

**Study Title**

**Bioinformatics Evaluation of the CP4 EPSPS Protein Utilizing the AD\_2010,  
TOX\_2010, and PRT\_2010 Databases**

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**Laboratory Project ID**

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

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Author Date: 2-23-10

### Quality Assurance Statement


**Study Title:** Bioinformatics Evaluation of the CP4 EPSPS Protein Utilizing the AD\_2010, TOX\_2010, and PRT\_2010 Databases

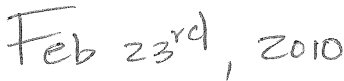
**Study Number:** REG-10-042

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
02/19/2010	Draft Report and Data Audit	02/19/2010	02/19/2010

  
Kanthasamy Karunanandaa, Ph.D.  
Quality Assurance Specialist  
Monsanto Regulatory, Monsanto Company

  
Date

**Study Certification Page**

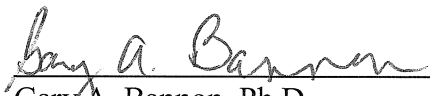
This report is an accurate and complete representation of the study/project activities.

**Signatures of Final Report Approval:**



Haidi Tu  
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Date: 2-23-10



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Date: Feb. 23, 2010

### **Study Information**

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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
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, 2009)
TOX_2010	Toxin protein sequence database (Release date January 22, 2010)



## 1.0 Summary

The bioinformatic evaluation of CP4 EPSPS has been conducted several times throughout the research and development process, with all reports concluding that the CP4 EPSPS protein was not similar to known allergens, toxins (Silvanovich, 2009), or other biologically active proteins (Tu and Silvanovich, 2009) that may adversely affect human or animal health. Periodically, the databases used to evaluate proteins are updated. The allergen database (AD\_2010) has been revised and published (FARRP, 2010; Tu and Silvanovich, 2010) and the new toxin (TOX\_2010) and protein (PRT\_2010) sequence databases have been assembled (Tu and Silvanovich, 2010). In order to determine if the CP4 EPSPS protein shares significant sequence similarity to new sequences contained in the updated allergen, toxin or protein databases, the CP4 EPSPS protein sequence was used as a query for a FASTA and Sliding Window search of the AD\_2010 database and a FASTA search of the TOX\_2010 and PRT\_2010 databases.

Results indicate there were no biologically relevant sequence similarities to allergens or toxins when the CP4 EPSPS 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 CP4 EPSPS protein sequence and proteins in the updated allergen database. When searching the PRT\_2010 database, results confirm that no biologically relevant structural similarity to proteins of concern was observed for CP4 EPSPS sequence. These data are consistent with those previously reported (Silvanovich, 2009; Tu and Silvanovich, 2009), where it was concluded that there was a lack of structurally relevant sequence similarity to allergens, toxins or other biologically active proteins that could be harmful to human or animal health.

## 2.0 Sequence Database Preparation

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 (December 15, 2009), 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).

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

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).

### **3.0 Sequence Database Searches**

The CP4 EPSPS sequence (Figure 1) used in this analysis was the same as that used previously as described in Silvanovich (2009). 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 algorithm (Lipman and Pearson, 1985; Pearson and Lipman, 1988). In the case of FASTA searches of the PRT\_2010 database performed using the CP4 EPSPS sequence, the Appendix 1 was truncated to display only the top 50 alignments.

FASTA comparisons are initiated by aligning the first match of a specific wordsize. The alignment is then extended based on the chosen scoring matrix. Specific FASTA comparison parameters used in this study included a wordsize (k-tuple) of two, a gap creation penalty of 10, and a gap extension penalty of two. The expectation score (*E*-score) was set to ten for searches of the AD\_2010 and TOX\_2010 databases and one for the PRT\_2010 database. 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 alignment is extensively analyzed for each database sequence. The BLOSUM50 matrix series (Henikoff and Henikoff, 1992) 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.

#### **4.0 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 CP4 EPSPS 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 CP4 EPSPS as the query sequence to search the AD\_2010 database, the top alignment was with GI-21725588 with an *E*-score of 1.5. Due to the high *E*-score value, this is not a meaningful alignment. No alignment met or exceeded the threshold of 35% identity over 80 amino acids recommended by Codex Alimentarius (2003). Furthermore, no eight contiguous amino acid identities were detected when the CP4 EPSPS protein sequence was compared to the AD\_2010 sequence database (Appendix 1).

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

Using CP4 EPSPS as the query sequence to search the TOX\_2010 database, the top alignment was with GI-267990064 with an *E*-score of 1.7. Due to the high *E*-score value, this is not a meaningful alignment (Appendix 1).

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

Using CP4 EPSPS as the query sequence to search the PRT\_2010 database, the top alignment positively identified CP4 EPSPS (GI: 27549260) with 100.00% identity over 455 amino acids with an *E*-score of 1.8e-173 (Appendix 1). The positive identification of CP4 EPSPS does not indicate potential adverse biological activity of the CP4 EPSPS protein.

## **6.0**    **Conclusions**

The results of these data indicate that no biologically relevant sequence similarities were observed between the CP4 EPSPS protein and allergen, toxin, or biologically active proteins. These results and conclusion are consistent with those previously reported by Silvanovich (2009) and Tu and Silvanovich (2009), which concluded that CP4 EPSPS demonstrated no structurally relevant sequence similarity to allergen, toxin, 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  
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Tu, H. and Silvanovich, A. 2009. Updated Bioinformatics Evaluation of the CP4 EPSPS Protein Utilizing the PRT\_2009 Database. Monsanto Regulatory Affair Response RAR-09-514, St. Louis, MO.

Tu, H. and Silvanovich, A. 2010. The Assembly of Databases Used for FASTA, BLAST and Sliding Window Searches in 2010. Monsanto Technical Report MSL0022498, St. Louis, MO.

1 MLHGASSRPA TARKSSGLSG TVRIPGDKSI SHRSFMFGGL ASGETRITGL  
51 LEGEDVINTG KAMQAMGARI RKEGDTWIID GVGNGGLLAP EAPLDFGNAA  
101 TGCRLTMGLV GYDFDSTFI GDASLTRPM GRVLNPLREM GVQVKSEDGD  
151 RLPVTLRGPK TPTPITYRVP MASAQVKS AV LLAGLNTPGI TTVIEPIMTR  
201 DHTEKMLQGF GANLTVETDA DGVRTIRLEG RGKLTGQVID VPGDPSSTAF  
251 PLVAALLVPG SDVTILNVLM NPTRTGLILT LQEMGADIEV INPRLAGGED  
301 VADLRVRSST LKGVTVPEDR APSMIDEYPI LAVAAFAEG ATVMNGLEEL  
351 RVKESDRLSA VANGLKLNGV DCDEGETSLV VRGRPDGKGL GNASGAAVAT  
401 HLDHRIAMSF LVMGLVSENP VTVDDATMIA TSFPEFMDLM AGLGAKIELS  
451 DTKAA

**Figure 1: The CP4 EPSPS Protein Sequence**

## Appendix 1. Bioinformatic analysis of polypeptide CP4\_EPSPS

```
>CP4_EPSPS
MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGKAMQAMGARIRKEGDT
WIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSIFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRL
PVTLRGPKTPTPTITYRVPMSAQVKSALLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETDADGVRTIRL
EGRGKLTGQVIDVPGDPSSAFPLVAALLVPGSDVTILNVLNMPTRTGLILTLQEMGADIEVINPRLAGGEDVADL
RVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGLKLVGDCDEGETSLV
VRGRPDGKGLGNASGAATHLDRHRIAMSFLVMGLVSENPTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
```

Sliding 8 amino acid window search  
Database searched = AD\_2010  
Query = CP4\_EPSPS

Start time: Fri Jan 22 19:50:55 GMT 2010 Finish time: Fri Jan 22 19:50:55  
GMT 2010

No 8 amino acid matches exist between CP4\_EPSPS and the AD\_2010 database

```
# fasta34 CP4_EPSPS.pep /genedata/1/db/AD_2010 -Q -E 10 -O
CP4_EPSPS.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
```

CP4\_EPSPS, 455 aa  
vs /genedata/1/db/AD\_2010 library

	opt	E()
< 20	3	0:==
22	0	0:
24	0	0:
26	0	0:
28	0	0:
30	2	2:*
32	5	8:==*
34	32	21:=====*
36	32	44:=====*
38	41	72:=====*
40	70	101:=====*
42	108	123:=====*
44	108	136:=====*
46	121	138:=====*
48	140	132:=====*
50	125	121:=====*
52	109	106:=====*

54	113	91:=====*
56	66	76:=====*
58	68	62:=====*
60	46	50:=====*
62	51	40:=====*
64	22	32:=====*
66	27	25:=====*
68	30	20:=====*
70	42	16:=====*
72	32	12:=====*
74	22	10:=====*
76	14	7:=====*
78	13	6:=====*
80	3	4:=====*
82	4	3:=====*
84	3	3:=====*
86	4	2:=====*
88	1	2:=====*
90	0	1:=====*
92	1	1:=====*
94	5	1:=====*
96	7	1:=====*
98	0	0:=====*
100	1	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))= 5.19540.00476; mu= 10.7535 0.252  
mean\_var=72.607822.942, 0's: 3 Z-trim: 3 B-trim: 219 in 1/42  
Lambda= 0.150516  
Kolmogorov-Smirnov statistic: 0.0856 (N=29) at 46

FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2  
join: 37, opt: 25, open/ext: -10/-2, width: 16

The best scores are:

	opt	bits	E(1471)
gi 21725588 emb CAD38375.1  unnamed protein produc ( 129)	78	25.8	1.5
gi 21725602 emb CAD38382.1  unnamed protein produc ( 129)	76	25.4	2
gi 21725604 emb CAD38383.1  unnamed protein produc ( 129)	76	25.4	2
gi 21725594 emb CAD38378.1  unnamed protein produc ( 129)	75	25.1	2.3
gi 21725596 emb CAD38379.1  unnamed protein produc ( 129)	75	25.1	2.3
gi 21725600 emb CAD38381.1  unnamed protein produc ( 129)	75	25.1	2.3
gi 21725592 emb CAD38377.1  unnamed protein produc ( 129)	75	25.1	2.3
gi 21725590 emb CAD38376.1  unnamed protein produc ( 129)	75	25.1	2.3



gi|1346568|sp|P49372.1|ALL1\_APIGR RecName: Full=Ma ( 154) 75 25.2 2.7  
gi|21725584|emb|CAD38373.1| unnamed protein produc ( 129) 74 24.9 2.7  
gi|21725586|emb|CAD38374.1| unnamed protein produc ( 129) 74 24.9 2.7  
gi|21725582|emb|CAD38372.1| unnamed protein produc ( 129) 74 24.9 2.7  
gi|224016002|gb|ACN32322.1| tropomyosin [Ascaris l ( 287) 78 26.0 2.8  
gi|17978844|gb|AAL47677.1| major Der f 2 isoform l ( 129) 73 24.7 3.2  
gi|21920|emb|CAA39099.1| CM2 protein [Triticum tur ( 145) 70 24.1 5.4  
gi|9280360|gb|AAF86369.1| major allergen I 18kDa a ( 150) 68 23.7 7.5  
gi|21713|emb|CAA35597.1| unnamed protein product l ( 168) 68 23.7 8.2  
gi|100834|pir||S16031 alpha-amylase inhibitor, tet ( 168) 68 23.7 8.2  
gi|54039254|sp|P67875.1|RNMG\_ASPFU RecName: Full=R ( 176) 68 23.7 8.5

>>gi|21725588|emb|CAD38375.1| unnamed protein product [D (129 aa)  
initn: 57 initl: 57 opt: 78 Z-score: 99.3 bits: 25.8 E(): 1.5  
Smith-Waterman score: 78; 25.882% identity (56.471% similar) in 85 aa  
overlap (224-303:48-129)

```

      200      210      220      230      240      250
CP4_EP IEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPG-DPSSSTAFPL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|217 VPGCHGNEPCIIGRGKPFQLEALFEANQNSKTAKIEIKASIDGLSVDVPGIDPNACHY--
      20      30      40      50      60      70
```

```

      260      270      280      290      300
CP4_EP VAALLVPGSDVTI---LNV-LMNPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      . : : : : : : : : : : : : : : : : : : : : : : :
gi|217 MNCPLVNGQQYDIKYTNWVPKIPNSENVVTVKVLG-DNGVLACAIATHAKIQD
      80      90      100      110      120
```

```

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGKLKLN
```

>>gi|21725602|emb|CAD38382.1| unnamed protein product [D (129 aa)  
initn: 54 initl: 54 opt: 76 Z-score: 96.9 bits: 25.4 E(): 2  
Smith-Waterman score: 76; 26.190% identity (55.952% similar) in 84 aa  
overlap (225-303:49-129)

```

      200      210      220      230      240      250
CP4_EP EPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPG-DPSSSTAFPLV
      : : : : : : : : : : : : : : : : : : : : : :
gi|217 PGCHGSEPCIHSGKPFQLEALFEANQNSATAKIEIKASIDGLSVDVPGIDPNACNY--M
      20      30      40      50      60      70
```

```

      260      270      280      290      300
CP4_EP AALLVPGSDVTI---LNV-LMNPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      : : : : : : : : : : : : : : : : : : : : : :
gi|217 KCPLVNGQQYDIKYTNWVPKIPNSENVVTVKVLG-DNGVLACAIATHAKIQD
      80      90      100      110      120
```

```

      310      320      330      340      350      360
```

CP4\_EP TLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGKLKLG

>>gi|21725604|emb|CAD38383.1| unnamed protein product [D (129 aa)  
initn: 54 initl: 54 opt: 76 Z-score: 96.9 bits: 25.4 E(): 2  
Smith-Waterman score: 76; 26.190% identity (55.952% similar) in 84 aa  
overlap (225-303:49-129)

```

      200      210      220      230      240      250
CP4_EP EPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPG-DPSSSTAFPLV
      : : : : : : : : : : : : : : : : : : : : : :
gi|217 PGCHGNEPCIHSGKPFQLEALFEANQNSATAKIEIKASIDGLSVDVPGIDPNACNY--M
      20      30      40      50      60      70
```

```

      260      270      280      290      300
CP4_EP AALLVPGSDVTI---LNV-LMNPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      : : : : : : : : : : : : : : : : : : : : : :
gi|217 KCPLVNGQQYDIKYTNWVPKIPNSENVVTVKVLG-DNGVLACAIATHAKIQD
      80      90      100      110      120
```

```

      310      320      330      340      350      360
CP4_EP TLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGKLKLG
```

>>gi|21725594|emb|CAD38378.1| unnamed protein product [D (129 aa)  
initn: 54 initl: 54 opt: 75 Z-score: 95.8 bits: 25.1 E(): 2.3  
Smith-Waterman score: 75; 26.190% identity (55.952% similar) in 84 aa  
overlap (225-303:49-129)

```

      200      210      220      230      240      250
CP4_EP EPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPG-DPSSSTAFPLV
      : : : : : : : : : : : : : : : : : : : : : :
gi|217 PGCHGNEPCIHSGKPFQLEALFEANQNSATAKIEIKASIDGLSVDVPGIDPNACNY--M
      20      30      40      50      60      70
```

```

      260      270      280      290      300
CP4_EP AALLVPGSDVTI---LNV-LMNPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      : : : : : : : : : : : : : : : : : : : : : :
gi|217 KCPLVNGQQYDIKYTNWVPKIPNSENVVTVKVLG-DNGVLACAIATHAKIRD
      80      90      100      110      120
```

```

      310      320      330      340      350      360
CP4_EP TLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGKLKLG
```

>>gi|21725596|emb|CAD38379.1| unnamed protein product [D (129 aa)  
initn: 54 initl: 54 opt: 75 Z-score: 95.8 bits: 25.1 E(): 2.3  
Smith-Waterman score: 75; 26.190% identity (54.762% similar) in 84 aa  
overlap (225-303:49-129)

```

      200      210      220      230      240      250
CP4_EP EPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPG-DPSSSTAFPLV
      : : : : : : : : : : : : : : : : : : : : : :
gi|217 PGCHGNEPCIHSGKPFQLEALFEANQNSATAKIEIKASIDGLSVDVPGIDPNACNY--M
```

```
>>gi|21725590|emb|CAD38376.1| unnamed protein product [D (129 aa)
  initn: 54 initl: 54 opt: 75 Z-score: 95.8 bits: 25.1 E(): 2.3
  Smith-Waterman score: 75; 26.190% identity (55.952% similar) in 84 aa
  overlap (225-303:49-129)

      200      210      220      230      240      250
CP4_EP EPIMTRDHTKEMKLQGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPG--DPSSTAFFLV
      : .. : .. : .. : .. : .. : .. : .. : .. : .. : .. : ..
gi|217 PGCHGSEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDGLSVDPGIDPNACHY--M
      20      30      40      50      60      70

      260      270      280      290      300
CP4_EP AALVLVPGSDVTI---LNV-LMNPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRSS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|217 NCPLVNGQQYDIKYTNWVPKIIAPNSENVVTVKVLG--DNGVLACAIATHAKIQD
      80      90      100      110      120

      310      320      330      340      350      360
CP4_EP TLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGLKLNG

>>gi|1346568|sp|P49372.1|ALL1_APIGR RecName: Full=Major (154 aa)
  initn: 38 initl: 38 opt: 75 Z-score: 94.7 bits: 25.2 E(): 2.7
  Smith-Waterman score: 75; 22.059% identity (50.735% similar) in 136 aa
  overlap (189-319:2-131)

      160      170      180      190      200      210
CP4_EP PKTPTPIITYRVPMASAQVKSAVLLAGLNTPGITTVIEPIMTRDHTKEMKLQGF--GANLTV
      : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 MGVTHTVLELTSSVSAEKIFQGFVIDVDVTVL
      10      20      30

      220      230      240      250      260      270
CP4_EP ETDADGV-RTIRLEGRG-KLTGQVIDVP-GDPSTAFPLVAALLVPGSDVTILNVLMNPT
      : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 PKAAPGAYKSVEIKDGGPGTLKIIITLPGGGPITT----MTLRIDGVNKEALTFDYSVI
      40      50      60      70      80

      280      290      300      310      320      330
CP4_EP RTGLILTLQEMGADIEVINPRLAGGEDVADLRVRSSTLKGVTVPEDRAPSMIDEYPILAV
      : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 DGDILLGFIESIENHVVLPVTADGG-SICKTTAIFHTKGDVAVPEENIKYANEQNTALFK
      90      100      110      120      130      140

      340      350      360      370      380      390
CP4_EP AAFAEGATVMNGLEELRVKESDRLSAVANGLKLNGVDCDEGETSLVVRGRPDGKGLGNA

gi|134 ALEAYLIAN
      150

>>gi|21725584|emb|CAD38373.1| unnamed protein product [D (129 aa)
  initn: 54 initl: 54 opt: 74 Z-score: 94.6 bits: 24.9 E(): 2.7
```

CP4\_EP AALLVPGSDVTI---LNV-LMNPTRTGLILTLOEMGADIEVINPRLAGGEDVADLRVRSS

```
>>gi|21920|emb|CAA39099.1| CM2 protein [Triticum turgidu (145 aa)
  initn: 54 initl: 54 opt: 70 Z-score: 89.2 bits: 24.1 E(): 5.4
Smith-Waterman score: 70; 24.771% identity (48.624% similar) in 109 aa
overlap (170-277:40-143)
```

```
140      150      160      170      180      190
CP4_EP  MGVSQKSEDDGRLPVTLRGPKITPTITYRVPMASQVKSALLAGLNTPGITTVIEPIMT
gi|219  LLLAAVLVSVFAAAAATGPYCYPGMGLPSNPLEGCREYVAQQTGCVGIVGSPVSTPEGNT
10      20      30      40      50      60

200      210      220      230      240      250
CP4_EP  -RDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSSTAFPLVAALLV
gi|219  PRDRCKEL--YDASQHCRCOA--VRYFIGRTSDPNSGVKLDLPGCPREPQRDFAKVLVT
70      80      90      100     110     120

260      270      280      290      300      310
CP4_EP  PGSDVTILNVLMNPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRSSTLKGVTVPE
gi|219  PGH-CNVMTVHNTPYCLGLDI
130      140
```

>>gi|9280360|gb|AAF86369.1| major allergen I 18kDa antig (150 aa)  
initn: 57 initl: 57 opt: 68 Z-score: 86.6 bits: 23.7 E(): 7.5  
Smith-Waterman score: 68; 41.667% identity (70.833% similar) in 24 aa  
overlap (77-99:50-73)

```
50      60      70      80      90      100
CP4_EP  ITGLLEGEDVINTGKAMQAMGARIRKEGDTWIIDGV-GNGGLLAPEAPLDFGNAATGCRL
gi|928  KRLLYNQAKAESNSHHAPLSDGKTGSSYAHWFTNGYDGNGLIKGRTPIKFGKADCDRPP
20      30      40      50      60      70

110     120     130     140     150     160
CP4_EP  TMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSSEDGDRPLPVTLRGPKITPTPI
gi|928  KHSQNGMGKDDHYLLEFPPTFPDGHDKFDSKNPKEDPGPARVIYTPNKFVFCGIVAHQR
80      90      100     110     120     130
```

>>gi|21713|emb|CAA35597.1| unnamed protein product [Trit (168 aa)  
initn: 61 initl: 61 opt: 68 Z-score: 85.9 bits: 23.7 E(): 8.2  
Smith-Waterman score: 68; 37.838% identity (62.162% similar) in 37 aa  
overlap (238-272:124-160)

```
210      220      230      240      250      260
CP4_EP  QGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSSTAFPLVAALLVPG--SDVTI
gi|217  CRCEALRYFIALPVPSQPVDPRSGNVGESGLIDLPGCPREMOWDFVRLLVAPGQCNLATI
100     110     120     130     140     150

270      280      290      300      310      320
CP4_EP  LNVLMNPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRSSTLKGVTVPEDRAPSMI
gi|217  HNVRYCPAVEQPLWI
```

```
160
>>gi|100834|pir|S16031 alpha-amylase inhibitor, tetrame (168 aa)
initn: 61 initl: 61 opt: 68 Z-score: 85.9 bits: 23.7 E(): 8.2
Smith-Waterman score: 68; 37.838% identity (62.162% similar) in 37 aa
overlap (238-272:124-160)
```

```
210      220      230      240      250      260
CP4_EP  QGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSSTAFPLVAALLVPG--SDVTI
gi|100  CRCEALRYFIALPVPSQPVDPRSGNVGESGLIDLPGCPREMOWDFVRLLVAPGQCNLATI
100     110     120     130     140     150

270      280      290      300      310      320
CP4_EP  LNVLMNPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRSSTLKGVTVPEDRAPSMI
gi|100  HNVRYCPAVEQPLWI
160
```

>>gi|54039254|sp|P67875.1|RNMG\_ASPFU RecName: Full=Ribon (176 aa)  
initn: 57 initl: 57 opt: 68 Z-score: 85.7 bits: 23.7 E(): 8.5  
Smith-Waterman score: 68; 41.667% identity (70.833% similar) in 24 aa  
overlap (77-99:77-100)

```
50      60      70      80      90      100
CP4_EP  ITGLLEGEDVINTGKAMQAMGARIRKEGDTWIIDGV-GNGGLLAPEAPLDFGNAATGCRL
gi|540  KRLLYSQAKAESNSHHAPLSDGKTGSSYPHWFTNGYDGNGLIKGRTPIKFGKADCDRPP
50      60      70      80      90      100

110     120     130     140     150     160
CP4_EP  TMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSSEDGDRPLPVTLRGPKITPTPI
gi|540  KHSQNGMGKDDHYLLEFPPTFPDGHDKFDSKKPKEDPGPARVIYTPNKFVFCGIVAHQRG
110     120     130     140     150     160
```

455 residues in 1 query sequences  
331323 residues in 1471 library sequences  
Scomplib [34t26]  
start: Fri Jan 22 19:50:54 2010 done: Fri Jan 22 19:50:54 2010  
Total Scan time: 0.060 Total Display time: 0.010  
Function used was FASTA [version 3.4t26 July 7, 2006]

# fasta34 CP4\_EPSPS.pep /genedata/1/db/TOX\_2010 -Q -E 10 -O  
CP4\_EPSPS.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

CP4\_EPSPS, 455 aa  
vs /genedata/1/db/TOX\_2010 library

```

      opt      E()
< 20    62    0:=====
 22     9    0:==          one = represents 13 library sequences
 24    15    0:==
 26     2    0:==
 28    43    2:*===
 30    78    12:*=====
 32    76    45:====*==
 34   304   122:=====*****
 36   283   250:=====*****
 38   412   414:=====*****
 40   539   577:=====***** *
 42   637   706:=====***** *
 44   509   779:=====*****
*
 46   628   793:=====*****
*
 48   644   759:=====*****
 50   725   693:=====*****
 52   659   609:=====*****
 54   661   520:=====*****
 56   409   435:=====***** *
 58   300   357:=====***** *
 60   382   289:=====*****
 62   276   232:=====*****
 64   211   184:=====*****
 66   183   146:=====*****
 68    87   115:===== *
 70    69    90:=====*
 72    47    70:===== *
 74    51    55:=====*
 76    13    43:== *
 78    12    33:== *
 80    16    26:==*
 82     6    20:==*
 84     1    16:==*
 86     3    12:*
 88    10     9:*          inset = represents 1 library sequences
 90     4     7:*
 92    19     6:*==      :=====*****
 94     4     4:*==      :==*
 96     2     3:*==      :==*
 98    13     3:*==      :==*****
```

```

100    22     2:*==      :==*****
102    12     2:*==      :==*****
104     0     1:*==      :*
106     0     1:*==      :*
108     1     1:*==      :*
110     0     1:*==      :*
112     4     0:==      :=====
114     0     0:==      :*
116     0     0:==      :*
118     0     0:==      :*
>120    0     0:==      :*
```

2069351 residues in 8448 sequences

Expectation\_n fit: rho(ln(x))= 7.55410.000701; mu= -2.1351 0.034  
mean\_var=58.010812.223, 0's: 60 Z-trim: 61 B-trim: 858 in 2/60  
Lambda= 0.168391  
Kolmogorov-Smirnov statistic: 0.0452 (N=29) at 36

FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2  
join: 37, opt: 25, open/ext: -10/-2, width: 16

The best scores are:

	opt	bits	E(8448)
gi 267990064 gb ACY86461.1  toxin addiction system ( 101)	80	27.8	1.7
gi 224470960 gb ACN48789.1  toxin [Salmonella ente ( 101)	80	27.8	1.7
gi 16445235 gb AAL23453.1  toxin addiction system: ( 101)	80	27.8	1.7
gi 169246228 gb ACA51202.1  toxin addiction system ( 101)	80	27.8	1.7
gi 256359207 gb ACU72704.1  Ricin B lectin [Catenu ( 943)	95	30.6	2.3
gi 68166314 gb AAY88075.1  toxin addiction system ( 101)	73	26.1	5.4
gi 52854778 gb AAU88259.1  cytolethal distending t ( 258)	80	27.4	5.5
gi 52854786 gb AAU88265.1  cytolethal distending t ( 258)	80	27.4	5.5
gi 73476869 gb AAZ76484.1  Post-segregation toxin ( 101)	72	25.9	6.4
gi 119951945 gb ABM10846.1  cytolethal distending ( 257)	79	27.2	6.4
gi 38154547 gb AAR12197.1  cytolethal distending t ( 258)	79	27.2	6.5
gi 23574038 emb CAD48849.1  cytolethal distending ( 258)	79	27.2	6.5
gi 38154551 gb AAR12200.1  cytolethal distending t ( 258)	79	27.2	6.5
gi 239793097 dbj BAH72979.1  cytolethal distending ( 258)	79	27.2	6.5
gi 38154555 gb AAR12203.1  cytolethal distending t ( 258)	79	27.2	6.5
gi 239835481 dbj BAH78166.1  cytolethal distending ( 258)	79	27.2	6.5
gi 253721255 gb ACT33564.1  type III cytolethal di ( 258)	79	27.2	6.5
gi 239835441 dbj BAH78136.1  cytolethal distending ( 258)	79	27.2	6.5
gi 38154559 gb AAR12206.1  cytolethal distending t ( 258)	79	27.2	6.5
gi 239835445 dbj BAH78139.1  cytolethal distending ( 258)	79	27.2	6.5
gi 2218089 gb AAC45442.1  cytolethal distending to ( 258)	79	27.2	6.5
gi 239793101 dbj BAH72982.1  cytolethal distending ( 258)	79	27.2	6.5
gi 239793081 dbj BAH72967.1  cytolethal distending ( 258)	79	27.2	6.5
gi 239835429 dbj BAH78127.1  cytolethal distending ( 258)	79	27.2	6.5
gi 197239660 gb ACH53456.1  cytolethal distending ( 134)	74	26.2	6.5
gi 197239658 gb ACH53455.1  cytolethal distending ( 134)	74	26.2	6.5
gi 218349870 emb CAQ87274.1  Cytotoxic protein [Es ( 110)	72	25.8	7.1
gi 218350096 emb CAQ87515.1  Cytotoxic protein [Es ( 110)	72	25.8	7.1
gi 218359346 emb CAU95832.1  Cytotoxic protein ccd ( 110)	72	25.8	7.1
gi 186703041 gb ACC91755.1  F-plasmid toxin [Cloni ( 101)	71	25.6	7.5
gi 62550776 emb CAH64699.1  toxin [uncultured bact ( 101)	71	25.6	7.5

```
gi|186703052|gb|ACC91764.1| F-plasmid toxin [Cloni ( 101) 71 25.6 7.5
gi|186703035|gb|ACC91751.1| F-plasmid toxin [Cloni ( 101) 71 25.6 7.5
gi|186703057|gb|ACC91768.1| F-plasmid toxin [Cloni ( 101) 71 25.6 7.5
gi|186703047|gb|ACC91760.1| F-plasmid toxin [Cloni ( 101) 71 25.6 7.5
gi|25988999|gb|AAN76305.1| gyrase target toxin [hi ( 101) 71 25.6 7.5
gi|3337026|dbj|BAA31785.1| cytotoxic protein LetB ( 101) 71 25.6 7.5
gi|186703038|gb|ACC91753.1| F-plasmid toxin [Cloni ( 101) 71 25.6 7.5
gi|52854782|gb|AAU88262.1| cytolethal distending t ( 258) 78 27.0 7.6
gi|81243901|gb|ABB64610.1| post-segregation toxin ( 101) 70 25.4 8.9
gi|197239662|gb|ACH53457.1| cytolethal distending ( 134) 72 25.8 9.1
gi|54145467|gb|AAV31087.1| cytolethal distending t ( 154) 73 25.9 9.2
gi|54145471|gb|AAV31089.1| cytolethal distending t ( 154) 73 25.9 9.2
gi|54145473|gb|AAV31090.1| cytolethal distending t ( 154) 73 25.9 9.2
gi|54145469|gb|AAV31088.1| cytolethal distending t ( 154) 73 25.9 9.2
gi|58045080|gb|AAW64850.1| post-segregation toxin ( 108) 70 25.3 9.7
gi|56383108|gb|AAL72356.2| post-segregation toxin ( 108) 70 25.3 9.7
gi|81248277|gb|ABB68984.1| post-segregation toxin ( 108) 70 25.3 9.7
gi|13310719|gb|AAK18543.1|AF348706_232 post-segreg ( 110) 70 25.3 9.9
gi|18654301|gb|AAL77581.1|L47837_1 cytotoxic prote ( 126) 71 25.5 10
gi|548212|gb|AAA98269.1| cytotoxic protein [Plasmi ( 126) 71 25.5 10
```

>>gi|267990064|gb|ACY86461.1| toxin addiction system: to (101 aa)  
initn: 53 initl: 53 opt: 80 Z-score: 112.1 bits: 27.8 E(): 1.7  
Smith-Waterman score: 94; 31.633% identity (55.102% similar) in 98 aa  
overlap (223-312:5-91)

```
200 210 220 230 240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKL----TGQVIDVPGDPSST
: : . : : : . : : : : :
gi|267 MQFKVYTCKRESRYRLFVVDVQSDIIDTPG--RRM
10 20 30

250 260 270 280 290 300
CP4_EP AFPLVAALL----VPGSDVTILNVLNMPTRTGLILTLQEMGADIEVINPRLAGGEDVADL
: : : : : : : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|267 AVPLVSARLLSEKVPRLDLYPVMHIGDEPYR---LLT-----TDMTSV-PATVIGEEVADL
40 50 60 70 80

310 320 330 340 350 360
CP4_EP RVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSAVANG
. : . : .
gi|267 SLRENDIKNAINLMFRGI
90 100
```

>>gi|224470960|gb|ACN48789.1| toxin [Salmonella enterica (101 aa)  
initn: 53 initl: 53 opt: 80 Z-score: 112.1 bits: 27.8 E(): 1.7  
Smith-Waterman score: 94; 31.633% identity (55.102% similar) in 98 aa  
overlap (223-312:5-91)

200 210 220 230 240

```
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKL----TGQVIDVPGDPSST
: : . : : : . : : : : :
gi|224 MQFKVYTCKRESRYRLFVVDVQSDIIDTPG--RRM
10 20 30

250 260 270 280 290 300
CP4_EP AFPLVAALL----VPGSDVTILNVLNMPTRTGLILTLQEMGADIEVINPRLAGGEDVADL
: : : : : : : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|224 AVPLVSARLLSEKVPRLDLYPVMHIGDEPYR---LLT-----TDMTSV-PATVIGEEVADL
40 50 60 70 80

310 320 330 340 350 360
CP4_EP RVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSAVANG
. : . : .
gi|224 SLRENDIKNAINLMFRGI
90 100

>>gi|16445235|gb|AAL23453.1| toxin addiction system: tox (101 aa)
initn: 53 initl: 53 opt: 80 Z-score: 112.1 bits: 27.8 E(): 1.7
Smith-Waterman score: 94; 31.633% identity (55.102% similar) in 98 aa
overlap (223-312:5-91)
```

```
200 210 220 230 240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKL----TGQVIDVPGDPSST
: : . : : : . : : : : :
gi|164 MQFKVYTCKRESRYRLFVVDVQSDIIDTPG--RRM
10 20 30

250 260 270 280 290 300
CP4_EP AFPLVAALL----VPGSDVTILNVLNMPTRTGLILTLQEMGADIEVINPRLAGGEDVADL
: : : : : : : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|164 AVPLVSARLLSEKVPRLDLYPVMHIGDEPYR---LLT-----TDMTSV-PATVIGEEVADL
40 50 60 70 80

310 320 330 340 350 360
CP4_EP RVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSAVANG
. : . : .
gi|164 SLRENDIKNAINLMFRGI
90 100
```

>>gi|169246228|gb|ACA51202.1| toxin addiction system tox (101 aa)  
initn: 53 initl: 53 opt: 80 Z-score: 112.1 bits: 27.8 E(): 1.7  
Smith-Waterman score: 94; 31.633% identity (55.102% similar) in 98 aa  
overlap (223-312:5-91)

```
200 210 220 230 240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKL----TGQVIDVPGDPSST
: : . : : : . : : : : :
gi|169 MQFKVYTCKRESRYRLFVVDVQSDIIDTPG--RRM
10 20 30
```

```

      250      260      270      280      290      300
CP4_EP AFPLVAALL---VPGSDVTILNVLNPNRTGLILTLQEMGADIEVINPRLAGGEDVADL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|169 AVPLVSARLLSEKVPDRDLYPVMHIGDEPYR---LLT-----TDMTSV-PATVIGEEVADL
      40      50      60      70      80

      310      320      330      340      350      360
CP4_EP RVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSAVANG
      : : : :
gi|169 SLRENDIKNAINLMFRGI
      90      100

>>gi|256359207|gb|ACU72704.1| Ricin B lectin [Catenulisp (943 aa)
      initn: 70 initl: 46 opt: 95 Z-score: 109.6 bits: 30.6 E(): 2.3
      Smith-Waterman score: 117; 24.430% identity (52.117% similar) in 307 aa
      overlap (11-310:609-886)

      10      20      30      40
CP4_EP MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|256 QANLYLPQVSPTTGWLEEWMTDPNLDTSDLTHRHLSPLVGL--FPGDRVTADQSP--AAL
      580      590      600      610      620      630

      50      60      70      80      90
CP4_EP ASGETRITGLL--EGEDVINTGKAMQAMG-ARIRKEGDTWIIDGVNGGLLAPEAPLDFG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|256 LTG---VTNLLTARGMNSFGWMAWRALCWARLNAGMAY--QAVTT--VLRP--SVNFS
      640      650      660      670      680

      100      110      120      130      140      150
CP4_EP NAATGCRLTMGLVGVDYFDST--FIGDASL-TKRPMPGRVLNPLREMGVQVKSEDGDRLPV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|256 NGAA-----INLFDMSYFGSSSVFQIDANFGTPSAMIEMLVYHRPGLVELLPALPDAWSV
      690      700      710      720      730      740

      160      170      180      190      200      210
CP4_EP TLRGPKTPITYRVPMASAVKSAVLLAGLN-TPGITTVEIPIMTRDHTKMLQGFGAN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|256 A--GSVTGVPVRGAMALDMAWSGGQVTTATLHGTPGAGTTVK---FGAWSQAVTIGSGGT
      750      760      770      780      790

      220      230      240      250      260      270
CP4_EP LTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSSTAFPLVAALLVPGSDVTILNVLNPN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|256 VTVVPPP---RATVFNVLNRRSGKAIDVPGSSTTAGTALIQTTLHNSPN---QWKFPAPA
      800      810      820      830      840

      280      290      300      310      320      330
CP4_EP RTGLILTLQEMGADIEVINPRLAGGEDVADLRVRSSTLKGVTVPEDRAPSMIDEYPILAV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|256 ATGYTVTNINSGMVADVNGGSTADGTAIVQWPANSGETNQEWTLADAGNGYVKLVCSRSGK
```

```

      850      860      870      880      890      900
CP4_EP AAFAEGATVMNGLEELRVKESDRLSAVANGLKLVDCDEGETSLVVRGRPDGKGLGNA

      340      350      360      370      380      390
gi|256 VLGVSQDSTSDLAGITQQTDTGDISQHWQRIAVR
      910      920      930      940

>>gi|68166314|gb|AAY88075.1| toxin addiction system toxi (101 aa)
      initn: 39 initl: 39 opt: 73 Z-score: 102.9 bits: 26.1 E(): 5.4
      Smith-Waterman score: 87; 30.208% identity (56.250% similar) in 96 aa
      overlap (225-312:7-91)

      200      210      220      230      240      250
CP4_EP EPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKL---TGQVIDVPGDPSSTAF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|681 MQFKGYTCKRESRYRLFVDVQSDIIDTPG--RRMAV
      10      20      30

      260      270      280      290      300
CP4_EP PLVAALL---VPGSDVTILNVLNPNRTGLILTLQEMGADIEVINPRLAGGEDVADLRV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|681 PLVSARLLSEKVPDRDLYPVMHIGDEPYR---LLT-----TDMTSV-PATVIGEVADLSL
      40      50      60      70      80

      310      320      330      340      350      360
CP4_EP RSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSAVANGLK
      : : : :
gi|681 RKTDIKNAINLMFRGI
      90      100

>>gi|52854778|gb|AAU88259.1| cytolethal distending toxin (258 aa)
      initn: 46 initl: 46 opt: 80 Z-score: 102.8 bits: 27.4 E(): 5.5
      Smith-Waterman score: 80; 38.298% identity (51.064% similar) in 47 aa
      overlap (132-176:34-80)

      110      120      130      140      150      160
CP4_EP GCRLTMGLVGVDYFDSTFIGDASLTKRPMPGRVLNPLREMGVQVKSEDGDRLPVTLRGPKT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|528 KRTSIFIAGVLIPILLNGCSSGKNKAYLDPKFVPPQVEGGPTVPSPDESGLPLPGPGPAL
      10      20      30      40      50      60

      170      180      190      200      210
CP4_EP PT--PITYRVPMASAVKSAVLLAGLNTPGITTVEIPIMTRDHTKMLQGFGANLTVETD
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|528 PTNAPIPIPVPGTAPAVSLMNMDSVLTMTWSRGAGSSSLWAYIYSDSNSFGELRNWQIMPG
      70      80      90      100      110      120

>>gi|52854786|gb|AAU88265.1| cytolethal distending toxin (258 aa)
      initn: 46 initl: 46 opt: 80 Z-score: 102.8 bits: 27.4 E(): 5.5
```

Smith-Waterman score: 80; 38.298% identity (51.064% similar) in 47 aa overlap (132-176:34-80)

```

      110      120      130      140      150      160
CP4_EP GCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      :: :: :: :: :: :: :: :: :: :: :: ::
gi|528 KRTSIFIAGVLIPILLNGCSSGKNKAYLDPKVFPQVEGGPTVPSDESGLPLPGGPAL
      10      20      30      40      50      60
```

```

      170      180      190      200      210
CP4_EP PT--PITYRVPMSAQVKS AVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD
      :: :: :: :: :: :: :: :: :: :: :: ::
gi|528 PTNAPIPIPVPGTAPAVSLMNMDSVLTMWSRGAGSSSLWAYIISDSNSFGELRNWQIMPG
      70      80      90      100     110     120
```

>>gi|73476869|gb|AAZ76484.1| Post-segregation toxin [Esc (101 aa)  
initn: 39 initl: 39 opt: 72 Z-score: 101.6 bits: 25.9 E(): 6.4  
Smith-Waterman score: 72; 29.787% identity (57.447% similar) in 94 aa overlap (223-312:5-91)

```

      200      210      220      230      240
CP4_EP VIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKL---TGQVIDVPGDPSST
      : : : : : : : : : : : : : : : : : :
gi|734      MQFKVYTYKRESRYRLFVDVQSDIIDTPG--RRM
      10      20      30
```

```

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLNMPTRTGLIITLQEMGADIEVINPRLAGGEDVADLRVRS
      ..... : : : : : : : : : : : : : : : : : :
gi|734 VIPLASARLL--SD-KVSRELYPVVHVGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
      40      50      60      70      80
```

```

      310      320      330      340      350      360
CP4_EP SILKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGLKLN
      . : :
gi|734 NDIKNAINLMFWGI
      90      100
```

>>gi|119951945|gb|ABM10846.1| cytolethal distending toxi (257 aa)  
initn: 47 initl: 47 opt: 79 Z-score: 101.5 bits: 27.2 E(): 6.4  
Smith-Waterman score: 79; 36.170% identity (48.936% similar) in 47 aa overlap (132-176:33-79)

```

      110      120      130      140      150      160
CP4_EP GCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      .. : : : : : : : : : : : :
gi|119 KCTSILIVGILIPILLNGCSSRKNAHLDPKVFPQVEGGPTIPSPDEPGLPLPGAGPAL
      10      20      30      40      50      60
```

```

      170      180      190      200      210
CP4_EP PT--PITYRVPMSAQVKS AVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD
```

```

      :: :: :: :: :
gi|119 PTNAPIPIPVPGTAPAVSLMNMDSVLTMWSRGAGSSSLWAYIISDSNSFGELRNWQIMPG
      70      80      90      100     110     120
```

>>gi|38154547|gb|AAR12197.1| cytolethal distending toxin (258 aa)  
initn: 47 initl: 47 opt: 79 Z-score: 101.5 bits: 27.2 E(): 6.5  
Smith-Waterman score: 79; 36.170% identity (48.936% similar) in 47 aa overlap (132-176:34-80)

```

      110      120      130      140      150      160
CP4_EP GCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      .. : : : : : : : : : : : :
gi|381 KYTPIFIAGILLPILLNGCSSGKNKAHLDPKVFPQVEGGPTIPSPDEPGLPLPGAGPAL
      10      20      30      40      50      60
```

```

      170      180      190      200      210
CP4_EP PT--PITYRVPMSAQVKS AVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD
      :: :: :: :: :
gi|381 PTNAPIPIPVPGTAPAVSLMNMDSVLTMWSRGAGSSSLWAYIISDSNSFGELRNWQIMPG
      70      80      90      100     110     120
```

>>gi|23574038|emb|CAD48849.1| cytolethal distending toxi (258 aa)  
initn: 47 initl: 47 opt: 79 Z-score: 101.5 bits: 27.2 E(): 6.5  
Smith-Waterman score: 79; 36.170% identity (48.936% similar) in 47 aa overlap (132-176:34-80)

```

      110      120      130      140      150      160
CP4_EP GCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      .. : : : : : : : : : : : :
gi|235 KYTPIFIAGILLPILLNGCSSGKNKAHLDPKVFPQVEGGPTIPSPDEPGLPLPGAGPAL
      10      20      30      40      50      60
```

```

      170      180      190      200      210
CP4_EP PT--PITYRVPMSAQVKS AVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD
      :: :: :: :: :
gi|235 PTNAPIPIPVPGTAPAVSLMNMDSVLTMWSRGAGSSSLWAYIISDSNSFGELRNWQIMPG
      70      80      90      100     110     120
```

>>gi|38154551|gb|AAR12200.1| cytolethal distending toxin (258 aa)  
initn: 47 initl: 47 opt: 79 Z-score: 101.5 bits: 27.2 E(): 6.5  
Smith-Waterman score: 79; 36.170% identity (48.936% similar) in 47 aa overlap (132-176:34-80)

```

      110      120      130      140      150      160
CP4_EP GCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      .. : : : : : : : : : : : :
gi|381 KYTPIFIAGILLPILLNGCSSGKNKAHLDPKVFPQVEGGPTIPSPDEPGLPLPGAGPAL
      10      20      30      40      50      60
```

```

      170      180      190      200      210
CP4_EP PT--PITYRVPMSAQVKS AVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD
```



```

      ::  ::  ::  ..  :
gi|381 PTNAPIPIPVPGTAPAVSLMNMDSVLTMWSRGAGSSSLWAYIISDSNSFGELRNWQIMPG
      70          80          90          100          110          120
```

>>gi|239793097|dbj|BAH72979.1| cytolethal distending tox (258 aa)  
 initn: 47 initl: 47 opt: 79 Z-score: 101.5 bits: 27.2 E(): 6.5  
Smith-Waterman score: 79; 36.170% identity (48.936% similar) in 47 aa  
overlap (132-176:34-80)

```

      110      120      130      140      150      160
CP4_EP GCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      ..  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|239 KYTPIFIAGILLPILLNGCSSGKNKAHLDPKVFPQVEGGPTIPSPDEPGLPLPGAGPAL
      10      20      30      40      50      60
```

```

      170      180      190      200      210
CP4_EP PT--PITYRVPMSAQVKSAVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD
      ::  ::  ::  ..  :
gi|239 PTNAPIPIPVPGTAPAVSLMNMDSVLTMWSRGAGSSSLWAYIISDSNSFGELRNWQIMPG
      70          80          90          100          110          120
```

>>gi|38154555|gb|AAR12203.1| cytolethal distending toxin (258 aa)  
 initn: 47 initl: 47 opt: 79 Z-score: 101.5 bits: 27.2 E(): 6.5  
Smith-Waterman score: 79; 36.170% identity (48.936% similar) in 47 aa  
overlap (132-176:34-80)

```

      110      120      130      140      150      160
CP4_EP GCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      ..  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|381 KCTSILIVGILIPILLNGCSSRKNRAHLDPKVFPQVEGGPTIPSPDEPGLPLPGAGPAL
      10      20      30      40      50      60
```

```

      170      180      190      200      210
CP4_EP PT--PITYRVPMSAQVKSAVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD
      ::  ::  ::  ..  :
gi|381 PTNAPIPIPVPGTAPAVSLMNMDSVLTMWSRGAGSSSLWAYIISDSNSFGELRNWQIMPG
      70          80          90          100          110          120
```

>>gi|239835481|dbj|BAH78166.1| cytolethal distending tox (258 aa)  
 initn: 47 initl: 47 opt: 79 Z-score: 101.5 bits: 27.2 E(): 6.5  
Smith-Waterman score: 79; 36.170% identity (48.936% similar) in 47 aa  
overlap (132-176:34-80)

```

      110      120      130      140      150      160
CP4_EP GCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      ..  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|239 KYTPIFIAGILLPILLNGCSSGKNKAHLDPKVFPQVEGGPTIPSPDEPGLPLPGAGPAL
      10      20      30      40      50      60
```

```

      170      180      190      200      210
CP4_EP PT--PITYRVPMSAQVKSAVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD
```

```

      ::  ::  ::  ..  :
gi|239 PTNAPIPIPVPGTAPAVSLMNMDSVLTMWSRGAGSSSLWAYIISDSNSFGELRNWQIMPG
      70          80          90          100          110          120
```

>>gi|253721255|gb|ACT33564.1| type III cytolethal disten (258 aa)  
 initn: 47 initl: 47 opt: 79 Z-score: 101.5 bits: 27.2 E(): 6.5  
Smith-Waterman score: 79; 36.170% identity (48.936% similar) in 47 aa  
overlap (132-176:34-80)

```

      110      120      130      140      150      160
CP4_EP GCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      ..  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|253 KCTSILIVGILIPILLNGCSSRKNRAHLDPKVFPQVEGGPTIPSPDEPGLPLPGAGPAL
      10      20      30      40      50      60
```

```

      170      180      190      200      210
CP4_EP PT--PITYRVPMSAQVKSAVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD
      ::  ::  ::  ..  :
gi|253 PTNAPIPIPVPGTAPAVSLMNMDSVLTMWSRGAGSSSLWAYIISDSNSFGELRNWQIMPG
      70          80          90          100          110          120
```

>>gi|239835441|dbj|BAH78136.1| cytolethal distending tox (258 aa)  
 initn: 47 initl: 47 opt: 79 Z-score: 101.5 bits: 27.2 E(): 6.5  
Smith-Waterman score: 79; 36.170% identity (48.936% similar) in 47 aa  
overlap (132-176:34-80)

```

      110      120      130      140      150      160
CP4_EP GCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      ..  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|239 KCTSILIVGILIPILLNGCSSRKNRAHLDPKVFPQVEGGPTIPSPDEPGLPLPGAGPAL
      10      20      30      40      50      60
```

```

      170      180      190      200      210
CP4_EP PT--PITYRVPMSAQVKSAVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD
      ::  ::  ::  ..  :
gi|239 PTNAPIPIPVPGTAPAVSLMNMDSVLTMWSRGAGSSSLWAYIISDSNSFGELRNWQIMPG
      70          80          90          100          110          120
```

>>gi|38154559|gb|AAR12206.1| cytolethal distending toxin (258 aa)  
 initn: 47 initl: 47 opt: 79 Z-score: 101.5 bits: 27.2 E(): 6.5  
Smith-Waterman score: 79; 36.170% identity (48.936% similar) in 47 aa  
overlap (132-176:34-80)

```

      110      120      130      140      150      160
CP4_EP GCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      ..  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|381 KYTPIFIAGILLPILLNGCSSGKNKAHLDPKVFPQVEGGPTIPSPDEPGLPLPGAGPAL
      10      20      30      40      50      60
```

```

      170      180      190      200      210
CP4_EP PT--PITYRVPMSAQVKSAVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD
```

```

      ::  ::  ::  ..  :
gi|381 PTNAPIPIPVPGTAPAVSLMNMDSVLTMWSRGAGSSSLWAYIISDSNSFGELRNWQIMPG
      70          80          90          100          110          120

>>gi|239835445|dbj|BAH78139.1| cytolethal distending tox (258 aa)
  initn: 47 initl: 47 opt: 79 Z-score: 101.5 bits: 27.2 E(): 6.5
Smith-Waterman score: 79; 36.170% identity (48.936% similar) in 47 aa
overlap (132-176:34-80)

      110          120          130          140          150          160
CP4_EP GCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      ..  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|239 KYTFIFIAGILLPILLNGCSSGKNKAHLDPKVFPQVEGGPTIPSPDEPGLPLPGAGPAL
      10          20          30          40          50          60

      170          180          190          200          210
CP4_EP PT--PITYRVPMASQVKSAVLLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETD
      ::  ::  ::  ..  :
gi|239 PTNAPIPIPVPGTAPAVSLMNMDSVLTMWSRGAGSSSLWAYIISDSNSFGELRNWQIMPG
      70          80          90          100          110          120

>>gi|2218089|gb|AAC45442.1| cytolethal distending toxin- (258 aa)
  initn: 47 initl: 47 opt: 79 Z-score: 101.5 bits: 27.2 E(): 6.5
Smith-Waterman score: 79; 36.170% identity (48.936% similar) in 47 aa
overlap (132-176:34-80)

      110          120          130          140          150          160
CP4_EP GCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      ..  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|221 KCTSILIVGILIPILLNGCSSRKNRAHLDPKVFPQVEGGPTIPSPDEPGLPLPGAGPAL
      10          20          30          40          50          60

      170          180          190          200          210
CP4_EP PT--PITYRVPMASQVKSAVLLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETD
      ::  ::  ::  ..  :
gi|221 PTNAPIPIPVPGTAPAVSLMNMDSVLTMWSRGAGSSSLWAYIISDSNSFGELRNWQIMPG
      70          80          90          100          110          120

>>gi|239793101|dbj|BAH72982.1| cytolethal distending tox (258 aa)
  initn: 47 initl: 47 opt: 79 Z-score: 101.5 bits: 27.2 E(): 6.5
Smith-Waterman score: 79; 36.170% identity (48.936% similar) in 47 aa
overlap (132-176:34-80)

      110          120          130          140          150          160
CP4_EP GCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      ..  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|239 KYTFIFIAGILLPILLNGCSSSEKNKAHLDPKVFPQVEGGPTIPSPDEPGLPLPGAGPAL
      10          20          30          40          50          60

      170          180          190          200          210
CP4_EP PT--PITYRVPMASQVKSAVLLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETD
```

```

      ::  ::  ::  ..  :
gi|239 PTNAPIPIPVPGTAPAVSLMNMDSVLTMWSRGAGSSSLWAYIISDSNSFGELRNWQIMPG
      70          80          90          100          110          120

>>gi|239793081|dbj|BAH72967.1| cytolethal distending tox (258 aa)
  initn: 47 initl: 47 opt: 79 Z-score: 101.5 bits: 27.2 E(): 6.5
Smith-Waterman score: 79; 36.170% identity (48.936% similar) in 47 aa
overlap (132-176:34-80)

      110          120          130          140          150          160
CP4_EP GCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      ..  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|239 KCTSILIVGILIPILLNGCSSRKNRAHLDPKVFPQVEGGPTIPSPDEPGLPLPGAGPAL
      10          20          30          40          50          60

      170          180          190          200          210
CP4_EP PT--PITYRVPMASQVKSAVLLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETD
      ::  ::  ::  ..  :
gi|239 PTNAPIPIPVPGTAPAVSLMNMDSVLTMWSRGAGSSSLWAYIISDSNSFGELRNWQIMPG
      70          80          90          100          110          120

>>gi|239835429|dbj|BAH78127.1| cytolethal distending tox (258 aa)
  initn: 47 initl: 47 opt: 79 Z-score: 101.5 bits: 27.2 E(): 6.5
Smith-Waterman score: 79; 36.170% identity (48.936% similar) in 47 aa
overlap (132-176:34-80)

      110          120          130          140          150          160
CP4_EP GCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      ..  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|239 KCTSILIVGILIPILLNGCSSRKNRAHLDPKVFPQVEGGPTIPSPDEPGLPLPGAGPAL
      10          20          30          40          50          60

      170          180          190          200          210
CP4_EP PT--PITYRVPMASQVKSAVLLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETD
      ::  ::  ::  ..  :
gi|239 PTNAPIPIPVPGTAPAVSLMNMDSVLTMWSRGAGSSSLWAYIISDSNSFGELRNWQIMPG
      70          80          90          100          110          120

>>gi|197239660|gb|ACH53456.1| cytolethal distending tox (134 aa)
  initn: 45 initl: 45 opt: 74 Z-score: 101.4 bits: 26.2 E(): 6.5
Smith-Waterman score: 74; 22.449% identity (59.184% similar) in 98 aa
overlap (235-327:17-113)

      210          220          230          240          250          260
CP4_EP KMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSSAFPLVAALLVPGSDVT
      ::  ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|197 ILAVQEAGSPPTAVDTGRVIPSPGPVIRELIWNLTNSRP--QQVY
      10          20          30          40

      270          280          290          300          310
CP4_EP ILNVLNMPT--RTGLILTLQEMGADIEVINPRLAGGEDVADLVRVRS---TLKGVTVPED
```

```
CP4_EP STLKGVTPEDRAPSMIDEYPI LavAAAFAGATVMNGLEELRVKESDRLSAVANGLKLN
      ..
gi|218 NDIKNAINLMFWGI
      100          110

>>gi|218350096|emb|CAQ87515.1| Cytotoxic protein [Escher (110 aa)
initn: 39 initl: 39 opt: 72 Z-score: 100.7 bits: 25.8 E(): 7.1
Smith-Waterman score: 72; 29.78% identity (57.44% similar) in 94 aa
overlap (223-312:14-100)

      200      210      220      230      240
CP4_EP VIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKL----TGQVIDVPGDPSST
      : : . : . : : .....
gi|218 MPMRTGTGEMQFKVITYKRESRYRLFVDVQSDIIDITPG--RRM
      10      20      30      40

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLMPNPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      ..... : : . : . .... : : . : . : ..... :
gi|218 VIPLASARLL--SD-KVSRELYPVVHVGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
      50      60      70      80      90

      310      320      330      340      350      360
CP4_EP STLKGVTPEDRAPSMIDEYPI LavAAAFAGATVMNGLEELRVKESDRLSAVANGLKLN
      ..
gi|218 NDIKNAINLMFWGI
      100          110

>>gi|218359346|emb|CAU59832.1| Cytotoxic protein ccdB (P (110 aa)
initn: 39 initl: 39 opt: 72 Z-score: 100.7 bits: 25.8 E(): 7.1
Smith-Waterman score: 72; 29.78% identity (57.44% similar) in 94 aa
overlap (223-312:14-100)

      200      210      220      230      240
CP4_EP VIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKL----TGQVIDVPGDPSST
      : : . : . : : .....
gi|218 MPMRTGTGEMQFKVITYKRESRYRLFVDVQSDIIDITPG--RRM
      10      20      30      40

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLMPNPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      ..... : : . : . .... : : . : . : ..... :
gi|218 VIPLASARLL--SD-KVSRELYPVVHVGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
      50      60      70      80      90

      310      320      330      340      350      360
CP4_EP STLKGVTPEDRAPSMIDEYPI LavAAAFAGATVMNGLEELRVKESDRLSAVANGLKLN
      ..
gi|218 NDIKNAINLMFWGI
      100          110
```

>>gi|186703041|gb|ACC91755.1| F-plasmid toxin [Cloning v (101 aa)  
initn: 39 init1: 39 opt: 71 Z-score: 100.2 bits: 25.6 E(): 7.5  
Smith-Waterman score: 71; 29.787% identity (56.383% similar) in 94 aa  
overlap (223-312:5-91)

```

      200      210      220      230      240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGK----TGQVIDVPGDPSST
      : : . : : : :
gi|186      MQFKVYTYKRESRYRLFVDVQSDIIDTPG--RRR
      10      20      30
```

```

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLNMPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      ..... : : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|186 VIPLASARLL--SD-KVSRELYPVVHIGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
      40      50      60      70      80
```

```

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGLKLN
      . :
gi|186 NDIKNAINLMFWGI
      90      100
```

>>gi|62550776|emb|CAH64699.1| toxin [uncultured bacteriu (101 aa)  
initn: 39 init1: 39 opt: 71 Z-score: 100.2 bits: 25.6 E(): 7.5  
Smith-Waterman score: 71; 29.787% identity (56.383% similar) in 94 aa  
overlap (223-312:5-91)

```

      200      210      220      230      240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGK----TGQVIDVPGDPSST
      : : . : : : :
gi|625      MQFKVYTYKRESRYRLFVDVQSDIIDTPG--RRR
      10      20      30
```

```

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLNMPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      ..... : : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|625 VIPLASARLL--SD-KVSRELYPVVHIGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
      40      50      60      70      80
```

```

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGLKLN
      . :
gi|625 NDIKNAINLMFWGI
      90      100
```

>>gi|186703052|gb|ACC91764.1| F-plasmid toxin [Cloning v (101 aa)  
initn: 39 init1: 39 opt: 71 Z-score: 100.2 bits: 25.6 E(): 7.5  
Smith-Waterman score: 71; 29.787% identity (56.383% similar) in 94 aa  
overlap (223-312:5-91)

```

      200      210      220      230      240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGK----TGQVIDVPGDPSST
      : : . : : : :
gi|186      MQFKVYTYKRESRYRLFVDVQSDIIDTPG--RRR
      10      20      30
```

```

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLNMPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      ..... : : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|186 VIPLASARLL--SD-KVSRELYPVVHIGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
      40      50      60      70      80
```

```

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGLKLN
      . :
gi|186 NDIKNAINLMFWGI
      90      100
```

>>gi|186703035|gb|ACC91751.1| F-plasmid toxin [Cloning v (101 aa)  
initn: 39 init1: 39 opt: 71 Z-score: 100.2 bits: 25.6 E(): 7.5  
Smith-Waterman score: 71; 29.787% identity (56.383% similar) in 94 aa  
overlap (223-312:5-91)

```

      200      210      220      230      240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGK----TGQVIDVPGDPSST
      : : . : : : :
gi|186      MQFKVYTYKRESRYRLFVDVQSDIIDTPG--RRR
      10      20      30
```

```

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLNMPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      ..... : : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|186 VIPLASARLL--SD-KVSRELYPVVHIGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
      40      50      60      70      80
```

```

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGLKLN
      . :
gi|186 NDIKNAINLMFWGI
      90      100
```

>>gi|186703057|gb|ACC91768.1| F-plasmid toxin [Cloning v (101 aa)  
initn: 39 init1: 39 opt: 71 Z-score: 100.2 bits: 25.6 E(): 7.5  
Smith-Waterman score: 71; 29.787% identity (56.383% similar) in 94 aa  
overlap (223-312:5-91)

```

      200      210      220      230      240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGK----TGQVIDVPGDPSST
      : : . : : : :
gi|186      MQFKVYTYKRESRYRLFVDVQSDIIDTPG--RRR
      10      20      30
```

```

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
.....: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|186 VIPLASARLL--SD-KVSRELYPVVHIGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
      40      50      60      70      80

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSAVANGKLKN
. .:
gi|186 NDIKNAINLMFWGI
      90      100

>>gi|186703047|gb|ACC91760.1| F-plasmid toxin [Cloning v (101 aa)
  initn: 39 initl: 39 opt: 71 Z-score: 100.2 bits: 25.6 E(): 7.5
Smith-Waterman score: 71; 29.787% identity (56.383% similar) in 94 aa
overlap (223-312:5-91)

      200      210      220      230      240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKL---TGQVIDVPGDPSST
      : . . : .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|186      MQFKVYTYKRESRYRLFVDVQSDIIDTPG--RRM
      10      20      30

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
.....: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|186 VIPLASARLL--SD-KVSRELYPVVHIGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
      40      50      60      70      80

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSAVANGKLKN
. .:
gi|186 NDIKNAINLMFWGI
      90      100

>>gi|25988999|gb|AAN76305.1| gyrase target toxin [his-3 (101 aa)
  initn: 39 initl: 39 opt: 71 Z-score: 100.2 bits: 25.6 E(): 7.5
Smith-Waterman score: 71; 29.787% identity (56.383% similar) in 94 aa
overlap (223-312:5-91)

      200      210      220      230      240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKL---TGQVIDVPGDPSST
      : . . : .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|259      MQFKVYTYKRESRYRLFVDVQSDIIDTPG--RRM
      10      20      30

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
.....: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|259 VIPLASARLL--SD-KVSRELYPVVHIGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
```

```

      40      50      60      70      80
      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSAVANGKLKN
. .:
gi|259 NDIKNAINLMFWGI
      90      100

>>gi|3337026|dbj|BAA31785.1| cytotoxic protein LetB [Esc (101 aa)
  initn: 39 initl: 39 opt: 71 Z-score: 100.2 bits: 25.6 E(): 7.5
Smith-Waterman score: 71; 29.787% identity (56.383% similar) in 94 aa
overlap (223-312:5-91)

      200      210      220      230      240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKL---TGQVIDVPGDPSST
      : . . : .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|333      MQFKVYTYKRESRYRLFVDVQSDIIDTPG--RRM
      10      20      30

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
.....: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|333 VIPLASARLL--SD-KVSRELYPVVHIGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
      40      50      60      70      80

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSAVANGKLKN
. .:
gi|333 NDIKNAINLMFWGI
      90      100

>>gi|186703038|gb|ACC91753.1| F-plasmid toxin [Cloning v (101 aa)
  initn: 39 initl: 39 opt: 71 Z-score: 100.2 bits: 25.6 E(): 7.5
Smith-Waterman score: 71; 29.787% identity (56.383% similar) in 94 aa
overlap (223-312:5-91)

      200      210      220      230      240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKL---TGQVIDVPGDPSST
      : . . : .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|186      MQFKVYTYKRESRYRLFVDVQSDIIDTPG--RRI
      10      20      30

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
.....: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|186 VIPLASARLL--SD-KVSRELYPVVHIGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
      40      50      60      70      80

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSAVANGKLKN
. .:
```

```

gi|197                                     ILVQEQAGSPSTAVDTGRVIPSPGIPVRELIWNLTNSRP--QQVY
                                         10      20      30      40

                               270      280      290      300      310
CP4_EP  ILNVLMNPT--RTGLILTLQEMGADIEVINPRLAGGEDVADLVRVRS---TLKGVTVPED
        :  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
gi|197  IYFSAVDALGGRVNLALVSNRRADDEVFVLRVPVRQGGRPLLGIRIGNDAFFTAHAIAAMRNN
        50      60      70      80      90      100

                               320      330      340      350      360      370
CP4_EP  RAPSMIDEYPIILAVAAAFAGATVMNGLEELRVKESDRLSAVANGLKLNQVDCDEGETSL
        :  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
gi|197  DAPALVEEVYNFFRDSRDPVHQALNWMIL
        110     120     130

>>gi|54145467|gb|AAV31087.1| cytolethal distending toxin (154 aa)
      initn: 45 initl: 45 opt: 73 Z-score: 98.7 bits: 25.9 E(): 9.2
Smith-Waterman score: 73; 22.449% identity (59.184% similar) in 98 aa
overlap (235-327:41-137)

                               210      220      230      240      250      260
CP4_EP  KMLQGGFANLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSSTAFPLVAALLVPGSDVT
        :  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
gi|541  INVRQLVSGENAVDILAVQEQAGSPSTAVDTGRVIPSPGIPVRELIWNLTNSRP--QQVY
        20      30      40      50      60

                               270      280      290      300      310
CP4_EP  ILNVLMNPT--RTGLILTLQEMGADIEVINPRLAGGEDVADLVRVRS---TLKGVTVPED
        :  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
gi|541  IYFSAVDALGGRVNLALVSNRQADEVFVLSVVRQGGRPLLGIRIGNDAFFTAHAIAARNN
        70      80      90      100     110     120

                               320      330      340      350      360      370
CP4_EP  RAPSMIDEYPIILAVAAAFAGATVMNGLEELRVKESDRLSAVANGLKLNQVDCDEGETSL
        :  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
gi|541  DAPELVEEVYSFFRDSRDPVHQALN
        130     140     150

>>gi|54145471|gb|AAV31089.1| cytolethal distending toxin (154 aa)
      initn: 45 initl: 45 opt: 73 Z-score: 98.7 bits: 25.9 E(): 9.2
Smith-Waterman score: 73; 22.449% identity (59.184% similar) in 98 aa
overlap (235-327:41-137)

                               210      220      230      240      250      260
CP4_EP  KMLQGGFANLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSSTAFPLVAALLVPGSDVT
        :  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
gi|541  INVRQLVSGENAVDILAVQEQAGSPSTAVDTGRVIPSPGIPVRELIWNLTNSRP--QQVY
        20      30      40      50      60

                               270      280      290      300      310
CP4_EP  ILNVLMNPT--RTGLILTLQEMGADIEVINPRLAGGEDVADLVRVRS---TLKGVTVPED

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```

CP4_EP RAPSMIDEYPIILAVAAAFEGATVMNGLEELRVKESDRLSAVANGKLNGVDCDEGETSL
      :: ....
gi|541 DAPELVVEEVYSFFRDSRDPVHQALN
      130      140      150

>>gi|58045080|gb|AAW64850.1| post-segregation toxin [Shi (108 aa)
initn: 39 initl: 39 opt: 70 Z-score: 98.3 bits: 25.3 E(): 9.7
Smith-Waterman score: 70; 28.723% identity (58.511% similar) in 94 aa
overlap (223-312:12-98)

      200      210      220      230      240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKL----TGQVIDVPGDPSST
      : . . : . : : . . . . .
gi|580 MRTGTGEMQFKVYAYKRESRYRLFVDVQSDIIDTPG--RRM
      10      20      30

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLNMPRTTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|580 VIPLASARLL--SD-KVSRELYPVVHVGD-ESWRMMTTDMASV-PIFVIGEEVADLSHRE
      40      50      60      70      80      90

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPIILAVAAAFEGATVMNGLEELRVKESDRLSAVANGKLN
      . :
gi|580 NDIKNAINLMFWGI
      100

>>gi|56383108|gb|AAL72356.2| post-segregation toxin [Shi (108 aa)
initn: 39 initl: 39 opt: 70 Z-score: 98.3 bits: 25.3 E(): 9.7
Smith-Waterman score: 70; 28.723% identity (58.511% similar) in 94 aa
overlap (223-312:12-98)

      200      210      220      230      240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKL----TGQVIDVPGDPSST
      : . . : . : : . . . . .
gi|563 MRTGTGEMQFKVYAYKRESRYRLFVDVQSDIIDTPG--RRM
      10      20      30

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLNMPRTTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|563 VIPLASARLL--SD-KVSRELYPVVHVGD-ESWRMMTTDMASV-PIFVIGEEVADLSHRE
      40      50      60      70      80      90

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPIILAVAAAFEGATVMNGLEELRVKESDRLSAVANGKLN
      . :
gi|563 NDIKNAINLMFWGI
      100

```

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```

      opt      E()
< 20 281432    0:=====
22   338      0:=          one = represents 27921 library sequences
24   859     17:*
26  2560     374:*
28  9356    4037:*
30 33052 24526:*
32 98385 94834:===*
34 238098 257179:=====*
36 500393 528185:=====*
38 837541 872893:=====*
```



```
40 1223914 1217609:=====*
42 1479515 1488379:=====*
44 1608426
1641821:=====*
46 1675230
1672235:=====*
48 1603961
1600972:=====*
50 1461509 1460894:=====*
52 1287205 1284369:=====*
54 1070076 1097077:=====*
56 882542 916395:=====*
58 731035 752343:=====*
60 587613 609442:=====*
62 471280 488592:=====*
64 373109 388574:=====*
66 295225 307117:=====*
68 227519 241572:=====*
70 178743 189310:=====*
72 141233 147928:=====*
74 109800 115334:=====*
76 86657 89767:=====*
78 66745 69775:=====*
80 50982 54179:=====*
82 40021 41446:=====*
84 30522 32830:=====*
86 24801 25402:=====*
88 18268 19655:=====*
90 14774 15208:=====*
92 11331 11767:=====*
94 8755 9105:=====*
96 6930 7045:=====*
98 5436 5451:=====*
100 4416 4218:=====*
102 3939 3263:=====*
104 9212 2525:=====*
106 2408 1954:=====*
108 1642 1512:=====*
110 1854 1170:=====*
112 1250 905:=====*
114 802 700:=====*
116 696 542:=====*
118 594 419:=====*
>120 9241 324:=====*
4761287459 residues in 17815538 sequences
statistics sampled from 60000 to 17802282 sequences
Expectation_n fit: rho(ln(x))= 5.99400.000185; mu= 7.2282 0.010
mean_var=79.266116.392, 0's: 959 Z-trim: 980 B-trim: 2811 in 1/62
Lambda= 0.144056
Kolmogorov-Smirnov statistic: 0.0165 (N=29) at 88
```

```
FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 37, opt: 25, open/ext: -10/-2, width: 16
The best scores are:
opt bits
E(17815538)
gi|27549260|gb|AAO17037.1| CP4EPSPS protein [synth ( 455) 2917 615.6 1.8e-173
gi|18266432|gb|AAL67577.1|AF464188_1 CP4EPSPS [Gly ( 455) 2917 615.6 1.8e-173
gi|144974765|gb|ABP12476.1| Sequence 70 from paten ( 455) 2917 615.6 1.8e-173
gi|281079467|gb|ADA36175.1| Sequence 15 from paten ( 455) 2917 615.6 1.8e-173
gi|197053766|gb|ACH25464.1| Sequence 16 from paten ( 455) 2909 613.9 5.7e-173
gi|2484147|gb|AAB72283.1|I49176 Sequence 3 from pa ( 455) 2909 613.9 5.7e-173
gi|2485224|gb|AAB73360.1|I44449 Sequence 3 from pa ( 455) 2909 613.9 5.7e-173
gi|5957547|gb|AAE08221.1| Sequence 3 from patent U ( 455) 2909 613.9 5.7e-173
gi|144974726|gb|ABP12437.1| Sequence 3 from patent ( 455) 2909 613.9 5.7e-173
gi|217243929|gb|ACK18296.1| Sequence 1 from patent ( 455) 2909 613.9 5.7e-173
gi|62318479|dbj|BAD94823.1| 5-enol-pyruvylshikimat ( 527) 2886 609.2 1.8e-171
gi|15073182|emb|CAC41690.1| Putative 3-phosphoshik ( 455) 2685 567.4 5.8e-159
gi|227343087|gb|ACP27305.1| 3-phosphoshikimate 1-c ( 448) 2670 564.3 5e-158
gi|150030157|gb|ABR62274.1| 3-phosphoshikimate 1-c ( 456) 2660 562.2 2.1e-157
gi|115254522|emb|CAK05596.1| putative 3-phosphoshi ( 452) 2563 542.0 2.5e-151
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gi 78363826 gb ABB41791.1  3-phosphoshikimate 1-ca ( 445) 1270 273.3 1.9e-70	gi 9107493 gb AAF85123.1 AE004043_7 3-phosphoshiki ( 454) 1198 258.3 6.3e-66
gi 183210388 gb ACC57786.1  5-enolpyruvylshikimate ( 756) 1273 274.0 2e-70	gi 167290928 gb ABE243792.1  Sequence 17730 from pa ( 454) 1198 258.3 6.3e-66
gi 53758016 gb AAU92307.1  3-phosphoshikimate 1-ca ( 422) 1269 273.1 2.1e-70	gi 198247672 gb ACH83265.1  3-phosphoshikimate 1-c ( 433) 1196 257.9 8e-66
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gi 219678890 gb EED35239.1  3-phosphoshikimate 1-c ( 433) 1267 272.7 2.9e-70	gi 78035677 emb CAJ23368.1  3-phosphoshikimate 1-c ( 440) 1196 257.9 8.1e-66
gi 148513208 gb ABQ80068.1  3-phosphoshikimate 1-c ( 746) 1270 273.4 3e-70	gi 21107840 gb AAM36518.1  3-phosphoshikimate 1-ca ( 440) 1194 257.5 1.1e-65
gi 169758566 gb ACA71882.1  3-phosphoshikimate 1-c ( 746) 1268 273.0 4e-70	gi 42681983 gb AAS28448.1  Sequence 3590 from pate ( 773) 1196 258.0 1.3e-65
gi 33703074 gb AAQ27549.1  Sequence 4521 from pate ( 758) 1268 273.0 4.1e-70	gi 222440562 gb EEE47241.1  EPSP synthase (3-phosp ( 289) 1189 256.4 1.5e-65
gi 68345959 gb AAY93565.1  prephenate dehydrogenas ( 741) 1267 272.8 4.6e-70	gi 167282500 gb ABZ35364.1  Sequence 9302 from pat ( 408) 1191 256.9 1.6e-65
gi 142060811 gb ECV26044.1  hypothetical protein G ( 437) 1263 271.8 5.2e-70	gi 167282697 gb ABZ35561.1  Sequence 9499 from pat ( 412) 1191 256.9 1.6e-65
gi 166858861 gb ABY97268.1  3-phosphoshikimate 1-c ( 746) 1265 272.4 6.2e-70	gi 167288949 gb ABZ41813.1  Sequence 15751 from pa ( 408) 1190 256.7 1.8e-65
gi 136410014 gb EBN98241.1  hypothetical protein G ( 445) 1261 271.4 7e-70	gi 167289333 gb ABZ42197.1  Sequence 16135 from pa ( 408) 1190 256.7 1.8e-65
gi 24983266 gb AAN67390.1 AE016365_5 prephenate de ( 746) 1264 272.2 7.1e-70	gi 148280723 gb ABQ54811.1  3-phosphoshikimate 1-c ( 433) 1189 256.5 2.2e-65
gi 95109658 emb CAK14359.1  putative prephenate de ( 746) 1264 272.2 7.1e-70	gi 218306685 emb CAU98758.1  unnamed protein produ ( 435) 1189 256.5 2.2e-65
gi 219996023 gb ACL72625.1  3-phosphoshikimate 1-c ( 441) 1256 270.4 1.4e-69	gi 52628760 gb AAU27501.1  3-phosphoshikimate 1-ca ( 433) 1187 256.0 2.9e-65
gi 262312455 gb EEY93540.1  conserved hypothetical ( 749) 1259 271.1 1.5e-69	gi 142559088 gb ECY95157.1  hypothetical protein G ( 431) 1185 255.6 3.9e-65
gi 91797377 gb ABE59516.1  3-phosphoshikimate 1-ca ( 750) 1259 271.1 1.5e-69	gi 143358135 gb EDE53806.1  hypothetical protein G ( 467) 1185 255.6 4.2e-65
gi 143443468 gb EDE98739.1  hypothetical protein G ( 422) 1255 270.2 1.6e-69	gi 92393712 gb ABE74987.1  prephenate dehydrogenas ( 780) 1188 256.4 4.2e-65
gi 148572136 gb ABQ94195.1  3-phosphoshikimate 1-c ( 770) 1256 270.5 2.3e-69	gi 188520832 gb ACD58777.1  3-phosphoshikimate 1-c ( 440) 1184 255.4 4.6e-65
gi 143957288 gb EDH84919.1  hypothetical protein G ( 499) 1250 269.2 3.8e-69	gi 58426603 gb AAW75640.1  3-phosphoshikimate 1-ca ( 440) 1184 255.4 4.6e-65
gi 121588771 gb ABM61351.1  3-phosphoshikimate 1-c ( 444) 1246 268.3 6.1e-69	gi 84367863 dbj BAE69021.1  3-phosphoshikimate 1-c ( 440) 1184 255.4 4.6e-65
gi 135102048 gb EBF50494.1  hypothetical protein G ( 383) 1244 267.9 7.2e-69	gi 214037923 gb EEB78587.1  3-phosphoshikimate 1-c ( 434) 1182 255.0 6e-65
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gi 89951391 gb ABD81406.1  prephenate dehydrogenas ( 745) 1246 268.4 9.5e-69	gi 53751114 emb CAH12525.1  3-phosphoshikimate 1-c ( 433) 1176 253.8 1.4e-64
gi 262299019 gb EEY86932.1  3-phosphoshikimate 1-c ( 748) 1246 268.4 9.6e-69	gi 56686249 dbj BAD79471.1  3-phosphoshikimate 1-c ( 448) 1165 251.5 7.2e-64
gi 145570888 gb ABP79994.1  3-phosphoshikimate 1-c ( 706) 1244 268.0 1.2e-68	gi 81167924 gb ABBS56264.1  3-phosphoshikimate 1-ca ( 448) 1165 251.5 7.2e-64
gi 49531306 emb CAG69018.1  bifunctional protein [ ( 748) 1244 268.0 1.3e-68	gi 142228751 gb ECW55704.1  hypothetical protein G ( 363) 1162 250.8 9.2e-64
gi 142461568 gb ECY24891.1  hypothetical protein G ( 433) 1238 266.6 1.9e-68	gi 147850559 emb CAK28053.1  3-phosphoshikimate 1- ( 437) 1160 250.4 1.4e-63
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gi 219677398 gb EED33763.1  3-phosphoshikimate 1-c ( 436) 1236 266.2 2.5e-68	gi 71038727 gb AAZ19035.1  3-phosphoshikimate 1-ca ( 778) 1163 251.2 1.5e-63

