933.1	hypothetical protein G ( 191)	142	40.6	0.75
gi 120594351 gb ABM37790.1	Rieske (2Fe-2S) domain ( 112)	140	40.0	0.65	gi 141837189 gb ECT59375.1	hypothetical protein G ( 230)	143	40.9	0.75
gi 74136889 gb AAZ93387.1	ferredoxin [Polaromonas ( 112)	140	40.0	0.65	gi 71916116 gb AAZ56018.1	putative dioxygenase [T ( 110)	139	39.8	0.75
gi 124400531 emb CAK66017.1	unnamed protein produ ( 594)	149	42.4	0.65	gi 143052138 gb EDC46398.1	hypothetical protein G ( 404)	146	41.7	0.75
gi 139544934 gb ECF80025.1	hypothetical protein G ( 238)	144	41.1	0.66	gi 144898345 emb CAM75209.1	assimilatory nitrite ( 111)	139	39.8	0.75
gi 137382206 gb EBT78360.1	hypothetical protein G ( 199)	143	40.8	0.66	gi 135939685 gb EBK84593.1	hypothetical protein G ( 407)	146	41.7	0.76
gi 209530745 gb ACI50682.1	Rieske (2Fe-2S) domain ( 504)	148	42.2	0.66	gi 138811869 gb ECB96911.1	hypothetical protein G ( 234)	143	40.9	0.76
gi 137231874 gb EBS94255.1	hypothetical protein G ( 202)	143	40.8	0.67	gi 136850860 gb EBQ82750.1	hypothetical protein G ( 162)	141	40.3	0.76
gi 3790104 gb AAC67588.1	ribulose-1,5-bisphosphat ( 168)	142	40.6	0.67	gi 134847465 gb EBB82193.1	hypothetical protein G ( 162)	141	40.3	0.76
gi 6409339 gb AAF07947.1	AF192778_1 ribulose-1,5-b ( 168)	142	40.6	0.67	gi 138378477 gb EB225812.1	hypothetical protein G ( 283)	144	41.1	0.76
gi 115285733 gb ABI91208.1	FAD-dependent pyridine ( 512)	148	42.2	0.67	gi 139892388 gb ECI17896.1	hypothetical protein G ( 283)	144	41.1	0.76
gi 135370924 gb EBH18580.1	hypothetical protein G ( 294)	145	41.4	0.67	gi 142015620 gb ECU85566.1	hypothetical protein G ( 344)	145	41.4	0.77
gi 141410765 gb ECR63927.1	hypothetical protein G ( 294)	145	41.4	0.67	gi 142628759 gb EC243898.1	hypothetical protein G ( 286)	144	41.1	0.77
gi 136486632 gb EBO47763.1	hypothetical protein G ( 170)	142	40.6	0.68	gi 161787038 emb CAP56624.1	putative benzene 1,2- ( 504)	147	42.0	0.77
gi 143938256 gb EDH71419.1	hypothetical protein G ( 249)	144	41.1	0.68	gi 139836876 gb ECH80667.1	hypothetical protein G ( 242)	143	40.9	0.78
gi 123963428 gb ABM78184.1	Rieske iron-sulfur pro ( 436)	147	41.9	0.69	gi 138213619 gb EBY45641.1	hypothetical protein G ( 96)	138	39.5	0.78
gi 221533690 gb EEE36678.1	rieske (2Fe-2S) protei ( 363)	146	41.7	0.69	gi 140908930 gb ECO31879.1	hypothetical protein G ( 202)	142	40.6	0.78
gi 139973043 gb ECT74013.1	hypothetical protein G ( 253)	144	41.1	0.69	gi 6573202 gb AAF17589.1	AF202645_1 ribulose-1,5-b ( 168)	141	40.4	0.78
gi 6272547 gb AAF06097.1	ribulose 1,5-bisphosphat ( 176)	142	40.6	0.7	gi 222438858 gb EEE45537.1	Ferric reductase like ( 355)	145	41.4	0.79



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gi 138087162 gb EBX67214.1	hypothetical protein G ( 205)	142	40.6	0.79	gi 154159113 gb ABS66329.1	nitrite reductase (NAD ( 110)	138	39.6	0.88
gi 140499022 gb ECM02651.1	hypothetical protein G ( 247)	143	40.9	0.79	gi 134692311 gb EBC85465.1	hypothetical protein G ( 278)	143	40.9	0.88
gi 143917103 gb EDH55818.1	hypothetical protein G ( 206)	142	40.6	0.8	gi 140385142 gb ECL41338.1	hypothetical protein G ( 231)	142	40.6	0.88
gi 140174529 gb ECK02504.1	hypothetical protein G ( 248)	143	40.9	0.8	gi 135254344 gb EBG45042.1	hypothetical protein G ( 160)	140	40.1	0.88
gi 215510884 gb EEC20337.1	conserved hypothetical ( 300)	144	41.2	0.8	gi 138011988 gb EBX26814.1	hypothetical protein G ( 193)	141	40.4	0.88
gi 157915736 gb ABV97163.1	Rieske (2Fe-2S) domain ( 119)	139	39.8	0.8	gi 139498804 gb ECF48574.1	hypothetical protein G ( 280)	143	40.9	0.88
gi 142328493 gb ECX29414.1	hypothetical protein G ( 362)	145	41.4	0.8	gi 82944472 dbj BAE49336.1	Ferredoxin subunits of ( 111)	138	39.6	0.88
gi 170769 gb AAA34301.1	ribulose-1,5-bisphosphate ( 174)	141	40.4	0.81	gi 142671327 gb EC273946.1	hypothetical protein G ( 282)	143	40.9	0.89
gi 143115926 gb EDC93001.1	hypothetical protein G ( 440)	146	41.7	0.81	gi 143027678 gb EDC28421.1	hypothetical protein G ( 236)	142	40.7	0.89
gi 136815094 gb EBQ58887.1	hypothetical protein G ( 306)	144	41.2	0.81	gi 135544240 gb EBI32759.1	hypothetical protein G ( 236)	142	40.7	0.89
gi 218963647 gb ACL13525.1	NidA [Diaphorobacter s ( 146)	140	40.1	0.81	gi 138525724 gb ECA19799.1	hypothetical protein G ( 136)	139	39.9	0.9
gi 142305122 gb ECX11974.1	hypothetical protein G ( 307)	144	41.2	0.82	gi 260419934 gb EEX13187.1	nitrite reductase [Cit ( 238)	142	40.7	0.9
gi 2286117 gb AAB64251.1	ribulose-1,5-bisphosphat ( 84)	137	39.3	0.82	gi 4038691 dbj BAA35162.1	ribulose-1,5-bisphospha ( 165)	140	40.1	0.9
gi 66771353 gb AAY54988.1	IP11909p [Drosophila me ( 536)	147	42.0	0.82	gi 155367243 gb ABU2848.1	Sequence 210317 from p ( 95)	137	39.3	0.91
gi 134427897 gb EBB29024.1	hypothetical protein G ( 256)	143	40.9	0.82	gi 144213950 gb EDJ69540.1	hypothetical protein G ( 289)	143	40.9	0.91
gi 2754835 gb AAB95211.1	ribulose 1,5 bisphosphat ( 147)	140	40.1	0.82	gi 24984804 gb AAN68783.1	AE016510_5 dioxygenase, ( 506)	146	41.7	0.91
gi 2754837 gb AAB95212.1	ribulose 1,5 bisphosphat ( 147)	140	40.1	0.82	gi 136176991 gb EBM40063.1	hypothetical protein G ( 242)	142	40.7	0.91
gi 2754847 gb AAB95217.1	ribulose 1,5 bisphosphat ( 147)	140	40.1	0.82	gi 3978511 gb AAC83372.1	ribulose-1,5-bisphosphat ( 168)	140	40.1	0.92
gi 2754839 gb AAB95213.1	ribulose 1,5 bisphosphat ( 147)	140	40.1	0.82	gi 142512945 gb ECY61963.1	hypothetical protein G ( 293)	143	40.9	0.92
gi 2754841 gb AAB95214.1	ribulose 1,5 bisphosphat ( 147)	140	40.1	0.82	gi 141940297 gb ECU31495.1	hypothetical protein G ( 170)	140	40.1	0.93
gi 2754843 gb AAB95215.1	ribulose 1,5 bisphosphat ( 147)	140	40.1	0.82	gi 151280246 gb ABR88656.1	nitrite reductase (NAD ( 118)	138	39.6	0.93
gi 7298536 gb AAF53755.1	CG10700 [Drosophila mela ( 539)	147	42.0	0.82	gi 138644790 gb ECB01469.1	hypothetical protein G ( 207)	141	40.4	0.94
gi 30420754 gb AAP30898.1	naphthalene dioxygenase ( 148)	140	40.1	0.82	gi 155342834 gb ABT98438.1	Sequence 185908 from p ( 99)	137	39.3	0.94
gi 4234996 gb AAD13058.1	naphthalene dioxygenase ( 149)	140	40.1	0.83	gi 189419803 gb ACD94201.1	Rieske (2Fe-2S) domain ( 99)	137	39.3	0.94
gi 17428101 emb CAD14790.1	probable ferredoxin su ( 103)	138	39.6	0.83	gi 139039379 gb ECC98930.1	hypothetical protein G ( 301)	143	40.9	0.94
gi 260644793 emb CBG67878.1	putative ring hydroxy ( 377)	145	41.4	0.83	gi 155362205 gb ABU17810.1	Sequence 205279 from p ( 120)	138	39.6	0.94
gi 37622233 gb AAQ95208.1	NidA [Mycobacterium sp. ( 455)	146	41.7	0.83	gi 155353316 gb ABU08921.1	Sequence 196390 from p ( 100)	137	39.3	0.95
gi 11038552 gb AAF75991.2	AF249301_1 naphthalene i ( 455)	146	41.7	0.83	gi 133737459 emb CAL60502.1	putative Choline mono ( 366)	144	41.2	0.95
gi 49072900 gb AAT51751.1	NidA [Mycobacterium van ( 455)	146	41.7	0.83	gi 4090293 emb CAA10497.1	hypothetical protein [S ( 175)	140	40.1	0.95
gi 119954328 gb ABM11333.1	ring hydroxylating dio ( 455)	146	41.7	0.83	gi 134508474 gb EBB76145.1	hypothetical protein G ( 255)	142	40.7	0.95
gi 73545026 gb AAZ78224.1	NidA [Mycobacterium sp. ( 455)	146	41.7	0.83	gi 144093320 gb EDI81757.1	hypothetical protein G ( 448)	145	41.5	0.96
gi 108743911 gb ABG02224.1	dioxygenase large alph ( 455)	146	41.7	0.83	gi 145216155 gb ABP45559.1	Rieske (2Fe-2S) domain ( 373)	144	41.2	0.96
gi 33333858 gb AAQ12023.1	putative initial ring-h ( 455)	146	41.7	0.83	gi 2605706 gb AAB84179.1	ribulose 1,5 bisphosphat ( 179)	140	40.1	0.97
gi 119697736 gb ABL94808.1	ring hydroxylating dio ( 458)	146	41.7	0.84	gi 2605708 gb AAB84180.1	ribulose 1,5 bisphosphat ( 179)	140	40.1	0.97
gi 26080259 gb AAN78314.1	dioxygenase large alpha ( 458)	146	41.7	0.84	gi 2605710 gb AAB84181.1	ribulose 1,5 bisphosphat ( 179)	140	40.1	0.97
gi 33333865 gb AAQ12029.1	putative ring-hydroxyla ( 459)	146	41.7	0.84	gi 2641205 gb AAB86854.1	ribulose 1,5 bisphosphat ( 179)	140	40.1	0.97
gi 134653470 gb EBC62795.1	hypothetical protein G ( 183)	141	40.4	0.84	gi 2641203 gb AAB86853.1	ribulose 1,5 bisphosphat ( 179)	140	40.1	0.97
gi 36958689 gb AAQ87157.1	Rieske-type ferredoxin ( 105)	138	39.6	0.84	gi 14027099 dbj BAB54053.1	putative Rieske-like f ( 103)	137	39.3	0.97
gi 227338942 gb ACP23161.1	putative Rieske-like f ( 105)	138	39.6	0.84	gi 142531519 gb ECY75464.1	hypothetical protein G ( 377)	144	41.2	0.97
gi 214028409 gb EEB69245.1	hypothetical protein R ( 384)	145	41.4	0.84	gi 26080255 gb AAN78312.1	dioxygenase large alpha ( 455)	145	41.5	0.97
gi 225680544 gb EEH18828.1	rhodocoxin reductase [ ( 670)	148	42.2	0.84	gi 145213747 gb ABP43151.1	ring hydroxylating dio ( 455)	145	41.5	0.97
gi 237825729 gb ACL13524.1	NidA [Pseudoxanthomona ( 385)	145	41.4	0.84	gi 142564523 gb ECY98950.1	hypothetical protein G ( 379)	144	41.2	0.97
gi 151359812 gb ABS02815.1	Rieske (2Fe-2S) domain ( 106)	138	39.6	0.85	gi 162946539 gb ABY21254.1	ribulose-1,5-bisphosph ( 181)	140	40.1	0.98
gi 156233996 gb ABU58779.1	Rieske (2Fe-2S) domain ( 107)	138	39.6	0.86	gi 162946541 gb ABY21255.1	ribulose-1,5-bisphosph ( 181)	140	40.1	0.98
gi 155343302 gb ABT98906.1	Sequence 186376 from p ( 156)	140	40.1	0.86	gi 14024925 dbj BAB51527.1	putative Rieske-like f ( 104)	137	39.3	0.98
gi 142344947 gb ECX41491.1	hypothetical protein G ( 272)	143	40.9	0.86	gi 21205493 dbj BAB96186.1	assimilatory nitrite r ( 104)	137	39.3	0.98
gi 142865556 gb EDB13128.1	hypothetical protein G ( 188)	141	40.4	0.86	gi 49245624 emb CAG44103.1	assimilatory nitrite r ( 104)	137	39.3	0.98
gi 155350884 gb ABU06489.1	Sequence 193958 from p ( 188)	141	40.4	0.86	gi 126234623 gb ABN98023.1	ring hydroxylating dio ( 458)	145	41.5	0.98
gi 143501238 gb EDF33352.1	hypothetical protein G ( 400)	145	41.4	0.87	gi 145213655 gb ABP43059.1	ring hydroxylating dio ( 458)	145	41.5	0.98
gi 138017042 gb EBX29345.1	hypothetical protein G ( 91)	137	39.3	0.87	gi 47563681 dbj BAD20297.1	polycyclic aromatic hy ( 458)	145	41.5	0.98
gi 72118588 gb AAZ60851.1	Rieske (2Fe-2S) region ( 110)	138	39.6	0.88	gi 26080263 gb AAN78316.1	dioxygenase large alpha ( 458)	145	41.5	0.98