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gi 147847907 emb CAK23458.1  3-phosphoshikimate 1- ( 439) 1157 249.8 2.2e-63	gi 257777792 gb ACV61686.1  3-phosphoshikimate 1-c ( 429) 1105 239.0 3.9e-60
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gi 218173786 gb ACK72519.1  3-phosphoshikimate 1-c ( 448) 1154 249.2 3.5e-63	gi 154355047 gb ABS76509.1  3-phosphoshikimate 1-c ( 438) 1091 236.1 3e-59
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gi 143267007 gb EDE01582.1  hypothetical protein G ( 382) 1150 248.3 5.4e-63	gi 169803915 gb ACA82533.1  3-phosphoshikimate 1-c ( 431) 1089 235.7 3.9e-59
gi 1653564 dbj BAA18477.1  3-phosphoshikimate 1-ca ( 447) 1149 248.2 7.2e-63	gi 135045054 gb EBF14105.1  hypothetical protein G ( 439) 1089 235.7 4e-59
gi 2484184 gb AAB72320.1 I49213 Sequence 67 from p ( 447) 1149 248.2 7.2e-63	gi 144072878 gb EDI67260.1  hypothetical protein G ( 416) 1085 234.8 6.8e-59
gi 167275962 gb ABZ28826.1  Sequence 2764 from pat ( 447) 1149 248.2 7.2e-63	gi 85773124 gb ABC79961.1  3-phosphoshikimate 1-ca ( 440) 1083 234.4 9.5e-59
gi 5957584 gb AAE08258.1  Sequence 67 from patent ( 447) 1149 248.2 7.2e-63	gi 77996387 gb ABB15286.1  3-phosphoshikimate 1-ca ( 428) 1081 234.0 1.2e-58
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gi 219993190 gb ACL69793.1  3-phosphoshikimate 1-c ( 430) 1142 246.7 1.9e-62	gi 143627605 gb EDF93941.1  hypothetical protein G ( 436) 1078 233.4 1.9e-58
gi 135895733 gb EBK54414.1  hypothetical protein G ( 435) 1142 246.7 1.9e-62	gi 135065714 gb EBF27273.1  hypothetical protein G ( 517) 1079 233.6 2e-58
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gi 86557342 gb ABD02299.1  3-phosphoshikimate 1-ca ( 434) 1138 245.9 3.4e-62	gi 141843988 gb ECT64267.1  hypothetical protein G ( 327) 1071 231.9 4.2e-58
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gi 269468607 gb EEZ80251.1  5-enolpyruvylshikimate ( 434) 1134 245.0 6.1e-62	gi 136626616 gb EBP36954.1  hypothetical protein G ( 349) 1069 231.5 5.9e-58
gi 86555472 gb ABD00430.1  3-phosphoshikimate 1-ca ( 444) 1131 244.4 9.5e-62	gi 22777464 dbj BAC13736.1  5-enolpyruvylshikimat ( 429) 1070 231.7 6.1e-58
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gi 143772965 gb EDG71093.1  hypothetical protein G ( 441) 1130 244.2 1.1e-61	gi 219953181 gb ACX63565.1  3-phosphoshikimate 1-c ( 440) 1070 231.7 6.2e-58
gi 135056108 gb EBF21159.1  hypothetical protein G ( 458) 1130 244.2 1.1e-61	gi 136112196 gb EBL99481.1  hypothetical protein G ( 353) 1067 231.1 7.9e-58
gi 135831629 gb EBK12121.1  hypothetical protein G ( 339) 1128 243.7 1.2e-61	gi 20516024 gb AAM24270.1  5-enolpyruvylshikimate- ( 423) 1067 231.1 9.2e-58
gi 146274052 dbj BAF59801.1  5-enolpyruvylshikimat ( 431) 1129 244.0 1.2e-61	gi 160360305 gb ABX31919.1  3-phosphoshikimate 1-c ( 432) 1067 231.1 9.4e-58
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gi 256589111 gb ACU99997.1  3-phosphoshikimate 1-c ( 448) 1127 243.6 1.7e-61	gi 261374423 gb ACX77166.1  3-phosphoshikimate 1-c ( 427) 1066 230.9 1.1e-57
gi 225643623 gb ACN98673.1  3-phosphoshikimate 1-c ( 431) 1125 243.2 2.2e-61	gi 35211601 dbj BAC88979.1  3-phosphoshikimate 1-c ( 432) 1066 230.9 1.1e-57
gi 158305702 gb ABW27319.1  3-phosphoshikimate 1-c ( 446) 1123 242.8 3e-61	gi 223698046 gb ACN18589.1  3-phosphoshikimate 1-c ( 428) 1065 230.7 1.2e-57
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gi 142682488 gb EC281982.1  hypothetical protein G ( 441) 1121 242.3 4e-61	gi 223698218 gb ACN18718.1  3-phosphoshikimate 1-c ( 428) 1065 230.7 1.2e-57
gi 142815727 gb EDA79221.1  hypothetical protein G ( 419) 1119 241.9 5.1e-61	gi 223698190 gb ACN18697.1  3-phosphoshikimate 1-c ( 428) 1065 230.7 1.2e-57
gi 134051714 gb ABO49685.1  3-phosphoshikimate 1-c ( 429) 1119 241.9 5.2e-61	gi 223697902 gb ACN18481.1  3-phosphoshikimate 1-c ( 428) 1065 230.7 1.2e-57
gi 167592737 gb ABZ84485.1  3-phosphoshikimate 1-c ( 424) 1117 241.5 6.9e-61	gi 223697898 gb ACN18478.1  3-phosphoshikimate 1-c ( 428) 1065 230.7 1.2e-57
gi 123963875 gb ABM78631.1  EPSP synthase (3-phosp ( 441) 1116 241.3 8.2e-61	gi 5957585 gb AAE08259.1  Sequence 69 from patent ( 443) 1065 230.7 1.3e-57
gi 33634587 emb CAE20573.1  EPSP synthase (3-phosp ( 441) 1116 241.3 8.2e-61	gi 2485262 gb AAB73398.1 I44487 Sequence 69 from p ( 443) 1065 230.7 1.3e-57
gi 113881454 gb ABI46412.1  3-phosphoshikimate 1-c ( 439) 1115 241.1 9.5e-61	gi 472932 emb CAA82544.1  enolpyruvylshikimate 3-p ( 443) 1065 230.7 1.3e-57
gi 212013111 gb ACJ20491.1  3-phosphoshikimate 1-c ( 438) 1114 240.9 1.1e-60	gi 2484185 gb AAB72321.1 I49214 Sequence 69 from p ( 443) 1065 230.7 1.3e-57
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gi 196183554 gb EDX78537.1  3-phosphoshikimate 1-c ( 453) 1111 240.3 1.7e-60	gi 196193797 gb EDX88756.1  3-phosphoshikimate 1-c ( 752) 1067 231.2 1.5e-57
gi 135817147 gb EBK02991.1  hypothetical protein G ( 333) 1108 239.6 2e-60	gi 189421466 gb ACD95864.1  3-phosphoshikimate 1-c ( 434) 1063 230.3 1.7e-57
gi 212011386 gb ACJ18767.1  3-phosphoshikimate 1-c ( 438) 1109 239.8 2.2e-60	gi 110169280 gb ABG53820.1  3-phosphoshikimate 1-c ( 462) 1062 230.1 2e-57
gi 22294064 dbj BAC07895.1  3-phosphoshikimate 1-c ( 440) 1108 239.6 2.6e-60	gi 212560430 gb ACJ33485.1  5-enolpyruvylshikimate ( 428) 1060 229.7 2.6e-57
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gi 142912654 gb EDB47050.1  hypothetical protein G ( 437) 1106 239.2 3.5e-60	gi 143040508 gb EDC37864.1  hypothetical protein G ( 324) 1056 228.8 3.6e-57

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gi 197088984 gb ACH40255.1	3-phosphoshikimate 1-c	( 429)	1057	229.0	4e-57	gi 187426429 gb ACD05708.1	3-phosphoshikimate 1-c	( 435)	1031	223.6	1.7e-55
gi 144049341 gb EDI49929.1	hypothetical protein G	( 434)	1057	229.0	4e-57	gi 144053315 gb EDI52883.1	hypothetical protein G	( 435)	1030	223.4	2e-55
gi 135675261 gb EBJ14661.1	hypothetical protein G	( 312)	1055	228.6	4e-57	gi 143212092 gb EDD62650.1	hypothetical protein G	( 440)	1030	223.4	2e-55
gi 139614992 gb ECG28587.1	hypothetical protein G	( 296)	1053	228.1	5.1e-57	gi 124514310 gb EAY55824.1	3-phosphoshikimate 1-c	( 454)	1030	223.4	2e-55
gi 144022190 gb EDI30532.1	hypothetical protein G	( 355)	1054	228.4	5.2e-57	gi 142267869 gb ECW84629.1	hypothetical protein G	( 424)	1029	223.2	2.2e-55
gi 143998481 gb EDI13750.1	hypothetical protein G	( 434)	1055	228.6	5.3e-57	gi 136251086 gb EBM89813.1	hypothetical protein G	( 439)	1029	223.2	2.3e-55
gi 72001739 gb AAZ57541.1	3-phosphoshikimate 1-ca	( 444)	1055	228.6	5.4e-57	gi 91070245 gb ABE11164.1	EPSP synthase [uncultur	( 436)	1028	223.0	2.6e-55
gi 56380573 dbj BAD76481.1	3-phosphoshikimate 1-c	( 427)	1054	228.4	6.1e-57	gi 143440288 gb EDE96880.1	hypothetical protein G	( 450)	1027	222.8	3.1e-55
gi 83573093 gb ABC19645.1	3-phosphoshikimate 1-ca	( 435)	1054	228.4	6.2e-57	gi 257820270 gb EEV47418.1	3-phosphoshikimate 1-c	( 431)	1026	222.6	3.5e-55
gi 196170465 gb ACG71438.1	3-phosphoshikimate 1-c	( 440)	1053	228.2	7.2e-57	gi 257836234 gb EEV61308.1	3-phosphoshikimate 1-c	( 431)	1026	222.6	3.5e-55
gi 197627301 gb EDY39860.1	3-phosphoshikimate 1-c	( 441)	1053	228.2	7.2e-57	gi 257832317 gb EEV58738.1	3-phosphoshikimate 1-c	( 431)	1026	222.6	3.5e-55
gi 142180162 gb ECW18900.1	hypothetical protein G	( 665)	1055	228.7	7.7e-57	gi 142796331 gb EDA64709.1	hypothetical protein G	( 436)	1026	222.6	3.5e-55
gi 136364387 gb EBN66848.1	hypothetical protein G	( 346)	1051	227.7	7.8e-57	gi 142700747 gb ECZ95072.1	hypothetical protein G	( 438)	1026	222.6	3.5e-55
gi 143140739 gb EDD11230.1	hypothetical protein G	( 437)	1051	227.8	9.5e-57	gi 142089244 gb ECV49966.1	hypothetical protein G	( 447)	1026	222.6	3.6e-55
gi 135394319 gb EBH34333.1	hypothetical protein G	( 446)	1051	227.8	9.7e-57	gi 134284387 gb ABO69382.1	5-enolpyruvylshikimate	( 429)	1025	222.4	4e-55
gi 77545564 gb ABA89126.1	3-phosphoshikimate 1-ca	( 431)	1050	227.6	1.1e-56	gi 142343370 gb ECX40386.1	hypothetical protein G	( 437)	1025	222.4	4e-55
gi 146232268 gb ABQ13246.1	3-phosphoshikimate 1-c	( 442)	1050	227.6	1.1e-56	gi 91070157 gb ABE11079.1	EPSP synthase 3-p [uncu	( 449)	1025	222.4	4.1e-55
gi 33238026 gb AAQ00093.1	5-enolpyruvylshikimate-	( 444)	1050	227.6	1.1e-56	gi 137453563 gb EBU18911.1	hypothetical protein G	( 299)	1022	221.7	4.5e-55
gi 116097111 gb ABJ62262.1	3-phosphoshikimate 1-c	( 434)	1048	227.2	1.5e-56	gi 242391389 dbj BAH81848.1	3-phosphoshikimate 1-	( 430)	1024	222.2	4.6e-55
gi 123198314 gb ABM69955.1	EPSP synthase (3-phosp	( 436)	1048	227.2	1.5e-56	gi 257823269 gb EEV50201.1	3-phosphoshikimate 1-c	( 431)	1024	222.2	4.6e-55
gi 143346942 gb EDE47625.1	hypothetical protein G	( 452)	1048	227.2	1.5e-56	gi 142552593 gb ECY90600.1	hypothetical protein G	( 432)	1024	222.2	4.6e-55
gi 55771839 dbj BAD70280.1	3-phosphoshikimate 1-c	( 427)	1047	226.9	1.7e-56	gi 142400398 gb ECX79396.1	hypothetical protein G	( 449)	1024	222.2	4.8e-55
gi 46196018 gb AAS80436.1	3-phosphoshikimate 1-ca	( 427)	1046	226.7	1.9e-56	gi 135374189 gb EBV20771.1	hypothetical protein G	( 414)	1023	222.0	5.1e-55
gi 39984592 gb AAR35978.1	3-phosphoshikimate 1-ca	( 429)	1046	226.7	1.9e-56	gi 142076285 gb ECV39284.1	hypothetical protein G	( 430)	1023	222.0	5.3e-55
gi 143061916 gb EDC53506.1	hypothetical protein G	( 432)	1045	226.5	2.2e-56	gi 146426078 emb CAM89510.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 159888754 gb ABX08968.1	EPSP synthase (3-phosp	( 445)	1045	226.5	2.3e-56	gi 146426070 emb CAM89501.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 140139249 gb ECJ80061.1	hypothetical protein G	( 293)	1042	225.8	2.5e-56	gi 146426954 emb CAM89870.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 226095016 dbj BAH43458.1	3-phosphoshikimate 1-	( 426)	1044	226.3	2.6e-56	gi 146426038 emb CAM89465.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 256791333 gb ACV22003.1	3-phosphoshikimate 1-c	( 439)	1044	226.3	2.6e-56	gi 146426994 emb CAM89915.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 146397030 gb ABQ25663.1	3-phosphoshikimate 1-c	( 428)	1042	225.9	3.4e-56	gi 146426086 emb CAM89519.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 138838604 gb ECC09871.1	hypothetical protein G	( 340)	1038	225.0	5e-56	gi 146426094 emb CAM89528.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 206602804 gb EDZ39285.1	3-phosphoshikimate 1-c	( 454)	1039	225.3	5.5e-56	gi 146426962 emb CAM89879.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 135494224 gb EBI00757.1	hypothetical protein G	( 385)	1038	225.1	5.6e-56	gi 146426978 emb CAM89897.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 123960447 gb ABM75230.1	EPSP synthase (3-phosp	( 422)	1038	225.1	6e-56	gi 146426938 emb CAM89852.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 207088576 gb EDZ65848.1	3-phosphoshikimate 1-c	( 444)	1038	225.1	6.3e-56	gi 146426102 emb CAM89537.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 76882029 gb ABA56710.1	3-phosphoshikimate 1-ca	( 444)	1038	225.1	6.3e-56	gi 146426046 emb CAM89474.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 143333051 gb EDE38631.1	hypothetical protein G	( 428)	1037	224.9	7e-56	gi 146426350 emb CAM89816.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 134267287 gb ABO67482.1	3-phosphoshikimate 1-c	( 432)	1037	224.9	7.1e-56	gi 146427026 emb CAM89951.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 143926783 gb EDH62981.1	hypothetical protein G	( 436)	1037	224.9	7.1e-56	gi 146426062 emb CAM89492.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 251774476 gb ACT17057.1	3-phosphoshikimate 1-c	( 429)	1036	224.7	8.1e-56	gi 146426030 emb CAM89456.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 136170720 gb EBM35960.1	hypothetical protein G	( 435)	1036	224.7	8.2e-56	gi 146427002 emb CAM89924.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 123200279 gb ABM71887.1	EPSP synthase (3-phosp	( 438)	1036	224.7	8.3e-56	gi 146427034 emb CAM89960.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 135777024 gb EBJ77664.1	hypothetical protein G	( 414)	1035	224.4	9.1e-56	gi 146426946 emb CAM89861.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 141174096 gb ECQ14403.1	hypothetical protein G	( 315)	1032	223.8	1.1e-55	gi 146427018 emb CAM89942.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 167282168 gb ABZ35032.1	Sequence 8970 from pat	( 424)	1033	224.0	1.2e-55	gi 146426054 emb CAM89483.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 167290440 gb ABZ43304.1	Sequence 17242 from pa	( 431)	1033	224.0	1.3e-55	gi 146426358 emb CAM89825.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 10174284 dbj BAB05386.1	5-enolpyruvoylshikimat	( 431)	1033	224.0	1.3e-55	gi 146426986 emb CAM89906.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 222447240 gb ACM51506.1	3-phosphoshikimate 1-c	( 435)	1033	224.0	1.3e-55	gi 146426022 emb CAM89447.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 163666945 gb ABY33311.1	3-phosphoshikimate 1-c	( 435)	1033	224.0	1.3e-55	gi 146427010 emb CAM89933.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 142953087 gb EDB75980.1	hypothetical protein G	( 446)	1032	223.8	1.5e-55	gi 146426930 emb CAM89843.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55
gi 143633398 gb EDF97125.1	hypothetical protein G	( 452)	1032	223.8	1.5e-55	gi 146426922 emb CAM89834.1	3-phosphoshikimate-1-	( 188)	1018	220.8	5.3e-55

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gi 143683282 gb EDG25451.1	hypothetical protein G	( 290)	1020	221.3	5.8e-55	gi 146427954 emb CAM90374.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 135970867 gb EBL05592.1	hypothetical protein G	( 449)	1022	221.8	6.4e-55	gi 146425934 emb CAM89348.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 83756719 gb ABC44832.1	3-phosphoshikimate 1-ca	( 430)	1021	221.5	7.1e-55	gi 146427178 emb CAM90122.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 262335582 gb ACY49379.1	3-phosphoshikimate 1-c	( 434)	1021	221.5	7.1e-55	gi 146426334 emb CAM89798.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 257474981 gb ACV55301.1	3-phosphoshikimate 1-c	( 442)	1020	221.3	8.4e-55	gi 146427282 emb CAM90239.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427218 emb CAM90167.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146425407 emb CAM89213.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427314 emb CAM90275.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146426254 emb CAM89708.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427330 emb CAM90293.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146425950 emb CAM89366.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427354 emb CAM90320.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427098 emb CAM90032.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427202 emb CAM90149.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146426214 emb CAM89663.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427930 emb CAM90347.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427226 emb CAM90176.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427058 emb CAM89987.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427298 emb CAM90257.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427042 emb CAM89969.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427346 emb CAM90311.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146426158 emb CAM89600.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146426126 emb CAM89564.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146425431 emb CAM89240.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427306 emb CAM90266.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 169402995 emb CAO99131.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146425918 emb CAM89330.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427210 emb CAM90158.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146426270 emb CAM89726.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427066 emb CAM89996.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146426166 emb CAM89609.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146425966 emb CAM89384.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427962 emb CAM90383.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146426182 emb CAM89627.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427130 emb CAM90068.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427290 emb CAM90248.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427970 emb CAM90392.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427146 emb CAM90086.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427170 emb CAM90113.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427074 emb CAM90005.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146426142 emb CAM89582.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427922 emb CAM90338.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146425423 emb CAM89231.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146426286 emb CAM89744.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146426150 emb CAM89591.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146425471 emb CAM89285.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146425447 emb CAM89258.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427234 emb CAM90185.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146426310 emb CAM89771.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146426198 emb CAM89645.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427938 emb CAM90356.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427082 emb CAM90014.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146425439 emb CAM89249.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427186 emb CAM90131.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146426262 emb CAM89717.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146425487 emb CAM89303.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427114 emb CAM90050.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146426342 emb CAM89807.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146426238 emb CAM89690.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427050 emb CAM89978.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146425958 emb CAM89375.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427162 emb CAM90104.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427154 emb CAM90095.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146426118 emb CAM89555.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427946 emb CAM90365.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146426206 emb CAM89654.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146426970 emb CAM89888.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146425998 emb CAM89420.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146426006 emb CAM89429.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146426294 emb CAM89753.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427258 emb CAM90212.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146426222 emb CAM89672.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427274 emb CAM90230.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146425415 emb CAM89222.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146426110 emb CAM89546.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 169402997 emb CAO99132.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427362 emb CAM90329.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146425391 emb CAM89195.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427322 emb CAM90284.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427106 emb CAM90041.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146425926 emb CAM89339.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146426174 emb CAM89618.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427338 emb CAM90302.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146426278 emb CAM89735.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427250 emb CAM90203.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146425982 emb CAM89402.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146426246 emb CAM89699.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146426302 emb CAM89762.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146425399 emb CAM89204.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427090 emb CAM90023.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146425495 emb CAM89312.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146425990 emb CAM89411.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146426014 emb CAM89438.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146426318 emb CAM89780.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146427138 emb CAM90077.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55
gi 146427122 emb CAM90059.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55	gi 146426326 emb CAM89789.1	3-phosphoshikimate-1-	( 188)	1014	219.9	9.5e-55

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gi 146425974 emb CAM89393.1	3-phosphoshikimate-1-	(188)	1014	219.9	9.5e-55	gi 146425239 emb CAM89024.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 146427194 emb CAM90140.1	3-phosphoshikimate-1-	(188)	1014	219.9	9.5e-55	gi 146425255 emb CAM89042.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 146425463 emb CAM89276.1	3-phosphoshikimate-1-	(188)	1014	219.9	9.5e-55	gi 146425247 emb CAM89033.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 146425455 emb CAM89267.1	3-phosphoshikimate-1-	(188)	1014	219.9	9.5e-55	gi 146425271 emb CAM89060.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 146425503 emb CAM89321.1	3-phosphoshikimate-1-	(188)	1014	219.9	9.5e-55	gi 146425287 emb CAM89078.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 146425479 emb CAM89294.1	3-phosphoshikimate-1-	(188)	1014	219.9	9.5e-55	gi 146425193 emb CAM88970.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 146426230 emb CAM89681.1	3-phosphoshikimate-1-	(188)	1014	219.9	9.5e-55	gi 146425295 emb CAM89087.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 146425942 emb CAM89357.1	3-phosphoshikimate-1-	(188)	1014	219.9	9.5e-55	gi 146425311 emb CAM89105.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 146426134 emb CAM89573.1	3-phosphoshikimate-1-	(188)	1014	219.9	9.5e-55	gi 146425263 emb CAM89051.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 146427242 emb CAM90194.1	3-phosphoshikimate-1-	(188)	1014	219.9	9.5e-55	gi 146425231 emb CAM89015.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 146427266 emb CAM90221.1	3-phosphoshikimate-1-	(188)	1014	219.9	9.5e-55	gi 146425215 emb CAM88997.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 146427978 emb CAM90401.1	3-phosphoshikimate-1-	(188)	1014	219.9	9.5e-55	gi 146425343 emb CAM89141.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 146426190 emb CAM89636.1	3-phosphoshikimate-1-	(188)	1014	219.9	9.5e-55	gi 146425199 emb CAM88979.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 157387605 gb ABV50342.1	EPSP synthase (3-phosp	(436)	1019	221.1	9.6e-55	gi 146425279 emb CAM89069.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 256583260 gb ACU94394.1	3-phosphoshikimate 1-c	(443)	1019	221.1	9.7e-55	gi 146425319 emb CAM89114.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 257818523 gb EEV45851.1	3-phosphoshikimate 1-c	(431)	1018	220.9	1.1e-54	gi 146425303 emb CAM89096.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 257825716 gb EEV52342.1	3-phosphoshikimate 1-c	(431)	1018	220.9	1.1e-54	gi 146425327 emb CAM89123.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54
gi 260073869 gb EEW62193.1	3-phosphoshikimate 1-c	(431)	1018	220.9	1.1e-54	gi 143387961 gb EDE69064.1	hypothetical protein G	(450)	1013	219.9	2.3e-54
gi 257830747 gb EEV57354.1	3-phosphoshikimate 1-c	(431)	1018	220.9	1.1e-54	gi 142420835 gb ECX94792.1	hypothetical protein G	(408)	1012	219.7	2.5e-54
gi 337495991 gb AAQ46605.1	Sequence 7163 from pate	(431)	1018	220.9	1.1e-54	gi 143006344 gb EDC12996.1	hypothetical protein G	(368)	1011	219.4	2.6e-54
gi 143005904 gb EDC12672.1	hypothetical protein G	(435)	1018	220.9	1.1e-54	gi 219541331 gb ACL23069.1	3-phosphoshikimate 1-c	(435)	1012	219.7	2.6e-54
gi 209540793 gb ACI61369.1	3-phosphoshikimate 1-c	(427)	1017	220.7	1.3e-54	gi 13622461 gb AAK34180.1	putative 3-phosphoshiki	(430)	1011	219.5	3e-54
gi 21904763 gb AAM79634.1	putative 3-phosphoshiki	(430)	1017	220.7	1.3e-54	gi 71853696 gb AAZ51719.1	3-phosphoshikimate 1-ca	(430)	1011	219.5	3e-54
gi 28810994 dbj BAC63928.1	putative 3-phosphoshik	(430)	1017	220.7	1.3e-54	gi 260552604 gb EEX25604.1	3-phosphoshikimate 1-c	(432)	1011	219.5	3e-54
gi 145411265 gb ABP68269.1	3-phosphoshikimate 1-c	(433)	1017	220.7	1.3e-54	gi 142511258 gb ECY60760.1	hypothetical protein G	(444)	1011	219.5	3.1e-54
gi 126543020 gb ABO17262.1	EPSP synthase (3-phosp	(436)	1017	220.7	1.3e-54	gi 78193339 gb ABB31106.1	3-phosphoshikimate 1-ca	(429)	1010	219.3	4.6e-54
gi 140350316 gb ECL17116.1	hypothetical protein G	(315)	1015	220.2	1.3e-54	gi 257812675 gb EEV41433.1	3-phosphoshikimate 1-c	(431)	1010	219.3	3.5e-54
gi 221564743 gb ACM20715.1	3-phosphoshikimate 1-c	(429)	1016	220.5	1.5e-54	gi 135521687 gb EBI18400.1	hypothetical protein G	(424)	1009	219.1	3.9e-54
gi 94546168 gb ABF36215.1	3-phosphoshikimate 1-ca	(430)	1016	220.5	1.5e-54	gi 142886839 gb EDB28223.1	hypothetical protein G	(437)	1009	219.1	4e-54
gi 134271853 emb CAM30088.1	3-phosphoshikimate 1-	(430)	1016	220.5	1.5e-54	gi 143595742 gb EDF78097.1	hypothetical protein G	(452)	1009	219.1	4.2e-54
gi 50903493 gb AAT87208.1	3-phosphoshikimate 1-ca	(430)	1016	220.5	1.5e-54	gi 16414538 emb CAC97267.1	aroE [Listeria innocua	(428)	1008	218.8	4.6e-54
gi 94542283 gb ABF32332.1	3-phosphoshikimate 1-ca	(430)	1016	220.5	1.5e-54	gi 94544175 gb ABF34223.1	3-phosphoshikimate 1-ca	(430)	1008	218.8	4.6e-54
gi 135062405 gb EBF25151.1	hypothetical protein G	(284)	1013	219.8	1.6e-54	gi 170015681 emb CAP05278.1	3-phosphoshikimate-1-	(188)	1003	217.6	4.6e-54
gi 142745913 gb EDA27571.1	hypothetical protein G	(427)	1015	220.3	1.7e-54	gi 142517542 gb ECY65289.1	hypothetical protein G	(329)	1005	218.2	5.6e-54
gi 2983892 gb AAC07443.1	5-enolpyruvylshikimate-3	(431)	1015	220.3	1.7e-54	gi 142714811 gb EDA05134.1	hypothetical protein G	(333)	1005	218.2	5.7e-54
gi 167273311 gb ABZ26175.1	Sequence 113 from pate	(431)	1015	220.3	1.7e-54	gi 56909911 dbj BAD64438.1	3-phosphoshikimate 1-c	(430)	1006	218.4	6.1e-54
gi 160429338 gb ABX42901.1	3-phosphoshikimate 1-c	(436)	1015	220.3	1.7e-54	gi 146425351 emb CAM89150.1	3-phosphoshikimate-1-	(188)	1001	217.2	6.2e-54
gi 221537862 gb EEE40315.1	3-phosphoshikimate 1-c	(436)	1015	220.3	1.7e-54	gi 225702144 emb CAW99831.1	3-phosphoshikimate 1-	(427)	1005	218.2	7.1e-54
gi 71802853 gb AAX72206.1	3-phosphoshikimate 1-ca	(427)	1014	220.1	1.9e-54	gi 143838364 gb EDG99243.1	hypothetical protein G	(449)	1004	218.0	8.5e-54
gi 19748517 gb AAL97960.1	putative 3-phosphoshiki	(427)	1014	220.1	1.9e-54	gi 152023794 gb ABS21564.1	3-phosphoshikimate 1-c	(424)	1003	217.8	9.3e-54
gi 94548104 gb ABF38150.1	3-phosphoshikimate 1-ca	(427)	1014	220.1	1.9e-54	gi 136143934 gb EBM18523.1	hypothetical protein G	(432)	1002	217.6	1.1e-53
gi 114337807 gb ABT68655.1	3-phosphoshikimate 1-c	(428)	1014	220.1	1.9e-54	gi 159890538 gb ABX03618.1	3-phosphoshikimate 1-c	(431)	1001	217.4	1.3e-53
gi 146425383 emb CAM89186.1	3-phosphoshikimate-1-	(188)	1009	218.9	2e-54	gi 142401851 gb ECX80480.1	hypothetical protein G	(435)	1001	217.4	1.3e-53
gi 146425375 emb CAM89177.1	3-phosphoshikimate-1-	(188)	1009	218.9	2e-54	gi 138829093 gb ECC05312.1	hypothetical protein G	(299)	998	216.7	1.4e-53
gi 146425359 emb CAM89159.1	3-phosphoshikimate-1-	(188)	1009	218.9	2e-54	gi 223698038 gb ACN18583.1	3-phosphoshikimate 1-c	(428)	1000	217.2	1.5e-53
gi 146425367 emb CAM89168.1	3-phosphoshikimate-1-	(188)	1009	218.9	2e-54	gi 223698102 gb ACN18631.1	3-phosphoshikimate 1-c	(428)	1000	217.2	1.5e-53
gi 78712497 gb ABB49674.1	3-phosphoshikimate 1-ca	(436)	1014	220.1	2e-54	gi 223697854 gb ACN18445.1	3-phosphoshikimate 1-c	(428)	1000	217.2	1.5e-53
gi 143578905 gb EDF73147.1	hypothetical protein G	(438)	1014	220.1	2e-54	gi 223697730 gb ACN18352.1	3-phosphoshikimate 1-c	(428)	1000	217.2	1.5e-53
gi 146425335 emb CAM89132.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54	gi 223698130 gb ACN18652.1	3-phosphoshikimate 1-c	(428)	1000	217.2	1.5e-53
gi 146425223 emb CAM89006.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54	gi 223698010 gb ACN18562.1	3-phosphoshikimate 1-c	(428)	1000	217.2	1.5e-53
gi 146425207 emb CAM88988.1	3-phosphoshikimate-1-	(188)	1008	218.7	2.3e-54	gi 223697738 gb ACN18358.1	3-phosphoshikimate 1-c	(428)	1000	217.2	1.5e-53



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gi 223697934 gb ACN18505.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 251849803 gb EES77762.1	conserved hypothetical	( 424)	993	215.7	3.9e-53
gi 223697726 gb ACN18349.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 222114137 emb CAR42616.1	3-phosphoshikimate	1- ( 427)	993	215.7	4e-53
gi 223698014 gb ACN18565.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697946 gb ACN18514.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223697834 gb ACN18430.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223698158 gb ACN18673.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223697734 gb ACN18355.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223698018 gb ACN18568.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223698138 gb ACN18658.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223698078 gb ACN18613.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223697782 gb ACN18391.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697870 gb ACN18457.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223698126 gb ACN18649.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223698006 gb ACN18559.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223698122 gb ACN18646.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223698058 gb ACN18598.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223698178 gb ACN18688.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697962 gb ACN18526.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223697818 gb ACN18418.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697894 gb ACN18475.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223697846 gb ACN18439.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697878 gb ACN18463.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223697786 gb ACN18394.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697954 gb ACN18520.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223697830 gb ACN18427.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697974 gb ACN18535.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223698142 gb ACN18661.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697926 gb ACN18499.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223698106 gb ACN18634.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223698150 gb ACN18667.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223697890 gb ACN18472.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697882 gb ACN18466.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223697806 gb ACN18409.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 16411376 emb CAD00001.1	aroE [Listeria monocyt	( 428)	993	215.7	4e-53
gi 223698098 gb ACN18628.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697742 gb ACN18361.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223697790 gb ACN18397.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697810 gb ACN18412.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223698134 gb ACN18655.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223698090 gb ACN18622.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223697798 gb ACN18403.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697850 gb ACN18442.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223697794 gb ACN18400.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223698042 gb ACN18586.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223698146 gb ACN18664.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697922 gb ACN18496.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223697754 gb ACN18370.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697814 gb ACN18415.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223698094 gb ACN18625.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 116742243 emb CAK21367.1	aroA [Listeria welshi	( 428)	993	215.7	4e-53
gi 223698202 gb ACN18706.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697914 gb ACN18490.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223697930 gb ACN18502.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697762 gb ACN18376.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223697822 gb ACN18421.1	3-phosphoshikimate	1-c	( 428)	1000	217.2	1.5e-53	gi 223697994 gb ACN18550.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 138083024 gb EBX64838.1	hypothetical protein G	( 304)	997	216.5	1.7e-53	gi 223697966 gb ACN18529.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53	
gi 183226926 dbj BAG27442.1	3-phosphoshikimate	1-	( 432)	998	216.8	2e-53	gi 223697942 gb ACN18511.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 142300251 gb ECX08327.1	hypothetical protein G	( 437)	998	216.8	2e-53	gi 223697998 gb ACN18553.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53	
gi 33639902 emb CAE19072.1	EPSP synthase (3-phosp	( 438)	998	216.8	2e-53	gi 223697858 gb ACN18448.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53	
gi 142082676 gb ECV44561.1	hypothetical protein G	( 438)	998	216.8	2e-53	gi 223698166 gb ACN18679.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53	
gi 143268164 gb EDE02418.1	hypothetical protein G	( 350)	996	216.3	2.2e-53	gi 223698070 gb ACN18607.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53	
gi 55738600 gb AAV62241.1	3-phosphoshikimate	1-ca	( 427)	997	216.6	2.2e-53	gi 223697982 gb ACN18541.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223698074 gb ACN18610.1	3-phosphoshikimate	1-c	( 428)	997	216.6	2.2e-53	gi 223697758 gb ACN18373.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 118417505 gb ABK85924.1	3-phosphoshikimate	1-c	( 429)	997	216.6	2.2e-53	gi 223698214 gb ACN18715.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 222455696 gb ACM59958.1	3-phosphoshikimate	1-c	( 433)	997	216.6	2.3e-53	gi 223697766 gb ACN18379.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 167282943 gb ABZ35807.1	Sequence 9745 from pat	( 417)	996	216.3	2.5e-53	gi 223697978 gb ACN18538.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53	
gi 140074666 gb ECJ36897.1	hypothetical protein G	( 299)	994	215.9	2.5e-53	gi 223698030 gb ACN18577.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53	
gi 55736709 gb AAV60351.1	3-phosphoshikimate	1-ca	( 427)	996	216.4	2.6e-53	gi 223697746 gb ACN18364.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 219539671 gb ACL21410.1	3-phosphoshikimate	1-c	( 435)	996	216.4	2.6e-53	gi 223698026 gb ACN18574.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 89334456 dbj BAE84051.1	hypothetical protein [	( 435)	996	216.4	2.6e-53	gi 223698222 gb ACN18721.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53	
gi 156232792 gb ABU57575.1	3-phosphoshikimate	1-c	( 431)	995	216.1	3e-53	gi 223698162 gb ACN18676.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 143233975 gb EDD78447.1	hypothetical protein G	( 437)	995	216.1	3e-53	gi 223698198 gb ACN18703.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53	
gi 143019553 gb EDC22663.1	hypothetical protein G	( 437)	995	216.1	3e-53	gi 223697918 gb ACN18493.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53	
gi 195974537 gb ACG62063.1	3-phosphoshikimate	1-c	( 427)	994	215.9	3.4e-53	gi 223697774 gb ACN18385.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 225699532 emb CAW93107.1	3-phosphoshikimate	1-	( 427)	994	215.9	3.4e-53	gi 223697938 gb ACN18508.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 223698086 gb ACN18619.1	3-phosphoshikimate	1-c	( 428)	994	215.9	3.4e-53	gi 223698034 gb ACN18580.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53
gi 42737974 gb AAS41905.1	3-phosphoshikimate	1-ca	( 429)	994	215.9	3.5e-53	gi 223697874 gb ACN18460.1	3-phosphoshikimate	1-c ( 428)	993	215.7	4e-53

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gi 223698210 gb ACN18712.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 229268332 gb ACQ49969.1	3-phosphoshikimate	1-c	( 429)	986	214.3	1.1e-52
gi 223698206 gb ACN18709.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 47551804 gb AAT32071.2	3-phosphoshikimate	1-ca	( 429)	986	214.3	1.1e-52
gi 223697770 gb ACN18382.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 227006491 gb ACP16234.1	3-phosphoshikimate	1-c	( 429)	986	214.3	1.1e-52
gi 223698182 gb ACN18691.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 49179677 gb AAT55053.1	3-phosphoshikimate	1-ca	( 429)	986	214.3	1.1e-52
gi 223697906 gb ACN18484.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 30257544 gb AAP26774.1	3-phosphoshikimate	1-ca	( 429)	986	214.3	1.1e-52
gi 223698066 gb ACN18604.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 270278481 gb EFA24327.1	3-phosphoshikimate	1-c	( 427)	985	214.1	1.3e-52
gi 223697862 gb ACN18451.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 223698118 gb ACN18643.1	3-phosphoshikimate	1-c	( 428)	985	214.1	1.3e-52
gi 223698110 gb ACN18637.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 217062913 gb ACJ77163.1	3-phosphoshikimate	1-c	( 429)	985	214.1	1.3e-52
gi 223698002 gb ACN18556.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 197205480 gb ACH47977.1	3-phosphoshikimate	1-c	( 427)	984	213.9	1.5e-52
gi 223697778 gb ACN18388.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 142478979 gb ECY37940.1	hypothetical protein G	( 434)	984	213.9	1.5e-52	
gi 223698154 gb ACN18670.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 136325414 gb EBN40361.1	hypothetical protein G	( 443)	984	213.9	1.5e-52	
gi 223697970 gb ACN18532.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 143475974 gb EDF19143.1	hypothetical protein G	( 425)	983	213.6	1.7e-52	
gi 223697990 gb ACN18547.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 262261195 gb EEY79894.1	3-phosphoshikimate	1-c	( 427)	983	213.6	1.7e-52
gi 223697986 gb ACN18544.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 139854247 gb ECH92990.1	hypothetical protein G	( 307)	981	213.2	1.7e-52	
gi 223698174 gb ACN18685.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 223698082 gb ACN18616.1	3-phosphoshikimate	1-c	( 428)	982	213.4	1.9e-52
gi 223698054 gb ACN18595.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 136028731 gb EBL43002.1	hypothetical protein G	( 418)	981	213.2	2.2e-52	
gi 223697838 gb ACN18433.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 142787199 gb EDA57892.1	hypothetical protein G	( 308)	979	212.8	2.3e-52	
gi 223698194 gb ACN18700.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 269788888 gb ACZ41029.1	3-phosphoshikimate	1-c	( 439)	981	213.2	2.3e-52
gi 223698170 gb ACN18682.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 136256857 gb EBM93634.1	hypothetical protein G	( 434)	980	213.0	2.6e-52	
gi 223697886 gb ACN18469.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 135032108 gb EBF05757.1	hypothetical protein G	( 416)	979	212.8	2.9e-52	
gi 223698022 gb ACN18571.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 157075738 gb ABV10421.1	3-phosphoshikimate	1-c	( 427)	979	212.8	3e-52
gi 223697866 gb ACN18454.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 257800017 gb EEV29069.1	3-phosphoshikimate	1-c	( 429)	979	212.8	3e-52
gi 223697910 gb ACN18487.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 257806578 gb EBN35400.1	3-phosphoshikimate	1-c	( 429)	979	212.8	3e-52
gi 223697958 gb ACN18523.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 182629665 gb ACB90613.1	3-phosphoshikimate	1-c	( 431)	979	212.8	3e-52
gi 223698050 gb ACN18592.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 143656521 gb EDG10782.1	hypothetical protein G	( 436)	979	212.8	3e-52	
gi 223697950 gb ACN18517.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 24377157 gb AAN58503.1	AE014920_1 5-enolpyruvyl	( 427)	978	212.6	3.4e-52	
gi 223698226 gb ACN18724.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 52348641 gb AAU41275.1	AroE [Bacillus lichenif	( 428)	978	212.6	3.5e-52	
gi 223698062 gb ACN18601.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 145903020 gb AAU23920.3	5-enolpyruvoylshikimat	( 428)	978	212.6	3.5e-52	
gi 223697842 gb ACN18436.1	3-phosphoshikimate	1-c	( 428)	993	215.7	4e-53	gi 257809882 gb EEV38702.1	3-phosphoshikimate	1-c	( 429)	978	212.6	3.5e-52
gi 135911255 gb EBK65191.1	hypothetical protein G	( 411)	992	215.5	4.4e-53	gi 228190727 gb ACP61997.1	Sequence 6491 from pat	( 464)	978	212.6	3.7e-52		
gi 49330610 gb AAT61256.1	3-phosphoshikimate	1-ca	( 429)	992	215.5	4.6e-53	gi 136404114 gb EBN94215.1	hypothetical protein G	( 389)	976	212.2	4.2e-52	
gi 136005759 gb EBL27605.1	hypothetical protein G	( 436)	992	215.5	4.7e-53	gi 163862888 gb ABY43947.1	3-phosphoshikimate	1-c	( 429)	976	212.2	4.6e-52	
gi 223697826 gb ACN18424.1	3-phosphoshikimate	1-c	( 428)	991	215.3	5.3e-53	gi 148569867 gb ABQ92012.1	3-phosphoshikimate	1-c	( 433)	976	212.2	4.7e-52
gi 218537723 gb ACK90121.1	3-phosphoshikimate	1-c	( 429)	991	215.3	5.3e-53	gi 160221349 gb ABX11283.1	5-enolpyruvylshikimate	( 454)	976	212.2	4.8e-52	
gi 225787055 gb ACO27272.1	3-phosphoshikimate	1-c	( 429)	991	215.3	5.3e-53	gi 144215829 gb EDJ70892.1	hypothetical protein G	( 390)	975	212.0	4.9e-52	
gi 51976038 gb AAU17588.1	3-phosphoshikimate	1-ca	( 429)	991	215.3	5.3e-53	gi 142484138 gb ECY41805.1	hypothetical protein G	( 408)	975	212.0	5.1e-52	
gi 139748663 gb ECH19156.1	hypothetical protein G	( 292)	988	214.6	5.9e-53	gi 168995736 gb ACA36348.1	3-phosphoshikimate	1-c	( 427)	975	212.0	5.3e-52	
gi 134964169 gb EBE59745.1	hypothetical protein G	( 425)	990	215.1	6.1e-53	gi 134873812 gb EBD99647.1	hypothetical protein G	( 284)	972	211.3	5.8e-52		
gi 225876989 emb CAS05698.1	Putative 5-enolpyruvy	( 428)	990	215.1	6.1e-53	gi 220674574 emb CAR69137.1	3-phosphoshikimate	1-	( 427)	974	211.8	6.1e-52	
gi 46881426 gb AAT04722.1	3-phosphoshikimate	1-ca	( 428)	990	215.1	6.1e-53	gi 225728344 gb ACO24195.1	3-phosphoshikimate	1-c	( 427)	974	211.8	6.1e-52
gi 217333195 gb ACK38989.1	3-phosphoshikimate	1-c	( 428)	990	215.1	6.1e-53	gi 225720612 gb AC016466.1	3-phosphoshikimate	1-c	( 427)	974	211.8	6.1e-52
gi 116100807 gb ABJ65953.1	3-phosphoshikimate	1-c	( 427)	989	214.9	7.1e-53	gi 225722753 gb ACO18606.1	3-phosphoshikimate	1-c	( 427)	974	211.8	6.1e-52
gi 218162110 gb ACK62102.1	3-phosphoshikimate	1-c	( 429)	989	214.9	7.1e-53	gi 254997648 dbj BAH88249.1	5-enolpyruvylshikimat	( 427)	974	211.8	6.1e-52	
gi 29896607 gb AAP09886.1	3-phosphoshikimate	1-ca	( 429)	989	214.9	7.1e-53	gi 225724804 gb ACO20656.1	3-phosphoshikimate	1-c	( 427)	974	211.8	6.1e-52
gi 223697802 gb ACN18406.1	3-phosphoshikimate	1-c	( 428)	988	214.7	8.2e-53	gi 194357091 gb ACE55539.1	3-phosphoshikimate	1-c	( 427)	974	211.8	6.1e-52
gi 223698114 gb ACN18640.1	3-phosphoshikimate	1-c	( 428)	988	214.7	8.2e-53	gi 56634435 gb AAW08901.1	Sequence 4297 from pate	( 459)	974	211.8	6.5e-52	
gi 218541446 gb ACK93840.1	3-phosphoshikimate	1-c	( 429)	988	214.7	8.2e-53	gi 239807780 gb ACS24845.1	3-phosphoshikimate	1-c	( 428)	973	211.6	7.1e-52
gi 136315089 gb EBN33493.1	hypothetical protein G	( 448)	988	214.7	8.5e-53	gi 14972856 gb AAK75469.1	3-phosphoshikimate	1-ca	( 427)	972	211.4	8.2e-52	
gi 135571448 gb EBI50213.1	hypothetical protein G	( 418)	987	214.5	9.3e-53	gi 135426956 gb EBH56298.1	hypothetical protein G	( 425)	971	211.2	9.4e-52		
gi 118502485 gb ABK98967.1	3-phosphoshikimate	1-c	( 431)	987	214.5	9.5e-53	gi 189906152 gb ACE58407.1	Sequence 3546 from pat	( 427)	971	211.2	9.4e-52	
gi 269100864 gb AC219851.1	3-phosphoshikimate	1-c	( 436)	987	214.5	9.6e-53	gi 189895504 gb ACE53085.1	Sequence 3546 from pat	( 427)	971	211.2	9.4e-52	

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gi 118850301 gb ABL27658.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 251815711 emb CAZ51311.1	3-phosphoshikimate 1-	(	426)	960	208.9	4.6e-51
gi 182938218 gb ACC20088.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 134904510 gb EBE20044.1	hypothetical protein G	(	325)	958	208.4	4.9e-51
gi 189900828 gb ACE55746.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 167776701 gb ABZ95002.1	3-phosphoshikimate 1-c	(	428)	959	208.7	5.3e-51
gi 189885049 gb ACE48254.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 167780379 gb ABZ98677.1	3-phosphoshikimate 1-c	(	428)	959	208.7	5.3e-51
gi 196983653 gb ACG90840.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 206739263 gb ACI18321.1	3-phosphoshikimate 1-c	(	435)	959	208.7	5.4e-51
gi 118841667 gb ABL24997.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 157681517 gb ABV62661.1	3-phosphoshikimate 1-c	(	428)	958	208.5	6.2e-51
gi 167338106 gb ABZ66405.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 139732520 gb ECH09244.1	hypothetical protein G	(	292)	955	207.8	6.8e-51
gi 217237720 gb ACK13966.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 683583 emb CAA55180.1	5-enolpyruvylshikimate-3	(	430)	957	208.2	7.1e-51
gi 259333339 gb ACW44685.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 124493516 emb CAL98495.1	3-phosphoshikimate 1-	(	430)	957	208.2	7.1e-51
gi 125115865 gb ABN23906.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 143334178 gb EDE39370.1	hypothetical protein G	(	484)	957	208.3	7.9e-51
gi 5616525 gb AAD45819.1 AF169483_1	5-enolpyruvyls	(	427)	971	211.2	9.4e-52	gi 195932969 gb ACG57669.1	3-phosphoshikimate 1-c	(	427)	955	207.8	9.5e-51			
gi 112096977 gb ABI08548.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 251771402 gb EES51981.1	3-phosphoshikimate 1-c	(	446)	955	207.8	9.8e-51
gi 118899388 gb ABL49226.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 143130375 gb EDD03631.1	hypothetical protein G	(	342)	953	207.4	1e-50
gi 281104388 gb ADA5902.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 196192722 gb ABX87686.1	3-phosphoshikimate 1-c	(	409)	952	207.2	1.4e-50
gi 182925979 gb ACC14532.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 143517608 gb EDF42079.1	hypothetical protein G	(	418)	952	207.2	1.4e-50
gi 115887011 gb ABJ49677.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 143823880 gb EDG88784.1	hypothetical protein G	(	442)	952	207.2	1.5e-50
gi 115811019 gb ABJ32064.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 140283581 gb ECK73924.1	hypothetical protein G	(	280)	949	206.5	1.6e-50
gi 14112362 gb AAE57779.1	Sequence 2 from patent	(	427)	971	211.2	9.4e-52	gi 239516843 gb EEQ56709.1	conserved hypothetical	(	425)	951	207.0	1.7e-50			
gi 47241604 gb AAT16176.1	Sequence	3546	from	pate	(	427)	971	211.2	9.4e-52	gi 226090387 dbj BAH38832.1	3-phosphoshikimate 1-	(	672)	953	207.5	1.9e-50
gi 189875194 gb ACE43394.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 24194817 gb AAN48457.1 AE011307_10	3-phosphoshi	(	440)	950	206.8	2e-50
gi 125085509 gb ABN18836.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 45601534 gb AAS71015.1	3-phosphoshikimate 1-ca	(	440)	950	206.8	2e-50
gi 197051730 gb ACH23628.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 189185917 gb ACD83102.1	5-enolpyruvylshikimate	(	695)	951	207.1	2.6e-50
gi 196999282 gb ACG98297.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 125498192 gb ABX44858.1	3-phosphoshikimate 1-c	(	427)	948	206.4	2.6e-50
gi 112079923 gb ABI03507.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 257803529 gb EEV32351.1	3-phosphoshikimate 1-c	(	429)	948	206.4	2.6e-50
gi 259339911 gb ACW47959.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 116108251 gb ABJ73391.1	3-phosphoshikimate 1-c	(	430)	947	206.2	3e-50
gi 196993017 gb ACG95251.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 140263796 gb ECK64233.1	hypothetical protein G	(	273)	944	205.5	3.1e-50
gi 182920657 gb ACC11871.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 142964063 gb EDB83665.1	hypothetical protein G	(	387)	945	205.7	3.7e-50
gi 118806535 gb ABL17420.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 141901632 gb ECU04596.1	hypothetical protein G	(	291)	943	205.3	3.8e-50
gi 197042232 gb ACH18866.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 116124307 gb ABJ75578.1	3-phosphoshikimate 1-c	(	440)	943	205.3	5.5e-50
gi 197018713 gb ACH07859.1	Sequence	3546	from	pat	(	427)	971	211.2	9.4e-52	gi 116121469 gb ABJ79512.1	3-phosphoshikimate 1-c	(	440)	943	205.3	5.5e-50
gi 167291680 gb ABZ44544.1	Sequence	18482	from	pa	(	430)	971	211.2	9.5e-52	gi 138056886 gb EBX50330.1	hypothetical protein G	(	317)	940	204.7	6.4e-50
gi 12724764 gb AAK05842.1 AE006404_9	3-phosphoshik	(	430)	971	211.2	9.5e-52	gi 143505071 gb EDF35219.1	hypothetical protein G	(	392)	941	204.9	6.6e-50			
gi 136611001 gb EBP27638.1	hypothetical protein G	(	365)	970	210.9	9.5e-52	gi 255968720 gb EET99342.1	3-phosphoshikimate 1-c	(	428)	939	204.5	9.5e-50			
gi 135896096 gb EBK54670.1	hypothetical protein G	(	394)	970	210.9	1e-51	gi 256998702 gb EEU85222.1	3-phosphoshikimate 1-c	(	428)	939	204.5	9.5e-50			
gi 138507712 gb ECA07901.1	hypothetical protein G	(	321)	968	210.5	1.1e-51	gi 142439106 gb ECY08464.1	hypothetical protein G	(	285)	936	203.8	1e-49			
gi 140758638 gb ECN32069.1	hypothetical protein G	(	299)	967	210.3	1.2e-51	gi 40806387 gb AAR92125.1	5-enolpyruvylshikimate-	(	426)	938	204.3	1.1e-49			
gi 139603541 gb ECG20683.1	hypothetical protein G	(	307)	967	210.3	1.3e-51	gi 217336546 gb ACK42339.1	3-phosphoshikimate 1-c	(	433)	937	204.1	1.3e-49			
gi 136814875 gb EBQ58741.1	hypothetical protein G	(	434)	969	210.7	1.3e-51	gi 142830212 gb EDA90204.1	hypothetical protein G	(	434)	936	203.9	1.5e-49			
gi 116076465 gb ABJ54185.1	3-phosphoshikimate 1-c	(	427)	968	210.5	1.5e-51	gi 135920803 gb EBK71830.1	hypothetical protein G	(	374)	935	203.6	1.5e-49			
gi 15458865 gb AAL00033.1	3-Enolpyruvylshikimate-	(	431)	968	210.5	1.5e-51	gi 257157926 gb EEU87886.1	3-phosphoshikimate 1-c	(	428)	935	203.7	1.7e-49			
gi 14106225 gb AAE55840.1	Sequence 2 from patent	(	427)	965	209.9	2.2e-51	gi 257164438 gb EEU94398.1	3-phosphoshikimate 1-c	(	428)	935	203.7	1.7e-49			
gi 134387655 gb EBB06773.1	hypothetical protein G	(	272)	962	209.2	2.3e-51	gi 255963810 gb EET96286.1	3-phosphoshikimate 1-c	(	428)	935	203.7	1.7e-49			
gi 167289692 gb ABZ42556.1	Sequence	16494	from	pa	(	417)	964	209.7	2.5e-51	gi 142615026 gb ECZ34221.1	hypothetical protein G	(	435)	935	203.7	1.7e-49
gi 149948344 gb ABR46872.1	3-phosphoshikimate 1-c	(	425)	963	209.5	3e-51	gi 136339509 gb EBN49907.1	hypothetical protein G	(	386)	934	203.4	1.8e-49			
gi 142551989 gb ECY90178.1	hypothetical protein G	(	415)	962	209.3	3.4e-51	gi 142274829 gb ECW89740.1	hypothetical protein G	(	354)	933	203.2	1.9e-49			
gi 138658485 gb ECB10957.1	hypothetical protein G	(	299)	960	208.8	3.4e-51	gi 145691253 gb ABP91758.1	5-enolpyruvylshikimate	(	426)	934	203.5	1.9e-49			
gi 170287625 dbj BAG14146.1	3-phosphoshikimate 1-	(	430)	962	209.3	3.5e-51	gi 256711589 gb EEU26627.1	3-phosphoshikimate 1-c	(	428)	934	203.5	2e-49			
gi 154352359 gb ABS74438.1	AroE [Bacillus amylo]	(	428)	961	209.1	4e-51	gi 142661801 gb ECZ67186.1	hypothetical protein G	(	360)	932	203.0	2.2e-49			
gi 124248218 emb CAL26234.1	5-enolpyruvylshikima	(	428)	961	209.1	4e-51	gi 12407967 gb AAG53678.1 AF318277_6	3-phosphoshik	(	428)	933	203.3	2.3e-49			
gi 251819569 emb CAR45232.1	3-phosphoshikimate 1-	(	426)	960	208.9	4.6e-51	gi 144993705 gb ABP15206.1	Sequence 45 from paten	(	428)	933	203.3	2.3e-49			
gi 251818311 emb CAZ56122.1	3-phosphoshikimate 1-	(	426)	960	208.9	4.6e-51	gi 257161129 gb EEU91089.1	3-phosphoshikimate 1-c	(	428)	933	203.3	2.3e-49			

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gi 256990575 gb EEU77777.1  3-phosphoshikimate 1-c ( 428)	933	203.3	2.3e-49	gi 134965637 gb EBE60728.1  hypothetical protein G ( 399)	897	195.8	3.8e-47
gi 256598595 gb EEU17771.1  3-phosphoshikimate 1-c ( 428)	933	203.3	2.3e-49	gi 139723826 gb ECH03396.1  hypothetical protein G ( 275)	894	195.1	4.2e-47
gi 29343591 gb AAO81353.1  3-phosphoshikimate 1-ca ( 428)	933	203.3	2.3e-49	gi 135056874 gb EBF21645.1  hypothetical protein G ( 329)	895	195.3	4.3e-47
gi 256993208 gb EEU80510.1  3-phosphoshikimate 1-c ( 428)	933	203.3	2.3e-49	gi 142365697 gb ECX55533.1  hypothetical protein G ( 395)	896	195.6	4.3e-47
gi 40130701 gb AAR58446.1  Sequence 4980 from pate ( 430)	933	203.3	2.3e-49	gi 143174862 gb EDD35554.1  hypothetical protein G ( 416)	896	195.6	4.5e-47
gi 256994769 gb EEU82071.1  3-phosphoshikimate 1-c ( 428)	932	203.0	2.6e-49	gi 140985559 gb ECO85428.1  hypothetical protein G ( 269)	893	194.9	4.8e-47
gi 144974744 gb ABP12455.1  Sequence 42 from paten ( 428)	930	202.6	3.5e-49	gi 143031825 gb EDC31489.1  hypothetical protein G ( 416)	895	195.4	5.3e-47
gi 143816 gb AAA20869.1  AroE [Bacillus subtilis] ( 428)	930	202.6	3.5e-49	gi 143138582 gb EDD09641.1  hypothetical protein G ( 313)	892	194.7	6.3e-47
gi 2634678 emb CAB14176.1  3-phosphoshikimate 1-ca ( 428)	930	202.6	3.5e-49	gi 136832462 gb EBQ70477.1  hypothetical protein G ( 371)	892	194.7	7.3e-47
gi 167296372 gb ABZ49236.1  Sequence 23174 from pa ( 428)	930	202.6	3.5e-49	gi 134860307 gb EBD90420.1  hypothetical protein G ( 369)	889	194.1	1.1e-46
gi 197053765 gb ACH25463.1  Sequence 15 from paten ( 428)	930	202.6	3.5e-49	gi 229263473 gb ACQ54506.1  3-phosphoshikimate 1-c ( 442)	890	194.3	1.1e-46
gi 2485242 gb AAB73378.1 I44467 Sequence 42 from p ( 428)	930	202.6	3.5e-49	gi 138397559 gb EBZ38708.1  hypothetical protein G ( 283)	887	193.6	1.2e-46
gi 5957565 gb AAE08239.1  Sequence 42 from patent ( 428)	930	202.6	3.5e-49	gi 221240501 gb ACM13211.1  3-phosphoshikimate 1-c ( 399)	889	194.1	1.2e-46
gi 2484165 gb AAB72301.1 I49194 Sequence 42 from p ( 428)	930	202.6	3.5e-49	gi 152930690 gb ABS36189.1  3-phosphoshikimate 1-c ( 442)	887	193.7	1.8e-46
gi 135415884 gb EBH48842.1  hypothetical protein G ( 390)	929	202.4	3.7e-49	gi 152928818 gb ABS34318.1  3-phosphoshikimate 1-c ( 442)	887	193.7	1.8e-46
gi 142583289 gb ECZ12035.1  hypothetical protein G ( 407)	929	202.4	3.8e-49	gi 148288929 emb CAL83016.1  3-phosphoshikimate 1- ( 442)	887	193.7	1.8e-46
gi 256952418 gb EEU69050.1  3-phosphoshikimate 1-c ( 428)	929	202.4	4e-49	gi 226841906 gb AC084572.1  3-phosphoshikimate 1-c ( 442)	886	193.5	2e-46
gi 142459624 gb ECY23468.1  hypothetical protein G ( 287)	926	201.7	4.4e-49	gi 142654970 gb ECZ62388.1  hypothetical protein G ( 433)	883	192.9	3.1e-46
gi 256683745 gb EEU23440.1  3-phosphoshikimate 1-c ( 428)	928	202.2	4.6e-49	gi 169120913 gb ACA44749.1  3-phosphoshikimate 1-c ( 442)	883	192.9	3.1e-46
gi 256987046 gb EEU74348.1  3-phosphoshikimate 1-c ( 428)	928	202.2	4.6e-49	gi 143688892 gb EDG29042.1  hypothetical protein G ( 432)	882	192.7	3.5e-46
gi 256949481 gb EEU66113.1  3-phosphoshikimate 1-c ( 428)	928	202.2	4.6e-49	gi 136830361 gb EBQ69080.1  hypothetical protein G ( 400)	880	192.2	4.4e-46
gi 256955616 gb EEU72248.1  3-phosphoshikimate 1-c ( 428)	928	202.2	4.6e-49	gi 142014592 gb ECU84573.1  hypothetical protein G ( 416)	880	192.2	4.6e-46
gi 142340264 gb ECX38084.1  hypothetical protein G ( 383)	926	201.8	5.6e-49	gi 125714526 gb ABN53018.1  3-phosphoshikimate 1-c ( 423)	879	192.0	5.3e-46
gi 134931800 gb EBE38163.1  hypothetical protein G ( 352)	923	201.1	8.1e-49	gi 116090991 gb ABJ56145.1  3-phosphoshikimate 1-c ( 437)	879	192.0	5.5e-46
gi 142736909 gb EDA21008.1  hypothetical protein G ( 372)	920	200.5	1.3e-48	gi 169407871 gb ACA56282.1  3-phosphoshikimate 1-c ( 442)	878	191.8	6.4e-46
gi 137336724 gb EBT52837.1  hypothetical protein G ( 305)	918	200.1	1.5e-48	gi 136052580 gb EBL59062.1  hypothetical protein G ( 390)	877	191.6	6.6e-46
gi 137500819 gb EBU43511.1  hypothetical protein G ( 307)	918	200.1	1.5e-48	gi 140596163 gb ECM33153.1  hypothetical protein G ( 280)	875	191.1	6.7e-46
gi 141275643 gb ECQ84034.1  hypothetical protein G ( 251)	915	199.4	1.9e-48	gi 144136414 gb EDJ12922.1  hypothetical protein G ( 485)	878	191.9	6.9e-46
gi 140262147 gb ECK63065.1  hypothetical protein G ( 251)	911	198.6	3.4e-48	gi 152936571 gb ABS42069.1  3-phosphoshikimate 1-c ( 442)	876	191.4	8.5e-46
gi 142241906 gb ECW65482.1  hypothetical protein G ( 400)	913	199.1	3.8e-48	gi 167041247 gb ABZ06003.1  putative EPSP synthase ( 446)	876	191.4	8.6e-46
gi 134555734 gb EBC04319.1  hypothetical protein G ( 344)	912	198.9	3.9e-48	gi 142703421 gb ECZ96994.1  hypothetical protein G ( 426)	874	191.0	1.1e-45
gi 76563325 gb ABA45909.1  3-phosphoshikimate 1-ca ( 427)	912	198.9	4.6e-48	gi 142560595 gb ECY96203.1  hypothetical protein G ( 308)	871	190.3	1.3e-45
gi 22533648 gb AAM99526.1 AE014219_18 3-phosphoshi ( 427)	912	198.9	4.6e-48	gi 135727138 gb EBJ46737.1  hypothetical protein G ( 331)	871	190.3	1.4e-45
gi 134892211 gb EBE11877.1  hypothetical protein G ( 363)	911	198.7	4.7e-48	gi 134974804 gb EBE66929.1  hypothetical protein G ( 392)	872	190.6	1.4e-45
gi 136313640 gb EBN32525.1  hypothetical protein G ( 435)	912	198.9	4.7e-48	gi 138292864 gb EBY83547.1  hypothetical protein G ( 260)	869	189.1	1.5e-45
gi 142307360 gb ECX13668.1  hypothetical protein G ( 436)	912	198.9	4.7e-48	gi 135630574 gb EBI87001.1  hypothetical protein G ( 283)	869	189.9	1.6e-45
gi 140523261 gb ECM09716.1  hypothetical protein G ( 291)	909	198.2	5.1e-48	gi 142707532 gb ECZ99900.1  hypothetical protein G ( 416)	871	190.4	1.7e-45
gi 138494665 gb EBZ99748.1  hypothetical protein G ( 269)	908	198.0	5.5e-48	gi 143510416 gb EDF38005.1  hypothetical protein G ( 415)	869	190.0	2.2e-45
gi 135903877 gb EBK60098.1  hypothetical protein G ( 419)	909	198.3	7e-48	gi 134855951 gb EBD87629.1  hypothetical protein G ( 254)	865	189.0	2.6e-45
gi 23095028 emb CAD46254.1  Unknown [Streptococcus ( 427)	907	197.9	9.5e-48	gi 138461639 gb EBZ83709.1  hypothetical protein G ( 290)	865	189.0	2.9e-45
gi 134898476 gb EBE16051.1  hypothetical protein G ( 405)	906	197.6	1.1e-47	gi 143906379 gb EBH48348.1  hypothetical protein G ( 599)	869	190.0	3e-45
gi 254045793 gb ACT62586.1  3-phosphoshikimate 1-c ( 432)	904	197.2	1.5e-47	gi 143129798 gb EDD03205.1  hypothetical protein G ( 431)	867	189.5	3.1e-45
gi 143452946 gb EDF04465.1  hypothetical protein G ( 281)	900	196.3	1.8e-47	gi 142417854 gb ECX92494.1  hypothetical protein G ( 660)	868	189.8	3.8e-45
gi 28271504 emb CAD64409.1  3-phosphoshikimate 1-c ( 432)	901	196.6	2.3e-47	gi 116229535 gb ABJ88244.1  3-phosphoshikimate 1-c ( 426)	865	189.1	4e-45
gi 143396673 gb EDB73613.1  hypothetical protein G ( 356)	899	196.2	2.6e-47	gi 142699976 gb ECZ94523.1  hypothetical protein G ( 326)	863	188.7	4.3e-45
gi 138568480 gb ECA49921.1  hypothetical protein G ( 294)	897	195.7	2.9e-47	gi 142019123 gb ECU88920.1  hypothetical protein G ( 414)	864	188.9	4.5e-45
gi 135491965 gb EBH99300.1  hypothetical protein G ( 289)	896	195.5	3.3e-47	gi 143234451 gb EDD78785.1  hypothetical protein G ( 366)	863	188.7	4.7e-45
gi 142246914 gb ECW69181.1  hypothetical protein G ( 296)	896	195.5	3.4e-47	gi 137267823 gb EBT14391.1  hypothetical protein G ( 276)	861	188.2	4.9e-45
gi 142577643 gb ECZ08109.1  hypothetical protein G ( 416)	898	196.0	3.4e-47	gi 206741482 gb ACI20539.1  3-phosphoshikimate 1-c ( 430)	863	188.7	5.4e-45
gi 158140591 gb ABW18903.1  3-phosphoshikimate 1-c ( 427)	898	196.0	3.5e-47	gi 135448115 gb EBH70436.1  hypothetical protein G ( 383)	860	188.1	7.6e-45
gi 142808318 gb EDA73669.1  hypothetical protein G ( 313)	896	195.5	3.6e-47	gi 136710153 gb EBP89355.1  hypothetical protein G ( 272)	856	187.2	1e-44

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gi 143575506 gb EDF71556.1	hypothetical protein G ( 358)	857	187.4	1.1e-44	gi 257271987 gb EEV04125.1	3-phosphoshikimate 1-c ( 432)	826	181.0	1.1e-42
gi 143445598 gb EDE99944.1	hypothetical protein G ( 366)	856	187.2	1.3e-44	gi 257284701 gb EEV14821.1	3-phosphoshikimate 1-c ( 432)	826	181.0	1.1e-42
gi 141751437 gb ECT10385.1	hypothetical protein G ( 240)	853	186.5	1.4e-44	gi 49241782 emb CAG40473.1	3-phosphoshikimate 1-c ( 432)	826	181.0	1.1e-42
gi 167045751 gb ABZ10397.1	putative EPSP synthase ( 443)	856	187.3	1.5e-44	gi 257278947 gb EEV09566.1	3-phosphoshikimate 1-c ( 432)	826	181.0	1.1e-42
gi 142502060 gb ECY54068.1	hypothetical protein G ( 274)	852	186.3	1.8e-44	gi 138508120 gb ECA08043.1	hypothetical protein G ( 264)	823	180.3	1.1e-42
gi 222120489 dbj BAH17824.1	3-phosphoshikimate 1- ( 433)	854	186.8	2e-44	gi 142552699 gb ECY90674.1	hypothetical protein G ( 425)	825	180.8	1.3e-42
gi 135770651 gb EBJ73691.1	hypothetical protein G ( 349)	852	186.4	2.2e-44	gi 142973132 gb EDB89862.1	hypothetical protein G ( 258)	822	180.1	1.3e-42
gi 141716480 gb ECS90978.1	hypothetical protein G ( 351)	852	186.4	2.2e-44	gi 139178038 gb ECD94124.1	hypothetical protein G ( 315)	822	180.1	1.5e-42
gi 161726857 emb CAP47298.1	unnamed protein produ ( 439)	853	186.6	2.3e-44	gi 139089271 gb ECD33698.1	hypothetical protein G ( 268)	821	179.9	1.5e-42
gi 28203719 gb AAO36160.1	3-phosphoshikimate 1-ca ( 439)	853	186.6	2.3e-44	gi 142941353 gb EDB67616.1	hypothetical protein G ( 419)	823	180.4	1.7e-42
gi 140153247 gb ECJ87824.1	hypothetical protein G ( 307)	850	185.9	2.6e-44	gi 143051067 gb EDC45621.1	hypothetical protein G ( 338)	821	179.9	1.9e-42
gi 163861631 gb ABY42690.1	3-phosphoshikimate 1-c ( 367)	850	186.0	3.1e-44	gi 135388286 gb EBH30252.1	hypothetical protein G ( 247)	819	179.5	1.9e-42
gi 225793440 gb ACO33530.1	3-phosphoshikimate 1-c ( 433)	847	185.4	5.5e-44	gi 143823138 gb EDG88250.1	hypothetical protein G ( 277)	819	179.5	2.1e-42
gi 138199350 gb EBY35873.1	hypothetical protein G ( 281)	844	184.7	5.8e-44	gi 158604933 gb ABW74752.1	3-phosphoshikimate 1-c ( 428)	821	180.0	2.3e-42
gi 142236410 gb ECW61386.1	hypothetical protein G ( 315)	844	184.7	6.4e-44	gi 143990770 gb EDI08126.1	hypothetical protein G ( 321)	819	179.5	2.4e-42
gi 229470142 gb ACQ71914.1	3-phosphoshikimate 1-c ( 416)	845	185.0	7.1e-44	gi 82656594 emb CAI81017.1	3-phosphoshikimate 1-c ( 432)	820	179.8	2.7e-42
gi 142521472 gb ECY68161.1	hypothetical protein G ( 443)	845	185.0	7.4e-44	gi 135341079 gb EBG98573.1	hypothetical protein G ( 269)	817	179.1	2.7e-42
gi 138683081 gb ECB28394.1	hypothetical protein G ( 246)	841	184.0	8e-44	gi 143505131 gb EDF35248.1	hypothetical protein G ( 381)	819	179.5	2.8e-42
gi 135924801 gb EBK74524.1	hypothetical protein G ( 368)	843	184.5	8.5e-44	gi 136274212 gb EBN05767.1	hypothetical protein G ( 343)	817	179.1	3.4e-42
gi 14106226 gb AAE55841.1	Sequence 4 from patent ( 415)	843	184.5	9.4e-44	gi 136878306 gb EBR00609.1	hypothetical protein G ( 266)	815	178.6	3.6e-42
gi 14112363 gb AAE57780.1	Sequence 4 from patent ( 415)	843	184.5	9.4e-44	gi 139609260 gb ECG24653.1	hypothetical protein G ( 267)	815	178.6	3.6e-42
gi 143143221 gb EDD13054.1	hypothetical protein G ( 343)	841	184.1	1.1e-43	gi 140734279 gb ECN15117.1	hypothetical protein G ( 219)	813	178.2	4.1e-42
gi 171990323 gb ACB61245.1	3-phosphoshikimate 1-c ( 417)	842	184.3	1.1e-43	gi 141829663 gb ECT53965.1	hypothetical protein G ( 306)	815	178.7	4.1e-42
gi 142975716 gb EDB91669.1	hypothetical protein G ( 334)	840	183.9	1.2e-43	gi 142963473 gb EDB83252.1	hypothetical protein G ( 432)	817	179.2	4.1e-42
gi 144047589 gb EDI48620.1	hypothetical protein G ( 354)	840	183.9	1.3e-43	gi 134338102 gb EBA73894.1	hypothetical protein G ( 291)	814	178.5	4.5e-42
gi 143651447 gb EDG07727.1	hypothetical protein G ( 334)	839	183.7	1.4e-43	gi 139248991 gb ECB35883.1	hypothetical protein G ( 293)	814	178.5	4.5e-42
gi 139093977 gb ECD37104.1	hypothetical protein G ( 289)	838	183.4	1.4e-43	gi 137063356 gb EBS00002.1	hypothetical protein G ( 249)	813	178.2	4.5e-42
gi 143260329 gb EDD96800.1	hypothetical protein G ( 256)	837	183.2	1.5e-43	gi 143533533 gb EDF49839.1	hypothetical protein G ( 445)	816	178.9	4.9e-42
gi 135647562 gb EBI97552.1	hypothetical protein G ( 338)	836	183.1	2.2e-43	gi 262080109 gb ACV16078.1	3-phosphoshikimate 1-c ( 459)	816	179.0	5e-42
gi 221571690 gb ACM22502.1	3-phosphoshikimate 1-c ( 421)	837	183.3	2.3e-43	gi 189341744 gb ACD91147.1	3-phosphoshikimate 1-c ( 434)	815	178.7	5.5e-42
gi 214040543 gb EEB81191.1	3-phosphoshikimate 1-c ( 421)	837	183.3	2.3e-43	gi 138329239 gb EBZ00337.1	hypothetical protein G ( 321)	813	178.3	5.7e-42
gi 170175891 gb ACB08943.1	3-phosphoshikimate 1-c ( 421)	837	183.3	2.3e-43	gi 143906650 gb EDH48541.1	hypothetical protein G ( 662)	817	179.2	5.9e-42
gi 147735256 gb ABQ46596.1	3-phosphoshikimate 1-c ( 421)	837	183.3	2.3e-43	gi 87125900 gb ABD20414.1	3-phosphoshikimate 1-ca ( 432)	814	178.5	6.3e-42
gi 138880837 gb ECC27684.1	hypothetical protein G ( 257)	834	182.6	2.3e-43	gi 269940957 emb CBI49341.1	3-phosphoshikimate 1- ( 432)	814	178.5	6.3e-42
gi 167276129 gb ABZ28993.1	Sequence 2931 from pat ( 410)	835	182.9	2.9e-43	gi 49244747 emb CAG43183.1	3-phosphoshikimate 1-c ( 432)	814	178.5	6.3e-42
gi 4980846 gb AAD35431.1	AE001715_7 3-phosphoshiki ( 410)	835	182.9	2.9e-43	gi 150374387 dbj BAF67647.1	3-phosphoshikimate 1- ( 432)	814	178.5	6.3e-42
gi 141303260 gb ECQ94812.1	hypothetical protein G ( 320)	833	182.4	3.2e-43	gi 21204523 dbj BAB95219.1	3-PHOSPHOSHIKIMATE 1-C ( 432)	814	178.5	6.3e-42
gi 27315616 gb AAO04750.1	AE016747_247 3-phosphosh ( 433)	833	182.5	4.1e-43	gi 87202756 gb ABD30566.1	3-phosphoshikimate 1-ca ( 432)	814	178.5	6.3e-42
gi 134562359 gb EBC08340.1	hypothetical protein G ( 318)	831	182.0	4.2e-43	gi 160368441 gb ABX29412.1	3-phosphoshikimate 1-c ( 432)	814	178.5	6.3e-42
gi 135489309 gb EBH97580.1	hypothetical protein G ( 350)	830	181.8	5.3e-43	gi 281032786 gb ADA18062.1	Sequence 5610 from pat ( 435)	814	178.5	6.4e-42
gi 68447173 dbj BAE04757.1	3-phosphoshikimate 1-c ( 432)	830	181.9	6.3e-43	gi 144188786 gb EDJ51597.1	hypothetical protein G ( 603)	815	178.8	7.3e-42
gi 142087282 gb ECV48343.1	hypothetical protein G ( 425)	829	181.6	7.2e-43	gi 57284605 gb AAW36699.1	3-phosphoshikimate 1-ca ( 432)	813	178.3	7.3e-42
gi 57637630 gb AAW54418.1	3-phosphoshikimate 1-ca ( 433)	829	181.6	7.3e-43	gi 136995971 gb EBR61979.1	hypothetical protein G ( 325)	811	177.8	7.6e-42
gi 281043957 gb ADA22685.1	Sequence 3223 from pat ( 436)	829	181.6	7.4e-43	gi 136354113 gb EBN59856.1	hypothetical protein G ( 283)	810	177.7	7.8e-42
gi 259269376 gb ACW29189.1	Sequence 3223 from pat ( 436)	829	181.6	7.4e-43	gi 138555285 gb ECA40675.1	hypothetical protein G ( 267)	809	177.4	8.6e-42
gi 217109301 gb ACJ93181.1	Sequence 3223 from pat ( 436)	829	181.6	7.4e-43	gi 262075379 gb ACY11352.1	3-phosphoshikimate 1-c ( 432)	811	177.9	9.8e-42
gi 143466480 gb EDF13416.1	hypothetical protein G ( 273)	825	180.7	8.7e-43	gi 14247235 dbj BAB57626.1	3-phosphoshikimate 1-c ( 432)	811	177.9	9.8e-42
gi 207084714 gb ED262001.1	3-phosphoshikimate 1-c ( 427)	827	181.2	9.6e-43	gi 156721918 dbj BAF78335.1	3-phosphoshikimate 1- ( 432)	811	177.9	9.8e-42
gi 135095629 gb EBF46390.1	hypothetical protein G ( 225)	823	180.3	9.9e-43	gi 13701263 dbj BAB42557.1	3-phosphoshikimate 1-c ( 432)	811	177.9	9.8e-42
gi 257281670 gb EEV11807.1	3-phosphoshikimate 1-c ( 432)	826	181.0	1.1e-42	gi 135176472 gb EBF98299.1	hypothetical protein G ( 278)	808	177.2	1e-41
gi 257275030 gb EEV06517.1	3-phosphoshikimate 1-c ( 432)	826	181.0	1.1e-42	gi 143913100 gb EDH52995.1	hypothetical protein G ( 479)	811	177.9	1.1e-41

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gi 142344653 gb ECX41282.1	hypothetical protein G ( 430)	809	177.5	1.3e-41	gi 135473041 gb EBH87124.1	hypothetical protein G ( 425)	783	172.1	5.4e-40
gi 194312559 gb ACF46954.1	3-phosphoshikimate 1-c ( 434)	809	177.5	1.3e-41	gi 143880166 gb EDH29665.1	hypothetical protein G ( 333)	781	171.6	5.9e-40
gi 142888789 gb EDB29602.1	hypothetical protein G ( 430)	808	177.3	1.5e-41	gi 142062898 gb ECV27877.1	hypothetical protein G ( 430)	782	171.9	6.3e-40
gi 189496532 gb ACE05080.1	3-phosphoshikimate 1-c ( 435)	808	177.3	1.5e-41	gi 193085440 gb ACF10716.1	3-phosphoshikimate 1-c ( 434)	782	171.9	6.4e-40
gi 134547100 gb EBB99141.1	hypothetical protein G ( 336)	806	176.8	1.6e-41	gi 143263748 gb EDD99246.1	hypothetical protein G ( 430)	781	171.7	7.3e-40
gi 142309197 gb ECX15063.1	hypothetical protein G ( 340)	806	176.8	1.6e-41	gi 256008713 gb ACU54280.1	3-phosphoshikimate 1-c ( 434)	781	171.7	7.4e-40
gi 142383766 gb ECX67542.1	hypothetical protein G ( 430)	807	177.1	1.7e-41	gi 32261686 gb AAP76736.1	3-phosphoshikimate 1-ca ( 438)	781	171.7	7.4e-40
gi 78497609 gb ABB44149.1	3-phosphoshikimate 1-ca ( 428)	806	176.9	2e-41	gi 136211928 gb EBM63318.1	hypothetical protein G ( 333)	779	171.2	7.8e-40
gi 144199065 gb EDJ59187.1	hypothetical protein G ( 246)	801	175.7	2.5e-41	gi 139841346 gb ECH83875.1	hypothetical protein G ( 258)	777	170.7	8.4e-40
gi 135033333 gb EBF06615.1	hypothetical protein G ( 414)	804	176.4	2.6e-41	gi 139163008 gb ECD83628.1	hypothetical protein G ( 312)	777	170.8	9.9e-40
gi 260078368 gb EEW66073.1	LOW QUALITY PROTEIN: 3 ( 266)	801	175.7	2.7e-41	gi 135319394 gb EBG83991.1	hypothetical protein G ( 333)	777	170.8	1e-39
gi 140334519 gb ECL05829.1	hypothetical protein G ( 270)	800	175.5	3.2e-41	gi 138154978 gb EBY06220.1	hypothetical protein G ( 209)	773	169.9	1.2e-39
gi 138262365 gb EBY65200.1	hypothetical protein G ( 238)	799	175.3	3.3e-41	gi 135240518 gb EBG36889.1	hypothetical protein G ( 311)	775	170.4	1.3e-39
gi 134990285 gb EBB77443.1	hypothetical protein G ( 300)	800	175.5	3.5e-41	gi 138397214 gb EBZ38470.1	hypothetical protein G ( 334)	775	170.4	1.4e-39
gi 137254189 gb EBT06708.1	hypothetical protein G ( 285)	799	175.3	3.8e-41	gi 144025250 gb EDI32680.1	hypothetical protein G ( 308)	774	170.1	1.5e-39
gi 137335428 gb EBT52086.1	hypothetical protein G ( 303)	798	175.1	4.7e-41	gi 141897414 gb ECU01571.1	hypothetical protein G ( 305)	773	169.9	1.7e-39
gi 144219781 gb EDJ73727.1	hypothetical protein G ( 428)	800	175.6	4.7e-41	gi 136622362 gb EBP34455.1	hypothetical protein G ( 328)	772	169.7	2.1e-39
gi 135781046 gb EBJ80223.1	hypothetical protein G ( 308)	798	175.1	4.7e-41	gi 140030681 gb ECJ12144.1	hypothetical protein G ( 246)	770	169.3	2.2e-39
gi 149946465 gb ABR52401.1	3-phosphoshikimate 1-c ( 432)	800	175.6	4.8e-41	gi 138700831 gb ECB40892.1	hypothetical protein G ( 314)	771	169.5	2.4e-39
gi 147741019 gb ABQ49317.1	3-phosphoshikimate 1-c ( 432)	800	175.6	4.8e-41	gi 139949518 gb ECI57412.1	hypothetical protein G ( 283)	770	169.3	2.5e-39
gi 151422271 dbj BAF69775.1	3-phosphoshikimate 1- ( 433)	800	175.6	4.8e-41	gi 142893869 gb EDB33252.1	hypothetical protein G ( 557)	774	170.3	2.5e-39
gi 135266853 gb EBG52393.1	hypothetical protein G ( 424)	799	175.4	5.4e-41	gi 135329585 gb EBG90868.1	hypothetical protein G ( 450)	772	169.8	2.8e-39
gi 139490738 gb ECF43051.1	hypothetical protein G ( 279)	796	174.7	5.8e-41	gi 134644279 gb EBG57396.1	hypothetical protein G ( 256)	768	168.9	3e-39
gi 136328373 gb EBN42356.1	hypothetical protein G ( 293)	796	174.7	6.1e-41	gi 134947939 gb EBE48938.1	hypothetical protein G ( 308)	769	169.1	3.1e-39
gi 143414697 gb EDE83057.1	hypothetical protein G ( 429)	798	175.2	6.3e-41	gi 135183725 gb EBG02913.1	hypothetical protein G ( 265)	768	168.9	3.1e-39
gi 119355398 gb ABL66269.1	3-phosphoshikimate 1-c ( 434)	798	175.2	6.4e-41	gi 143093399 gb EDC76589.1	hypothetical protein G ( 228)	767	168.6	3.2e-39
gi 141355624 gb ECR25075.1	hypothetical protein G ( 303)	795	174.5	7.2e-41	gi 5957566 gb AAE08240.1	Sequence 44 from patent ( 430)	770	169.4	3.6e-39
gi 135098087 gb EBF47962.1	hypothetical protein G ( 222)	793	174.0	7.3e-41	gi 2485243 gb AAB73379.1	I44468 Sequence 44 from p ( 430)	770	169.4	3.6e-39
gi 143971097 gb EDH94528.1	hypothetical protein G ( 570)	798	175.3	8.1e-41	gi 2484166 gb AAB72302.1	I49195 Sequence 44 from p ( 430)	770	169.4	3.6e-39
gi 137854115 gb EBW38016.1	hypothetical protein G ( 286)	793	174.1	9.1e-41	gi 152956 gb AAA71897.1	3-phosphoshikimate-1-carb ( 430)	770	169.4	3.6e-39
gi 141976830 gb ECU56929.1	hypothetical protein G ( 330)	793	174.1	1e-40	gi 144974745 gb ABP12456.1	Sequence 44 from paten ( 430)	770	169.4	3.6e-39
gi 142680915 gb ECZ80867.1	hypothetical protein G ( 338)	793	174.1	1.1e-40	gi 142011761 gb ECU81815.1	hypothetical protein G ( 440)	770	169.4	3.6e-39
gi 141101489 gb ECP63549.1	hypothetical protein G ( 294)	792	173.9	1.1e-40	gi 136955165 gb EBR38869.1	hypothetical protein G ( 311)	767	168.7	4.2e-39
gi 141097662 gb ECP60818.1	hypothetical protein G ( 301)	792	173.9	1.1e-40	gi 142971616 gb EDB88788.1	hypothetical protein G ( 317)	767	168.7	4.2e-39
gi 137395150 gb EBT85818.1	hypothetical protein G ( 319)	792	173.9	1.2e-40	gi 144037176 gb EDI41070.1	hypothetical protein G ( 544)	770	169.4	4.4e-39
gi 142090737 gb ECV51207.1	hypothetical protein G ( 425)	793	174.2	1.3e-40	gi 142331844 gb ECX31901.1	hypothetical protein G ( 430)	768	169.0	4.8e-39
gi 139921163 gb ECI38192.1	hypothetical protein G ( 235)	789	173.2	1.4e-40	gi 142267558 gb ECW84392.1	hypothetical protein G ( 313)	766	168.5	4.8e-39
gi 194310012 gb ACF44712.1	3-phosphoshikimate 1-c ( 433)	792	174.0	1.5e-40	gi 144212823 gb EDJ68735.1	hypothetical protein G ( 445)	768	169.0	4.9e-39
gi 34483387 emb CAE10385.1	3-PHOSPHOSHIKIMATE 1-C ( 437)	792	174.0	1.5e-40	gi 143877405 gb EDH27656.1	hypothetical protein G ( 447)	768	169.0	4.9e-39
gi 142643653 gb ECZ54421.1	hypothetical protein G ( 339)	790	173.5	1.6e-40	gi 144075303 gb EDI68980.1	hypothetical protein G ( 474)	768	169.0	5.2e-39
gi 142006350 gb ECU77442.1	hypothetical protein G ( 324)	789	173.3	1.8e-40	gi 142403788 gb ECX81944.1	hypothetical protein G ( 333)	765	168.3	5.9e-39
gi 139420983 gb ECE99819.1	hypothetical protein G ( 337)	788	173.1	2.2e-40	gi 138571481 gb ECA52062.1	hypothetical protein G ( 245)	763	167.8	6e-39
gi 144105457 gb EDI90364.1	hypothetical protein G ( 242)	786	172.6	2.2e-40	gi 135364074 gb EBH13997.1	hypothetical protein G ( 441)	766	168.6	6.5e-39
gi 143978542 gb EDH99586.1	hypothetical protein G ( 260)	786	172.6	2.3e-40	gi 142133901 gb ECV83825.1	hypothetical protein G ( 430)	765	168.3	7.3e-39
gi 216479401 gb AAM73137.1	3-phosphoshikimate 1-ca ( 434)	789	173.3	2.3e-40	gi 145205328 gb ABP36371.1	3-phosphoshikimate 1-c ( 433)	765	168.3	7.4e-39
gi 94552691 gb ABF42615.1	3-phosphoshikimate 1-ca ( 435)	789	173.3	2.3e-40	gi 138840709 gb ECC10949.1	hypothetical protein G ( 342)	763	167.9	8e-39
gi 253510676 gb EES89335.1	5-enolpyruvylshikimate ( 436)	789	173.3	2.3e-40	gi 157700108 gb ABY68268.1	3-phosphoshikimate 1-c ( 425)	764	168.1	8.4e-39
gi 140902672 gb ECO27576.1	hypothetical protein G ( 290)	786	172.6	2.5e-40	gi 142585981 gb ECZ13884.1	hypothetical protein G ( 441)	764	168.1	8.7e-39
gi 135918291 gb EBK70077.1	hypothetical protein G ( 307)	785	172.4	3.1e-40	gi 144051266 gb EDI51354.1	hypothetical protein G ( 327)	762	167.7	8.9e-39
gi 142317432 gb ECX21250.1	hypothetical protein G ( 454)	786	172.7	3.7e-40	gi 139284870 gb ECE45110.1	hypothetical protein G ( 241)	760	167.2	9.2e-39
gi 139662994 gb ECG60888.1	hypothetical protein G ( 279)	782	171.8	4.4e-40	gi 135647573 gb EBI97559.1	hypothetical protein G ( 298)	759	167.0	1.3e-38

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gi 143992208 gb EDI09178.1	hypothetical protein G ( 432)	761	167.5	1.3e-38	gi 136860454 gb EBQ89188.1	hypothetical protein G ( 246)	736	162.2	3e-37
gi 143696214 gb EDG32946.1	hypothetical protein G ( 434)	761	167.5	1.3e-38	gi 140955798 gb ECO64828.1	hypothetical protein G ( 273)	736	162.2	3.2e-37
gi 141935581 gb ECU28288.1	hypothetical protein G ( 226)	757	166.6	1.3e-38	gi 139768554 gb ECH32813.1	hypothetical protein G ( 278)	736	162.2	3.3e-37
gi 139664047 gb ECG61621.1	hypothetical protein G ( 258)	757	166.6	1.5e-38	gi 135103443 gb EBF51389.1	hypothetical protein G ( 418)	738	162.7	3.5e-37
gi 141064495 gb ECP38367.1	hypothetical protein G ( 306)	758	166.8	1.5e-38	gi 139134351 gb ECD63724.1	hypothetical protein G ( 301)	736	162.2	3.5e-37
gi 137335317 gb EBT52025.1	hypothetical protein G ( 306)	758	166.8	1.5e-38	gi 140036702 gb ECJ16354.1	hypothetical protein G ( 301)	736	162.2	3.5e-37
gi 134622016 gb EBC44186.1	hypothetical protein G ( 314)	758	166.8	1.5e-38	gi 140729862 gb ECN11951.1	hypothetical protein G ( 304)	736	162.2	3.5e-37
gi 142656427 gb EC263418.1	hypothetical protein G ( 445)	760	167.3	1.6e-38	gi 140364603 gb ECL26871.1	hypothetical protein G ( 219)	734	161.8	3.6e-37
gi 143830277 gb EDG93382.1	hypothetical protein G ( 449)	760	167.3	1.6e-38	gi 143449513 gb EDF02359.1	hypothetical protein G ( 444)	738	162.7	3.7e-37
gi 139939562 gb ECI51111.1	hypothetical protein G ( 308)	757	166.6	1.7e-38	gi 143676349 gb EDG21217.1	hypothetical protein G ( 446)	738	162.7	3.7e-37
gi 78171788 gb ABB28884.1	3-phosphoshikimate 1-ca ( 435)	759	167.1	1.8e-38	gi 139696294 gb ECG83976.1	hypothetical protein G ( 287)	735	162.0	3.9e-37
gi 136821916 gb EBQ63445.1	hypothetical protein G ( 319)	757	166.6	1.8e-38	gi 135562484 gb EBI44473.1	hypothetical protein G ( 293)	735	162.0	4e-37
gi 134801092 gb EBD52793.1	hypothetical protein G ( 446)	759	167.1	1.8e-38	gi 134813827 gb EBD60698.1	hypothetical protein G ( 286)	734	161.8	4.5e-37
gi 134675387 gb EBP75542.1	hypothetical protein G ( 306)	755	166.2	2.3e-38	gi 222421192 emb CAL28006.1	3-phosphoshikimate 1- ( 432)	736	162.3	4.8e-37
gi 140528515 gb ECM11387.1	hypothetical protein G ( 318)	755	166.2	2.4e-38	gi 142156622 gb ECW00862.1	hypothetical protein G ( 222)	732	161.4	4.8e-37
gi 143006221 gb EDC12907.1	hypothetical protein G ( 448)	757	166.7	2.4e-38	gi 142220950 gb ECW49934.1	hypothetical protein G ( 747)	739	163.0	5e-37
gi 141860322 gb EC275628.1	hypothetical protein G ( 283)	754	166.0	2.5e-38	gi 141163007 gb ECQ06591.1	hypothetical protein G ( 235)	732	161.4	5.1e-37
gi 136630657 gb EBP39342.1	hypothetical protein G ( 335)	755	166.2	2.5e-38	gi 137000351 gb EBR64461.1	hypothetical protein G ( 305)	733	161.6	5.5e-37
gi 134775377 gb EBD34861.1	hypothetical protein G ( 406)	756	166.5	2.6e-38	gi 72495104 dbj BAE18425.1	5-enolpyruvylshikimate ( 432)	735	162.1	5.6e-37
gi 136302090 gb EBN24661.1	hypothetical protein G ( 430)	756	166.5	2.7e-38	gi 193088545 gb ACF13820.1	3-phosphoshikimate 1-c ( 435)	735	162.1	5.6e-37
gi 142888313 gb EDB29243.1	hypothetical protein G ( 321)	754	166.0	2.8e-38	gi 137930097 gb EBW81399.1	hypothetical protein G ( 306)	732	161.4	6.4e-37
gi 141233117 gb ECQ54347.1	hypothetical protein G ( 228)	751	165.3	3.2e-38	gi 142971459 gb EDB88674.1	hypothetical protein G ( 315)	732	161.4	6.5e-37
gi 223588889 gb ACM92625.1	3-phosphoshikimate 1-c ( 431)	754	166.1	3.6e-38	gi 141382713 gb ECA44145.1	hypothetical protein G ( 233)	730	160.9	6.7e-37
gi 135502733 gb EBI06227.1	hypothetical protein G ( 271)	751	165.3	3.7e-38	gi 262223840 gb EEY74299.1	3-phosphoshikimate 1-c ( 665)	735	162.2	8.1e-37
gi 141024369 gb ECP11205.1	hypothetical protein G ( 274)	751	165.3	3.7e-38	gi 141192666 gb ECQ26680.1	hypothetical protein G ( 258)	729	160.8	8.4e-37
gi 138011480 gb EBX26531.1	hypothetical protein G ( 292)	751	165.4	4e-38	gi 141378761 gb ECR41291.1	hypothetical protein G ( 221)	728	160.5	8.5e-37
gi 134407854 gb EBB17419.1	hypothetical protein G ( 293)	750	165.2	4.6e-38	gi 135969735 gb EBL04825.1	hypothetical protein G ( 263)	729	160.8	8.6e-37
gi 138073518 gb EBX59366.1	hypothetical protein G ( 289)	749	164.9	5.2e-38	gi 143031842 gb EDC31502.1	hypothetical protein G ( 316)	730	161.0	8.7e-37
gi 135097328 gb EBF47474.1	hypothetical protein G ( 314)	749	165.0	5.6e-38	gi 137889644 gb EBW58374.1	hypothetical protein G ( 275)	729	160.8	8.9e-37
gi 141494611 gb ECS06053.1	hypothetical protein G ( 234)	747	164.5	5.8e-38	gi 140991096 gb ECO89414.1	hypothetical protein G ( 280)	729	160.8	9.1e-37
gi 138660172 gb ECB12113.1	hypothetical protein G ( 276)	747	164.5	6.7e-38	gi 139558026 gb ECF89335.1	hypothetical protein G ( 296)	729	160.8	9.5e-37
gi 141299754 gb ECQ93545.1	hypothetical protein G ( 286)	747	164.5	6.9e-38	gi 229376059 gb EEO26150.1	3-phosphoshikimate 1-c ( 434)	731	161.3	9.9e-37
gi 143240990 gb EDD83029.1	hypothetical protein G ( 430)	749	165.0	7.4e-38	gi 144082397 gb EDI74102.1	hypothetical protein G ( 515)	732	161.5	1e-36
gi 139617327 gb ECG29769.1	hypothetical protein G ( 270)	746	164.3	7.6e-38	gi 142096572 gb ECV56061.1	hypothetical protein G ( 434)	730	161.1	1.1e-36
gi 138602361 gb ECA73437.1	hypothetical protein G ( 300)	746	164.3	8.3e-38	gi 134767569 gb EBD29449.1	hypothetical protein G ( 449)	730	161.1	1.2e-36
gi 142294047 gb ECX03786.1	hypothetical protein G ( 323)	746	164.3	8.9e-38	gi 134325002 gb EBA65155.1	hypothetical protein G ( 299)	727	160.4	1.3e-36
gi 136830709 gb EBQ69311.1	hypothetical protein G ( 327)	746	164.3	9e-38	gi 140765239 gb ECN35318.1	hypothetical protein G ( 307)	727	160.4	1.3e-36
gi 135080385 gb EBF36631.1	hypothetical protein G ( 253)	744	163.9	9.6e-38	gi 143559332 gb EDF63130.1	hypothetical protein G ( 439)	729	160.9	1.3e-36
gi 140702862 gb ECM93365.1	hypothetical protein G ( 286)	744	163.9	1.1e-37	gi 134912557 gb EBE25355.1	hypothetical protein G ( 281)	726	160.2	1.4e-36
gi 138281250 gb EBY78010.1	hypothetical protein G ( 302)	744	163.9	1.1e-37	gi 138267882 gb EBY68980.1	hypothetical protein G ( 284)	726	160.2	1.4e-36
gi 139974108 gb ECI74764.1	hypothetical protein G ( 304)	744	163.9	1.1e-37	gi 140299537 gb ECL81908.1	hypothetical protein G ( 286)	726	160.2	1.4e-36
gi 143234938 gb EDD79123.1	hypothetical protein G ( 270)	743	163.7	1.2e-37	gi 239523935 gb EEQ63801.1	3-phosphoshikimate 1-c ( 431)	728	160.7	1.5e-36
gi 138290616 gb EBY82177.1	hypothetical protein G ( 295)	743	163.7	1.3e-37	gi 136822130 gb EBQ63589.1	hypothetical protein G ( 444)	728	160.7	1.6e-36
gi 142666850 gb EC270721.1	hypothetical protein G ( 334)	743	163.7	1.4e-37	gi 112803452 gb EAU00796.1	3-phosphoshikimate 1-c ( 424)	727	160.4	1.7e-36
gi 141489620 gb ECS04477.1	hypothetical protein G ( 301)	742	163.5	1.5e-37	gi 142993753 gb EDC04217.1	hypothetical protein G ( 275)	724	159.7	1.8e-36
gi 139845582 gb ECH86898.1	hypothetical protein G ( 305)	742	163.5	1.5e-37	gi 136028828 gb EBL43065.1	hypothetical protein G ( 409)	726	160.2	1.9e-36
gi 138465274 gb EBZ86300.1	hypothetical protein G ( 214)	739	162.8	1.7e-37	gi 144224364 gb EDU77028.1	hypothetical protein G ( 348)	725	160.0	1.9e-36
gi 142767462 gb EDA43227.1	hypothetical protein G ( 445)	743	163.8	1.8e-37	gi 137891350 gb EBW59332.1	hypothetical protein G ( 287)	723	159.5	2.2e-36
gi 135744571 gb EBJ57515.1	hypothetical protein G ( 301)	740	163.1	2e-37	gi 142525284 gb ECY70920.1	hypothetical protein G ( 304)	723	159.5	2.3e-36
gi 140289895 gb ECK77037.1	hypothetical protein G ( 307)	740	163.1	2e-37	gi 134510091 gb EBB77103.1	hypothetical protein G ( 264)	722	159.3	2.4e-36
gi 141103301 gb ECP64813.1	hypothetical protein G ( 309)	740	163.1	2e-37	gi 137383188 gb EBT78926.1	hypothetical protein G ( 286)	722	159.3	2.5e-36

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gi 141523746 gb ECS14701.1	hypothetical protein G ( 291)	722	159.3	2.6e-36	gi 138564576 gb ECA47108.1	hypothetical protein G ( 312)	706	156.0	2.7e-35
gi 139645346 gb ECG48218.1	hypothetical protein G ( 275)	721	159.1	2.8e-36	gi 139434088 gb ECF08737.1	hypothetical protein G ( 287)	705	155.8	2.9e-35
gi 135522926 gb EBI19182.1	hypothetical protein G ( 293)	721	159.1	3e-36	gi 142010327 gb ECU80421.1	hypothetical protein G ( 394)	706	156.1	3.3e-35
gi 135150889 gb EBF81845.1	hypothetical protein G ( 293)	721	159.1	3e-36	gi 2313507 gb AAD07470.1	3-phosphoshikimate 1-car ( 429)	706	156.1	3.6e-35
gi 142113139 gb ECV68675.1	hypothetical protein G ( 416)	723	159.6	3e-36	gi 210133180 gb ACJ08171.1	3-phosphoshikimate 1-c ( 429)	706	156.1	3.6e-35
gi 140728099 gb ECN10681.1	hypothetical protein G ( 300)	721	159.1	3e-36	gi 136044945 gb EBL53876.1	hypothetical protein G ( 439)	706	156.1	3.7e-35
gi 139742010 gb ECH15842.1	hypothetical protein G ( 291)	720	158.9	3.4e-36	gi 135295582 gb EBG69224.1	hypothetical protein G ( 221)	701	154.9	4.2e-35
gi 134795852 gb EBD49110.1	hypothetical protein G ( 412)	722	159.4	3.5e-36	gi 141929650 gb ECU24164.1	hypothetical protein G ( 278)	702	155.2	4.4e-35
gi 109714282 emb CAJ99290.1	3-phosphoshikimate 1- ( 429)	722	159.4	3.6e-36	gi 142551449 gb ECY89791.1	hypothetical protein G ( 284)	702	155.2	4.5e-35
gi 138415605 gb EBZ51637.1	hypothetical protein G ( 246)	718	158.5	4e-36	gi 135312851 gb EBG79579.1	hypothetical protein G ( 300)	701	155.0	5.4e-35
gi 140237179 gb ECK45858.1	hypothetical protein G ( 265)	718	158.5	4.2e-36	gi 1398989525 gb ECI15914.1	hypothetical protein G ( 221)	699	154.5	5.6e-35
gi 142655804 gb ECZ62978.1	hypothetical protein G ( 388)	720	159.0	4.4e-36	gi 139189085 gb ECE01980.1	hypothetical protein G ( 262)	700	154.7	5.6e-35
gi 141829660 gb ECT53963.1	hypothetical protein G ( 311)	718	158.5	4.8e-36	gi 140284595 gb ECK74389.1	hypothetical protein G ( 287)	700	154.8	6e-35
gi 144036682 gb EDI40729.1	hypothetical protein G ( 312)	718	158.5	4.9e-36	gi 142271427 gb ECW87239.1	hypothetical protein G ( 291)	700	154.8	6.1e-35
gi 143683511 gb EDG25599.1	hypothetical protein G ( 449)	720	159.0	5e-36	gi 135379194 gb EBH24154.1	hypothetical protein G ( 443)	702	155.3	6.6e-35
gi 261839786 gb ACX99551.1	3-phosphoshikimate 1-c ( 429)	719	158.8	5.5e-36	gi 134894864 gb EBE13658.1	hypothetical protein G ( 289)	699	154.5	7e-35
gi 139047127 gb ECD04427.1	hypothetical protein G ( 259)	715	157.9	6.4e-36	gi 136833675 gb EBQ71286.1	hypothetical protein G ( 413)	701	155.0	7.2e-35
gi 143487900 gb EDF25456.1	hypothetical protein G ( 443)	718	158.6	6.6e-36	gi 143151911 gb EDD19366.1	hypothetical protein G ( 215)	696	153.9	8.4e-35
gi 142554361 gb ECY91840.1	hypothetical protein G ( 282)	715	157.9	6.9e-36	gi 268617282 gb ACZ11647.1	3-phosphoshikimate 1-c ( 428)	700	154.8	8.5e-35
gi 136230222 gb EBM75731.1	hypothetical protein G ( 279)	714	157.7	7.8e-36	gi 137912650 gb EBW1582.1	hypothetical protein G ( 271)	696	153.9	1e-34
gi 142520919 gb ECY67749.1	hypothetical protein G ( 435)	716	158.2	8.6e-36	gi 143273185 gb EDE05978.1	hypothetical protein G ( 423)	698	154.4	1.1e-34
gi 118414572 gb ABK82992.1	3-phosphoshikimate 1-c ( 425)	715	157.9	9.8e-36	gi 142397546 gb ECX77275.1	hypothetical protein G ( 437)	698	154.4	1.2e-34
gi 134743795 gb EBD15255.1	hypothetical protein G ( 283)	712	157.2	1.1e-35	gi 140715196 gb ECN01656.1	hypothetical protein G ( 277)	695	153.7	1.2e-34
gi 134831338 gb EBD71836.1	hypothetical protein G ( 283)	712	157.2	1.1e-35	gi 136942528 gb EBR31747.1	hypothetical protein G ( 291)	695	153.7	1.3e-34
gi 137700970 gb EBV53502.1	hypothetical protein G ( 289)	712	157.3	1.1e-35	gi 34558834 gb AAQ75178.1	3-phosphoshikimate 1-ca ( 431)	697	154.2	1.3e-34
gi 135540996 gb EBI30679.1	hypothetical protein G ( 294)	712	157.3	1.1e-35	gi 142845608 gb EDB01702.1	hypothetical protein G ( 443)	697	154.2	1.4e-34
gi 136769707 gb EBQ28730.1	hypothetical protein G ( 259)	711	157.0	1.1e-35	gi 135936082 gb EBK82171.1	hypothetical protein G ( 254)	693	153.3	1.5e-34
gi 261838386 gb ACX98152.1	3-phosphoshikimate 1-c ( 429)	714	157.7	1.1e-35	gi 134524270 gb EBB85548.1	hypothetical protein G ( 302)	694	153.5	1.5e-34
gi 107837189 gb ABF85058.1	3-phosphoshikimate 1-c ( 429)	714	157.7	1.1e-35	gi 142032131 gb ECV01025.1	hypothetical protein G ( 432)	695	153.8	1.8e-34
gi 141103360 gb ECP64854.1	hypothetical protein G ( 262)	711	157.0	1.1e-35	gi 78166074 gb ABB23172.1	3-phosphoshikimate 1-ca ( 433)	695	153.8	1.8e-34
gi 135815796 gb EBK02149.1	hypothetical protein G ( 389)	713	157.5	1.2e-35	gi 137866498 gb EBW45118.1	hypothetical protein G ( 278)	692	153.1	1.9e-34
gi 140461717 gb ECL90174.1	hypothetical protein G ( 208)	709	156.6	1.3e-35	gi 140201840 gb ECK21774.1	hypothetical protein G ( 211)	690	152.6	2e-34
gi 4155563 gb AAD06557.1	3-PHOSPHOSHIKIMATE 1-CAR ( 429)	713	157.5	1.3e-35	gi 143597077 gb EDF78773.1	hypothetical protein G ( 439)	694	153.6	2.1e-34
gi 143103963 gb EDC84209.1	hypothetical protein G ( 262)	710	156.8	1.3e-35	gi 142744348 gb EDA26459.1	hypothetical protein G ( 383)	693	153.4	2.1e-34
gi 139513223 gb ECF58552.1	hypothetical protein G ( 273)	710	156.8	1.4e-35	gi 140869145 gb ECO05746.1	hypothetical protein G ( 276)	690	152.7	2.5e-34
gi 142716191 gb EDA06118.1	hypothetical protein G ( 299)	710	156.8	1.5e-35	gi 138176812 gb EBY21559.1	hypothetical protein G ( 292)	690	152.7	2.6e-34
gi 254001519 emb CAX29537.1	3-phosphoshikimate 1- ( 429)	712	157.3	1.5e-35	gi 141310217 gb ECQ97279.1	hypothetical protein G ( 272)	689	152.5	2.8e-34
gi 140210178 gb ECK27766.1	hypothetical protein G ( 216)	707	156.2	1.7e-35	gi 134662035 gb EBC67782.1	hypothetical protein G ( 298)	689	152.5	3e-34
gi 188144074 gb ACD48491.1	3-phosphoshikimate 1-c ( 429)	711	157.1	1.8e-35	gi 136619536 gb EBP32785.1	hypothetical protein G ( 324)	689	152.5	3.3e-34
gi 208432878 gb ACI27749.1	3-phosphoshikimate 1-c ( 429)	711	157.1	1.8e-35	gi 134922415 gb EBE31913.1	hypothetical protein G ( 456)	691	153.0	3.3e-34
gi 141113013 gb ECP71635.1	hypothetical protein G ( 281)	708	156.4	1.9e-35	gi 135868048 gb EBK35027.1	hypothetical protein G ( 234)	687	152.0	3.3e-34
gi 142651615 gb ECZ60006.1	hypothetical protein G ( 423)	710	156.9	2e-35	gi 136260802 gb EBM96358.1	hypothetical protein G ( 404)	690	152.7	3.4e-34
gi 138605445 gb ECA75646.1	hypothetical protein G ( 264)	707	156.2	2e-35	gi 142629081 gb ECZ44128.1	hypothetical protein G ( 413)	690	152.7	3.5e-34
gi 139129981 gb ECD60708.1	hypothetical protein G ( 290)	707	156.2	2.2e-35	gi 135009399 gb EBE90409.1	hypothetical protein G ( 216)	686	151.8	3.5e-34
gi 141081650 gb ECP49597.1	hypothetical protein G ( 247)	706	156.0	2.2e-35	gi 134888104 gb EBE09153.1	hypothetical protein G ( 441)	690	152.8	3.7e-34
gi 140841479 gb ECN88442.1	hypothetical protein G ( 292)	707	156.2	2.2e-35	gi 140327911 gb ECL01330.1	hypothetical protein G ( 236)	686	151.8	3.8e-34
gi 137901546 gb EBW65266.1	hypothetical protein G ( 302)	707	156.2	2.3e-35	gi 137921162 gb EBW76361.1	hypothetical protein G ( 304)	687	152.1	4.1e-34
gi 27262190 gb AAN87376.1	3-phosphoshikimate 1-ca ( 256)	706	156.0	2.3e-35	gi 141089428 gb ECP54985.1	hypothetical protein G ( 266)	686	151.8	4.2e-34
gi 142239293 gb ECW63535.1	hypothetical protein G ( 442)	709	156.7	2.4e-35	gi 134720376 gb EBD01873.1	hypothetical protein G ( 255)	685	151.6	4.7e-34
gi 135409824 gb EBH44760.1	hypothetical protein G ( 450)	709	156.7	2.4e-35	gi 135875132 gb EBK39974.1	hypothetical protein G ( 444)	688	152.3	5e-34
gi 135830394 gb EBK11348.1	hypothetical protein G ( 423)	708	156.5	2.7e-35	gi 141879530 gb ECT88967.1	hypothetical protein G ( 278)	685	151.6	5.1e-34



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gi 137736100 gb EBV72455.1	hypothetical protein G ( 294)	685	151.6	5.3e-34	gi 141389048 gb ECR48542.1	hypothetical protein G ( 192)	667	147.8	5e-33
gi 137812730 gb EBW14044.1	hypothetical protein G ( 259)	684	151.4	5.5e-34	gi 143516129 gb EDF41123.1	hypothetical protein G ( 394)	671	148.8	5.2e-33
gi 138564577 gb ECA47109.1	hypothetical protein G ( 321)	685	151.7	5.8e-34	gi 138970089 gb ECC63836.1	hypothetical protein G ( 251)	668	148.1	5.4e-33
gi 136572401 gb EBP02753.1	hypothetical protein G ( 285)	684	151.4	6e-34	gi 137356768 gb EBT64149.1	hypothetical protein G ( 305)	669	148.3	5.5e-33
gi 138825029 gb ECC03218.1	hypothetical protein G ( 287)	684	151.4	6.1e-34	gi 140971289 gb ECO75475.1	hypothetical protein G ( 267)	668	148.1	5.7e-33
gi 135036247 gb EBF08483.1	hypothetical protein G ( 261)	683	151.2	6.4e-34	gi 134586542 gb EBC22942.1	hypothetical protein G ( 254)	667	147.9	6.3e-33
gi 140055201 gb ECJ26753.1	hypothetical protein G ( 317)	684	151.4	6.6e-34	gi 139351418 gb ECE59394.1	hypothetical protein G ( 260)	667	147.9	6.4e-33
gi 143162244 gb EDD26590.1	hypothetical protein G ( 394)	685	151.7	6.9e-34	gi 143636057 gb EDF98691.1	hypothetical protein G ( 268)	667	147.9	6.6e-33
gi 134355864 gb EBA85489.1	hypothetical protein G ( 401)	685	151.7	7e-34	gi 142540256 gb ECY81791.1	hypothetical protein G ( 443)	670	148.6	6.6e-33
gi 135952956 gb EBK93503.1	hypothetical protein G ( 444)	684	151.5	8.8e-34	gi 137904507 gb EBW66910.1	hypothetical protein G ( 270)	667	147.9	6.6e-33
gi 135382585 gb EBH26426.1	hypothetical protein G ( 445)	684	151.5	8.8e-34	gi 134587137 gb EBC23302.1	hypothetical protein G ( 238)	666	147.7	6.9e-33
gi 138197142 gb EBY34330.1	hypothetical protein G ( 194)	679	150.3	8.9e-34	gi 137316119 gb EBT41367.1	hypothetical protein G ( 265)	666	147.7	7.6e-33
gi 140294305 gb ECK79442.1	hypothetical protein G ( 210)	679	150.3	9.5e-34	gi 143869852 gb EDH22124.1	hypothetical protein G ( 441)	668	148.2	8.8e-33
gi 136006587 gb EBL28090.1	hypothetical protein G ( 304)	681	150.8	9.8e-34	gi 142945309 gb EBB70428.1	hypothetical protein G ( 330)	665	147.8	1.1e-32
gi 139762490 gb ECH28616.1	hypothetical protein G ( 258)	680	150.6	9.8e-34	gi 139807489 gb ECH60285.1	hypothetical protein G ( 208)	662	146.8	1.1e-32
gi 136503636 gb EBO58780.1	hypothetical protein G ( 377)	681	150.9	1.2e-33	gi 135007077 gb EBE88844.1	hypothetical protein G ( 407)	666	147.8	1.1e-32
gi 140796557 gb ECN57125.1	hypothetical protein G ( 229)	678	150.1	1.2e-33	gi 152939223 gb ABS43964.1	3-phosphoshikimate 1-c ( 423)	666	147.8	1.1e-32
gi 137877407 gb EBW51396.1	hypothetical protein G ( 275)	679	150.4	1.2e-33	gi 136812901 gb EBQ57436.1	hypothetical protein G ( 442)	666	147.8	1.2e-32
gi 141425814 gb ECR74107.1	hypothetical protein G ( 239)	678	150.1	1.2e-33	gi 136798838 gb EBQ48122.1	hypothetical protein G ( 227)	662	146.8	1.2e-32
gi 136080841 gb EBL78109.1	hypothetical protein G ( 285)	679	150.4	1.2e-33	gi 143435399 gb EDE94044.1	hypothetical protein G ( 443)	666	147.8	1.2e-32
gi 136694506 gb EBP79131.1	hypothetical protein G ( 288)	679	150.4	1.2e-33	gi 139835846 gb ECH79917.1	hypothetical protein G ( 269)	663	147.1	1.2e-32
gi 143027028 gb EDC27946.1	hypothetical protein G ( 443)	681	150.9	1.4e-33	gi 136262713 gb EBM97691.1	hypothetical protein G ( 388)	665	147.5	1.2e-32
gi 137295367 gb EBT29790.1	hypothetical protein G ( 269)	678	150.2	1.4e-33	gi 139775304 gb EBH37500.1	hypothetical protein G ( 292)	663	147.1	1.3e-32
gi 137577482 gb EBU85349.1	hypothetical protein G ( 253)	677	150.0	1.5e-33	gi 153804313 gb ABS51320.1	3-phosphoshikimate 1-c ( 424)	665	147.6	1.3e-32
gi 135410539 gb EBH45247.1	hypothetical protein G ( 393)	679	150.5	1.6e-33	gi 57166528 gb AAW35307.1	3-phosphoshikimate 1-ca ( 428)	665	147.6	1.3e-32
gi 141725526 gb ECS96576.1	hypothetical protein G ( 296)	677	150.0	1.7e-33	gi 135835370 gb EBK14477.1	hypothetical protein G ( 278)	662	146.9	1.4e-32
gi 143179993 gb EDD39182.1	hypothetical protein G ( 421)	679	150.5	1.7e-33	gi 136331028 gb EBN44134.1	hypothetical protein G ( 432)	664	147.4	1.5e-32
gi 137706785 gb EBV56572.1	hypothetical protein G ( 223)	675	149.5	1.8e-33	gi 140352336 gb ECL18584.1	hypothetical protein G ( 266)	661	146.6	1.6e-32
gi 139539653 gb ECF76318.1	hypothetical protein G ( 228)	675	149.5	1.8e-33	gi 134346473 gb EBA79510.1	hypothetical protein G ( 441)	664	147.4	1.6e-32
gi 134953240 gb EBE52444.1	hypothetical protein G ( 305)	676	149.8	2e-33	gi 141168333 gb ECQ10384.1	hypothetical protein G ( 258)	660	146.4	1.8e-32
gi 136286814 gb EBN14262.1	hypothetical protein G ( 276)	675	149.6	2.1e-33	gi 135879561 gb EBK43089.1	hypothetical protein G ( 260)	660	146.4	1.8e-32
gi 136080172 gb EBL77651.1	hypothetical protein G ( 352)	676	149.8	2.3e-33	gi 135306712 gb EBG75775.1	hypothetical protein G ( 382)	662	146.9	1.8e-32
gi 137723714 gb EBV65818.1	hypothetical protein G ( 262)	674	149.3	2.4e-33	gi 142505282 gb ECY56360.1	hypothetical protein G ( 386)	662	146.9	1.9e-32
gi 142251381 gb ECW72468.1	hypothetical protein G ( 368)	676	149.8	2.4e-33	gi 139374135 gb ECE67784.1	hypothetical protein G ( 277)	660	146.4	1.9e-32
gi 136044545 gb EBL53611.1	hypothetical protein G ( 439)	677	150.1	2.4e-33	gi 140092149 gb ECU47988.1	hypothetical protein G ( 279)	660	146.4	1.9e-32
gi 137473914 gb EBU29669.1	hypothetical protein G ( 242)	673	149.1	2.5e-33	gi 143183876 gb EDD42018.1	hypothetical protein G ( 396)	662	146.9	1.9e-32
gi 140986458 gb ECO86073.1	hypothetical protein G ( 289)	674	149.4	2.6e-33	gi 137852058 gb EBW36821.1	hypothetical protein G ( 276)	659	146.2	2.1e-32
gi 142131720 gb ECV82212.1	hypothetical protein G ( 413)	676	149.8	2.6e-33	gi 134797263 gb EBD50100.1	hypothetical protein G ( 398)	661	146.7	2.2e-32
gi 139938553 gb ECI50387.1	hypothetical protein G ( 254)	673	149.1	2.7e-33	gi 135390469 gb EBH31737.1	hypothetical protein G ( 441)	661	146.7	2.4e-32
gi 141443180 gb ECR86430.1	hypothetical protein G ( 255)	673	149.1	2.7e-33	gi 137457344 gb EBU20973.1	hypothetical protein G ( 239)	657	145.8	2.5e-32
gi 139973384 gb ECI74252.1	hypothetical protein G ( 265)	673	149.1	2.8e-33	gi 136053553 gb EBL59732.1	hypothetical protein G ( 362)	659	146.3	2.7e-32
gi 140047126 gb ECJ22456.1	hypothetical protein G ( 272)	673	149.1	2.8e-33	gi 144040383 gb EDT43271.1	hypothetical protein G ( 442)	660	146.5	2.8e-32
gi 142012462 gb ECU82503.1	hypothetical protein G ( 395)	675	149.6	2.9e-33	gi 143988677 gb EDI06566.1	hypothetical protein G ( 218)	655	145.3	3.1e-32
gi 136042971 gb EBL52555.1	hypothetical protein G ( 395)	675	149.6	2.9e-33	gi 112360221 emb CAL35016.1	3-phosphoshikimate 1- ( 428)	659	146.3	3.1e-32
gi 143907191 gb EDH48930.1	hypothetical protein G ( 418)	674	149.4	3.5e-33	gi 136808575 gb EBQ54561.1	hypothetical protein G ( 442)	659	146.3	3.2e-32
gi 138520674 gb ECA16304.1	hypothetical protein G ( 265)	671	148.7	3.7e-33	gi 135009040 gb EBE90157.1	hypothetical protein G ( 395)	658	146.1	3.4e-32
gi 138932794 gb ECC47942.1	hypothetical protein G ( 272)	671	148.7	3.8e-33	gi 142813782 gb EDA77762.1	hypothetical protein G ( 433)	658	146.1	3.7e-32
gi 143099253 gb EDC80882.1	hypothetical protein G ( 274)	671	148.7	3.8e-33	gi 143789403 gb EDG79192.1	hypothetical protein G ( 407)	657	145.9	4e-32
gi 139543375 gb ECF78911.1	hypothetical protein G ( 236)	670	148.5	3.8e-33	gi 141975165 gb ECU55743.1	hypothetical protein G ( 254)	654	145.2	4.1e-32
gi 142970879 gb EDB88270.1	hypothetical protein G ( 299)	670	148.5	4.7e-33	gi 121504279 gb EAQ72379.2	3-phosphoshikimate 1-c ( 423)	657	145.9	4.1e-32
gi 135658881 gb EBJ04539.1	hypothetical protein G ( 262)	669	148.3	4.9e-33	gi 135461960 gb EBH79689.1	hypothetical protein G ( 258)	654	145.2	4.2e-32

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gi 143680111 gb EDG23778.1	hypothetical protein G ( 443)	657	145.9	4.3e-32	gi 142280802 gb ECW94104.1	hypothetical protein G ( 280)	640	142.3	3.4e-31
gi 143598405 gb EDF79423.1	hypothetical protein G ( 394)	656	145.7	4.5e-32	gi 134781214 gb EBD38889.1	hypothetical protein G ( 352)	641	142.5	3.5e-31
gi 139088179 gb ECD32916.1	hypothetical protein G ( 239)	653	145.0	4.5e-32	gi 135690666 gb EBJ24138.1	hypothetical protein G ( 283)	639	142.1	3.9e-31
gi 142675360 gb ECZ76848.1	hypothetical protein G ( 395)	656	145.7	4.5e-32	gi 138043293 gb EBX43263.1	hypothetical protein G ( 306)	639	142.1	4.2e-31
gi 142684538 gb ECZ83443.1	hypothetical protein G ( 293)	654	145.2	4.6e-32	gi 134787001 gb EBD42903.1	hypothetical protein G ( 265)	638	141.9	4.3e-31
gi 135845413 gb EBK20780.1	hypothetical protein G ( 213)	652	144.7	4.7e-32	gi 134976758 gb EBE68251.1	hypothetical protein G ( 386)	640	142.3	4.4e-31
gi 138398823 gb EBZ39594.1	hypothetical protein G ( 274)	653	145.0	5.1e-32	gi 137922726 gb EBW77238.1	hypothetical protein G ( 281)	638	141.9	4.5e-31
gi 141732305 gb ECT00772.1	hypothetical protein G ( 300)	653	145.0	5.5e-32	gi 135275881 gb EBG57715.1	hypothetical protein G ( 204)	636	141.4	4.5e-31
gi 140820936 gb ECN74293.1	hypothetical protein G ( 215)	651	144.5	5.5e-32	gi 140822463 gb ECN75406.1	hypothetical protein G ( 229)	636	141.4	5e-31
gi 141934358 gb ECU27467.1	hypothetical protein G ( 262)	652	144.8	5.6e-32	gi 137358507 gb EBT65149.1	hypothetical protein G ( 271)	637	141.7	5e-31
gi 144114347 gb EDT96759.1	hypothetical protein G ( 511)	656	145.7	5.6e-32	gi 137110893 gb EBS26319.1	hypothetical protein G ( 278)	637	141.7	5.1e-31
gi 139557236 gb ECF88763.1	hypothetical protein G ( 288)	652	144.8	6.1e-32	gi 139743346 gb ECH16606.1	hypothetical protein G ( 215)	635	141.2	5.5e-31
gi 139734911 gb ECH10883.1	hypothetical protein G ( 218)	650	144.3	6.4e-32	gi 136359784 gb EBN63723.1	hypothetical protein G ( 255)	636	141.4	5.5e-31
gi 139005441 gb ECT75437.1	hypothetical protein G ( 261)	651	144.6	6.5e-32	gi 141859518 gb ECT75045.1	hypothetical protein G ( 265)	636	141.4	5.7e-31
gi 139498116 gb ECF48108.1	hypothetical protein G ( 310)	652	144.8	6.5e-32	gi 207083516 gb EDZ60942.1	3-phosphoshikimate 1-c ( 439)	639	142.2	5.7e-31
gi 143179362 gb EDD38720.1	hypothetical protein G ( 441)	654	145.3	6.6e-32	gi 135487726 gb EBH96571.1	hypothetical protein G ( 381)	638	141.9	5.8e-31
gi 143388359 gb EDF69270.1	hypothetical protein G ( 272)	651	144.6	6.7e-32	gi 135846862 gb EBG21692.1	hypothetical protein G ( 387)	638	141.9	5.9e-31
gi 138689266 gb ECB32656.1	hypothetical protein G ( 277)	651	144.6	6.8e-32	gi 140501840 gb ECM03625.1	hypothetical protein G ( 284)	636	141.5	6e-31
gi 140305932 gb ECK86014.1	hypothetical protein G ( 267)	650	144.3	7.6e-32	gi 135666846 gb EBJ09495.1	hypothetical protein G ( 249)	635	141.2	6.2e-31
gi 140994978 gb ECO92196.1	hypothetical protein G ( 213)	648	143.9	8.4e-32	gi 136407897 gb EBN96812.1	hypothetical protein G ( 213)	634	141.0	6.3e-31
gi 140268029 gb ECK67239.1	hypothetical protein G ( 214)	648	143.9	8.4e-32	gi 135721677 gb EBJ43342.1	hypothetical protein G ( 361)	637	141.7	6.4e-31
gi 141883047 gb ECT91467.1	hypothetical protein G ( 257)	649	144.1	8.5e-32	gi 143495182 gb EDF30165.1	hypothetical protein G ( 390)	637	141.7	6.9e-31
gi 143460504 gb EDF09805.1	hypothetical protein G ( 384)	651	144.6	9e-32	gi 141235790 gb ECQ56283.1	hypothetical protein G ( 244)	634	141.0	7.1e-31
gi 139635959 gb ECG41765.1	hypothetical protein G ( 249)	648	143.9	9.6e-32	gi 143253346 gb EDD91725.1	hypothetical protein G ( 249)	634	141.0	7.2e-31
gi 134796922 gb EBD49853.1	hypothetical protein G ( 299)	649	144.2	9.7e-32	gi 142795846 gb EDA64359.1	hypothetical protein G ( 403)	636	141.5	8.2e-31
gi 138675605 gb ECB23156.1	hypothetical protein G ( 300)	649	144.2	9.7e-32	gi 141580814 gb ECS46000.1	hypothetical protein G ( 250)	633	140.8	8.3e-31
gi 134579288 gb EBC18564.1	hypothetical protein G ( 222)	647	143.7	1e-31	gi 136098922 gb EBL90401.1	hypothetical protein G ( 413)	636	141.5	8.3e-31
gi 141310782 gb EQ97441.1	hypothetical protein G ( 276)	648	143.9	1e-31	gi 141370926 gb ECR35647.1	hypothetical protein G ( 258)	633	140.8	8.6e-31
gi 140306938 gb ECK86704.1	hypothetical protein G ( 289)	648	143.9	1.1e-31	gi 142223275 gb ECW51657.1	hypothetical protein G ( 439)	636	141.5	8.8e-31
gi 139645545 gb ECG48352.1	hypothetical protein G ( 259)	647	143.7	1.1e-31	gi 141226948 gb ECQ49886.1	hypothetical protein G ( 270)	633	140.8	8.9e-31
gi 138280102 gb EBY77418.1	hypothetical protein G ( 268)	647	143.7	1.2e-31	gi 137316621 gb EBT41642.1	hypothetical protein G ( 296)	633	140.8	9.6e-31
gi 138196756 gb EBY34068.1	hypothetical protein G ( 263)	646	143.5	1.3e-31	gi 137070063 gb EBS03773.1	hypothetical protein G ( 298)	633	140.8	9.7e-31
gi 134704854 gb EBC93118.1	hypothetical protein G ( 242)	645	143.3	1.4e-31	gi 137335226 gb EBT51972.1	hypothetical protein G ( 276)	632	140.6	1e-30
gi 157386116 gb ABV52431.1	3-phosphoshikimate 1-c ( 423)	648	144.0	1.5e-31	gi 135856354 gb EBK27680.1	hypothetical protein G ( 408)	634	141.1	1.1e-30
gi 895778 emb CAA61554.1	5-enolpyruvinylshikimate ( 428)	648	144.0	1.5e-31	gi 143245592 gb EDD86275.1	hypothetical protein G ( 435)	634	141.1	1.2e-30
gi 142537980 gb ECY80156.1	hypothetical protein G ( 442)	648	144.0	1.6e-31	gi 141856808 gb ECT73158.1	hypothetical protein G ( 265)	631	140.4	1.2e-30
gi 143980116 gb EDI00633.1	hypothetical protein G ( 379)	647	143.8	1.6e-31	gi 138656624 gb ECB09665.1	hypothetical protein G ( 305)	631	140.4	1.3e-30
gi 142143916 gb ECV91266.1	hypothetical protein G ( 182)	642	142.6	1.7e-31	gi 141237285 gb ECQ57366.1	hypothetical protein G ( 200)	628	139.7	1.4e-30
gi 140945922 gb ECO57780.1	hypothetical protein G ( 255)	644	143.1	1.7e-31	gi 143886715 gb EDH34407.1	hypothetical protein G ( 441)	632	140.7	1.6e-30
gi 143510567 gb EDF38097.1	hypothetical protein G ( 307)	645	143.3	1.8e-31	gi 139108648 gb ECD47280.1	hypothetical protein G ( 272)	629	140.0	1.6e-30
gi 136620139 gb EBP33148.1	hypothetical protein G ( 271)	644	143.1	1.8e-31	gi 135216672 gb EBG22887.1	hypothetical protein G ( 166)	626	139.3	1.6e-30
gi 137180732 gb EBS65453.1	hypothetical protein G ( 215)	641	142.4	2.3e-31	gi 137078632 gb EBS08614.1	hypothetical protein G ( 199)	627	139.5	1.6e-30
gi 134887599 gb EBE08816.1	hypothetical protein G ( 440)	645	143.4	2.4e-31	gi 141882967 gb ECT91409.1	hypothetical protein G ( 236)	628	139.8	1.6e-30
gi 139689782 gb ECG79632.1	hypothetical protein G ( 240)	641	142.5	2.5e-31	gi 143115386 gb EDC92602.1	hypothetical protein G ( 409)	631	140.5	1.7e-30
gi 138251002 gb EBY57235.1	hypothetical protein G ( 260)	641	142.5	2.7e-31	gi 140055200 gb ECJ26752.1	hypothetical protein G ( 180)	626	139.3	1.7e-30
gi 140473337 gb ECL94305.1	hypothetical protein G ( 262)	641	142.5	2.7e-31	gi 137898190 gb EBW63309.1	hypothetical protein G ( 268)	628	139.8	1.8e-30
gi 137295054 gb EBT29629.1	hypothetical protein G ( 281)	641	142.5	2.9e-31	gi 142296833 gb ECX05822.1	hypothetical protein G ( 403)	630	140.3	1.9e-30
gi 137002628 gb EBR65772.1	hypothetical protein G ( 286)	641	142.5	3e-31	gi 141718414 gb ECS92174.1	hypothetical protein G ( 356)	628	139.8	2.3e-30
gi 137369411 gb EBT71302.1	hypothetical protein G ( 243)	640	142.3	3e-31	gi 136926330 gb EBR22646.1	hypothetical protein G ( 328)	627	139.6	2.5e-30
gi 141387612 gb ECR47580.1	hypothetical protein G ( 221)	639	142.0	3.2e-31	gi 143186318 gb EDD43806.1	hypothetical protein G ( 333)	627	139.6	2.5e-30
gi 135292728 gb EBG67583.1	hypothetical protein G ( 447)	643	143.0	3.3e-31	gi 142343455 gb ECX40449.1	hypothetical protein G ( 351)	627	139.6	2.7e-30

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gi 139942801 gb ECI53440.1	hypothetical protein G ( 263)	625	139.2	2.8e-30	gi 142886453 gb EDB28141.1	hypothetical protein G ( 379)	610	136.1	3.3e-29
gi 143465264 gb EDF12656.1	hypothetical protein G ( 377)	626	139.4	3.3e-30	gi 135644105 gb EBI95407.1	hypothetical protein G ( 276)	608	135.6	3.3e-29
gi 134508435 gb EBB76121.1	hypothetical protein G ( 272)	624	138.9	3.3e-30	gi 143113848 gb EDC91473.1	hypothetical protein G ( 334)	609	135.9	3.4e-29
gi 139929141 gb ECI43695.1	hypothetical protein G ( 272)	624	138.9	3.3e-30	gi 140209892 gb ECK27558.1	hypothetical protein G ( 210)	606	135.2	3.5e-29
gi 141034040 gb ECP17849.1	hypothetical protein G ( 272)	624	138.9	3.3e-30	gi 138372334 gb EBZ21784.1	hypothetical protein G ( 261)	607	135.4	3.7e-29
gi 141181800 gb ECQ19627.1	hypothetical protein G ( 248)	623	138.7	3.5e-30	gi 144041930 gb EDI44427.1	hypothetical protein G ( 441)	610	136.1	3.7e-29
gi 139450633 gb ECF18656.1	hypothetical protein G ( 261)	623	138.7	3.7e-30	gi 142731161 gb EDA16839.1	hypothetical protein G ( 379)	609	135.9	3.8e-29
gi 142618019 gb ECZ36310.1	hypothetical protein G ( 276)	623	138.7	3.8e-30	gi 141349373 gb ECR20756.1	hypothetical protein G ( 247)	606	135.2	4e-29
gi 135008910 gb EBE90069.1	hypothetical protein G ( 431)	625	139.2	4.2e-30	gi 135303110 gb EBG73663.1	hypothetical protein G ( 300)	607	135.4	4.1e-29
gi 135301778 gb EBG72877.1	hypothetical protein G ( 346)	623	138.8	4.7e-30	gi 138288446 gb EBY80873.1	hypothetical protein G ( 259)	606	135.2	4.2e-29
gi 138733010 gb ECB63289.1	hypothetical protein G ( 267)	621	138.3	5e-30	gi 134722639 gb EBD03170.1	hypothetical protein G ( 276)	605	135.0	5.1e-29
gi 143710497 gb EDG39549.1	hypothetical protein G ( 439)	623	138.8	5.7e-30	gi 139146426 gb ECD72028.1	hypothetical protein G ( 284)	605	135.0	5.3e-29
gi 136294048 gb EBN19181.1	hypothetical protein G ( 281)	620	138.1	6e-30	gi 143837477 gb EDG98597.1	hypothetical protein G ( 252)	603	134.6	6.3e-29
gi 139100964 gb ECD41990.1	hypothetical protein G ( 263)	619	137.9	6.5e-30	gi 143644718 gb EDG03752.1	hypothetical protein G ( 253)	603	134.6	6.3e-29
gi 140415147 gb ECL60719.1	hypothetical protein G ( 275)	619	137.9	6.8e-30	gi 143509311 gb EDF37468.1	hypothetical protein G ( 363)	605	135.1	6.5e-29
gi 139248676 gb ECE35811.1	hypothetical protein G ( 200)	617	137.4	6.9e-30	gi 142445939 gb ECY13527.1	3-phosphoshikimate 1-ca ( 395)	600	133.9	7.9e-29
gi 143916848 gb EDH55629.1	hypothetical protein G ( 339)	620	138.2	7.1e-30	gi 71062313 gb AAZ21316.1	3-phosphoshikimate 1-ca ( 395)	604	134.9	8.1e-29
gi 29727034 gb AAD47362.2 AF038578_5 cyclohexadien	( 505)	622	138.7	7.5e-30	gi 143249054 gb EDD88694.1	hypothetical protein G ( 344)	603	134.6	8.3e-29
gi 136976536 gb EBR50991.1	hypothetical protein G ( 309)	618	137.7	8.7e-30	gi 134563621 gb EBG09100.1	hypothetical protein G ( 348)	602	134.4	9.6e-29
gi 141216849 gb ECQ42758.1	hypothetical protein G ( 263)	617	137.5	8.7e-30	gi 136317320 gb EBN34967.1	hypothetical protein G ( 349)	602	134.4	9.7e-29
gi 136637387 gb EBP43347.1	hypothetical protein G ( 230)	616	137.3	9e-30	gi 143387950 gb EDE69059.1	hypothetical protein G ( 364)	602	134.4	1e-28
gi 141067369 gb ECP39770.1	hypothetical protein G ( 206)	615	137.0	9.4e-30	gi 144034658 gb EDI39332.1	hypothetical protein G ( 222)	599	133.7	1e-28
gi 136480496 gb EBD43798.1	hypothetical protein G ( 404)	619	138.0	9.5e-30	gi 142973874 gb EDG90380.1	hypothetical protein G ( 374)	602	134.4	1e-28
gi 142392190 gb ECX73356.1	hypothetical protein G ( 299)	617	137.5	9.7e-30	gi 134915661 gb EBE27413.1	hypothetical protein G ( 279)	600	134.0	1.1e-28
gi 135475610 gb EBH88835.1	hypothetical protein G ( 279)	616	137.3	1.1e-29	gi 142353791 gb ECX47379.1	hypothetical protein G ( 253)	599	133.7	1.1e-28
gi 143914669 gb EDH54067.1	hypothetical protein G ( 392)	618	137.8	1.1e-29	gi 141519084 gb ECS13650.1	hypothetical protein G ( 195)	597	133.3	1.2e-28
gi 134425336 gb EBB27523.1	hypothetical protein G ( 294)	616	137.3	1.1e-29	gi 134407016 gb EBB16951.1	hypothetical protein G ( 276)	599	133.8	1.2e-28
gi 135575756 gb EBI52970.1	hypothetical protein G ( 162)	612	136.4	1.2e-29	gi 135723033 gb EBU44194.1	hypothetical protein G ( 367)	600	134.0	1.3e-28
gi 134326213 gb EBA65879.1	hypothetical protein G ( 271)	615	137.1	1.2e-29	gi 135016962 gb EBE95506.1	hypothetical protein G ( 377)	600	134.0	1.4e-28
gi 139402158 gb ECE86608.1	hypothetical protein G ( 239)	614	136.8	1.2e-29	gi 140834228 gb ECN83709.1	hypothetical protein G ( 234)	597	133.3	1.4e-28
gi 143744226 gb EDG56728.1	hypothetical protein G ( 398)	617	137.6	1.2e-29	gi 136764304 gb EBQ25053.1	hypothetical protein G ( 405)	600	134.0	1.5e-28
gi 135188909 gb EBG06240.1	hypothetical protein G ( 244)	614	136.8	1.3e-29	gi 135033042 gb EBF06409.1	hypothetical protein G ( 382)	599	133.8	1.6e-28
gi 139179376 gb ECD95073.1	hypothetical protein G ( 247)	614	136.9	1.3e-29	gi 139809562 gb ECH61775.1	hypothetical protein G ( 236)	596	133.1	1.6e-28
gi 143681911 gb EDG24746.1	hypothetical protein G ( 376)	616	137.4	1.4e-29	gi 135169736 gb EBF93991.1	hypothetical protein G ( 337)	598	133.6	1.7e-28
gi 137007600 gb EBR68605.1	hypothetical protein G ( 199)	612	136.4	1.4e-29	gi 138544954 gb ECA33332.1	hypothetical protein G ( 281)	596	133.1	1.9e-28
gi 138396080 gb EBZ37708.1	hypothetical protein G ( 279)	614	136.9	1.4e-29	gi 135462160 gb EBH79820.1	hypothetical protein G ( 241)	595	132.9	1.9e-28
gi 143823139 gb EDG88251.1	hypothetical protein G ( 206)	612	136.4	1.5e-29	gi 141387610 gb ECR47578.1	hypothetical protein G ( 286)	596	133.1	1.9e-28
gi 143592271 gb EDF76017.1	hypothetical protein G ( 381)	615	137.1	1.6e-29	gi 140430189 gb ECL69708.1	hypothetical protein G ( 249)	595	132.9	2e-28
gi 135328530 gb EBG90150.1	hypothetical protein G ( 341)	614	136.9	1.7e-29	gi 135735463 gb EBJ51874.1	hypothetical protein G ( 270)	595	132.9	2.1e-28
gi 143227632 gb EDD73899.1	hypothetical protein G ( 346)	614	136.9	1.7e-29	gi 140007059 gb ECI96257.1	hypothetical protein G ( 226)	593	132.5	2.4e-28
gi 136662556 gb EBP58336.1	hypothetical protein G ( 190)	610	136.0	1.8e-29	gi 141198878 gb ECQ30289.1	hypothetical protein G ( 227)	593	132.5	2.4e-28
gi 139012268 gb ECC79849.1	hypothetical protein G ( 277)	611	136.3	2.2e-29	gi 140711280 gb ECM98898.1	hypothetical protein G ( 228)	593	132.5	2.4e-28
gi 143764419 gb EDG66830.1	hypothetical protein G ( 335)	612	136.5	2.2e-29	gi 138799428 gb ECB91382.1	hypothetical protein G ( 302)	594	132.7	2.7e-28
gi 222539413 gb ACM64514.1	3-phosphoshikimate 1-c ( 428)	613	136.8	2.4e-29	gi 142782139 gb EDA54172.1	hypothetical protein G ( 227)	592	132.3	2.8e-28
gi 143718994 gb EDG43389.1	hypothetical protein G ( 379)	612	136.5	2.5e-29	gi 138307154 gb EBY90044.1	hypothetical protein G ( 233)	592	132.3	2.9e-28
gi 140907696 gb ECO31017.1	hypothetical protein G ( 282)	610	136.0	2.5e-29	gi 140995634 gb ECO92668.1	hypothetical protein G ( 171)	590	131.8	2.9e-28
gi 137284545 gb EBT23794.1	hypothetical protein G ( 271)	609	135.8	2.8e-29	gi 134426111 gb EBB27979.1	hypothetical protein G ( 309)	593	132.5	3.2e-28
gi 139332513 gb ECE53914.1	hypothetical protein G ( 273)	609	135.8	2.9e-29	gi 134961005 gb EBE57619.1	hypothetical protein G ( 270)	592	132.3	3.3e-28
gi 134855060 gb EBD7065.1	hypothetical protein G ( 394)	611	136.3	2.9e-29	gi 141691249 gb ECS83238.1	hypothetical protein G ( 167)	589	131.6	3.3e-28
gi 142204276 gb ECW37281.1	hypothetical protein G ( 249)	608	135.6	3e-29	gi 136211953 gb EBM63336.1	hypothetical protein G ( 310)	592	132.3	3.7e-28
gi 139891102 gb ECI17002.1	hypothetical protein G ( 218)	607	135.4	3.1e-29	gi 140624511 gb ECM41483.1	hypothetical protein G ( 232)	590	131.9	3.8e-28