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gi|134411853|gb|EBB19670.1| hypothetical protein G ( 263) 142 40.7 0.98
gi|142906654|gb|EDB42626.1| hypothetical protein G ( 317) 143 40.9 0.98
gi|143787900|gb|EDG78461.1| hypothetical protein G ( 384) 144 41.2 0.99
gi|142375854|gb|ECX62160.1| hypothetical protein G ( 385) 144 41.2 0.99
gi|214038278|gb|EEB78941.1| Rieske (2Fe-2S) domain ( 386) 144 41.2 0.99
gi|137524793|gb|EBU55908.1| hypothetical protein G ( 222) 141 40.4 0.99
gi|155108041|gb|ABT05661.1| Sequence 74 from paten ( 88) 136 39.1 0.99
gi|142272188|gb|ECW87803.1| hypothetical protein G ( 185) 140 40.1 0.99
gi|150412529|gb|EDN07916.1| conserved hypothetical ( 563) 146 41.7 1
gi|118167734|gb|ABK68631.1| Rieske [2Fe-2S] domain ( 389) 144 41.2 1
gi|155342875|gb|ABT98479.1| Sequence 185949 from p ( 186) 140 40.1 1
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## First 50 DMO Alignments

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>>gi|55584974|gb|AAV53699.1| DdmC [Stenotrophomonas malt (339 aa)
  initn: 2306 init1: 2306 opt: 2306 Z-score: 2824.5 bits: 531.1 E(): 2.9e-
  148
Smith-Waterman score: 2306; 99.704% identity (99.704% similar) in 338 aa
overlap (30-367:2-339)
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      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      .....
gi|555      MTFVRNAWYVAALPEELSEKPLGRTILDTPLA
      10      20      30

      70      80      90      100     110     120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNGARPA
      .....
gi|555 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNGARPA
      40      50      60      70      80      90

      130     140     150     160     170     180
DMO+27 SLNVRSPVVERDALIWIICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD
      .....
gi|555 SLNVRSPVVERDALIWIWPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD
      100     110     120     130     140     150

      190     200     210     220     230     240
DMO+27 NLMDLGHAQYVHRANAQTDAFDRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGANTP
      .....
gi|555 NLMDLGHAQYVHRANAQTDAFDRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGANTP
      160     170     180     190     200     210

      250     260     270     280     290     300
DMO+27 VDAWNDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTHILTPETEASCHYFFGSSRNFGI
      .....
gi|555 VDAWNDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTHILTPETEASCHYFFGSSRNFGI
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      220      230      240      250      260      270
      310      320      330      340      350      360
DMO+27 DDPEMDGVLRSWQAQALVKEDKVVVEAIEERRRAYVEANGIRPAMLSCEAAVVRVSREIEK
      .....
gi|555 DDPEMDGVLRSWQAQALVKEDKVVVEAIEERRRAYVEANGIRPAMLSCEAAVVRVSREIEK
      280      290      300      310      320      330

DMO+27 LEQLEAA
      .....
gi|555 LEQLEAA

>>gi|91175995|gb|ABE26579.1| Sequence 4 from patent US 7 (339 aa)
  initn: 2306 init1: 2306 opt: 2306 Z-score: 2824.5 bits: 531.1 E(): 2.9e-
  148
Smith-Waterman score: 2306; 99.704% identity (99.704% similar) in 338 aa
overlap (30-367:2-339)

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      .....
gi|911      MTFVRNAWYVAALPEELSEKPLGRTILDTPLA
      10      20      30

      70      80      90      100     110     120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNGARPA
      .....
gi|911 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNGARPA
      40      50      60      70      80      90

      130     140     150     160     170     180
DMO+27 SLNVRSPVVERDALIWIICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD
      .....
gi|911 SLNVRSPVVERDALIWIWPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD
      100     110     120     130     140     150

      190     200     210     220     230     240
DMO+27 NLMDLGHAQYVHRANAQTDAFDRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGANTP
      .....
gi|911 NLMDLGHAQYVHRANAQTDAFDRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGANTP
      160     170     180     190     200     210

      250     260     270     280     290     300
DMO+27 VDAWNDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTHILTPETEASCHYFFGSSRNFGI
      .....
gi|911 VDAWNDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTHILTPETEASCHYFFGSSRNFGI
      220     230     240     250     260     270

      310     320     330     340     350     360
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DMO+27 DDPEMDGVLRSWQAQALVKEDKVVVEAIERRRAYVEANGIRPAMLSCEAAVRVSREIEK
      .....
gi|911 DDPEMDGVLRSWQAQALVKEDKVVVEAIERRRAYVEANGIRPAMLSCEAAVRVSREIEK
      280      290      300      310      320      330

DMO+27 LEQLEAA
      .....
gi|911 LEQLEAA

>>gi|115833518|gb|ABJ40820.1| Sequence 3 from patent US (339 aa)
      initn: 2306 initl: 2306 opt: 2306 Z-score: 2824.5 bits: 531.1 E(): 2.9e-
      148
      Smith-Waterman score: 2306; 99.704% identity (99.704% similar) in 338 aa
      overlap (30-367:2-339)

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      .....
gi|115 MTFVRNAWYVAALPEELSEKPLGRTILDTPLA
      10      20      30

      70      80      90      100     110     120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNGARPA
      .....
gi|115 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNGARPA
      40      50      60      70      80      90

      130     140     150     160     170     180
DMO+27 SLNVRSPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD
      .....
gi|115 SLNVRSPVVERDALIWIPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD
      100     110     120     130     140     150

      190     200     210     220     230     240
DMO+27 NLMDLGHAQYVHRANAQTDAFDRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGANTP
      .....
gi|115 NLMDLGHAQYVHRANAQTDAFDRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGANTP
      160     170     180     190     200     210

      250     260     270     280     290     300
DMO+27 VDAWNDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTHILTPETEASCHYFFGSSSRNFGI
      .....
gi|115 VDAWNDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTHILTPETEASCHYFFGSSSRNFGI
      220     230     240     250     260     270

      310     320     330     340     350     360
DMO+27 DDPEMDGVLRSWQAQALVKEDKVVVEAIERRRAYVEANGIRPAMLSCEAAVRVSREIEK
      .....
gi|115 DDPEMDGVLRSWQAQALVKEDKVVVEAIERRRAYVEANGIRPAMLSCEAAVRVSREIEK
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      280      290      300      310      320      330

DMO+27 LEQLEAA
      .....
gi|115 LEQLEAA

>>gi|148502355|gb|ABQ70609.1| Vanillate monooxygenase [S (351 aa)
      initn: 881 initl: 344 opt: 912 Z-score: 1117.0 bits: 215.2 E(): 3.7e-53
      Smith-Waterman score: 912; 42.813% identity (68.807% similar) in 327 aa
      overlap (31-356:9-330)

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      .....
gi|148 MGGETSGNFLRNAWYMFAGGEEVADAPLGRTIAGEELV
      10      20      30

      70      80      90      100     110     120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNGARPA
      .....
gi|148 CFRGKDGVLV-LADRCPHRFVPLSLGVSADGVLECAHYGLRFSGDGRCMFNPLGDP--PE
      40      50      60      70      80      90

      130     140     150     160     170     180
DMO+27 SLNVRSPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD
      .....
gi|148 RAVVRSPVVERDRVIWVWTGDPALADPDGIADFSFLADPARATVIGYAHVRADYQLAID
      100     110     120     130     140     150

      190     200     210     220     230
DMO+27 NLMDLGHAQYVHRANAQTDAFDRLEREVIVGDGEI-QALMKIPGGTPSVLMAKFLRGANT
      .....
gi|148 NLSDLTHVQFVHRDYQASEAYHRLVDDTW-QDGDVVHRSITFPNGRPAPFLQSFL-GPDK
      160     170     180     190     200     210

      240     250     260     270     280     290
DMO+27 PVDAWNDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTHILTPETEASCHYFFGSSSRNFG
      .....
gi|148 LIDFTMETRWTLPSNIKLSATVTEPGAPDQYLIQNSAHLVTPHADGSCHYFYAHSRDYG
      220     230     240     250     260     270

      300     310     320     330     340     350
DMO+27 IDDPMDGVLRSWQAQALVKEDKVVVEAIERRRAYVEANGIRPAMLSCEAAVRVSREIE
      .....
gi|148 VGDPEADEKIREWQRVGFGEQDKPVLEAQQRVVGHRDIMELEPVLPTDAGGVARRILA
      280     290     300     310     320     330