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gi 137824042 gb EBW20669.1	hypothetical protein G ( 203)	589	131.6	3.9e-28	gi 137512952 gb EBU49685.1	hypothetical protein G ( 231)	577	129.1	2.5e-27
gi 139811438 gb ECH63106.1	hypothetical protein G ( 241)	590	131.9	4e-28	gi 134492839 gb EBB67196.1	hypothetical protein G ( 258)	577	129.2	2.7e-27
gi 142721012 gb EDA09566.1	hypothetical protein G ( 424)	593	132.6	4.2e-28	gi 138858289 gb ECC17909.1	hypothetical protein G ( 275)	577	129.2	2.9e-27
gi 47250293 gb AAT20236.1	Sequence 1608 from pate ( 309)	591	132.1	4.2e-28	gi 143058690 gb EDC51173.1	hypothetical protein G ( 257)	576	129.0	3.1e-27
gi 135649501 gb EBI98752.1	hypothetical protein G ( 371)	592	132.4	4.3e-28	gi 136253248 gb EBM91261.1	hypothetical protein G ( 304)	577	129.2	3.1e-27
gi 141720170 gb ECS93268.1	hypothetical protein G ( 346)	591	132.1	4.7e-28	gi 141132797 gb ECP85624.1	hypothetical protein G ( 322)	577	129.2	3.3e-27
gi 135901397 gb EBK58397.1	hypothetical protein G ( 223)	588	131.4	4.9e-28	gi 134492761 gb EBB67150.1	hypothetical protein G ( 205)	574	128.5	3.4e-27
gi 137342847 gb EBT56305.1	hypothetical protein G ( 272)	589	131.7	5.1e-28	gi 142019072 gb ECU88872.1	hypothetical protein G ( 248)	575	128.7	3.5e-27
gi 140677547 gb ECM75559.1	hypothetical protein G ( 237)	588	131.4	5.2e-28	gi 138387052 gb EBZ31733.1	hypothetical protein G ( 294)	576	129.0	3.5e-27
gi 135393586 gb EBH33843.1	hypothetical protein G ( 379)	590	131.9	5.8e-28	gi 134347423 gb EBA80130.1	hypothetical protein G ( 359)	577	129.2	3.6e-27
gi 143372153 gb EDB62339.1	hypothetical protein G ( 438)	590	132.0	6.6e-28	gi 141338252 gb ECR14195.1	hypothetical protein G ( 265)	575	128.8	3.7e-27
gi 137160598 gb EBS54177.1	hypothetical protein G ( 225)	586	131.0	6.6e-28	gi 141935579 gb ECU28286.1	hypothetical protein G ( 164)	572	128.0	3.8e-27
gi 135428951 gb EBH57631.1	hypothetical protein G ( 227)	586	131.0	6.7e-28	gi 139715639 gb ECG97589.1	hypothetical protein G ( 197)	573	128.3	3.8e-27
gi 141272822 gb ECQ82078.1	hypothetical protein G ( 278)	587	131.3	6.9e-28	gi 136318277 gb EBN35598.1	hypothetical protein G ( 325)	576	129.0	3.8e-27
gi 135744269 gb EBJ57327.1	hypothetical protein G ( 285)	587	131.3	7e-28	gi 140780154 gb ECN45628.1	hypothetical protein G ( 245)	574	128.5	4e-27
gi 139450953 gb ECF18884.1	hypothetical protein G ( 252)	586	131.0	7.3e-28	gi 140265299 gb ECP85629.1	hypothetical protein G ( 178)	572	128.1	4.1e-27
gi 142804270 gb EDA70643.1	hypothetical protein G ( 256)	586	131.0	7.4e-28	gi 136290187 gb EBN16555.1	hypothetical protein G ( 258)	574	128.5	4.2e-27
gi 141418805 gb ECR69222.1	hypothetical protein G ( 257)	586	131.0	7.4e-28	gi 141308402 gb ECQ96556.1	hypothetical protein G ( 258)	574	128.5	4.2e-27
gi 144126252 gb EDJ05420.1	hypothetical protein G ( 233)	585	130.8	7.9e-28	gi 141109595 gb ECP69313.1	hypothetical protein G ( 187)	572	128.1	4.2e-27
gi 139383908 gb ECE74599.1	hypothetical protein G ( 201)	584	130.6	8e-28	gi 143635271 gb EDF98232.1	hypothetical protein G ( 375)	576	129.0	4.4e-27
gi 135544424 gb EBI32879.1	hypothetical protein G ( 396)	588	131.5	8.1e-28	gi 136929793 gb EBR24575.1	hypothetical protein G ( 270)	574	128.6	4.4e-27
gi 139799834 gb ECH54843.1	hypothetical protein G ( 254)	585	130.8	8.5e-28	gi 135208488 gb EBG18075.1	hypothetical protein G ( 230)	573	128.3	4.4e-27
gi 137230117 gb EBS93243.1	hypothetical protein G ( 236)	584	130.6	9.2e-28	gi 139479977 gb ECP36832.1	hypothetical protein G ( 233)	573	128.3	4.4e-27
gi 138264744 gb EBY66746.1	hypothetical protein G ( 221)	583	130.4	1e-27	gi 144118385 gb EDI99657.1	hypothetical protein G ( 344)	575	128.8	4.7e-27
gi 137600689 gb EBU98255.1	hypothetical protein G ( 198)	582	130.2	1.1e-27	gi 138473826 gb EBZ92124.1	hypothetical protein G ( 187)	571	127.9	4.9e-27
gi 137606050 gb EBV01280.1	hypothetical protein G ( 235)	583	130.4	1.1e-27	gi 138410663 gb EBZ48146.1	hypothetical protein G ( 221)	572	128.1	4.9e-27
gi 135468157 gb EBH83851.1	hypothetical protein G ( 343)	585	130.9	1.1e-27	gi 139206262 gb ECE13862.1	hypothetical protein G ( 225)	572	128.1	5e-27
gi 139197803 gb ECE08220.1	hypothetical protein G ( 250)	583	130.4	1.1e-27	gi 136438974 gb EB016938.1	hypothetical protein G ( 254)	572	128.1	5.5e-27
gi 20905696 gb AAM30934.1	3-phosphoshikimate 1-ca ( 430)	586	131.1	1.2e-27	gi 140760372 gb ECN33022.1	hypothetical protein G ( 188)	570	127.7	5.7e-27
gi 161726859 emb CAP47299.1	unnamed protein produ ( 430)	586	131.1	1.2e-27	gi 140425672 gb ECL67335.1	hypothetical protein G ( 252)	571	127.9	6.3e-27
gi 197053761 gb ACH25459.1	Sequence 11 from paten ( 430)	586	131.1	1.2e-27	gi 139040218 gb ECC99544.1	hypothetical protein G ( 258)	571	127.9	6.5e-27
gi 138511461 gb ECA10116.1	hypothetical protein G ( 262)	583	130.4	1.2e-27	gi 140296649 gb ECC80535.1	hypothetical protein G ( 267)	571	127.9	6.7e-27
gi 142626295 gb EC242151.1	hypothetical protein G ( 270)	583	130.4	1.2e-27	gi 141975411 gb ECU55913.1	hypothetical protein G ( 246)	570	127.7	7.2e-27
gi 135500999 gb EBI05114.1	hypothetical protein G ( 325)	584	130.7	1.2e-27	gi 136884800 gb EBR04358.1	hypothetical protein G ( 184)	568	127.2	7.5e-27
gi 142202639 gb ECW36029.1	hypothetical protein G ( 236)	582	130.2	1.2e-27	gi 142623014 gb ECZ39816.1	hypothetical protein G ( 333)	571	128.0	8.1e-27
gi 140948059 gb EC059318.1	hypothetical protein G ( 222)	581	130.0	1.3e-27	gi 139492061 gb ECF43960.1	hypothetical protein G ( 205)	568	127.3	8.2e-27
gi 135169737 gb EBF93992.1	hypothetical protein G ( 317)	583	130.5	1.4e-27	gi 143225744 gb EDD72527.1	hypothetical protein G ( 346)	571	128.0	8.3e-27
gi 137232547 gb EBS94634.1	hypothetical protein G ( 237)	581	130.0	1.4e-27	gi 139119268 gb ECD54583.1	hypothetical protein G ( 249)	569	127.5	8.4e-27
gi 142266870 gb ECW83884.1	hypothetical protein G ( 185)	579	129.5	1.5e-27	gi 136616380 gb EBP30906.1	hypothetical protein G ( 354)	571	128.0	8.5e-27
gi 137557613 gb EBU74085.1	hypothetical protein G ( 192)	579	129.5	1.6e-27	gi 139865703 gb ECI00815.1	hypothetical protein G ( 254)	569	127.5	8.5e-27
gi 141393185 gb ECR51347.1	hypothetical protein G ( 271)	581	130.0	1.6e-27	gi 139687054 gb ECG77816.1	hypothetical protein G ( 217)	568	127.3	8.6e-27
gi 139040947 gb ECD00081.1	hypothetical protein G ( 204)	579	129.5	1.7e-27	gi 134872290 gb EBB98647.1	hypothetical protein G ( 383)	571	128.0	9.1e-27
gi 136231925 gb EBM76868.1	hypothetical protein G ( 230)	579	129.6	1.9e-27	gi 136075621 gb EBL74549.1	hypothetical protein G ( 396)	571	128.0	9.4e-27
gi 136346125 gb EBM54406.1	hypothetical protein G ( 228)	578	129.4	2.1e-27	gi 135964875 gb EBL01570.1	hypothetical protein G ( 339)	570	127.8	9.5e-27
gi 136568435 gb EBP00216.1	hypothetical protein G ( 379)	581	130.1	2.1e-27	gi 140139580 gb ECJ80221.1	hypothetical protein G ( 184)	566	126.8	9.9e-27
gi 137068138 gb EBS02685.1	hypothetical protein G ( 198)	577	129.1	2.2e-27	gi 138159520 gb EBY09503.1	hypothetical protein G ( 227)	567	127.1	1e-26
gi 136184878 gb EBM45270.1	hypothetical protein G ( 202)	577	129.1	2.2e-27	gi 142653024 gb ECZ61002.1	hypothetical protein G ( 229)	567	127.1	1e-26
gi 136609934 gb EBP26903.1	hypothetical protein G ( 394)	581	130.1	2.2e-27	gi 143392869 gb EDE71678.1	hypothetical protein G ( 331)	569	127.6	1.1e-26
gi 144114617 gb EDI96951.1	hypothetical protein G ( 245)	578	129.4	2.3e-27	gi 135377215 gb EBH22814.1	hypothetical protein G ( 340)	569	127.6	1.1e-26
gi 136484986 gb EB046689.1	hypothetical protein G ( 259)	578	129.4	2.4e-27	gi 142389451 gb ECX71311.1	hypothetical protein G ( 247)	567	127.1	1.1e-26
gi 135790786 gb EBJ86387.1	hypothetical protein G ( 225)	577	129.1	2.4e-27	gi 137889824 gb EBW58476.1	hypothetical protein G ( 260)	567	127.1	1.2e-26

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gi 134339575 gb EBA74899.1	hypothetical protein G ( 199)	565	126.6	1.2e-26	gi 138798250 gb ECB90802.1	hypothetical protein G ( 239)	555	124.6	6.1e-26
gi 135121196 gb EBF62739.1	hypothetical protein G ( 199)	565	126.6	1.2e-26	gi 140882192 gb ECO14647.1	hypothetical protein G ( 183)	553	124.1	6.4e-26
gi 143038670 gb EDC36519.1	hypothetical protein G ( 389)	569	127.6	1.2e-26	gi 135373751 gb EBH20476.1	hypothetical protein G ( 359)	557	125.1	6.5e-26
gi 134863258 gb EBD92485.1	hypothetical protein G ( 172)	564	126.4	1.3e-26	gi 139196107 gb ECE07005.1	hypothetical protein G ( 218)	554	124.4	6.5e-26
gi 140309242 gb ECK88285.1	hypothetical protein G ( 285)	567	127.1	1.3e-26	gi 136321702 gb EBN37871.1	hypothetical protein G ( 322)	556	124.9	6.8e-26
gi 135914634 gb EBK67553.1	hypothetical protein G ( 250)	566	126.9	1.3e-26	gi 137023050 gb EBR77234.1	hypothetical protein G ( 197)	553	124.1	6.9e-26
gi 138424579 gb EBZ57865.1	hypothetical protein G ( 257)	566	126.9	1.3e-26	gi 137920165 gb EBW75787.1	hypothetical protein G ( 200)	553	124.1	7e-26
gi 137468525 gb EBU26841.1	hypothetical protein G ( 240)	565	126.7	1.4e-26	gi 135576705 gb EBI53580.1	hypothetical protein G ( 346)	556	124.9	7.2e-26
gi 143691937 gb EDG30929.1	hypothetical protein G ( 336)	567	127.1	1.4e-26	gi 143557400 gb EDF62059.1	hypothetical protein G ( 254)	554	124.4	7.4e-26
gi 136969398 gb EBR46933.1	hypothetical protein G ( 213)	564	126.4	1.5e-26	gi 198037329 emb CAR53255.1	3-phosphoshikimate 1- ( 434)	557	125.1	7.6e-26
gi 134551651 gb EBC01843.1	hypothetical protein G ( 326)	566	126.9	1.6e-26	gi 169815598 gb ACA90181.1	3-phosphoshikimate 1-c ( 434)	557	125.1	7.6e-26
gi 142551184 gb ECY89604.1	hypothetical protein G ( 290)	565	126.7	1.7e-26	gi 137968623 gb EBX03144.1	hypothetical protein G ( 233)	553	124.2	7.9e-26
gi 142423272 gb ECX96633.1	hypothetical protein G ( 259)	564	126.5	1.8e-26	gi 143843065 gb EDH02621.1	hypothetical protein G ( 387)	556	124.9	8e-26
gi 143371316 gb EDK61828.1	hypothetical protein G ( 260)	564	126.5	1.8e-26	gi 135893800 gb EBK53064.1	hypothetical protein G ( 207)	552	123.9	8.3e-26
gi 138340797 gb EBZ07170.1	hypothetical protein G ( 188)	562	126.0	1.8e-26	gi 124870769 gb EAY62485.1	5-enolpyruvylshikimate ( 479)	557	125.1	8.3e-26
gi 139696462 gb ECG84095.1	hypothetical protein G ( 226)	563	126.2	1.8e-26	gi 139071862 gb ECD21725.1	hypothetical protein G ( 232)	552	124.0	9.1e-26
gi 135716657 gb EBU40232.1	hypothetical protein G ( 326)	565	126.7	1.9e-26	gi 187716173 gb ACD17397.1	3-phosphoshikimate 1-c ( 434)	555	124.7	1e-25
gi 137948089 gb EBW91495.1	hypothetical protein G ( 201)	562	126.0	1.9e-26	gi 137566498 gb EBU79105.1	hypothetical protein G ( 225)	551	123.7	1e-25
gi 138908490 gb ECC37780.1	hypothetical protein G ( 241)	563	126.2	1.9e-26	gi 134551891 gb EBC01982.1	hypothetical protein G ( 329)	553	124.2	1.1e-25
gi 142922285 gb EDB53971.1	hypothetical protein G ( 362)	565	126.7	2.1e-26	gi 139245948 gb ECE35232.1	hypothetical protein G ( 215)	550	123.5	1.1e-25
gi 135240692 gb EBG36991.1	hypothetical protein G ( 283)	563	126.3	2.2e-26	gi 135226702 gb EBG28755.1	hypothetical protein G ( 310)	552	124.0	1.2e-25
gi 138795144 gb ECB89357.1	hypothetical protein G ( 240)	562	126.0	2.2e-26	gi 91688767 gb ABE31967.1	3-phosphoshikimate 1-ca ( 434)	554	124.5	1.2e-25
gi 135941869 gb EBK86062.1	hypothetical protein G ( 402)	565	126.8	2.3e-26	gi 134952781 gb EBE52351.1	hypothetical protein G ( 377)	553	124.3	1.2e-25
gi 134868092 gb EBD95850.1	hypothetical protein G ( 246)	562	126.0	2.3e-26	gi 135604263 gb EBI70715.1	hypothetical protein G ( 320)	552	124.0	1.2e-25
gi 138512645 gb ECA10915.1	hypothetical protein G ( 247)	562	126.0	2.3e-26	gi 135483426 gb EBH93800.1	hypothetical protein G ( 347)	552	124.0	1.3e-25
gi 141158183 gb ECQ03135.1	hypothetical protein G ( 233)	561	125.8	2.5e-26	gi 139636870 gb ECC42399.1	hypothetical protein G ( 253)	550	123.6	1.3e-25
gi 135590928 gb EBI62468.1	hypothetical protein G ( 298)	562	126.1	2.7e-26	gi 138847143 gb ECC13990.1	hypothetical protein G ( 217)	549	123.3	1.3e-25
gi 72395592 gb AAZ69865.1	3-phosphoshikimate 1-ca ( 443)	564	126.6	2.8e-26	gi 105892312 gb ABF75477.1	3-phosphoshikimate 1-c ( 434)	553	124.3	1.4e-25
gi 141894282 gb ECT99316.1	hypothetical protein G ( 237)	560	125.6	2.9e-26	gi 136947697 gb EBR34653.1	hypothetical protein G ( 240)	549	123.3	1.4e-25
gi 137705280 gb EBV55748.1	hypothetical protein G ( 244)	560	125.6	3e-26	gi 134979326 gb EBE69999.1	hypothetical protein G ( 212)	548	123.1	1.5e-25
gi 139477785 gb ECF35725.1	hypothetical protein G ( 179)	558	125.2	3.1e-26	gi 237875728 gb ACR28061.1	Prephenate dehydrogena ( 432)	552	124.1	1.6e-25
gi 167284551 gb ABZ37415.1	Sequence 11353 from pa ( 424)	563	126.4	3.1e-26	gi 142836321 gb EDA94821.1	hypothetical protein G ( 438)	552	124.1	1.6e-25
gi 143559119 gb EDF62999.1	hypothetical protein G ( 319)	561	125.9	3.3e-26	gi 143696142 gb EDG32910.1	hypothetical protein G ( 270)	549	123.4	1.6e-25
gi 141656055 gb ECS67288.1	hypothetical protein G ( 242)	559	125.4	3.5e-26	gi 137405532 gb EBT91789.1	hypothetical protein G ( 308)	549	123.4	1.8e-25
gi 138863194 gb ECC19987.1	hypothetical protein G ( 245)	559	125.4	3.5e-26	gi 140684627 gb ECM80425.1	hypothetical protein G ( 188)	546	122.7	1.8e-25
gi 136107740 gb EBL96408.1	hypothetical protein G ( 251)	559	125.4	3.6e-26	gi 140227603 gb ECK39251.1	hypothetical protein G ( 192)	546	122.7	1.8e-25
gi 134961533 gb EBE57972.1	hypothetical protein G ( 364)	561	125.9	3.7e-26	gi 137807735 gb EBW11120.1	hypothetical protein G ( 227)	547	122.9	1.8e-25
gi 141118072 gb ECP75106.1	hypothetical protein G ( 266)	559	125.4	3.7e-26	gi 139664048 gb ECG61622.1	hypothetical protein G ( 174)	545	122.4	2e-25
gi 143233038 gb EDD77786.1	hypothetical protein G ( 304)	559	125.5	4.2e-26	gi 135486766 gb EBH95950.1	hypothetical protein G ( 350)	549	123.4	2e-25
gi 143554952 gb EDF60809.1	hypothetical protein G ( 325)	559	125.5	4.5e-26	gi 138799594 gb ECB91450.1	hypothetical protein G ( 188)	545	122.5	2.1e-25
gi 140786812 gb ECN50244.1	hypothetical protein G ( 233)	557	125.0	4.5e-26	gi 116647157 gb ABK07798.1	3-phosphoshikimate 1-c ( 434)	550	123.7	2.1e-25
gi 142807522 gb EDA73087.1	hypothetical protein G ( 335)	559	125.5	4.6e-26	gi 141904797 gb ECU06828.1	hypothetical protein G ( 225)	546	122.7	2.1e-25
gi 139608209 gb ECG23917.1	hypothetical protein G ( 241)	557	125.0	4.6e-26	gi 137657757 gb EBV28937.1	hypothetical protein G ( 277)	547	123.0	2.2e-25
gi 136366647 gb EBN68381.1	hypothetical protein G ( 305)	558	125.3	4.9e-26	gi 142502870 gb ECY54666.1	hypothetical protein G ( 244)	546	122.7	2.3e-25
gi 136116511 gb EBM02403.1	hypothetical protein G ( 311)	558	125.3	5e-26	gi 135619300 gb EBT80064.1	hypothetical protein G ( 216)	545	122.5	2.4e-25
gi 136336798 gb EBN48052.1	hypothetical protein G ( 321)	558	125.3	5.1e-26	gi 135336253 gb EBG95349.1	hypothetical protein G ( 222)	545	122.5	2.4e-25
gi 139515305 gb ECF59981.1	hypothetical protein G ( 284)	557	125.0	5.3e-26	gi 144092979 gb EDT81512.1	hypothetical protein G ( 224)	545	122.5	2.4e-25
gi 136526549 gb EB073484.1	hypothetical protein G ( 337)	558	125.3	5.3e-26	gi 134905326 gb EBE20586.1	hypothetical protein G ( 322)	547	123.0	2.5e-25
gi 141806782 gb ECT38147.1	hypothetical protein G ( 247)	556	124.8	5.4e-26	gi 139718797 gb ECG99847.1	hypothetical protein G ( 282)	546	122.7	2.6e-25
gi 138537975 gb ECA28323.1	hypothetical protein G ( 183)	554	124.3	5.6e-26	gi 141939792 gb ECU31133.1	hypothetical protein G ( 241)	545	122.5	2.6e-25
gi 140158907 gb ECJ91707.1	hypothetical protein G ( 264)	556	124.8	5.7e-26	gi 142174489 gb ECW14547.1	hypothetical protein G ( 215)	544	122.3	2.7e-25

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gi 142106223 gb ECV63468.1	hypothetical protein G ( 260)	545	122.5	2.8e-25	gi 135239148 gb EBG36086.1	hypothetical protein G ( 260)	536	120.7	1e-24
gi 141370398 gb ECR35261.1	hypothetical protein G ( 229)	544	122.3	2.9e-25	gi 167281782 gb ABZ34646.1	Sequence 8584 from pat ( 435)	539	121.4	1e-24
gi 139693729 gb ECG82133.1	hypothetical protein G ( 231)	544	122.3	2.9e-25	gi 93353516 gb ABF07605.1	3-phosphoshikimate 1-ca ( 452)	539	121.4	1.1e-24
gi 135961619 gb EBK99364.1	hypothetical protein G ( 334)	546	122.8	3e-25	gi 140909158 gb ECO32037.1	hypothetical protein G ( 197)	534	120.2	1.1e-24
gi 137265443 gb EBT13073.1	hypothetical protein G ( 285)	545	122.5	3e-25	gi 136287602 gb EBN14795.1	hypothetical protein G ( 240)	535	120.4	1.1e-24
gi 141829576 gb ECT53906.1	hypothetical protein G ( 246)	544	122.3	3e-25	gi 140346704 gb ECL14523.1	hypothetical protein G ( 289)	536	120.7	1.1e-24
gi 139685248 gb ECG76510.1	hypothetical protein G ( 210)	543	122.1	3.1e-25	gi 171992497 gb ACB63416.1	3-phosphoshikimate 1-c ( 434)	538	121.2	1.2e-24
gi 136941044 gb EBR30919.1	hypothetical protein G ( 316)	545	122.6	3.3e-25	gi 139681527 gb ECG73843.1	hypothetical protein G ( 233)	534	120.2	1.2e-24
gi 141897485 gb ECU01623.1	hypothetical protein G ( 270)	544	122.3	3.3e-25	gi 141468959 gb ECS00232.1	hypothetical protein G ( 280)	535	120.5	1.2e-24
gi 142659509 gb EC265576.1	hypothetical protein G ( 383)	546	122.8	3.3e-25	gi 138983048 gb ECC68255.1	hypothetical protein G ( 312)	535	120.5	1.4e-24
gi 141433718 gb ECR75057.1	hypothetical protein G ( 199)	542	121.8	3.4e-25	gi 222452024 gb ACM56289.1	3-phosphoshikimate 1-c ( 453)	537	121.0	1.4e-24
gi 141866828 gb ECT80295.1	hypothetical protein G ( 172)	541	121.6	3.4e-25	gi 142861145 gb EDB09899.1	hypothetical protein G ( 338)	535	120.5	1.5e-24
gi 137239164 gb EBS98164.1	hypothetical protein G ( 242)	543	122.1	3.5e-25	gi 135288143 gb EBG64892.1	hypothetical protein G ( 207)	532	119.8	1.5e-24
gi 143916119 gb EDH55081.1	hypothetical protein G ( 216)	542	121.9	3.6e-25	gi 139853911 gb EBH92771.1	hypothetical protein G ( 292)	534	120.3	1.5e-24
gi 135865254 gb EBK33280.1	hypothetical protein G ( 313)	544	122.4	3.7e-25	gi 136661056 gb EBP57372.1	hypothetical protein G ( 184)	531	119.5	1.5e-24
gi 139589323 gb ECG10868.1	hypothetical protein G ( 225)	542	121.9	3.8e-25	gi 141709826 gb ECS86859.1	hypothetical protein G ( 234)	532	119.8	1.6e-24
gi 141665863 gb ECG70196.1	hypothetical protein G ( 226)	542	121.9	3.8e-25	gi 139040948 gb ECD00082.1	hypothetical protein G ( 237)	532	119.8	1.7e-24
gi 138530901 gb ECA23368.1	hypothetical protein G ( 287)	543	122.1	4e-25	gi 135317778 gb EBG82900.1	hypothetical protein G ( 410)	535	120.5	1.7e-24
gi 135896558 gb EBK54995.1	hypothetical protein G ( 345)	544	122.4	4.1e-25	gi 140690954 gb ECM84840.1	hypothetical protein G ( 298)	533	120.1	1.7e-24
gi 140405936 gb ECL55694.1	hypothetical protein G ( 232)	541	121.7	4.5e-25	gi 140343196 gb ECL11994.1	hypothetical protein G ( 304)	533	120.1	1.8e-24
gi 134450625 gb EBB42108.1	hypothetical protein G ( 201)	540	121.4	4.5e-25	gi 135393659 gb EBH33889.1	hypothetical protein G ( 261)	532	119.8	1.8e-24
gi 134533954 gb EBB91312.1	hypothetical protein G ( 242)	541	121.7	4.6e-25	gi 139064451 gb ECD16608.1	hypothetical protein G ( 223)	531	119.6	1.8e-24
gi 137214519 gb EBS84393.1	hypothetical protein G ( 295)	542	121.9	4.7e-25	gi 138276283 gb EBH74911.1	hypothetical protein G ( 308)	532	119.9	2.1e-24
gi 134849254 gb EBD83358.1	hypothetical protein G ( 275)	541	121.7	5.2e-25	gi 140028597 gb ECJ10751.1	hypothetical protein G ( 312)	532	119.9	2.1e-24
gi 136206440 gb EBM59627.1	hypothetical protein G ( 245)	540	121.5	5.4e-25	gi 136443021 gb EBO19562.1	hypothetical protein G ( 457)	534	120.3	2.2e-24
gi 134981203 gb EBE71267.1	hypothetical protein G ( 292)	541	121.7	5.4e-25	gi 142905356 gb EDB41681.1	hypothetical protein G ( 199)	529	119.1	2.2e-24
gi 83655416 gb ABC39479.1	prephenate dehydrogenas ( 805)	547	123.2	5.5e-25	gi 136315894 gb EBN34015.1	hypothetical protein G ( 280)	531	119.6	2.2e-24
gi 138641254 gb ECA99072.1	hypothetical protein G ( 302)	541	121.7	5.6e-25	gi 143715743 gb EDG41937.1	hypothetical protein G ( 243)	530	119.4	2.3e-24
gi 140654805 gb ECM59434.1	hypothetical protein G ( 256)	540	121.5	5.6e-25	gi 141915818 gb ECL14327.1	hypothetical protein G ( 249)	530	119.4	2.3e-24
gi 139967027 gb ECI69743.1	hypothetical protein G ( 306)	541	121.7	5.7e-25	gi 138116427 gb EBX83452.1	hypothetical protein G ( 297)	531	119.6	2.3e-24
gi 137329713 gb EBT48905.1	hypothetical protein G ( 223)	539	121.2	5.7e-25	gi 134967391 gb EBE61919.1	hypothetical protein G ( 354)	532	119.9	2.3e-24
gi 141333425 gb ECR11074.1	hypothetical protein G ( 296)	540	121.5	6.3e-25	gi 141188377 gb ECQ24336.1	hypothetical protein G ( 306)	531	119.6	2.4e-24
gi 141882968 gb ECT91410.1	hypothetical protein G ( 185)	537	120.8	6.5e-25	gi 184191968 gb ACC69933.1	3-phosphoshikimate 1-c ( 434)	533	120.1	2.4e-24
gi 135645619 gb EBI96344.1	hypothetical protein G ( 306)	540	121.5	6.5e-25	gi 135670495 gb EBJ11737.1	hypothetical protein G ( 316)	531	119.7	2.5e-24
gi 140178654 gb ECK05494.1	hypothetical protein G ( 222)	538	121.0	6.6e-25	gi 137178927 gb EBS64474.1	hypothetical protein G ( 249)	529	119.2	2.7e-24
gi 77966375 gb ABB07755.1	3-phosphoshikimate 1-ca ( 434)	542	122.0	6.6e-25	gi 134138234 gb ABO53977.1	3-phosphoshikimate 1-c ( 434)	532	119.9	2.8e-24
gi 141671849 gb ECS73496.1	hypothetical protein G ( 314)	540	121.5	6.7e-25	gi 139824132 gb ECH71785.1	hypothetical protein G ( 238)	528	119.0	3e-24
gi 141048681 gb ECP27929.1	hypothetical protein G ( 290)	539	121.3	7.2e-25	gi 139196108 gb ECE07006.1	hypothetical protein G ( 207)	527	118.7	3e-24
gi 135841164 gb EBK18114.1	hypothetical protein G ( 312)	539	121.3	7.7e-25	gi 141545034 gb ECS26839.1	hypothetical protein G ( 254)	528	119.0	3.1e-24
gi 142998533 gb EDC07332.1	hypothetical protein G ( 227)	537	120.8	7.8e-25	gi 135871899 gb EBK37709.1	hypothetical protein G ( 255)	528	119.0	3.1e-24
gi 142109868 gb ECV66243.1	hypothetical protein G ( 524)	542	122.0	7.8e-25	gi 135564677 gb EBT45872.1	hypothetical protein G ( 306)	529	119.2	3.2e-24
gi 141927970 gb ECU22932.1	hypothetical protein G ( 327)	539	121.3	8e-25	gi 115280963 gb ABT86480.1	3-phosphoshikimate 1-c ( 434)	531	119.7	3.2e-24
gi 138499014 gb ECA02780.1	hypothetical protein G ( 237)	537	120.8	8.1e-25	gi 137171985 gb EBS60590.1	hypothetical protein G ( 272)	528	119.0	3.3e-24
gi 55274195 gb AAV48979.1	hypothetical carboxyvin ( 202)	536	120.6	8.1e-25	gi 135477171 gb EBH89817.1	hypothetical protein G ( 384)	530	119.5	3.4e-24
gi 139629194 gb ECG37093.1	hypothetical protein G ( 306)	538	121.1	8.7e-25	gi 140788599 gb ECN51475.1	hypothetical protein G ( 235)	527	118.8	3.4e-24
gi 189333856 dbj BAG42926.1	3-phosphoshikimate 1- ( 434)	540	121.6	8.8e-25	gi 143039536 gb EDC37155.1	hypothetical protein G ( 336)	529	119.2	3.5e-24
gi 160342858 gb ABX15944.1	3-phosphoshikimate 1-c ( 434)	540	121.6	8.8e-25	gi 141712157 gb ECS88316.1	hypothetical protein G ( 216)	526	118.5	3.6e-24
gi 222436771 gb EEB43450.1	hypothetical protein S ( 136)	533	119.9	8.9e-25	gi 139732419 gb ECH09173.1	hypothetical protein G ( 227)	526	118.5	3.8e-24
gi 135327266 gb EBG89302.1	hypothetical protein G ( 357)	538	121.1	9.9e-25	gi 134604121 gb EBC33250.1	hypothetical protein G ( 325)	528	119.0	3.9e-24
gi 137591925 gb EBU93376.1	hypothetical protein G ( 256)	536	120.6	1e-24	gi 140472221 gb ECL93917.1	hypothetical protein G ( 284)	527	118.8	4e-24
gi 142105249 gb ECV62774.1	hypothetical protein G ( 305)	537	120.9	1e-24	gi 138558264 gb ECA42657.1	hypothetical protein G ( 291)	527	118.8	4.1e-24

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gi 140118856 gb ECJ66743.1	hypothetical protein G ( 210)	525	118.3	4.1e-24	gi 254218017 gb EET07401.1	prephenate dehydrogena ( 753)	525	118.6	1.2e-23
gi 142394074 gb ECX74728.1	hypothetical protein G ( 296)	527	118.8	4.1e-24	gi 242138323 gb EES24725.1	prephenate dehydrogena ( 753)	525	118.6	1.2e-23
gi 137547042 gb EBU68034.1	hypothetical protein G ( 312)	527	118.8	4.3e-24	gi 143839650 gb EDH00163.1	hypothetical protein G ( 302)	519	117.1	1.3e-23
gi 136980766 gb EBR53373.1	hypothetical protein G ( 285)	526	118.6	4.6e-24	gi 140119424 gb ECJ67138.1	hypothetical protein G ( 227)	517	116.7	1.4e-23
gi 138110485 gb EBX80097.1	hypothetical protein G ( 218)	524	118.1	4.9e-24	gi 135489518 gb EBH97714.1	hypothetical protein G ( 271)	518	116.9	1.4e-23
gi 139494432 gb ECF45603.1	hypothetical protein G ( 305)	526	118.6	4.9e-24	gi 184211626 gb EDU08669.1	prephenate dehydrogena ( 749)	524	118.4	1.4e-23
gi 141385612 gb ECR46209.1	hypothetical protein G ( 187)	523	117.9	4.9e-24	gi 138996659 gb ECC72241.1	hypothetical protein G ( 201)	516	116.4	1.4e-23
gi 113525597 emb CAJ91942.1	3-Enolpyruvylshikimat ( 434)	528	119.1	5e-24	gi 136324373 gb EBN39656.1	hypothetical protein G ( 337)	519	117.2	1.5e-23
gi 139454002 gb ECF21045.1	hypothetical protein G ( 284)	525	118.4	5.3e-24	gi 139441542 gb ECG12258.1	hypothetical protein G ( 242)	517	116.7	1.5e-23
gi 143591543 gb EDF75609.1	hypothetical protein G ( 219)	523	117.9	5.7e-24	gi 135491229 gb EBH98820.1	hypothetical protein G ( 208)	516	116.5	1.5e-23
gi 136364219 gb EBN66733.1	hypothetical protein G ( 310)	525	118.4	5.7e-24	gi 167277472 gb ABZ30336.1	Sequence 4274 from pat ( 415)	520	117.4	1.5e-23
gi 137657142 gb EBV28587.1	hypothetical protein G ( 276)	524	118.2	6e-24	gi 140215327 gb ECK31464.1	hypothetical protein G ( 216)	516	116.5	1.5e-23
gi 141543043 gb ECS25410.1	hypothetical protein G ( 294)	524	118.2	6.3e-24	gi 150011975 gb ABR54427.1	3-phosphoshikimate 1-c ( 429)	520	117.4	1.6e-23
gi 138799362 gb ECB91357.1	hypothetical protein G ( 298)	524	118.2	6.4e-24	gi 142702742 gb ECZ96501.1	hypothetical protein G ( 231)	516	116.5	1.6e-23
gi 136969921 gb EBR47225.1	hypothetical protein G ( 306)	524	118.2	6.5e-24	gi 142823924 gb EDA85437.1	hypothetical protein G ( 332)	518	117.0	1.7e-23
gi 135489629 gb EBH97784.1	hypothetical protein G ( 363)	525	118.4	6.6e-24	gi 143159217 gb EDD24462.1	hypothetical protein G ( 283)	517	116.7	1.7e-23
gi 140748856 gb ECN25154.1	hypothetical protein G ( 312)	524	118.2	6.7e-24	gi 140985159 gb ECC085137.1	hypothetical protein G ( 283)	517	116.7	1.7e-23
gi 137375246 gb EBT74514.1	hypothetical protein G ( 226)	522	117.7	6.7e-24	gi 141847270 gb ECT66591.1	hypothetical protein G ( 241)	516	116.5	1.7e-23
gi 142865504 gb EDB13092.1	hypothetical protein G ( 227)	522	117.7	6.7e-24	gi 135215196 gb EBG22013.1	hypothetical protein G ( 259)	516	116.5	1.8e-23
gi 138613133 gb ECA81107.1	hypothetical protein G ( 326)	524	118.2	6.9e-24	gi 136230377 gb EBM75834.1	hypothetical protein G ( 307)	517	116.7	1.8e-23
gi 142607018 gb ECZ28589.1	hypothetical protein G ( 202)	521	117.5	7e-24	gi 139643880 gb ECG47198.1	hypothetical protein G ( 301)	516	116.5	2e-23
gi 139995621 gb ECI89691.1	hypothetical protein G ( 284)	523	118.0	7.1e-24	gi 135686333 gb EBJ21480.1	hypothetical protein G ( 304)	516	116.5	2.1e-23
gi 137691967 gb EBV48315.1	hypothetical protein G ( 286)	523	118.0	7.1e-24	gi 141110942 gb ECZ70249.1	hypothetical protein G ( 196)	513	115.8	2.2e-23
gi 135845227 gb EBK20663.1	hypothetical protein G ( 303)	523	118.0	7.5e-24	gi 142656925 gb ECZ63763.1	hypothetical protein G ( 197)	513	115.8	2.2e-23
gi 142543985 gb ECY84528.1	hypothetical protein G ( 268)	522	117.7	7.8e-24	gi 169652329 gb EDS85022.1	prephenate dehydrogena ( 749)	521	117.7	2.2e-23
gi 135854902 gb EBK26763.1	hypothetical protein G ( 236)	521	117.5	8.1e-24	gi 134442483 gb EBB37469.1	hypothetical protein G ( 285)	515	116.3	2.3e-23
gi 138005019 gb EBX23095.1	hypothetical protein G ( 288)	522	117.8	8.3e-24	gi 139920801 gb ECI37947.1	hypothetical protein G ( 156)	511	115.4	2.4e-23
gi 138091258 gb EBX69473.1	hypothetical protein G ( 175)	519	117.0	8.3e-24	gi 138180415 gb EBY24121.1	hypothetical protein G ( 314)	515	116.3	2.4e-23
gi 137912933 gb EBW71741.1	hypothetical protein G ( 279)	521	117.5	9.3e-24	gi 139647519 gb ECA49757.1	hypothetical protein G ( 225)	513	115.8	2.4e-23
gi 138660060 gb ECB12035.1	hypothetical protein G ( 284)	521	117.6	9.5e-24	gi 237503144 gb ACQ95462.1	prephenate dehydrogena ( 749)	520	117.5	2.5e-23
gi 134549068 gb EBC00317.1	hypothetical protein G ( 241)	520	117.3	9.5e-24	gi 137703414 gb EBV54784.1	hypothetical protein G ( 279)	514	116.1	2.6e-23
gi 138550260 gb ECA37196.1	hypothetical protein G ( 251)	520	117.3	9.8e-24	gi 139914190 gb ECI33276.1	hypothetical protein G ( 294)	514	116.1	2.7e-23
gi 138878119 gb ECC26539.1	hypothetical protein G ( 255)	520	117.3	9.9e-24	gi 143760794 gb EDG64991.1	hypothetical protein G ( 317)	514	116.1	2.8e-23
gi 142411096 gb ECX87359.1	hypothetical protein G ( 436)	523	118.1	1e-23	gi 134531717 gb EBB89974.1	hypothetical protein G ( 201)	511	115.4	3e-23
gi 137078318 gb EBS08436.1	hypothetical protein G ( 314)	521	117.6	1e-23	gi 138115352 gb EBX38289.1	hypothetical protein G ( 238)	512	115.6	3e-23
gi 141123386 gb ECP78845.1	hypothetical protein G ( 245)	519	117.1	1.1e-23	gi 138840632 gb ECC10892.1	hypothetical protein G ( 289)	513	115.9	3e-23
gi 52428212 gb AAU48805.1	prephenate dehydrogenas ( 673)	525	118.6	1.1e-23	gi 135795613 gb EBJ89439.1	hypothetical protein G ( 209)	511	115.4	3.1e-23
gi 142771693 gb EDA46374.1	hypothetical protein G ( 179)	517	116.6	1.1e-23	gi 141139548 gb ECP90029.1	hypothetical protein G ( 249)	512	115.7	3.1e-23
gi 76581095 gb ABA50570.1	prephenate dehydrogenas ( 714)	525	118.6	1.2e-23	gi 136509201 gb EBO62385.1	hypothetical protein G ( 297)	513	115.9	3.1e-23
gi 157805514 gb ED082684.1	prephenate dehydrogena ( 740)	525	118.6	1.2e-23	gi 136178233 gb EBM40882.1	hypothetical protein G ( 213)	511	115.4	3.1e-23
gi 126219744 gb ABN83250.1	prephenate dehydrogena ( 749)	525	118.6	1.2e-23	gi 135713521 gb EBJ38289.1	hypothetical protein G ( 353)	514	116.1	3.1e-23
gi 121227083 gb ABM49601.1	prephenate dehydrogena ( 749)	525	118.6	1.2e-23	gi 135495643 gb EBI01665.1	hypothetical protein G ( 384)	514	116.2	3.4e-23
gi 148029278 gb EDK87183.1	prephenate dehydrogena ( 749)	525	118.6	1.2e-23	gi 141373745 gb ECR37668.1	hypothetical protein G ( 236)	511	115.4	3.4e-23
gi 147745439 gb EDK52519.1	prephenate dehydrogena ( 749)	525	118.6	1.2e-23	gi 138618036 gb ECA84358.1	hypothetical protein G ( 281)	512	115.7	3.4e-23
gi 126243949 gb ABO07042.1	prephenate dehydrogena ( 749)	525	118.6	1.2e-23	gi 139219178 gb ECE22826.1	hypothetical protein G ( 290)	512	115.7	3.5e-23
gi 126226820 gb ABN90360.1	prephenate dehydrogena ( 749)	525	118.6	1.2e-23	gi 136214158 gb EBM64824.1	hypothetical protein G ( 183)	509	115.0	3.6e-23
gi 124294618 gb ABN03887.1	prephenate dehydrogena ( 749)	525	118.6	1.2e-23	gi 140388086 gb ECL43376.1	hypothetical protein G ( 304)	512	115.7	3.7e-23
gi 160697699 gb EDP87669.1	prephenate dehydrogena ( 749)	525	118.6	1.2e-23	gi 143397410 gb EDE73971.1	hypothetical protein G ( 270)	511	115.5	3.8e-23
gi 147750783 gb EDK57852.1	prephenate dehydrogena ( 749)	525	118.6	1.2e-23	gi 142916528 gb EDB49892.1	hypothetical protein G ( 218)	509	115.0	4.2e-23
gi 157987840 gb ED095605.1	prephenate dehydrogena ( 753)	525	118.6	1.2e-23	gi 134548409 gb EBB99923.1	hypothetical protein G ( 317)	511	115.5	4.4e-23
gi 52210541 emb CAH36524.1	putative bifunctional ( 753)	525	118.6	1.2e-23	gi 139132650 gb ECD62535.1	hypothetical protein G ( 231)	509	115.0	4.5e-23

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gi 142699289 gb ECZ94025.1	hypothetical protein G ( 199)	508	114.8	4.5e-23	gi 137829749 gb EBW24000.1	hypothetical protein G ( 258)	501	113.4	1.6e-22
gi 135742000 gb EBJ55937.1	hypothetical protein G ( 336)	511	115.5	4.6e-23	gi 76558044 emb CAI49630.1	3-phosphoshikimate 1-c ( 438)	504	114.1	1.6e-22
gi 134788582 gb EBD44017.1	hypothetical protein G ( 150)	506	114.3	4.7e-23	gi 138810206 gb ECB96158.1	hypothetical protein G ( 201)	499	112.9	1.7e-22
gi 179351349 gb ACB85619.1	3-phosphoshikimate 1-c ( 484)	513	116.0	4.7e-23	gi 141404015 gb ECR59067.1	hypothetical protein G ( 286)	501	113.4	1.7e-22
gi 137536874 gb EBU62471.1	hypothetical protein G ( 271)	509	115.0	5.1e-23	gi 135562509 gb EBI44489.1	hypothetical protein G ( 348)	502	113.6	1.7e-22
gi 142277937 gb ECW92013.1	hypothetical protein G ( 234)	508	114.8	5.2e-23	gi 142592013 gb ECZ18106.1	hypothetical protein G ( 213)	499	112.9	1.8e-22
gi 141879126 gb ECT88675.1	hypothetical protein G ( 237)	508	114.8	5.3e-23	gi 141673429 gb ECS74370.1	hypothetical protein G ( 303)	501	113.4	1.8e-22
gi 142775989 gb EDA49581.1	hypothetical protein G ( 335)	510	115.3	5.3e-23	gi 135589703 gb EBI61715.1	hypothetical protein G ( 305)	501	113.4	1.8e-22
gi 141219643 gb ECQ44682.1	hypothetical protein G ( 291)	509	115.1	5.4e-23	gi 187724763 gb ACD25928.1	3-phosphoshikimate 1-c ( 434)	503	113.9	1.8e-22
gi 134400710 gb EBB13457.1	hypothetical protein G ( 303)	509	115.1	5.6e-23	gi 135570872 gb EBI49844.1	hypothetical protein G ( 275)	500	113.2	1.9e-22
gi 136273877 gb EBN05547.1	hypothetical protein G ( 220)	507	114.6	5.7e-23	gi 140714513 gb ECN01171.1	hypothetical protein G ( 281)	500	113.2	1.9e-22
gi 193222745 emb CAQ68748.1	3-enolpyruvylshikimat ( 434)	511	115.6	5.8e-23	gi 139789418 gb ECH47697.1	hypothetical protein G ( 204)	498	112.7	2e-22
gi 137333376 gb EBT50948.1	hypothetical protein G ( 265)	508	114.8	5.8e-23	gi 140794555 gb ECN55677.1	hypothetical protein G ( 215)	498	112.7	2e-22
gi 136805390 gb EBQ52454.1	hypothetical protein G ( 225)	507	114.6	5.8e-23	gi 136659405 gb EBP56376.1	hypothetical protein G ( 310)	500	113.2	2.1e-22
gi 138147023 gb EBY00725.1	hypothetical protein G ( 239)	507	114.6	6.1e-23	gi 143324668 gb EDE33761.1	hypothetical protein G ( 198)	497	112.5	2.2e-22
gi 138838260 gb ECC09710.1	hypothetical protein G ( 205)	506	114.4	6.2e-23	gi 135216633 gb EBG22867.1	hypothetical protein G ( 147)	495	112.0	2.3e-22
gi 138822185 gb ECC01789.1	hypothetical protein G ( 244)	507	114.6	6.2e-23	gi 135334320 gb EBG94059.1	hypothetical protein G ( 290)	499	113.0	2.3e-22
gi 140173956 gb ECK02082.1	hypothetical protein G ( 291)	508	114.9	6.3e-23	gi 138094881 gb EBX71452.1	hypothetical protein G ( 293)	499	113.0	2.3e-22
gi 141978626 gb ECU58234.1	hypothetical protein G ( 184)	505	114.1	6.5e-23	gi 137319505 gb EBT43281.1	hypothetical protein G ( 279)	498	112.8	2.6e-22
gi 72119670 gb AAZ61933.1	3-phosphoshikimate 1-ca ( 434)	510	115.3	6.6e-23	gi 137697594 gb EBV51548.1	hypothetical protein G ( 239)	497	112.5	2.6e-22
gi 139531150 gb ECF70548.1	hypothetical protein G ( 241)	506	114.4	7.1e-23	gi 136961265 gb EBR42313.1	hypothetical protein G ( 240)	497	112.5	2.6e-22
gi 135888366 gb EBK49261.1	hypothetical protein G ( 208)	505	114.2	7.2e-23	gi 138945048 gb ECC53187.1	hypothetical protein G ( 249)	497	112.5	2.7e-22
gi 124895538 gb EAY69418.1	5-enolpyruvylshikimate ( 434)	509	115.1	7.7e-23	gi 134404891 gb EBB15769.1	hypothetical protein G ( 296)	498	112.8	2.7e-22
gi 137246014 gb EBT02032.1	hypothetical protein G ( 268)	506	114.4	7.8e-23	gi 240864488 gb ACS62149.1	3-phosphoshikimate 1-c ( 434)	500	113.3	2.8e-22
gi 141653377 gb ECS66510.1	hypothetical protein G ( 279)	506	114.4	8.1e-23	gi 254589820 gb ACT69182.1	putative 3-phosphoshik ( 440)	500	113.3	2.8e-22
gi 137929679 gb EBW81155.1	hypothetical protein G ( 200)	504	113.9	8.1e-23	gi 138445398 gb EBZ72305.1	hypothetical protein G ( 174)	494	111.8	3e-22
gi 139453942 gb ECF21003.1	hypothetical protein G ( 205)	504	114.0	8.3e-23	gi 135382545 gb EBH26399.1	hypothetical protein G ( 290)	497	112.6	3.1e-22
gi 143057941 gb EDC50622.1	hypothetical protein G ( 296)	506	114.4	8.5e-23	gi 139190333 gb ECE02883.1	hypothetical protein G ( 300)	497	112.6	3.1e-22
gi 139195857 gb ECE06823.1	hypothetical protein G ( 298)	506	114.4	8.6e-23	gi 144206042 gb EDJ63793.1	hypothetical protein G ( 218)	495	112.1	3.2e-22
gi 141592162 gb ECS49928.1	hypothetical protein G ( 315)	506	114.5	9e-23	gi 142325118 gb ECX26898.1	hypothetical protein G ( 207)	494	111.9	3.5e-22
gi 140673199 gb ECM72415.1	hypothetical protein G ( 227)	504	114.0	9e-23	gi 138737512 gb ECB66482.1	hypothetical protein G ( 292)	496	112.4	3.5e-22
gi 140999785 gb ECO95579.1	hypothetical protein G ( 168)	502	113.5	9.3e-23	gi 134674198 gb EBC74845.1	hypothetical protein G ( 218)	494	111.9	3.7e-22
gi 137849920 gb EBW35596.1	hypothetical protein G ( 238)	504	114.0	9.4e-23	gi 135066400 gb EBF27712.1	hypothetical protein G ( 187)	493	111.7	3.7e-22
gi 142560062 gb ECY95832.1	hypothetical protein G ( 296)	505	114.2	9.8e-23	gi 141235824 gb ECQ56308.1	hypothetical protein G ( 189)	493	111.7	3.8e-22
gi 142690999 gb ECZ88084.1	hypothetical protein G ( 220)	503	113.8	1e-22	gi 134587656 gb EBC23605.1	hypothetical protein G ( 190)	493	111.7	3.8e-22
gi 141723183 gb ECS95130.1	hypothetical protein G ( 197)	502	113.5	1.1e-22	gi 140456535 gb ECL88213.1	hypothetical protein G ( 161)	492	111.4	3.8e-22
gi 141903494 gb ECU05918.1	hypothetical protein G ( 235)	503	113.8	1.1e-22	gi 139895987 gb ECI20390.1	hypothetical protein G ( 236)	494	111.9	3.9e-22
gi 141081658 gb ECP49602.1	hypothetical protein G ( 200)	502	113.5	1.1e-22	gi 141391411 gb ECR50083.1	hypothetical protein G ( 236)	494	111.9	3.9e-22
gi 140248541 gb ECK53972.1	hypothetical protein G ( 295)	504	114.0	1.1e-22	gi 56387797 gb AAV86384.1	3-phosphoshikimate 1-ca ( 462)	498	112.9	4e-22
gi 197053762 gb ACH25460.1	Sequence 12 from paten ( 430)	506	114.5	1.2e-22	gi 137942810 gb EBW88522.1	hypothetical protein G ( 173)	492	111.4	4e-22
gi 19918689 gb AAO7883.1	3-phosphoshikimate 1-ca ( 430)	506	114.5	1.2e-22	gi 137048868 gb EBR91792.1	hypothetical protein G ( 182)	492	111.4	4.2e-22
gi 139559346 gb ECF90294.1	hypothetical protein G ( 223)	502	113.6	1.2e-22	gi 138566080 gb ECA48176.1	hypothetical protein G ( 303)	495	112.2	4.2e-22
gi 136628519 gb EBP38073.1	hypothetical protein G ( 229)	502	113.6	1.2e-22	gi 136876301 gb EBQ99430.1	hypothetical protein G ( 227)	493	111.7	4.4e-22
gi 134737900 gb EBD11884.1	hypothetical protein G ( 239)	502	113.6	1.3e-22	gi 140108073 gb ECJ59094.1	hypothetical protein G ( 122)	489	110.7	4.6e-22
gi 137863209 gb EBW43227.1	hypothetical protein G ( 283)	503	113.8	1.3e-22	gi 143115784 gb EDC92899.1	hypothetical protein G ( 338)	495	112.2	4.7e-22
gi 134518053 gb EBB81858.1	hypothetical protein G ( 176)	500	113.1	1.3e-22	gi 141104379 gb ECP65577.1	hypothetical protein G ( 297)	494	111.9	4.8e-22
gi 135427488 gb EBH56660.1	hypothetical protein G ( 307)	503	113.8	1.4e-22	gi 137527307 gb EBU57304.1	hypothetical protein G ( 155)	490	111.0	4.9e-22
gi 134602901 gb EBC32497.1	hypothetical protein G ( 311)	503	113.8	1.4e-22	gi 141656057 gb ECS67290.1	hypothetical protein G ( 224)	492	111.5	5e-22
gi 137036578 gb EBR84858.1	hypothetical protein G ( 237)	501	113.4	1.4e-22	gi 138008762 gb EBX25078.1	hypothetical protein G ( 191)	491	111.2	5.1e-22
gi 142717897 gb EDA07347.1	hypothetical protein G ( 282)	502	113.6	1.5e-22	gi 141452906 gb ECR92796.1	hypothetical protein G ( 271)	493	111.7	5.1e-22
gi 137009311 gb EBR69583.1	hypothetical protein G ( 300)	502	113.6	1.5e-22	gi 141160798 gb ECQ05001.1	hypothetical protein G ( 203)	491	111.3	5.3e-22



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gi 140375918 gb ECL34759.1	hypothetical protein G ( 290)	493	111.7	5.4e-22	gi 141360607 gb ECR28514.1	hypothetical protein G ( 313)	483	109.7	2.5e-21
gi 140676988 gb ECM75154.1	hypothetical protein G ( 137)	488	110.5	5.8e-22	gi 139699914 gb ECG86528.1	hypothetical protein G ( 265)	482	109.4	2.5e-21
gi 137324469 gb EBT46018.1	hypothetical protein G ( 274)	492	111.5	6e-22	gi 135162903 gb EBF89585.1	hypothetical protein G ( 163)	479	108.7	2.5e-21
gi 141899038 gb ECU02730.1	hypothetical protein G ( 285)	492	111.5	6.2e-22	gi 137214394 gb EBS84325.1	hypothetical protein G ( 291)	482	109.5	2.7e-21
gi 143255766 gb EDD93469.1	hypothetical protein G ( 298)	492	111.5	6.4e-22	gi 134835060 gb EBD74225.1	hypothetical protein G ( 295)	482	109.5	2.7e-21
gi 139669584 gb ECG65360.1	hypothetical protein G ( 219)	490	111.1	6.6e-22	gi 138860211 gb ECC18701.1	hypothetical protein G ( 259)	481	109.2	2.8e-21
gi 134446918 gb EBB39935.1	hypothetical protein G ( 234)	490	111.1	7e-22	gi 142969511 gb EDB87361.1	hypothetical protein G ( 266)	481	109.2	2.8e-21
gi 140887583 gb EC018446.1	hypothetical protein G ( 242)	490	111.1	7.2e-22	gi 134635372 gb EBC52105.1	hypothetical protein G ( 205)	479	108.8	3e-21
gi 137834745 gb EBW26918.1	hypothetical protein G ( 289)	491	111.3	7.2e-22	gi 137576321 gb EBU84711.1	hypothetical protein G ( 292)	481	109.2	3.1e-21
gi 137322978 gb EBT45218.1	hypothetical protein G ( 293)	491	111.3	7.3e-22	gi 141073413 gb ECP43912.1	hypothetical protein G ( 300)	481	109.2	3.2e-21
gi 134804078 gb EBD54578.1	hypothetical protein G ( 211)	489	110.8	7.3e-22	gi 140438418 gb ECL75365.1	hypothetical protein G ( 182)	478	108.5	3.2e-21
gi 136393960 gb EBN87219.1	hypothetical protein G ( 312)	491	111.3	7.7e-22	gi 140053257 gb ECU25908.1	hypothetical protein G ( 225)	479	108.8	3.3e-21
gi 68346293 gb AAAY3899.1	prephenate dehydrogenas ( 447)	493	111.8	7.9e-22	gi 135799699 gb EBJ92019.1	hypothetical protein G ( 271)	480	109.0	3.3e-21
gi 139998431 gb ECI91715.1	hypothetical protein G ( 271)	490	111.1	7.9e-22	gi 137030492 gb EBR81435.1	hypothetical protein G ( 171)	477	108.3	3.5e-21
gi 141955051 gb ECU42041.1	hypothetical protein G ( 165)	487	110.4	7.9e-22	gi 138586257 gb ECA62165.1	hypothetical protein G ( 288)	480	109.0	3.5e-21
gi 136262507 gb EBM97543.1	hypothetical protein G ( 237)	489	110.9	8.1e-22	gi 141713106 gb ECS88901.1	hypothetical protein G ( 346)	481	109.3	3.6e-21
gi 139052693 gb EC08205.1	hypothetical protein G ( 298)	490	111.1	8.6e-22	gi 143098825 gb EDC80571.1	hypothetical protein G ( 309)	480	109.0	3.7e-21
gi 143287006 gb EDE12905.1	hypothetical protein G ( 145)	485	109.9	9.5e-22	gi 142218889 gb ECW48454.1	hypothetical protein G ( 223)	478	108.6	3.8e-21
gi 138419111 gb EBZ53968.1	hypothetical protein G ( 247)	488	110.7	9.7e-22	gi 138251176 gb EBY57356.1	hypothetical protein G ( 233)	478	108.6	3.9e-21
gi 140838036 gb ECN85960.1	hypothetical protein G ( 292)	489	110.9	9.7e-22	gi 137014132 gb EBR72273.1	hypothetical protein G ( 244)	478	108.6	4.1e-21
gi 141898445 gb ECU02305.1	hypothetical protein G ( 256)	488	110.7	1e-21	gi 140523504 gb ECM09797.1	hypothetical protein G ( 245)	478	108.6	4.1e-21
gi 136637899 gb EBP43656.1	hypothetical protein G ( 273)	488	110.7	1.1e-21	gi 137719292 gb EBV63298.1	hypothetical protein G ( 180)	476	108.1	4.2e-21
gi 134902958 gb EBE19018.1	hypothetical protein G ( 336)	489	110.9	1.1e-21	gi 138030261 gb EBX36003.1	hypothetical protein G ( 263)	478	108.6	4.3e-21
gi 137129035 gb EBS36550.1	hypothetical protein G ( 214)	486	110.2	1.1e-21	gi 171193469 gb ACB44430.1	3-phosphoshikimate 1-c ( 442)	481	109.3	4.4e-21
gi 143069597 gb EDC59159.1	hypothetical protein G ( 303)	488	110.7	1.2e-21	gi 142962907 gb EDB82861.1	hypothetical protein G ( 150)	474	107.7	4.7e-21
gi 135579519 gb EBT55375.1	hypothetical protein G ( 329)	488	110.7	1.2e-21	gi 168992012 gb ACA39552.1	3-phosphoshikimate 1-c ( 187)	475	107.9	5e-21
gi 136994338 gb EBR61028.1	hypothetical protein G ( 280)	487	110.5	1.3e-21	gi 135982409 gb EBL13409.1	hypothetical protein G ( 309)	478	108.6	5e-21
gi 257046992 gb ACV36180.1	3-phosphoshikimate 1-c ( 655)	492	111.7	1.3e-21	gi 141790910 gb ECT30914.1	hypothetical protein G ( 168)	474	107.7	5.2e-21
gi 141927329 gb ECU22470.1	hypothetical protein G ( 289)	487	110.5	1.3e-21	gi 139532469 gb ECF71502.1	hypothetical protein G ( 279)	477	108.4	5.3e-21
gi 139717854 gb ECG99181.1	hypothetical protein G ( 231)	485	110.0	1.4e-21	gi 141940271 gb ECU31475.1	hypothetical protein G ( 213)	475	107.9	5.6e-21
gi 139910655 gb ECI30758.1	hypothetical protein G ( 235)	485	110.0	1.4e-21	gi 137963940 gb EBX00422.1	hypothetical protein G ( 305)	477	108.4	5.7e-21
gi 140066777 gb ECJ32528.1	hypothetical protein G ( 282)	486	110.3	1.5e-21	gi 139409852 gb ECE91909.1	hypothetical protein G ( 260)	476	108.2	5.7e-21
gi 140973901 gb ECO77339.1	hypothetical protein G ( 290)	486	110.3	1.5e-21	gi 142711155 gb EDA02482.1	hypothetical protein G ( 226)	475	107.9	5.9e-21
gi 140297850 gb ECK81100.1	hypothetical protein G ( 260)	485	110.1	1.6e-21	gi 226458362 gb EEH55659.1	predicted protein [Mic ( 459)	479	108.9	6.1e-21
gi 137717949 gb EBV62551.1	hypothetical protein G ( 230)	484	109.8	1.6e-21	gi 138319895 gb EBY95130.1	hypothetical protein G ( 282)	476	108.2	6.1e-21
gi 138602658 gb ECA73649.1	hypothetical protein G ( 273)	485	110.1	1.6e-21	gi 134629694 gb EBC48725.1	hypothetical protein G ( 288)	476	108.2	6.3e-21
gi 139026437 gb ECC89644.1	hypothetical protein G ( 293)	485	110.1	1.7e-21	gi 140656566 gb ECM60669.1	hypothetical protein G ( 250)	475	108.0	6.4e-21
gi 137195758 gb EBS73722.1	hypothetical protein G ( 210)	483	109.6	1.7e-21	gi 142100413 gb ECV59278.1	hypothetical protein G ( 308)	476	108.2	6.6e-21
gi 140786534 gb ECN50058.1	hypothetical protein G ( 295)	485	110.1	1.7e-21	gi 141687467 gb ECS81421.1	hypothetical protein G ( 262)	475	108.0	6.7e-21
gi 135680007 gb EBJ17574.1	hypothetical protein G ( 311)	485	110.1	1.8e-21	gi 17427919 emb CAD14609.1	probable 3-phosphoshik ( 436)	478	108.7	6.7e-21
gi 141989319 gb ECU65887.1	hypothetical protein G ( 264)	484	109.8	1.8e-21	gi 138135881 gb EBX94279.1	hypothetical protein G ( 268)	475	108.0	6.8e-21
gi 137804261 gb EBW09125.1	hypothetical protein G ( 273)	484	109.9	1.9e-21	gi 134908887 gb EBE22927.1	hypothetical protein G ( 308)	475	108.0	7.7e-21
gi 136078872 gb EBL76774.1	hypothetical protein G ( 199)	482	109.4	1.9e-21	gi 137259371 gb EBT09655.1	hypothetical protein G ( 221)	473	107.5	7.7e-21
gi 161165740 emb CAN97045.1	3-phosphoshikimate 1- ( 461)	487	110.6	1.9e-21	gi 141106614 gb ECP67175.1	hypothetical protein G ( 270)	474	107.8	7.9e-21
gi 138607890 gb ECA77386.1	hypothetical protein G ( 181)	481	109.1	2e-21	gi 137243061 gb EBT00335.1	hypothetical protein G ( 245)	473	107.5	8.4e-21
gi 139918049 gb ECI36047.1	hypothetical protein G ( 260)	483	109.6	2.1e-21	gi 141407006 gb ECR61199.1	hypothetical protein G ( 262)	473	107.6	8.9e-21
gi 142266198 gb ECW83397.1	hypothetical protein G ( 325)	484	109.9	2.2e-21	gi 18376380 emb CAD21207.1	probable PENTAFUNCTION (1563)	483	110.0	9.8e-21
gi 140442914 gb ECL78527.1	hypothetical protein G ( 242)	482	109.4	2.3e-21	gi 139371007 gb ECE65615.1	hypothetical protein G ( 304)	473	107.6	1e-20
gi 138159519 gb EBY09502.1	hypothetical protein G ( 205)	481	109.2	2.3e-21	gi 142507077 gb ECY57668.1	hypothetical protein G ( 305)	473	107.6	1e-20
gi 136332752 gb EBN45289.1	hypothetical protein G ( 209)	481	109.2	2.3e-21	gi 157321714 gb ABY40811.1	3-phosphoshikimate 1-c ( 428)	475	108.1	1e-20
gi 139820926 gb ECH69481.1	hypothetical protein G ( 223)	481	109.2	2.4e-21	gi 136431133 gb EB011861.1	hypothetical protein G ( 262)	472	107.4	1e-20

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gi 137000978 gb EBR64813.1	hypothetical protein G ( 230)	471	107.1	1.1e-20	gi 144582815 gb ABP00889.1	predicted protein [Ost ( 436)	467	106.4	3.3e-20
gi 137293075 gb EBT28512.1	hypothetical protein G ( 272)	472	107.4	1.1e-20	gi 141964658 gb ECU48472.1	hypothetical protein G ( 268)	464	105.7	3.3e-20
gi 139621692 gb ECG31968.1	hypothetical protein G ( 272)	472	107.4	1.1e-20	gi 135455852 gb EBH75607.1	hypothetical protein G ( 235)	463	105.5	3.4e-20
gi 139023907 gb ECC87913.1	hypothetical protein G ( 166)	469	106.6	1.1e-20	gi 139579623 gb ECG03907.1	hypothetical protein G ( 281)	464	105.7	3.4e-20
gi 134884660 gb EBE06854.1	hypothetical protein G ( 276)	472	107.4	1.1e-20	gi 141317497 gb ECR00630.1	hypothetical protein G ( 283)	464	105.7	3.5e-20
gi 140795522 gb ECN56376.1	hypothetical protein G ( 280)	472	107.4	1.1e-20	gi 140510912 gb ECM06926.1	hypothetical protein G ( 208)	462	105.2	3.5e-20
gi 141302923 gb ECQ94687.1	hypothetical protein G ( 281)	472	107.4	1.1e-20	gi 141939310 gb ECU30795.1	hypothetical protein G ( 251)	463	105.5	3.6e-20
gi 138657864 gb ECB10524.1	hypothetical protein G ( 283)	472	107.4	1.1e-20	gi 136694505 gb EBP79130.1	hypothetical protein G ( 183)	461	105.0	3.7e-20
gi 136993434 gb EBR60509.1	hypothetical protein G ( 284)	472	107.4	1.1e-20	gi 1146414 gb AAA85091.1	3-phosphoshikimate 1-car ( 432)	466	106.2	3.7e-20
gi 143672084 gb EDG18795.1	hypothetical protein G ( 419)	474	107.9	1.2e-20	gi 141809387 gb ECT39920.1	hypothetical protein G ( 270)	463	105.5	3.8e-20
gi 139122965 gb ECD57240.1	hypothetical protein G ( 306)	472	107.4	1.2e-20	gi 134629207 gb EBC48440.1	hypothetical protein G ( 272)	463	105.5	3.9e-20
gi 134407858 gb EBB17421.1	hypothetical protein G ( 314)	472	107.4	1.2e-20	gi 134464347 gb EBB50178.1	hypothetical protein G ( 197)	461	105.0	3.9e-20
gi 143053685 gb EDC47513.1	hypothetical protein G ( 266)	471	107.1	1.2e-20	gi 88176432 gb EAQ83900.1	hypothetical protein CH (1464)	473	107.9	3.9e-20
gi 136268536 gb EBN01805.1	hypothetical protein G ( 315)	472	107.4	1.2e-20	gi 142577198 gb ECZ07785.1	hypothetical protein G ( 482)	466	106.2	4.1e-20
gi 140469715 gb ECL93060.1	hypothetical protein G ( 231)	470	106.9	1.2e-20	gi 134557217 gb EBC05219.1	hypothetical protein G ( 296)	463	105.5	4.2e-20
gi 138080088 gb EBX63139.1	hypothetical protein G ( 281)	471	107.2	1.3e-20	gi 136996308 gb EBR62166.1	hypothetical protein G ( 181)	460	104.8	4.2e-20
gi 134464839 gb EBB50457.1	hypothetical protein G ( 177)	468	106.4	1.3e-20	gi 140328230 gb ECU01542.1	hypothetical protein G ( 182)	460	104.8	4.2e-20
gi 139905975 gb ECI27361.1	hypothetical protein G ( 248)	470	106.9	1.3e-20	gi 188029313 emb CAO97190.1	3-phosphoshikimate 1- ( 428)	465	106.0	4.3e-20
gi 138620417 gb ECA85940.1	hypothetical protein G ( 312)	471	107.2	1.4e-20	gi 135851336 gb EBK24502.1	hypothetical protein G ( 161)	459	104.6	4.4e-20
gi 139654368 gb ECG54707.1	hypothetical protein G ( 147)	466	106.0	1.5e-20	gi 140032122 gb ECJ13099.1	hypothetical protein G ( 194)	460	104.8	4.5e-20
gi 134728264 gb EBD06387.1	hypothetical protein G ( 253)	469	106.7	1.5e-20	gi 137176800 gb EBS63254.1	hypothetical protein G ( 271)	462	105.3	4.5e-20
gi 137182909 gb EBS66675.1	hypothetical protein G ( 260)	469	106.7	1.6e-20	gi 141186881 gb ECQ23250.1	hypothetical protein G ( 206)	460	104.8	4.7e-20
gi 148551350 gb ABQ86478.1	EPSP synthase (3-phosp ( 438)	472	107.5	1.6e-20	gi 135208489 gb EBG18076.1	hypothetical protein G ( 206)	460	104.8	4.7e-20
gi 137424329 gb EBU02368.1	hypothetical protein G ( 278)	469	106.7	1.7e-20	gi 138340796 gb EBZ07169.1	hypothetical protein G ( 125)	457	104.1	4.7e-20
gi 140787776 gb ECN50901.1	hypothetical protein G ( 287)	469	106.7	1.7e-20	gi 139748675 gb ECH19163.1	hypothetical protein G ( 288)	462	105.3	4.7e-20
gi 206590606 emb CAQ37568.1	3-phosphoshikimate 1- ( 435)	471	107.2	1.8e-20	gi 137091767 gb EBS15725.1	hypothetical protein G ( 214)	460	104.8	4.9e-20
gi 140676899 gb ECM75091.1	hypothetical protein G ( 168)	465	105.8	1.9e-20	gi 135343553 gb EBH00233.1	hypothetical protein G ( 300)	462	105.3	4.9e-20
gi 136917542 gb EBR18692.1	hypothetical protein G ( 289)	468	106.5	2e-20	gi 140995635 gb ECO92669.1	hypothetical protein G ( 157)	458	104.3	5e-20
gi 134775968 gb EBD35272.1	hypothetical protein G ( 297)	468	106.5	2e-20	gi 139568311 gb ECF96248.1	hypothetical protein G ( 264)	461	105.1	5e-20
gi 139227125 gb ECE28521.1	hypothetical protein G ( 268)	467	106.3	2.1e-20	gi 137278631 gb EBT20527.1	hypothetical protein G ( 136)	457	104.1	5.1e-20
gi 138030771 gb EBX36292.1	hypothetical protein G ( 275)	467	106.3	2.2e-20	gi 134745606 gb EBD16293.1	hypothetical protein G ( 197)	459	104.6	5.2e-20
gi 138150939 gb EBY03425.1	hypothetical protein G ( 202)	465	105.8	2.2e-20	gi 141460123 gb ECR97455.1	hypothetical protein G ( 278)	461	105.1	5.3e-20
gi 136724096 gb EBP98532.1	hypothetical protein G ( 180)	464	105.6	2.3e-20	gi 135951103 gb EBK92257.1	hypothetical protein G ( 282)	461	105.1	5.3e-20
gi 138014097 gb EBX27907.1	hypothetical protein G ( 256)	466	106.1	2.4e-20	gi 140503041 gb ECM04119.1	hypothetical protein G ( 288)	461	105.1	5.4e-20
gi 139974702 gb ECI75189.1	hypothetical protein G ( 157)	463	105.4	2.4e-20	gi 141018576 gb ECP05967.1	hypothetical protein G ( 248)	460	104.8	5.5e-20
gi 142058446 gb ECV24053.1	hypothetical protein G ( 439)	469	106.8	2.5e-20	gi 139397227 gb ECE83225.1	hypothetical protein G ( 305)	461	105.1	5.7e-20
gi 139682895 gb ECG74820.1	hypothetical protein G ( 274)	466	106.1	2.5e-20	gi 91712081 gb ABE52008.1	3-phosphoshikimate 1-ca ( 427)	463	105.6	5.7e-20
gi 137260499 gb EBT10295.1	hypothetical protein G ( 274)	466	106.1	2.5e-20	gi 142982566 gb EDB96566.1	hypothetical protein G ( 310)	461	105.1	5.8e-20
gi 136231923 gb EBM76866.1	hypothetical protein G ( 197)	464	105.6	2.5e-20	gi 140111307 gb ECJ61391.1	hypothetical protein G ( 265)	460	104.9	5.8e-20
gi 136408371 gb EBN97136.1	hypothetical protein G ( 286)	466	106.1	2.6e-20	gi 134663080 gb EBC68366.1	hypothetical protein G ( 140)	456	103.9	6e-20
gi 141056695 gb ECP33646.1	hypothetical protein G ( 179)	463	105.4	2.7e-20	gi 138161925 gb EBY11146.1	hypothetical protein G ( 202)	458	104.4	6.2e-20
gi 138140452 gb EBX96828.1	hypothetical protein G ( 302)	466	106.1	2.8e-20	gi 137916341 gb EBW73633.1	hypothetical protein G ( 284)	460	104.9	6.2e-20
gi 140421950 gb ECL64775.1	hypothetical protein G ( 256)	465	105.9	2.8e-20	gi 135811093 gb EBJ99203.1	hypothetical protein G ( 247)	459	104.6	6.3e-20
gi 88600955 gb ABD46423.1	putative 3-phosphoshiki ( 435)	468	106.6	2.8e-20	gi 139806318 gb ECB59786.1	hypothetical protein G ( 292)	460	104.9	6.3e-20
gi 136146607 gb EBM20258.1	hypothetical protein G ( 190)	463	105.4	2.8e-20	gi 143480854 gb EDP21802.1	hypothetical protein G ( 250)	459	104.6	6.4e-20
gi 142249738 gb ECW71259.1	hypothetical protein G ( 439)	468	106.6	2.8e-20	gi 135346262 gb EBH02057.1	hypothetical protein G ( 304)	460	104.9	6.6e-20
gi 136631260 gb EBP39693.1	hypothetical protein G ( 209)	463	105.4	3.1e-20	gi 142930364 gb EDB59786.1	hypothetical protein G ( 262)	459	104.7	6.7e-20
gi 141822654 gb ECT49103.1	hypothetical protein G ( 293)	465	105.9	3.1e-20	gi 139455460 gb ECF22083.1	hypothetical protein G ( 268)	459	104.7	6.8e-20
gi 256729198 gb EEU42552.1	predicted protein [Nec (1569)	475	108.3	3.1e-20	gi 142575612 gb ECZ06674.1	hypothetical protein G ( 196)	457	104.2	6.9e-20
gi 135910595 gb EBK64732.1	hypothetical protein G ( 305)	465	105.9	3.2e-20	gi 141222898 gb ECQ46942.1	hypothetical protein G ( 237)	458	104.4	7.1e-20
gi 206595339 emb CAQ62266.1	3-phosphoshikimate 1- ( 435)	467	106.4	3.3e-20	gi 139075902 gb ECD24383.1	hypothetical protein G ( 281)	459	104.7	7.1e-20

gi 139188816 gb ECE01784.1	hypothetical protein G ( 245)	458	104.4	7.3e-20	gi 134852959 gb EBD85720.1	hypothetical protein G ( 307)	451	103.0	2.4e-19
gi 135804817 gb EBJ95270.1	hypothetical protein G ( 248)	458	104.4	7.3e-20	gi 140227605 gb ECK39253.1	hypothetical protein G ( 307)	451	103.0	2.4e-19
gi 138660385 gb ECB12258.1	hypothetical protein G ( 221)	457	104.2	7.7e-20	gi 134872021 gb EBD98471.1	hypothetical protein G ( 270)	450	102.8	2.5e-19
gi 168827279 gb ACA32650.1	3-phosphoshikimate 1-c ( 432)	461	105.2	7.7e-20	gi 140036373 gb ECJ16119.1	hypothetical protein G ( 279)	450	102.8	2.6e-19
gi 137942191 gb EBW88167.1	hypothetical protein G ( 200)	456	104.0	8.1e-20	gi 138956668 gb ECC58149.1	hypothetical protein G ( 287)	450	102.8	2.6e-19
gi 137958827 gb EBW97523.1	hypothetical protein G ( 284)	458	104.5	8.3e-20	gi 139642797 gb ECG46468.1	hypothetical protein G ( 249)	449	102.6	2.7e-19
gi 141314678 gb ECQ98633.1	hypothetical protein G ( 296)	458	104.5	8.6e-20	gi 134872282 gb EBD98642.1	hypothetical protein G ( 269)	449	102.6	2.9e-19
gi 139068047 gb ECD19190.1	hypothetical protein G ( 260)	457	104.2	8.8e-20	gi 140933952 gb ECO49463.1	hypothetical protein G ( 279)	449	102.6	3e-19
gi 140658132 gb ECM61746.1	hypothetical protein G ( 198)	455	103.8	9.3e-20	gi 137360628 gb EBT66371.1	hypothetical protein G ( 286)	449	102.6	3e-19
gi 137004591 gb EBR66887.1	hypothetical protein G ( 281)	457	104.2	9.5e-20	gi 139739230 gb ECH13944.1	hypothetical protein G ( 261)	448	102.4	3.2e-19
gi 135477800 gb EBH90218.1	hypothetical protein G ( 282)	457	104.2	9.5e-20	gi 114307433 gb ABI58676.1	3-phosphoshikimate 1-c ( 433)	451	103.1	3.3e-19
gi 143251258 gb EDD90204.1	hypothetical protein G ( 295)	457	104.3	9.9e-20	gi 138941425 gb ECC51619.1	hypothetical protein G ( 231)	447	102.1	3.4e-19
gi 139916408 gb ECI34864.1	hypothetical protein G ( 256)	456	104.0	1e-19	gi 136808175 gb EBQ54259.1	hypothetical protein G ( 275)	448	102.4	3.4e-19
gi 140772822 gb ECN40516.1	hypothetical protein G ( 189)	454	103.5	1e-19	gi 139354446 gb ECE60428.1	hypothetical protein G ( 325)	449	102.6	3.4e-19
gi 139076956 gb ECD25149.1	hypothetical protein G ( 278)	456	104.0	1.1e-19	gi 137557298 gb EBU73902.1	hypothetical protein G ( 277)	448	102.4	3.4e-19
gi 137755595 gb EBV82450.1	hypothetical protein G ( 281)	456	104.0	1.1e-19	gi 144114046 gb EDJ96547.1	hypothetical protein G ( 200)	446	101.9	3.4e-19
gi 138685421 gb ECB29910.1	hypothetical protein G ( 240)	455	103.8	1.1e-19	gi 139152261 gb ECD76059.1	hypothetical protein G ( 285)	448	102.4	3.5e-19
gi 136830333 gb EBQ69060.1	hypothetical protein G ( 158)	452	103.1	1.2e-19	gi 139991868 gb ECI87059.1	hypothetical protein G ( 248)	447	102.1	3.6e-19
gi 189915141 gb ACE61393.1	3-phosphoshikimate 1-c ( 432)	458	104.5	1.2e-19	gi 139188209 gb ECE01339.1	hypothetical protein G ( 187)	445	101.7	3.7e-19
gi 165876218 gb ABY69266.1	3-phosphoshikimate 1-c ( 432)	458	104.5	1.2e-19	gi 139750669 gb ECH20532.1	hypothetical protein G ( 262)	447	102.2	3.8e-19
gi 141749797 gb ECT09608.1	hypothetical protein G ( 135)	451	102.9	1.2e-19	gi 140114936 gb ECJ63978.1	hypothetical protein G ( 286)	447	102.2	4.1e-19
gi 136650971 gb EBP51388.1	hypothetical protein G ( 266)	455	103.8	1.2e-19	gi 137264374 gb EBT12455.1	hypothetical protein G ( 245)	446	101.9	4.1e-19
gi 135507167 gb EBI09057.1	hypothetical protein G ( 192)	453	103.3	1.2e-19	gi 138907009 gb ECC37100.1	hypothetical protein G ( 177)	444	101.5	4.1e-19
gi 141123028 gb ECP78588.1	hypothetical protein G ( 273)	455	103.8	1.2e-19	gi 140380447 gb ECL38000.1	hypothetical protein G ( 292)	447	102.2	4.1e-19
gi 137030922 gb EBR81678.1	hypothetical protein G ( 276)	455	103.8	1.2e-19	gi 137450070 gb EBU16913.1	hypothetical protein G ( 251)	446	101.9	4.2e-19
gi 140653578 gb ECM58585.1	hypothetical protein G ( 171)	452	103.1	1.3e-19	gi 135666691 gb EBJ09399.1	hypothetical protein G ( 164)	443	101.2	4.5e-19
gi 89345096 gb ABD69299.1	3-phosphoshikimate 1-ca ( 669)	460	105.0	1.3e-19	gi 138677357 gb ECB24420.1	hypothetical protein G ( 279)	446	102.0	4.6e-19
gi 139760239 gb ECH27080.1	hypothetical protein G ( 253)	454	103.6	1.3e-19	gi 134673469 gb EBC74420.1	hypothetical protein G ( 181)	443	101.3	4.9e-19
gi 137426729 gb EBU03730.1	hypothetical protein G ( 261)	454	103.6	1.4e-19	gi 141113089 gb ECP71687.1	hypothetical protein G ( 155)	442	101.0	4.9e-19
gi 112822801 gb ABI24890.1	3-phosphoshikimate 1-c ( 432)	457	104.3	1.4e-19	gi 1890139 gb AAB86439.1	AroA [Mannheimia haemoly ( 432)	448	102.5	5e-19
gi 197698457 gb EDY45390.1	PlmJK [Streptomyces sp ( 995)	462	105.5	1.4e-19	gi 138636499 gb ECA95841.1	hypothetical protein G ( 271)	445	101.7	5.2e-19
gi 138139693 gb EBX96411.1	hypothetical protein G ( 264)	454	103.6	1.4e-19	gi 139498755 gb ECF48542.1	hypothetical protein G ( 209)	443	101.3	5.5e-19
gi 138691138 gb ECB33980.1	hypothetical protein G ( 137)	450	102.7	1.4e-19	gi 140648727 gb ECM55237.1	hypothetical protein G ( 292)	445	101.8	5.5e-19
gi 145047091 gb ABP33718.1	3-phosphoshikimate 1-c ( 442)	457	104.3	1.4e-19	gi 139454391 gb ECF21324.1	hypothetical protein G ( 258)	444	101.5	5.7e-19
gi 134886066 gb EBE07800.1	hypothetical protein G ( 299)	454	103.6	1.5e-19	gi 135640463 gb EBI93148.1	hypothetical protein G ( 310)	445	101.8	5.8e-19
gi 126096971 gb ABN73799.1	3-phosphoshikimate 1-c ( 432)	456	104.1	1.6e-19	gi 142005931 gb ECU77145.1	hypothetical protein G ( 271)	444	101.5	6e-19
gi 144034657 gb EDI39331.1	hypothetical protein G ( 193)	451	102.9	1.6e-19	gi 48995007 gb AAT48249.1	chloroplast CP4-EPSPS f ( 141)	440	100.6	6e-19
gi 139051627 gb ECD07438.1	hypothetical protein G ( 276)	453	103.4	1.7e-19	gi 138335879 gb EBZ03751.1	hypothetical protein G ( 198)	442	101.1	6.1e-19
gi 139643546 gb ECG46969.1	hypothetical protein G ( 125)	448	102.2	1.7e-19	gi 140303989 gb ECK84652.1	hypothetical protein G ( 282)	444	101.5	6.2e-19
gi 137863910 gb EBW43621.1	hypothetical protein G ( 253)	452	103.2	1.8e-19	gi 224964543 emb CAX50053.1	3-phosphoshikimate 1- ( 428)	446	102.0	6.6e-19
gi 142318022 gb ECX21690.1	hypothetical protein G ( 257)	452	103.2	1.8e-19	gi 143035975 gb EDC34531.1	hypothetical protein G ( 169)	440	100.6	7.1e-19
gi 137821808 gb EBW19362.1	hypothetical protein G ( 191)	450	102.7	1.9e-19	gi 139018177 gb ECC83955.1	hypothetical protein G ( 200)	441	100.9	7.1e-19
gi 137040706 gb EBR87177.1	hypothetical protein G ( 231)	451	103.0	1.9e-19	gi 138430761 gb EBZ62251.1	hypothetical protein G ( 255)	442	101.1	7.5e-19
gi 139125728 gb ECD58839.1	hypothetical protein G ( 167)	449	102.5	1.9e-19	gi 194682094 emb CAR41667.1	3-phosphoshikimate 1- ( 428)	445	101.8	7.7e-19
gi 141894283 gb ECT99317.1	hypothetical protein G ( 202)	450	102.7	1.9e-19	gi 37199250 dbj BAC95082.1	3-phosphoshikimate 1-c ( 428)	445	101.8	7.7e-19
gi 136801771 gb EBQ50060.1	hypothetical protein G ( 294)	452	103.2	2e-19	gi 153093746 gb EDN74689.1	3-phosphoshikimate 1-c ( 432)	445	101.8	7.7e-19
gi 134628386 gb EBC47961.1	hypothetical protein G ( 265)	451	103.0	2.1e-19	gi 138542053 gb ECA31262.1	hypothetical protein G ( 262)	442	101.1	7.7e-19
gi 139408555 gb ECE90996.1	hypothetical protein G ( 275)	451	103.0	2.2e-19	gi 139450344 gb ECP18445.1	hypothetical protein G ( 139)	438	100.2	7.9e-19
gi 269848851 gb ACZ49495.1	3-phosphoshikimate 1-c ( 458)	454	103.7	2.2e-19	gi 141128430 gb ECP82499.1	hypothetical protein G ( 284)	442	101.1	8.3e-19
gi 136936196 gb EBR28143.1	hypothetical protein G ( 178)	448	102.3	2.3e-19	gi 138972884 gb ECC65105.1	hypothetical protein G ( 184)	439	100.4	8.8e-19
gi 137060732 gb EBR98539.1	hypothetical protein G ( 215)	449	102.5	2.4e-19	gi 141367144 gb ECR33007.1	hypothetical protein G ( 258)	441	100.9	8.8e-19

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gi 140334517 gb ECL05827.1	hypothetical protein G ( 158)	438	100.2	8.9e-19	gi 134544087 gb EBB97350.1	hypothetical protein G ( 226)	435	99.6	1.9e-18
gi 138153319 gb EBY05062.1	hypothetical protein G ( 271)	441	100.9	9.2e-19	gi 144146470 gb EDJ20240.1	hypothetical protein G ( 163)	433	99.2	1.9e-18
gi 138520206 gb ECA15974.1	hypothetical protein G ( 277)	441	100.9	9.4e-19	gi 138382720 gb EBZ28752.1	hypothetical protein G ( 193)	434	99.4	1.9e-18
gi 138911546 gb ECC39123.1	hypothetical protein G ( 256)	440	100.7	1e-18	gi 134711099 gb EBC96621.1	hypothetical protein G ( 236)	435	99.6	1.9e-18
gi 28806007 dbj BAC59283.1	3-phosphoshikimate 1-c ( 426)	443	101.4	1e-18	gi 142459623 gb ECY23467.1	hypothetical protein G ( 144)	432	98.9	1.9e-18
gi 3008973 gb AAC10319.1	I72834 Sequence 4 from pa ( 434)	443	101.4	1e-18	gi 139957031 gb ECI62788.1	hypothetical protein G ( 175)	433	99.2	2e-18
gi 3015354 gb AAC12234.1	I79200 Sequence 4 from pa ( 434)	443	101.4	1e-18	gi 91696897 gb ABE43726.1	3-phosphoshikimate 1-ca ( 668)	441	101.1	2e-18
gi 3940967 gb AAC81966.1	I96497 Sequence 4 from pa ( 434)	443	101.4	1e-18	gi 140083489 gb ECJ43144.1	hypothetical protein G ( 254)	435	99.7	2.1e-18
gi 1830395 gb AAB44849.1	Sequence 4 from patent U ( 434)	443	101.4	1e-18	gi 141776609 gb ECT23341.1	hypothetical protein G ( 185)	433	99.2	2.1e-18
gi 451485 gb AA21529.1	5-enolpyruvylshikimate 3- ( 434)	443	101.4	1e-18	gi 141987601 gb ECU64667.1	hypothetical protein G ( 219)	434	99.4	2.1e-18
gi 56616713 gb AAW04888.1	Sequence 2 from patent ( 434)	443	101.4	1e-18	gi 142732836 gb EDA18046.1	hypothetical protein G ( 259)	435	99.7	2.1e-18
gi 5972478 gb AAE12369.1	Sequence 4 from patent U ( 434)	443	101.4	1e-18	gi 148719663 gb ABR00791.1	3-phosphoshikimate 1-c ( 432)	438	100.4	2.1e-18
gi 135561916 gb EBI44110.1	hypothetical protein G ( 270)	440	100.7	1.1e-18	gi 139888767 gb ECI15397.1	hypothetical protein G ( 161)	432	98.9	2.1e-18
gi 143482336 gb EDF22566.1	hypothetical protein G ( 275)	440	100.7	1.1e-18	gi 142596803 gb ECZ21432.1	hypothetical protein G ( 233)	434	99.4	2.2e-18
gi 134932131 gb EBE38383.1	hypothetical protein G ( 144)	436	99.8	1.1e-18	gi 139777013 gb ECH38737.1	hypothetical protein G ( 202)	433	99.2	2.3e-18
gi 137275963 gb EBT19032.1	hypothetical protein G ( 207)	438	100.2	1.1e-18	gi 140304325 gb ECK84887.1	hypothetical protein G ( 202)	433	99.2	2.3e-18
gi 146453322 gb EDK47578.1	pentafunctional AROM p (1551)	450	103.1	1.1e-18	gi 135717215 gb EBJ40588.1	hypothetical protein G ( 251)	434	99.4	2.4e-18
gi 139639483 gb ECG44207.1	hypothetical protein G ( 255)	439	100.5	1.2e-18	gi 135377759 gb EBH23190.1	hypothetical protein G ( 183)	432	99.0	2.4e-18
gi 2485256 gb AAB73392.1	I44481 Sequence 61 from p ( 432)	442	101.2	1.2e-18	gi 163259926 emb CAP42227.1	3-phosphoshikimate 1- ( 447)	437	100.2	2.5e-18
gi 2484179 gb AAB72315.1	I49208 Sequence 61 from p ( 432)	442	101.2	1.2e-18	gi 139865705 gb ECI00817.1	hypothetical protein G ( 165)	431	98.7	2.5e-18
gi 148865 gb AA24943.1	enolpyruvylshikimatephosp ( 432)	442	101.2	1.2e-18	gi 260220855 emb CBA28839.1	3-phosphoshikimate 1- ( 665)	439	100.7	2.7e-18
gi 5957579 gb AAE08253.1	Sequence 61 from patent ( 432)	442	101.2	1.2e-18	gi 141512033 gb ECJ11482.1	hypothetical protein G ( 213)	432	99.0	2.7e-18
gi 144974758 gb ABP122469.1	Sequence 61 from paten ( 432)	442	101.2	1.2e-18	gi 84372628 gb ABC56898.1	AroA [Methanosphaera st ( 426)	436	100.0	2.8e-18
gi 40083323 gb AAR41877.1	Sequence 5147 from pate ( 434)	442	101.2	1.2e-18	gi 145317961 gb ABP60108.1	3-phosphoshikimate 1-c ( 427)	436	100.0	2.8e-18
gi 139606942 gb ECG23026.1	hypothetical protein G ( 269)	439	100.5	1.2e-18	gi 143715077 gb EDG41632.1	hypothetical protein G ( 266)	433	99.2	2.9e-18
gi 138968495 gb ECC63182.1	hypothetical protein G ( 193)	437	100.0	1.2e-18	gi 167323336 gb ABZ59929.1	Sequence 10728 from pa ( 443)	436	100.0	2.9e-18
gi 138376657 gb EBZ24565.1	hypothetical protein G ( 201)	437	100.0	1.3e-18	gi 150837793 gb ABR71769.1	Prephenate dehydrogena ( 748)	439	100.7	2.9e-18
gi 141291390 gb ECQ89981.1	hypothetical protein G ( 149)	435	99.6	1.3e-18	gi 139552854 gb ECF85640.1	hypothetical protein G ( 279)	433	99.3	3e-18
gi 140196807 gb ECK18245.1	hypothetical protein G ( 249)	438	100.3	1.3e-18	gi 136829266 gb EBQ68345.1	hypothetical protein G ( 280)	433	99.3	3e-18
gi 140940783 gb ECO54306.1	hypothetical protein G ( 213)	437	100.0	1.3e-18	gi 139736854 gb ECH12243.1	hypothetical protein G ( 283)	433	99.3	3e-18
gi 262338316 gb ACY52111.1	5-Enolpyruvylshikimate ( 426)	441	101.0	1.4e-18	gi 163774845 gb EDQ88471.1	predicted protein [Mon (1520)	443	101.7	3.1e-18
gi 142004810 gb ECU76380.1	hypothetical protein G ( 306)	439	100.5	1.4e-18	gi 134548028 gb EBB99698.1	hypothetical protein G ( 176)	430	98.5	3.1e-18
gi 138538470 gb ECA28678.1	hypothetical protein G ( 278)	438	100.3	1.4e-18	gi 139807487 gb ECH60283.1	hypothetical protein G ( 153)	429	98.3	3.2e-18
gi 138337633 gb EBZ04990.1	hypothetical protein G ( 241)	437	100.1	1.5e-18	gi 139918409 gb ECI36300.1	hypothetical protein G ( 262)	432	99.0	3.3e-18
gi 136617331 gb EBP31472.1	hypothetical protein G ( 287)	438	100.3	1.5e-18	gi 140679635 gb ECM77044.1	hypothetical protein G ( 136)	428	98.1	3.3e-18
gi 136829494 gb EBQ68499.1	hypothetical protein G ( 245)	437	100.1	1.5e-18	gi 141831946 gb ECT55589.1	hypothetical protein G ( 161)	429	98.3	3.3e-18
gi 143161428 gb EDD26007.1	hypothetical protein G ( 246)	437	100.1	1.5e-18	gi 138293084 gb EBY83709.1	hypothetical protein G ( 230)	431	98.8	3.4e-18
gi 143553814 gb EDF60157.1	hypothetical protein G ( 295)	438	100.3	1.5e-18	gi 138544070 gb ECA32707.1	hypothetical protein G ( 298)	432	99.1	3.6e-18
gi 136327210 gb EBN41578.1	hypothetical protein G ( 182)	435	99.6	1.5e-18	gi 138500221 gb ECA03654.1	hypothetical protein G ( 256)	431	98.8	3.7e-18
gi 148716269 gb ABQ98479.1	3-phosphoshikimate 1-c ( 432)	440	100.8	1.6e-18	gi 156525456 gb ABU70542.1	hypothetical protein V ( 426)	434	99.6	3.7e-18
gi 68058025 gb AAX88278.1	3-phosphoshikimate 1-ca ( 432)	440	100.8	1.6e-18	gi 218322092 emb CAV18185.1	3-phosphoshikimate 1- ( 426)	434	99.6	3.7e-18
gi 137262673 gb EBT11508.1	hypothetical protein G ( 262)	437	100.1	1.6e-18	gi 139955470 gb ECI61700.1	hypothetical protein G ( 160)	428	98.1	3.8e-18
gi 138671510 gb ECB20197.1	hypothetical protein G ( 268)	437	100.1	1.6e-18	gi 142699709 gb ECZ94320.1	hypothetical protein G ( 270)	431	98.8	3.9e-18
gi 137492420 gb EBU39211.1	hypothetical protein G ( 276)	437	100.1	1.7e-18	gi 141373757 gb ECR37676.1	hypothetical protein G ( 152)	427	97.9	4.2e-18
gi 146453336 gb EDK47592.1	pentafunctional AROM p (1551)	447	102.5	1.7e-18	gi 139552257 gb ECF85214.1	hypothetical protein G ( 261)	430	98.6	4.3e-18
gi 135614522 gb EBI77073.1	hypothetical protein G ( 298)	437	100.1	1.8e-18	gi 139974316 gb ECI74913.1	hypothetical protein G ( 240)	429	98.4	4.7e-18
gi 136650301 gb EBP50987.1	hypothetical protein G ( 254)	436	99.9	1.8e-18	gi 139711446 gb ECG94601.1	hypothetical protein G ( 287)	430	98.6	4.7e-18
gi 138659889 gb ECB11911.1	hypothetical protein G ( 255)	436	99.9	1.8e-18	gi 140907504 gb ECO30880.1	hypothetical protein G ( 287)	430	98.6	4.7e-18
gi 138065352 gb EBX54709.1	hypothetical protein G ( 155)	433	99.1	1.8e-18	gi 138558546 gb ECA42855.1	hypothetical protein G ( 253)	429	98.4	4.9e-18
gi 122088811 emb CAL11617.1	3-phosphoshikimate 1- ( 428)	439	100.6	1.8e-18	gi 139688350 gb ECG78743.1	hypothetical protein G ( 217)	428	98.2	4.9e-18
gi 143040406 gb EDC37793.1	hypothetical protein G ( 431)	439	100.6	1.8e-18	gi 238546281 dbj BAH62632.1	3-phosphoshikimate 1- ( 427)	432	99.1	5e-18

gi 138813436 gb ECB97627.1	hypothetical protein G ( 189)	427	97.9	5.1e-18	gi 139074825 gb ECD23598.1	hypothetical protein G ( 255)	424	97.4	1e-17
gi 141561788 gb ECS38612.1	hypothetical protein G ( 264)	429	98.4	5.1e-18	gi 164415617 gb ABY53228.1	3-phosphoshikimate 1-c ( 437)	427	98.1	1e-17
gi 143330502 gb EDE37121.1	hypothetical protein G ( 437)	432	99.1	5.1e-18	gi 142831753 gb EDA91373.1	hypothetical protein G ( 193)	422	96.9	1.1e-17
gi 86569313 gb ABD13122.1	3-phosphoshikimate 1-ca ( 446)	432	99.1	5.2e-18	gi 141595259 gb ECS50998.1	hypothetical protein G ( 198)	422	96.9	1.1e-17
gi 141100594 gb ECP62927.1	hypothetical protein G ( 230)	428	98.2	5.2e-18	gi 135499961 gb EBI04446.1	hypothetical protein G ( 168)	421	96.7	1.1e-17
gi 135954943 gb EBK94850.1	hypothetical protein G ( 237)	428	98.2	5.3e-18	gi 134900083 gb EBE17116.1	hypothetical protein G ( 278)	424	97.4	1.1e-17
gi 143973333 gb EDH96102.1	hypothetical protein G ( 179)	426	97.7	5.6e-18	gi 237624944 gb ACR01634.1	3-phosphoshikimate 1-c ( 653)	429	98.6	1.1e-17
gi 138953444 gb ECC56703.1	hypothetical protein G ( 250)	428	98.2	5.6e-18	gi 143027515 gb EDC28300.1	hypothetical protein G ( 244)	423	97.2	1.1e-17
gi 139361912 gb ECE62605.1	hypothetical protein G ( 257)	428	98.2	5.7e-18	gi 140734280 gb ECN15118.1	hypothetical protein G ( 178)	421	96.7	1.1e-17
gi 119767369 gb ABL99939.1	3-phosphoshikimate 1-c ( 428)	431	98.9	5.8e-18	gi 136101807 gb EBL92381.1	hypothetical protein G ( 216)	422	96.9	1.2e-17
gi 169751429 gb ACA68947.1	3-phosphoshikimate 1-c ( 428)	431	98.9	5.8e-18	gi 138842884 gb ECC12012.1	hypothetical protein G ( 256)	423	97.2	1.2e-17
gi 152961130 gb ABS48591.1	3-phosphoshikimate 1-c ( 428)	431	98.9	5.8e-18	gi 140331781 gb ECL03954.1	hypothetical protein G ( 136)	419	96.2	1.2e-17
gi 186697859 gb ACC88488.1	3-phosphoshikimate 1-c ( 428)	431	98.9	5.8e-18	gi 136184571 gb EBM45065.1	hypothetical protein G ( 198)	421	96.7	1.2e-17
gi 51589037 emb CAH20655.1	3-phosphoshikimate 1-c ( 428)	431	98.9	5.8e-18	gi 136760214 gb EBQ22187.1	hypothetical protein G ( 277)	423	97.2	1.3e-17
gi 141265029 gb ECQ76941.1	hypothetical protein G ( 220)	427	98.0	5.8e-18	gi 137684839 gb EBV44401.1	hypothetical protein G ( 252)	422	97.0	1.3e-17
gi 119536596 gb ABL81213.1	3-phosphoshikimate 1-c ( 430)	431	98.9	5.8e-18	gi 143575841 gb EDF71719.1	hypothetical protein G ( 156)	419	96.2	1.4e-17
gi 120594658 gb AMC38097.1	3-phosphoshikimate 1-c ( 667)	433	99.4	6.3e-18	gi 125622565 gb EAG50884.1	3-phosphoshikimate 1-c ( 426)	425	97.7	1.4e-17
gi 160365739 gb ABX37352.1	3-phosphoshikimate 1-c ( 675)	433	99.4	6.4e-18	gi 2485255 gb AAB73391.1	I44480 Sequence 60 from p ( 427)	425	97.7	1.4e-17
gi 135460444 gb EBH78673.1	hypothetical protein G ( 178)	425	97.5	6.4e-18	gi 144974757 gb ABP12468.1	Sequence 60 from paten ( 427)	425	97.7	1.4e-17
gi 1161308 gb AAB48057.1	5-enolpyruvylshikimate-3 ( 424)	430	98.7	6.6e-18	gi 2484178 gb AAB72314.1	I49207 Sequence 60 from p ( 427)	425	97.7	1.4e-17
gi 108776396 gb ABG18915.1	3-phosphoshikimate 1-c ( 428)	430	98.7	6.6e-18	gi 155523 gb AAA27666.1	5-enolpyruvylshikimate 3- ( 427)	425	97.7	1.4e-17
gi 145211273 gb ABP40680.1	3-phosphoshikimate 1-c ( 428)	430	98.7	6.6e-18	gi 5957578 gb AAE08252.1	Sequence 60 from patent ( 427)	425	97.7	1.4e-17
gi 115347149 emb CAL20042.1	3-phosphoshikimate 1-c ( 428)	430	98.7	6.6e-18	gi 168992013 gb ACA39553.1	3-phosphoshikimate 1-c ( 186)	420	96.5	1.4e-17
gi 45435889 gb AAS61446.1	3-phosphoshikimate 1-ca ( 428)	430	98.7	6.6e-18	gi 135914933 gb EBK67763.1	hypothetical protein G ( 261)	422	97.0	1.4e-17
gi 108778591 gb ABG12649.1	3-phosphoshikimate 1-c ( 428)	430	98.7	6.6e-18	gi 1574434 gb AAC23237.1	3-phosphoshikimate-1-car ( 432)	425	97.7	1.4e-17
gi 2623655043 gb ACY61600.1	3-phosphoshikimate 1-c ( 428)	430	98.7	6.6e-18	gi 142684103 gb EC283120.1	hypothetical protein G ( 223)	421	96.7	1.4e-17
gi 74056467 gb AAZ96907.1	3-phosphoshikimate 1-ca ( 428)	430	98.7	6.6e-18	gi 139177896 gb ECD94031.1	hypothetical protein G ( 269)	422	97.0	1.4e-17
gi 262361421 gb ACY58142.1	3-phosphoshikimate 1-c ( 428)	430	98.7	6.6e-18	gi 138646184 gb ECB02436.1	hypothetical protein G ( 269)	422	97.0	1.4e-17
gi 162351017 gb ABX84965.1	3-phosphoshikimate 1-c ( 428)	430	98.7	6.6e-18	gi 140412812 gb ECL59115.1	hypothetical protein G ( 270)	422	97.0	1.4e-17
gi 270344367 gb AC277132.1	3-phosphoshikimate 1-c ( 429)	430	98.7	6.7e-18	gi 141109424 gb ECP69193.1	hypothetical protein G ( 230)	421	96.7	1.4e-17
gi 21959675 gb AAM86335.1	AE013881_5 5-enolpyruvyl ( 443)	430	98.7	6.8e-18	gi 134346105 gb EBA79260.1	hypothetical protein G ( 272)	422	97.0	1.4e-17
gi 54208741 gb AAV31127.1	5-enolpyruvylshikimate- ( 393)	429	98.5	7.1e-18	gi 139452944 gb ECF20286.1	hypothetical protein G ( 283)	422	97.0	1.5e-17
gi 137209058 gb EBS81261.1	hypothetical protein G ( 251)	426	97.8	7.5e-18	gi 119669775 emb CAL93688.1	3-phosphoshikimate 1- ( 653)	427	98.2	1.5e-17
gi 139435660 gb ECF09838.1	hypothetical protein G ( 252)	426	97.8	7.5e-18	gi 142646574 gb ECZ56461.1	hypothetical protein G ( 172)	419	96.3	1.5e-17
gi 227009768 gb ACP05980.1	3-phosphoshikimate 1-c ( 426)	429	98.5	7.6e-18	gi 140015718 gb ECJ02171.1	hypothetical protein G ( 284)	422	97.0	1.5e-17
gi 254844554 gb EET22968.1	3-phosphoshikimate 1-c ( 426)	429	98.5	7.6e-18	gi 140456534 gb ECL88212.1	hypothetical protein G ( 146)	418	96.0	1.5e-17
gi 229370390 gb ACQ60813.1	5-Enolpyruvylshikimate ( 426)	429	98.5	7.6e-18	gi 197317472 gb ACH66919.1	3-phosphoshikimate 1-c ( 426)	424	97.5	1.6e-17
gi 150420105 gb EDN12408.1	3-phosphoshikimate 1-c ( 426)	429	98.5	7.6e-18	gi 141204390 gb ECQ34073.1	hypothetical protein G ( 186)	419	96.3	1.6e-17
gi 9656253 gb AAF94882.1	3-phosphoshikimate 1-car ( 426)	429	98.5	7.6e-18	gi 40109989 gb AAR52369.1	Sequence 12086 from pat ( 429)	424	97.5	1.6e-17
gi 150954342 gb ABR76372.1	3-phosphoshikimate 1-c ( 427)	429	98.5	7.7e-18	gi 109701064 gb ABG40984.1	3-phosphoshikimate 1-c ( 429)	424	97.5	1.6e-17
gi 141883060 gb ECT91476.1	hypothetical protein G ( 277)	426	97.8	8.1e-18	gi 141581759 gb ECS46281.1	hypothetical protein G ( 263)	421	96.8	1.6e-17
gi 140674293 gb ECM73199.1	hypothetical protein G ( 236)	425	97.6	8.2e-18	gi 134676029 gb EBC75916.1	hypothetical protein G ( 190)	419	96.3	1.6e-17
gi 61396468 gb AAX45933.1	5-enolpyruvylshikimate ( 413)	428	98.3	8.6e-18	gi 135704029 gb EBJ32424.1	hypothetical protein G ( 267)	421	96.8	1.6e-17
gi 61396470 gb AAX45934.1	5-enolpyruvylshikimate ( 413)	428	98.3	8.6e-18	gi 134844834 gb EBB80509.1	hypothetical protein G ( 270)	421	96.8	1.6e-17
gi 150424595 gb EDN16531.1	3-phosphoshikimate 1-c ( 426)	428	98.3	8.8e-18	gi 141338053 gb ECL14097.1	hypothetical protein G ( 139)	417	95.8	1.6e-17
gi 142755731 gb EDA34694.1	hypothetical protein G ( 266)	425	97.6	9.1e-18	gi 134502363 gb EBB72442.1	hypothetical protein G ( 273)	421	96.8	1.6e-17
gi 140315571 gb ECK92797.1	hypothetical protein G ( 268)	425	97.6	9.1e-18	gi 138149138 gb EBY02188.1	hypothetical protein G ( 201)	419	96.3	1.7e-17
gi 139820786 gb ECH69383.1	hypothetical protein G ( 200)	423	97.1	9.4e-18	gi 61396474 gb AAX45936.1	5-enolpyruvylshikimate ( 413)	423	97.3	1.8e-17
gi 141162624 gb ECQ06320.1	hypothetical protein G ( 170)	422	96.9	9.5e-18	gi 76875277 emb CAI86498.1	3-phosphoshikimate 1-c ( 425)	423	97.3	1.8e-17
gi 140837662 gb ECN85695.1	hypothetical protein G ( 246)	424	97.4	9.8e-18	gi 229465653 gb ACQ67427.1	3-enolpyruvylshikimate ( 428)	423	97.3	1.8e-17
gi 139887326 gb ECI14382.1	hypothetical protein G ( 154)	421	96.6	1e-17	gi 253781755 emb CAQ84918.1	3-phosphoshikimate 1- ( 431)	423	97.3	1.8e-17

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gi 223692065 gb ACN15348.1	AroA [Desulfobacterium	( 439)	423	97.3	1.9e-17	gi 140677578 gb ECM75581.1	hypothetical protein G	( 179)	412	94.8	4.2e-17
gi 134889936 gb EBE10360.1	hypothetical protein G	( 137)	416	95.6	1.9e-17	gi 61396462 gb AAX45930.1	5-enolpyruvylshikimate	( 413)	417	96.0	4.2e-17
gi 137874616 gb EBW49779.1	hypothetical protein G	( 196)	418	96.1	1.9e-17	gi 247538562 gb ACT07183.1	3-phosphoshikimate 1-c	( 429)	417	96.0	4.3e-17
gi 61396478 gb AAX45938.1	5-enolpyruvylshikimate	( 413)	422	97.1	2e-17	gi 141587996 gb ECS48226.1	hypothetical protein G	( 278)	414	95.3	4.6e-17
gi 139491037 gb ECF43255.1	hypothetical protein G	( 252)	419	96.3	2.1e-17	gi 138872276 gb ECC23886.1	hypothetical protein G	( 242)	413	95.1	4.7e-17
gi 134542621 gb EBB96479.1	hypothetical protein G	( 258)	419	96.3	2.1e-17	gi 139504738 gb ECF52676.1	hypothetical protein G	( 244)	413	95.1	4.7e-17
gi 137699902 gb EBV52881.1	hypothetical protein G	( 188)	417	95.9	2.1e-17	gi 61396486 gb AAX45942.1	5-enolpyruvylshikimate	( 413)	416	95.8	4.8e-17
gi 111152891 emb CAJ64639.1	3-phosphoshikimate 1-	( 439)	422	97.1	2.2e-17	gi 140540312 gb ECM15770.1	hypothetical protein G	( 183)	411	94.6	4.9e-17
gi 138274656 gb EBY73771.1	hypothetical protein G	( 267)	419	96.3	2.2e-17	gi 206569939 gb ACI11715.1	3-phosphoshikimate 1-c	( 427)	416	95.8	5e-17
gi 135809669 gb EBJ98309.1	hypothetical protein G	( 270)	419	96.3	2.2e-17	gi 36784993 emb CAE13913.1	3-phosphoshikimate 1-c	( 428)	416	95.8	5e-17
gi 143212084 gb EDD62644.1	hypothetical protein G	( 194)	417	95.9	2.2e-17	gi 139938907 gb ECI50641.1	hypothetical protein G	( 268)	413	95.1	5.1e-17
gi 139386082 gb ECE76188.1	hypothetical protein G	( 139)	415	95.4	2.2e-17	gi 144195827 gb EDJ56799.1	hypothetical protein G	( 405)	415	95.6	5.5e-17
gi 139584109 gb ECG07146.1	hypothetical protein G	( 277)	419	96.3	2.2e-17	gi 140385024 gb ECL41258.1	hypothetical protein G	( 178)	410	94.4	5.6e-17
gi 140698605 gb ECM90303.1	hypothetical protein G	( 240)	418	96.1	2.3e-17	gi 138403520 gb EBZ43001.1	hypothetical protein G	( 183)	410	94.4	5.7e-17
gi 140799955 gb ECN59593.1	hypothetical protein G	( 147)	415	95.4	2.3e-17	gi 226906411 gb EEH92329.1	5-enolpyruvylshikimate	( 427)	415	95.6	5.8e-17
gi 134420848 gb EBB24938.1	hypothetical protein G	( 210)	417	95.9	2.3e-17	gi 251754698 gb ACT12774.1	3-phosphoshikimate 1-c	( 429)	415	95.6	5.8e-17
gi 227013635 gb ACP09845.1	3-phosphoshikimate 1-c	( 426)	421	96.8	2.4e-17	gi 122937807 gb ABM68632.1	plastid EPSP synthase	( 514)	416	95.8	5.8e-17
gi 146315739 gb ABQ20278.1	3-phosphoshikimate 1-c	( 426)	421	96.8	2.4e-17	gi 135003079 gb EBE86104.1	hypothetical protein G	( 194)	410	94.4	6e-17
gi 137214858 gb EBS84591.1	hypothetical protein G	( 162)	415	95.4	2.5e-17	gi 136022122 gb EBL38615.1	hypothetical protein G	( 240)	411	94.7	6.2e-17
gi 141041963 gb ECP23312.1	hypothetical protein G	( 163)	415	95.4	2.5e-17	gi 141161546 gb ECC05541.1	hypothetical protein G	( 242)	411	94.7	6.3e-17
gi 36786091 emb CAE15143.1	unnamed protein produc	( 451)	421	96.9	2.5e-17	gi 140419894 gb ECL63396.1	hypothetical protein G	( 243)	411	94.7	6.3e-17
gi 71846535 gb AAZ46031.1	cytidylate kinase / 3-p	( 643)	423	97.3	2.6e-17	gi 61396464 gb AAX45931.1	5-enolpyruvylshikimate	( 413)	414	95.4	6.5e-17
gi 143269600 gb EDE03471.1	hypothetical protein G	( 283)	418	96.1	2.6e-17	gi 140374552 gb ECL33774.1	hypothetical protein G	( 153)	408	93.9	6.5e-17
gi 142982479 gb EDB96508.1	hypothetical protein G	( 215)	416	95.7	2.8e-17	gi 143280338 gb EDE09543.1	hypothetical protein G	( 155)	408	93.9	6.6e-17
gi 139522890 gb ECF65242.1	hypothetical protein G	( 218)	416	95.7	2.8e-17	gi 111969689 gb ABH78640.1	Sequence 8483 from pat	( 431)	414	95.4	6.7e-17
gi 5957577 gb AAE08251.1	Sequence 59 from patent	( 427)	420	96.6	2.8e-17	gi 142870290 gb EDB16562.1	hypothetical protein G	( 266)	411	94.7	6.8e-17
gi 562760 emb CAA57812.1	3-phosphoshikimate 1-car	( 427)	420	96.6	2.8e-17	gi 141087172 gb ECP53417.1	hypothetical protein G	( 162)	408	94.0	6.8e-17
gi 2485254 gb AAB73390.1	I44479 Sequence 59 from p	( 427)	420	96.6	2.8e-17	gi 139894040 gb ECI19042.1	hypothetical protein G	( 199)	409	94.2	7.1e-17
gi 144974756 gb ABP12467.1	Sequence 59 from paten	( 427)	420	96.6	2.8e-17	gi 140238212 gb ECK46609.1	hypothetical protein G	( 211)	409	94.2	7.4e-17
gi 2484177 gb AAB72313.1	I49206 Sequence 59 from p	( 427)	420	96.6	2.8e-17	gi 136855918 gb EBQ86151.1	hypothetical protein G	( 254)	410	94.5	7.6e-17
gi 157083610 gb ABV13288.1	hypothetical protein C	( 427)	420	96.6	2.8e-17	gi 139621088 gb ECG31545.1	hypothetical protein G	( 182)	408	94.0	7.6e-17
gi 49612043 emb CAG75492.1	3-phosphoshikimate 1-c	( 429)	420	96.6	2.8e-17	gi 136961527 gb EBR42455.1	hypothetical protein G	( 184)	408	94.0	7.6e-17
gi 135408047 gb EBH43560.1	hypothetical protein G	( 263)	417	95.9	2.8e-17	gi 139153582 gb ECD76894.1	hypothetical protein G	( 219)	409	94.2	7.7e-17
gi 140173280 gb ECK01590.1	hypothetical protein G	( 267)	417	95.9	2.9e-17	gi 167322676 gb ABZ59269.1	Sequence 10068 from pa	( 428)	413	95.2	7.7e-17
gi 61396476 gb AAX45937.1	5-enolpyruvylshikimate	( 413)	419	96.4	3.1e-17	gi 135668636 gb EBJ10592.1	hypothetical protein G	( 281)	410	94.5	8.2e-17
gi 61396466 gb AAX45932.1	5-enolpyruvylshikimate	( 413)	419	96.4	3.1e-17	gi 139007276 gb ECC76408.1	hypothetical protein G	( 243)	409	94.2	8.4e-17
gi 61396472 gb AAX45935.1	5-enolpyruvylshikimate	( 413)	419	96.4	3.1e-17	gi 239801199 gb ACS18266.1	3-phosphoshikimate 1-c	( 670)	415	95.7	8.5e-17
gi 61396460 gb AAX45929.1	5-enolpyruvylshikimate	( 413)	419	96.4	3.1e-17	gi 456205 emb CAA54317.1	5-enolpyruvylshikimate-3	( 409)	412	95.0	8.5e-17
gi 61396458 gb AAX45928.1	5-enolpyruvylshikimate	( 413)	419	96.4	3.1e-17	gi 135856027 gb EBK27473.1	hypothetical protein G	( 215)	408	94.0	8.7e-17
gi 135610065 gb EBI74288.1	hypothetical protein G	( 181)	414	95.2	3.2e-17	gi 134747467 gb EBD17355.1	hypothetical protein G	( 183)	407	93.8	8.8e-17
gi 59480469 gb AAW86256.1	5-enolpyruvylshikimate-	( 426)	419	96.4	3.2e-17	gi 226714722 gb ACO73860.1	AroA [Laribacter hongk	( 428)	412	95.0	8.9e-17
gi 229378861 gb EE028952.1	prephenate dehydrogena	( 439)	419	96.4	3.3e-17	gi 139023026 gb ECC87309.1	hypothetical protein G	( 161)	406	93.5	9.1e-17
gi 140301825 gb ECK83158.1	hypothetical protein G	( 273)	416	95.7	3.4e-17	gi 137282407 gb EBT22623.1	hypothetical protein G	( 118)	404	93.1	9.2e-17
gi 140667355 gb ECM68197.1	hypothetical protein G	( 175)	413	95.0	3.6e-17	gi 139604357 gb EBE21255.1	hypothetical protein G	( 240)	408	94.0	9.6e-17
gi 18957974 gb AAL79610.1	3-phosphoshikimate 1-ca	( 428)	418	96.2	3.7e-17	gi 136604454 gb EBP23203.1	hypothetical protein G	( 401)	411	94.8	9.7e-17
gi 135678884 gb EBJ16882.1	hypothetical protein G	( 222)	414	95.3	3.8e-17	gi 167294414 gb ABZ47278.1	Sequence 21216 from pa	( 421)	411	94.8	1e-16
gi 158270965 gb EDO96795.1	5-enolpyruvylshikimate	( 512)	419	96.5	3.8e-17	gi 138274368 gb EBY73567.1	hypothetical protein G	( 256)	408	94.0	1e-16
gi 35186983 gb AAQ84158.1	PlmJK [Streptomyces sp.	(1003)	423	97.4	3.8e-17	gi 141051049 gb ECP29554.1	hypothetical protein G	( 223)	407	93.8	1e-16
gi 138432976 gb EBZ63840.1	hypothetical protein G	( 232)	414	95.3	3.9e-17	gi 138296295 gb EBY85353.1	hypothetical protein G	( 139)	404	93.1	1.1e-16
gi 140740736 gb ECN19673.1	hypothetical protein G	( 175)	412	94.8	4.1e-17	gi 134914016 gb EBE26328.1	hypothetical protein G	( 175)	405	93.3	1.1e-16
gi 136039035 gb EBL49925.1	hypothetical protein G	( 179)	412	94.8	4.2e-17	gi 141069352 gb ECP41137.1	hypothetical protein G	( 183)	405	93.4	1.2e-16

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gi 88187784 gb ABD40781.1	3-phosphoshikimate 1-ca	( 430)	410	94.6	1.2e-16	gi 124260205 gb ABM95199.1	3-phosphoshikimate 1-c	( 674)	406	93.8	3.1e-16
gi 138340681 gb EBZ07096.1	hypothetical protein G	( 136)	403	92.9	1.2e-16	gi 135610492 gb EBI74558.1	hypothetical protein G	( 211)	399	92.1	3.1e-16
gi 137329660 gb EBT48876.1	hypothetical protein G	( 161)	404	93.1	1.2e-16	gi 61396490 gb AAAX45944.1	5-enolpyruvylshikimate	( 413)	403	93.1	3.2e-16
gi 135465600 gb EBH82121.1	hypothetical protein G	( 266)	407	93.8	1.2e-16	gi 61396488 gb AAAX45943.1	5-enolpyruvylshikimate	( 413)	403	93.1	3.2e-16
gi 229378960 gb EEO29051.1	prephenate dehydrogena	( 440)	410	94.6	1.2e-16	gi 137219979 gb EBS87529.1	hypothetical protein G	( 255)	400	92.4	3.2e-16
gi 141402472 gb ECR57949.1	hypothetical protein G	( 228)	406	93.6	1.2e-16	gi 71914680 gb AAZ54582.1	3-phosphoshikimate 1-ca	( 424)	403	93.1	3.2e-16
gi 139132738 gb ECD62600.1	hypothetical protein G	( 164)	404	93.1	1.2e-16	gi 136582315 gb EBP09076.1	hypothetical protein G	( 218)	399	92.1	3.2e-16
gi 140169499 gb ECJ98961.1	hypothetical protein G	( 237)	406	93.6	1.3e-16	gi 261372470 gb ACX75215.1	3-phosphoshikimate 1-c	( 442)	403	93.1	3.3e-16
gi 140049962 gb ECJ24138.1	hypothetical protein G	( 240)	406	93.6	1.3e-16	gi 142661590 gb ECZ67038.1	hypothetical protein G	( 163)	397	91.7	3.4e-16
gi 143037211 gb EDC35437.1	hypothetical protein G	( 174)	404	93.1	1.3e-16	gi 137401562 gb EBT89526.1	hypothetical protein G	( 229)	399	92.2	3.4e-16
gi 49651207 emb CAG78144.1	YALIOF12639p [Yarrowia	(1556)	417	96.3	1.3e-16	gi 141869737 gb ECT82397.1	hypothetical protein G	( 238)	399	92.2	3.5e-16
gi 61396480 gb AAAX45939.1	5-enolpyruvylshikimate	( 413)	409	94.3	1.3e-16	gi 140165244 gb ECJ96063.1	hypothetical protein G	( 241)	399	92.2	3.5e-16
gi 135945291 gb EBK88343.1	hypothetical protein G	( 254)	406	93.6	1.3e-16	gi 143418238 gb EDE85044.1	hypothetical protein G	( 243)	399	92.2	3.5e-16
gi 137398175 gb EBT87602.1	hypothetical protein G	( 257)	406	93.6	1.4e-16	gi 143173373 gb EDD34522.1	hypothetical protein G	( 182)	397	91.7	3.7e-16
gi 140869146 gb ECO05747.1	hypothetical protein G	( 169)	403	92.9	1.5e-16	gi 134895707 gb EBE14212.1	hypothetical protein G	( 184)	397	91.7	3.7e-16
gi 135370189 gb EBH18092.1	hypothetical protein G	( 254)	405	93.4	1.6e-16	gi 167353991 gb ABZ76604.1	3-phosphoshikimate 1-c	( 426)	402	92.9	3.7e-16
gi 140317761 gb ECK94388.1	hypothetical protein G	( 257)	405	93.4	1.6e-16	gi 58417478 emb CAI26682.1	3-phosphoshikimate 1-c	( 427)	402	92.9	3.7e-16
gi 15420539 gb AAK97382.1	AF360730_1 5-enolpyruvyl	( 427)	408	94.1	1.6e-16	gi 57160999 emb CAH57905.1	3-phosphoshikimate 1-c	( 427)	402	92.9	3.7e-16
gi 88599102 gb ABD44571.1	putative 3-phosphoshiki	( 428)	408	94.1	1.6e-16	gi 135563740 gb EBI45267.1	hypothetical protein G	( 260)	399	92.2	3.8e-16
gi 56311966 emb CAI06611.1	3-phosphoshikimate 1-c	( 646)	410	94.6	1.7e-16	gi 139566690 gb ECP95076.1	hypothetical protein G	( 262)	399	92.2	3.8e-16
gi 61396482 gb AAAX45940.1	5-enolpyruvylshikimate	( 413)	407	93.9	1.8e-16	gi 142002556 gb ECU74821.1	hypothetical protein G	( 265)	399	92.2	3.8e-16
gi 140953256 gb ECO62988.1	hypothetical protein G	( 256)	404	93.2	1.8e-16	gi 140710317 gb ECM98211.1	hypothetical protein G	( 227)	398	91.9	3.9e-16
gi 261605294 gb ACX87780.1	3-phosphoshikimate 1-c	( 429)	407	93.9	1.8e-16	gi 257477369 gb EDF75688.1	3-phosphoshikimate 1-c	( 450)	402	92.9	3.9e-16
gi 137400223 gb EBT88769.1	hypothetical protein G	( 262)	404	93.2	1.8e-16	gi 135898935 gb EBK56671.1	hypothetical protein G	( 277)	399	92.2	4e-16
gi 61396484 gb AAAX45941.1	5-enolpyruvylshikimate	( 413)	406	93.7	2e-16	gi 141085446 gb ECP52224.1	hypothetical protein G	( 204)	397	91.7	4.1e-16
gi 61396496 gb AAAX45947.1	5-enolpyruvylshikimate	( 413)	406	93.7	2e-16	gi 141091027 gb ECP56087.1	hypothetical protein G	( 206)	397	91.7	4.1e-16
gi 142770656 gb EDA45614.1	hypothetical protein G	( 186)	401	92.5	2.1e-16	gi 33148677 gb AAP96196.1	3-phosphoshikimate 1-ca	( 435)	401	92.7	4.4e-16
gi 139589854 gb ECG11246.1	hypothetical protein G	( 160)	400	92.3	2.1e-16	gi 138749005 gb ECB73949.1	hypothetical protein G	( 225)	397	91.7	4.4e-16
gi 134455928 gb EBB45238.1	hypothetical protein G	( 267)	403	93.0	2.2e-16	gi 135398882 gb EBH37393.1	hypothetical protein G	( 267)	398	92.0	4.4e-16
gi 139078368 gb ECD26173.1	hypothetical protein G	( 227)	402	92.8	2.2e-16	gi 138076915 gb EBX61317.1	hypothetical protein G	( 162)	395	91.3	4.4e-16
gi 137841823 gb EBW30955.1	hypothetical protein G	( 230)	402	92.8	2.2e-16	gi 34104358 gb AAQ60717.1	3-phosphoshikimate 1-ca	( 456)	401	92.7	4.6e-16
gi 138139300 gb EBX96194.1	hypothetical protein G	( 275)	403	93.0	2.2e-16	gi 135141355 gb EBF75716.1	hypothetical protein G	( 169)	395	91.3	4.6e-16
gi 140449002 gb ECL82972.1	hypothetical protein G	( 288)	403	93.0	2.3e-16	gi 140570131 gb ECM24965.1	hypothetical protein G	( 204)	396	91.5	4.7e-16
gi 144124603 gb EDJ04217.1	hypothetical protein G	( 180)	400	92.3	2.4e-16	gi 134767539 gb EBD29427.1	hypothetical protein G	( 257)	397	91.8	5e-16
gi 138542215 gb ECA31380.1	hypothetical protein G	( 252)	402	92.8	2.4e-16	gi 143544422 gb EDF55404.1	hypothetical protein G	( 189)	395	91.3	5.1e-16
gi 157317811 gb ABV36909.1	3-phosphoshikimate 1-c	( 426)	405	93.5	2.4e-16	gi 140438577 gb ECL75479.1	hypothetical protein G	( 268)	397	91.8	5.1e-16
gi 217498375 gb ACK46568.1	3-phosphoshikimate 1-c	( 426)	405	93.5	2.4e-16	gi 139560754 gb ECF91299.1	hypothetical protein G	( 227)	396	91.5	5.2e-16
gi 84779489 dbj BAE74266.1	3-phosphoshikimate 1-c	( 435)	405	93.5	2.5e-16	gi 139398702 gb ECE84262.1	hypothetical protein G	( 229)	396	91.5	5.2e-16
gi 140575918 gb ECM27279.1	hypothetical protein G	( 268)	402	92.8	2.5e-16	gi 141988235 gb ECU65125.1	hypothetical protein G	( 150)	393	90.8	5.5e-16
gi 139772528 gb ECH35546.1	hypothetical protein G	( 269)	402	92.8	2.5e-16	gi 197053763 gb ACH25461.1	Sequence 13 from paten	( 419)	399	92.3	5.7e-16
gi 138964745 gb ECC61414.1	hypothetical protein G	( 164)	399	92.1	2.5e-16	gi 2621856 gb AAB85269.1	5-enolpyruvylshikimate 3	( 419)	399	92.3	5.7e-16
gi 135066978 gb EBF28079.1	hypothetical protein G	( 119)	397	91.6	2.6e-16	gi 167274362 gb ABZ27226.1	Sequence 1164 from pat	( 419)	399	92.3	5.7e-16
gi 137241746 gb EBS99587.1	hypothetical protein G	( 241)	401	92.6	2.6e-16	gi 134823747 gb EBD66995.1	hypothetical protein G	( 255)	396	91.6	5.7e-16
gi 140283088 gb ECK73670.1	hypothetical protein G	( 241)	401	92.6	2.6e-16	gi 145564830 gb ABP75765.1	3-phosphoshikimate 1-c	( 426)	399	92.3	5.8e-16
gi 61396494 gb AAAX45946.1	5-enolpyruvylshikimate	( 413)	404	93.3	2.7e-16	gi 134462524 gb EBB49131.1	hypothetical protein G	( 220)	395	91.3	5.8e-16
gi 138522325 gb ECA17436.1	hypothetical protein G	( 215)	400	92.3	2.8e-16	gi 218355966 emb CAQ88582.1	5-enolpyruvylshikimat	( 434)	399	92.3	5.9e-16
gi 46914055 emb CAG20835.1	putative 3-phosphoshik	( 428)	404	93.3	2.8e-16	gi 142902212 gb EDB39353.1	hypothetical protein G	( 228)	395	91.3	6e-16
gi 142199015 gb ECW33272.1	hypothetical protein G	( 439)	404	93.3	2.9e-16	gi 120590404 gb ABM33844.1	3-phosphoshikimate 1-c	( 679)	401	92.8	6.5e-16
gi 141442027 gb ECR85618.1	hypothetical protein G	( 163)	398	91.9	2.9e-16	gi 125997494 gb ABN61569.1	3-phosphoshikimate 1-c	( 426)	398	92.1	6.7e-16
gi 138219010 gb EBY49364.1	hypothetical protein G	( 193)	399	92.1	2.9e-16	gi 151424006 dbj BAF71509.1	3-phosphoshikimate 1-	( 427)	398	92.1	6.7e-16
gi 139917801 gb ECI35869.1	hypothetical protein G	( 239)	400	92.4	3e-16	gi 33113261 gb AAP94212.1	3-phosphoshikimate 1-ca	( 427)	398	92.1	6.7e-16

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gi 156532856 gb ABU77682.1	hypothetical protein E ( 428)	398	92.1	6.7e-16	gi 140767972 gb ECN37198.1	hypothetical protein G ( 204)	389	90.1	1.3e-15
gi 142194251 gb ECW29626.1	hypothetical protein G ( 439)	398	92.1	6.8e-16	gi 139024443 gb ECC88277.1	hypothetical protein G ( 242)	390	90.3	1.3e-15
gi 142196972 gb ECW31688.1	hypothetical protein G ( 439)	398	92.1	6.8e-16	gi 140374206 gb ECL33521.1	hypothetical protein G ( 253)	390	90.3	1.3e-15
gi 170945047 emb CAP71158.1	unnamed protein produ (1567)	405	93.8	7.5e-16	gi 135683728 gb EBJ19875.1	hypothetical protein G ( 215)	389	90.1	1.3e-15
gi 61396492 gb AA45945.1	5-enolpyruvylshikimate ( 413)	397	91.9	7.5e-16	gi 81241720 gb ABB62430.1	5-enolpyruvylshikimate- ( 424)	393	91.0	1.4e-15
gi 141237520 gb ECQ57535.1	hypothetical protein G ( 217)	393	90.9	7.6e-16	gi 208009607 emb CAQ79903.1	3-phosphoshikimate 1- ( 427)	393	91.0	1.4e-15
gi 157846892 gb ABV87391.1	3-phosphoshikimate 1-c ( 426)	397	91.9	7.7e-16	gi 91709413 gb ABE49341.1	3-phosphoshikimate 1-ca ( 429)	393	91.0	1.4e-15
gi 120558876 gb ABM24803.1	3-phosphoshikimate 1-c ( 426)	397	91.9	7.7e-16	gi 91709269 gb ABE49197.1	3-phosphoshikimate 1-ca ( 429)	393	91.0	1.4e-15
gi 141399647 gb ECR55895.1	hypothetical protein G ( 160)	391	90.4	7.8e-16	gi 137852928 gb EBW37332.1	hypothetical protein G ( 221)	389	90.1	1.4e-15
gi 115422436 emb CAJ48961.1	3-phosphoshikimate 1- ( 439)	397	91.9	7.9e-16	gi 85816343 gb ABC84481.1	putative 5-enolpyruvyls ( 160)	387	89.6	1.4e-15
gi 142200197 gb ECW34167.1	hypothetical protein G ( 439)	397	91.9	7.9e-16	gi 138831281 gb ECC06379.1	hypothetical protein G ( 136)	386	89.3	1.4e-15
gi 142068853 gb ECV33175.1	hypothetical protein G ( 449)	397	91.9	8e-16	gi 135593367 gb EBI63979.1	hypothetical protein G ( 269)	390	90.3	1.4e-15
gi 138521898 gb ECA17149.1	hypothetical protein G ( 236)	393	90.9	8.2e-16	gi 135512902 gb EBI12761.1	hypothetical protein G ( 271)	390	90.3	1.4e-15
gi 142099007 gb ECV58104.1	hypothetical protein G ( 173)	391	90.4	8.4e-16	gi 142263836 gb ECW81652.1	hypothetical protein G ( 140)	386	89.4	1.4e-15
gi 136122103 gb EBM06235.1	hypothetical protein G ( 253)	393	90.9	8.7e-16	gi 140889253 gb ECO19651.1	hypothetical protein G ( 273)	390	90.3	1.4e-15
gi 139732399 gb ECH09160.1	hypothetical protein G ( 255)	393	90.9	8.8e-16	gi 138641134 gb ECA98992.1	hypothetical protein G ( 197)	388	89.8	1.4e-15
gi 167294358 gb ABZ47222.1	Sequence 21160 from pa ( 425)	396	91.7	8.9e-16	gi 137525040 gb EBU56039.1	hypothetical protein G ( 286)	390	90.3	1.5e-15
gi 136993418 gb EBR60500.1	hypothetical protein G ( 222)	392	90.7	9e-16	gi 139365969 gb ECE63735.1	hypothetical protein G ( 206)	388	89.8	1.5e-15
gi 33504186 emb CAD83448.1	3-phosphoshikimate 1-c ( 433)	396	91.7	9e-16	gi 137098844 gb EB819574.1	hypothetical protein G ( 208)	388	89.8	1.5e-15
gi 142171806 gb ECW12483.1	hypothetical protein G ( 435)	396	91.7	9e-16	gi 139515492 gb ECF60106.1	hypothetical protein G ( 149)	386	89.4	1.5e-15
gi 2484182 gb AAB72318.1	I49211 Sequence 64 from p ( 442)	396	91.7	9.2e-16	gi 257758305 dbj BAI29802.1	5-enolpyruvylshikimat ( 427)	392	90.8	1.6e-15
gi 2485259 gb AAB73395.1	I44484 Sequence 64 from p ( 442)	396	91.7	9.2e-16	gi 218360262 emb CAQ97812.1	5-enolpyruvylshikimat ( 427)	392	90.8	1.6e-15
gi 5957582 gb AAE08256.1	Sequence 64 from patent ( 442)	396	91.7	9.2e-16	gi 1787137 gb AAC73994.1	5-enolpyruvylshikimate-3 ( 427)	392	90.8	1.6e-15
gi 144037 gb AAA22968.1	5-enolpyruvylshikimate-3- ( 442)	396	91.7	9.2e-16	gi 197053764 gb ACH25462.1	Sequence 14 from paten ( 427)	392	90.8	1.6e-15
gi 144974761 gb ABP12472.1	Sequence 64 from paten ( 442)	396	91.7	9.2e-16	gi 209774902 gb ACT85763.1	5-enolpyruvylshikimate ( 427)	392	90.8	1.6e-15
gi 857227501 gb ABC77693.1	3-phosphoshikimate-1-ca ( 446)	396	91.7	9.2e-16	gi 209911417 dbj BAG76491.1	3-phosphoshikimate 1- ( 427)	392	90.8	1.6e-15
gi 167281308 gb ABZ34172.1	Sequence 8110 from pat ( 416)	395	91.4	1e-15	gi 209161693 gb ACI39126.1	3-phosphoshikimate 1-c ( 427)	392	90.8	1.6e-15
gi 141190121 gb ECQ25416.1	hypothetical protein G ( 253)	392	90.7	1e-15	gi 209774900 gb ACT85762.1	5-enolpyruvylshikimate ( 427)	392	90.8	1.6e-15
gi 141918038 gb ECU15844.1	hypothetical protein G ( 257)	392	90.7	1e-15	gi 238859881 gb ACR61879.1	5-enolpyruvylshikimate ( 427)	392	90.8	1.6e-15
gi 194342310 gb EDX23276.1	3-phosphoshikimate 1-c ( 428)	395	91.4	1e-15	gi 73854941 gb AAZ87648.1	5-enolpyruvylshikimate- ( 427)	392	90.8	1.6e-15
gi 242131724 gb ACS86026.1	3-phosphoshikimate 1-c ( 429)	395	91.4	1e-15	gi 157077738 gb ABV17446.1	3-phosphoshikimate 1-c ( 427)	392	90.8	1.6e-15
gi 139696464 gb ECG84097.1	hypothetical protein G ( 188)	390	90.2	1e-15	gi 12514074 gb AAG55393.1	AE005280_4 5-enolpyruvyl ( 427)	392	90.8	1.6e-15
gi 150840321 gb ABR74292.1	3-phosphoshikimate 1-c ( 433)	395	91.4	1e-15	gi 1651430 dbj BAA35643.1	5-enolpyruvylshikimate- ( 427)	392	90.8	1.6e-15
gi 138904179 gb ECC35826.1	hypothetical protein G ( 242)	391	90.5	1.1e-15	gi 81246057 gb ABB66765.1	5-enolpyruvylshikimate- ( 427)	392	90.8	1.6e-15
gi 139089556 gb ECD33905.1	hypothetical protein G ( 244)	391	90.5	1.1e-15	gi 254591507 gb ACT70868.1	3-phosphoshikimate 1-c ( 427)	392	90.8	1.6e-15
gi 138376143 gb EBZ24210.1	hypothetical protein G ( 214)	390	90.3	1.2e-15	gi 13360450 dbj BAB34414.1	5-enolpyruvylshikimate ( 427)	392	90.8	1.6e-15
gi 212556775 gb ACJ29229.1	3-phosphoshikimate 1-c ( 426)	394	91.2	1.2e-15	gi 260449946 gb ACX40368.1	3-phosphoshikimate 1-c ( 427)	392	90.8	1.6e-15
gi 135134197 gb EBF71145.1	hypothetical protein G ( 430)	394	91.2	1.2e-15	gi 218431432 emb CAR12310.1	5-enolpyruvylshikimat ( 427)	392	90.8	1.6e-15
gi 262091733 gb ACY25322.1	3-phosphoshikimate 1-c ( 370)	393	91.0	1.2e-15	gi 15113316 gb AAE68900.1	Sequence 7 from patent ( 427)	392	90.8	1.6e-15
gi 140011396 gb ECI99246.1	hypothetical protein G ( 226)	390	90.3	1.2e-15	gi 209774898 gb ACI85761.1	5-enolpyruvylshikimate ( 427)	392	90.8	1.6e-15
gi 157935342 gb EDO91012.1	3-phosphoshikimate 1-c ( 451)	394	91.2	1.2e-15	gi 26107333 gb AAN79516.1	AE016758_120 3-phosphosh ( 427)	392	90.8	1.6e-15
gi 169653245 gb EDS85938.1	3-phosphoshikimate 1-c ( 451)	394	91.2	1.2e-15	gi 218351113 emb CAU96817.1	5-enolpyruvylshikimat ( 427)	392	90.8	1.6e-15
gi 76581267 gb ABA50742.1	3-phosphoshikimate 1-ca ( 451)	394	91.2	1.2e-15	gi 209774906 gb ACI85765.1	5-enolpyruvylshikimate ( 427)	392	90.8	1.6e-15
gi 157805653 gb EDO82823.1	3-phosphoshikimate 1-c ( 451)	394	91.2	1.2e-15	gi 187430562 gb ACD09836.1	3-phosphoshikimate 1-c ( 427)	392	90.8	1.6e-15
gi 126219794 gb ABN83300.1	3-phosphoshikimate 1-c ( 451)	394	91.2	1.2e-15	gi 169888401 gb ACB02108.1	5-enolpyruvylshikimate ( 427)	392	90.8	1.6e-15
gi 237506815 gb ACQ99133.1	3-phosphoshikimate 1-c ( 451)	394	91.2	1.2e-15	gi 257752848 dbj BAI24350.1	5-enolpyruvylshikimat ( 427)	392	90.8	1.6e-15
gi 242139654 gb EES26056.1	3-phosphoshikimate 1-c ( 451)	394	91.2	1.2e-15	gi 257763436 dbj BAI34931.1	5-enolpyruvylshikimat ( 427)	392	90.8	1.6e-15
gi 254219427 gb EET08811.1	3-phosphoshikimate 1-c ( 451)	394	91.2	1.2e-15	gi 167273981 gb ABZ26845.1	Sequence 783 from pate ( 427)	392	90.8	1.6e-15
gi 184212268 gb EDU09311.1	3-phosphoshikimate 1-c ( 451)	394	91.2	1.2e-15	gi 115250880 emb CAJ68705.1	3-phosphoshikimate 1- ( 437)	392	90.8	1.6e-15
gi 126227113 gb ABN90653.1	3-phosphoshikimate 1-c ( 451)	394	91.2	1.2e-15	gi 82411256 gb ABB75365.1	3-phosphoshikimate 1-ca ( 437)	392	90.8	1.6e-15
gi 138333550 gb EBZ02342.1	hypothetical protein G ( 238)	390	90.3	1.3e-15	gi 143954156 gb EDH82710.1	hypothetical protein G ( 136)	385	89.1	1.6e-15



gi 88598075 gb ABD43545.1  putative 3-phosphoshiki ( 440)	392	90.8	1.6e-15	gi 140676897 gb ECM75089.1  hypothetical protein G ( 127)	381	88.3	2.7e-15
gi 139449952 gb ECF18163.1  hypothetical protein G ( 239)	388	89.9	1.7e-15	gi 135772951 gb EBJ75107.1  hypothetical protein G ( 255)	385	89.3	2.8e-15
gi 140917730 gb ECO37955.1  hypothetical protein G ( 256)	388	89.9	1.8e-15	gi 138122745 gb EBX87000.1  hypothetical protein G ( 262)	385	89.3	2.8e-15
gi 135036529 gb EBF08664.1  hypothetical protein G ( 423)	391	90.6	1.8e-15	gi 142161969 gb ECW04955.1  hypothetical protein G ( 372)	387	89.8	2.9e-15
gi 151365419 gb ABS08419.1  3-phosphoshikimate 1-c ( 426)	391	90.6	1.8e-15	gi 33571749 emb CAE41250.1  3-phosphoshikimate 1-c ( 442)	388	90.0	2.9e-15
gi 209774904 gb ACI85764.1  5-enolpyruvylshikimate ( 427)	391	90.6	1.8e-15	gi 33576881 emb CAE33961.1  3-phosphoshikimate 1-c ( 442)	388	90.0	2.9e-15
gi 3859585 gb AAC72854.1  3-enolpyruvylshikimate-5 ( 427)	391	90.6	1.8e-15	gi 52208740 emb CAH34676.1  putative 3-phosphoshik ( 451)	388	90.0	3e-15
gi 91715109 gb ABE55035.1  3-phosphoshikimate 1-ca ( 428)	391	90.6	1.8e-15	gi 140345209 gb ECL13444.1  hypothetical protein G ( 196)	383	88.8	3e-15
gi 139203617 gb ECE11938.1  hypothetical protein G ( 260)	388	89.9	1.8e-15	gi 143576125 gb EDF71819.1  hypothetical protein G ( 172)	382	88.6	3e-15
gi 149905851 gb ABR36684.1  3-phosphoshikimate 1-c ( 435)	391	90.6	1.9e-15	gi 137822467 gb EBW19744.1  hypothetical protein G ( 110)	379	87.9	3.2e-15
gi 136974924 gb EBR50068.1  hypothetical protein G ( 190)	386	89.4	1.9e-15	gi 137006884 gb EBR68201.1  hypothetical protein G ( 215)	383	88.8	3.2e-15
gi 139984221 gb ECI81817.1  hypothetical protein G ( 100)	382	88.5	1.9e-15	gi 134610603 gb EBC37222.1  hypothetical protein G ( 258)	384	89.1	3.2e-15
gi 134450405 gb EBB41981.1  hypothetical protein G ( 174)	385	89.2	2e-15	gi 281178039 dbj BAI54369.1  3-phosphoshikimate 1- ( 427)	387	89.8	3.3e-15
gi 135784761 gb EBJ82581.1  hypothetical protein G ( 250)	387	89.7	2e-15	gi 253977137 gb ACT42807.1  3-phosphoshikimate 1-c ( 427)	387	89.8	3.3e-15
gi 141500557 gb ECS07759.1  hypothetical protein G ( 212)	386	89.4	2.1e-15	gi 157066110 gb ABV05365.1  3-phosphoshikimate 1-c ( 427)	387	89.8	3.3e-15
gi 142771453 gb EDA46198.1  hypothetical protein G ( 253)	387	89.7	2.1e-15	gi 253325107 gb ACT29709.1  3-phosphoshikimate 1-c ( 427)	387	89.8	3.3e-15
gi 137204744 gb EBJ78807.1  hypothetical protein G ( 155)	384	89.0	2.1e-15	gi 242376723 emb CAQ31436.1  aroA [Escherichia col ( 427)	387	89.8	3.3e-15
gi 30040688 gb AAP16419.1  5-enolpyruvylshikimate- ( 427)	390	90.4	2.1e-15	gi 218370560 emb CAR18367.1  5-enolpyruvylshikimat ( 427)	387	89.8	3.3e-15
gi 110614463 gb ABF03130.1  5-enolpyruvylshikimate ( 427)	390	90.4	2.1e-15	gi 253972923 gb ACT38594.1  3-phosphoshikimate 1-c ( 427)	387	89.8	3.3e-15
gi 24051176 gb AAN42533.1  5-enolpyruvylshikimate- ( 427)	390	90.4	2.1e-15	gi 170521635 gb ACB18913.1  3-phosphoshikimate 1-c ( 427)	387	89.8	3.3e-15
gi 260216483 emb CBA29637.1  3-phosphoshikimate 1- ( 428)	390	90.4	2.1e-15	gi 169755618 gb ACA78317.1  3-phosphoshikimate 1-c ( 427)	387	89.8	3.3e-15
gi 138644794 gb ECB01472.1  hypothetical protein G ( 262)	387	89.7	2.1e-15	gi 142851614 gb ABO89935.1  3-phosphoshikimate 1-c ( 427)	387	89.8	3.3e-15
gi 52307682 gb AAU38182.1  AroA protein [Mannheimi ( 433)	390	90.4	2.1e-15	gi 2947033 gb AAC05428.1  3-enolpyruvylshikimate-5 ( 428)	387	89.8	3.3e-15
gi 6013215 gb AAF01290.1 AF182427_3 5-enolpyruvyls ( 442)	390	90.4	2.2e-15	gi 21623205 gb AAM67855.1  3-phosphoshikimate 1-ca ( 428)	387	89.8	3.3e-15
gi 139068739 gb ECD19686.1  hypothetical protein G ( 163)	384	89.0	2.2e-15	gi 134963519 gb EBE59309.1  hypothetical protein G ( 263)	384	89.1	3.3e-15
gi 138900787 gb ECC34332.1  hypothetical protein G ( 232)	386	89.5	2.2e-15	gi 135563570 gb EBT45165.1  hypothetical protein G ( 189)	382	88.6	3.3e-15
gi 140993087 gb ECO90844.1  hypothetical protein G ( 152)	383	88.7	2.4e-15	gi 142367329 gb ECX56585.1  hypothetical protein G ( 438)	387	89.8	3.3e-15
gi 110342697 gb ABG68934.1  3-phosphoshikimate 1-c ( 427)	389	90.2	2.4e-15	gi 140310203 gb ECK88940.1  hypothetical protein G ( 137)	380	88.1	3.3e-15
gi 215264105 emb CAS08449.1  5-enolpyruvylshikimat ( 427)	389	90.2	2.4e-15	gi 33574090 emb CAE38415.1  3-phosphoshikimate 1-c ( 442)	387	89.8	3.3e-15
gi 226898314 gb EEH84573.1  AroA [Escherichia sp. ( 427)	389	90.2	2.4e-15	gi 141395406 gb ECR52919.1  hypothetical protein G ( 125)	379	87.9	3.6e-15
gi 218426312 emb CAR07137.1  5-enolpyruvylshikimat ( 427)	389	90.2	2.4e-15	gi 139774292 gb ECH36762.1  hypothetical protein G ( 177)	381	88.4	3.6e-15
gi 91071583 gb ABE06464.1  3-phosphoshikimate 1-ca ( 427)	389	90.2	2.4e-15	gi 2484150 gb AAB72286.1 I49179 Sequence 8 from pa ( 423)	386	89.6	3.7e-15
gi 218364582 emb CAR02268.1  5-enolpyruvylshikimat ( 427)	389	90.2	2.4e-15	gi 2485227 gb AAB73363.1 I44452 Sequence 8 from pa ( 423)	386	89.6	3.7e-15
gi 115512250 gb ABJ00325.1  AroA [Escherichia coli ( 427)	389	90.2	2.4e-15	gi 144974729 gb ABP12440.1  Sequence 8 from patent ( 423)	386	89.6	3.7e-15
gi 138258528 gb EBY62639.1  hypothetical protein G ( 260)	386	89.5	2.4e-15	gi 5957550 gb AAE08224.1  Sequence 8 from patent U ( 423)	386	89.6	3.7e-15
gi 144114020 gb EDI96529.1  hypothetical protein G ( 438)	389	90.2	2.5e-15	gi 40966 emb CAA25223.1  unnamed protein product [ ( 427)	386	89.6	3.8e-15
gi 151280371 gb ABR88781.1  3-phosphoshikimate 1-c ( 441)	389	90.2	2.5e-15	gi 4731170 gb AAD28375.1 AF110153_2 5-enolpyruvoyl ( 428)	386	89.6	3.8e-15
gi 148029460 gb EDK87365.1  3-phosphoshikimate 1-c ( 451)	389	90.2	2.6e-15	gi 238869916 gb ACR69627.1  3-phosphoshikimate 1-c ( 428)	386	89.6	3.8e-15
gi 147750604 gb EDK57673.1  3-phosphoshikimate 1-c ( 451)	389	90.2	2.6e-15	gi 71554514 gb AAZ33725.1  prephenate dehydrogenas ( 366)	385	89.3	3.8e-15
gi 126241624 gb ABO04717.1  3-phosphoshikimate 1-c ( 451)	389	90.2	2.6e-15	gi 141329021 gb ECR07965.1  hypothetical protein G ( 264)	383	88.9	3.8e-15
gi 124291356 gb ABN00625.1  3-phosphoshikimate 1-c ( 451)	389	90.2	2.6e-15	gi 141168332 gb ECQ10383.1  hypothetical protein G ( 147)	379	87.9	4.1e-15
gi 121229589 gb ABM52107.1  3-phosphoshikimate 1-c ( 451)	389	90.2	2.6e-15	gi 134685548 gb EBC81580.1  hypothetical protein G ( 151)	379	87.9	4.2e-15
gi 160697726 gb EDP87696.1  3-phosphoshikimate 1-c ( 451)	389	90.2	2.6e-15	gi 140659527 gb ECM62702.1  hypothetical protein G ( 253)	382	88.6	4.3e-15
gi 147745264 gb EDK52344.1  3-phosphoshikimate 1-c ( 451)	389	90.2	2.6e-15	gi 169212099 gb ACA49855.1  enoylpyrovyl-shikimate ( 427)	385	89.4	4.3e-15
gi 52428112 gb AAU48705.1  3-phosphoshikimate-1-ca ( 451)	389	90.2	2.6e-15	gi 226935015 gb AC092617.1  AroA [Edwardsiella tar ( 428)	385	89.4	4.3e-15
gi 28852194 gb AAO55268.1  prephenate dehydrogenas ( 535)	390	90.5	2.6e-15	gi 143270564 gb EDE04150.1  hypothetical protein G ( 428)	385	89.4	4.3e-15
gi 139229948 gb ECE30111.1  hypothetical protein G ( 234)	385	89.2	2.6e-15	gi 142089203 gb ECV49931.1  hypothetical protein G ( 198)	380	88.2	4.6e-15
gi 140079528 gb ECJ40341.1  hypothetical protein G ( 242)	385	89.3	2.7e-15	gi 139503952 gb ECF52132.1  hypothetical protein G ( 240)	381	88.4	4.7e-15
gi 141003112 gb ECO97873.1  hypothetical protein G ( 242)	385	89.3	2.7e-15	gi 135563091 gb EBI44861.1  hypothetical protein G ( 243)	381	88.4	4.7e-15
gi 136855917 gb EBQ86150.1  hypothetical protein G ( 243)	385	89.3	2.7e-15	gi 137396460 gb EBT86593.1  hypothetical protein G ( 247)	381	88.4	4.8e-15
gi 137366429 gb EBT69661.1  hypothetical protein G ( 245)	385	89.3	2.7e-15	gi 221730036 gb ACM32856.1  3-phosphoshikimate 1-c ( 673)	387	89.9	4.8e-15