      360
DMO+27 KLEQLEAA
```

gi|148 QRIARERKGMLEAVGDQ  
340 350

>>gi|148500390|gb|ABQ68644.1| Vanillate monooxygenase [S (367 aa)  
initn: 754 initl: 572 opt: 832 Z-score: 1018.7 bits: 197.1 E(): 1.1e-47  
Smith-Waterman score: 832; 38.841% identity (66.377% similar) in 345 aa  
overlap (31-367:3-347)

	10	20	30	40	50	60
DMO+27	MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRN	AWYVAALPEELSEKPLGRTILDTPLA				
		.....	.....	.....	.....	.....
gi 148			MVYLRNAWYVAAWSDEVSDNLLTRILNEQVL			
			10 20 30			

	70	80	90	100	110	120
DMO+27	LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHNGGARPA					
	...	...	.....	.....	.....	.....
gi 148	LYRTEAGELVATANTCPHRFAPLHLGKVVGDAIECPYHGLRFNGEGRCVFNPDGDGRIPA					
	40 50 60 70 80 90					

	130	140	150	160	170	180
DMO+27	SLNVRSPVPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD					
	.....	.....	.....	.....	.....	.....
gi 148	GARLRTYPIITERLGAAWIWMGDPARADLAMIPDFEFLEDPSYRTVKGLVHVRANYRYIND					
	100 110 120 130 140 150					

	190	200	210	220	230
DMO+27	NLMDLGHAGYVHRANAQTDADFRLEREVIVGDG-EIQA-LMKIPGGTPSV--LMAKFLRG				
	....	...	.....	.....	.....
gi 148	NLMDEAHLHMVHHNSLACDMVRRAKTELVKDEGGTIWANRYGRDGAPPAIFDMMWRMTRG				
	160 170 180 190 200 210				

	240	250	260	270	280	290
DMO+27	A-NTPVDANWDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTHILTPETEASCHYFFGSS					
	.....	.....	.....	.....	.....	.....
gi 148	DYEGTMDHWVEGGWKAPCFVRNNTGVVLHGRPRDEGLETKNAHLTPETDTTTHYFWAIC					
	220 230 240 250 260 270					

	300	310	320	330	340	350
DMO+27	RNFGIDDPEDMGVLRWQAQALVKEDKVVEAIEERRRAYVEANGIRPAMLSCEAAVRVS					
	.....	.....	.....	.....	.....	.....
gi 148	RNFRITDDAELDQGIQTGYEAFVHDEDEVMLNAVQEAMGDFWFSMKPALLQADIGAVELR					
	280 290 300 310 320 330					

	360
DMO+27	REIEKL---EQLEAA
	.....
gi 148	RTLDRMIAAEQAEQAGQADRPQPARSAEAVG
	340 350 360

>>gi|148499658|gb|ABQ67912.1| Vanillate monooxygenase [S (359 aa)  
initn: 800 initl: 800 opt: 816 Z-score: 999.3 bits: 193.5 E(): 1.3e-46  
Smith-Waterman score: 816; 40.785% identity (67.069% similar) in 331 aa  
overlap (30-356:2-328)

	10	20	30	40	50	60
DMO+27	MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRN	AWYVAALPEELSEKPLGRTILDTPLA				
		.....	.....	.....	.....	.....
gi 148			MTFLRNAWYAAAWSSELADGTLARTFLDEPVV			
			10 20 30			

	70	80	90	100	110	120
DMO+27	LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHNGGARPA					
	...	...	.....	.....	.....	.....
gi 148	LFRGEDGKAVALADMCPHRFAPLSLGRIGGDTIRCPYHGLVFDKMGACVHNPHGRGVRS					
	40 50 60 70 80 90					

	130	140	150	160	170	180
DMO+27	SLNVRSPVPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD					
	.....	.....	.....	.....	.....	.....
gi 148	SLSVRSYPVLERDSVLWIWMGDAALAGATPPPSFAFLDKDGWATIRGMLGVGANYELVTD					
	100 110 120 130 140 150					

	190	200	210	220	230
DMO+27	NLMDLGHAGYVHRANAQTDADFRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGAN-T				
	.....	.....	.....	.....	.....
gi 148	NLMDLSHAEFLHPFIAPEGSAAGIRYRAEQDDDRVAIIHDMPD-QPNTPLFELLGKTVT				
	160 170 180 190 200 210				

	240	250	260	270	280	290
DMO+27	PVDANWDIRWNKVSAM-LNFIAVA--PEGTPKEQSIHSRGTHILTPETEASCHYFFGSSR					
	.....	.....	.....	.....	.....	.....
gi 148	RIDGYANTYWEAPANMRLETCAIAIEPADGGRAEMLQA--HLLTPETETSTHYFWAISR					
	220 230 240 250 260					

	300	310	320	330	340	350
DMO+27	NFGIDDPEDMGVLRWQAQALVKEDKVVEAIEERRRAYVEANGIRPAMLSCEAAVRVSR					
	.....	.....	.....	.....	.....	.....
gi 148	DLCLDDQEAMLRFGIDAARNEDEPMIQAQVQGRMRGRPLMDMSPALLPMDEAAVRARR					
	270 280 290 300 310 320					

	360
DMO+27	EIEKLEQLEAA
gi 148	ILARRIAEEQKARAVEARDEGQPAAHACAAE
	330 340 350

>>gi|148499796|gb|ABQ68050.1| Vanillate monooxygenase [S (338 aa)  
initn: 762 initl: 338 opt: 813 Z-score: 996.0 bits: 192.8 E(): 2e-46  
Smith-Waterman score: 813; 39.535% identity (65.407% similar) in 344 aa  
overlap (28-365:1-335)

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      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      .. .. : : : : : : : : : : : : : : : : : :
gi|148      MSKDIRNLWYVAALSTEIADGPVGRRICSLPVV
      10      20      30

      70      80      90      100     110     120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNARPA
      .. .. : : : : : : : : : : : : : : : : : :
gi|148 LYRERSGAVAALFDRCPHRFVPLSRGCEGDRLCVGYHGLAYDGAGKCVANPQGTVTR--
      40      50      60      70      80      90

      130     140     150     160     170     180
DMO+27 SLNVRSFPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD
      .. .. : : : : : : : : : : : : : : : : : :
gi|148 SLDVRSFPVEERHGLVWIWMGDPALRDTVAIPDFSLLDRPAMPQYGYMWTAAHFELMTD
      100     110     120     130     140     150

      190     200     210     220     230
DMO+27 NLMDLGHAQYVHRANAQTDAFD-----RLEREVIVGDGEIQALMKIPGGTPSVLMAKFL
      .. .. : : . : : : : : : : : : : : : : : :
gi|148 NIMDLSHIEFLHADTLGTEKIRDAKVQARVEGETVYSGRTVHDEI-----LPPFLEGSFQ
      160     170     180     190     200

      240     250     260     270     280     290
DMO+27 RGANTPVDAWNDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTHILTPETEASCHYFFGSGS
      .. .. : : : : : : : : : : : : : : : : : :
gi|148 TGGR-PVTRSLSVRWNPALMLLTVGVDPA-PEKAPRETfNMHfITPETSTtCHYfWAA
      210     220     230     240     250     260

      300     310     320     330     340     350
DMO+27 SRNFGIDDPEDMGVLRSWQAQALVKEDKVVVEAIERRRAYVEANGIRPAMLSCEAAVRV
      .. .. : : : : : : : : : : : : : : : : : :
gi|148 TRPYGPDDPEWDRRLREGLERAFRTEDKPMIEAQQLVTGEADLLDLKPALFRGDGAATHA
      270     280     290     300     310     320

      360
DMO+27 SREIEKLEQLEAA
      . . . . .
gi|148 RRILTQLRRRAEEEA
      330

>>gi|148502359|gb|ABQ70613.1| Vanillate monooxygenase [S (350 aa)
  initn: 770 init1: 418 opt: 799 Z-score: 978.6 bits: 189.6 E(): 1.9e-45
Smith-Waterman score: 799; 37.278% identity (65.385% similar) in 338 aa
overlap (30-365:5-336)

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      .. : : : : : : . . : : . . : :

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gi|148      MSDRSFPLNCWYMAAWADEVRDILLARRLFGRPIV
      10      20      30

      70      80      90      100     110     120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNARPA
      . : : : : : : : : : : : : : : : : : : :
gi|148 MARFHDGAAVAFDDRCPHRFAPLSLGRKGDRIECGYHGLQFGRSGACIANPGGGGHFPP
      40      50      60      70      80      90

      130     140     150     160     170
DMO+27 SLNVRSFPVVERDALIWICPGDPALADPGAIPDFGCRVDPAA--YRTVGGYGHVDCNYKLL
      . : : : : : : : : : : : : : : : : : : :
gi|148 GTRTRAYPLVERHRILWIWPGDPALADEGTIPDLAL-IPPAGGHDNIGNYLHVKANWLLLE
      100     110     120     130     140     150

      180     190     200     210     220     230
DMO+27 VDNLMDLGHAQYVHRANAQTDAFDRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGAN
      .. : : . . . . . : : : : : : : : : :
gi|148 TDNIMDLTHVGFLHDGSLGNATMRAAEVKVSEQDGTIRAVLWMPD-----TLCGFGPMQG
      160     170     180     190     200

      240     250     260     270     280     290
DMO+27 TPVDAWNDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTHILTPETEASCHYFFGSSRNf
      : : : : : : : : : : : : : : : : : : : :
gi|148 QPCDQWNNVVMWMAPIIMMDFGAVPPGAEPIDKGAYAFHIFTPETEQSTHYFFGSSGSY
      210     220     230     240     250     260

      300     310     320     330     340     350
DMO+27 GIDDPEDMGVLRSWQAQALVKEDKVVVEAIERRRAYVEANGIRPAMLSCEAAVRVSREI
      : : . . . : : : : : : : : : : : : : :
gi|148 GDDEAWIPAMVREAQSRVFLAEDNPMVEGVADRMGGEDFWSLKPAILPSDAAAIRVRRRI
      270     280     290     300     310     320

      360
DMO+27 EKLEQLEAA
      . . . :

gi|148 AQMCREERSAVIADKVNLVTA
      330     340     350

>>gi|148500415|gb|ABQ68669.1| Vanillate monooxygenase [S (362 aa)
  initn: 776 init1: 776 opt: 793 Z-score: 971.0 bits: 188.3 E(): 5e-45
Smith-Waterman score: 793; 38.166% identity (65.385% similar) in 338 aa
overlap (30-367:2-339)

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      .. : : : : : : . . : : . . : :
gi|148      MSFLRNAWYVAGWSGDLGPAPRRIRVLGEWIA
      10      20      30

      70      80      90      100     110     120

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DMO+27 GQC<sup>VH</sup>NPHGNGARPASLNVRSFPVVERDALIWIICPGDPALADPGAIPDFGCRVDPA-YRT  
.:.:. .:..: . :.:.:.:. .:..: . :.:.:. .:..: .:..: .:..:

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gi|148 GKCVLNPHGNRILPTAAVRAFPVIERHGMIIWMGEHDLADPSRIPDFS-YLDAADQRT
160      170      180      190      200      210

      170      180      190      200      210      220
DMO+27 VG-GYGHVDCNYKLLVDNLMDLGHAQYVHRANAQTDADFRLEREVI--VGdgeIQALMKI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|148 RGAGYLPTRANYQLLTDNILDASHADYLNH-ALLDSGGTRHEAPRVQELGDGSVEVSWTW
220      230      240      250      260      270

      230      240      250      260      270      280
DMO+27 PGGTPSVLMAKFLRGANTPVDANDIRWNKVSAMLNFIAPAEGTPKEQSIHSRGTHILT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|148 GPASPMKFLSH--MYAPGAEVHTRLAVRWHPASAMHLRISSAAEGEELDQGLQAEAMHMT
280      290      300      310      320      330

      290      300      310      320      330      340
DMO+27 PETEASCHYFFGSSRNFGIDDPEDMGVLRSWQAQALVKEDKVVVEAIERRA--YVEANGI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|148 PETARQTHYFYGGVRSFDVANDAYTAAFLEGARRAFADKPMIEAVQANMGDETDIFAM
340      350      360      370      380      390

      350      360
DMO+27 RPAMLSCEAAVRVSREIEKLEQLEAA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|148 RPLGLIGDAGGVVRERLRRLIAAERHP
400      410      420

>>gi|87135570|gb|ABD26312.1| Rieske (2Fe-2S) protein [No (356 aa)
  initn: 768 init1: 357 opt: 757 Z-score: 927.1 bits: 180.1 E(): 1.4e-42
Smith-Waterman score: 757; 36.571% identity (66.000% similar) in 350 aa
overlap (18-365:7-350)

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILTDTPLA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|871 MSGGEPVFKLS--AKPAATYLRNTWYVAGWASDLAGEPQQRTFLEEPVA
10      20      30      40

      70      80      90      100      110      120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNGARPA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|871 LFRDGHGEAKAIGGRCPHRFAPLGHGSVVDGALMCPYHGLRFDDGGRVHNPHPGGHLFD
50      60      70      80      90      100

      130      140      150      160      170      180
DMO+27 SLNVRSFPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|871 ARQ-RVYPLVERHALLWIWMGDAKADPASIPDFSWLSDPWEAVRGATVAEGHFELYSD
110      120      130      140      150      160

      190      200      210      220      230
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DMO+27 NLMDLGHQAQYVHRANAQTDADFRLEREVI--GDGEIQALMKIPGGTPSVLMAKFLRGANT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|871 NILDLSHANFVHPALVAS-AFTEGERKFWQDGDNVFAEYVRL--NDELSVGISAVMGTEGR
170      180      190      200      210      220

      240      250      260      270      280      290
DMO+27 PVDANDIRWNKVSAM-LNFIAPAEGTPKEQSIHSRGTHILTPEEASCHYFFGSSRN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|871 PQDFYGMVWHAPAVLYDFRAGEP-GTPREQCTLLPSLHAFPTPTDTHYFWATARDY
230      240      250      260      270      280

      300      310      320      330      340      350
DMO+27 GIDDPEDMGVLRSWQAQALVKEDKVVVEAIERRRAYVEANGIRPAMLSCEAAVRVSREI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|871 RLGDAEFTAGMRAALEFAFEQEDMPIIRDShRLMRGEDFWALRPLILGGGGGVARRML
290      300      310      320      330      340

      360
DMO+27 EKLEQLEAA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|871 QRLIERERQDDAA
350

>>gi|115284366|gb|ABI89882.1| Vanillate monooxygenase [B (366 aa)
  initn: 743 init1: 478 opt: 756 Z-score: 925.7 bits: 179.9 E(): 1.7e-42
Smith-Waterman score: 756; 37.101% identity (65.217% similar) in 345 aa
overlap (31-367:11-351)

      10      20      30      40      50
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPL--GRTILTDTPL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 MRPQGNMKRPFLRNAWYVAAWDSEVKADELFFQRTLLNESV
10      20      30      40

      60      70      80      90      100      110
DMO+27 ALYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNGAR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 LLFRNDRGEVQAVSNRCPHRFAPLHLGKKLPNGVQCPYHGLEFDGSGQCTRNPHG
50      60      70      80      90      100

      120      130      140      150      160      170
DMO+27 ASLNVRSFVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGG--YGHVDCNYKLL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 KAAQLKTYPVVEKYSLIWIWMGEASIDSSKIPDFSC-LDPQLSHVAKRYLHVKNYVLE
110      120      130      140      150

      180      190      200      210      220      230
DMO+27 VDNLMDLGHQAQYVHRANAQTDADFRLEREVI--GDGEIQALMKIPGGT--PSVLMAKFLRGA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 TDNILDLSHIQVLPHTLGSSSVADAITSVVQEGNTVYSMRQTVGDMPEFLYRQRRIPV
160      170      180      190      200      210
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      240      250      260      270      280      290
DMO+27 NTPVDAWNDIRWNKVSAMLNFI AVAPEGTPKEQSIHSRGTHILTPETEASCHYFFGSSRN
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115  GTPVDRWIDVRWDAPAHMLLDAGSVATGKPRSEGVSNKIAHIFSPETASTTHYWFVAVSNP
      220      230      240      250      260      270

      300      310      320      330      340      350
DMO+27 FGIDDPEDMGVLRWQ-AQALVK---EDKVVVEAIERRRAYVEANGIRPAMLSCDEAAV
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115  LSMGD---DGMQRAEDFVSGLVHFPQNE DLPMLEAQQH MIGEADFWSLKPVLLAGDAAA
      280      290      300      310      320      330

      360
DMO+27 RVSREIEKLEQLEAA
      . : : : : : : :
gi|115  RARRILDKLLADEEATMQTIVSKSEQRFNK
      340      350      360

>>gi|148501501|gb|ABQ69755.1| Vanillate monooxygenase [S (347 aa)
      initn: 701 initl: 465 opt: 739 Z-score: 905.2 bits: 176.0 E(): 2.3e-41
Smith-Waterman score: 739; 36.070% identity (66.569% similar) in 341 aa
overlap (31-367:3-340)

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|148  MAYLLNRWYAAAWSGEVAREPFMRVLFDPKPVL
      10      20      30

      70      80      90      100      110      120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNGARPA
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|148  FYRTESGDVTALSNVCPHRFAPLNRGKLFGDAIRCPYHGLRFGPDGRCVQNPIGKGLLPA
      40      50      60      70      80      90

      130      140      150      160      170
DMO+27 SLNVRSPVVERDALIWICPGDPALADPGA-IP-DFGCRVDPAYRTVGGYGHVDCNYKLL
      . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|148  KAQLTRYATIEAHGVIWVHG-PAPADATKLVPPDFLDEHD-RYDFVDGYIAIDANYALV
      100      110      120      130      140      150

      180      190      200      210      220      230
DMO+27 VDNLMDLGHQAQYVHRANAQTDAFDRLEREVIVGDGE-IQALMKIPGGTPSVLM-AKFLRG
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|148  SDNLIDLSHAFLHPNLNPGANQVR-RFTAQTDGETVRALNARPGEPPTVLLRAALGDG
      160      170      180      190      200

      240      250      260      270      280      290
DMO+27 ANTPVDAWNDIRWNKVSAMLNFI AVAPEGTPKEQSIHSRGTHILTPETEASCHYFFGSSR
      . . : : : : : : . . . : : : : : : : : : : : : : : : : : : : : : . :

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gi|148  VGDITIDMWSNVTNPPALLCVEVGGTARGAPKEAGVNTMAAHLITPETAVRSHYFWKLGR
      210      220      230      240      250      260

      300      310      320      330      340      350
DMO+27 NFGIDDPEDMGVLRWQQAALVKEDKVVVEAIERRRAYVEANGIRPAMLSCDEAAVRVSR
      . : : : : : . : : : : : : : : : : : . : : : : : : : : : : : : : : : :
gi|148  TYRRGDPDFSARVQAMVSSAFVEEDKPIIEAQQHNMGDVGFQQLDPVYLES DGAAARARR
      270      280      290      300      310      320

      360
DMO+27 EIEKLEQLEAA
      . : : : : : : :
gi|148  IMNRLLAENAADALIAPV
      330      340

>>gi|148501508|gb|ABQ69762.1| Vanillate monooxygenase [S (342 aa)
      initn: 696 initl: 652 opt: 727 Z-score: 890.6 bits: 173.3 E(): 1.5e-40
Smith-Waterman score: 727; 36.471% identity (63.529% similar) in 340 aa
overlap (31-367:3-340)

      10      20      30      40      50
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEEL-SEKPLGRTILDTP
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|148  MPFLRNCWYVAAWDDEIPAEGTFHRRILNEDI
      10      20      30

      60      70      80      90      100      110
DMO+27 ALYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNGARP
      . : . : : : : : : : : : : : : : : : : . : . : : : : : : : : : : : : :
gi|148  LLARDGEGEVRLNRNRCPHRFAPLSIGTRTGDAIECAYHGLRFGLDGRCLSNPHGSGQIP
      40      50      60      70      80      90

      120      130      140      150      160      170
DMO+27 ASLNVRSPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVG-YGYHVDNYKLL
      . : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|148  ANARVQTYPPVVRHLLAWIWMGDPDKADPSAIPDL-VGLDPERFAINRGYMHPTANYEYM
      100      110      120      130      140      150

      180      190      200      210      220      230
DMO+27 VDNLMDLGHQAQYVHRANAQTDAFDRLEREVIVGDGEIQA-LMKIPGGTPSVLMAKFLRGA
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|148  ADNIMDLGHIEFLHKGLLGSEAVRRAEIEVKQAGNVVHSNRLTRDEILPTALELLY-ETE
      160      170      180      190      200      210

      240      250      260      270      280      290
DMO+27 NTPVDAWNDIRWNKVSAMLNFI AVAPEGTPKEQSIHSRGTHILTPETEASCHYFFGSSRN
      . : : : : : . : : : : : . : : : : : . : : : : : . : : : : : . : : : :
gi|148  GKPVDRLDVTWYPGNMQLVVGVTGAGQPERIGREAPGAHLMTPETDDSTHYFWSNARD
      220      230      240      250      260      270

      300      310      320      330      340      350

```



```
DMO+27 FGIDDPEDMGVLRWQAQALVKEDKVVVEAIEERRRAYVEANGIRPAMLSCEAAVRVSRE
      :  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
gi|148 FRRDDQLHAALDQGFQLAFEDHDKPMIMAQHDAIGGEDFWEMHVPVILEGDAGAVRARRI
      280      290      300      310      320      330

      360
DMO+27 IEKLEQLEAA
      ....  ::  ::
gi|148 LRKLIKEEQAVG
      340

>>gi|206587490|emb|CAQ18072.1| vanillate o-demethylase o (342 aa)
      initn: 660 init1: 324 opt: 727 Z-score: 890.6 bits: 173.3 E(): 1.5e-40
      Smith-Waterman score: 727; 38.040% identity (62.824% similar) in 347 aa
      overlap (31-365:2-340)

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      .....  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
gi|206      MFLKNAWYVACTPDEIADKPLGRRICGERMV
      10      20      30

      70      80      90      100      110      120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHNGNARPA
      ..  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
gi|206 FYRGPEGKVAALEDFCPHRGAPLSLGFVRDGHVCGYHGLTMKADGKCASMP---GQRVG
      40      50      60      70      80

      130      140      150      160      170
DMO+27 SLN-VRSFPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLV
      ..  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
gi|206 GFPCIRQFPVVERYGFIWVWPGDAELADPAQIHHLWEAESKAWAYGGGLYHIQCDYRLMI
      90      100      110      120      130      140

      180      190      200      210      220      230
DMO+27 DNLMDLGHQAQYVHRAN-AQTDAFDRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGA-
      ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
gi|206 DNLMDLTHETYVHATSIGQPEIEEAAPQTRVEGDTVVTSRF-MENIMPPFPWATALRGAG
      150      160      170      180      190      200

      240      250      260      270      280
DMO+27 ---NTPVDAWDIRWNKVSAMLNFIAVAPEG-----TPKEQSIHSRGTHILTPETEASCH
      ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
gi|206 LADNVPCDRWQICRFTPPSHVLIIEVGVAHAGKGGYDAGPEHRVGSIVVDFITPETETSIW
      210      220      230      240      250      260

      290      300      310      320      330      340
DMO+27 YFFGSSRNFGIDDPEDMGVLRWQAQALVKEDKVVVEAIEERRR-AYVEANGIRPAMLSCD
      ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
gi|206 YFWGMARNFRVDDAALTDITRQGGQK-IFGEDLDMLESQQRNLLAYPERNLLK---LNID
      270      280      290      300      310      320
```

```
      350      360
DMO+27 EAAVRSREIEKLEQLEAA
      ....  ::  ::  ::
gi|206 AGGVQSRRVLERLLEREQQ
      330      340

>>gi|148501505|gb|ABQ69759.1| Vanillate monooxygenase [S (345 aa)
      initn: 431 init1: 431 opt: 721 Z-score: 883.2 bits: 171.9 E(): 3.9e-40
      Smith-Waterman score: 721; 35.756% identity (64.826% similar) in 344 aa
      overlap (30-367:2-339)

      10      20      30      40      50
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSE-KPLGRTILDTPL
      .....  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
gi|148      MSFLRNCWYVAGWADELAEGAPLARTIAGEAI
      10      20      30

      60      70      80      90      100      110
DMO+27 ALYRQPDGV--VAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDG-GGQCVHNPHNGNA
      ..  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
gi|148 LFWR--DGASLFAVADRCPHRLAPLHMGRTDGATVRCGYHGLAFDGVSGRCTDNPH--GA
      40      50      60      70      80

      120      130      140      150      160      170
DMO+27 RPASLNVRSPFVVERDALIWICPGDPALADPGAIPDFGCRVDPAA--YRTVGGYGHVDCNY
      ..  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
gi|148 ITSALAIRTYPCVERHRILWVWTGDPDRADPADIPDMGF-VDRAGEHAFSGGYMHTAAGH
      90      100      110      120      130      140

      180      190      200      210      220      230
DMO+27 KLLVDNLMDLGHAQYVHRANAQTDAFDRLEREVIVGDGEIQALMKIPGGTPSV-LMAKFL
      ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
gi|148 KLLLEDNILDLSHADYLHPATLGGSITRT-RAHVEERGDAVFVQWLASGEPAPIFRPEM
      150      160      170      180      190      200

      240      250      260      270      280      290
DMO+27 RGANTPVDAWDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTHILTPETEASCHYFFGS
      ..  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
gi|148 PDPLIDTDMWTEVLWHPDGMILRTGATPMGRPRAEGIDTWNHVMTPETATTTTHYFYCN
      210      220      230      240      250      260

      300      310      320      330      340      350
DMO+27 SRNFGIDDPEDMGVLRWQAQALVKEDKVVVEAIEERRRAYVEANGIRPAMLSCEAAVRV
      ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
gi|148 SRNYRTDDPAYNAAMAAGLRIAFEQEDKPMIEAQQRALGEADLFDLRPALLAIDNGSTRA
      270      280      290      300      310      320

      360
DMO+27 SREIEKLEQLEAA
      :  ::  ::
```

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```

initn: 653 initl1: 320 opt: 717 Z-score: 878.3 bits: 171.0 E(): 7.3e-40
Smith-Waterman score: 717; 37.752% identity (62.248% similar) in 347 aa
overlap (31-365:2-340)

      10          20          30          40          50          60
DMO>27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRITLDTPLA
      .....: .....: .....: .....: .....: .....: .....: .....:
gi|206          MFLKNAWYVACTPDEIADKPLGRRICGERMV
              10          20          30

      70          80          90          100         110         120
DMO>27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGLHQCYPYHGLEFDGGGQCVHNPHNGARPA
      .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|206 FYRGPPEGKMAALEDPCPHRGAPLSLGFVRDGHLCVGYHGLTMKADGKCASMP---GQRVVG
              40          50          60          70          80

      130         140         150         160         170
DMO>27 SLN-VRSFPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLV
      .. .....: .....: .....: .....: .....: .....: .....: .....:
gi|206 GFPCIRQFPFVVERYGFIEWVWPGDAELADPAQIIHLEWAESKAWAYGGGLYHIQCDYRLMI
              90          100         110         120         130         140

      180         190         200         210         220         230
DMO>27 DNLMDLGHAAQYVHRAN-AQTDAFDRLEREVVGDEIGIQLMKIPGGTPSVLMAKFLRGA-
      :.....: .....: .....: .....: .....: .....: .....: .....:
gi|206 DNLMDLTHETYVHATSIGQPEIEEAAPQTRVEGDTVTSRFR-MENIMPPFPFWATALRGAG
              150         160         170         180         190         200

      240         250         260         270         280
DMO>27 ---NTPVDAWNDIRWNKVSAMLNFIAVA---PEGTPKEQSIHSRGTI---LTPPETEASCH
      :.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|206 LADNVPCDRWQICRFTPPSHVLIEVGVAHASKGGYDAGPEHRVGSIVVDFIIPETETSIW
              210         220         230         240         250         260

      290         300         310         320         330         340
DMO>27 YFFGSSRRNFGIDDPEDMGVLRSWQAQALVKEDKVVEAIERRR-AYVEANGIRPAMLSCD
      :.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|206 YFWGMARNFRVDDAALTDTRIQQGQK-IFGEDLDMLESQQRNLLAYPERNLLK---LNID
              270         280         290         300         310         320

      350         360
DMO>27 EAAVRVSREIEKLEQLEAA
      .: .: .: .: .: .:
gi|206 AGGVQSRRLVERLLERERQ
              330         340

>>gi|171996652|gb|ACB67570.1| Vanillate monooxygenase [B (359 aa)
initn: 650 initl1: 306 opt: 710 Z-score: 869.4 bits: 169.5 E(): 2.3e-39
Smith-Waterman score: 710; 37.356% identity (61.494% similar) in 348 aa
overlap (31-367:2-342)

```

>>gi|171996652|gb|ACB67570.1| Vanillate monooxygenase [B (359 aa)  
initn: 650 init1: 306 opt: 710 Z-score: 869.4 bits: 169.5 E(): 2.3e-39  
Smith-Waterman score: 710; 37.356% identity (61.494% similar) in 348 aa  
overlap (31-367:2-342)

```

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|171      MFLKNAWYVACTPDEIDGKPLGRKICNEPMV
      10      20      30
```

```

      70      80      90      100     110     120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHNGGARPA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|171 FYRAADGGQVAALEDFCPHRGAPLSLGFVRDGLVLCGYHGLEMGCGNGKATGMP---GQRVVG
      40      50      60      70      80
```

```

      130     140     150     160     170
DMO+27 SLN-VRSFPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|171 GFPPIRSFPVVERYGF IWVWPGDASEADPARLPALSWAEDPAWAHGGGLYHIRCDYRLMI
      90      100     110     120     130     140
```

```

      180     190     200     210     220     230
DMO+27 DNLMDLGHAQYVHRANAQTDAFDRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGA--
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|171 DNLMDLTHETVYHATSIGQKEIDEAPPKTTANGDEVVTSRFMQNVMPPPFWRMALRGNGL
      150     160     170     180     190     200
```

```

      240     250     260     270     280     290
DMO+27 --NTPVDANWDIRWNKVSAMNFIAPAPEG-----TPKEQSIHSRGTHILTPETEASCHY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|171 ADDVPVDRWQICRFTPPSHVMIEVGVAHAGGGYDAPAEKASSIVVDFITPETDTSIWY
      210     220     230     240     250     260
```

```

      300     310     320     330     340
DMO+27 FFGSSRNFGIDDPMDGVLRSWQAQALVKEDKVVVEAIERRRAYVEANGIRPAM-LSCDE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|171 FWGMARNFRPDDHALTAETIREGQGKIFA-ED---LEMLERQQLNLEQWPDRLKLLKNIDA
      270     280     290     300     310     320
```

```

      350     360
DMO+27 AAVRVSREIEKLEQLEAA
      : : : : : : : :
gi|171 GGVLSRKVIERLLAAEQASSPQRPRVIPVAQIKEAS
      330     340     350
```

>>gi|91795567|gb|ABE57706.1| Rieske (2Fe-2S) protein [Ch (353 aa)  
initn: 631 init1: 299 opt: 707 Z-score: 865.9 bits: 168.8 E(): 3.6e-39  
Smith-Waterman score: 707; 35.942% identity (62.319% similar) in 345 aa  
overlap (31-366:2-341)

```

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|917      MFPKNTWYVACTPDEIEEKPLGRTICNEQIV
```

```

      10      20      30
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHNGGARPA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|917 FFRAEGGQVAAVEDFCPHRGAPLSLGFVRDGLVLCGYHGLEMGCDGKCSSMP-GQRVRGF
      40      50      60      70      80      90
```

```

      130     140     150     160     170     180
DMO+27 SLNVRSPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|917 P-SIHAYPVVERHGFIWVWPGDAEQADPDQIPELHWANDPEWAYGGGLYHINCDYRLMID
      100     110     120     130     140
```

```

      190     200     210     220     230
DMO+27 NLMDLGHQAQYVHRANAQTDAFDRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGA--
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|917 NLMDLTHETVYHASSIGQPEIEEAAPETKVNNGDEVLTIRHMENIPAPPFQWSALRGNNLA
      150     160     170     180     190     200
```

```

      240     250     260     270     280     290
DMO+27 --TPVDANWDIRWNKVSAMNFIAPAPEG-----TPKEQSIHSRGTHILTPETEASCHY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|917 DDVPVDRWQICRFTPPSHVILIEVGVAHAGGGYDAPADAKASSIVVDFITPETETSIWY
      210     220     230     240     250     260
```

```

      300     310     320     330     340     350
DMO+27 FFGSSRNFGIDDPMDGVLRSWQAQALVKEDKVVVEAIERRRAYVEANGIRPAMLSCEAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|917 WGMARNFNPQDEALTEQIREGQGKIFA-EDLEMLLES--QQRNLLRYPDRRLMLNIDGGG
      270     280     290     300     310     320
```

```

      360
DMO+27 VRVSREIEKLEQLEAA
      : : : : : : : :
gi|917 VQARRVIDRILKAEAEANAQPPQAATAS
      330     340     350
```

>>gi|91693685|gb|ABE36882.1| Vanillate demethylase [Burk (353 aa)  
initn: 638 init1: 262 opt: 706 Z-score: 864.7 bits: 168.6 E(): 4.2e-39  
Smith-Waterman score: 706; 36.095% identity (66.272% similar) in 338 aa  
overlap (31-356:3-336)