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gi 137245288 gb EBT01614.1	hypothetical protein G ( 215)	380	88.2	4.9e-15	gi 141443182 gb ECR86432.1	hypothetical protein G ( 146)	372	86.5	1.1e-14
gi 125715790 gb ABN54282.1	3-phosphoshikimate 1-c ( 423)	384	89.2	5e-15	gi 135597997 gb EBI66840.1	hypothetical protein G ( 244)	375	87.2	1.1e-14
gi 24348389 gb AAN55438.1	AE015681_2 3-phosphoshik ( 426)	384	89.2	5e-15	gi 142746219 gb EDA27786.1	hypothetical protein G ( 211)	374	86.9	1.2e-14
gi 138615794 gb ECA82879.1	hypothetical protein G ( 225)	380	88.2	5.1e-15	gi 141055602 gb ECP32851.1	hypothetical protein G ( 179)	373	86.7	1.2e-14
gi 134893001 gb EBE12405.1	hypothetical protein G ( 137)	377	87.5	5.1e-15	gi 261246194 emb CBG23998.1	3-phosphoshikimate 1- ( 427)	378	87.9	1.2e-14
gi 137545103 gb EBU66926.1	hypothetical protein G ( 116)	376	87.2	5.1e-15	gi 267992715 gb ACY87600.1	3-phosphoshikimate 1-c ( 427)	378	87.9	1.2e-14
gi 138880582 gb ECC27596.1	hypothetical protein G ( 270)	381	88.4	5.2e-15	gi 16419490 gb AAL19912.1	3-enolpyruvylshikimate- ( 427)	378	87.9	1.2e-14
gi 63257580 gb AAAY38676.1	Prephenate dehydrogenas ( 534)	385	89.4	5.3e-15	gi 138264743 gb EBY66745.1	hypothetical protein G ( 161)	372	86.5	1.2e-14
gi 138512522 gb ECA10830.1	hypothetical protein G ( 235)	380	88.2	5.3e-15	gi 139521800 gb ECF64621.1	hypothetical protein G ( 271)	375	87.2	1.2e-14
gi 167273444 gb ABZ26308.1	Sequence 246 from pate ( 341)	382	88.7	5.5e-15	gi 137798212 gb EBW05651.1	hypothetical protein G ( 232)	374	87.0	1.2e-14
gi 17978913 gb AAL47682.1	5-enolpyruvylshikimate ( 426)	383	89.0	5.8e-15	gi 256363216 gb ACU76713.1	3-phosphoshikimate 1-c ( 454)	378	87.9	1.3e-14
gi 160865242 gb ABX21865.1	hypothetical protein S ( 427)	383	89.0	5.8e-15	gi 140433318 gb ECL71874.1	hypothetical protein G ( 233)	374	87.0	1.3e-14
gi 253985497 gb ACT50354.1	3-phosphoshikimate 1-c ( 432)	383	89.0	5.8e-15	gi 140890066 gb ECO20239.1	hypothetical protein G ( 143)	371	86.2	1.3e-14
gi 260213106 emb CBE04506.1	3-phosphoshikimate 1- ( 437)	383	89.0	5.9e-15	gi 141889995 gb ECT96217.1	hypothetical protein G ( 237)	374	87.0	1.3e-14
gi 260209657 emb CBA63357.1	3-phosphoshikimate 1- ( 437)	383	89.0	5.9e-15	gi 136315848 gb EBN33986.1	hypothetical protein G ( 172)	372	86.5	1.3e-14
gi 247534368 gb ACS97614.1	3-phosphoshikimate 1-c ( 441)	383	89.0	5.9e-15	gi 137234142 gb EBS95536.1	hypothetical protein G ( 242)	374	87.0	1.3e-14
gi 136238252 gb EBM81150.1	hypothetical protein G ( 195)	378	87.8	6e-15	gi 140182536 gb ECK08290.1	hypothetical protein G ( 206)	373	86.7	1.3e-14
gi 138795121 gb ECB89349.1	hypothetical protein G ( 235)	379	88.0	6.1e-15	gi 143676232 gb EDG21149.1	hypothetical protein G ( 152)	371	86.3	1.3e-14
gi 140301223 gb ECK82759.1	hypothetical protein G ( 210)	378	87.8	6.4e-15	gi 142342306 gb ECX39599.1	hypothetical protein G ( 214)	373	86.7	1.3e-14
gi 155109881 gb ABT06556.1	Sequence 10 from paten ( 426)	382	88.7	6.7e-15	gi 137786059 gb EBV98729.1	hypothetical protein G ( 156)	371	86.3	1.4e-14
gi 111913995 gb ABH66278.1	Sequence 10 from paten ( 426)	382	88.7	6.7e-15	gi 62127135 gb AAX64838.1	3-enolpyruvylshikimate- ( 427)	377	87.7	1.4e-14
gi 3452007 gb AAC32745.1	EPSP synthase AroA [Shig ( 427)	382	88.7	6.7e-15	gi 161364150 gb ABX67918.1	hypothetical protein S ( 427)	377	87.7	1.4e-14
gi 190687453 gb ACE85131.1	3-phosphoshikimate 1-c ( 428)	382	88.7	6.7e-15	gi 194404814 gb ACT65036.1	3-phosphoshikimate 1-c ( 427)	377	87.7	1.4e-14
gi 140343211 gb ECL12005.1	hypothetical protein G ( 262)	379	88.0	6.7e-15	gi 224467314 gb ACN45144.1	3-phosphoshikimate 1-c ( 427)	377	87.7	1.4e-14
gi 139532179 gb ECF71291.1	hypothetical protein G ( 222)	378	87.8	6.8e-15	gi 142942923 gb EDB68713.1	hypothetical protein G ( 264)	374	87.0	1.4e-14
gi 137447190 gb EBU15268.1	hypothetical protein G ( 268)	379	88.0	6.9e-15	gi 142317060 gb ECX20980.1	hypothetical protein G ( 119)	369	85.8	1.4e-14
gi 140209686 gb ECK27413.1	hypothetical protein G ( 176)	376	87.3	7.4e-15	gi 140013850 gb ECJ00937.1	hypothetical protein G ( 203)	372	86.5	1.5e-14
gi 262109647 gb EEY67699.1	pentafunctional AROM p (1548)	389	90.5	7.4e-15	gi 126638175 gb ABO23818.1	3-phosphoshikimate 1-c ( 426)	376	87.5	1.6e-14
gi 160861032 gb ABX49566.1	3-phosphoshikimate 1-c ( 426)	381	88.5	7.7e-15	gi 139996187 gb ECT90104.1	hypothetical protein G ( 158)	370	86.1	1.6e-14
gi 267985183 gb ACY85012.1	3-phosphoshikimate 1-c ( 428)	381	88.5	7.7e-15	gi 261413785 gb ACX83156.1	3-phosphoshikimate 1-c ( 443)	376	87.5	1.6e-14
gi 134570021 gb EBC13008.1	hypothetical protein G ( 262)	378	87.8	7.8e-15	gi 183580816 dbj BAG29287.1	3-phosphoshikimate 1- ( 445)	376	87.5	1.6e-14
gi 139589855 gb ECG11247.1	hypothetical protein G ( 162)	375	87.1	7.9e-15	gi 194343512 gb EDX24478.1	3-phosphoshikimate 1-c ( 450)	376	87.5	1.7e-14
gi 229374383 gb EE024774.1	3-phosphoshikimate 1-c ( 443)	381	88.5	8e-15	gi 134745039 gb EBD15968.1	hypothetical protein G ( 248)	372	86.6	1.8e-14
gi 139590611 gb ECG11788.1	hypothetical protein G ( 126)	373	86.6	8.5e-15	gi 135581832 gb EBI56856.1	hypothetical protein G ( 211)	371	86.3	1.8e-14
gi 135392272 gb EBH32957.1	hypothetical protein G ( 215)	376	87.4	8.8e-15	gi 137056263 gb EBR96016.1	hypothetical protein G ( 254)	372	86.6	1.8e-14
gi 141407657 gb ECR61667.1	hypothetical protein G ( 257)	377	87.6	8.9e-15	gi 142778570 gb EDA51511.1	hypothetical protein G ( 154)	369	85.8	1.8e-14
gi 138839333 gb ECC10257.1	hypothetical protein G ( 156)	374	86.9	8.9e-15	gi 197213620 gb ACH51017.1	3-phosphoshikimate 1-c ( 427)	375	87.3	1.8e-14
gi 593745 gb AAA55352.1	Sequence 4 from Patent EP ( 427)	380	88.3	8.9e-15	gi 143182082 gb EDD40705.1	hypothetical protein G ( 188)	370	86.1	1.9e-14
gi 125595950 gb EA235730.1	hypothetical protein O ( 506)	381	88.6	8.9e-15	gi 143912469 gb EDH52565.1	hypothetical protein G ( 434)	375	87.3	1.9e-14
gi 141828747 gb ECT53330.1	hypothetical protein G ( 161)	374	86.9	9.1e-15	gi 137553390 gb EBU71649.1	hypothetical protein G ( 224)	371	86.3	1.9e-14
gi 140376762 gb ECL35372.1	hypothetical protein G ( 191)	375	87.1	9.1e-15	gi 140215326 gb ECK31463.1	hypothetical protein G ( 168)	369	85.9	1.9e-14
gi 134567711 gb EBC11607.1	hypothetical protein G ( 226)	376	87.4	9.2e-15	gi 139503982 gb ECF52152.1	hypothetical protein G ( 240)	371	86.3	2e-14
gi 135681953 gb EBJ18772.1	hypothetical protein G ( 170)	374	86.9	9.5e-15	gi 140386793 gb ECL42479.1	hypothetical protein G ( 147)	368	85.6	2e-14
gi 136386119 gb EBN81787.1	hypothetical protein G ( 171)	374	86.9	9.6e-15	gi 136199323 gb EBM54861.1	hypothetical protein G ( 175)	369	85.9	2e-14
gi 136202243 gb EBM56814.1	hypothetical protein G ( 203)	375	87.1	9.6e-15	gi 141237519 gb ECQ57534.1	hypothetical protein G ( 211)	370	86.1	2e-14
gi 140259294 gb ECK61125.1	hypothetical protein G ( 244)	376	87.4	9.8e-15	gi 261354892 gb EEY17320.1	pentafunctional AROM p (1574)	382	89.0	2.1e-14
gi 194407735 gb ACF67954.1	3-phosphoshikimate 1-c ( 427)	379	88.1	1e-14	gi 150837332 gb ABR71308.1	3-phosphoshikimate 1-c ( 425)	374	87.1	2.1e-14
gi 194712899 gb ACF92120.1	3-phosphoshikimate 1-c ( 427)	379	88.1	1e-14	gi 269413 gb AAA01407.1	Sequence 3 from Patent US ( 427)	374	87.1	2.1e-14
gi 142607846 gb ECZ29157.1	hypothetical protein G ( 192)	374	86.9	1.1e-14	gi 138754029 gb ECB75799.1	hypothetical protein G ( 263)	371	86.4	2.1e-14
gi 140146263 gb ECJ83303.1	hypothetical protein G ( 167)	373	86.7	1.1e-14	gi 141350069 gb ECR21238.1	hypothetical protein G ( 160)	368	85.6	2.2e-14
gi 137244587 gb EBT01212.1	hypothetical protein G ( 238)	375	87.2	1.1e-14	gi 142827467 gb EDA88112.1	hypothetical protein G ( 265)	371	86.4	2.2e-14

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gi 140428372 gb ECL68838.1	hypothetical protein G ( 236)	370	86.1	2.3e-14	gi 219624517 gb ACL30672.1	3-phosphoshikimate 1-c ( 427)	369	86.0	4.3e-14
gi 137239733 gb EBS98468.1	hypothetical protein G ( 174)	368	85.7	2.3e-14	gi 142950535 gb EDB74156.1	hypothetical protein G ( 159)	363	84.6	4.4e-14
gi 141550593 gb ECS30851.1	hypothetical protein G ( 209)	369	85.9	2.3e-14	gi 134379630 gb EBB01558.1	hypothetical protein G ( 434)	369	86.0	4.4e-14
gi 135964545 gb EBL01341.1	hypothetical protein G ( 178)	368	85.7	2.4e-14	gi 145689057 gb ABP89563.1	5-enolpyruvylshikimate ( 164)	363	84.6	4.5e-14
gi 142038696 gb ECV07294.1	hypothetical protein G ( 426)	373	86.9	2.4e-14	gi 142660287 gb ECZ66125.1	hypothetical protein G ( 171)	363	84.6	4.7e-14
gi 113884944 gb ABI38996.1	3-phosphoshikimate 1-c ( 426)	373	86.9	2.4e-14	gi 140955222 gb ECO64409.1	hypothetical protein G ( 240)	365	85.1	4.7e-14
gi 113888993 gb ABI43044.1	3-phosphoshikimate 1-c ( 426)	373	86.9	2.4e-14	gi 135256647 gb EBG46395.1	hypothetical protein G ( 263)	365	85.1	5.1e-14
gi 117612752 gb ABK48206.1	3-phosphoshikimate 1-c ( 426)	373	86.9	2.4e-14	gi 197702692 gb EDY48504.1	3-phosphoshikimate 1-c ( 440)	368	85.8	5.2e-14
gi 143454987 gb EDF05938.1	hypothetical protein G ( 186)	368	85.7	2.4e-14	gi 140310865 gb ECK89393.1	hypothetical protein G ( 226)	364	84.9	5.2e-14
gi 137987089 gb EBX13684.1	hypothetical protein G ( 221)	369	85.9	2.5e-14	gi 193222394 emb CAL62698.2	3-phosphoshikimate 1- ( 442)	368	85.8	5.2e-14
gi 137016135 gb EBR73396.1	hypothetical protein G ( 230)	369	85.9	2.5e-14	gi 136044801 gb EBL53783.1	hypothetical protein G ( 269)	365	85.1	5.2e-14
gi 138907006 gb ECC37097.1	hypothetical protein G ( 149)	366	85.2	2.7e-14	gi 138037253 gb EBX39901.1	hypothetical protein G ( 232)	364	84.9	5.3e-14
gi 120606889 gb AMM42629.1	3-phosphoshikimate 1-c ( 673)	375	87.4	2.7e-14	gi 137883640 gb EBW54936.1	hypothetical protein G ( 243)	364	84.9	5.5e-14
gi 220975650 gb EED93978.1	predicted protein [Tha ( 486)	373	86.9	2.7e-14	gi 253983562 gb ACT48420.1	3-phosphoshikimate 1-c ( 426)	367	85.6	5.8e-14
gi 135052511 gb EBF18868.1	hypothetical protein G ( 422)	372	86.7	2.8e-14	gi 142544985 gb ECY85240.1	hypothetical protein G ( 137)	360	83.9	6e-14
gi 140303484 gb ECK84310.1	hypothetical protein G ( 256)	369	85.9	2.8e-14	gi 256686562 gb ACV09455.1	3-phosphoshikimate 1-c ( 446)	367	85.6	6e-14
gi 17147195 gb AAZ27668.1	3-phosphoshikimate 1-ca ( 426)	372	86.7	2.8e-14	gi 137524207 gb EBU55586.1	hypothetical protein G ( 164)	361	84.2	6e-14
gi 153876 gb AAA27028.1	5-enolpyruvylshikimate-3- ( 427)	372	86.7	2.8e-14	gi 139462417 gb ECF27014.1	hypothetical protein G ( 229)	363	84.7	6e-14
gi 1781351 emb CAA71382.1	aroA [Salmonella typhim ( 427)	372	86.7	2.8e-14	gi 142757194 gb EDA35755.1	hypothetical protein G ( 229)	363	84.7	6e-14
gi 140064591 gb ECJ31472.1	hypothetical protein G ( 222)	368	85.9	2.9e-14	gi 139532178 gb ECF71290.1	hypothetical protein G ( 235)	363	84.7	6.2e-14
gi 139934982 gb ECI47822.1	hypothetical protein G ( 239)	368	85.7	3e-14	gi 222419069 gb ACM49092.1	3-phosphoshikimate 1-c ( 462)	367	85.6	6.2e-14
gi 138215696 gb EBY47061.1	hypothetical protein G ( 128)	364	84.8	3.2e-14	gi 140315884 gb ECK93023.1	hypothetical protein G ( 242)	363	84.7	6.3e-14
gi 593743 gb AAA55350.1	Sequence 2 from Patent EP ( 427)	371	86.5	3.3e-14	gi 135427661 gb EBT56773.1	hypothetical protein G ( 127)	359	83.7	6.4e-14
gi 135273602 gb EBG56384.1	hypothetical protein G ( 263)	368	85.7	3.3e-14	gi 138393430 gb EBZ36056.1	hypothetical protein G ( 152)	360	84.0	6.5e-14
gi 143181940 gb EDD40611.1	hypothetical protein G ( 223)	367	85.5	3.3e-14	gi 240857213 gb ACS54880.1	3-phosphoshikimate 1-c ( 420)	366	85.4	6.6e-14
gi 137056967 gb EBR96418.1	hypothetical protein G ( 226)	367	85.5	3.3e-14	gi 124364003 gb ABN07811.1	3-phosphoshikimate 1-c ( 422)	366	85.4	6.6e-14
gi 141381885 gb ECR43532.1	hypothetical protein G ( 198)	366	85.3	3.4e-14	gi 141682065 gb ECS79110.1	hypothetical protein G ( 223)	362	84.5	6.8e-14
gi 139161830 gb ECD82757.1	hypothetical protein G ( 174)	365	85.0	3.6e-14	gi 136460127 gb EBO30630.1	hypothetical protein G ( 383)	365	85.2	7e-14
gi 141159028 gb ECQ03748.1	hypothetical protein G ( 245)	367	85.5	3.6e-14	gi 140421747 gb ECL64640.1	hypothetical protein G ( 175)	360	84.0	7.4e-14
gi 140604008 gb ECM35576.1	hypothetical protein G ( 183)	365	85.0	3.7e-14	gi 136145599 gb EBM19604.1	hypothetical protein G ( 409)	365	85.2	7.4e-14
gi 2485252 gb AAB73388.1	I44477 Sequence 57 from p ( 427)	370	86.2	3.8e-14	gi 136106430 gb EBL95515.1	hypothetical protein G ( 110)	357	83.3	7.6e-14
gi 5957575 gb AAE08249.1	Sequence 57 from patent ( 427)	370	86.2	3.8e-14	gi 169812004 gb ACA86588.1	3-phosphoshikimate 1-c ( 426)	365	85.2	7.7e-14
gi 154366 gb AAA27223.1	5-enolpyruvylshikimate 3- ( 427)	370	86.2	3.8e-14	gi 29138009 gb AAO69570.1	3-phosphoshikimate 1-ca ( 427)	365	85.2	7.7e-14
gi 15113317 gb AAE68901.1	Sequence 8 from patent ( 427)	370	86.2	3.8e-14	gi 56128229 gb AAV77735.1	3-phosphoshikimate 1-ca ( 427)	365	85.2	7.7e-14
gi 219621962 gb ACL30118.1	3-phosphoshikimate 1-c ( 427)	370	86.2	3.8e-14	gi 197094372 emb CAR59885.1	3-phosphoshikimate 1- ( 427)	365	85.2	7.7e-14
gi 2484175 gb AAB72311.1	I49204 Sequence 57 from p ( 427)	370	86.2	3.8e-14	gi 16502141 emb CAD05378.1	3-phosphoshikimate 1-c ( 427)	365	85.2	7.7e-14
gi 144974754 gb ABP12465.1	Sequence 57 from paten ( 427)	370	86.2	3.8e-14	gi 193084121 gb ACF09788.1	3-phosphoshikimate 1-c ( 429)	365	85.2	7.8e-14
gi 197940547 gb ACH77880.1	3-phosphoshikimate 1-c ( 427)	370	86.2	3.8e-14	gi 135253730 gb EBG44676.1	hypothetical protein G ( 442)	365	85.2	8e-14
gi 206708172 emb CAR32465.1	3-phosphoshikimate 1- ( 427)	370	86.2	3.8e-14	gi 140302847 gb ECK83869.1	hypothetical protein G ( 227)	361	84.3	8e-14
gi 205271966 emb CAR36810.1	3-phosphoshikimate 1- ( 427)	370	86.2	3.8e-14	gi 108765521 gb ABG04440.1	3-phosphoshikimate 1-c ( 447)	365	85.2	8e-14
gi 136877422 gb EBR00100.1	hypothetical protein G ( 262)	367	85.5	3.8e-14	gi 197720164 gb EDY64072.1	3-phosphoshikimate 1-c ( 453)	365	85.2	8.1e-14
gi 137656038 gb EBV27947.1	hypothetical protein G ( 160)	364	84.8	3.8e-14	gi 134799090 gb EBD51377.1	hypothetical protein G ( 141)	358	83.5	8.1e-14
gi 136301860 gb EBN24503.1	hypothetical protein G ( 236)	366	85.3	4e-14	gi 141365559 gb ECR31937.1	hypothetical protein G ( 235)	361	84.3	8.2e-14
gi 167277430 gb ABZ30294.1	Sequence 4232 from pat (1542)	377	88.0	4.2e-14	gi 138406922 gb EBZ45453.1	hypothetical protein G ( 237)	361	84.3	8.3e-14
gi 137340742 gb EBT55118.1	hypothetical protein G ( 210)	365	85.1	4.2e-14	gi 143923175 gb EDH60320.1	hypothetical protein G ( 244)	361	84.3	8.5e-14
gi 138153842 gb EBY05412.1	hypothetical protein G ( 179)	364	84.8	4.2e-14	gi 139154621 gb ECD77605.1	hypothetical protein G ( 301)	362	84.5	8.8e-14
gi 135336773 gb EBG95699.1	hypothetical protein G ( 253)	366	85.3	4.3e-14	gi 137794484 gb EBW03536.1	hypothetical protein G ( 220)	360	84.0	9e-14
gi 142105911 gb ECV63243.1	hypothetical protein G ( 131)	362	84.4	4.3e-14	gi 141205783 gb ECQ35040.1	hypothetical protein G ( 221)	360	84.0	9e-14
gi 139222176 gb ECE24995.1	hypothetical protein G ( 256)	366	85.3	4.3e-14	gi 137796550 gb EBW04720.1	hypothetical protein G ( 222)	360	84.0	9e-14
gi 143926832 gb EDH63014.1	hypothetical protein G ( 426)	369	86.0	4.3e-14	gi 142554251 gb ECY91763.1	hypothetical protein G ( 188)	359	83.8	9e-14
gi 10038984 dbj BAB13019.1	3-phosphoshikimate 1-c ( 427)	369	86.0	4.3e-14	gi 117648862 gb ABK52964.1	3-phosphoshikimate 1-c (1004)	369	86.2	9.1e-14

gi 138629106 gb ECA92062.1	hypothetical protein G ( 224)	360	84.0	9.1e-14	gi 143362591 gb EDE564421.1	hypothetical protein G ( 410)	359	84.0	1.8e-13
gi 144012226 gb EDI23677.1	hypothetical protein G ( 272)	361	84.3	9.3e-14	gi 138490939 gb EBZ98202.1	hypothetical protein G ( 220)	355	83.0	1.8e-13
gi 141398247 gb ECR54893.1	hypothetical protein G ( 119)	356	83.1	9.4e-14	gi 140733658 gb ECN14670.1	hypothetical protein G ( 260)	356	83.2	1.8e-13
gi 138109040 gb EBX79294.1	hypothetical protein G ( 246)	360	84.1	9.9e-14	gi 145305567 gb ABP56149.1	3-phosphoshikimate 1-c ( 433)	359	84.0	1.9e-13
gi 136866671 gb EBQ93382.1	hypothetical protein G ( 246)	360	84.1	9.9e-14	gi 134912975 gb EBE25634.1	hypothetical protein G ( 223)	355	83.0	1.9e-13
gi 135744502 gb EBJ57473.1	hypothetical protein G ( 211)	359	83.8	1e-13	gi 137115528 gb EBS28958.1	hypothetical protein G ( 160)	353	82.5	1.9e-13
gi 142010326 gb ECU80420.1	hypothetical protein G ( 180)	358	83.6	1e-13	gi 138740065 gb ECB68288.1	hypothetical protein G ( 160)	353	82.5	1.9e-13
gi 142080005 gb ECV42334.1	hypothetical protein G ( 352)	362	84.5	1e-13	gi 12721147 gb AAK02923.1	AroA [Pasteurella multo ( 440)	359	84.0	1.9e-13
gi 137165195 gb EBS56765.1	hypothetical protein G ( 182)	358	83.6	1e-13	gi 140482318 gb ECL96816.1	hypothetical protein G ( 226)	355	83.0	1.9e-13
gi 135179383 gb EBG00170.1	hypothetical protein G ( 155)	357	83.3	1e-13	gi 197710217 gb EDY54251.1	3-phosphoshikimate 1-c ( 441)	359	84.0	1.9e-13
gi 219547426 gb ACL17876.1	3-phosphoshikimate 1-c ( 423)	363	84.8	1e-13	gi 139459145 gb ECF24711.1	hypothetical protein G ( 228)	355	83.0	1.9e-13
gi 135951288 gb EBK92380.1	hypothetical protein G ( 205)	358	83.6	1.1e-13	gi 137634728 gb EBV17335.1	hypothetical protein G ( 232)	355	83.0	1.9e-13
gi 137326809 gb EBT47329.1	hypothetical protein G ( 250)	359	83.9	1.2e-13	gi 138811671 gb ECB96825.1	hypothetical protein G ( 232)	355	83.0	1.9e-13
gi 136647641 gb EBP49413.1	hypothetical protein G ( 257)	359	83.9	1.2e-13	gi 11525367 emb CAK06442.1	putative 3-phosphoshi ( 420)	358	83.8	2.1e-13
gi 140376968 gb ECL35520.1	hypothetical protein G ( 219)	358	83.6	1.2e-13	gi 8546878 emb CAB94597.1	3-phosphoshikimate 1-ca ( 438)	358	83.8	2.2e-13
gi 138112315 gb EBX81121.1	hypothetical protein G ( 133)	355	82.9	1.2e-13	gi 137500712 gb EBU43450.1	hypothetical protein G ( 138)	351	82.1	2.2e-13
gi 227453530 gb ACP32283.1	3-phosphoshikimate 1-c ( 434)	362	84.6	1.2e-13	gi 144102999 gb EDT88610.1	hypothetical protein G ( 118)	350	81.8	2.2e-13
gi 137840358 gb EBW30125.1	hypothetical protein G ( 142)	355	82.9	1.3e-13	gi 141573502 gb ECS42616.1	hypothetical protein G ( 141)	351	82.1	2.2e-13
gi 135600560 gb EBI68434.1	hypothetical protein G ( 235)	358	83.6	1.3e-13	gi 135777069 gb EBJ77694.1	hypothetical protein G ( 237)	354	82.8	2.3e-13
gi 138737749 gb ECB66651.1	hypothetical protein G ( 182)	356	83.2	1.4e-13	gi 135965679 gb EBL02113.1	hypothetical protein G ( 174)	352	82.3	2.3e-13
gi 136940074 gb EBR30361.1	hypothetical protein G ( 217)	357	83.4	1.4e-13	gi 140820545 gb ECN74010.1	hypothetical protein G ( 206)	353	82.6	2.3e-13
gi 135035087 gb EBF07763.1	hypothetical protein G ( 426)	361	84.4	1.4e-13	gi 141429392 gb ECR76550.1	hypothetical protein G ( 251)	354	82.8	2.4e-13
gi 47637 emb CAA38417.1	unnamed protein product [ ( 427)	361	84.4	1.4e-13	gi 209533895 gb ACT53830.1	3-phosphoshikimate 1-c ( 420)	357	83.5	2.4e-13
gi 2484183 gb AAB72319.1	I49212 Sequence 65 from p ( 427)	361	84.4	1.4e-13	gi 137072304 gb EBS05031.1	hypothetical protein G ( 224)	353	82.6	2.5e-13
gi 2485260 gb AAB73396.1	I44485 Sequence 65 from p ( 427)	361	84.4	1.4e-13	gi 141156551 gb ECQ01946.1	hypothetical protein G ( 227)	353	82.6	2.5e-13
gi 5957576 gb AAE08250.1	Sequence 58 from patent ( 427)	361	84.4	1.4e-13	gi 141794130 gb ECT32615.1	hypothetical protein G ( 145)	350	81.9	2.6e-13
gi 237500387 gb ACQ92980.1	3-phosphoshikimate 1-c ( 427)	361	84.4	1.4e-13	gi 167292847 gb ABZ45711.1	Sequence 19649 from pa ( 426)	356	83.3	2.8e-13
gi 144974762 gb ABP12473.1	Sequence 65 from paten ( 427)	361	84.4	1.4e-13	gi 30180948 emb CAD85875.1	EPSP synthase (3-phosp ( 431)	356	83.3	2.8e-13
gi 2485253 gb AAB73389.1	I44478 Sequence 58 from p ( 427)	361	84.4	1.4e-13	gi 260647047 emb CBG70146.1	3-phosphoshikimate 1- ( 443)	356	83.3	2.9e-13
gi 5957583 gb AAE08257.1	Sequence 65 from patent ( 427)	361	84.4	1.4e-13	gi 143570931 gb EDF69343.1	hypothetical protein G ( 138)	349	81.7	2.9e-13
gi 2484176 gb AAB72312.1	I49205 Sequence 58 from p ( 427)	361	84.4	1.4e-13	gi 140395644 gb ECL48451.1	hypothetical protein G ( 235)	352	82.4	3e-13
gi 144974755 gb ABP12466.1	Sequence 58 from paten ( 427)	361	84.4	1.4e-13	gi 217410917 gb EEC50846.1	3-phosphoshikimate 1-c ( 483)	356	83.4	3.1e-13
gi 142221780 gb ECW50540.1	hypothetical protein G ( 434)	361	84.4	1.4e-13	gi 140960254 gb ECO68025.1	hypothetical protein G ( 254)	352	82.4	3.2e-13
gi 140996322 gb ECO93156.1	hypothetical protein G ( 194)	356	83.2	1.4e-13	gi 114334589 gb ABI71971.1	3-phosphoshikimate 1-c ( 426)	355	83.1	3.3e-13
gi 142660118 gb ECZ66009.1	hypothetical protein G ( 143)	354	82.7	1.5e-13	gi 119863478 gb ABM02955.1	3-phosphoshikimate 1-c ( 428)	355	83.1	3.3e-13
gi 137413372 gb EBT96140.1	hypothetical protein G ( 205)	356	83.2	1.5e-13	gi 238871683 gb ACR71393.1	3-phosphoshikimate 1-c ( 431)	355	83.1	3.3e-13
gi 135145339 gb EBF78282.1	hypothetical protein G ( 410)	360	84.2	1.5e-13	gi 135347203 gb EBH02679.1	hypothetical protein G ( 222)	351	82.2	3.3e-13
gi 255924589 gb ACU40100.1	3-phosphoshikimate 1-c ( 420)	360	84.2	1.6e-13	gi 143892353 gb EDH38461.1	hypothetical protein G ( 433)	355	83.1	3.3e-13
gi 140238213 gb ECK46610.1	hypothetical protein G ( 219)	356	83.2	1.6e-13	gi 137594212 gb EBU94648.1	hypothetical protein G ( 190)	350	81.9	3.3e-13
gi 72393962 gb AAZ68239.1	3-phosphoshikimate 1-ca ( 428)	360	84.2	1.6e-13	gi 256796396 gb ACV27052.1	3-phosphoshikimate 1-c ( 442)	355	83.1	3.4e-13
gi 140263797 gb ECK64234.1	hypothetical protein G ( 134)	353	82.5	1.6e-13	gi 135950277 gb EBK91698.1	hypothetical protein G ( 230)	351	82.2	3.4e-13
gi 141051576 gb ECP29931.1	hypothetical protein G ( 263)	357	83.5	1.6e-13	gi 140932293 gb ECO48252.1	hypothetical protein G ( 195)	350	81.9	3.4e-13
gi 138368034 gb EBZ19603.1	hypothetical protein G ( 266)	357	83.5	1.6e-13	gi 140915160 gb ECO36180.1	hypothetical protein G ( 142)	348	81.5	3.5e-13
gi 142532130 gb ECY75910.1	hypothetical protein G ( 137)	353	82.5	1.6e-13	gi 140442678 gb ECL78355.1	hypothetical protein G ( 201)	350	81.9	3.5e-13
gi 139077328 gb ECD25425.1	hypothetical protein G ( 226)	356	83.2	1.6e-13	gi 137655461 gb EBV27620.1	hypothetical protein G ( 201)	350	81.9	3.5e-13
gi 135111798 gb EBF56743.1	hypothetical protein G ( 138)	353	82.5	1.6e-13	gi 139613416 gb ECG27637.1	hypothetical protein G ( 211)	350	82.0	3.7e-13
gi 142175064 gb ECW14980.1	hypothetical protein G ( 138)	353	82.5	1.6e-13	gi 138983487 gb ECC68508.1	hypothetical protein G ( 179)	349	81.7	3.7e-13
gi 143855585 gb EDH11623.1	hypothetical protein G ( 118)	352	82.3	1.7e-13	gi 142329282 gb ECK29996.1	hypothetical protein G ( 185)	349	81.7	3.8e-13
gi 135240693 gb EBG36992.1	hypothetical protein G ( 166)	354	82.7	1.7e-13	gi 140188819 gb ECK12796.1	hypothetical protein G ( 191)	349	81.7	3.9e-13
gi 140972874 gb ECO76607.1	hypothetical protein G ( 236)	356	83.2	1.7e-13	gi 137854155 gb EBW38038.1	hypothetical protein G ( 227)	350	82.0	3.9e-13
gi 139355526 gb ECE60735.1	hypothetical protein G ( 205)	355	83.0	1.7e-13	gi 141822648 gb ECT49099.1	hypothetical protein G ( 194)	349	81.7	3.9e-13

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gi 137525237 gb EBU56150.1	hypothetical protein G ( 234)	350	82.0	4e-13	gi 143324225 gb EDE33520.1	hypothetical protein G ( 402)	346	81.3	1.1e-12
gi 137080837 gb EBS09819.1	hypothetical protein G ( 205)	349	81.7	4.1e-13	gi 134378823 gb EBB01013.1	hypothetical protein G ( 359)	345	81.0	1.2e-12
gi 143973504 gb EDH96220.1	hypothetical protein G ( 125)	346	81.0	4.1e-13	gi 19887052 gb AAM01843.1	5-enolpyruvylshikimate- ( 428)	346	81.3	1.2e-12
gi 135466250 gb EBH82554.1	hypothetical protein G ( 477)	354	82.9	4.1e-13	gi 197053760 gb ACH25458.1	Sequence 10 from paten ( 428)	346	81.3	1.2e-12
gi 141447794 gb ECR89501.1	hypothetical protein G ( 250)	350	82.0	4.2e-13	gi 161726853 emb CAP47297.1	unnamed protein produ ( 428)	346	81.3	1.2e-12
gi 141931434 gb ECU25456.1	hypothetical protein G ( 251)	350	82.0	4.2e-13	gi 142160570 gb ECW03887.1	hypothetical protein G ( 512)	347	81.5	1.2e-12
gi 38199572 emb CAE49223.1	3-phosphoshikimate 1-c ( 431)	353	82.7	4.4e-13	gi 63334427 gb AAY40476.1	5-enol-pyruvylshikimate ( 444)	346	81.3	1.2e-12
gi 135841015 gb EBK18020.1	hypothetical protein G ( 196)	348	81.5	4.6e-13	gi 143017653 gb EDC21271.1	hypothetical protein G ( 195)	341	80.1	1.2e-12
gi 143142368 gb EDD12423.1	hypothetical protein G ( 383)	352	82.5	4.6e-13	gi 136365694 gb EBN67728.1	hypothetical protein G ( 231)	342	80.3	1.2e-12
gi 141547228 gb ECS28434.1	hypothetical protein G ( 199)	348	81.5	4.6e-13	gi 140120371 gb ECJ67812.1	hypothetical protein G ( 242)	342	80.3	1.3e-12
gi 136452097 gb EBO25416.1	hypothetical protein G ( 204)	348	81.5	4.7e-13	gi 139972695 gb ECI73769.1	hypothetical protein G ( 243)	342	80.3	1.3e-12
gi 139065978 gb ECD17692.1	hypothetical protein G ( 247)	349	81.8	4.8e-13	gi 137897622 gb EBW62970.1	hypothetical protein G ( 175)	340	79.8	1.3e-12
gi 46400157 emb CAF23606.1	putative 3-phosphoshik ( 939)	357	83.7	4.8e-13	gi 134491078 gb EBB66101.1	hypothetical protein G ( 153)	339	79.6	1.3e-12
gi 141823036 gb ECT49373.1	hypothetical protein G ( 211)	348	81.5	4.9e-13	gi 142080142 gb ECV42444.1	hypothetical protein G ( 428)	345	81.1	1.4e-12
gi 141358226 gb ECR26863.1	hypothetical protein G ( 218)	348	81.5	5e-13	gi 139798315 gb ECH53759.1	hypothetical protein G ( 310)	343	80.6	1.4e-12
gi 138464932 gb EBZ86060.1	hypothetical protein G ( 165)	346	81.1	5.3e-13	gi 138213505 gb EBY45565.1	hypothetical protein G ( 190)	340	79.9	1.4e-12
gi 135957341 gb EBK96478.1	hypothetical protein G ( 180)	346	81.1	5.7e-13	gi 136401218 gb EBN92222.1	hypothetical protein G ( 98)	338	79.6	1.4e-12
gi 86280632 gb ABC89695.1	3-phosphoshikimate 1-ca ( 420)	351	82.3	5.7e-13	gi 140119422 gb ECJ67136.1	hypothetical protein G ( 165)	339	79.6	1.4e-12
gi 135660988 gb EBJ05847.1	hypothetical protein G ( 216)	347	81.3	5.7e-13	gi 138071564 gb EBX58228.1	hypothetical protein G ( 239)	341	80.1	1.5e-12
gi 118135516 gb ABK62560.1	3-phosphoshikimate 1-c ( 435)	351	82.3	5.9e-13	gi 135434940 gb EBH61643.1	hypothetical protein G ( 209)	340	79.9	1.5e-12
gi 135311115 gb EBG78396.1	hypothetical protein G ( 162)	345	80.9	6e-13	gi 270512698 gb ACZ90976.1	3-phosphoshikimate 1-c ( 425)	344	80.8	1.6e-12
gi 135475974 gb EBH89065.1	hypothetical protein G ( 242)	347	81.4	6.3e-13	gi 207102480 emb CAR82020.1	unnamed protein produ ( 425)	344	80.8	1.6e-12
gi 140555709 gb ECM20146.1	hypothetical protein G ( 207)	346	81.1	6.4e-13	gi 137102829 gb EBS21784.1	hypothetical protein G ( 112)	336	78.9	1.6e-12
gi 190695875 gb ACE89960.1	3-phosphoshikimate 1-c ( 420)	350	82.1	6.6e-13	gi 75702201 gb ABA21877.1	3-phosphoshikimate 1-ca ( 426)	344	80.8	1.6e-12
gi 218301274 emb CAU98622.1	unnamed protein produ ( 450)	350	82.1	7e-13	gi 71796266 gb AAZ41017.1	3-phosphoshikimate 1-ca ( 432)	344	80.8	1.6e-12
gi 139395594 gb ECE82263.1	hypothetical protein G ( 198)	345	80.9	7.1e-13	gi 139775941 gb ECH37969.1	hypothetical protein G ( 159)	338	79.4	1.6e-12
gi 136291219 gb EBN17253.1	hypothetical protein G ( 252)	346	81.2	7.6e-13	gi 136662565 gb EBP58343.1	hypothetical protein G ( 159)	338	79.4	1.6e-12
gi 135324770 gb EBG87629.1	hypothetical protein G ( 135)	342	80.2	7.9e-13	gi 5957580 gb AAE08254.1	Sequence 62 from patent ( 441)	344	80.9	1.6e-12
gi 136446532 gb EBQ21828.1	hypothetical protein G ( 191)	344	80.7	8e-13	gi 144974759 gb ABP12470.1	Sequence 62 from paten ( 441)	344	80.9	1.6e-12
gi 138997581 gb ECC72530.1	hypothetical protein G ( 230)	345	80.9	8.1e-13	gi 2485257 gb AAB73393.1	I44482 Sequence 62 from p ( 441)	344	80.9	1.6e-12
gi 136805392 gb EBQ52456.1	hypothetical protein G ( 197)	344	80.7	8.2e-13	gi 581456 emb CAA78480.1	aroA [Pasteurella multoc ( 441)	344	80.9	1.6e-12
gi 135667198 gb EBJ09710.1	hypothetical protein G ( 238)	345	80.9	8.3e-13	gi 2484180 gb AAB72316.1	I49209 Sequence 62 from p ( 441)	344	80.9	1.6e-12
gi 137196438 gb EBS74082.1	hypothetical protein G ( 149)	342	80.2	8.6e-13	gi 136293903 gb EBN19081.1	hypothetical protein G ( 193)	339	79.7	1.6e-12
gi 137513759 gb EBU50081.1	hypothetical protein G ( 179)	343	80.5	8.7e-13	gi 138088359 gb EBX67891.1	hypothetical protein G ( 241)	340	79.9	1.7e-12
gi 136113324 gb EBM00254.1	hypothetical protein G ( 182)	343	80.5	8.8e-13	gi 135635389 gb EBI89991.1	hypothetical protein G ( 129)	336	78.9	1.8e-12
gi 139407942 gb ECE90556.1	hypothetical protein G ( 132)	341	80.0	8.9e-13	gi 137893657 gb EBW60674.1	hypothetical protein G ( 95)	334	78.5	1.8e-12
gi 143377822 gb EDE65681.1	hypothetical protein G ( 428)	348	81.7	9e-13	gi 198260919 gb EDY85227.1	3-phosphoshikimate 1-c ( 446)	343	80.6	1.9e-12
gi 137214083 gb EBS84150.1	hypothetical protein G ( 222)	344	80.7	9.1e-13	gi 139395595 gb ECE82264.1	hypothetical protein G ( 230)	339	79.7	1.9e-12
gi 138935690 gb ECC49156.1	hypothetical protein G ( 162)	342	80.2	9.2e-13	gi 139117329 gb ECD53219.1	hypothetical protein G ( 196)	338	79.4	1.9e-12
gi 189428021 gb ACD98169.1	5-enolpyruvylshikimate ( 445)	348	81.7	9.3e-13	gi 23326204 gb AAN24780.1	3-phosphoshikimate 1-ca ( 455)	343	80.7	1.9e-12
gi 138501049 gb ECA04254.1	hypothetical protein G ( 242)	344	80.7	9.8e-13	gi 136951000 gb EBR36509.1	hypothetical protein G ( 276)	340	79.9	1.9e-12
gi 135569263 gb EBT48826.1	hypothetical protein G ( 149)	341	80.0	9.9e-13	gi 135035458 gb EBF07996.1	hypothetical protein G ( 405)	342	80.4	2e-12
gi 141045191 gb ECP25528.1	hypothetical protein G ( 149)	341	80.0	9.9e-13	gi 135522927 gb EBI19183.1	hypothetical protein G ( 129)	335	78.7	2.1e-12
gi 138146322 gb EBY00264.1	hypothetical protein G ( 150)	341	80.0	9.9e-13	gi 91202313 emb CAJ75373.1	strongly similar to 3- ( 424)	342	80.4	2.1e-12
gi 138224534 gb EBY53274.1	hypothetical protein G ( 212)	343	80.5	1e-12	gi 138800588 gb ECB91870.1	hypothetical protein G ( 156)	336	79.0	2.1e-12
gi 161985195 gb ABX80844.1	3-phosphoshikimate 1-c ( 418)	347	81.5	1e-12	gi 237882706 gb EEP71534.1	3-phosphoshikimate 1-c ( 433)	342	80.4	2.2e-12
gi 221155485 gb ACM04612.1	3-phosphoshikimate 1-c ( 434)	347	81.5	1e-12	gi 134841298 gb EBD78239.1	hypothetical protein G ( 225)	338	79.5	2.2e-12
gi 142404151 gb ECX82212.1	hypothetical protein G ( 228)	343	80.5	1.1e-12	gi 135109078 gb EBF55010.1	hypothetical protein G ( 452)	342	80.4	2.2e-12
gi 41817616 gb AAS12201.1	3-phosphoshikimate 1-ca ( 449)	347	81.5	1.1e-12	gi 137475361 gb EBU30443.1	hypothetical protein G ( 121)	334	78.5	2.3e-12
gi 141709852 gb ECS86876.1	hypothetical protein G ( 143)	340	79.8	1.1e-12	gi 137271986 gb EBT16720.1	hypothetical protein G ( 202)	337	79.2	2.3e-12
gi 141398250 gb ECR54896.1	hypothetical protein G ( 122)	339	79.6	1.1e-12	gi 141879835 gb ECT89188.1	hypothetical protein G ( 207)	337	79.2	2.3e-12

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gi 137527344 gb EBU57324.1	hypothetical protein G ( 217)	337	79.3	2.4e-12	gi 135966631 gb EBL02759.1	hypothetical protein G ( 214)	331	78.0	5.7e-12
gi 141808595 gb ECT39392.1	hypothetical protein G ( 134)	334	78.5	2.5e-12	gi 17134157 dbj BAB76718.1	3-phosphoshikimate 1-c ( 425)	335	79.0	5.8e-12
gi 213504188 emb CAS92805.1	unnamed protein produ ( 431)	341	80.2	2.5e-12	gi 213504190 emb CAS92806.1	unnamed protein produ ( 431)	335	79.0	5.9e-12
gi 134362434 gb EBA89872.1	hypothetical protein G ( 163)	335	78.8	2.5e-12	gi 218301288 emb CAU98636.1	unnamed protein produ ( 431)	335	79.0	5.9e-12
gi 239515101 gb EEQ54968.1	3-phosphoshikimate 1-c ( 445)	341	80.2	2.5e-12	gi 135013362 gb EBE93072.1	hypothetical protein G ( 165)	329	77.5	6.1e-12
gi 136288662 gb EBN15525.1	hypothetical protein G ( 202)	336	79.0	2.6e-12	gi 139543335 gb ECF78883.1	hypothetical protein G ( 141)	328	77.3	6.1e-12
gi 139540931 gb ECF77151.1	hypothetical protein G ( 177)	335	78.8	2.7e-12	gi 140194355 gb ECK16491.1	hypothetical protein G ( 142)	328	77.3	6.2e-12
gi 137927027 gb EBW79646.1	hypothetical protein G ( 150)	334	78.6	2.7e-12	gi 139776743 gb ECH38540.1	hypothetical protein G ( 236)	331	78.0	6.2e-12
gi 142504418 gb ECY55742.1	hypothetical protein G ( 249)	337	79.3	2.7e-12	gi 141975410 gb ECZ55912.1	hypothetical protein G ( 107)	326	76.8	6.4e-12
gi 118193930 gb ABK76848.1	5-enolpyruvylshikimate ( 414)	340	80.0	2.8e-12	gi 137625100 gb EBV12215.1	hypothetical protein G ( 161)	328	77.3	6.9e-12
gi 137873963 gb EBW49399.1	hypothetical protein G ( 262)	337	79.3	2.9e-12	gi 140674338 gb ECM73231.1	hypothetical protein G ( 236)	330	77.8	7.2e-12
gi 135280343 gb EBG60330.1	hypothetical protein G ( 188)	335	78.8	2.9e-12	gi 142981403 gb EDB95732.1	hypothetical protein G ( 122)	326	76.9	7.2e-12
gi 136799237 gb EBQ48383.1	hypothetical protein G ( 263)	337	79.3	2.9e-12	gi 142806346 gb EDA72212.1	hypothetical protein G ( 240)	330	77.8	7.3e-12
gi 137961021 gb EBW98740.1	hypothetical protein G ( 230)	336	79.1	3e-12	gi 137601619 gb EBU98561.1	hypothetical protein G ( 146)	327	77.1	7.3e-12
gi 143735046 gb EDG51254.1	hypothetical protein G ( 237)	336	79.1	3e-12	gi 142914613 gb EDB48485.1	hypothetical protein G ( 106)	325	76.6	7.4e-12
gi 140469806 gb ECL93098.1	hypothetical protein G ( 240)	336	79.1	3.1e-12	gi 136051934 gb EBL58617.1	hypothetical protein G ( 207)	329	77.6	7.4e-12
gi 142007150 gb ECU78011.1	hypothetical protein G ( 248)	336	79.1	3.2e-12	gi 140878389 gb ECC12061.1	hypothetical protein G ( 211)	329	77.6	7.5e-12
gi 145017901 gb EDK02180.1	hypothetical protein M (1575)	347	81.7	3.2e-12	gi 134820000 gb EBD64619.1	hypothetical protein G ( 130)	326	76.9	7.6e-12
gi 142028027 gb ECU97300.1	hypothetical protein G ( 420)	339	79.8	3.2e-12	gi 269786272 gb ACZ38415.1	3-phosphoshikimate 1-c ( 435)	333	78.6	7.9e-12
gi 137268762 gb EBT14925.1	hypothetical protein G ( 187)	334	78.6	3.3e-12	gi 51856246 dbj BAD40404.1	3-phosphoshikimate-1-c ( 449)	333	78.6	8.1e-12
gi 136645114 gb EBP47908.1	hypothetical protein G ( 132)	331	77.9	3.8e-12	gi 137698489 gb EBV52072.1	hypothetical protein G ( 151)	326	76.9	8.7e-12
gi 140758228 gb ECN31786.1	hypothetical protein G ( 220)	334	78.6	3.8e-12	gi 139913576 gb ECI32833.1	hypothetical protein G ( 214)	328	77.4	8.8e-12
gi 68264311 emb CAI37799.1	3-phosphoshikimate 1-c ( 429)	338	79.6	3.8e-12	gi 140309628 gb ECH88544.1	hypothetical protein G ( 98)	323	76.2	9.2e-12
gi 135852837 gb EBK25457.1	hypothetical protein G ( 226)	334	78.6	3.9e-12	gi 143904377 gb EDH46982.1	hypothetical protein G ( 343)	330	77.9	9.9e-12
gi 137020450 gb EBR75785.1	hypothetical protein G ( 120)	330	77.7	4e-12	gi 140182762 gb ECK08451.1	hypothetical protein G ( 184)	326	76.9	1e-11
gi 213524060 gb ACJ52807.1	3-phosphoshikimate 1-c ( 461)	338	79.6	4e-12	gi 135943313 gb EBK87033.1	hypothetical protein G ( 190)	326	76.9	1.1e-11
gi 137606007 gb EBV01255.1	hypothetical protein G ( 208)	333	78.4	4.2e-12	gi 141954027 gb ECU41298.1	hypothetical protein G ( 225)	327	77.2	1.1e-11
gi 134412896 gb EBB20265.1	hypothetical protein G ( 152)	331	77.9	4.2e-12	gi 137887915 gb EBW57387.1	hypothetical protein G ( 168)	325	76.7	1.1e-11
gi 139752541 gb ECH21814.1	hypothetical protein G ( 182)	332	78.2	4.3e-12	gi 134700209 gb EBC90411.1	hypothetical protein G ( 169)	325	76.7	1.1e-11
gi 137113514 gb EBS27820.1	hypothetical protein G ( 301)	335	78.9	4.3e-12	gi 134380743 gb EBB02262.1	hypothetical protein G ( 200)	326	77.0	1.1e-11
gi 140674336 gb ECM73229.1	hypothetical protein G ( 220)	333	78.4	4.4e-12	gi 136357207 gb EBN61951.1	hypothetical protein G ( 204)	326	77.0	1.1e-11
gi 138956670 gb ECC58151.1	hypothetical protein G ( 134)	330	77.7	4.4e-12	gi 138839332 gb ECC10256.1	hypothetical protein G ( 155)	324	76.5	1.2e-11
gi 6855375 emb CAB71266.1	3-phosphoshikimate 1-ca ( 440)	337	79.4	4.5e-12	gi 138510310 gb ECA09339.1	hypothetical protein G ( 160)	324	76.5	1.2e-11
gi 197697271 gb EDY44204.1	3-phosphoshikimate 1-c ( 443)	337	79.4	4.5e-12	gi 138006824 gb EBX24048.1	hypothetical protein G ( 164)	324	76.5	1.2e-11
gi 269305959 gb ACZ31509.1	3-phosphoshikimate 1-c ( 444)	337	79.4	4.5e-12	gi 142858079 gb EDB07673.1	hypothetical protein G ( 141)	323	76.3	1.3e-11
gi 134510774 gb EBB77501.1	hypothetical protein G ( 120)	329	77.5	4.6e-12	gi 138288445 gb EBY80872.1	hypothetical protein G ( 143)	323	76.3	1.3e-11
gi 139695641 gb ECG83504.1	hypothetical protein G ( 235)	333	78.4	4.6e-12	gi 141666967 gb ECS70781.1	hypothetical protein G ( 238)	326	77.0	1.3e-11
gi 138908492 gb ECC37782.1	hypothetical protein G ( 123)	329	77.5	4.7e-12	gi 167288349 gb ABZ41213.1	Sequence 15151 from pa ( 400)	329	77.7	1.3e-11
gi 143051684 gb EDC46069.1	hypothetical protein G ( 151)	330	77.7	4.9e-12	gi 167287866 gb ABZ40730.1	Sequence 14668 from pa ( 410)	329	77.7	1.3e-11
gi 136377067 gb EBN75527.1	hypothetical protein G ( 152)	330	77.7	4.9e-12	gi 167287577 gb ABZ40441.1	Sequence 14379 from pa ( 410)	329	77.7	1.3e-11
gi 140538314 gb ECM15202.1	hypothetical protein G ( 153)	330	77.7	4.9e-12	gi 167284960 gb ABZ37824.1	Sequence 11762 from pa ( 410)	329	77.7	1.3e-11
gi 142221795 gb ECW50550.1	hypothetical protein G ( 356)	335	78.9	5e-12	gi 141201113 gb ECQ31813.1	hypothetical protein G ( 184)	324	76.5	1.4e-11
gi 136108377 gb EBL96850.1	hypothetical protein G ( 216)	332	78.2	5e-12	gi 15155591 gb AAK86449.1	3-phosphoshikimate 1-ca ( 425)	329	77.7	1.4e-11
gi 137249529 gb EBT04003.1	hypothetical protein G ( 132)	329	77.5	5e-12	gi 209409579 emb CAR82016.1	unnamed protein produ ( 425)	329	77.7	1.4e-11
gi 142176534 gb ECW16103.1	hypothetical protein G ( 441)	336	79.2	5.2e-12	gi 136532719 gb EB077403.1	hypothetical protein G ( 375)	328	77.5	1.4e-11
gi 139957029 gb ECI62786.1	hypothetical protein G ( 165)	330	77.7	5.3e-12	gi 237878972 gb ACR31304.1	5-enolpyruvylshikimate ( 451)	329	77.7	1.4e-11
gi 141561787 gb ECS38611.1	hypothetical protein G ( 196)	331	78.0	5.3e-12	gi 139751825 gb ECH21337.1	hypothetical protein G ( 201)	324	76.5	1.5e-11
gi 141357056 gb ECR26055.1	hypothetical protein G ( 198)	331	78.0	5.3e-12	gi 134549606 gb EBC00642.1	hypothetical protein G ( 111)	320	75.6	1.6e-11
gi 138599473 gb ECA71366.1	hypothetical protein G ( 200)	331	78.0	5.4e-12	gi 135506999 gb EBI08954.1	hypothetical protein G ( 220)	324	76.6	1.6e-11
gi 138685422 gb ECB22911.1	hypothetical protein G ( 288)	333	78.5	5.5e-12	gi 139137061 gb ECP65571.1	hypothetical protein G ( 114)	320	75.6	1.6e-11
gi 143120591 gb EDC96442.1	hypothetical protein G ( 210)	331	78.0	5.6e-12	gi 108768752 gb ABG07474.1	3-phosphoshikimate 1-c ( 438)	328	77.5	1.6e-11

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gi 119693519 gb ABL90592.1	3-phosphoshikimate 1-c ( 438)	328	77.5	1.6e-11	gi 140922142 gb ECO40954.1	hypothetical protein G ( 127)	315	74.6	3.6e-11
gi 137007196 gb EBR68377.1	hypothetical protein G ( 98)	319	75.4	1.6e-11	gi 139300510 gb ECE48466.1	hypothetical protein G ( 180)	317	75.1	3.7e-11
gi 142196767 gb ECW31538.1	hypothetical protein G ( 325)	326	77.1	1.7e-11	gi 239679351 gb ACS07601.1	Sequence 23 from paten ( 419)	322	76.3	3.7e-11
gi 135220220 gb EBG24982.1	hypothetical protein G ( 234)	324	76.6	1.7e-11	gi 117576145 emb CAL68907.1	unnamed protein produ ( 419)	322	76.3	3.7e-11
gi 137815339 gb EBW15583.1	hypothetical protein G ( 172)	322	76.1	1.7e-11	gi 226911720 gb EEH96921.1	3-phosphoshikimate 1-c ( 431)	322	76.3	3.8e-11
gi 117576131 emb CAL68900.1	unnamed protein produ ( 419)	327	77.3	1.8e-11	gi 139125726 gb ECD58837.1	hypothetical protein G ( 114)	314	74.4	3.8e-11
gi 239679344 gb ACS07594.1	Sequence 9 from patent ( 419)	327	77.3	1.8e-11	gi 141531454 gb ECS17387.1	hypothetical protein G ( 162)	316	74.8	3.9e-11
gi 94220102 gb ABF14261.1	3-phosphoshikimate 1-ca ( 428)	327	77.3	1.8e-11	gi 218301271 emb CAU98620.1	unnamed protein produ ( 442)	322	76.3	3.9e-11
gi 144123245 gb EDJ03229.1	hypothetical protein G ( 438)	327	77.3	1.9e-11	gi 27361607 gb AAO10514.1	AE016804_24 3-phosphoshi ( 376)	321	76.0	3.9e-11
gi 137439907 gb EBU11139.1	hypothetical protein G ( 139)	320	75.6	1.9e-11	gi 126219902 gb ABN83408.1	5-enolpyruvylshikimate ( 448)	322	76.3	3.9e-11
gi 135301369 gb EBG72638.1	hypothetical protein G ( 142)	320	75.6	2e-11	gi 139512332 gb ECF57947.1	hypothetical protein G ( 122)	314	74.4	4.1e-11
gi 134789146 gb EBD44416.1	hypothetical protein G ( 147)	320	75.6	2e-11	gi 141358068 gb ECR26755.1	hypothetical protein G ( 172)	316	74.8	4.1e-11
gi 141436523 gb ECR81656.1	hypothetical protein G ( 179)	321	75.9	2.1e-11	gi 141571591 gb ECS42100.1	hypothetical protein G ( 124)	314	74.4	4.1e-11
gi 138189835 gb EBY30590.1	hypothetical protein G ( 213)	322	76.1	2.1e-11	gi 138538608 gb ECA28773.1	hypothetical protein G ( 174)	316	74.9	4.1e-11
gi 135798487 gb EBJ91258.1	hypothetical protein G ( 132)	319	75.4	2.1e-11	gi 139459143 gb ECF24709.1	hypothetical protein G ( 179)	316	74.9	4.2e-11
gi 139445388 gb ECF14877.1	hypothetical protein G ( 219)	322	76.1	2.1e-11	gi 154698953 gb EDN98691.1	hypothetical protein S (1576)	329	78.0	4.3e-11
gi 126233798 gb ABN97198.1	3-phosphoshikimate 1-c ( 438)	326	77.1	2.2e-11	gi 117576137 emb CAL68903.1	unnamed protein produ ( 419)	321	76.1	4.3e-11
gi 140647368 gb ECM54294.1	hypothetical protein G ( 191)	321	75.9	2.2e-11	gi 239679350 gb ACS07600.1	Sequence 21 from paten ( 419)	321	76.1	4.3e-11
gi 141076390 gb ECP45929.1	hypothetical protein G ( 195)	321	75.9	2.2e-11	gi 239679347 gb ACS07597.1	Sequence 15 from paten ( 419)	321	76.1	4.3e-11
gi 138267880 gb EBY68978.1	hypothetical protein G ( 130)	318	75.2	2.4e-11	gi 117576143 emb CAL68906.1	unnamed protein produ ( 419)	321	76.1	4.3e-11
gi 53854589 gb AAU95677.1	arom [Sclerotinia scler (1590)	333	78.8	2.4e-11	gi 143683392 gb EDG25520.1	hypothetical protein G ( 155)	315	74.6	4.3e-11
gi 218086784 emb CAT03395.1	unnamed protein produ ( 419)	325	76.9	2.4e-11	gi 134974650 gb EBE66821.1	hypothetical protein G ( 198)	316	74.9	4.6e-11
gi 141784517 gb ECT27521.1	hypothetical protein G ( 218)	321	75.9	2.4e-11	gi 140242114 gb ECA49397.1	hypothetical protein G ( 201)	316	74.9	4.7e-11
gi 137551557 gb EBU70622.1	hypothetical protein G ( 135)	318	75.2	2.5e-11	gi 143612207 gb EDF86144.1	hypothetical protein G ( 334)	319	75.6	4.7e-11
gi 137514998 gb EBU50711.1	hypothetical protein G ( 194)	320	75.7	2.6e-11	gi 137082794 gb EBS10909.1	hypothetical protein G ( 242)	317	75.1	4.8e-11
gi 137434272 gb EBU08031.1	hypothetical protein G ( 231)	321	75.9	2.6e-11	gi 135819476 gb EBK04465.1	hypothetical protein G ( 182)	315	74.7	5e-11
gi 117561405 gb ABK38353.1	3-phosphoshikimate 1-c ( 455)	325	76.9	2.6e-11	gi 182634487 gb ACB95261.1	3-phosphoshikimate 1-c ( 424)	320	75.9	5e-11
gi 134678975 gb EBC77637.1	hypothetical protein G ( 200)	320	75.7	2.6e-11	gi 138033807 gb EBX38001.1	hypothetical protein G ( 97)	311	73.7	5.1e-11
gi 135767474 gb EBJ71737.1	hypothetical protein G ( 237)	321	76.0	2.6e-11	gi 141796891 gb ECT33585.1	hypothetical protein G ( 161)	314	74.4	5.2e-11
gi 140278343 gb ECK71234.1	hypothetical protein G ( 145)	318	75.2	2.7e-11	gi 139753549 gb ECH22504.1	hypothetical protein G ( 227)	316	74.9	5.2e-11
gi 136051935 gb EBL58618.1	hypothetical protein G ( 206)	320	75.7	2.7e-11	gi 138575184 gb ECA54711.1	hypothetical protein G ( 193)	315	74.7	5.2e-11
gi 135848766 gb EBK22892.1	hypothetical protein G ( 148)	318	75.2	2.7e-11	gi 136047742 gb EBL55766.1	hypothetical protein G ( 199)	315	74.7	5.4e-11
gi 143489039 gb EDF26103.1	hypothetical protein G ( 153)	318	75.2	2.8e-11	gi 143086208 gb EDC71322.1	hypothetical protein G ( 200)	315	74.7	5.4e-11
gi 137183149 gb EBS66811.1	hypothetical protein G ( 140)	317	75.0	3e-11	gi 136310120 gb EBN30164.1	hypothetical protein G ( 390)	319	75.6	5.4e-11
gi 140945347 gb ECO57367.1	hypothetical protein G ( 198)	319	75.5	3e-11	gi 229383027 gb EEO33118.1	3-phosphoshikimate 1-c ( 426)	319	75.7	5.8e-11
gi 135582507 gb EBI57266.1	hypothetical protein G ( 202)	319	75.5	3.1e-11	gi 136446530 gb EBO21826.1	hypothetical protein G ( 187)	314	74.4	5.9e-11
gi 213504180 emb CAS92801.1	unnamed protein produ ( 467)	324	76.7	3.1e-11	gi 157918462 gb ABV99889.1	3-phosphoshikimate 1-c ( 433)	319	75.7	5.9e-11
gi 76782132 gb ABA54838.1	3-phosphoshikimate 1-ca ( 403)	323	76.5	3.1e-11	gi 137251448 gb EBT05121.1	hypothetical protein G ( 198)	314	74.5	6.2e-11
gi 144197942 gb EDJ58366.1	hypothetical protein G ( 482)	324	76.7	3.2e-11	gi 140795564 gb ECN56407.1	hypothetical protein G ( 216)	314	74.5	6.7e-11
gi 2649064 gb AAB89746.1	5-enolpyruvylshikimate 3 ( 416)	323	76.5	3.2e-11	gi 268312873 gb ACY99247.1	3-phosphoshikimate 1-c ( 425)	318	75.4	6.7e-11
gi 197053754 gb ACH25452.1	Sequence 4 from patent ( 416)	323	76.5	3.2e-11	gi 141070657 gb ECP42029.1	hypothetical protein G ( 157)	312	74.0	6.7e-11
gi 167294559 gb ABZ47423.1	Sequence 21361 from pa ( 416)	323	76.5	3.2e-11	gi 135696052 gb EBJ27471.1	hypothetical protein G ( 190)	313	74.2	6.9e-11
gi 239679345 gb ACS07595.1	Sequence 11 from paten ( 419)	323	76.5	3.2e-11	gi 134843697 gb EBD79778.1	hypothetical protein G ( 122)	310	73.5	7.2e-11
gi 117576125 emb CAL68897.1	unnamed protein produ ( 419)	323	76.5	3.2e-11	gi 143157320 gb EDD23165.1	hypothetical protein G ( 205)	313	74.3	7.4e-11
gi 117576123 emb CAL68666.1	unnamed protein produ ( 419)	323	76.5	3.2e-11	gi 139909706 gb ECJ30075.1	hypothetical protein G ( 205)	313	74.3	7.4e-11
gi 239679341 gb ACS07591.1	Sequence 3 from patent ( 419)	323	76.5	3.2e-11	gi 117576135 emb CAL68902.1	unnamed protein produ ( 419)	317	75.2	7.7e-11
gi 209571207 emb CAR82018.1	unnamed protein produ ( 419)	323	76.5	3.2e-11	gi 239679346 gb ACS07596.1	Sequence 13 from paten ( 419)	317	75.2	7.7e-11
gi 239679343 gb ACS07593.1	Sequence 7 from patent ( 419)	323	76.5	3.2e-11	gi 158510786 gb ABW67753.1	3-phosphoshikimate 1-c ( 423)	317	75.2	7.7e-11
gi 117576129 emb CAL68899.1	unnamed protein produ ( 419)	323	76.5	3.2e-11	gi 137183088 gb EBS66775.1	hypothetical protein G ( 187)	312	74.0	7.8e-11
gi 134740074 gb EBD13133.1	hypothetical protein G ( 240)	319	75.5	3.5e-11	gi 257050668 gb ACV39852.1	3-phosphoshikimate 1-c ( 431)	317	75.2	7.8e-11
gi 140050235 gb ECJ24330.1	hypothetical protein G ( 107)	314	74.3	3.6e-11	gi 139308929 gb ECE49564.1	hypothetical protein G ( 120)	309	73.3	8.2e-11

gi 135933536 gb EBK80451.1	hypothetical protein G ( 168)	311	73.8	8.3e-11	gi 139731566 gb ECH08565.1	hypothetical protein G ( 180)	306	72.8	1.8e-10
gi 143344597 gb EDE46223.1	hypothetical protein G ( 328)	315	74.8	8.3e-11	gi 140064590 gb ECJ31471.1	hypothetical protein G ( 184)	306	72.8	1.8e-10
gi 135162902 gb EBF89584.1	hypothetical protein G ( 124)	309	73.3	8.5e-11	gi 134392972 gb EBB09817.1	hypothetical protein G ( 185)	306	72.8	1.8e-10
gi 135111849 gb EBF56773.1	hypothetical protein G ( 294)	314	74.5	8.7e-11	gi 138081070 gb EBX63704.1	hypothetical protein G ( 235)	307	73.0	2e-10
gi 160339357 gb ABX12444.1	3-phosphoshikimate 1-c ( 422)	316	75.0	8.9e-11	gi 207102476 emb CAR82015.1	unnamed protein produ ( 418)	310	73.8	2.1e-10
gi 142836951 gb EDA95298.1	hypothetical protein G ( 184)	311	73.8	8.9e-11	gi 28851495 gb AAO54572.1	3-phosphoshikimate 1-ca ( 418)	310	73.8	2.1e-10
gi 138324259 gb EBY97937.1	hypothetical protein G ( 218)	312	74.1	9e-11	gi 117648206 gb ABK52308.1	3-phosphoshikimate 1-c ( 423)	310	73.8	2.1e-10
gi 137533283 gb EBU60530.1	hypothetical protein G ( 162)	310	73.6	9.2e-11	gi 142545689 gb ECY85744.1	hypothetical protein G ( 188)	305	72.6	2.2e-10
gi 145689056 gb ABP89562.1	5-enolpyruvylshikimate ( 101)	307	72.9	9.5e-11	gi 137813443 gb EBW14469.1	hypothetical protein G ( 191)	305	72.6	2.2e-10
gi 140659905 gb ECM62959.1	hypothetical protein G ( 124)	308	73.1	9.8e-11	gi 137272029 gb EBT16745.1	hypothetical protein G ( 162)	304	72.3	2.2e-10
gi 141116592 gb ECP74054.1	hypothetical protein G ( 147)	309	73.4	9.8e-11	gi 134457901 gb EBB46412.1	hypothetical protein G ( 201)	305	72.6	2.3e-10
gi 137996781 gb EBX18771.1	hypothetical protein G ( 210)	311	73.8	1e-10	gi 218301285 emb CAU98633.1	unnamed protein produ ( 412)	309	73.6	2.4e-10
gi 134917544 gb EBE28661.1	hypothetical protein G ( 180)	310	73.6	1e-10	gi 207102482 emb CAR82021.1	unnamed protein produ ( 418)	309	73.6	2.4e-10
gi 117576133 emb CAL68901.1	unnamed protein produ ( 419)	315	74.8	1e-10	gi 63254850 gb AAY35946.1	3-phosphoshikimate 1-ca ( 418)	309	73.6	2.4e-10
gi 135491966 gb EBH99301.1	hypothetical protein G ( 112)	307	72.9	1e-10	gi 221722512 gb ACM25668.1	3-phosphoshikimate 1-c ( 418)	309	73.6	2.4e-10
gi 259027640 gb ACV91084.1	5-enolpyruvylshikimate ( 427)	315	74.8	1e-10	gi 207102488 emb CAR82024.1	unnamed protein produ ( 418)	309	73.6	2.4e-10
gi 121052443 emb CAM08779.1	5-enolpyruvylshikima ( 433)	315	74.8	1.1e-10	gi 226184786 dbj BAH32890.1	3-phosphoshikimate 1- ( 437)	309	73.6	2.5e-10
gi 140082999 gb ECJ42830.1	hypothetical protein G ( 191)	310	73.6	1.1e-10	gi 142078992 gb ECV41483.1	hypothetical protein G ( 439)	309	73.6	2.5e-10
gi 135594207 gb EBI64500.1	hypothetical protein G ( 99)	306	72.7	1.1e-10	gi 138151161 gb EBY03576.1	hypothetical protein G ( 118)	301	71.7	2.6e-10
gi 143355421 gb EDS52319.1	hypothetical protein G ( 448)	315	74.8	1.1e-10	gi 143081824 gb EDC68127.1	hypothetical protein G ( 196)	304	72.4	2.6e-10
gi 184212201 gb EDU09244.1	putative 3-phosphoshik ( 448)	315	74.8	1.1e-10	gi 139814833 gb ECH65564.1	hypothetical protein G ( 196)	304	72.4	2.6e-10
gi 137658590 gb EBV29424.1	hypothetical protein G ( 101)	306	72.7	1.1e-10	gi 137819489 gb EBW18017.1	hypothetical protein G ( 170)	303	72.1	2.6e-10
gi 143437003 gb EDE94972.1	hypothetical protein G ( 635)	317	75.3	1.1e-10	gi 140182535 gb ECX08289.1	hypothetical protein G ( 148)	302	71.9	2.7e-10
gi 141725760 gb ECS96726.1	hypothetical protein G ( 144)	308	73.2	1.1e-10	gi 138014336 gb EBX28033.1	hypothetical protein G ( 294)	306	72.9	2.8e-10
gi 134753000 gb EBD20520.1	hypothetical protein G ( 180)	309	73.4	1.2e-10	gi 117576139 emb CAL68904.1	unnamed protein produ ( 419)	308	73.4	2.8e-10
gi 239679342 gb ACS07592.1	Sequence 5 from patent ( 419)	314	74.6	1.2e-10	gi 239679348 gb ACS07598.1	Sequence 17 from paten ( 419)	308	73.4	2.8e-10
gi 117576141 emb CAL68905.1	unnamed protein produ ( 419)	314	74.6	1.2e-10	gi 136360811 gb EBN64427.1	hypothetical protein G ( 131)	301	71.7	2.8e-10
gi 117576127 emb CAL68898.1	unnamed protein produ ( 419)	314	74.6	1.2e-10	gi 229362102 emb CAY49004.1	putative 3-phosphoshi ( 425)	308	73.4	2.8e-10
gi 239679349 gb ACS07599.1	Sequence 19 from paten ( 419)	314	74.6	1.2e-10	gi 186464230 gb ACC80031.1	3-phosphoshikimate 1-c ( 426)	308	73.4	2.8e-10
gi 141920457 gb ECU17551.1	hypothetical protein G ( 221)	310	73.7	1.2e-10	gi 118765287 dbj BAF39466.1	3-phosphoshikimate 1- ( 450)	308	73.4	3e-10
gi 261392307 emb CAX49833.1	3-phosphoshikimate 1- ( 433)	314	74.6	1.2e-10	gi 138697010 gb ECB38164.1	hypothetical protein G ( 208)	303	72.2	3.1e-10
gi 138733009 gb ECB63288.1	hypothetical protein G ( 135)	307	72.9	1.2e-10	gi 209571213 emb CAR82026.1	unnamed protein produ ( 412)	307	73.1	3.2e-10
gi 141515914 gb ECS12618.1	hypothetical protein G ( 194)	309	73.4	1.2e-10	gi 209571209 emb CAR82019.1	unnamed protein produ ( 412)	307	73.1	3.2e-10
gi 135882330 gb EBK45024.1	hypothetical protein G ( 201)	309	73.4	1.3e-10	gi 169157002 emb CAQ02172.1	3-phosphoshikimate 1- ( 487)	308	73.4	3.2e-10
gi 169653664 gb EDS86357.1	putative 3-phosphoshik ( 469)	314	74.6	1.3e-10	gi 134676963 gb EBC76457.1	hypothetical protein G ( 179)	302	71.9	3.2e-10
gi 143243535 gb EDD84840.1	hypothetical protein G ( 177)	308	73.2	1.3e-10	gi 209571211 emb CAR82025.1	unnamed protein produ ( 444)	307	73.2	3.4e-10
gi 138052107 gb EBX47852.1	hypothetical protein G ( 130)	306	72.7	1.4e-10	gi 135603657 gb EBI70337.1	hypothetical protein G ( 197)	302	72.0	3.5e-10
gi 137453946 gb EBU19127.1	hypothetical protein G ( 182)	308	73.2	1.4e-10	gi 143277548 gb EDE08112.1	hypothetical protein G ( 149)	300	71.5	3.6e-10
gi 141182843 gb ECQ20365.1	hypothetical protein G ( 134)	306	72.7	1.4e-10	gi 136066746 gb EBL68557.1	hypothetical protein G ( 177)	301	71.7	3.6e-10
gi 109626980 emb CAJ53455.1	3-phosphoshikimate 1- ( 432)	313	74.4	1.4e-10	gi 141993398 gb ECU68756.1	hypothetical protein G ( 178)	301	71.7	3.7e-10
gi 138717870 gb ECB52618.1	hypothetical protein G ( 311)	311	73.9	1.4e-10	gi 135811094 gb EBY99204.1	hypothetical protein G ( 153)	300	71.5	3.7e-10
gi 509519401 gb AAT89641.1	3-phosphoshikimate 1-ca ( 436)	313	74.4	1.4e-10	gi 136291221 gb EBN17255.1	hypothetical protein G ( 181)	301	71.7	3.7e-10
gi 140269326 gb ECK68180.1	hypothetical protein G ( 123)	305	72.5	1.5e-10	gi 144119343 gb EDJ00333.1	hypothetical protein G ( 133)	299	71.3	3.8e-10
gi 161595853 gb ABX73513.1	5-enolpyruvylshikimat ( 399)	312	74.2	1.5e-10	gi 226512689 gb EEH62034.1	3-phosphoshikimate 1-c ( 433)	306	73.0	3.8e-10
gi 71556208 gb AAZ35419.1	3-phosphoshikimate 1-ca ( 418)	312	74.2	1.6e-10	gi 268624509 gb EEZ56909.1	3-phosphoshikimate 1-c ( 433)	306	73.0	3.8e-10
gi 207102484 emb CAR82022.1	unnamed protein produ ( 418)	312	74.2	1.6e-10	gi 256559915 gb ACU85762.1	3-phosphoshikimate 1-c ( 441)	306	73.0	3.9e-10
gi 137751638 gb EBV80445.1	hypothetical protein G ( 131)	305	72.5	1.6e-10	gi 138737167 gb ECB66241.1	hypothetical protein G ( 206)	301	71.8	4.2e-10
gi 137485375 gb EBU35622.1	hypothetical protein G ( 102)	303	72.0	1.7e-10	gi 134471594 gb EBB54403.1	hypothetical protein G ( 209)	301	71.8	4.2e-10
gi 136050609 gb EBL57707.1	hypothetical protein G ( 389)	311	74.0	1.7e-10	gi 167293329 gb ABZ46193.1	Sequence 20131 from pa ( 411)	305	72.7	4.2e-10
gi 140226600 gb ECK38548.1	hypothetical protein G ( 236)	308	73.2	1.7e-10	gi 139521188 gb ECP64171.1	hypothetical protein G ( 155)	299	71.3	4.3e-10
gi 134385480 gb EBB05348.1	hypothetical protein G ( 107)	303	72.1	1.8e-10	gi 268550754 gb EEZ45773.1	3-phosphoshikimate 1-c ( 433)	305	72.7	4.4e-10