```

      10      20      30      40      50
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKP-LGRTILDTPLA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|916      MEFLRNTWYAAGWSQDLAAGAMLGRTMLNLEQL
      10      20      30
```

```

      60      70      80      90      100     110
DMO+27 ALYRQPDGVVAALLDICPHRFAPLSDGILVNG-HLQCPYHGLEFDGGGQCVHNPHNGGAR
```

```

      .:.:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:
gi|916  VLFRADDGTVSALSDDICPHRFAPLHLGKIVDGCRIQCAYHALEFDGTGACVKNPHGQKI
      40          50          60          70          80          90

      120      130      140      150      160      170
DMO+27  PASLNVRSFPVVERDALIWICPGDPALADPGAIPDFGCRVDP--AYR-TVGGYGHVDCNY
      .:.:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:
gi|916  PAAAKLQAYPVVEKHSLIWVWMGEQAAADPSVIPDFSM-LDPDSGFQVSRDLHMDASY
      100      110      120      130      140      150

      180      190      200      210      220      230
DMO+27  KLLVDNLMDLGHQAQYVHRANAQTDADFRLEREVIVGDGEIQALMKIPG-GTPSVLMAKFL
      .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:
gi|916  DLVVDNLMDLSHTAFLHDGILGSKYTIKADTSLEQTGETVKVTRLMPNVPVPGFFDLMFN
      160      170      180      190      200      210

      240      250      260      270      280      290
DMO+27  RGANTPVDAWNDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTHILTPETEASCHYFFGS
      .:.:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:
gi|916  RDGGI-VDYWTEIRWNLPGLMNNNTGVTLPGAPRSEGTGVYGMHFLTPTETDVCWYHFAA
      220      230      240      250      260      270

      300      310      320      330      340
DMO+27  ----SRNFGID-DPEMDGVLRWSQAQALVKEDKVVVEAIERRRAYVEANG-IRPAMLSCD
      .:.:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:
gi|916  VRQNPRTWGEPIDEIKESIDLRRYAFEEQDQWIIKA--QQQTILRAKGNLQPVSLSTD
      280      290      300      310      320

      350      360
DMO+27  EAAVRVSREIEKLEQLEAA
      .:.:  .:.:

gi|916  IGIERYKRILKAALVAERSGSTMAA
      330      340      350

>>gi|198040316|emb|CAR56301.1| vanillate O-demethylase o (359 aa)
      initn: 649 init1: 303 opt: 706 Z-score: 864.5 bits: 168.6 E(): 4.3e-39
Smith-Waterman score: 706; 36.494% identity (61.494% similar) in 348 aa
overlap (31-367:2-342)

      10      20      30      40      50      60
DMO+27  MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:
gi|198  MFLKNAWYVACTPDEIDGKPLGRKICNESMV
      10      20      30

      70      80      90      100      110      120
DMO+27  LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPNGHNGARPA
      .:.:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:
gi|198  LYRATDGQVAALEDFCPHRGAPLSLGVVRDGVLCGYHGLEMGCGNKGTAGMP---GQRVVG
      40      50      60      70      80
```

```

      130      140      150      160      170
DMO+27  SL-NVRSFPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLV
      .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:
gi|198  GFPSIRSFPFAVERYGFVWVWPGDPSEADPAKLPALAWAEDPAWAHGGGLYHIRCDYRLMI
      90      100      110      120      130      140

      180      190      200      210      220      230
DMO+27  DNLMDLGHQAQYVHRANAQTDADFRLEREVIVGDGEIQALMKIPGGTSPVLMAKFLRGA--
      .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:
gi|198  DNLMDLTHETYVHASSIGQKEIDEAPPKTTSHGDEVVTSRFMENVMPPPFWRMALRGNGL
      150      160      170      180      190      200

      240      250      260      270      280      290
DMO+27  --NTPVDAWNDIRWNKVSAMLNFIAVAPEG-----TPKEQSIHSRGTHILTPETEASCHY
      .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:
gi|198  ADDVPVDRWQICRFTPPSHVMIEVGVVAHAGHGGYDAPANKKASSIVVDFITPETDTSIWY
      210      220      230      240      250      260

      300      310      320      330      340
DMO+27  FFGSSRNFGIDPEMDGVLRWSQAQALVKEDKVVVEAIERRRAYVEANGIRPAM-LSCDE
      .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:
gi|198  FWGMARNFRPDDHALTAEIREGQGKIFA-ED---LEMLERQQRNLEQWPERTLLKLNIDA
      270      280      290      300      310      320

      350      360
DMO+27  AAVRVSREIEKLEQLEAA
      .:.:  .:.:..:  .:.:

gi|198  GGVLSRKVIDRLLAEENAAARPQRPAIPVAHAREAS
      330      340      350

>>gi|134135372|gb|ABO56486.1| Vanillate monooxygenase [B (359 aa)
      initn: 635 init1: 295 opt: 701 Z-score: 858.4 bits: 167.4 E(): 9.4e-39
Smith-Waterman score: 701; 36.782% identity (60.920% similar) in 348 aa
overlap (31-367:2-342)

      10      20      30      40      50      60
DMO+27  MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:
gi|134  MFLKNAWYVACTPDEIDGKPLGRKICNESMV
      10      20      30

      70      80      90      100      110
DMO+27  LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPNGHNGARP
      .:.:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:
gi|134  FYRAADGRVAALEDFCPHRGAPLSLGFVRDGVLCGYHGLEMGCGNKGTAMPGQVRVGFP
      40      50      60      70      80      90