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gi 7226672 gb AAF41793.1  3-phosphoshikimate 1-car ( 433)	305	72.7	4.4e-10	gi 141778677 gb ECT24444.1  hypothetical protein G ( 147)	291	69.6	1.3e-09
gi 268622298 gb EEZ54698.1  3-phosphoshikimate 1-c ( 433)	305	72.7	4.4e-10	gi 147830428 emb CAN01363.1  3-phosphoshikimate 1- ( 487)	298	71.3	1.3e-09
gi 268585344 gb EEZ50020.1  3-phosphoshikimate 1-c ( 433)	305	72.7	4.4e-10	gi 141399981 gb ECR56140.1  hypothetical protein G ( 182)	292	69.9	1.4e-09
gi 268587665 gb EEZ52341.1  3-phosphoshikimate 1-c ( 433)	305	72.7	4.4e-10	gi 137016683 gb EBR73704.1  hypothetical protein G ( 99)	288	68.9	1.4e-09
gi 268548093 gb EEZ43511.1  3-phosphoshikimate 1-c ( 433)	305	72.7	4.4e-10	gi 140604009 gb ECM35577.1  hypothetical protein G ( 194)	292	69.9	1.4e-09
gi 136405337 gb EBN95052.1  hypothetical protein G ( 97)	296	70.6	4.5e-10	gi 141952739 gb ECU40371.1  hypothetical protein G ( 171)	291	69.7	1.5e-09
gi 141594961 gb ECS50891.1  hypothetical protein G ( 194)	300	71.5	4.6e-10	gi 138587156 gb ECA62809.1  hypothetical protein G ( 181)	291	69.7	1.6e-09
gi 138262361 gb EBY65197.1  hypothetical protein G ( 166)	299	71.3	4.6e-10	gi 116699210 gb ABK18398.1  3-phosphoshikimate 1-c ( 423)	296	70.9	1.6e-09
gi 137396650 gb EBT86710.1  hypothetical protein G ( 129)	297	70.8	4.9e-10	gi 56179475 gb AAV82197.1  5-enolpyruvylshikimate- ( 429)	296	70.9	1.6e-09
gi 135849858 gb EBK23583.1  hypothetical protein G ( 95)	295	70.4	5.1e-10	gi 120866826 emb CAM10584.1  5-enolpyruvylshikima ( 433)	296	70.9	1.6e-09
gi 151359694 gb ABS02697.1  3-phosphoshikimate 1-c ( 449)	304	72.5	5.3e-10	gi 193933758 gb ACF29582.1  3-phosphoshikimate 1-c ( 433)	296	70.9	1.6e-09
gi 139642795 gb ECG46466.1  hypothetical protein G ( 199)	299	71.3	5.4e-10	gi 59718193 gb AAW89598.1  putative 5-enolpyruvyl ( 433)	296	70.9	1.6e-09
gi 138011315 gb EBX26442.1  hypothetical protein G ( 174)	298	71.1	5.5e-10	gi 136634439 gb EBP41578.1  hypothetical protein G ( 136)	289	69.2	1.6e-09
gi 135680289 gb EBJ17747.1  hypothetical protein G ( 126)	296	70.6	5.6e-10	gi 139832401 gb ECH77500.1  hypothetical protein G ( 289)	293	70.2	1.8e-09
gi 135898933 gb EBK56669.1  hypothetical protein G ( 181)	298	71.1	5.7e-10	gi 139968913 gb ECI71100.1  hypothetical protein G ( 132)	288	69.0	1.8e-09
gi 136430441 gb EBO11415.1  hypothetical protein G ( 256)	300	71.6	5.8e-10	gi 137394998 gb EBT85728.1  hypothetical protein G ( 159)	289	69.2	1.9e-09
gi 247545418 gb ACT02437.1  3-phosphoshikimate 1-c ( 430)	303	72.3	5.9e-10	gi 141325309 gb ECR05885.1  hypothetical protein G ( 97)	286	68.5	1.9e-09
gi 254672959 emb CBA07392.1  3-phosphoshikimate 1- ( 433)	303	72.3	5.9e-10	gi 135833976 gb EBK13589.1  hypothetical protein G ( 143)	288	69.0	2e-09
gi 254668754 emb CBA06624.1  3-phosphoshikimate 1- ( 433)	303	72.3	5.9e-10	gi 141393186 gb ECR51348.1  hypothetical protein G ( 103)	286	68.5	2e-09
gi 137446725 gb EBU15001.1  hypothetical protein G ( 115)	295	70.4	6e-10	gi 142712954 gb EDF03778.1  hypothetical protein G ( 170)	289	69.2	2e-09
gi 207102486 emb CAR82023.1  unnamed protein produ ( 444)	303	72.3	6.1e-10	gi 139552759 gb ECF85571.1  hypothetical protein G ( 178)	289	69.2	2.1e-09
gi 120400573 gb ABM21481.1  5'-enolpyruvylshikimat ( 444)	303	72.3	6.1e-10	gi 141711640 gb ECS87995.1  hypothetical protein G ( 184)	289	69.2	2.1e-09
gi 157272154 gb ABY26712.1  5-enolpyruvylshikimate ( 444)	303	72.3	6.1e-10	gi 136634441 gb EBP41580.1  hypothetical protein G ( 132)	287	68.8	2.1e-09
gi 141787258 gb ECT28985.1  hypothetical protein G ( 140)	296	70.7	6.1e-10	gi 142319596 gb ECX22834.1  hypothetical protein G ( 133)	287	68.8	2.1e-09
gi 138502658 gb ECA05423.1  hypothetical protein G ( 152)	296	70.7	6.6e-10	gi 161161889 emb CAN93194.1  3-phosphoshikimate 1- ( 428)	294	70.5	2.1e-09
gi 268582986 gb EEZ47662.1  3-phosphoshikimate 1-c ( 433)	302	72.1	6.8e-10	gi 134397597 gb EBB11730.1  hypothetical protein G ( 186)	289	69.3	2.1e-09
gi 268626765 gb EEZ59165.1  3-phosphoshikimate 1-c ( 433)	302	72.1	6.8e-10	gi 135714631 gb EBJ38978.1  hypothetical protein G ( 115)	286	68.5	2.2e-09
gi 134977338 gb EBE68641.1  hypothetical protein G ( 114)	294	70.2	6.8e-10	gi 139936889 gb ECT49196.1  hypothetical protein G ( 192)	289	69.3	2.2e-09
gi 134136777 gb ABO57891.1  3-phosphoshikimate 1-c ( 460)	302	72.1	7.2e-10	gi 136580598 gb EBP07978.1  hypothetical protein G ( 329)	292	70.0	2.3e-09
gi 134357023 gb EBA86222.1  hypothetical protein G ( 126)	294	70.2	7.5e-10	gi 138381148 gb EBZ27658.1  hypothetical protein G ( 103)	285	68.3	2.3e-09
gi 197710309 gb EDY54343.1  3-phosphoshikimate 1-c ( 415)	301	71.9	7.6e-10	gi 136931619 gb EBR25604.1  hypothetical protein G ( 203)	289	69.3	2.3e-09
gi 143023313 gb EDC25299.1  hypothetical protein G ( 131)	294	70.2	7.7e-10	gi 140795452 gb ECN56325.1  hypothetical protein G ( 172)	288	69.0	2.3e-09
gi 142130241 gb ECV81111.1  hypothetical protein G ( 133)	294	70.2	7.8e-10	gi 142053474 gb ECV20051.1  hypothetical protein G ( 362)	292	70.0	2.5e-09
gi 254670251 emb CBA05487.1  3-phosphoshikimate 1- ( 433)	301	71.9	7.9e-10	gi 137380099 gb EBT77156.1  hypothetical protein G ( 246)	289	69.3	2.7e-09
gi 139859200 gb ECH96267.1  hypothetical protein G ( 195)	296	70.7	8.2e-10	gi 141038491 gb ECP20912.1  hypothetical protein G ( 180)	287	68.8	2.8e-09
gi 139968357 gb ECI70702.1  hypothetical protein G ( 201)	296	70.7	8.4e-10	gi 136715732 gb EBP93040.1  hypothetical protein G ( 417)	292	70.0	2.8e-09
gi 116256981 gb ABJ90663.1  3-phosphoshikimate 1-c ( 435)	300	71.7	9.2e-10	gi 141831272 gb ECT55097.1  hypothetical protein G ( 190)	287	68.8	2.9e-09
gi 142419593 gb ECX93837.1  hypothetical protein G ( 420)	299	71.5	1e-09	gi 139417854 gb ECE97583.1  hypothetical protein G ( 137)	285	68.4	2.9e-09
gi 141235823 gb ECQ56307.1  hypothetical protein G ( 131)	292	69.8	1e-09	gi 138274369 gb EBY73568.1  hypothetical protein G ( 192)	287	68.8	2.9e-09
gi 139934981 gb ECI47821.1  hypothetical protein G ( 184)	294	70.3	1e-09	gi 138621767 gb ECA86898.1  hypothetical protein G ( 193)	287	68.8	3e-09
gi 139449963 gb ECF18170.1  hypothetical protein G ( 194)	294	70.3	1.1e-09	gi 136508745 gb EB062095.1  hypothetical protein G ( 195)	287	68.8	3e-09
gi 508779900 emb CAG37740.1  related to 3-phosphosh ( 451)	299	71.5	1.1e-09	gi 135327870 gb EBG89709.1  hypothetical protein G ( 196)	287	68.8	3e-09
gi 270259768 emb CBI38901.1  unnamed protein produ ( 463)	299	71.5	1.1e-09	gi 3893083 emb CAA10164.1  5-enolpyruvylshikimate ( 332)	290	69.6	3.1e-09
gi 141805848 gb ECT37496.1  hypothetical protein G ( 174)	293	70.1	1.1e-09	gi 136829493 gb EBG68498.1  hypothetical protein G ( 307)	289	69.4	3.3e-09
gi 138461383 gb EBZ83526.1  hypothetical protein G ( 178)	293	70.1	1.2e-09	gi 170231 gb AAA34072.1  5-enolpyruvylshikimate-3- ( 338)	289	69.4	3.6e-09
gi 139740652 gb ECH14977.1  hypothetical protein G ( 183)	293	70.1	1.2e-09	gi 143203778 gb EDD56578.1  hypothetical protein G ( 89)	281	67.4	3.6e-09
gi 220000157 gb ACL76758.1  3-phosphoshikimate 1-c ( 422)	298	71.3	1.2e-09	gi 141668834 gb ECS71793.1  hypothetical protein G ( 150)	284	68.2	3.7e-09
gi 136414763 gb EBO01321.1  hypothetical protein G ( 423)	298	71.3	1.2e-09	gi 140448493 gb ECL82608.1  hypothetical protein G ( 109)	282	67.7	3.7e-09
gi 257170988 gb ACV48747.1  3-phosphoshikimate 1-c ( 430)	298	71.3	1.2e-09	gi 141342655 gb ECR16143.1  hypothetical protein G ( 187)	285	68.4	3.8e-09
gi 259420526 emb CBF57577.1  unnamed protein produ ( 447)	298	71.3	1.3e-09	gi 139214786 gb ECL19726.1  hypothetical protein G ( 310)	288	69.1	3.9e-09
gi 218301277 emb CAU98625.1  unnamed protein produ ( 447)	298	71.3	1.3e-09	gi 142629045 gb ECZ44103.1  hypothetical protein G ( 188)	285	68.4	3.9e-09

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gi 141309322 gb ECQ97031.1	hypothetical protein G ( 190)	285	68.4	3.9e-09	gi 254257728 emb CAZ91473.1	unnamed protein produ ( 436)	283	68.2	1.1e-08
gi 119955588 gb ABM12593.1	3-phosphoshikimate 1-c ( 446)	290	69.6	4e-09	gi 158064938 emb CAP11431.1	unnamed protein produ ( 436)	283	68.2	1.1e-08
gi 141771908 gb ECT20846.1	hypothetical protein G ( 118)	282	67.7	4e-09	gi 136149188 gb EBM21932.1	hypothetical protein G ( 313)	281	67.7	1.1e-08
gi 142537102 gb ECY79515.1	hypothetical protein G ( 165)	284	68.2	4e-09	gi 256356896 gb ACU70393.1	UDP-N-acetylglucosamin ( 450)	283	68.2	1.1e-08
gi 140904031 gb ECO28501.1	hypothetical protein G ( 174)	284	68.2	4.2e-09	gi 137322029 gb EBT44686.1	hypothetical protein G ( 178)	277	66.7	1.2e-08
gi 137287625 gb EBT25443.1	hypothetical protein G ( 179)	284	68.2	4.3e-09	gi 146407374 gb ABQ35880.1	3-phosphoshikimate 1-c ( 418)	282	68.0	1.2e-08
gi 218760993 gb ACL03459.1	3-phosphoshikimate 1-c ( 419)	289	69.4	4.3e-09	gi 261370679 gb ACX73428.1	3-phosphoshikimate 1-c ( 426)	282	68.0	1.2e-08
gi 221734706 gb ACM35669.1	3-phosphoshikimate 1-c ( 423)	289	69.4	4.4e-09	gi 141714720 gb ECS89901.1	hypothetical protein G ( 186)	277	66.8	1.2e-08
gi 138333549 gb EBZ02341.1	hypothetical protein G ( 184)	284	68.2	4.4e-09	gi 167727088 emb CAP13874.1	3-phosphoshikimate 1- ( 430)	282	68.0	1.2e-08
gi 136109563 gb EBL97675.1	hypothetical protein G ( 158)	283	68.0	4.4e-09	gi 137504641 gb EBU45451.1	hypothetical protein G ( 188)	277	66.8	1.2e-08
gi 261282220 gb ACX64191.1	3-phosphoshikimate 1-c ( 430)	289	69.4	4.4e-09	gi 54018070 dbj BAD59440.1	putative 5-enolpyruvyl ( 437)	282	68.0	1.2e-08
gi 144179424 gb EDJ44599.1	hypothetical protein G ( 236)	285	68.5	4.7e-09	gi 137129293 gb EBS36687.1	hypothetical protein G ( 225)	278	67.0	1.2e-08
gi 3410961 dbj BAA32276.1	3-phosphoshikimate 1-ca ( 391)	288	69.2	4.7e-09	gi 167291814 gb ABZ44678.1	Sequence 18616 from pa ( 439)	282	68.0	1.2e-08
gi 138211244 gb EBY44003.1	hypothetical protein G ( 126)	281	67.5	4.9e-09	gi 10580760 gb AAG19594.1	3-phosphoshikimate 1-ca ( 439)	282	68.0	1.2e-08
gi 134641468 gb EBC55730.1	hypothetical protein G ( 128)	281	67.5	4.9e-09	gi 197053758 gb ACH25456.1	Sequence 8 from patent ( 439)	282	68.0	1.2e-08
gi 138316610 gb EBY93784.1	hypothetical protein G ( 154)	282	67.8	5e-09	gi 46448291 gb AAS94946.1	3-phosphoshikimate 1-ca ( 439)	282	68.0	1.2e-08
gi 218444766 gb EEG72779.1	3-phosphoshikimate 1-c ( 430)	288	69.2	5.1e-09	gi 140867415 gb ECO04516.1	hypothetical protein G ( 165)	276	66.5	1.3e-08
gi 143911526 gb EDH51939.1	hypothetical protein G ( 366)	287	69.0	5.1e-09	gi 143304386 gb EDE21860.1	hypothetical protein G ( 416)	281	67.7	1.4e-08
gi 135193457 gb EBG09189.1	hypothetical protein G ( 195)	283	68.0	5.3e-09	gi 167043753 gb ABZ08445.1	putative EPSP synthase ( 422)	281	67.8	1.4e-08
gi 134857212 gb EBD88436.1	hypothetical protein G ( 166)	282	67.8	5.3e-09	gi 137062259 gb EBR99387.1	hypothetical protein G ( 190)	276	66.6	1.4e-08
gi 136863779 gb EBQ91435.1	hypothetical protein G ( 124)	280	67.3	5.5e-09	gi 226244298 dbj BAH54646.1	3-phosphoshikimate 1- ( 438)	281	67.8	1.4e-08
gi 141711572 gb ECS87954.1	hypothetical protein G ( 181)	282	67.8	5.7e-09	gi 140677546 gb ECM75558.1	hypothetical protein G ( 117)	273	65.8	1.4e-08
gi 262193245 gb ACY30625.1	EPSP synthase [Ginkgo ( 353)	286	68.8	5.7e-09	gi 29606692 dbj BAC70753.1	putative 3-phosphoshik ( 446)	281	67.8	1.4e-08
gi 139026901 gb ECC89959.1	hypothetical protein G ( 131)	280	67.3	5.8e-09	gi 141347116 gb ECR19224.1	hypothetical protein G ( 100)	272	65.6	1.5e-08
gi 32397219 emb CAD72526.1	3-phosphoshikimate 1-c ( 501)	288	69.2	5.8e-09	gi 135601197 gb EBI68833.1	hypothetical protein G ( 195)	276	66.6	1.5e-08
gi 262086810 gb ACY22778.1	3-phosphoshikimate 1-c ( 421)	286	68.8	6.7e-09	gi 142307382 gb ECL13686.1	hypothetical protein G ( 167)	275	66.3	1.5e-08
gi 141103300 gb ECP64812.1	hypothetical protein G ( 132)	279	67.1	6.7e-09	gi 137781568 gb EBV96306.1	hypothetical protein G ( 289)	278	67.1	1.5e-08
gi 138859647 gb ECC18477.1	hypothetical protein G ( 188)	281	67.6	6.9e-09	gi 141055410 gb ECP32712.1	hypothetical protein G ( 177)	275	66.3	1.5e-08
gi 136894582 gb EBR09947.1	hypothetical protein G ( 161)	280	67.4	6.9e-09	gi 143120588 gb EDC96439.1	hypothetical protein G ( 178)	275	66.3	1.6e-08
gi 145217759 gb ABP47163.1	3-phosphoshikimate 1-c ( 446)	286	68.8	7e-09	gi 2826287 gb AAB98493.1	3-phosphoshikimate-1-car ( 429)	280	67.5	1.6e-08
gi 137439612 gb EBU10974.1	hypothetical protein G ( 194)	281	67.6	7e-09	gi 167294666 gb ABZ47530.1	Sequence 21468 from pa ( 429)	280	67.5	1.6e-08
gi 218602333 emb CAV32035.1	unnamed protein produ ( 413)	285	68.6	7.6e-09	gi 197053759 gb ACH25457.1	Sequence 9 from patent ( 429)	280	67.5	1.6e-08
gi 254257746 emb CAZ91482.1	unnamed protein produ ( 413)	285	68.6	7.6e-09	gi 136997668 gb EBR62935.1	hypothetical protein G ( 189)	275	66.3	1.6e-08
gi 158064957 emb CAP11440.1	unnamed protein produ ( 413)	285	68.6	7.6e-09	gi 136122790 gb EBM06705.1	hypothetical protein G ( 163)	274	66.1	1.7e-08
gi 137613393 gb EBV05490.1	hypothetical protein G ( 110)	277	66.7	7.7e-09	gi 137991869 gb EBX16769.1	hypothetical protein G ( 167)	274	66.1	1.7e-08
gi 135246787 gb EBG40574.1	hypothetical protein G ( 396)	284	68.4	8.5e-09	gi 139557235 gb ECF88762.1	hypothetical protein G ( 120)	272	65.6	1.7e-08
gi 138115862 gb EBX83138.1	hypothetical protein G ( 205)	280	67.4	8.5e-09	gi 140878388 gb ECO12060.1	hypothetical protein G ( 171)	274	66.1	1.7e-08
gi 141718967 gb ECS92519.1	hypothetical protein G ( 177)	279	67.2	8.7e-09	gi 134993483 gb EBE79617.1	hypothetical protein G ( 174)	274	66.1	1.8e-08
gi 138705585 gb ECB44304.1	hypothetical protein G ( 183)	279	67.2	8.9e-09	gi 23492616 dbj BAC17589.1	5-enolpyruvylshikimate ( 408)	279	67.3	1.8e-08
gi 139308621 gb ECE49455.1	hypothetical protein G ( 185)	279	67.2	9e-09	gi 143421907 gb EDE86867.1	hypothetical protein G ( 252)	276	66.6	1.8e-08
gi 139600607 gb ECG18735.1	hypothetical protein G ( 115)	276	66.5	9.2e-09	gi 139742666 gb ECL16215.1	hypothetical protein G ( 130)	272	65.6	1.8e-08
gi 120563746 gb ABM29490.1	3-phosphoshikimate 1-c ( 439)	284	68.4	9.3e-09	gi 140266570 gb ECK66195.1	hypothetical protein G ( 223)	275	66.4	1.9e-08
gi 256586404 gb ACU97537.1	3-phosphoshikimate 1-c ( 444)	284	68.4	9.3e-09	gi 8163275 gb AAF73581.1	3-phosphoshikimate 1-car ( 441)	279	67.3	1.9e-08
gi 140340030 gb ECL09713.1	hypothetical protein G ( 151)	277	66.7	1e-08	gi 143286973 gb EDE12890.1	hypothetical protein G ( 330)	277	66.9	2e-08
gi 135862908 gb EBK31807.1	hypothetical protein G ( 181)	278	67.0	1e-08	gi 134403526 gb EBB15016.1	hypothetical protein G ( 171)	273	65.9	2e-08
gi 135775967 gb EBJ77004.1	hypothetical protein G ( 181)	278	67.0	1e-08	gi 141281733 gb ECQ86790.1	hypothetical protein G ( 239)	275	66.4	2e-08
gi 135076564 gb EBF34204.1	hypothetical protein G ( 215)	279	67.2	1e-08	gi 218602347 emb CAV32047.1	unnamed protein produ ( 413)	278	67.1	2.1e-08
gi 73660021 emb CAI82628.1	3-phosphoshikimate 1-c ( 420)	283	68.2	1e-08	gi 218602343 emb CAV32045.1	unnamed protein produ ( 413)	278	67.1	2.1e-08
gi 146270033 gb ABQ17025.1	3-phosphoshikimate 1-c ( 420)	283	68.2	1e-08	gi 142965654 gb EDB84756.1	hypothetical protein G ( 134)	271	65.4	2.2e-08
gi 138212148 gb EBY44623.1	hypothetical protein G ( 131)	276	66.5	1e-08	gi 269096620 gb ACZ221056.1	UDP-N-acetylglucosamin ( 438)	278	67.1	2.2e-08
gi 183174668 gb ACC39778.1	3-phosphoshikimate 1-c ( 431)	283	68.2	1.1e-08	gi 110822831 gb ABG98115.1	3-phosphoshikimate 1-c ( 438)	278	67.1	2.2e-08

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gi 140795343 gb ECN56244.1	hypothetical protein G ( 162)	272	65.7	2.2e-08	gi 158064949 emb CAP11436.1	unnamed protein produ ( 413)	273	66.1	4.3e-08
gi 135937496 gb EBK83135.1	hypothetical protein G ( 169)	272	65.7	2.3e-08	gi 254257738 emb CAZ91478.1	unnamed protein produ ( 413)	273	66.1	4.3e-08
gi 137598092 gb EBU96799.1	hypothetical protein G ( 88)	268	64.7	2.3e-08	gi 158064965 emb CAP11444.1	unnamed protein produ ( 413)	273	66.1	4.3e-08
gi 139983349 gb ECI81241.1	hypothetical protein G ( 284)	275	66.4	2.3e-08	gi 218602325 emb CAV32028.1	unnamed protein produ ( 413)	273	66.1	4.3e-08
gi 140962513 gb ECO69651.1	hypothetical protein G ( 127)	270	65.2	2.4e-08	gi 158064963 emb CAP11443.1	unnamed protein produ ( 413)	273	66.1	4.3e-08
gi 218602331 emb CAV32033.1	unnamed protein produ ( 413)	277	66.9	2.4e-08	gi 218602341 emb CAV32044.1	unnamed protein produ ( 413)	273	66.1	4.3e-08
gi 158064955 emb CAP11439.1	unnamed protein produ ( 413)	277	66.9	2.4e-08	gi 254257754 emb CAZ91486.1	unnamed protein produ ( 413)	273	66.1	4.3e-08
gi 254257744 emb CAZ91481.1	unnamed protein produ ( 413)	277	66.9	2.4e-08	gi 218602321 emb CAV32026.1	unnamed protein produ ( 413)	273	66.1	4.3e-08
gi 144221934 gb EDJ75270.1	hypothetical protein G ( 415)	277	66.9	2.4e-08	gi 254257752 emb CAZ91485.1	unnamed protein produ ( 413)	273	66.1	4.3e-08
gi 139916023 gb ECI34592.1	hypothetical protein G ( 133)	270	65.2	2.5e-08	gi 138393082 gb EBZ35835.1	hypothetical protein G ( 183)	268	64.9	4.4e-08
gi 552297801 gb AAV45199.1	3-phosphoshikimate 1-ca ( 429)	277	66.9	2.5e-08	gi 139715640 gb ECG97590.1	hypothetical protein G ( 94)	264	63.9	4.4e-08
gi 260078369 gb EEW60674.1	3-phosphoshikimate 1-c ( 135)	270	65.2	2.5e-08	gi 141443969 gb ECR86984.1	hypothetical protein G ( 137)	266	64.4	4.5e-08
gi 134563127 gb EBC08803.1	hypothetical protein G ( 99)	268	64.8	2.6e-08	gi 222136865 gb ACM45082.1	5-enolpyruvylshikimate ( 317)	271	65.6	4.5e-08
gi 140607098 gb ECM36324.1	hypothetical protein G ( 232)	273	66.0	2.6e-08	gi 136937780 gb EBR29049.1	hypothetical protein G ( 169)	267	64.7	4.7e-08
gi 88783188 gb EAR14361.1	3-phosphoshikimate 1-ca ( 409)	276	66.7	2.8e-08	gi 139801494 gb ECH56019.1	hypothetical protein G ( 172)	267	64.7	4.8e-08
gi 254257740 emb CAZ91479.1	unnamed protein produ ( 413)	276	66.7	2.8e-08	gi 143840587 gb EDH00849.1	hypothetical protein G ( 90)	263	63.7	4.9e-08
gi 218602349 emb CAV32048.1	unnamed protein produ ( 413)	276	66.7	2.8e-08	gi 139765372 gb ECH30618.1	hypothetical protein G ( 126)	265	64.2	4.9e-08
gi 218602327 emb CAV32029.1	unnamed protein produ ( 413)	276	66.7	2.8e-08	gi 143754925 gb EDG61826.1	hypothetical protein G ( 177)	267	64.7	4.9e-08
gi 158064943 emb CAP11433.1	unnamed protein produ ( 413)	276	66.7	2.8e-08	gi 143715076 gb EDG41631.1	hypothetical protein G ( 150)	266	64.4	4.9e-08
gi 254257742 emb CAZ91480.1	unnamed protein produ ( 413)	276	66.7	2.8e-08	gi 137599818 gb EBU97767.1	hypothetical protein G ( 78)	262	63.5	5e-08
gi 218602319 emb CAV32025.1	unnamed protein produ ( 413)	276	66.7	2.8e-08	gi 138181735 gb EBY25008.1	hypothetical protein G ( 180)	267	64.7	5e-08
gi 254257732 emb CAZ91475.1	unnamed protein produ ( 413)	276	66.7	2.8e-08	gi 135654046 gb EBU01552.1	hypothetical protein G ( 187)	267	64.7	5.1e-08
gi 158064953 emb CAP11438.1	unnamed protein produ ( 413)	276	66.7	2.8e-08	gi 41398263 gb AAS05884.1	AroA [Mycobacterium avi ( 435)	272	65.9	5.2e-08
gi 218602329 emb CAV32031.1	unnamed protein produ ( 413)	276	66.7	2.8e-08	gi 135117332 gb EBF60283.1	hypothetical protein G ( 86)	262	63.5	5.4e-08
gi 158064951 emb CAP11437.1	unnamed protein produ ( 413)	276	66.7	2.8e-08	gi 135805402 gb EBJ95639.1	hypothetical protein G ( 168)	266	64.5	5.4e-08
gi 193083953 gb ACF09630.1	3-phosphoshikimate 1-c ( 426)	276	66.7	2.9e-08	gi 164454856 dbj BAF96973.1	putative 5-enolpyruvyl ( 122)	264	64.0	5.5e-08
gi 143138581 gb EDD09640.1	hypothetical protein G ( 84)	266	64.3	3e-08	gi 139675536 gb ECG69534.1	hypothetical protein G ( 92)	262	63.5	5.7e-08
gi 134557848 gb EBC05598.1	hypothetical protein G ( 407)	275	66.5	3.2e-08	gi 57225151 gb AAW40208.1	3-phosphoshikimate 1-ca ( 420)	271	65.7	5.8e-08
gi 134423121 gb EBB26248.1	hypothetical protein G ( 182)	270	65.3	3.3e-08	gi 139349149 gb ECE58652.1	hypothetical protein G ( 136)	264	64.0	6e-08
gi 139189020 gb ECE01933.1	hypothetical protein G ( 182)	270	65.3	3.3e-08	gi 139602942 gb ECG20278.1	hypothetical protein G ( 266)	268	65.0	6e-08
gi 110620656 emb CAJ35934.1	putative 3-phosphoshi ( 422)	275	66.5	3.3e-08	gi 138589959 gb ECA64753.1	hypothetical protein G ( 273)	268	65.0	6.2e-08
gi 256690345 gb ACV10682.1	3-phosphoshikimate 1-c ( 428)	275	66.5	3.3e-08	gi 27651558 emb CAD36891.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 141573503 gb ECS42617.1	hypothetical protein G ( 114)	267	64.6	3.3e-08	gi 27651530 emb CAD36877.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 118171644 gb ABK72540.1	3-phosphoshikimate 1-c ( 443)	275	66.5	3.4e-08	gi 27651514 emb CAD36869.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 261373400 gb ACX76145.1	EPSP synthase (3-phosp ( 455)	275	66.5	3.5e-08	gi 27651568 emb CAD36896.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 164454854 dbj BAF96972.1	putative 5-enolpyruvyl ( 122)	267	64.6	3.5e-08	gi 27651544 emb CAD36884.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 219860009 gb ACL40351.1	3-phosphoshikimate 1-c ( 475)	275	66.5	3.6e-08	gi 27651548 emb CAD36886.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 158064959 emb CAP11441.1	unnamed protein produ ( 413)	274	66.3	3.7e-08	gi 27651536 emb CAD36880.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 254257748 emb CAZ91483.1	unnamed protein produ ( 413)	274	66.3	3.7e-08	gi 27651564 emb CAD36894.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 218602335 emb CAV32038.1	unnamed protein produ ( 413)	274	66.3	3.7e-08	gi 27651534 emb CAD36879.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 114337300 gb ABT68148.1	UDP-N-acetylglucosamin ( 416)	274	66.3	3.7e-08	gi 27651542 emb CAD36883.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 178464619 dbj BAG19139.1	putative 5-enolpyruvyl ( 450)	274	66.3	4e-08	gi 27651532 emb CAD36878.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 145751285 gb ABP96766.1	putative 5-enolpyruvyl ( 122)	266	64.4	4.1e-08	gi 27651538 emb CAD36881.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 27651526 emb CAD36875.1	putative 5-enolpyruvyl ( 122)	266	64.4	4.1e-08	gi 27651528 emb CAD36876.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 134322213 gb EBA63460.1	hypothetical protein G ( 283)	271	65.6	4.1e-08	gi 27651546 emb CAD36885.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 144012227 gb EDI23678.1	hypothetical protein G ( 173)	268	64.9	4.1e-08	gi 27651570 emb CAD36897.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 254257734 emb CAZ91476.1	unnamed protein produ ( 413)	273	66.1	4.3e-08	gi 145751141 gb ABP96759.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 158064945 emb CAP11434.1	unnamed protein produ ( 413)	273	66.1	4.3e-08	gi 27651506 emb CAD36865.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 254257730 emb CAZ91474.1	unnamed protein produ ( 413)	273	66.1	4.3e-08	gi 27651522 emb CAD36873.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 218602339 emb CAV32043.1	unnamed protein produ ( 413)	273	66.1	4.3e-08	gi 145750944 gb ABP96750.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08
gi 158064940 emb CAP11432.1	unnamed protein produ ( 413)	273	66.1	4.3e-08	gi 164454852 dbj BAF96971.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08

gi 27651524 emb CAD36874.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08	gi 27651502 emb CAD36863.1	putative 5-enolpyruvyl ( 122)	259	62.9	1.1e-07
gi 27651508 emb CAD36866.1	putative 5-enolpyruvyl ( 122)	263	63.8	6.3e-08	gi 27651540 emb CAD36882.1	putative 5-enolpyruvyl ( 122)	259	62.9	1.1e-07
gi 167044926 gb ABZ09592.1	putative EPSP synthase ( 394)	270	65.5	6.3e-08	gi 27651512 emb CAD36868.1	putative 5-enolpyruvyl ( 122)	259	62.9	1.1e-07
gi 134554900 gb EBC03811.1	hypothetical protein G ( 173)	265	64.2	6.4e-08	gi 142748549 gb EDA29468.1	hypothetical protein G ( 238)	263	63.9	1.1e-07
gi 256793860 gb ACV24529.1	3-phosphoshikimate 1-c ( 427)	270	65.5	6.8e-08	gi 136501410 gb EBO57343.1	hypothetical protein G ( 287)	264	64.1	1.1e-07
gi 269096461 gb ACZ20897.1	3-phosphoshikimate 1-c ( 448)	270	65.5	7.1e-08	gi 142081421 gb ECV43511.1	hypothetical protein G ( 106)	258	62.7	1.1e-07
gi 136187309 gb EBM46881.1	hypothetical protein G ( 279)	267	64.8	7.2e-08	gi 136076477 gb EBL75135.1	hypothetical protein G ( 149)	260	63.2	1.2e-07
gi 145750758 gb ABP96741.1	putative 5-enolpyruvyl ( 122)	262	63.6	7.3e-08	gi 143380471 gb EDE67259.1	hypothetical protein G ( 212)	262	63.7	1.2e-07
gi 27651498 emb CAD36861.1	putative 5-enolpyruvyl ( 122)	262	63.6	7.3e-08	gi 136649531 gb EBP50530.1	hypothetical protein G ( 110)	258	62.7	1.2e-07
gi 27651510 emb CAD36867.1	putative 5-enolpyruvyl ( 122)	262	63.6	7.3e-08	gi 110673799 gb ABG82786.1	3-phosphoshikimate 1-c ( 424)	266	64.6	1.2e-07
gi 27651494 emb CAD36948.1	putative 5-enolpyruvyl ( 122)	262	63.6	7.3e-08	gi 197053755 gb ACH25453.1	Sequence 5 from patent ( 428)	266	64.6	1.2e-07
gi 62948560 gb AAY22964.1	putative 5-enolpyruvyls ( 122)	262	63.6	7.3e-08	gi 15023793 gb AAK78871.1	AE007605_4 5-enolpyruvyl ( 428)	266	64.6	1.2e-07
gi 76577727 gb ABA54134.1	putative 5-enolpyruvyls ( 122)	262	63.6	7.3e-08	gi 188499339 gb ACD52475.1	3-phosphoshikimate 1-c ( 433)	266	64.6	1.2e-07
gi 27651552 emb CAD36888.1	putative 5-enolpyruvyl ( 122)	262	63.6	7.3e-08	gi 136661055 gb EBP57371.1	hypothetical protein G ( 102)	257	62.5	1.3e-07
gi 155369179 dbj BAF75638.1	putative 5-enolpyruvyl ( 122)	262	63.6	7.3e-08	gi 140161022 gb ECJ93154.1	hypothetical protein G ( 171)	260	63.2	1.3e-07
gi 145751418 gb ABP96773.1	putative 5-enolpyruvyl ( 122)	262	63.6	7.3e-08	gi 153999656 gb ABS56079.1	3-phosphoshikimate 1-c ( 421)	265	64.4	1.4e-07
gi 27651562 emb CAD36893.1	putative 5-enolpyruvyl ( 122)	262	63.6	7.3e-08	gi 139710378 gb ECC93826.1	hypothetical protein G ( 131)	258	62.7	1.4e-07
gi 27651554 emb CAD36889.1	putative 5-enolpyruvyl ( 122)	262	63.6	7.3e-08	gi 197053756 gb ACH25454.1	Sequence 6 from patent ( 424)	265	64.4	1.4e-07
gi 137383382 gb EBT79041.1	hypothetical protein G ( 151)	263	63.8	7.6e-08	gi 181443551 dbj BAB80402.1	3-phosphoshikimate 1-c ( 424)	265	64.4	1.4e-07
gi 254257750 emb CAZ91484.1	unnamed protein produ ( 413)	269	65.3	7.6e-08	gi 137626582 gb EBV13018.1	hypothetical protein G ( 188)	260	63.2	1.4e-07
gi 218602337 emb CAV32040.1	unnamed protein produ ( 413)	269	65.3	7.6e-08	gi 135307869 gb EBG76462.1	hypothetical protein G ( 167)	259	63.0	1.5e-07
gi 158064961 emb CAP11442.1	unnamed protein produ ( 413)	269	65.3	7.6e-08	gi 27651560 emb CAD36892.1	putative 5-enolpyruvyl ( 122)	257	62.5	1.5e-07
gi 270153723 gb ACZ61561.1	3-phosphoshikimate 1-c ( 420)	269	65.3	7.7e-08	gi 27651518 emb CAD36871.1	putative 5-enolpyruvyl ( 122)	257	62.5	1.5e-07
gi 238876015 gb ACR75722.1	3-phosphoshikimate 1-c ( 427)	269	65.3	7.8e-08	gi 136265415 gb EBM99606.1	hypothetical protein G ( 129)	257	62.5	1.6e-07
gi 143832006 gb EDG94622.1	hypothetical protein G ( 162)	263	63.8	8.1e-08	gi 143352053 gb EDE50399.1	hypothetical protein G ( 300)	262	63.7	1.6e-07
gi 135286490 gb EBG63923.1	hypothetical protein G ( 164)	263	63.8	8.1e-08	gi 140653357 gb ECM58430.1	hypothetical protein G ( 304)	262	63.7	1.6e-07
gi 139901711 gb ECI24311.1	hypothetical protein G ( 118)	261	63.3	8.2e-08	gi 137897728 gb EBW63033.1	hypothetical protein G ( 112)	256	62.3	1.6e-07
gi 27651520 emb CAD36872.1	putative 5-enolpyruvyl ( 122)	261	63.3	8.4e-08	gi 5104222 dbj BAA79537.1	3-phosphoshikimate 1-ca ( 427)	264	64.2	1.6e-07
gi 140482317 gb ECL96815.1	hypothetical protein G ( 171)	263	63.8	8.4e-08	gi 167296048 gb ABZ48912.1	Sequence 22850 from pa ( 427)	264	64.2	1.6e-07
gi 218602323 emb CAV32027.1	unnamed protein produ ( 413)	268	65.0	8.8e-08	gi 197053753 gb ACH25451.1	Sequence 3 from patent ( 427)	264	64.2	1.6e-07
gi 254257736 emb CAZ91477.1	unnamed protein produ ( 413)	268	65.0	8.8e-08	gi 13883144 gb AAK47667.1	3-phosphoshikimate 1-ca ( 450)	264	64.2	1.7e-07
gi 158064947 emb CAP11435.1	unnamed protein produ ( 413)	268	65.0	8.8e-08	gi 2072694 emb CAB08328.1	3-PHOSPHOSHIKIMATE 1-CA ( 450)	264	64.2	1.7e-07
gi 137240909 gb EBS99122.1	hypothetical protein G ( 111)	260	63.1	9e-08	gi 1061198 emb CAA36510.1	unnamed protein product ( 450)	264	64.2	1.7e-07
gi 135097052 gb EBF47290.1	hypothetical protein G ( 367)	267	64.8	9.2e-08	gi 148722956 gb ABR07581.1	3-phosphoshikimate 1-c ( 450)	264	64.2	1.7e-07
gi 137289947 gb EBT26741.1	hypothetical protein G ( 121)	260	63.1	9.6e-08	gi 253321772 gb ACT26375.1	3-phosphoshikimate 1-c ( 450)	264	64.2	1.7e-07
gi 27651496 emb CAD36949.1	putative 5-enolpyruvyl ( 122)	260	63.1	9.7e-08	gi 121494765 emb CAL73246.1	3-phosphoshikimate 1- ( 450)	264	64.2	1.7e-07
gi 208968957 dbj BAG74299.1	putative 5-enolpyruvyl ( 122)	260	63.1	9.7e-08	gi 224774724 dbj BAH27530.1	3-phosphoshikimate 1- ( 450)	264	64.2	1.7e-07
gi 27651550 emb CAD36887.1	putative 5-enolpyruvyl ( 122)	260	63.1	9.7e-08	gi 148507242 gb ABQ75051.1	3-phosphoshikimate 1-c ( 450)	264	64.2	1.7e-07
gi 27651500 emb CAD36862.1	putative 5-enolpyruvyl ( 122)	260	63.1	9.7e-08	gi 121494857 emb CAL73339.1	3-phosphoshikimate 1- ( 450)	264	64.2	1.7e-07
gi 27651566 emb CAD36895.1	putative 5-enolpyruvyl ( 122)	260	63.1	9.7e-08	gi 124599370 gb EAY58474.1	3-phosphoshikimate 1-c ( 450)	264	64.2	1.7e-07
gi 134801291 gb EBD52889.1	hypothetical protein G ( 398)	267	64.8	9.8e-08	gi 1499281 gb AAA25356.1	key enzyme from the shiki ( 450)	264	64.2	1.7e-07
gi 140356997 gb ECL21447.1	hypothetical protein G ( 126)	260	63.1	1e-07	gi 141690760 gb ECS82975.1	hypothetical protein G ( 166)	258	62.8	1.7e-07
gi 138607893 gb ECA77389.1	hypothetical protein G ( 127)	260	63.1	1e-07	gi 27651556 emb CAD36890.1	putative 5-enolpyruvyl ( 122)	256	62.3	1.7e-07
gi 137572843 gb EBU82720.1	hypothetical protein G ( 91)	258	62.7	1e-07	gi 229419569 gb EEO34616.1	3-phosphoshikimate 1-c ( 422)	263	64.0	1.8e-07
gi 218602345 emb CAV32046.1	unnamed protein produ ( 413)	267	64.8	1e-07	gi 137063681 gb EBS00190.1	hypothetical protein G ( 112)	255	62.1	1.9e-07
gi 110682538 gb ABG85908.1	3-phosphoshikimate 1-c ( 424)	267	64.8	1e-07	gi 135856457 gb EBK27747.1	hypothetical protein G ( 157)	257	62.6	1.9e-07
gi 118570151 gb ABL04902.1	3-phosphoshikimate 1-c ( 431)	267	64.8	1.1e-07	gi 137691378 gb EBV47987.1	hypothetical protein G ( 135)	256	62.3	1.9e-07
gi 137440713 gb EBU11589.1	hypothetical protein G ( 140)	260	63.2	1.1e-07	gi 135563245 gb EBT44958.1	hypothetical protein G ( 321)	261	63.5	1.9e-07
gi 142613449 gb ECZ33107.1	hypothetical protein G ( 101)	258	62.7	1.1e-07	gi 37359246 gb AAN77867.1	5-enolpyruvylshikimate- ( 330)	261	63.5	2e-07
gi 140222712 gb ECK35845.1	hypothetical protein G ( 169)	261	63.4	1.1e-07	gi 135501503 gb EBT05440.1	hypothetical protein G ( 144)	256	62.3	2e-07
gi 139117331 gb ECD53221.1	hypothetical protein G ( 201)	262	63.7	1.1e-07	gi 137064853 gb EBS00850.1	hypothetical protein G ( 172)	257	62.6	2e-07

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gi 143123363 gb EDC98470.1	hypothetical protein G ( 407)	262	63.8	2.1e-07	gi 139635409 gb ECG41393.1	hypothetical protein G ( 171)	251	61.3	4.8e-07
gi 136331388 gb EBN44372.1	hypothetical protein G ( 264)	259	63.1	2.2e-07	gi 144018831 gb EDI28211.1	hypothetical protein G ( 104)	248	60.6	4.8e-07
gi 138955423 gb ECC57612.1	hypothetical protein G ( 312)	260	63.3	2.2e-07	gi 140108183 gb ECJ59174.1	hypothetical protein G ( 124)	249	60.9	4.8e-07
gi 138588318 gb ECA63615.1	hypothetical protein G ( 170)	256	62.4	2.3e-07	gi 262208075 gb ACY32173.1	3-phosphoshikimate 1-c ( 690)	259	63.3	5e-07
gi 27651504 emb CAD36864.1	putative 5-enolpyruvyl ( 122)	254	61.9	2.3e-07	gi 140449001 gb ECL82971.1	hypothetical protein G ( 154)	250	61.1	5e-07
gi 140006705 gb ECI96016.1	hypothetical protein G ( 180)	256	62.4	2.4e-07	gi 141008389 gb ECP01391.1	hypothetical protein G ( 255)	253	61.8	5e-07
gi 49645101 emb CAG98673.1	KLLA0F19712p [Kluyvero (1578)	269	65.5	2.4e-07	gi 257792900 gb ACV67278.1	5-enolpyruvylshikimate ( 518)	257	62.8	5.2e-07
gi 159887343 gb ABX02280.1	3-phosphoshikimate 1-c ( 429)	261	63.6	2.5e-07	gi 143030018 gb EDC30145.1	hypothetical protein G ( 269)	253	61.8	5.3e-07
gi 140047125 gb ECJ22455.1	hypothetical protein G ( 119)	253	61.7	2.6e-07	gi 141952437 gb ECU40153.1	hypothetical protein G ( 166)	250	61.1	5.4e-07
gi 219690818 gb ACL32041.1	3-phosphoshikimate 1-c ( 385)	260	63.4	2.6e-07	gi 135861318 gb EBK30804.1	hypothetical protein G ( 101)	247	60.4	5.4e-07
gi 141988236 gb ECU65126.1	hypothetical protein G ( 102)	252	61.4	2.6e-07	gi 137238418 gb EBS97769.1	hypothetical protein G ( 172)	250	61.1	5.5e-07
gi 141584608 gb ECS47173.1	hypothetical protein G ( 171)	255	62.2	2.7e-07	gi 141430667 gb ECR77456.1	hypothetical protein G ( 64)	244	59.7	5.6e-07
gi 135293978 gb EBG68304.1	hypothetical protein G ( 397)	260	63.4	2.7e-07	gi 256581891 gb ACU93026.1	3-phosphoshikimate 1-c ( 409)	255	62.3	5.7e-07
gi 136534380 gb EBG78463.1	hypothetical protein G ( 175)	255	62.2	2.7e-07	gi 137391662 gb EBT83813.1	hypothetical protein G ( 108)	247	60.4	5.7e-07
gi 134806237 gb EBD55969.1	hypothetical protein G ( 176)	255	62.2	2.7e-07	gi 110279818 gb ABG58004.1	3-phosphoshikimate 1-c ( 415)	255	62.3	5.7e-07
gi 143336668 gb EDE41053.1	hypothetical protein G ( 252)	257	62.7	2.8e-07	gi 139510525 gb ECF56688.1	hypothetical protein G ( 155)	249	60.9	5.8e-07
gi 150013290 gb ABX55741.1	3-phosphoshikimate 1-c ( 433)	260	63.4	2.9e-07	gi 139853511 gb ECH92492.1	hypothetical protein G ( 184)	250	61.1	5.9e-07
gi 139775605 gb ECH37721.1	hypothetical protein G ( 160)	254	61.9	2.9e-07	gi 89144043 emb CAJ79291.1	3-phosphoshikimate 1-c ( 425)	255	62.3	5.9e-07
gi 137831221 gb EBW24864.1	hypothetical protein G ( 164)	254	62.0	3e-07	gi 115129578 gb ABI82765.1	3-phosphoshikimate 1-c ( 425)	255	62.3	5.9e-07
gi 140133038 gb ECJ76373.1	hypothetical protein G ( 100)	251	61.2	3e-07	gi 134253354 gb EBA52448.1	3-phosphoshikimate 1-c ( 425)	255	62.3	5.9e-07
gi 167273761 gb ABZ26625.1	Sequence 563 from pate ( 462)	260	63.4	3.1e-07	gi 156252874 gb ABU61380.1	3-phosphoshikimate 1-c ( 425)	255	62.3	5.9e-07
gi 6458826 gb AAF10666.1 AE001959_6	3-phosphoshiki ( 462)	260	63.4	3.1e-07	gi 151570774 gb EDN36428.1	3-phosphoshikimate 1-c ( 425)	255	62.3	5.9e-07
gi 138145249 gb EBX99526.1	hypothetical protein G ( 144)	253	61.7	3.1e-07	gi 142647091 gb ECW63816.1	hypothetical protein G ( 117)	247	60.4	6.1e-07
gi 136179936 gb EBM42003.1	hypothetical protein G ( 283)	257	62.7	3.1e-07	gi 137267092 gb EBT13999.1	hypothetical protein G ( 117)	247	60.4	6.1e-07
gi 134811217 gb EBD59044.1	hypothetical protein G ( 470)	260	63.4	3.1e-07	gi 143596894 gb EDF78687.1	hypothetical protein G ( 331)	253	61.9	6.3e-07
gi 138516940 gb ECA13844.1	hypothetical protein G ( 177)	254	62.0	3.2e-07	gi 142239667 gb ECW63816.1	hypothetical protein G ( 172)	249	60.9	6.4e-07
gi 135740077 gb EBJ54747.1	hypothetical protein G ( 182)	254	62.0	3.3e-07	gi 136895041 gb EBR10177.1	hypothetical protein G ( 75)	244	59.7	6.4e-07
gi 138175700 gb EBY20773.1	hypothetical protein G ( 216)	255	62.2	3.3e-07	gi 141074770 gb ECP44839.1	hypothetical protein G ( 150)	248	60.7	6.5e-07
gi 136514553 gb EBQ65808.1	hypothetical protein G ( 111)	251	61.3	3.3e-07	gi 135475905 gb EBH89025.1	hypothetical protein G ( 298)	252	61.7	6.7e-07
gi 125862039 gb ABN57228.1	3-phosphoshikimate 1-c ( 422)	259	63.2	3.3e-07	gi 151572218 gb EDN37872.1	3-phosphoshikimate 1-c ( 425)	254	62.1	6.8e-07
gi 139813738 gb ECH64771.1	hypothetical protein G ( 156)	253	61.7	3.3e-07	gi 118423587 gb ABK89977.1	3-phosphoshikimate 1-c ( 425)	254	62.1	6.8e-07
gi 139864844 gb ECI00209.1	hypothetical protein G ( 265)	256	62.5	3.4e-07	gi 134049878 gb ABO46949.1	3-phosphoshikimate 1-c ( 425)	254	62.1	6.8e-07
gi 257228991 gb ACV53022.1	5-enolpyruvylshikimate ( 518)	260	63.4	3.4e-07	gi 257792898 gb ACV67277.1	5-enolpyruvylshikimate ( 518)	255	62.4	7e-07
gi 136423872 gb EBO07160.1	hypothetical protein G ( 378)	258	62.9	3.4e-07	gi 143429820 gb EDE90925.1	hypothetical protein G ( 165)	248	60.7	7.1e-07
gi 134606507 gb EBC34706.1	hypothetical protein G ( 118)	251	61.3	3.5e-07	gi 141358911 gb ECR27338.1	hypothetical protein G ( 231)	250	61.2	7.1e-07
gi 141081778 gb ECP49687.1	hypothetical protein G ( 102)	250	61.0	3.5e-07	gi 140986024 gb ECO85762.1	hypothetical protein G ( 141)	247	60.5	7.2e-07
gi 135401199 gb EBH38962.1	hypothetical protein G ( 391)	258	63.0	3.5e-07	gi 138433557 gb EBZ64253.1	hypothetical protein G ( 169)	248	60.7	7.3e-07
gi 134563693 gb EBC09142.1	hypothetical protein G ( 284)	256	62.5	3.6e-07	gi 142847470 gb EDB03074.1	hypothetical protein G ( 89)	244	59.8	7.4e-07
gi 138206680 gb EBY40866.1	hypothetical protein G ( 293)	256	62.5	3.7e-07	gi 142029705 gb ECU98902.1	hypothetical protein G ( 107)	245	60.0	7.5e-07
gi 136650521 gb EBP51121.1	hypothetical protein G ( 152)	252	61.5	3.7e-07	gi 157122156 gb EDO66296.1	3-phosphoshikimate 1-c ( 425)	253	61.9	7.8e-07
gi 138088436 gb EBX67931.1	hypothetical protein G ( 93)	249	60.8	3.7e-07	gi 254842865 gb EET21279.1	3-phosphoshikimate 1-c ( 426)	253	61.9	7.8e-07
gi 140638840 gb ECM48477.1	hypothetical protein G ( 134)	251	61.3	3.9e-07	gi 167597744 gb ABZ87742.1	3-phosphoshikimate 1-c ( 426)	253	61.9	7.8e-07
gi 140136930 gb ECJ78639.1	hypothetical protein G ( 82)	248	60.6	3.9e-07	gi 257228989 gb ACV53021.1	5-enolpyruvylshikimate ( 518)	254	62.2	8e-07
gi 94555387 gb ABF45301.1	3-phosphoshikimate 1-ca ( 440)	258	63.0	3.9e-07	gi 189170087 gb ACB80082.1	5-enolpyruvylshikimate ( 520)	254	62.2	8.1e-07
gi 137155531 gb EBS51327.1	hypothetical protein G ( 166)	252	61.5	4e-07	gi 142052471 gb ECV19283.1	hypothetical protein G ( 117)	245	60.0	8.1e-07
gi 27651516 emb CAD36870.1	putative 5-enolpyruvyl ( 122)	250	61.1	4.1e-07	gi 138143615 gb EBX98782.1	hypothetical protein G ( 272)	250	61.2	8.2e-07
gi 118164840 gb ABK65737.1	3-phosphoshikimate 1-c ( 419)	257	62.8	4.3e-07	gi 136951562 gb EBR36833.1	hypothetical protein G ( 85)	243	59.5	8.2e-07
gi 150033408 gb ABR65521.1	3-phosphoshikimate 1-c ( 429)	257	62.8	4.4e-07	gi 135519158 gb EBT16781.1	hypothetical protein G ( 142)	246	60.3	8.3e-07
gi 137153403 gb EBS50130.1	hypothetical protein G ( 97)	248	60.6	4.5e-07	gi 139910522 gb ECI30664.1	hypothetical protein G ( 171)	247	60.5	8.5e-07
gi 141842424 gb ECT63134.1	hypothetical protein G ( 165)	251	61.3	4.6e-07	gi 141936386 gb ECU28820.1	hypothetical protein G ( 105)	244	59.8	8.6e-07
gi 31620004 emb CAD95348.1	3-PHOSPHOSHIKIMATE 1-C ( 450)	257	62.8	4.6e-07	gi 135097282 gb EBF47442.1	hypothetical protein G ( 106)	244	59.8	8.6e-07

gi 239838503 gb ACS30300.1	3-phosphoshikimate 1-c	( 476)	253	62.0	8.6e-07	gi 137262334 gb EBT11318.1	hypothetical protein G	( 99)	240	58.9	1.4e-06
gi 138638232 gb ECA97023.1	hypothetical protein G	( 150)	246	60.3	8.7e-07	gi 143445595 gb EDE99941.1	hypothetical protein G	( 84)	239	58.7	1.5e-06
gi 141196850 gb ECQ28892.1	hypothetical protein G	( 129)	245	60.0	8.8e-07	gi 256579750 gb ACU90886.1	3-phosphoshikimate 1-c	( 448)	249	61.1	1.5e-06
gi 116665787 gb ABK14814.1	3-phosphoshikimate 1-c	( 421)	252	61.7	9e-07	gi 138379540 gb EBZ26536.1	hypothetical protein G	( 118)	241	59.2	1.5e-06
gi 139588193 gb ECG10061.1	hypothetical protein G	( 155)	246	60.3	9e-07	gi 141006545 gb ECP00155.1	hypothetical protein G	( 280)	246	60.4	1.5e-06
gi 254840528 gb EET18964.1	3-phosphoshikimate 1-c	( 425)	252	61.7	9e-07	gi 141867175 gb ECT80548.1	hypothetical protein G	( 107)	240	59.0	1.5e-06
gi 151568465 gb EDN34119.1	hypothetical protein F	( 425)	252	61.7	9e-07	gi 134557324 gb EBC05284.1	hypothetical protein G	( 212)	244	59.9	1.6e-06
gi 110320519 emb CAL08604.1	3-phosphoshikimate 1-	( 425)	252	61.7	9e-07	gi 142394073 gb ECX74727.1	hypothetical protein G	( 153)	242	59.4	1.6e-06
gi 56604207 emb CAG45221.1	3-phosphoshikimate 1-c	( 425)	252	61.7	9e-07	gi 142143769 gb ECV91152.1	hypothetical protein G	( 132)	241	59.2	1.6e-06
gi 132663055 gb ABO34701.1	3-phosphoshikimate 1-c	( 429)	252	61.7	9.1e-07	gi 187723900 gb ACD25121.1	3-phosphoshikimate 1-c	( 433)	248	60.9	1.6e-06
gi 138209136 gb EBY42538.1	hypothetical protein G	( 160)	246	60.3	9.2e-07	gi 143676556 gb EDG21358.1	hypothetical protein G	( 443)	248	60.9	1.7e-06
gi 170783792 gb ACB37380.1	5-enolpyruvylshikimate	( 520)	253	62.0	9.3e-07	gi 140342741 gb ECL11664.1	hypothetical protein G	( 193)	243	59.7	1.7e-06
gi 193230774 gb ACF16410.1	5-enolpyruvylshikimate	( 521)	253	62.0	9.3e-07	gi 140213869 gb ECK30436.1	hypothetical protein G	( 100)	239	58.7	1.7e-06
gi 164564335 gb EBY61050.1	5-enolpyruvylshikimate	( 521)	253	62.0	9.3e-07	gi 218757794 gb ACL08693.1	3-phosphoshikimate 1-c	( 450)	248	60.9	1.7e-06
gi 15113313 gb AAE68897.1	Sequence 4 from patent	( 446)	252	61.7	9.4e-07	gi 139588191 gb ECG10059.1	hypothetical protein G	( 169)	242	59.5	1.7e-06
gi 226317774 gb ACO45770.1	putative 3-phosphoshik	( 446)	252	61.7	9.4e-07	gi 213504186 emb CAS92804.1	unnamed protein produ	( 461)	248	60.9	1.7e-06
gi 139526428 gb ECF67652.1	hypothetical protein G	( 165)	246	60.3	9.5e-07	gi 137313236 gb EBT39796.1	hypothetical protein G	( 148)	241	59.2	1.8e-06
gi 137707930 gb EBV57186.1	hypothetical protein G	( 72)	241	59.1	9.5e-07	gi 142092265 gb ECV52480.1	hypothetical protein G	( 149)	241	59.2	1.8e-06
gi 134453802 gb EBB43977.1	hypothetical protein G	( 119)	244	59.8	9.5e-07	gi 137181885 gb EBS66113.1	hypothetical protein G	( 151)	241	59.2	1.8e-06
gi 139774290 gb ECH36760.1	hypothetical protein G	( 120)	244	59.8	9.6e-07	gi 394748 emb CAA51291.1	3-phosphoshikimate 1-car	( 92)	238	58.5	1.8e-06
gi 218301283 emb CAU98630.1	unnamed protein produ	( 463)	252	61.7	9.7e-07	gi 475972 gb AAA17839.1	pentafunctional enzyme [P	(1581)	255	62.6	1.8e-06
gi 218301280 emb CAU98627.1	unnamed protein produ	( 468)	252	61.7	9.8e-07	gi 170775096 gb ACB33235.1	3-phosphoshikimate 1-c	( 699)	250	61.4	1.9e-06
gi 138636289 gb ECA95687.1	hypothetical protein G	( 150)	245	60.1	1e-06	gi 146346304 gb EDK32840.1	AroA [Clostridium klyu	( 426)	247	60.7	1.9e-06
gi 139975788 gb ECI75973.1	hypothetical protein G	( 210)	247	60.5	1e-06	gi 219567771 dbj BAH05755.1	hypothetical protein	( 426)	247	60.7	1.9e-06
gi 140359360 gb ECL23139.1	hypothetical protein G	( 111)	243	59.6	1e-06	gi 45047634 emb CAF30761.1	3-phosphoshikimate-1-c	( 429)	247	60.7	1.9e-06
gi 58416522 emb CAI27635.1	3-phosphoshikimate 1-c	( 427)	251	61.5	1e-06	gi 136246949 gb EBM87035.1	hypothetical protein G	( 115)	239	58.8	1.9e-06
gi 142291970 gb ECX02262.1	hypothetical protein G	( 116)	243	59.6	1.1e-06	gi 139022251 gb ECC86765.1	hypothetical protein G	( 161)	241	59.2	1.9e-06
gi 136354624 gb EBN60202.1	hypothetical protein G	( 99)	242	59.4	1.1e-06	gi 187712349 gb ACD30646.1	3-phosphoshikimate 1-c	( 425)	246	60.5	2.1e-06
gi 141063525 gb ECP37936.1	hypothetical protein G	( 319)	249	61.0	1.1e-06	gi 76782198 gb ABA54869.1	putative 5-enolpyruvyls	( 520)	247	60.7	2.2e-06
gi 63334331 gb AAY40472.1	5-enol-pyruvylshikimate	( 447)	251	61.5	1.1e-06	gi 48526086 gb AAT45244.1	5-enol-pyruvylshikimate	( 523)	247	60.7	2.2e-06
gi 167283499 gb ABZ36363.1	Sequence 10301 from pa	( 392)	250	61.3	1.1e-06	gi 140786127 gb ECN49774.1	hypothetical protein G	( 166)	240	59.0	2.3e-06
gi 138705584 gb ECB44303.1	hypothetical protein G	( 172)	245	60.1	1.1e-06	gi 144157096 gb EDJ28064.1	hypothetical protein G	( 460)	246	60.5	2.3e-06
gi 219867914 gb ACL48249.1	3-phosphoshikimate 1-c	( 484)	251	61.5	1.2e-06	gi 141358868 gb ECR27311.1	hypothetical protein G	( 146)	239	58.8	2.3e-06
gi 237907951 gb EEP82352.1	pentafunctional AROM p	(1580)	258	63.2	1.2e-06	gi 140365320 gb ECL27383.1	hypothetical protein G	( 107)	237	58.3	2.4e-06
gi 139761003 gb ECH27597.1	hypothetical protein G	( 154)	244	59.9	1.2e-06	gi 137034169 gb EBR83523.1	hypothetical protein G	( 127)	238	58.6	2.4e-06
gi 135666238 gb EBJ09113.1	hypothetical protein G	( 157)	244	59.9	1.2e-06	gi 167294770 gb ABZ47634.1	Sequence 21572 from pa	( 410)	245	60.3	2.4e-06
gi 143922947 gb EDH60152.1	hypothetical protein G	( 96)	241	59.1	1.2e-06	gi 5457888 emb CAB49378.1	aroA 3-phosphoshikimate	( 410)	245	60.3	2.4e-06
gi 137776675 gb EBV93594.1	hypothetical protein G	( 264)	247	60.6	1.2e-06	gi 142798898 gb EDA66645.1	hypothetical protein G	( 179)	240	59.1	2.4e-06
gi 2485248 gb AAB73384.1	I44473 Sequence 53 from p	( 444)	250	61.3	1.3e-06	gi 139597835 gb ECG16899.1	hypothetical protein G	( 157)	239	58.8	2.5e-06
gi 5957571 gb AAE08245.1	Sequence 53 from patent	( 444)	250	61.3	1.3e-06	gi 138386372 gb EBZ31255.1	hypothetical protein G	( 222)	241	59.3	2.5e-06
gi 2484171 gb AAB72307.1	I49200 Sequence 53 from p	( 444)	250	61.3	1.3e-06	gi 137956336 gb EBW96154.1	hypothetical protein G	( 142)	238	58.6	2.6e-06
gi 144974750 gb ABP12461.1	Sequence 53 from paten	( 444)	250	61.3	1.3e-06	gi 139225737 gb ECE27527.1	hypothetical protein G	( 299)	242	59.6	2.8e-06
gi 63334354 gb AAY40473.1	5-enol-pyruvylshikimate	( 447)	250	61.3	1.3e-06	gi 50840349 gb AAT83016.1	3-phosphoshikimate 1-ca	( 429)	244	60.1	2.9e-06
gi 140055797 gb ECJ27025.1	hypothetical protein G	( 90)	240	58.9	1.3e-06	gi 141003111 gb ECO97872.1	hypothetical protein G	( 138)	237	58.4	3e-06
gi 145689058 gb ABP89564.1	5-enolpyruvylshikimate	( 151)	243	59.7	1.4e-06	gi 137645515 gb EBV22535.1	hypothetical protein G	( 99)	235	57.9	3e-06
gi 197068384 gb ACH29559.1	Sequence 178 from pate	( 129)	242	59.4	1.4e-06	gi 63334403 gb AAY40475.1	5-enol-pyruvylshikimate	( 446)	244	60.1	3e-06
gi 136491500 gb EBO50896.1	hypothetical protein G	( 299)	247	60.6	1.4e-06	gi 136844649 gb EBQ78580.1	hypothetical protein G	( 165)	238	58.6	3e-06
gi 170229 gb AAA34071.1	5-enolpyruvylshikimate-3-	( 518)	250	61.3	1.4e-06	gi 142194442 gb ECW29770.1	hypothetical protein G	( 339)	242	59.6	3.1e-06
gi 157142998 gb ABV24481.1	5-enolpyruvylshikimate	( 521)	250	61.3	1.4e-06	gi 140436263 gb ECL73891.1	hypothetical protein G	( 287)	241	59.4	3.1e-06
gi 116054912 emb CAL56989.1	5-enolpyruvylshikimat	( 316)	247	60.6	1.4e-06	gi 140728122 gb ECN10699.1	hypothetical protein G	( 90)	234	57.7	3.2e-06
gi 281079464 gb ADA36172.1	Sequence 5 from patent	( 525)	250	61.4	1.4e-06	gi 157805890 gb EDO83060.1	3-phosphoshikimate 1-c	( 435)	243	59.9	3.4e-06