      120      130      140      150      160      170
DMO+27  ASLNVRSFPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLV
      .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:  .:.:..:
gi|134  A---IRSFVPVERYGFVWVWPGDASRADPAALPALTWADDPVWAHGGGLYHIRCDYRLMI
```

[illegible]

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210          220          230          240          250          260
      300      310          320      330          340      350
DMO+27 R-NFGIDDPEDMGVLRWSQAQ----ALVKEDKVVVEAIERRRAYVEANGIRPAMLSCEA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|148 RMNPIDHDPERDAEIRDQLSRVRKMAFAEQDGPMMEAQORLIQDPAVDTSRPALFDIDLG
      270      280      290      300      310      320

      360
DMO+27 AVRVSREIEKLEQLEAA
      : : : : :
gi|148 ASRFARRHDKMLKADVSA
      330      340

>>gi|89343834|gb|ABD68037.1| Rieske (2Fe-2S) protein [Rh (351 aa)
      initn: 596 initl: 289 opt: 690 Z-score: 845.1 bits: 164.9 E(): 5.2e-38
Smith-Waterman score: 690; 36.337% identity (63.372% similar) in 344 aa
overlap (31-361:2-336)

      10          20          30          40          50          60
DMO+27 MQVWPPIGKKKFETLSYLPLLTRDSRAMATFVRNAWYVAALPEELSEKPLGRITILDTPLA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|893      MFPKNTWYVAATPNEIDEKPLGRITICGERIA
      10          20          30

      70          80          90          100          110
DMO+27 LYRQDPDGVVAALLDICPHRFAPLSDSGILVNGHLQCPYHGLEFDGGGQCVHNPHNGAR--
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|893 FYRGEENKVAAVEDFCPHRGAPLSLGYVSEGLKVCYHGLEMGCQGKTIAMP-GQVRVGRF
      40          50          60          70          80          90

      120          130          140          150          160          170
DMO+27 PASLNVRSPFVVERDALIWIICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|893 PA---IKAYPVVERYGFIWVWPGDAAQADEAKIPHMAWYDNPEWAYGGGLYHINCDYRLM
      100          110          120          130          140

      180          190          200          210          220          230
DMO+27 VDNLMDLGHQAQYVHRANAQTDAFDRLE-REVIVGDGEIQALMKIPGGTSPVLMAKFLRGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|893 IDNLMDLTHETVHASSIGQKEIDETPCKTTVEGDTVVISRF-MSGIQQPPFVQWQMALRAN
      150          160          170          180          190          200

      240          250          260          270          280
DMO+27 ----NTPVDAWNDIRWNKVSAMLNFIAPAPEG-----TPKEQSIHSRGTHILTPETEASC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|893 HLADDPVPDRWQICRFTPPSHVMIEVGVAHQHGGGYDAPNDKKAYSVVVDFITPETETSI
      210          220          230          240          250          260

      290          300          310          320          330          340
DMO+27 HYFFGSSSRNFGIDDPEDMGVLRWSQAQALVKEDKVVVEAIERRRAYVEANGIRPA-MLSC

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360
DMO>27 AAVRVSREIEKLEQLEAA
... : : : : :
gi|142 GGVLSRKVIERLLADENASSPQRVPVIPVAQIKEAS
350 360 370 380

>>gi|105894856|gb|ABF78020.1| Rieske (2Fe-2S) region [Bu (359 aa)
initn: 632 initl: 296 opt: 688 Z-score: 842.5 bits: 164.5 E(): 7.2e-38
Smith-Waterman score: 688; 36.207% identity (60.920% similar) in 348 aa
overlap (31-367:2-342)

10 20 30 40 50 60
DMO>27 MQVWPPIGKKKFETLSYLPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
... : : : : :
gi|105 MFLKNAWYVACTPDEIDGKPLGRKICNESMV
10 20 30

70 80 90 100 110 120
DMO>27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCQVHNPHNGARPA
... : : : : :
gi|105 LYRAADGQVAALEDPCPHRGAPLSLGFVRDGVLCGYHGLEMGCGKPGAGMP---GQRVG
40 50 60 70 80

130 140 150 160 170
DMO>27 SL-NVRSEFPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLV
.. : : : : :
gi|105 GFPSIRSFPFAVERYGFVWVWPGDASEADPAKLPAWAEADPAWAHGGGLYHIRCDYRLMI
90 100 110 120 130 140

180 190 200 210 220 230
DMO>27 DNLMDLGHAAQYVHRANAQTDAFDRLEREIVGDGEIQALMKIPGGTPSVLMAKFLRGA--
... : : : : :
gi|105 DNLMDLTHETVYHASSIGQKEIDEAPPKTTSHGDEVVTSRFMENVMPPPFWRMALRGNGL
150 160 170 180 190 200

240 250 260 270 280 290
DMO>27 --NTPVDAWNDIRWNKVSAMLNFIAVAPEG----TPKEQSIHSRGTHILTPETEASCHY
. : : : . : : : :
gi|105 ADDIPVDRWQICRFTPPSHVMIEVGVAHAGHGGYDAPPNKKASSIVVDFITPETDTSIWY
210 220 230 240 250 260

300 310 320 330 340
DMO>27 FFGSSRNFGIDDPMDGVLRSWQAQALVKEDKVVEAIEERRRAYVEANGIRPAM-LSCDE
. : : : . : : : :
gi|105 FWGMARNFRPDDAALTAEIREGQKIFA-ED---LEMLERQQRNLEQWPERTLLKLNIDA
270 280 290 300 310 320

350 360
DMO>27 AAVRVSREIEKLEQLEAA
... : : : : :
gi|105 GGVLSRKVIDRLLAAEHAASSPQRVPVIPVAQVKAAS

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330      340      350

>>gi|116651336|gb|ABK11976.1| Rieske (2Fe-2S) domain pro (359 aa)
  initn: 632 init1: 296 opt: 688 Z-score: 842.5 bits: 164.5 E(): 7.2e-38
Smith-Waterman score: 688; 36.207% identity (60.920% similar) in 348 aa
overlap (31-367;2-342)

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      ..... :... :... :. . .
gi|116      MFLKNAWYVACTPDEIDGKPLGRKICNESMV
      10      20      30

      70      80      90      100     110     120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHNGGARPA
      :: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|116 LYRAADGQVALEDFCPHRGAPLSLGFVRDGVLCGYHGLEMGCNGKPAGMP---GQRVG
      40      50      60      70      80

      130     140     150     160     170
DMO+27 SL-NVRSFPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLV
      .. : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|116 GFPSIRSFPFAVERYGFVWVWPGDASEADPAKLPAWAEADPAWAGGGLYHIRCDYRLMI
      90      100     110     120     130     140

      180     190     200     210     220     230
DMO+27 DNLMDLGHQAQYVHRANAQTDADFRLEREVIVGDGEIQALMKIPGGTSPVLMKFLRGA--
      : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|116 DNLMDLTHETYVHASSIGQKEIDEAPPKTTSHGDEVVTSRFMENVMPPPFWRMALRGNGL
      150     160     170     180     190     200

      240     250     260     270     280     290
DMO+27 --NTPVDANWDIRWNKVSAMLNFIAPAPEG-----TPKEQSIHSGTHILTPETEASCHY
      . : : : . : : : . : : : : : : : : : : : : : : : : :
gi|116 ADDIPVDRWQICRFTPPSHVMIEVGVAHAGHGGYDAPPNKKASSIVVDFITPETDTSIWY
      210     220     230     240     250     260

      300     310     320     330     340
DMO+27 FFGSSRNFGIDDPEDMGVLRSWQAQALVKEDKVVVEAIEERRAYVEANGIRPAM-LSCDE
      : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|116 FWGMARNFRPDAAALTAIEIREGQKIFA-ED---LEMLERQQRNLEQWPERTLLKLNIDA
      270     280     290     300     310     320

      350     360
DMO+27 AAVRVSREIEKLEQLEAA
      . : . : : : : :
gi|116 GGVLSRKVIDRLLAAEHAASQRPVIPAQVKAAS
      330     340     350

>>gi|124876389|gb|EAY66379.1| Phenylpropionate dioxygena (359 aa)
  initn: 631 init1: 295 opt: 687 Z-score: 841.3 bits: 164.3 E(): 8.4e-38
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Smith-Waterman score: 687; 35.920% identity (60.920% similar) in 348 aa
overlap (31-367;2-342)

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      ..... :... :... :. . .
gi|124      MFLKNAWYVACTPDEIDGKPLGRKICNESMV
      10      20      30

      70      80      90      100     110     120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHNGGARPA
      :: : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|124 LYRTADGQIAALEDFCPHRGAPLSLGFVRDGVLCGYHGLEMGCNGKPAGMP---GQRVG
      40      50      60      70      80

      130     140     150     160     170
DMO+27 SL-NVRSFPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLV
      .. : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|124 GFPSIRSFPFAVERYGFVWVWPGDASEADPAKLPAWAEADPAWAGGGLYHIRCDYRLMI
      90      100     110     120     130     140

      180     190     200     210     220     230
DMO+27 DNLMDLGHQAQYVHRANAQTDADFRLEREVIVGDGEIQALMKIPGGTSPVLMKFLRGA--
      : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|124 DNLMDLTHETYVHASSIGQKEIDEAPPKTTSHGDEVVTSRFMENVMPPPFWRMALRGNGL
      150     160     170     180     190     200

      240     250     260     270     280     290
DMO+27 --NTPVDANWDIRWNKVSAMLNFIAPAPEG-----TPKEQSIHSGTHILTPETEASCHY
      . : : : . : : : . : : : : : : : : : : : : : : : : :
gi|124 ADDIPVDRWQICRFTPPSHVMIEVGVAHAGHGGYDAPPNKKASSIVVDFITPETDTSIWY
      210     220     230     240     250     260

      300     310     320     330     340
DMO+27 FFGSSRNFGIDDPEDMGVLRSWQAQALVKEDKVVVEAIEERRAYVEANGIRPAM-LSCDE
      : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|124 FWGMARNFRPDAAALTAIEIREGQKIFA-ED---LEMLERQQRNLEQWPERTLLKLNIDA
      270     280     290     300     310     320

      350     360
DMO+27 AAVRVSREIEKLEQLEAA
      . : . : : : : :
gi|124 GGVLSRKVIDRLLAAEHAASQRPVIPAQVKAAS
      330     340     350

>>gi|124899433|gb|EAY71276.1| Phenylpropionate dioxygena (347 aa)
  initn: 651 init1: 302 opt: 686 Z-score: 840.3 bits: 164.0 E(): 9.6e-38
Smith-Waterman score: 686; 35.613% identity (62.678% similar) in 351 aa
overlap (31-367;2-343)

      10      20      30      40      50      60
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DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      ..... :..... : ..
gi|124      MFLKNTWYVACTPDEFADKPLGRQICGERMV
              10      20      30

              70      80      90      100      110
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNP-HGNGARP
      ..... :..... : .. :..... : .. : ..
gi|124 FFRDANGTVAALEDFCPHRGAPLSLGTVRDGRLLVCGYHGLTMGADGKCVSMPCQRVGGIP
      40      50      60      70      80      90

      120      130      140      150      160      170
DMO+27 ASLNVRSPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLV
      : .. :..... :..... : .. : .. : .. : .. : .. : ..
gi|124 A---IRRYPAVERYGFVWVWPGDPAQADPATIHLRHWADDPGWAYGGGLYHIDCDYRLMI
      100      110      120      130      140

      180      190      200      210      220      230
DMO+27 DNLMDLGHQAQYVHRANAQTDAFDRLEREVIVGDGEIQALMK-IPGGTPSVLMAKFLRGA-
      :..... : .. : .. : .. : .. : .. : .. : .. : .. : ..
gi|124 DNLMDLTHETVYHASSIGQPEIEEAPPTTKV-DGDTVTTSRFMEGIVPPPFWAAALRGNG
      150      160      170      180      190      200

      240      250      260      270      280
DMO+27 ---NTPVDANWDIRWNKVSAMLNFIAVAPEGT-----PKEQSIHSRGTHILTPETEASC
      : .. : .. : .. : .. : .. : .. : .. : .. : .. : ..
gi|124 LADDVRCRDWQICHFTPPSHVMIEVGVAHAGKGGYHADPRDK-VSSIVVDFITPETDTSI
      210      220      230      240      250      260

      290      300      310      320      330      340
DMO+27 HYFFGSSRNFGIDDPMDGVLRSWQAQALVKEDKVVEAIERRRAYVEANGIRPAM-LSC
      :..... : .. : .. : .. : .. : .. : .. : .. : .. : ..
gi|124 WYFWGMARSAFVDDRALDRTIRKGGQ-AIFAEDLEMLEAQQRNLLRWPDP---RPLLKLNI
      270      280      290      300      310      320

      350      360
DMO+27 DEAAVRVSREIEKL-EQLEAA
      : .. : .. : .. : .. : ..
gi|124 DAGGVQSRRLDRLIDQERAAALSC
      330      340

>>gi|146191733|emb|CAL75738.1| vanillate O-demethylase o (347 aa)
      initn: 626 initl: 271 opt: 685 Z-score: 839.0 bits: 163.8 E(): 1.1e-37
Smith-Waterman score: 685; 36.391% identity (62.722% similar) in 338 aa
overlap (29-361:3-335)

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      : .. :..... : .. : .. : .. : ..
gi|146      MAASFPMNAWYAAAWDAEVKQALLPRITICGKHVV
              10      20      30
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              70      80      90      100      110      120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPNGARPA
      : .. :..... : .. : .. : .. : .. : .. : .. : .. : .. : ..
gi|146 MYRKADGATAALEDACWHRLVPLSKGRLEGDTVCCGYHGLKFSPOGRCTYMPQSQETINP-
      40      50      60      70      80      90

      130      140      150      160      170      180
DMO+27 SLNVRSPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD
      : .. :..... : .. :..... : .. : .. : .. : .. : .. : ..
gi|146 SACVRAYPAPERHRFIWLWMGDPALADPATIPDMHWNHDPAWAGDGKTIQVKCDYRLVVD
      100      110      120      130      140      150

      190      200      210      220      230      240
DMO+27 NLMDLGHQAQYVHRANAQTDAFDRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGANTP
      : .. : .. : .. : .. : .. : .. : .. : .. : .. : ..
gi|146 NLMDLTHETVHGGSSIGNDAVAEAPFDVTHGERTATVTRWMRGIEPPPFWAKQL-GKPG
      160      170      180      190      200      210

      250      260      270      280      290
DMO+27 VDAWDIRWNKVSAMLNFIAVAPEGTPEKQSIHSRGTH----ILTPETEASCHYFFGSS
      : .. : .. : .. : .. : .. : .. : .. : .. : .. : ..
gi|146 VDRWQIRFESPCVTITDVGVAPTGTGAPEGDRSQGVNGMVLNTIIPETDKTCHYFWAFA
      220      230      240      250      260      270

      300      310      320      330      340      350
DMO+27 RNFGIDDPMDGVLRSWQAQALVKEDKVVEAIERRRAYVEANGIRPAMLSCEAAVRVS
      : .. : .. : .. : .. : .. : .. : .. : .. : .. : ..
gi|146 RNYKLEQRLTTEIRE-GVSGIFREDEFLEA--QQRAMDENPGRVFYNLIDAGAMWAR
      280      290      300      310      320

      360
DMO+27 REIEKLEQLEAA
      : ....
gi|146 RIIDRMIARETPLREAAE
      330      340

>>gi|77969157|gb|ABB10536.1| Rieske (2Fe-2S) protein [Bu (373 aa)
      initn: 611 initl: 279 opt: 684 Z-score: 837.3 bits: 163.6 E(): 1.4e-37
Smith-Waterman score: 684; 36.494% identity (60.920% similar) in 348 aa
overlap (31-367:16-356)

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      :..... :..... :..... : .. : .. : ..
gi|779      MPRTGGIDLKETTNNVFLKNAWYVAGTPDEIDGKPLGRKICNESMV
              10      20      30      40

      70      80      90      100      110      120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPNGARPA
      : .. : .. : .. : .. : .. : .. : .. : .. : .. : ..
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DMO+27 SLNVRSPFPVVERDALIWCIPGDPALADPGAIPDFGCRVDPAAYRTVGGYGHVDCNYKLLVD  
:  
gi|121 SACVRAFFIVERHRFVWIWPGDPALADPTLVDPDLRWMNDPAWTGDGRMTEVKADYRLVID  
100 110 120 130 140 150

190 200 210 220 230  
DMO+27 NLMDLGHAGQYVHRANAQTDAFDRLEREIVIGDGEIQALMK---IPGGTFSVLMAKFLRGA  
:  
gi|121 NLMDLTHTYTVHGSSIGNELAKAPFDAV--HGETTATIRRVVLNEDAPPFWGAQL--GK  
160 170 180 190 200 210

240 250 260 270 280 290  
DMO+27 NTPVDAWNDIRWNKVSAMLNFIAVAPEGT--P---KEQSIHSRGTHILTPETEASCHYFF  
:  
gi|121 PGPVDRWQIIHFKA PSTIVLDVGVA PAGSGAPEGHREAGVMWVIHIPTSTAKSCYYFW  
220 230 240 250 260 270

300 310 320 330 340 350  
DMO+27 GSSRNFGIDDPEDMG-VLRSWQAQALVKEDKVVVVEAIERRRAYVEANGIRPAMLSCDEAA  
:  
gi|121 CHLRNRYRVHEQRVTREILQG--AGGILLEDEIVIEAQGRAIDKNPDRDFYNMNIDAGSLW  
280 290 300 310 320

360  
DMO+27 VRVSREIEKLEQLEAA

gi|121 ARRLIDAMIEKETRRRPIPIAAA  
330 340 350

>>gi|86572059|gb|ABD06616.1| Rieske (2Fe-2S) protein [Rh (347 aa)  
initn: 401 initl: 272 opt: 680 Z-score: 832.9 bits: 162.7 E(): 2.5e-37  
Smith-Waterman score: 680; 35.362% identity (61.159% similar) in 345 aa  
overlap (28-367:1-340)

10 20 30 40 50 60  
DMO+27 MQVWPPIGKKKFETLSYLPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA  
:  
gi|865 MPAFPLNAWYAAAWDADIKHALFPRTICNKHVV  
10 20 30

70 80 90 100 110 120  
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQC VHNPHGNARPA  
:  
gi|865 MYRKADGSVAALLEDACWHRLVPLSKGRLEGDTVVCYHGLKFSPQGRCTYMPSETINP-  
40 50 60 70 80 90

130 140 150 160 170 180  
DMO+27 SLNVRSPFPVVERDALIWCIPGDPALADPGAIPDFGCRVDPAAYRTVGGYGHVDCNYKLLVD  
:  
gi|865 SACVRSYPVVERHRFVWLWMGDPALADPALVPDMHWNDPAWAGDGKTIHARCDWRLLVVD  
100 110 120 130 140 150

```

      190      200      210      220      230      240
DMO+27 NLMDLGHAQYVHRANAQTDADFRLEREIVGDGEIQALMKIPGGTPSVLMAKFLRGANTP
      :::: : ::: .. .:: . : : : : : : : : : : : : : : : :
gi|865 NLMDLTHETYYVHGSSIGNEAVAEAPFDVTHGDRVTVTWRMRGIEAPPFWAAQLRKP-G
      160      170      180      190      200      210

      250      260      270      280      290
DMO+27 VDAWDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTH----ILTPETEASCHYFFGSS
      : : : : . . . . : : : : . . . . : : : : : : : : : : : :
gi|865 VDRWQIIRFEAPGTVTIDVGVPAGSGAPEGDRSQGVNGFVLNTMTPETDITTCYFWAFV
      220      230      240      250      260      270

      300      310      320      330      340      350
DMO+27 RNFGIDDPMDGVLRWSQAQALVKEDKVVVEAIERRRAYVEANGIRPAMLSCEAAVRVS
      : : : : . : : : : : : : : : : : : : : : : : : : : : :
gi|865 RNYRLGDQRLTTEIRE-GVSGIFGEDEIILEA--QQRRAISENPDRVFYNLNIDAGAMWSR
      280      290      300      310      320

      360
DMO+27 REIEKLEQLEAA
      . .... : :
gi|865 KLIDRMVAKEAAPRLQAAE
      330      340

>>gi|87134412|gb|ABD25154.1| Rieske (2Fe-2S) protein [No (341 aa)
      initn: 655 initl: 236 opt: 678 Z-score: 830.6 bits: 162.2 E(): 3.3e-37
      Smith-Waterman score: 678; 36.103% identity (63.324% similar) in 349 aa
      overlap (28-366:1-333)

      10      20      30      40      50
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKP-LGRTILDTP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|871 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      10      20      30

      60      70      80      90      100      110
DMO+27 ALYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNGARP
      ..... : : . : : : : : : : : : : : : : : : : : : : : : :
gi|871 VIWRKADGTPVIMADRCPHRFVPLSRGQRDGMRCGYHGLAFSSSGGCVHNPFDEALP
      40      50      60      70      80      90

      120      130      140      150      160      170
DMO+27 ASLNVRSPFVVERDALIWICPGDPALADPGAIPDFGCRVD---PAYRTVGGYGHVDCNYK
      . : . : : : . : : : : : : : : : : : : : : : : : : : : :
gi|871 LA-RVEVLFPVVEKHTGLWFPGDADRADPALIPDFGF-LDVERPLHR---GHLKMDAGYE
      100      110      120      130      140

      180      190      200      210      220      230
DMO+27 LLVDNLMDLGHAQYVHRANAQTDADFRLEREIVGDG-EIQALMKIPGGTP-SVLMAK
      : : : : : : : : : : . . . . : : : : : : : : : : : :

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gi|871 LVTDNLMDLSHAEFIHRDSFGVNGSLLTCGQHEVVQDEGGAIWNNWTMPDSEPPSWAVAM
      150      160      170      180      190      200

      240      250      260      270      280      290
DMO+27 FLRGANTPVDANDIRWNKVSAMLNFIAVAPEGTPKEQSI--HSRGTHILTPETEASCHY
      . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|871 LPEGART--DQWLHMRWNAPSCLALFLGLARSGTDRKDMVVPMPADPHILTPETVITSHY
      210      220      230      240      250      260

      300      310      320      330      340      350
DMO+27 FFGSSRNFGIDDPMDGVLRWSQAQALVKEDKVVVEAIERRRAYVEANGIRPAMLSCEA
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|871 FYTHE-----PTPEAHALLE---KAFLEEDHPMLHAQQEAMGSADFWDLRPVVLPSDAG
      270      280      290      300      310

      360
DMO+27 AVRVSREIEKLEQLEAA
      : : : : . . . : : : : :
gi|871 AIRVRRMMQLRRAEAGLEEEAAA
      320      330      340

>>gi|160343813|gb|ABX16898.1| Rieske (2Fe-2S) domain pro (347 aa)
      initn: 651 initl: 308 opt: 678 Z-score: 830.5 bits: 162.2 E(): 3.4e-37
      Smith-Waterman score: 678; 35.897% identity (61.823% similar) in 351 aa
      overlap (31-367:2-343)

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTP
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|160 : : : : : : : : : : : : : : : : : : : : : : : : : : :
      10      20      30

      70      80      90      100      110
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNGARP
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|160 FFRDGEGETVAALDFCPHRGAPLSLGTVRDGHVLCGYHGLTMGADGKCTSMPCQVRVGIP
      40      50      60      70      80      90

      120      130      140      150      160      170
DMO+27 ASLNVRSPFVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLV
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|160 A---IRRYPAVERYGFVWVWPGDPAQADSATIHPLHWADDPGWAYGGGLYHIDCDYRLMI
      100      110      120      130      140

      180      190      200      210      220      230
DMO+27 DNLMDLGHAQYVHRANAQTDADFRLEREIVGDGEIQALMK-IPGGTPSVLMAKFLRGA-
      : : : : : : : : : : . . . . : : : : : : : : : : : :
gi|160 DNLMDLTHETYYVHASSIGQPEIEEAPPTTKV-DGDTVTTSRFMEGIVPPPFWAAALRGNG
      150      160      170      180      190      200

      240      250      260      270      280

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```
gi|167 RDYQLGEQKVTIQIREAITKVFA-EDEVIVEA--QQRAIDDPHDVFNLYNLIDAGAMWAR
      280      290      300      310      320      330

      360
DMO+27 REIEKLEQLEAA
      : .... :
gi|167 RLIDRMVAAEAPPVIAIAE
      340      350

>>gi|170775464|gb|ACB33603.1| Rieske (2Fe-2S) domain pro (351 aa)
      initn: 623 init1: 317 opt: 675 Z-score: 826.7 bits: 161.5 E(): 5.4e-37
Smith-Waterman score: 675; 37.135% identity (61.696% similar) in 342 aa
overlap (31-360:2-335)

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      ..... : ..... :
gi|170 MFARNAWYVACTPDEFADKPLGRTICGEPLV
      10      20      30

      70      80      90      100      110
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHNGAR--
      ..... : ..... : ..... : ..... : ..... :
gi|170 FYRDGSGAVAALDFCPHRGAPLSLGRVCEGRLVCGYHGLEMGCDGKTIAMP-GQVRVGF
      40      50      60      70      80      90

      120      130      140      150      160      170
DMO+27 PASLNVRSFPVVERDALIWIICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLL
      :: ..... : ..... : ..... : ..... : ..... :
gi|170 PA---IRSFPVIERHGFVWVWPGDAARADAALLPALPWADHPEWAYGGGLYNIGCDYRLM
      100      110      120      130      140

      180      190      200      210      220      230
DMO+27 VDNLMDLGHAAQYVHRANAQTDAFDRLEREVIVGDGEIQALMKIPG--GTPSVLMAKFLRG
      ..... : ..... : ..... : ..... : ..... :
gi|170 IDNLMDLTHETVYHATSIGQKEIDEVPCSTRVDGDEVITSRFMNGIEAPPFWKMLRMNG
      150      160      170      180      190      200

      240      250      260      270      280
DMO+27 A--NTPVDANNDIRWNKVSAMLNFIAVAPEG-----TPKEQSIHSRGTHILTPETEASCH
      . .... : ..... : ..... : ..... : ..... :
gi|170 LPDDQFVDRWQICHFTPPSHVLIEVGVALAGHGGAAPAEVKASSIVVDFIIPETDGSIW
      210      220      230      240      250      260

      290      300      310      320      330      340
DMO+27 YFFGSSRNFGIDDPEMDGVLSWQAQALVKEDKVVVEAIERRRAYVEANGIRPAM-LSCD
      ::: ..... : ..... : ..... : ..... : ..... :
gi|170 YFGMARHFKPHDPSLTQIRDGQGRIFA-EDR---EMLERQANLRTWPDRKLLALNID
      270      280      290      300      310      320

      350      360
```

```
DMO+27 EAAVRVSREIEKLEQLEAA
      ..... :
gi|170 SGGVQARRVIDRKIAEERAPSGAPESSW
      330      340      350

>>gi|192286254|gb|ACF02635.1| Vanillate monooxygenase [R (347 aa)
      initn: 389 init1: 266 opt: 674 Z-score: 825.6 bits: 161.3 E(): 6.3e-37
Smith-Waterman score: 674; 34.783% identity (61.739% similar) in 345 aa
overlap (28-367:1-340)

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      : .. : ..... : ..... : ..... :
gi|192 MPAPPLNAWYAAAWDADIKHALFPRTICGKHVV
      10      20      30

      70      80      90      100      110      120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHNGARPA
      ..... : ..... : ..... : ..... : ..... :
gi|192 MYRKADGNVAALDACAWHRLVPLSKGRLEGDTVVCYHGLKFNPGQGRCTYMPSQETINP-
      40      50      60      70      80      90

      130      140      150      160      170      180
DMO+27 SLNVRSFPVVERDALIWIICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD
      : ..... : ..... : ..... : ..... : ..... :
gi|192 SACVRSYPVVERHRFVWLWMGDPVLADPALVPDMHWNDDPAWAGDGKTIYAKCDWRLVVD
      100      110      120      130      140      150

      190      200      210      220      230      240
DMO+27 NLMDLGHAAQYVHRANAQTDAFDRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGANTP
      ..... : ..... : ..... : ..... : ..... :
gi|192 NLMDLTHETVYHGGSSIGNEAFAEPFDVTHGDRVTVTTRWMKGIEPPPFWAAQL-GKPLG
      160      170      180      190      200      210

      250      260      270      280      290
DMO+27 VDAWNDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTH----ILTPETEASCHYFFGSS
      :: ..... : ..... : ..... : ..... :
gi|192 VDRWQIIRFEAPGTVIDVGVAPAGTGAPEGDRSQGVNGFVLNTMTPTDTHYFWAFV
      220      230      240      250      260      270

      300      310      320      330      340      350
DMO+27 RNFGIDDPEDMGVLSWQAQALVKEDKVVVEAIERRRAYVEANGIRPAMLSCEAAVRVS
      :: ..... : ..... : ..... : ..... :
gi|192 RNYRLSDQRLTTEIRE-GVSGIFREDEIIIEA--QQRAMLENPDRVFNLYNLIDAGAMWSR
      280      290      300      310      320

      360
DMO+27 REIEKLEQLEAA
      : .... :
gi|192 KLIDRMVAQESAPKLQAAE
      330      340
```

>>gi|146405860|gb|ABQ34366.1| vanillate O-demethylase ox (347 aa)  
initn: 390 initl: 272 opt: 674 Z-score: 825.6 bits: 161.3 E(): 6.3e-37  
Smith-Waterman score: 674; 36.578% identity (62.537% similar) in 339 aa  
overlap (29-361:3-335)

```

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      :: ::::: ::::: ::::: ::::: :::::
gi|146      MAASFPMNAWYAAAWDAEVKQALLPRTICGKHVV
      10      20      30
```

```

      70      80      90     100     110     120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHNGGARPA
      ::::: ::::: ::::: ::::: ::::: :::::
gi|146 MYRKADGSIAALEDACWHRLVPLSKGRLEGDTVVCGYHGLKFSPQGRCTFMPSQETINP-
      40      50      60      70      80      90
```

```

     130     140     150     160     170     180
DMO+27 SLNVRSPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD
      ::::: ::::: ::::: ::::: ::::: :::::
gi|146 SACVRAYPAVERHRFIWLMGDPALADPATIPDMHWNHDPWAGDGKTIQVKCDYRLVVD
     100     110     120     130     140     150
```

```

     190     200     210     220     230     240
DMO+27 NLMDLGHQYVHRANAQTDADFRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGANTP
      ::::: ::::: ::::: ::::: ::::: :::::
gi|146 NLMDLTHTFVHGSSIGNDAVAEAPFDVTHGERTATVTRWMRGIEPPPFWAKQL-GKPG
     160     170     180     190     200     210
```

```

     250     260     270     280     290
DMO+27 VDAWNDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTH-----ILTPETEASCHYFFGSS
      ::::: ::::: ::::: ::::: :::::
gi|146 VDRWQIIRFEAPCTVTIDVGVAPTGTGAPEGDRSQGVNGMVLNTITPETDKTCHYFWAFA
     220     230     240     250     260     270
```

```

     300     310     320     330     340     350
DMO+27 RNFGIDDPEDMGVLRSWQAQALVKEDKVVEAIERRRAYVEANGIRPAM-LSCDEAAVRV
      ::::: ::::: ::::: ::::: :::::
gi|146 RNYQLTEQRLTTEIRE-GVSGIFREDELILEA--QQRAMDANPGRVFYNLNIDAGAMWA
     280     290     300     310     320
```

```

     360
DMO+27 SREIEKLEQLEAA
      :::::
gi|146 RRIIDRMIARETPLEAAE
     330     340
```

>>gi|39650537|emb|CAE29060.1| putative vanillate O-demet (347 aa)  
initn: 383 initl: 266 opt: 670 Z-score: 820.7 bits: 160.4 E(): 1.2e-36

Smith-Waterman score: 670; 34.493% identity (62.029% similar) in 345 aa  
overlap (28-367:1-340)

```

      10      20      30      40      50      60
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRTILDTPLA
      : : ::::: ::::: ::::: :::::
gi|396      MPAFPLNAWYAAAWDADIKHALFPRTICGKHVV
      10      20      30
```

```

      70      80      90     100     110     120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHNGGARPA
      ::::: ::::: ::::: ::::: ::::: :::::
gi|396 MYRKADGTVAELEDACWHRLVPLSKGRLEGDTVVCGYHGLKFNPQGRCTYMPQSQETINP-
      40      50      60      70      80      90
```

```

     130     140     150     160     170     180
DMO+27 SLNVRSPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD
      : ::::: ::::: ::::: ::::: :::::
gi|396 SACVRSPVVERHRFVWLWMGDPVLADPALVPDMHWNDDPAWAGDGKTIYAKCDWRLVVD
     100     110     120     130     140     150
```

```

     190     200     210     220     230     240
DMO+27 NLMDLGHQYVHRANAQTDADFRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGANTP
      ::::: ::::: ::::: ::::: :::::
gi|396 NLMDLTHTYVHGSSIGNEAVAEAPFDVTHGDRVTVTTRWMMKIEPPPFWAAQL-GKPG
     160     170     180     190     200     210
```

```

     250     260     270     280     290
DMO+27 VDAWNDIRWNKVSAMLNFIAVAPEGTPKEQSIHSRGTH-----ILTPETEASCHYFFGSS
      ::::: ::::: ::::: :::::
gi|396 VDRWQIIRFEAPGTVIDVGVAPAGTRAPEGDRSQGVNGFVLNTITPETDTTCHYFWAFV
     220     230     240     250     260     270
```

```

     300     310     320     330     340     350
DMO+27 RNFGIDDPEDMGVLRSWQAQALVKEDKVVEAIERRRAYVEANGIRPAMLSCEAAVRVS
      ::::: ::::: ::::: :::::
gi|396 RNYRLSEQRLTTEIRE-GVSGIFREDEIILEA--QQRAMLENPDRVFYNLNIDAGAMWSR
     280     290     300     310     320
```

```

     360
DMO+27 REIEKLEQLEAA
      :::::
gi|396 KLIDRMVAQESAPKQLQAAE
     330     340
```

>>gi|121553096|gb|ABM57245.1| Rieske (2Fe-2S) domain pro (343 aa)  
initn: 630 initl: 278 opt: 665 Z-score: 814.6 bits: 159.3 E(): 2.6e-36  
Smith-Waterman score: 665; 34.783% identity (59.710% similar) in 345 aa  
overlap (31-365:2-340)

```

      10      20      30      40      50      60
```

```

70      80      90      100     110     120
DMO+27 LYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNGARPA
gi|273 MYRKADGVAALLEDACWHLVPLSKGRLEGDTVVCGYHGLKYNAQGRCTFMPSQETINP-
40      50      60      70      80      90

130      140      150      160      170      180
DMO+27 SLNVRSPVVERDALIWICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLVD
gi|273 SACVRAYPVVERHRYIWLWMGDPALADPALVPMHWNHDPAWAGDGKTIRVNC DYRLVLD
100     110     120     130     140     150

190      200      210      220      230      240
DMO+27 NLMDLGHAYQVHRANAQTDAFDRLEREIVGDGEIQALMKIPGGTSPVLMAKFLRGANTP
gi|273 NLMDLTHTETVHGSSIGNDAVAEAPFDVTHGEKTVTVTRWMRNIEPPFWAKQL-GKPLG
160     170     180     190     200     210

250      260      270      280      290
DMO+27 VDAWNDIRWNKVSAMNFIAVAPEGTPKEQSIHSRGTH----ILTPETEASCHYFFGSS
gi|273 VDRWQIIRFEAPCTIAIDVGVAPTGTGAPEGDRSQGVNGFVLNTITPETEKTCHYFWAFV
220     230     240     250     260     270

300      310      320      330      340      350
DMO+27 RNFGIDDPEDMGVLRSWQAQALVKEDKVVVEAIERRRAYVEANGIRPAMLSCEAAVRVS
gi|273 RNYQIGEQRIITTEIRE-GVSGIFHEDELILEA--QGRAMDENPD RVFYNLNIDAGAMWTR
280     290     300     310     320     330

360
DMO+27 REIEKLEQLEAA
gi|273 KLIDKMVAKENAPQHLQAAE
340     350

>>gi|124258972|gb|ABM93966.1| putative vanillate O-demet (353 aa)
initn: 612 initl: 400 opt: 662 Z-score: 810.8 bits: 158.6 E(): 4.2e-36
Smith-Waterman score: 662; 35.159% identity (62.536% similar) in 347 aa
overlap (30-366:10-350)

10      20      30      40      50
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDSRAMATFVRNAWYVAALPEELSEKPL-GRITILDTP
gi|124 MEQKIELKQSYLTNAWYVAALSTEVGAQALFHRKILDTSI
10      20      30      40

60      70      80      90      100     110
DMO+27 ALYRPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHGNGARP

```

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```

DMO+27 ASLNVRSPFVVERDALIWIICPGDPALADPGAIPDFGCRVDPAYRTVGGYGHVDCNYKLLV
      .  :: :..... :: : :: : :: : :: : :: : ..:: : ..:: : ..:: :
gi|721 PQARVRVLPVVERNRNIWIWMGDPEAADPALIPDTHWLADPAWRSLDGYIHYDVNYLLIA
      100          110          120          130          140          150

      180          190          200          210          220          230
DMO+27 DNLMDLGHAGYVHRAN-AQTDAFDRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGAN
      ::::: :: : ..:: : ..:: : ..:: : ..:: : ..:: : ..:: : ..:: :
gi|721 DNLLDFSHLPFVHPTTLGGSEAYAAQPKVERLDDGVG-ITRWLTNTEAPPFAKQVKNWP
      160          170          180          190          200

      240          250          260          270          280          290
DMO+27 TPVDAWNDIRWNKVSAMLNFIAVAPEGT--PKEQSIHS--RGTHILTPETEASCHYFFG
      :: : :: : ..:: : ..:: : ..:: : ..:: : ..:: : ..:: : ..:: :
gi|721 GKVDWRNIYNFTIPAILLMDSGMAPTGTGAPEGQRIDAAEFRGCQALTPETENSTHYFFA
      210          220          230          240          250          260

      300          310          320          330          340          350
DMO+27 SSRNFGIDDPEDMGVLRSWQAQALVK---EDKVVVEAIERRRAYVEANGIRPAMLSCEA
      ::::: :: : ..:: : ..:: : ..:: : ..:: : ..:: : ..:: : ..:: :
gi|721 HPHNFAIDNPE---VTRSIH-QSVVTAFFEDERDIIITAQQRSLALAPDFKMVP--FSIDAA
      270          280          290          300          310          320

      360
DMO+27 AVRVSREIEKLEQLEAA
      .  ..  ::
gi|721 LSQFRWVVERRVADEAAQAQQRQAKEA
      330          340          350

>>gi|219951453|gb|ACL61845.1| Rieske (2Fe-2S) domain pro (361 aa)
  initn: 401 initl: 310 opt: 661 Z-score: 809.4 bits: 158.4 E(): 5e-36
Smith-Waterman score: 661; 37.574% identity (61.834% similar) in 338 aa
overlap (34-361:10-342)

      10          20          30          40          50          60
DMO+27 WPPIGKKKFETLSYLPLTRDSRAMATFVRNAWYVAALPEELSEKPLGRITLDTPLALYR
      ::::: ..:: : ..:: : ..:: : ..:: : ..:: :
gi|219          MAGAKPYPLNAWYAVAWDHEIKRELTARTICDTGIVLYR
      10          20          30

      70          80          90          100          110          120
DMO+27 QPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGGGQCVHNPHNGNARPASLN
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|219 RTDQVVAALDEDACWHRLPLSLGLHLHGDEVVCGYHGLIFNPAGRCTFMPAQETINP-SAC
      40          50          60          70          80          90

      130          140          150          160          170          180
DMO+27 VRSPFVVERDALIWIICPGDPALADPGAIPDFGCRVDPAYRTVGG-YGHVDCNYKLLVDNL
      ::::: :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :
gi|219 VRAFPVVERYRLIWWMGDPALADPDTPDFHWNDSAPWVGEGGTFYSLQCDYRLVIDNL
      100          110          120          130          140          150

```



```

      190      200      210      220      230      240
DMO+27 MDLGHQYVHRANAQTDAFDRLEREVIVGDGEIQALMKIPGGTPSVLMAKFLRGANTPVD
      ::: :   ::: ..   .:: :   ::   : ..   . .   : . : .:: :   ::
gi|219 MDLTHETYVHAGSIGDEAITRNPFEVTHTRKVTVERWMENIEPPPFWARLL-GRPGHVD
      160      170      180      190      200      210

      250      260      270      280      290
DMO+27 AWNDRWNKVSAMLNFIAPAEGTPKEQSIHSRGTH-----ILTPETEASCHYFFGSSRN
      : . . . .   . . . .:: : .: . . . .   . . . . : . . . .:: :
gi|219 RWQIIHFEAPCVVAGDVGVALTGTGARQGDRSQGVNGFFLAAITPETGTSCHYFWNFVRN
      220      230      240      250      260      270

      300      310      320      330      340      350
DMO+27 FGIDDPMDGVL---RSWQAQALVKEDKVVVEAIERRRAYVEANGIRPAM-LSCDEAAVR
      : : : . .   : . : . . . . .: : : : :   : : : : : : : : : :
gi|219 FRTDDAELTRSLNLAHVNOGRGVYDQDHDVLEAQQRA---ISKNRPQPFYNLNI DAGALW
      280      290      300      310      320      330

      360
DMO+27 VSREIEKLEQLEAA
      . : : .
gi|219 AHRLLIDGMCAEGRQTQAGTSSDLAAAE
      340      350      360
```

### First 8 Ribulose Bisphosphate Carboxy Alignments

>>gi|169156|gb|AAA33686.1| ribulose 1,5-bisphosphate car (156 aa)  
initn: 172 initl: 172 opt: 187 Z-score: 234.9 bits: 50.9 E(): 0.0005  
Smith-Waterman score: 187; 50.725% identity (65.217% similar) in 69 aa  
overlap (1-67:34-97)

```

      10      20
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDS--RAM
      : . . . . .
gi|169 GGLKFMTGFPVKVNTDITSITSNGGRVKCMQVWPPIGKKKFETLSYLPPLTRDQLLKEV
      10      20      30      40      50      60

      30      40      50      60      70      80
DMO+27 ATFVRNAWYVAALPEELSEKPLGRTILDTPALYRQPDGVVAALLDICPHRFAPLSDGIL
      . . . . : : : . : : : :
gi|169 EYLLRKGW-VPCLEFELEKGFVYREHNKSP---RYYDGRYWTMWKLPMTGTTDASQVLK
      70      80      90      100      110

      90      100      110      120      130      140
DMO+27 VNGHLQCPYHGLEFDGGGQCVHNPHGNGARPASLNVRSFVVERDALIWICPGDPALADP
      120      130      140      150

gi|169 ELDEVVAAYPQAFVRIIGFDNVRQVQCISFIAHTPESY
      120      130      140      150
```

>>gi|217075090|gb|ACJ85905.1| unknown [Medicago truncatu (181 aa)  
initn: 168 initl: 168 opt: 187 Z-score: 233.9 bits: 50.9 E(): 0.00057  
Smith-Waterman score: 187; 51.667% identity (71.667% similar) in 60 aa  
overlap (1-58:59-117)

```

      10      20
DMO+27 MQVWPPIGKKKFETLSYLPPLTRD--SRAM
      : . . . . .
gi|217 VGLKSMAGFPVTKVNDITSITSNGGRVNCMQVWPPIGKKKFETLSYLPPLTREQLAKEV
      30      40      50      60      70      80

      30      40      50      60      70      80
DMO+27 ATFVRNAWYVAALPEELSEKPLGRTILDTPALYRQPDGVVAALLDICPHRFAPLSDGIL
      . . . . : : : . : : : :
gi|217 EYLIRKGW-VACLEFETEKGFVYRENHSSPGYYDGRYWTMWKLPPLFGATDASQVLKELDE
      90      100      110      120      130      140
```

>>gi|169148|gb|AAA33684.1| ribulose-1,5-bisphosphate car (136 aa)  
initn: 172 initl: 172 opt: 185 Z-score: 233.4 bits: 50.4 E(): 0.00061  
Smith-Waterman score: 185; 63.830% identity (78.723% similar) in 47 aa  
overlap (1-45:14-59)

```

      10      20      30      40
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDS--RAMATFVRNAWYVAALPEEL
      : . . . . .
gi|169 NTDITSNGERVKCMQVWPPIGKKKFETLSYLPPLTRDQLLKEVEYLLRKGW-VPCLEFEL
      10      20      30      40      50

      50      60      70      80      90      100
DMO+27 SEKPLGRTILDTPALYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEFDGG
      60      70      80      90      100      110

gi|169 LKGFVYGEHNKSPRYDGRYWTMWKLPMTGTTDPAQVVKEVDEVVAAYPEAFVRVIGFNN
      60      70      80      90      100      110
```

>>gi|12019640|gb|AAA33685.2| ribulose 1,5 bisphosphate c (139 aa)  
initn: 172 initl: 172 opt: 185 Z-score: 233.2 bits: 50.4 E(): 0.00062  
Smith-Waterman score: 185; 53.333% identity (68.333% similar) in 60 aa  
overlap (1-58:17-75)

```

      10      20      30      40
DMO+27 MQVWPPIGKKKFETLSYLPPLTRDS--RAMATFVRNAWYVAALP
      : . . . . .
gi|120 NTDITSITSNGGRVKCMQVWPPIGKKKFETLSYLPPLTRDQLLKEVEYLLRKWP-VPCLE
      10      20      30      40      50

      50      60      70      80      90      100
DMO+27 EELSEKPLGRTILDTPALYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEF
      : : . . : :
gi|120 FELEKGFVYREHNKSPGYDGRYWTMWKLPMTGTTDASQVLKELDEVVAAYPQAFVRIIG
      60      70      80      90      100      110
```

>>gi|20859|emb|CAA25390.1| ribulose biphosphate carboxy (180 aa)  
initn: 172 initl: 172 opt: 186 Z-score: 232.7 bits: 50.7 E(): 0.00066  
Smith-Waterman score: 186; 53.333% identity (70.000% similar) in 60 aa  
overlap (1-58:58-116)

```

                                10      20
DMO+27      MQVWPPIGKKKFETLSYLPPLTRDS--RAM
            :::::::::::::::::::::::::::: . .
gi|208      GGLKSMTGFPVKVNTDITSITSNGGRVKCMQVWPPIGKKKFETLSYLPPLTRDQLLKEV
            30      40      50      60      70      80

            30      40      50      60      70      80
DMO+27      ATFVRNAWYVAALPEELSEKPLGRTILDTPALYRQPDGVVAALLDICPHRFAPLSDGIL
            ..... : : :: . . : :
gi|208      EYLLRKGW-VPCLEFELEKGFVYREHNKSPGYDGRYWTMWKLPFGTTDASQVLKELDE
            90      100     110     120     130     140
```

>>gi|20855|emb|CAA27864.1| ribulose biphosphate carboxy (180 aa)  
initn: 172 initl: 172 opt: 186 Z-score: 232.7 bits: 50.7 E(): 0.00066  
Smith-Waterman score: 186; 53.333% identity (70.000% similar) in 60 aa  
overlap (1-58:58-116)

```

                                10      20
DMO+27      MQVWPPIGKKKFETLSYLPPLTRDS--RAM
            :::::::::::::::::::::::::::: . .
gi|208      GGLKSMTGFPVKVNTDITSITSNGGRVKCMQVWPPIGKKKFETLSYLPPLTRDQLLKEV
            30      40      50      60      70      80

            30      40      50      60      70      80
DMO+27      ATFVRNAWYVAALPEELSEKPLGRTILDTPALYRQPDGVVAALLDICPHRFAPLSDGIL
            ..... : : :: . . : :
gi|208      EYLLRKGW-VPCLEFELEKGFVYREHNKSPGYDGRYWTMWKLPFGTTDASQVLKELDE
            90      100     110     120     130     140
```

>>gi|20857|emb|CAA27865.1| ribulose 1.5-bisphosphate car (180 aa)  
initn: 172 initl: 172 opt: 186 Z-score: 232.7 bits: 50.7 E(): 0.00066  
Smith-Waterman score: 186; 53.333% identity (70.000% similar) in 60 aa  
overlap (1-58:58-116)

```

                                10      20
DMO+27      MQVWPPIGKKKFETLSYLPPLTRDS--RAM
            :::::::::::::::::::::::::::: . .
gi|208      GGLKSMTGFPVKVNTDITSITSNGGRVKCMQVWPPIGKKKFETLSYLPPLTRDQLLKEV
            30      40      50      60      70      80

            30      40      50      60      70      80
DMO+27      ATFVRNAWYVAALPEELSEKPLGRTILDTPALYRQPDGVVAALLDICPHRFAPLSDGIL
            ..... : : :: . . : :
gi|208      EYLLRKGW-VPCLEFELEKGFVYREHNKSPGYDGRYWTMWKLPFGTTDASQVLKELDE
            90      100     110     120     130     140
```

>>gi|12019640|gb|AAA33685.2| ribulose 1,5 bisphosphate c (139 aa)  
initn: 172 initl: 172 opt: 185 Z-score: 233.2 bits: 50.4 E(): 0.00062  
Smith-Waterman score: 185; 53.333% identity (68.333% similar) in 60 aa  
overlap (1-58:17-75)

```

                                10      20      30      40
DMO+27      MQVWPPIGKKKFETLSYLPPLTRDS--RAMATFVRNAWYVAALP
            :::::::::::::::::::::::::::: . . .... : :
gi|120      NTDITSITSNGGRVKCMQVWPPIGKKKFETLSYLPPLTRDQLLKEVEYLLRKPW-VPCLE
            10      20      30      40      50

            50      60      70      80      90      100
DMO+27      EELSEKPLGRTILDTPALYRQPDGVVAALLDICPHRFAPLSDGILVNGHLQCPYHGLEF
            :: . . : :
gi|120      FELEKGFVYREHNKSPGYDGRYWTMWKLPFGTTDASQVLKELDEVVAAYPQAFVRIIG
```

367 residues in 1 query sequences  
4761287459 residues in 17815538 library sequences  
Scomplib [34t26]  
start: Tue Feb 16 16:23:49 2010 done: Tue Feb 16 16:36:27 2010  
Total Scan time: 622.850 Total Display time: 3.840

Function used was FASTA [version 3.4t26 July 7, 2006]

Database checksum values:

Tue Feb 16 16:36:28 GMT 2010	a184245745a6ed8c6ecde45b26637bba
/genedata/1/db/AD_2010	
Tue Feb 16 16:36:28 GMT 2010	17c3a19148dfb0163e270cf41e2aa437
/genedata/1/db/TOX_2010	
Tue Feb 16 16:37:20 GMT 2010	e657d3127c1aad11f9f7df8dcc5e448c
/genedata/1/db/PRT_2010	