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gi 126220435 gb ABN83941.1  3-phosphoshikimate 1-c ( 435)	243	59.9	3.4e-06	gi 170374 gb AAA34136.1  5-enolpyruvylshikimate-3- ( 520)	241	59.5	5.2e-06
gi 169653402 gb EDS86095.1  3-phosphoshikimate 1-c ( 435)	243	59.9	3.4e-06	gi 136810426 gb EBQ55796.1  hypothetical protein G ( 142)	233	57.6	5.4e-06
gi 237505533 gb ACQ97851.1  3-phosphoshikimate 1-c ( 435)	243	59.9	3.4e-06	gi 134923875 gb EBE32883.1  hypothetical protein G ( 103)	231	57.1	5.5e-06
gi 157935341 gb EDO91011.1  3-phosphoshikimate 1-c ( 435)	243	59.9	3.4e-06	gi 139483444 gb ECF39330.1  hypothetical protein G ( 104)	231	57.1	5.5e-06
gi 126226989 gb ABN90529.1  3-phosphoshikimate 1-c ( 435)	243	59.9	3.4e-06	gi 137771645 gb EBV90851.1  hypothetical protein G ( 246)	236	58.3	5.7e-06
gi 242139779 gb EES26181.1  3-phosphoshikimate 1-c ( 435)	243	59.9	3.4e-06	gi 13375567 gb AAK20397.1 AF349754_1 5-enolpyruvyl ( 347)	238	58.8	5.7e-06
gi 141920103 gb ECU17301.1  hypothetical protein G ( 162)	237	58.4	3.4e-06	gi 135696355 gb EBJ27660.1  hypothetical protein G ( 151)	233	57.6	5.7e-06
gi 15113311 gb AAE68895.1  Sequence 2 from patent ( 444)	243	59.9	3.4e-06	gi 143619097 gb EDF89452.1  hypothetical protein G ( 350)	238	58.8	5.7e-06
gi 63334366 gb AAQ40474.1  5-enol-pyruvylshikimate ( 446)	243	59.9	3.4e-06	gi 140710291 gb ECM98191.1  hypothetical protein G ( 152)	233	57.6	5.7e-06
gi 143084014 gb EDC69721.1  hypothetical protein G ( 165)	237	58.4	3.5e-06	gi 143289772 gb EDE14254.1  hypothetical protein G ( 415)	239	59.0	5.8e-06
gi 137626704 gb EBV13083.1  hypothetical protein G ( 166)	237	58.4	3.5e-06	gi 135670534 gb EBJ11760.1  hypothetical protein G ( 111)	231	57.1	5.8e-06
gi 77862401 gb ABBO4469.1  5-enolpyruvylshikimate ( 235)	239	58.9	3.5e-06	gi 138345236 gb EBZ10124.1  hypothetical protein G ( 155)	233	57.6	5.8e-06
gi 141562291 gb ECS38975.1  hypothetical protein G ( 122)	235	57.9	3.6e-06	gi 135418683 gb EBH50720.1  hypothetical protein G ( 425)	239	59.0	5.9e-06
gi 139813737 gb ECH64770.1  hypothetical protein G ( 175)	237	58.4	3.6e-06	gi 194344913 gb EDX25879.1  UDP-N-acetylglucosamin ( 509)	240	59.3	5.9e-06
gi 135591171 gb EBI62617.1  hypothetical protein G ( 176)	237	58.4	3.7e-06	gi 134268433 gb ABO68628.1  UDP-N-acetylglucosamin ( 434)	239	59.0	6e-06
gi 178464133 dbj BAG18653.1  putative 5-enolpyruvyl ( 415)	242	59.6	3.7e-06	gi 144061091 gb ED158614.1  hypothetical protein G ( 72)	228	56.4	6.2e-06
gi 141309321 gb ECQ97030.1  hypothetical protein G ( 153)	236	58.2	3.7e-06	gi 139178037 gb ECF94123.1  hypothetical protein G ( 274)	236	58.3	6.2e-06
gi 135648868 gb EBI98362.1  hypothetical protein G ( 133)	235	58.0	3.8e-06	gi 167324427 gb ABZ61020.1  Sequence 11819 from pa ( 392)	238	58.8	6.3e-06
gi 139756385 gb ECH24426.1  hypothetical protein G ( 187)	237	58.4	3.9e-06	gi 140103800 gb ECJ56094.1  hypothetical protein G ( 147)	232	57.4	6.4e-06
gi 142178523 gb ECW17637.1  hypothetical protein G ( 87)	232	57.3	4.1e-06	gi 57117457 gb AAW33954.1  AROM pentafunctional en (1539)	246	60.7	6.5e-06
gi 134899027 gb EBE16415.1  hypothetical protein G ( 170)	236	58.2	4.1e-06	gi 238032531 emb CAY70554.1  Pentafunctional arom (1545)	246	60.7	6.5e-06
gi 143836029 gb EDG97541.1  hypothetical protein G ( 173)	236	58.2	4.2e-06	gi 143131822 gb EDD04677.1  hypothetical protein G ( 408)	238	58.8	6.6e-06
gi 57158522 dbj BAD84452.1  5-enolpyruvylshikimate ( 399)	241	59.4	4.2e-06	gi 223643106 emb CX41980.1  pentafunctional AROM (1550)	246	60.7	6.6e-06
gi 134840320 gb EBD77599.1  hypothetical protein G ( 147)	235	58.0	4.2e-06	gi 134661181 gb EBC67295.1  hypothetical protein G ( 210)	234	57.8	6.6e-06
gi 139920800 gb ECI37946.1  hypothetical protein G ( 174)	236	58.2	4.2e-06	gi 124417311 emb CAK82326.1  unnamed protein produ (1118)	244	60.3	6.6e-06
gi 85821331 gb EAQ42478.1  3-phosphoshikimate 1-ca ( 409)	241	59.4	4.3e-06	gi 137677308 gb EBV40060.1  hypothetical protein G ( 112)	230	56.9	6.8e-06
gi 218093860 emb CAT71432.1  unnamed protein produ ( 415)	241	59.4	4.3e-06	gi 140455535 gb ECL87542.1  hypothetical protein G ( 259)	235	58.1	6.8e-06
gi 161726851 emb CAP47296.1  unnamed protein produ ( 424)	241	59.4	4.4e-06	gi 184212267 gb EDU09310.1  3-phosphoshikimate 1-c ( 435)	238	58.8	6.9e-06
gi 19714500 gb AAL95129.1  3-phosphoshikimate 1-ca ( 424)	241	59.4	4.4e-06	gi 55740769 gb AAV64030.1  5-enolpyruvylshikimate ( 519)	239	59.1	7e-06
gi 197053757 gb ACH25455.1  Sequence 7 from patent ( 424)	241	59.4	4.4e-06	gi 134675150 gb EBC75402.1  hypothetical protein G ( 83)	228	56.4	7e-06
gi 137935241 gb EBW84278.1  hypothetical protein G ( 260)	238	58.7	4.4e-06	gi 2485250 gb AAB73386.1 I44475 Sequence 55 from p ( 444)	238	58.8	7.1e-06
gi 229468460 gb ACQ70232.1  UDP-N-acetylglucosamin ( 433)	241	59.4	4.5e-06	gi 144974752 gb ABP12463.1  Sequence 55 from paten ( 444)	238	58.8	7.1e-06
gi 139453944 gb ECF21005.1  hypothetical protein G ( 97)	232	57.3	4.5e-06	gi 2484173 gb AAB72309.1 I49202 Sequence 55 from p ( 444)	238	58.8	7.1e-06
gi 16751567 gb AAL27697.1  5-enolpyruvylshikimate- ( 516)	242	59.7	4.5e-06	gi 15113310 gb AAE68894.1  Sequence 1 from patent ( 444)	238	58.8	7.1e-06
gi 2484172 gb AAB72308.1 I49201 Sequence 54 from p ( 444)	241	59.4	4.6e-06	gi 5957573 gb AAE08247.1  Sequence 55 from patent ( 444)	238	58.8	7.1e-06
gi 144974751 gb ABP12462.1  Sequence 54 from paten ( 444)	241	59.4	4.6e-06	gi 135805587 gb EBJ95757.1  hypothetical protein G ( 102)	229	56.7	7.2e-06
gi 2485249 gb AAB73385.1 I44474 Sequence 54 from p ( 444)	241	59.4	4.6e-06	gi 141550051 gb ECS30458.1  hypothetical protein G ( 144)	231	57.1	7.3e-06
gi 5957572 gb AAE08246.1  Sequence 54 from patent ( 444)	241	59.4	4.6e-06	gi 139559348 gb ECF90296.1  hypothetical protein G ( 105)	229	56.7	7.4e-06
gi 141894557 gb ECT99515.1  hypothetical protein G ( 140)	234	57.8	4.6e-06	gi 138456986 gb EBZ80350.1  hypothetical protein G ( 174)	232	57.4	7.5e-06
gi 136243804 gb EBM84904.1  hypothetical protein G ( 85)	231	57.0	4.6e-06	gi 140465850 gb ECL91459.1  hypothetical protein G ( 302)	235	58.1	7.8e-06
gi 134846736 gb EBD81731.1  hypothetical protein G ( 275)	238	58.7	4.7e-06	gi 2485258 gb AAB73394.1 I44483 Sequence 63 from p ( 426)	237	58.6	7.9e-06
gi 48526088 gb AAT45245.1  5-enol-pyruvylshikimate ( 454)	241	59.5	4.7e-06	gi 141872 gb AAA21937.1  3-phosphoshikimate-1-carb ( 426)	237	58.6	7.9e-06
gi 143575554 gb EDF71579.1  hypothetical protein G ( 145)	234	57.8	4.8e-06	gi 144974760 gb ABP12471.1  Sequence 63 from paten ( 426)	237	58.6	7.9e-06
gi 141074771 gb ECP44840.1  hypothetical protein G ( 147)	234	57.8	4.8e-06	gi 2484181 gb AAB72317.1 I49210 Sequence 63 from p ( 426)	237	58.6	7.9e-06
gi 135039257 gb EBF10408.1  hypothetical protein G ( 342)	239	59.0	4.9e-06	gi 5957581 gb AAE08255.1  Sequence 63 from patent ( 426)	237	58.6	7.9e-06
gi 139575354 gb ECG01163.1  hypothetical protein G ( 245)	237	58.5	4.9e-06	gi 12541842 emb CAC25305.1  unnamed protein produc ( 430)	237	58.6	7.9e-06
gi 140431938 gb ECL70931.1  hypothetical protein G ( 295)	238	58.7	5e-06	gi 41324987 emb CAF19468.1  3-PHOSPHOSHIKIMATE 1-C ( 430)	237	58.6	7.9e-06
gi 141040121 gb ECP22036.1  hypothetical protein G ( 213)	236	58.3	5e-06	gi 217229978 gb ACK11087.1  Sequence 412 from pate ( 430)	237	58.6	7.9e-06
gi 137839327 gb EBW29556.1  hypothetical protein G ( 110)	232	57.3	5e-06	gi 140844847 dbj BAF53846.1  hypothetical protein ( 430)	237	58.6	7.9e-06
gi 138377687 gb EBZ25278.1  hypothetical protein G ( 154)	234	57.8	5e-06	gi 21323530 dbj BAB98157.1  5-enolpyruvylshikimate ( 430)	237	58.6	7.9e-06
gi 140029257 gb ECJ11191.1  hypothetical protein G ( 98)	231	57.1	5.2e-06	gi 169191 gb AAA33699.1  5-enolpyruvylshikimate-3- ( 516)	238	58.9	8e-06

gi 62786941 gb AA06820.1	Sequence 27 from patent	( 516)	238	58.9	8e-06	gi 121228841 gb ABM51359.1	putative 3-phosphoshik	( 435)	234	58.0	1.2e-05
gi 6732247 emb CAB69241.1	unnamed protein product	( 516)	238	58.9	8e-06	gi 147745265 gb EDK52345.1	3-phosphoshikimate 1-c	( 435)	234	58.0	1.2e-05
gi 223548872 gb EEF50361.1	3-phosphoshikimate 1-c	( 518)	238	58.9	8.1e-06	gi 148029459 gb EDK87364.1	3-phosphoshikimate 1-c	( 435)	234	58.0	1.2e-05
gi 48526084 gb AAT45243.1	5-enol-pyruvylshikimate	( 519)	238	58.9	8.1e-06	gi 147750605 gb EDK57674.1	3-phosphoshikimate 1-c	( 435)	234	58.0	1.2e-05
gi 139820928 gb ECH69483.1	hypothetical protein G	( 116)	229	56.7	8.1e-06	gi 50951139 gb AAT88840.1	UDP-N-acetylglucosamine	( 456)	234	58.0	1.3e-05
gi 135710441 gb EBJ36390.1	hypothetical protein G	( 116)	229	56.7	8.1e-06	gi 142229932 gb ECW56578.1	hypothetical protein G	( 144)	227	56.3	1.3e-05
gi 135107136 gb EBF53752.1	hypothetical protein G	( 441)	237	58.6	8.1e-06	gi 142028895 gb ECU98128.1	hypothetical protein G	( 392)	233	57.8	1.3e-05
gi 140849292 gb ECN91757.1	hypothetical protein G	( 268)	234	57.9	8.1e-06	gi 135733489 gb EBJ50660.1	hypothetical protein G	( 123)	226	56.1	1.3e-05
gi 139849794 gb ECH89899.1	hypothetical protein G	( 163)	231	57.2	8.1e-06	gi 138846965 gb ECC13935.1	hypothetical protein G	( 205)	229	56.8	1.3e-05
gi 138831381 gb ECC06430.1	hypothetical protein G	( 139)	230	56.9	8.2e-06	gi 141533718 gb ECS18963.1	hypothetical protein G	( 148)	227	56.3	1.3e-05
gi 142748550 gb EDA29469.1	hypothetical protein G	( 198)	232	57.4	8.3e-06	gi 135588646 gb EBI61023.1	hypothetical protein G	( 91)	224	55.6	1.3e-05
gi 116611308 gb ABK04032.1	3-phosphoshikimate 1-c	( 460)	237	58.6	8.4e-06	gi 48526066 gb AAT45234.1	5-enol-pyruvylshikimate	( 357)	232	57.5	1.4e-05
gi 138910924 gb ECC38856.1	hypothetical protein G	( 103)	228	56.5	8.4e-06	gi 48526070 gb AAT45236.1	5-enol-pyruvylshikimate	( 358)	232	57.5	1.4e-05
gi 135939139 gb EBK84238.1	hypothetical protein G	( 332)	235	58.1	8.5e-06	gi 48526072 gb AAT45237.1	5-enol-pyruvylshikimate	( 360)	232	57.5	1.4e-05
gi 135040418 gb EBF11141.1	hypothetical protein G	( 335)	235	58.1	8.5e-06	gi 143663997 gb EDG14715.1	hypothetical protein G	( 112)	225	55.9	1.4e-05
gi 182908332 gb ACC04216.1	Sequence 4351 from pat	( 471)	237	58.6	8.6e-06	gi 241914647 gb EER87791.1	hypothetical protein S	( 506)	234	58.0	1.4e-05
gi 137781153 gb EBV96078.1	hypothetical protein G	( 154)	230	57.0	8.9e-06	gi 229565672 gb ACQ79523.1	3-phosphoshikimate 1-c	( 434)	233	57.8	1.4e-05
gi 4235097 gb AAD13108.1	5-enolpyruvylshikimate 3	( 498)	237	58.6	9e-06	gi 139938554 gb ECI50388.1	hypothetical protein G	( 82)	223	55.4	1.4e-05
gi 229431757 gb EE041969.1	3-phosphoshikimate 1-c	( 424)	236	58.4	9e-06	gi 16751569 gb AAL27698.1	AF371966_1 5-enolpyruvyl	( 516)	234	58.0	1.4e-05
gi 256035894 gb ACU59469.1	3-phosphoshikimate 1-c	( 426)	236	58.4	9.1e-06	gi 18893860 gb AAL81823.1	3-phosphoshikimate 1-ca	( 440)	233	57.8	1.4e-05
gi 141225757 gb ECQ49018.1	hypothetical protein G	( 113)	228	56.5	9.1e-06	gi 197053768 gb ACH25466.1	Sequence 18 from paten	( 521)	234	58.0	1.4e-05
gi 254219555 gb EET08939.1	3-phosphoshikimate 1-c	( 435)	236	58.4	9.2e-06	gi 21555078 gb AAM63771.1	5-enolpyruvylshikimate-	( 521)	234	58.0	1.4e-05
gi 52208741 emb CAH34677.1	putative 3-phosphoskim	( 435)	236	58.4	9.2e-06	gi 143159253 gb EDD24485.1	hypothetical protein G	( 279)	230	57.1	1.5e-05
gi 76579593 gb ABA49068.1	putative 3-phosphoskimi	( 435)	236	58.4	9.2e-06	gi 142514368 gb ECY62998.1	hypothetical protein G	( 105)	224	55.6	1.5e-05
gi 137256208 gb EBT07853.1	hypothetical protein G	( 166)	230	57.0	9.5e-06	gi 138740714 gb ECB87755.1	hypothetical protein G	( 90)	232	55.4	1.5e-05
gi 137080022 gb EBS09377.1	hypothetical protein G	( 121)	228	56.5	9.7e-06	gi 30268138 emb CAC82655.1	5-enolpyruvylshikimate	( 409)	232	57.6	1.6e-05
gi 139813261 gb ECH64420.1	hypothetical protein G	( 104)	227	56.3	9.8e-06	gi 149770891 emb CAL42356.1	3-phosphoshikimate 1-	( 409)	232	57.6	1.6e-05
gi 136153838 gb EBM24965.1	hypothetical protein G	( 173)	230	57.0	9.9e-06	gi 138146448 gb EBY00346.1	hypothetical protein G	( 153)	226	56.1	1.6e-05
gi 155262583 gb ABT18187.1	Sequence 105657 from p	( 411)	235	58.2	1e-05	gi 167042884 gb ABZ07600.1	putative EPSP synthase	( 183)	227	56.4	1.6e-05
gi 260198061 gb EEW95577.1	3-phosphoshikimate 1-c	( 421)	235	58.2	1e-05	gi 136927795 gb EBR23477.1	hypothetical protein G	( 157)	226	56.1	1.6e-05
gi 268614908 gb ACZ09276.1	3-phosphoshikimate 1-c	( 424)	235	58.2	1e-05	gi 178463819 dbj BAG18339.1	putative UDP-N-acetyl	( 509)	233	57.8	1.6e-05
gi 207087579 gb EDZ64862.1	3-phosphoshikimate 1-c	( 432)	235	58.2	1.1e-05	gi 134894270 gb EBE13265.1	hypothetical protein G	( 135)	225	55.9	1.6e-05
gi 18251236 gb AAL65913.1	AF440389_1 5-enolpyruvyl	( 518)	236	58.4	1.1e-05	gi 13430624 gb AAK25934.1	AF360224_1 putative 5-en	( 521)	233	57.8	1.7e-05
gi 257796482 gb ACV67419.1	3-phosphoshikimate 1-c	( 444)	235	58.2	1.1e-05	gi 12321113 gb AAG50661.1	AC084242_5 5-enolpyruvyl	( 521)	233	57.8	1.7e-05
gi 141801247 gb ECT35781.1	hypothetical protein G	( 165)	229	56.8	1.1e-05	gi 11094810 gb AAG29739.1	AC084414_7 5-enolpyruvyl	( 521)	233	57.8	1.7e-05
gi 124402111 emb CAK67586.1	unnamed protein produ	(1468)	242	59.9	1.1e-05	gi 270259770 emb CBI38903.1	unnamed protein produ	( 521)	233	57.8	1.7e-05
gi 135886415 gb EBK47897.1	hypothetical protein G	( 168)	229	56.8	1.1e-05	gi 14532882 gb AAK64123.1	putative 5-enolpyruvyls	( 521)	233	57.8	1.7e-05
gi 139807552 gb ECH60329.1	hypothetical protein G	( 173)	229	56.8	1.1e-05	gi 5957574 gb AAE08248.1	Sequence 56 from patent	( 444)	232	57.6	1.7e-05
gi 137498472 gb EBU42283.1	hypothetical protein G	( 64)	223	55.3	1.1e-05	gi 2485251 gb AAB73387.1	I44476 Sequence 56 from p	( 444)	232	57.6	1.7e-05
gi 143196767 gb EDD51467.1	hypothetical protein G	( 64)	223	55.3	1.1e-05	gi 2484174 gb AAB72310.1	I49203 Sequence 56 from p	( 444)	232	57.6	1.7e-05
gi 142121563 gb ECV74769.1	hypothetical protein G	( 411)	234	58.0	1.2e-05	gi 144974753 gb ABP12464.1	Sequence 56 from paten	( 444)	232	57.6	1.7e-05
gi 143421721 gb EDB86769.1	hypothetical protein G	( 352)	233	57.7	1.2e-05	gi 136514494 gb EB065771.1	hypothetical protein G	( 270)	229	56.9	1.7e-05
gi 138609960 gb ECA78837.1	hypothetical protein G	( 299)	232	57.5	1.2e-05	gi 135571691 gb EBI50372.1	hypothetical protein G	( 232)	228	56.6	1.7e-05
gi 142813513 gb EDA77564.1	hypothetical protein G	( 303)	232	57.5	1.2e-05	gi 138887693 gb ECC30776.1	hypothetical protein G	( 146)	225	55.9	1.8e-05
gi 135290345 gb EBG66194.1	hypothetical protein G	( 132)	227	56.3	1.2e-05	gi 136124879 gb EBM08135.1	hypothetical protein G	( 80)	221	55.0	1.9e-05
gi 136974431 gb EBR49789.1	hypothetical protein G	( 113)	226	56.1	1.2e-05	gi 46095337 gb AAS80163.1	5-enolpyruvylshikimate-	( 514)	232	57.6	1.9e-05
gi 136968507 gb EBR46423.1	hypothetical protein G	( 113)	226	56.1	1.2e-05	gi 136717696 gb EBP94335.1	hypothetical protein G	( 225)	227	56.4	1.9e-05
gi 261377205 gb ACX79948.1	UDP-N-acetylglucosamin	( 434)	234	58.0	1.2e-05	gi 213504182 emb CAS92802.1	unnamed protein produ	( 464)	231	57.4	2e-05
gi 126242614 gb ABO05707.1	putative 3-phosphoshik	( 435)	234	58.0	1.2e-05	gi 142533801 gb ECY77123.1	hypothetical protein G	( 106)	222	55.2	2.1e-05
gi 160697916 gb EDP87886.1	putative 3-phosphoshik	( 435)	234	58.0	1.2e-05	gi 137643716 gb EBV21662.1	hypothetical protein G	( 95)	221	55.0	2.2e-05
gi 124291405 gb ABN00674.1	putative 3-phosphoshik	( 435)	234	58.0	1.2e-05	gi 137729195 gb EBV68871.1	hypothetical protein G	( 226)	226	56.2	2.2e-05



gi 123965218 gb ABE77393.4	EPSP synthase [Allium	( 522)	231	57.4	2.2e-05	gi 144974749 gb ABP12460.1	Sequence 52 from paten	( 444)	227	56.5	3.4e-05
gi 20226493 gb AAE88870.1	Sequence 3 from patent	( 444)	230	57.2	2.2e-05	gi 5957570 gb AAE08244.1	Sequence 52 from patent	( 444)	227	56.5	3.4e-05
gi 15113314 gb AAE68898.1	Sequence 5 from patent	( 444)	230	57.2	2.2e-05	gi 15113312 gb AAE68896.1	Sequence 3 from patent	( 444)	227	56.5	3.4e-05
gi 3714672 emb CAA03525.1	unnamed protein product	( 444)	230	57.2	2.2e-05	gi 2485247 gb AAB73383.1	I44472 Sequence 52 from p	( 444)	227	56.5	3.4e-05
gi 62786942 gb AAY06821.1	Sequence 28 from patent	( 444)	230	57.2	2.2e-05	gi 135651047 gb EBI99696.1	hypothetical protein G	( 100)	218	54.4	3.5e-05
gi 33724442 gb AAQ32651.1	Sequence 3 from patent	( 444)	230	57.2	2.2e-05	gi 134600018 gb EBC30786.1	hypothetical protein G	( 275)	224	55.8	3.5e-05
gi 197053767 gb ACH25465.1	Sequence 17 from paten	( 444)	230	57.2	2.2e-05	gi 134880266 gb EBE03915.1	hypothetical protein G	( 399)	226	56.3	3.6e-05
gi 3714738 emb CAA03538.1	unnamed protein product	( 444)	230	57.2	2.2e-05	gi 238936984 emb CAR25163.1	KLTH0G13090p [Lachanc	(1579)	234	58.2	3.8e-05
gi 21886542 emb CAD2174.1	unnamed protein produc	( 444)	230	57.2	2.2e-05	gi 141888249 gb ECT95030.1	hypothetical protein G	( 115)	218	54.4	3.9e-05
gi 1524383 emb CAA44974.1	3-phosphoshikimate 1-ca	( 444)	230	57.2	2.2e-05	gi 140614574 gb ECM38495.1	hypothetical protein G	( 314)	224	55.8	3.9e-05
gi 4774185 emb CAB42493.1	unnamed protein product	( 445)	230	57.2	2.2e-05	gi 63003818 gb AAY25438.1	At2g45300 [Arabidopsis	( 520)	227	56.6	3.9e-05
gi 141298247 gb ECQ92973.1	hypothetical protein G	( 139)	223	55.5	2.2e-05	gi 110742505 dbj BAE99170.1	5-enolpyruvylshikimat	( 520)	227	56.6	3.9e-05
gi 228266275 gb ACP96948.1	Sequence 29166 from pa	( 535)	231	57.4	2.3e-05	gi 62786929 gb AAY06808.1	Sequence 2 from patent	( 520)	227	56.6	3.9e-05
gi 135654047 gb EBJ01553.1	hypothetical protein G	( 122)	222	55.2	2.3e-05	gi 2583124 gb AAB82633.1	5-enolpyruvylshikimate-3	( 520)	227	56.6	3.9e-05
gi 143177389 gb EDD37310.1	hypothetical protein G	( 399)	229	56.9	2.4e-05	gi 295790 emb CAA29828.1	EPSP [Arabidopsis thalia	( 520)	227	56.6	3.9e-05
gi 144033885 gb EDI38787.1	hypothetical protein G	( 155)	223	55.5	2.5e-05	gi 281108574 gb ADA52832.1	Sequence 7 from patent	( 521)	227	56.6	3.9e-05
gi 2151836138 gb EE564675.1	3-phosphoshikimate 1-c	( 423)	229	56.9	2.5e-05	gi 56909232 dbj BAD63759.1	3-phosphoshikimate 1-c	( 446)	226	56.3	4e-05
gi 138035180 gb EBX38754.1	hypothetical protein G	( 136)	222	55.3	2.5e-05	gi 143337878 gb EDE41942.1	hypothetical protein G	( 165)	220	54.9	4e-05
gi 143940857 gb EDH73332.1	hypothetical protein G	( 371)	228	56.7	2.6e-05	gi 139041852 gb ECD00736.1	hypothetical protein G	( 165)	220	54.9	4e-05
gi 226520702 gb ACO66690.1	predicted protein [Mic	( 229)	225	56.0	2.6e-05	gi 140240697 gb ECK48383.1	hypothetical protein G	( 273)	223	55.6	4e-05
gi 138952139 gb ECC56131.1	hypothetical protein G	( 141)	222	55.3	2.6e-05	gi 170934465 gb ACB39726.1	3-phosphoshikimate 1-c	( 399)	225	56.1	4.2e-05
gi 140094177 gb ECJ49446.1	hypothetical protein G	( 142)	222	55.3	2.6e-05	gi 138445397 gb EBZ72304.1	hypothetical protein G	( 76)	215	53.7	4.2e-05
gi 136595080 gb EBP17208.1	hypothetical protein G	( 472)	229	57.0	2.7e-05	gi 143010366 gb EDC15947.1	hypothetical protein G	( 406)	225	56.1	4.2e-05
gi 140662460 gb ECM64704.1	hypothetical protein G	( 148)	222	55.3	2.7e-05	gi 137372418 gb EBT72999.1	hypothetical protein G	( 128)	218	54.4	4.3e-05
gi 142606038 gb EC227895.1	hypothetical protein G	( 413)	228	56.7	2.8e-05	gi 121554705 gb ABM58854.1	3-phosphoshikimate 1-c	( 705)	228	56.8	4.4e-05
gi 140645644 gb ECM53119.1	hypothetical protein G	( 297)	226	56.3	2.8e-05	gi 56381718 dbj BAD77626.1	UDP-N-acetylglucosamin	( 434)	225	56.1	4.5e-05
gi 139701374 gb ECG87541.1	hypothetical protein G	( 154)	222	55.3	2.8e-05	gi 141196760 gb ECQ28828.1	hypothetical protein G	( 137)	218	54.4	4.6e-05
gi 143209192 gb EDD60527.1	hypothetical protein G	( 357)	227	56.5	2.8e-05	gi 3714674 emb CAA03526.1	unnamed protein product	( 444)	225	56.1	4.6e-05
gi 134406690 gb EBB16764.1	hypothetical protein G	( 95)	219	54.6	2.9e-05	gi 21886544 emb CAD42175.1	unnamed protein produc	( 444)	225	56.1	4.6e-05
gi 143692754 gb EDG31345.1	hypothetical protein G	( 260)	225	56.0	2.9e-05	gi 3714740 emb CAA03539.1	unnamed protein product	( 444)	225	56.1	4.6e-05
gi 197709166 gb ACH72672.1	5-enolpyruvylshikimate	( 510)	229	57.0	2.9e-05	gi 33724443 gb AAQ32652.1	Sequence 5 from patent	( 444)	225	56.1	4.6e-05
gi 239808863 gb ACS25928.1	UDP-N-acetylglucosamin	( 435)	228	56.7	2.9e-05	gi 20226494 gb AAE88871.1	Sequence 9 from patent	( 444)	225	56.1	4.6e-05
gi 141110776 gb ECP70130.1	hypothetical protein G	( 163)	222	55.3	3e-05	gi 4774187 emb CAB42494.1	unnamed protein product	( 445)	225	56.1	4.6e-05
gi 5957569 gb AAE08243.1	Sequence 51 from patent	( 444)	228	56.7	3e-05	gi 262272507 gb ACY40415.1	3-phosphoshikimate 1-c	( 385)	224	55.9	4.7e-05
gi 2484169 gb AAB72305.1	I49198 Sequence 51 from p	( 444)	228	56.7	3e-05	gi 142492368 gb ECY47510.1	hypothetical protein G	( 147)	218	54.4	4.8e-05
gi 2485246 gb AAB73382.1	I44471 Sequence 51 from p	( 444)	228	56.7	3e-05	gi 140435310 gb ECL73227.1	hypothetical protein G	( 125)	217	54.2	4.9e-05
gi 144974748 gb ABP12459.1	Sequence 51 from paten	( 444)	228	56.7	3e-05	gi 117576868 emb CAL65337.1	3-phosphoshikimate 1-	( 405)	224	55.9	4.9e-05
gi 143204891 gb EDD57396.1	hypothetical protein G	( 389)	227	56.5	3.1e-05	gi 139194383 gb ECE05764.1	hypothetical protein G	( 131)	217	54.2	5.1e-05
gi 139764010 gb ECH29671.1	hypothetical protein G	( 143)	221	55.1	3.1e-05	gi 139524990 gb ECF66675.1	hypothetical protein G	( 94)	215	53.7	5.1e-05
gi 143435517 gb EDE94112.1	hypothetical protein G	( 332)	226	56.3	3.1e-05	gi 138383307 gb EBZ229157.1	hypothetical protein G	( 133)	217	54.2	5.1e-05
gi 138065413 gb EBX54745.1	hypothetical protein G	( 64)	216	53.9	3.2e-05	gi 111979103 gb ABH83340.1	Sequence 9 from patent	( 506)	225	56.1	5.1e-05
gi 256718776 gb EEU32331.1	3-phosphoshikimate 1-c	( 421)	227	56.5	3.3e-05	gi 281079465 gb ADA36173.1	Sequence 8 from patent	( 506)	225	56.1	5.1e-05
gi 229429522 gb EEO39734.1	3-phosphoshikimate 1-c	( 424)	227	56.5	3.3e-05	gi 134887116 gb EBE08499.1	hypothetical protein G	( 136)	217	54.2	5.2e-05
gi 141325310 gb ECR05886.1	hypothetical protein G	( 95)	218	54.4	3.3e-05	gi 135556587 gb EDP40658.1	hypothetical protein G	( 151)	217	54.2	5.7e-05
gi 512545 emb CAA01426.1	aroA [Aeromonas salmonic	( 427)	227	56.5	3.3e-05	gi 44889967 emb CAD29607.2	pentafunctional arom p	(1582)	231	57.6	5.8e-05
gi 134867908 gb EBD95726.1	hypothetical protein G	( 369)	226	56.3	3.4e-05	gi 136069640 gb EBL70519.1	hypothetical protein G	( 154)	217	54.3	5.8e-05
gi 17815 emb CAA35839.1	5-enolpyruvylshikimate-3-	( 516)	228	56.8	3.4e-05	gi 159131499 gb EDP56612.1	pentafunctional polype	(1605)	231	57.6	5.9e-05
gi 62786940 gb AAY06819.1	Sequence 26 from patent	( 516)	228	56.8	3.4e-05	gi 137127816 gb EBS35887.1	hypothetical protein G	( 133)	216	54.0	5.9e-05
gi 136143958 gb EBM18538.1	hypothetical protein G	( 370)	226	56.3	3.4e-05	gi 281108576 gb ADA52834.1	Sequence 9 from patent	( 506)	224	55.9	5.9e-05
gi 111979101 gb ABH83338.1	Sequence 7 from patent	( 521)	228	56.8	3.4e-05	gi 14549196 dbj BAB61062.1	3-phosphoshikimate 1-c	( 511)	224	55.9	6e-05
gi 2484170 gb AAB72306.1	I49199 Sequence 52 from p	( 444)	227	56.5	3.4e-05	gi 254256567 emb CAZ91430.1	unnamed protein produ	( 511)	224	55.9	6e-05

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gi 15778436 gb AAL07437.1 AF413082_1 EPSP synthase ( 511)	224	55.9	6e-05	gi 143054617 gb EDC48197.1 hypothetical protein G ( 335)	217	54.4	0.00011
gi 15724392 gb AAL06593.1 5-enolpyruvylshikimate ( 511)	224	55.9	6e-05	gi 135802331 gb EBJ93691.1 hypothetical protein G ( 75)	208	52.2	0.00011
gi 55297191 dbj BAD68865.1 putative 5-enolpyruvyl ( 515)	224	55.9	6e-05	gi 141447793 gb ECR89500.1 hypothetical protein G ( 147)	212	53.2	0.00011
gi 55296169 dbj BAD67887.1 putative 5-enolpyruvyl ( 515)	224	55.9	6e-05	gi 256578504 gb ACU89640.1 UDP-N-acetylglucosamin ( 416)	218	54.7	0.00012
gi 125553934 gb EAY99539.1 hypothetical protein O ( 515)	224	55.9	6e-05	gi 139497159 gb ECF47452.1 hypothetical protein G ( 94)	209	52.5	0.00012
gi 113594752 dbj BAF18626.1 Os06g0133900 [Oryza s ( 515)	224	55.9	6e-05	gi 135290648 gb EBG66366.1 hypothetical protein G ( 220)	214	53.7	0.00012
gi 187973283 gb EDU40782.1 pentafunctional AROM p ( 864)	227	56.7	6.1e-05	gi 143352907 gb EDE50882.1 hypothetical protein G ( 429)	218	54.7	0.00012
gi 140099644 gb ECJ53238.1 hypothetical protein G ( 269)	220	55.0	6.1e-05	gi 134840321 gb EBD77600.1 hypothetical protein G ( 135)	211	53.0	0.00012
gi 135507166 gb EBI09056.1 hypothetical protein G ( 101)	214	53.5	6.2e-05	gi 281079463 gb ADA36171.1 Sequence 1 from patent ( 515)	219	54.9	0.00012
gi 144065936 gb EDI62214.1 hypothetical protein G ( 121)	215	53.8	6.3e-05	gi 24850309 gb AAN63155.1 5-enolpyruvylshikimate- ( 445)	218	54.7	0.00013
gi 119950797 gb ABM09708.1 putative UDP-N-acetylgl ( 467)	223	55.7	6.4e-05	gi 16415786 emb CAD01096.1 5-enolpyruvylshikimate ( 445)	218	54.7	0.00013
gi 137552102 gb EBU70915.1 hypothetical protein G ( 124)	215	53.8	6.4e-05	gi 141795168 gb ECT33018.1 hypothetical protein G ( 139)	211	53.0	0.00013
gi 56569933 gb AAV99867.1 Sequence 5 from patent ( 570)	224	56.0	6.6e-05	gi 139755777 gb ECH24015.1 hypothetical protein G ( 118)	210	52.7	0.00013
gi 167249310 gb ABZ25917.1 Sequence 5 from patent ( 570)	224	56.0	6.6e-05	gi 140152196 gb ECJ87114.1 hypothetical protein G ( 140)	211	53.0	0.00013
gi 210071512 gb EEA25601.1 3-dehydroquinone synth (1571)	230	57.4	6.6e-05	gi 142887871 gb EDB28923.1 hypothetical protein G ( 394)	217	54.4	0.00013
gi 144189617 gb EDJ52210.1 hypothetical protein G ( 180)	217	54.3	6.7e-05	gi 137648475 gb EBV23980.1 hypothetical protein G ( 173)	212	53.2	0.00013
gi 119412546 gb EAA22487.1 pentafunctional polype (1578)	230	57.4	6.7e-05	gi 138618826 gb ECA84865.1 hypothetical protein G ( 76)	207	52.0	0.00013
gi 49529154 emb CAG62820.1 unnamed protein produc (1579)	230	57.4	6.7e-05	gi 141081748 gb ECP49664.1 hypothetical protein G ( 152)	211	53.0	0.00014
gi 141443548 gb ECR86688.1 hypothetical protein G ( 153)	216	54.0	6.7e-05	gi 218722059 gb EED21477.1 pentafunctional polype (1577)	225	56.4	0.00014
gi 139064301 gb ECD16501.1 hypothetical protein G ( 254)	219	54.8	6.7e-05	gi 139335289 gb ECE54589.1 hypothetical protein G ( 252)	214	53.7	0.00014
gi 143026908 gb EDC27859.1 hypothetical protein G ( 159)	216	54.0	6.9e-05	gi 135766604 gb EBJ71201.1 hypothetical protein G ( 155)	211	53.0	0.00014
gi 137722143 gb EBV64909.1 hypothetical protein G ( 115)	214	53.6	7e-05	gi 144098861 gb EDI85676.1 hypothetical protein G ( 363)	216	54.2	0.00014
gi 136049990 gb EBL57288.1 hypothetical protein G ( 202)	217	54.3	7.4e-05	gi 140096140 gb ECJ80823.1 hypothetical protein G ( 115)	209	52.5	0.00014
gi 139610443 gb ECG25482.1 hypothetical protein G ( 286)	219	54.8	7.4e-05	gi 136465730 gb EBO34255.1 hypothetical protein G ( 136)	210	52.8	0.00014
gi 136459333 gb EBO30109.1 hypothetical protein G ( 244)	218	54.5	7.5e-05	gi 141209606 gb ECQ37721.1 hypothetical protein G ( 137)	210	52.8	0.00014
gi 141676308 gb ECS75854.1 hypothetical protein G ( 151)	215	53.8	7.6e-05	gi 40557113 gb AAR87844.1 5-enolpyruvylshikimate- ( 445)	217	54.5	0.00015
gi 136654155 gb EBP53271.1 hypothetical protein G ( 348)	220	55.0	7.6e-05	gi 136447507 gb EBO22455.1 hypothetical protein G ( 232)	213	53.5	0.00015
gi 134912558 gb EBE25356.1 hypothetical protein G ( 128)	214	53.6	7.6e-05	gi 134364163 gb EBA91033.1 hypothetical protein G ( 102)	208	52.3	0.00015
gi 44985944 gb AAS54555.1 AGR066Wp [Ashbya gossyp (1577)	229	57.2	7.7e-05	gi 140486597 gb ECJ97657.1 hypothetical protein G ( 74)	206	51.8	0.00015
gi 137478171 gb EBU31918.1 hypothetical protein G ( 154)	215	53.8	7.8e-05	gi 142003656 gb ECU75568.1 hypothetical protein G ( 238)	213	53.5	0.00015
gi 225214557 gb ACN83291.1 3-phosphoshikimate 1-c ( 420)	221	55.3	7.8e-05	gi 142393793 gb ECX74526.1 hypothetical protein G ( 466)	217	54.5	0.00015
gi 281108575 gb ADA52833.1 Sequence 8 from patent ( 520)	222	55.5	8.1e-05	gi 138825030 gb ECC03219.1 hypothetical protein G ( 105)	208	52.3	0.00015
gi 111979102 gb ABH83339.1 Sequence 8 from patent ( 520)	222	55.5	8.1e-05	gi 143729176 gb EDG48487.1 hypothetical protein G ( 338)	215	54.0	0.00015
gi 138640927 gb ECA98853.1 hypothetical protein G ( 171)	215	53.9	8.5e-05	gi 135319190 gb EBG38385.1 hypothetical protein G ( 77)	206	51.8	0.00016
gi 143364680 gb EDE57647.1 hypothetical protein G ( 123)	213	53.4	8.5e-05	gi 135261549 gb EBG49250.1 hypothetical protein G ( 248)	213	53.5	0.00016
gi 143907468 gb EDH49131.1 hypothetical protein G ( 209)	216	54.1	8.8e-05	gi 148323442 gb EDK88692.1 3-phosphoshikimate 1-c ( 420)	216	54.2	0.00016
gi 138388666 gb EBZ32841.1 hypothetical protein G ( 127)	213	53.4	8.8e-05	gi 27904180 gb AAO27013.1 3-phosphoshikimate 1-ca ( 427)	216	54.2	0.00016
gi 136692287 gb EBP77687.1 hypothetical protein G ( 273)	217	54.4	9.5e-05	gi 142582794 gb ECZ11702.1 hypothetical protein G ( 114)	208	52.3	0.00016
gi 141883580 gb ECT91843.1 hypothetical protein G ( 241)	216	54.1	9.9e-05	gi 138629390 gb ECA92270.1 hypothetical protein G ( 99)	207	52.1	0.00017
gi 143881431 gb EDH30581.1 hypothetical protein G ( 107)	211	52.9	0.0001	gi 137761629 gb EBV85571.1 hypothetical protein G ( 278)	213	53.5	0.00017
gi 255342376 gb ACU08489.1 5-Enolpyruvylshikimate ( 410)	219	54.9	0.0001	gi 138258529 gb EBY62640.1 hypothetical protein G ( 147)	209	52.6	0.00018
gi 143294031 gb EDE16453.1 hypothetical protein G ( 211)	215	53.9	0.0001	gi 116792410 gb ABK26355.1 unknown [Picea sitchen ( 148)	209	52.6	0.00018
gi 134985130 gb EBE73942.1 hypothetical protein G ( 152)	213	53.4	0.0001	gi 210064464 gb EEA18560.1 pentafunctional polype (1573)	223	56.0	0.00018
gi 135513466 gb EBI13124.1 hypothetical protein G ( 152)	213	53.4	0.0001	gi 261497413 gb ACX83863.1 3-phosphoshikimate 1-c ( 416)	215	54.0	0.00018
gi 269095297 gb AC225288.1 3-phosphoshikimate 1-c ( 422)	219	54.9	0.0001	gi 238939610 emb CAR27785.1 ZYR00D06578p [Zygosc (1589)	223	56.0	0.00018
gi 51858127 dbj BAD42285.1 UDP-N-acetylglucosamin ( 424)	219	54.9	0.0001	gi 141847271 gb ECT66592.1 hypothetical protein G ( 112)	207	52.1	0.00019
gi 113376729 gb AAZ79230.2 plastid 5-enolpyruvyls ( 437)	219	54.9	0.00011	gi 119537558 gb ABL82175.1 UDP-N-acetylglucosamin ( 508)	216	54.3	0.00019
gi 141329022 gb ECR07966.1 hypothetical protein G ( 161)	213	53.4	0.00011	gi 135733488 gb EBJ50659.1 hypothetical protein G ( 160)	209	52.6	0.00019
gi 40557115 gb AAR87845.1 5-enolpyruvylshikimate- ( 445)	219	54.9	0.00011	gi 138609959 gb ECA78836.1 hypothetical protein G ( 115)	207	52.1	0.00019
gi 239795036 dbj BAH74025.1 3-phosphoshikimate 1- ( 445)	219	54.9	0.00011	gi 29605907 dbj BAC69971.1 putative UDP-N-acetylgl ( 437)	215	54.0	0.00019
gi 136028772 gb EBL43028.1 hypothetical protein G ( 143)	212	53.2	0.00011	gi 143365722 gb EDE58318.1 hypothetical protein G ( 375)	214	53.8	0.00019

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gi 134077312 emb CAK45651.1  unnamed protein produ (1031)	220	55.2	0.0002	gi 256559742 gb ACU85589.1  UDP-N-acetylglucosamin ( 517)	212	53.5	0.00034
gi 136116509 gb EBM02401.1  hypothetical protein G ( 118)	207	52.1	0.0002	gi 135651046 gb EBI99695.1  hypothetical protein G ( 117)	203	51.3	0.00035
gi 213504184 emb CAS92803.1  unnamed protein produ ( 455)	215	54.0	0.0002	gi 139191265 gb ECE03543.1  hypothetical protein G ( 166)	205	51.8	0.00035
gi 135659439 gb EBJ04885.1  hypothetical protein G ( 127)	207	52.1	0.00021	gi 144194317 gb EDJ55692.1  hypothetical protein G ( 232)	207	52.3	0.00035
gi 143268167 gb EDE02421.1  hypothetical protein G ( 77)	204	51.4	0.00021	gi 136950192 gb EBR36051.1  hypothetical protein G ( 143)	204	51.5	0.00036
gi 138629391 gb ECA92271.1  hypothetical protein G ( 91)	205	51.7	0.00021	gi 143855993 gb EDH11923.1  hypothetical protein G ( 648)	213	53.7	0.00036
gi 140771259 gb ECN39459.1  hypothetical protein G ( 130)	207	52.1	0.00021	gi 119674666 gb ABL88922.1  3-phosphoshikimate 1-c ( 399)	210	53.0	0.00036
gi 137414679 gb EBT96858.1  hypothetical protein G ( 154)	208	52.4	0.00021	gi 197628303 gb EDY40847.1  3-phosphoshikimate 1-c ( 403)	210	53.0	0.00037
gi 144092537 gb EDI81200.1  hypothetical protein G ( 81)	204	51.4	0.00022	gi 135856458 gb EBK27748.1  hypothetical protein G ( 110)	202	51.1	0.00038
gi 141892373 gb ECT97923.1  hypothetical protein G ( 308)	212	53.3	0.00022	gi 116062764 dbj BAA80401.2  3-phosphoshikimate 1- ( 419)	210	53.0	0.00038
gi 143335933 gb EDE40536.1  hypothetical protein G ( 430)	214	53.8	0.00022	gi 135662774 gb EBJ06959.1  hypothetical protein G ( 303)	208	52.5	0.00038
gi 137589221 gb EBU91870.1  hypothetical protein G ( 134)	207	52.1	0.00022	gi 167296094 gb ABZ48958.1  Sequence 22896 from pa ( 427)	210	53.0	0.00039
gi 137848316 gb EBW34665.1  hypothetical protein G ( 135)	207	52.1	0.00022	gi 137646588 gb EBV23065.1  hypothetical protein G ( 224)	206	52.0	0.00039
gi 140413732 gb ECL59758.1  hypothetical protein G ( 137)	207	52.1	0.00022	gi 16415784 emb CAD01095.1  5-enolpyruvylshikimate ( 445)	210	53.0	0.0004
gi 167290545 gb ABZ43409.1  Sequence 17347 from pa ( 447)	214	53.8	0.00023	gi 24850311 gb AAN63156.1  5-enolpyruvylshikimate- ( 445)	210	53.0	0.0004
gi 10175334 dbj BAB06432.1  3-phosphoshikimate 1-c ( 447)	214	53.8	0.00023	gi 56638357 gb AAW10629.1  Sequence 7 from patent ( 445)	210	53.0	0.0004
gi 140672153 gb EBT71666.1  hypothetical protein G ( 141)	207	52.2	0.00023	gi 137313646 gb EBT40020.1  hypothetical protein G ( 140)	203	51.3	0.0004
gi 140810164 gb ECN66826.1  hypothetical protein G ( 278)	211	53.1	0.00023	gi 137327459 gb EBT47689.1  hypothetical protein G ( 143)	203	51.3	0.00041
gi 141798088 gb ECT34142.1  hypothetical protein G ( 144)	207	52.2	0.00023	gi 2484168 gb AAB72304.1 I49197 Sequence 50 from p ( 460)	210	53.0	0.00041
gi 141546046 gb ECS27575.1  hypothetical protein G ( 124)	206	51.9	0.00024	gi 144974747 gb ABP12458.1  Sequence 50 from paten ( 460)	210	53.0	0.00041
gi 138611211 gb ECA79728.1  hypothetical protein G ( 286)	211	53.1	0.00024	gi 5957568 gb AAE08242.1  Sequence 50 from patent ( 460)	210	53.0	0.00041
gi 139498756 gb ECF48543.1  hypothetical protein G ( 64)	202	51.0	0.00024	gi 2485245 gb AAB73381.1 I44470 Sequence 50 from p ( 460)	210	53.0	0.00041
gi 141992988 gb ECU68466.1  hypothetical protein G ( 149)	207	52.2	0.00024	gi 143659900 gb EDG12514.1  hypothetical protein G ( 64)	198	50.1	0.00042
gi 140455536 gb ECL87543.1  hypothetical protein G ( 247)	210	52.9	0.00024	gi 139177681 gb ECD93905.1  hypothetical protein G ( 288)	207	52.3	0.00042
gi 140236302 gb ECK45224.1  hypothetical protein G ( 154)	207	52.2	0.00025	gi 142857706 gb EDB07392.1  hypothetical protein G ( 486)	210	53.0	0.00043
gi 170174741 gb ACB07794.1  3-phosphoshikimate 1-c ( 423)	213	53.6	0.00025	gi 141954719 gb ECU41802.1  hypothetical protein G ( 349)	208	52.5	0.00043
gi 140654303 gb ECM59089.1  hypothetical protein G ( 112)	205	51.7	0.00025	gi 141580813 gb ECS45999.1  hypothetical protein G ( 78)	199	50.4	0.00043
gi 142142776 gb ECV90405.1  hypothetical protein G ( 138)	206	51.9	0.00026	gi 143866695 gb EDH19810.1  hypothetical protein G ( 352)	208	52.5	0.00043
gi 143205281 gb EDD57686.1  hypothetical protein G ( 140)	206	51.9	0.00026	gi 135343554 gb EBH00234.1  hypothetical protein G ( 155)	203	51.3	0.00044
gi 140413370 gb ECL59501.1  hypothetical protein G ( 231)	209	52.7	0.00026	gi 13092893 emb CAC30301.1  putative 3-phosphoshik ( 430)	209	52.8	0.00045
gi 138878118 gb ECC26538.1  hypothetical protein G ( 120)	205	51.7	0.00026	gi 219932929 emb CAR70886.1  putative 3-phosphoshi ( 430)	209	52.8	0.00045
gi 143270309 gb EDE03964.1  hypothetical protein G ( 408)	212	53.4	0.00028	gi 138437383 gb EBZ67000.1  hypothetical protein G ( 221)	205	51.8	0.00045
gi 262181543 gb ACY29662.1  5-enolpyruvylshikimate ( 248)	209	52.7	0.00028	gi 144034478 gb EDI39203.1  hypothetical protein G ( 69)	198	50.1	0.00045
gi 143970801 gb EDH94315.1  hypothetical protein G ( 110)	204	51.5	0.00028	gi 135913705 gb EBR66907.1  hypothetical protein G ( 136)	202	51.1	0.00045
gi 136531748 gb EBO76792.1  hypothetical protein G ( 185)	207	52.2	0.00029	gi 160707495 gb EAT91093.2  hypothetical protein S (1661)	217	54.7	0.00045
gi 142893931 gb EDB33295.1  hypothetical protein G ( 427)	212	53.4	0.00029	gi 136570079 gb EBP01271.1  hypothetical protein G ( 195)	204	51.6	0.00046
gi 110729299 gb ABG88197.1  EPSP synthase [Phaseol ( 522)	213	53.7	0.0003	gi 139968256 gb ECI70629.1  hypothetical protein G ( 140)	202	51.1	0.00047
gi 119948400 gb ABM07311.1  3-Phosphoshikimate-1-c ( 456)	212	53.4	0.00031	gi 135693637 gb EBJ25980.1  hypothetical protein G ( 200)	204	51.6	0.00047
gi 142478397 gb ECY37505.1  hypothetical protein G ( 63)	200	50.5	0.00031	gi 140473336 gb ECL94304.1  hypothetical protein G ( 75)	198	50.2	0.00048
gi 142582261 gb ECZ11328.1  hypothetical protein G ( 104)	203	51.3	0.00031	gi 29339497 gb AAO77293.1  3-phosphoshikimate 1-ca ( 410)	208	52.6	0.0005
gi 593744 gb AAA55351.1  Sequence 3 from Patent EP ( 469)	212	53.4	0.00031	gi 7019762 emb CAB75770.1  pentafunctional aromati (1573)	216	54.5	0.0005
gi 137781507 gb EBV96275.1  hypothetical protein G ( 206)	207	52.2	0.00032	gi 139125658 gb ECD58797.1  hypothetical protein G ( 181)	203	51.4	0.0005
gi 137013318 gb EBR71823.1  hypothetical protein G ( 126)	204	51.5	0.00032	gi 76876364 emb CAI87586.1  UDP-N-acetylglucosamin ( 419)	208	52.6	0.00051
gi 2485244 gb AAB73380.1 I44469 Sequence 49 from p ( 480)	212	53.4	0.00032	gi 139101794 gb ECD42558.1  hypothetical protein G ( 132)	201	50.9	0.00051
gi 2484167 gb AAB72303.1 I49196 Sequence 49 from p ( 480)	212	53.4	0.00032	gi 141179292 gb ECQ17891.1  hypothetical protein G ( 112)	200	50.7	0.00051
gi 144974746 gb ABP12457.1  Sequence 49 from paten ( 480)	212	53.4	0.00032	gi 257472973 gb ACV51092.1  3-phosphoshikimate 1-c ( 426)	208	52.6	0.00051
gi 5957567 gb AAE08241.1  Sequence 49 from patent ( 480)	212	53.4	0.00032	gi 135589340 gb EBT61491.1  hypothetical protein G ( 68)	197	49.9	0.00051
gi 229422320 gb EE037367.1  3-phosphoshikimate 1-c ( 418)	211	53.2	0.00033	gi 222843005 gb EEE80552.1  3-phosphoshikimate 1-c ( 518)	209	52.8	0.00053
gi 142608246 gb ECZ29452.1  hypothetical protein G ( 419)	211	53.2	0.00033	gi 143231890 gb EDD76949.1  hypothetical protein G ( 398)	207	52.4	0.00056
gi 197053769 gb ACH25467.1  Sequence 19 from paten ( 506)	212	53.4	0.00033	gi 136481378 gb EBO44369.1  hypothetical protein G ( 108)	199	50.4	0.00057
gi 136314634 gb EBN33187.1  hypothetical protein G ( 514)	212	53.4	0.00034	gi 238851221 gb EQ40685.1  hypothetical protein C (1568)	215	54.3	0.00058

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gi 119397025 gb EAW07456.1	pentafunctional polypeptide (1587)	215	54.3	0.00058	gi 139957028 gb ECI62785.1	hypothetical protein G ( 95)	194	49.4	0.0011
gi 114335818 gb ABI73200.1	UDP-N-acetylglucosamin ( 419)	207	52.4	0.00058	gi 138719578 gb ECB53769.1	hypothetical protein G ( 137)	196	49.9	0.0011
gi 134719113 gb EBD01143.1	hypothetical protein G ( 136)	200	50.7	0.00061	gi 138838259 gb ECC09709.1	hypothetical protein G ( 99)	194	49.4	0.0011
gi 141537327 gb ECS21320.1	hypothetical protein G ( 70)	196	49.7	0.00061	gi 138404715 gb EBZ43876.1	hypothetical protein G ( 229)	199	50.6	0.0011
gi 256686438 gb ACV09331.1	UDP-N-acetylglucosamin ( 439)	207	52.4	0.00061	gi 140235542 gb ECK44673.1	hypothetical protein G ( 273)	200	50.8	0.0011
gi 141670245 gb ECS72593.1	hypothetical protein G ( 275)	204	51.7	0.00062	gi 139593930 gb ECG14149.1	hypothetical protein G ( 141)	196	49.9	0.0011
gi 137252226 gb EBT05562.1	hypothetical protein G ( 123)	199	50.5	0.00064	gi 137153595 gb EBS50236.1	hypothetical protein G ( 103)	194	49.4	0.0011
gi 142456675 gb ECY21312.1	hypothetical protein G ( 405)	206	52.2	0.00065	gi 141970069 gb ECU52289.1	hypothetical protein G ( 286)	200	50.8	0.0012
gi 144203151 gb EDJ61880.1	hypothetical protein G ( 108)	198	50.2	0.00066	gi 138254743 gb EBY59922.1	hypothetical protein G ( 90)	193	49.2	0.0012
gi 143081548 gb EDC67931.1	hypothetical protein G ( 411)	206	52.2	0.00066	gi 220698176 gb EED54516.1	pentafunctional polypeptide (1578)	210	53.3	0.0012
gi 139902023 gb ECI24529.1	hypothetical protein G ( 211)	202	51.2	0.00066	gi 211586138 emb CAP93886.1	Pcl6g12160 [Penicilli] (1586)	210	53.3	0.0012
gi 114197527 gb EAU39227.1	hypothetical protein A (1581)	214	54.1	0.00067	gi 3834343 emb CAA28836.1	arom polypeptide [Emeri] (1586)	210	53.3	0.0012
gi 15113315 gb AAE68899.1	Sequence 6 from patent ( 423)	206	52.2	0.00068	gi 83770536 dbj BAE60669.1	unnamed protein product (1595)	210	53.3	0.0012
gi 143094736 gb EDV77565.1	hypothetical protein G ( 306)	204	51.7	0.00069	gi 137958190 gb EBW97170.1	hypothetical protein G ( 111)	194	49.4	0.0012
gi 258554844 gb ACV77786.1	3-phosphoshikimate 1-c ( 428)	206	52.2	0.00069	gi 135657735 gb EBJ03832.1	hypothetical protein G ( 94)	193	49.2	0.0012
gi 140981503 gb ECO82557.1	hypothetical protein G ( 237)	202	51.2	0.00073	gi 140722456 gb ECN06632.1	hypothetical protein G ( 157)	196	49.9	0.0012
gi 240135769 gb EER35322.1	pentafunctional polypeptide (1551)	213	53.9	0.00076	gi 138452474 gb EBZ77315.1	hypothetical protein G ( 157)	196	49.9	0.0012
gi 218675784 gb ACL00597.1	5-enolpyruvylshikimate ( 410)	205	52.0	0.00076	gi 141051574 gb ECP29929.1	hypothetical protein G ( 158)	196	49.9	0.0012
gi 134759239 gb EBD23750.1	hypothetical protein G ( 416)	205	52.0	0.00077	gi 257811704 gb EEV40524.1	UDP-N-acetylglucosamin ( 430)	202	51.3	0.0012
gi 136574586 gb EBP04142.1	hypothetical protein G ( 67)	194	49.3	0.00078	gi 141916054 gb ECU14493.1	hypothetical protein G ( 82)	192	48.9	0.0012
gi 136132486 gb EBM13199.1	hypothetical protein G ( 256)	202	51.2	0.00078	gi 135163783 gb EBF90152.1	hypothetical protein G ( 165)	196	49.9	0.0013
gi 136333268 gb EBN45633.1	hypothetical protein G ( 136)	198	50.3	0.00081	gi 135099842 gb EBF49079.1	hypothetical protein G ( 322)	200	50.9	0.0013
gi 140268788 gb ECK67789.1	hypothetical protein G ( 137)	198	50.3	0.00081	gi 136947037 gb EBR34275.1	hypothetical protein G ( 143)	195	49.7	0.0013
gi 78220930 gb ABB40279.1	3-phosphoshikimate 1-ca ( 442)	205	52.0	0.00082	gi 18160470 gb AAL63821.1	3-phosphoshikimate 1-ca ( 400)	201	51.1	0.0013
gi 190347323 gb EDK39572.2	hypothetical protein P (1210)	211	53.4	0.00082	gi 226289074 gb EEH44586.1	pentafunctional AROM p (1538)	209	53.0	0.0013
gi 138953443 gb ECC56702.1	hypothetical protein G ( 120)	197	50.0	0.00084	gi 145304842 gb ABP55424.1	3-phosphoshikimate 1-c ( 414)	201	51.1	0.0014
gi 136253249 gb EBM91262.1	hypothetical protein G ( 143)	198	50.3	0.00084	gi 189420145 gb ACD94543.1	UDP-N-acetylglucosamin ( 419)	201	51.1	0.0014
gi 142257629 gb ECW77085.1	hypothetical protein G ( 410)	204	51.7	0.00088	gi 257807952 gb EEV36774.1	UDP-N-acetylglucosamin ( 430)	201	51.1	0.0014
gi 142876278 gb EDB20907.1	hypothetical protein G ( 151)	198	50.3	0.00088	gi 257801515 gb EEV30445.1	UDP-N-acetylglucosamin ( 430)	201	51.1	0.0014
gi 238842364 gb EEQ32026.1	pentafunctional AROM p (1571)	212	53.7	0.00089	gi 169242594 emb CAM63622.1	3-phosphoshikimate 1- ( 431)	201	51.1	0.0014
gi 157921240 gb ABW02667.1	3-phosphoshikimate 1-c ( 414)	204	51.7	0.00089	gi 142110315 gb ECV66589.1	hypothetical protein G ( 366)	200	50.9	0.0014
gi 167274833 gb ABZ27697.1	Sequence 1635 from patent (1588)	212	53.7	0.0009	gi 142201089 gb ECW34849.1	hypothetical protein G ( 453)	201	51.1	0.0015
gi 3381 emb CAA29458.1	unnamed protein product [S (1588)	212	53.7	0.0009	gi 142559146 gb ECY95199.1	hypothetical protein G ( 146)	194	49.5	0.0015
gi 665659 emb CAA88208.1	AroIp [Saccharomyces cerevisiae] (1588)	212	53.7	0.0009	gi 226281118 gb EEH36684.1	pentafunctional AROM p (1523)	208	52.8	0.0015
gi 136136795 gb EBM15292.1	hypothetical protein G ( 255)	201	51.0	0.0009	gi 140706516 gb ECM95928.1	hypothetical protein G ( 65)	189	48.3	0.0016
gi 139197802 gb ECE08219.1	hypothetical protein G ( 80)	194	49.3	0.00091	gi 263254749 gb EEZ26183.1	3-phosphoshikimate 1-c ( 410)	200	50.9	0.0016
gi 171991199 gb ACB62121.1	UDP-N-acetylglucosamin ( 434)	204	51.8	0.00093	gi 225681904 gb EEH20188.1	pentafunctional AROM p (1603)	208	52.8	0.0016
gi 135669319 gb EBJ11015.1	hypothetical protein G ( 136)	197	50.1	0.00093	gi 136640296 gb EBP45062.1	hypothetical protein G ( 132)	193	49.2	0.0016
gi 134562746 gb EBC08575.1	hypothetical protein G ( 164)	198	50.3	0.00095	gi 134553252 gb EBC02793.1	hypothetical protein G ( 114)	192	49.0	0.0016
gi 143141346 gb EDD11677.1	hypothetical protein G ( 100)	195	49.6	0.00095	gi 139664636 gb ECG62011.1	hypothetical protein G ( 263)	197	50.2	0.0016
gi 136789549 gb EBQ41934.1	hypothetical protein G ( 63)	192	48.9	0.00099	gi 141113012 gb ECP71634.1	hypothetical protein G ( 83)	190	48.5	0.0017
gi 140376969 gb ECL35521.1	hypothetical protein G ( 149)	197	50.1	0.001	gi 143868004 gb EDH20779.1	hypothetical protein G ( 167)	194	49.5	0.0017
gi 142704948 gb ECZ98083.1	hypothetical protein G ( 107)	195	49.6	0.001	gi 139379779 gb ECE71675.1	hypothetical protein G ( 120)	192	49.0	0.0017
gi 136760213 gb EBQ22186.1	hypothetical protein G ( 150)	197	50.1	0.001	gi 137964772 gb EBX00908.1	hypothetical protein G ( 151)	193	49.3	0.0018
gi 229452487 gb EE058278.1	3-phosphoshikimate 1-c ( 409)	203	51.5	0.001	gi 142072287 gb ECV36024.1	hypothetical protein G ( 419)	199	50.7	0.0018
gi 137954036 gb EBW94853.1	hypothetical protein G ( 178)	198	50.3	0.001	gi 138687742 gb ECB31567.1	hypothetical protein G ( 215)	195	49.7	0.0018
gi 135010860 gb EBE91396.1	hypothetical protein G ( 93)	194	49.4	0.001	gi 135739268 gb EBU54246.1	hypothetical protein G ( 131)	192	49.0	0.0019
gi 267983528 gb ACY83357.1	UDP-N-acetylglucosamin ( 418)	203	51.5	0.001	gi 140653063 gb ECM58227.1	hypothetical protein G ( 132)	192	49.0	0.0019
gi 143444815 gb EDE99481.1	hypothetical protein G ( 419)	203	51.5	0.001	gi 224465099 gb EEF81352.1	UDP-N-acetylglucosamin ( 427)	199	50.7	0.0019
gi 137468274 gb EBU26710.1	hypothetical protein G ( 131)	196	49.9	0.001	gi 140033355 gb ECJ13975.1	hypothetical protein G ( 98)	190	48.6	0.0019
gi 135347204 gb EBH02680.1	hypothetical protein G ( 95)	194	49.4	0.0011	gi 139727823 gb ECH06066.1	hypothetical protein G ( 163)	193	49.3	0.0019

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gi 242123418 gb ACS81114.1	3-phosphoshikimate 1-c ( 444)	199	50.7	0.0019	gi 193089610 gb ACF14885.1	UDP-N-acetylglucosamin ( 429)	195	49.9	0.0034
gi 138751797 gb ECB75063.1	hypothetical protein G ( 273)	196	50.0	0.002	gi 116612514 gb ABK05238.1	UDP-N-acetylglucosamin ( 507)	196	50.1	0.0034
gi 138114114 gb EBX82134.1	hypothetical protein G ( 144)	192	49.0	0.002	gi 115789082 gb ABJ22152.1	Sequence 7120 from pat ( 430)	195	49.9	0.0034
gi 134469016 gb EBB52900.1	hypothetical protein G ( 74)	188	48.1	0.002	gi 143911586 gb EDH51981.1	hypothetical protein G ( 261)	192	49.2	0.0034
gi 138198542 gb EBY35312.1	hypothetical protein G ( 63)	187	47.8	0.002	gi 138307153 gb EBY90043.1	hypothetical protein G ( 96)	186	47.7	0.0034
gi 229445205 gb EE050996.1	3-phosphoshikimate 1-c ( 409)	198	50.5	0.0021	gi 139363992 gb ECE63192.1	hypothetical protein G ( 82)	185	47.5	0.0034
gi 143462007 gb EDF10728.1	hypothetical protein G ( 178)	193	49.3	0.0021	gi 135681712 gb EBJ18625.1	hypothetical protein G ( 124)	187	48.0	0.0036
gi 262355555 gb EE204646.1	3-phosphoshikimate 1-c ( 410)	198	50.5	0.0021	gi 150414167 gb EDN09532.1	3-dehydroquinase synth (1538)	202	51.6	0.0037
gi 142562795 gb ECY97747.1	hypothetical protein G ( 151)	192	49.1	0.0021	gi 143610523 gb EDF85316.1	hypothetical protein G ( 419)	194	49.7	0.0038
gi 251947714 gb EE587996.1	3-phosphoshikimate 1-c ( 412)	198	50.5	0.0021	gi 134382056 gb EBB03106.1	hypothetical protein G ( 67)	183	47.0	0.0038
gi 149386230 gb ABN65979.2	predicted protein [Pic (1571)	206	52.4	0.0021	gi 142882449 gb EDB25460.1	hypothetical protein G ( 80)	184	47.3	0.0038
gi 190404911 gb EDV08178.1	3-dehydroquinase dehyd (1588)	206	52.4	0.0021	gi 143644117 gb EDG03371.1	hypothetical protein G ( 96)	185	47.5	0.0039
gi 259145368 emb CAY78632.1	Aro1p [Saccharomyces (1588)	206	52.4	0.0021	gi 212561985 gb ACJ35040.1	UDP-N-acetylglucosamin ( 439)	194	49.7	0.004
gi 143307135 gb EDE23454.1	hypothetical protein G ( 419)	198	50.5	0.0021	gi 239838602 gb ACS30399.1	UDP-N-acetylglucosamin ( 442)	194	49.7	0.004
gi 143690268 gb EDG29963.1	hypothetical protein G ( 256)	195	49.8	0.0021	gi 137532653 gb EBU60183.1	hypothetical protein G ( 140)	187	48.0	0.004
gi 134945150 gb EBE47064.1	hypothetical protein G ( 133)	191	48.8	0.0022	gi 143224629 gb EDD71741.1	hypothetical protein G ( 413)	193	49.5	0.0043
gi 135692503 gb EBJ25287.1	hypothetical protein G ( 133)	191	48.8	0.0022	gi 137415456 gb EBT97288.1	hypothetical protein G ( 255)	190	48.7	0.0044
gi 134454271 gb EBB44255.1	hypothetical protein G ( 133)	191	48.8	0.0022	gi 219953367 gb ACL63751.1	UDP-N-acetylglucosamin ( 422)	193	49.5	0.0044
gi 139589325 gb ECG10870.1	hypothetical protein G ( 113)	190	48.6	0.0022	gi 136087910 gb EBL82913.1	hypothetical protein G ( 134)	186	47.8	0.0045
gi 141588775 gb ECS48489.1	hypothetical protein G ( 262)	195	49.8	0.0022	gi 140607099 gb ECM36325.1	hypothetical protein G ( 136)	186	47.8	0.0045
gi 141118077 gb ECP75109.1	hypothetical protein G ( 69)	187	47.9	0.0022	gi 134455209 gb EBB44828.1	hypothetical protein G ( 137)	186	47.8	0.0046
gi 140222713 gb ECK35846.1	hypothetical protein G ( 160)	192	49.1	0.0022	gi 137268607 gb EBT14833.1	hypothetical protein G ( 269)	190	48.7	0.0046
gi 141303147 gb ECQ94769.1	hypothetical protein G ( 264)	195	49.8	0.0022	gi 223512251 gb EEF23969.1	3-phosphoshikimate 1-c ( 193)	188	48.3	0.0046
gi 134859754 gb EBD90063.1	hypothetical protein G ( 62)	186	47.6	0.0023	gi 139030135 gb ECC92270.1	hypothetical protein G ( 100)	184	47.3	0.0047
gi 126249231 gb ABO08322.1	3-phosphoshikimate 1-c ( 403)	197	50.3	0.0024	gi 149390731 gb ABR25383.1	5-enolpyruvylshikimate ( 273)	190	48.8	0.0047
gi 238868104 gb ACR67815.1	UDP-N-acetylglucosamin ( 413)	197	50.3	0.0024	gi 142495350 gb ECY49520.1	hypothetical protein G ( 276)	190	48.8	0.0047
gi 239593894 gb EEQ76475.1	3-dehydroquinase synth (1597)	205	52.2	0.0025	gi 137462153 gb EBU23533.1	hypothetical protein G ( 120)	185	47.6	0.0047
gi 239607236 gb EEQ84223.1	3-dehydroquinase synth (1597)	205	52.2	0.0025	gi 136139207 gb EBM16318.1	hypothetical protein G ( 169)	187	48.0	0.0048
gi 136051312 gb EBL58189.1	hypothetical protein G ( 370)	196	50.1	0.0026	gi 146152689 gb ABQ03543.1	3-phosphoshikimate 1-c ( 409)	192	49.2	0.005
gi 138684318 gb ECB29207.1	hypothetical protein G ( 137)	190	48.6	0.0026	gi 167291322 gb ABZ44186.1	Sequence 18124 from pa ( 410)	192	49.2	0.005
gi 143709062 gb EDG38906.1	hypothetical protein G ( 376)	196	50.1	0.0026	gi 10639425 emb CAC11427.1	3-phosphoshikimate 1-c ( 410)	192	49.2	0.005
gi 240250963 gb ACS47902.1	3-phosphoshikimate 1-c ( 448)	197	50.3	0.0026	gi 141745506 gb ECT07595.1	hypothetical protein G ( 128)	185	47.6	0.005
gi 240249395 gb ACS46335.1	3-phosphoshikimate 1-c ( 448)	197	50.3	0.0026	gi 155262582 gb ABT18186.1	Sequence 105656 from p ( 155)	186	47.8	0.0051
gi 139199645 gb ECE09358.1	hypothetical protein G ( 322)	195	49.8	0.0026	gi 139689781 gb ECG79631.1	hypothetical protein G ( 94)	183	47.1	0.0051
gi 219621611 gb EBH14043.1	3-phosphoshikimate 1-c ( 462)	197	50.3	0.0027	gi 135390495 gb EBH31755.1	hypothetical protein G ( 133)	185	47.6	0.0052
gi 139957153 gb ECI62875.1	hypothetical protein G ( 203)	192	49.1	0.0027	gi 162953230 gb ABY22745.1	UDP-N-acetylglucosamin ( 515)	193	49.5	0.0052
gi 241995660 gb ACS75029.1	AroA [Methylophilus me ( 126)	189	48.4	0.0028	gi 135692660 gb EBJ25383.1	hypothetical protein G ( 140)	185	47.6	0.0054
gi 135364141 gb EBH14043.1	hypothetical protein G ( 91)	187	47.9	0.0028	gi 139513765 gb ECF58913.1	hypothetical protein G ( 124)	184	47.4	0.0056
gi 141272693 gb ECQ81987.1	hypothetical protein G ( 152)	190	48.6	0.0028	gi 134677879 gb EBC77000.1	hypothetical protein G ( 243)	188	48.3	0.0056
gi 140905310 gb ECO29373.1	hypothetical protein G ( 298)	194	49.6	0.0028	gi 138371238 gb EBZ21040.1	hypothetical protein G ( 76)	181	46.6	0.0057
gi 240278751 gb EER42257.1	pentafunctional AROM p (1595)	204	52.0	0.0029	gi 136629195 gb EBP38477.1	hypothetical protein G ( 76)	181	46.6	0.0057
gi 225560322 gb EEH08604.1	pentafunctional AROM p (1595)	204	52.0	0.0029	gi 134764306 gb EBD27211.1	hypothetical protein G ( 246)	188	48.3	0.0057
gi 136292074 gb EBN17837.1	hypothetical protein G ( 259)	193	49.4	0.0029	gi 15623398 dbj BAB67386.1	408aa long hypothetica ( 408)	191	49.0	0.0057
gi 135540756 gb EBI30520.1	hypothetical protein G ( 371)	195	49.9	0.003	gi 143133776 gb EDD06103.1	hypothetical protein G ( 296)	189	48.6	0.0058
gi 141117651 gb ECP74806.1	hypothetical protein G ( 267)	193	49.4	0.003	gi 157917592 gb ABY99019.1	3-phosphoshikimate 1-c ( 414)	191	49.0	0.0058
gi 142827402 gb EDA88063.1	hypothetical protein G ( 124)	188	48.2	0.0031	gi 143916751 gb EDH55551.1	hypothetical protein G ( 418)	191	49.0	0.0058
gi 139013401 gb ECC80641.1	hypothetical protein G ( 248)	192	49.1	0.0032	gi 138176813 gb EBY21560.1	hypothetical protein G ( 79)	181	46.6	0.0058
gi 60491659 emb CAH06411.1	putative 3-phosphoshik ( 410)	195	49.9	0.0032	gi 114338910 gb ABT69758.1	UDP-N-acetylglucosamin ( 419)	191	49.0	0.0058
gi 195933610 gb ACG58310.1	UDP-N-acetylglucosamin ( 421)	195	49.9	0.0033	gi 140904032 gb ECO28502.1	hypothetical protein G ( 135)	184	47.4	0.006
gi 53956243 gb AAV06240.1	Sequence 18197 from pat ( 421)	195	49.9	0.0033	gi 136500904 gb EBO57015.1	hypothetical protein G ( 370)	190	48.8	0.0061
gi 196170661 gb ACG71634.1	UDP-N-acetylglucosamin ( 422)	195	49.9	0.0033	gi 138544955 gb ECA33333.1	hypothetical protein G ( 86)	181	46.7	0.0063

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gi 137393308 gb EBT84756.1	hypothetical protein G ( 335)	189	48.6	0.0064	gi 139487309 gb ECF41573.1	hypothetical protein G ( 98)	179	46.3	0.0094
gi 145284076 gb ABP51658.1	3-phosphoshikimate 1-c ( 398)	190	48.8	0.0065	gi 141885008 gb ECT92840.1	hypothetical protein G ( 192)	183	47.2	0.0094
gi 138700454 gb ECB40624.1	hypothetical protein G ( 105)	182	46.9	0.0065	gi 138764060 gb ECB78675.1	hypothetical protein G ( 117)	180	46.5	0.0095
gi 135215041 gb EBG21926.1	hypothetical protein G ( 76)	180	46.4	0.0065	gi 29834829 gb AAP05464.1	3-phosphoshikimate 1-ca ( 446)	188	48.4	0.0095
gi 142452999 gb ECY18640.1	hypothetical protein G ( 417)	190	48.8	0.0067	gi 162953604 gb ABY23119.1	3-phosphoshikimate 1-c ( 461)	188	48.4	0.0098
gi 89335099 dbj BAE84694.1	hypothetical protein [ ( 419)	190	48.8	0.0068	gi 139188211 gb ECE01341.1	hypothetical protein G ( 63)	176	45.6	0.0099
gi 141433721 gb ECR79660.1	hypothetical protein G ( 80)	180	46.4	0.0068	gi 143745983 gb EDG57607.1	hypothetical protein G ( 150)	181	46.8	0.01
gi 135009318 gb EBE90352.1	hypothetical protein G ( 362)	189	48.6	0.0069	gi 15103454 gb AAE65493.1	Sequence 2 from patent (1551)	195	50.1	0.01
gi 197030981 gb ACH14982.1	Sequence 2 from patent ( 431)	190	48.8	0.0069	gi 20239787 gb AAE91809.1	Sequence 2 from patent (1551)	195	50.1	0.01
gi 207102478 emb CAR82017.1	unnamed protein produ ( 431)	190	48.8	0.0069	gi 143042478 gb EDC39310.1	hypothetical protein G ( 212)	183	47.2	0.01
gi 218086749 emb CAT03393.1	unnamed protein produ ( 431)	190	48.8	0.0069	gi 135121308 gb EBF62811.1	hypothetical protein G ( 296)	185	47.7	0.01
gi 213501391 emb CAS92774.1	unnamed protein produ ( 431)	190	48.8	0.0069	gi 140045594 gb ECJ21510.1	hypothetical protein G ( 78)	177	45.8	0.01
gi 161726847 emb CAP47295.1	unnamed protein produ ( 431)	190	48.8	0.0069	gi 137218459 gb EBS86662.1	hypothetical protein G ( 109)	179	46.3	0.01
gi 51587625 emb CAH19218.1	3-phosphoshikimate 1-c ( 431)	190	48.8	0.0069	gi 92394696 gb ABE75971.1	UDP-N-acetylglucosamine ( 422)	187	48.2	0.01
gi 218301238 emb CAU98558.1	unnamed protein produ ( 431)	190	48.8	0.0069	gi 138140870 gb EBX97063.1	hypothetical protein G ( 136)	180	46.5	0.011
gi 213501389 emb CAS92773.1	unnamed protein produ ( 431)	190	48.8	0.0069	gi 139739266 gb ECH13970.1	hypothetical protein G ( 317)	185	47.7	0.011
gi 213501387 emb CAS92772.1	unnamed protein produ ( 431)	190	48.8	0.0069	gi 139770468 gb ECH34129.1	hypothetical protein G ( 121)	179	46.3	0.011
gi 197053752 gb ACH25450.1	Sequence 2 from patent ( 431)	190	48.8	0.0069	gi 136211954 gb EBM63337.1	hypothetical protein G ( 122)	179	46.3	0.011
gi 218301240 emb CAU98560.1	unnamed protein produ ( 431)	190	48.8	0.0069	gi 142166301 gb ECW08274.1	hypothetical protein G ( 400)	186	48.0	0.012
gi 270507581 gb AC285859.1	UDP-N-acetylglucosamin ( 438)	190	48.8	0.007	gi 142351900 gb ECX46155.1	hypothetical protein G ( 91)	177	45.8	0.012
gi 134468282 gb EBB52463.1	hypothetical protein G ( 70)	179	46.2	0.007	gi 256689084 gb ACV06886.1	5-enolpyruvylshikimate ( 348)	185	47.8	0.012
gi 142900876 gb EDB38366.1	hypothetical protein G ( 317)	188	48.4	0.0071	gi 140383974 gb ECL40532.1	hypothetical protein G ( 251)	183	47.3	0.012
gi 141808592 gb ECT39389.1	hypothetical protein G ( 117)	182	46.9	0.0071	gi 137419753 gb EBT99762.1	hypothetical protein G ( 111)	178	46.1	0.012
gi 138138563 gb EBX95779.1	hypothetical protein G ( 140)	183	47.2	0.0072	gi 135556520 gb EBI40613.1	hypothetical protein G ( 94)	177	45.8	0.012
gi 142331408 gb ECX31573.1	hypothetical protein G ( 324)	188	48.4	0.0072	gi 135320669 gb EBG84854.1	hypothetical protein G ( 132)	179	46.3	0.012
gi 136480862 gb EB044034.1	hypothetical protein G ( 325)	188	48.4	0.0072	gi 139391913 gb EC79640.1	hypothetical protein G ( 133)	179	46.3	0.012
gi 141983563 gb ECU61776.1	hypothetical protein G ( 64)	178	46.0	0.0075	gi 16412014 emb CAD00604.1	UDP-N-acetylglucosamin ( 430)	186	48.0	0.012
gi 142476987 gb ECY36457.1	hypothetical protein G ( 149)	183	47.2	0.0076	gi 116742768 emb CAK21892.1	murA-1 [Listeria wels ( 430)	186	48.0	0.012
gi 140208878 gb ECK26833.1	hypothetical protein G ( 79)	179	46.2	0.0078	gi 217332641 gb ACK38435.1	UDP-N-acetylglucosamin ( 430)	186	48.0	0.012
gi 46914771 emb CAG21548.1	putative UDP-N-acetylgl ( 420)	189	48.6	0.0078	gi 16415206 emb CAC97896.1	UDP-N-acetylglucosamin ( 430)	186	48.0	0.012
gi 137740525 gb EBV74756.1	hypothetical protein G ( 133)	182	46.9	0.0079	gi 21702575 gb AAM75972.1	AF481102_8 5-enolpyruvyl ( 432)	186	48.0	0.012
gi 108461643 gb ABF86828.1	putative 3-phosphoshik ( 430)	189	48.6	0.008	gi 142637013 gb ECZ49717.1	hypothetical protein G ( 369)	185	47.8	0.012
gi 139513224 gb ECF58553.1	hypothetical protein G ( 69)	178	46.0	0.008	gi 140808226 gb ECN65512.1	hypothetical protein G ( 136)	179	46.3	0.012
gi 134598959 gb EBC30184.1	hypothetical protein G ( 160)	183	47.2	0.0081	gi 140185524 gb ECK10449.1	hypothetical protein G ( 137)	179	46.3	0.013
gi 119947437 gb ABM06348.1	UDP-N-acetylglucosamin ( 441)	189	48.6	0.0082	gi 62148370 emb CAH64137.1	3-phosphoshikimate 1-c ( 445)	186	48.0	0.013
gi 143620960 gb EDF90404.1	hypothetical protein G ( 331)	187	48.2	0.0085	gi 260649506 emb CBG72621.1	UDP-N-acetylglucosami ( 448)	186	48.0	0.013
gi 212009244 gb ACJ16626.1	5-enolpyruvylshikimate ( 402)	188	48.4	0.0087	gi 142928836 gb EDB58683.1	hypothetical protein G ( 322)	184	47.5	0.013
gi 135309098 gb EBG77172.1	hypothetical protein G ( 288)	186	47.9	0.0087	gi 52214895 dbj BAD47488.1	3-phosphoshikimate 1-c ( 410)	185	47.8	0.014
gi 256689097 gb ACV06899.1	3-phosphoshikimate 1-c ( 476)	189	48.7	0.0087	gi 138198137 gb EBY35030.1	hypothetical protein G ( 180)	180	46.6	0.014
gi 140624510 gb ECM41482.1	hypothetical protein G ( 76)	178	46.0	0.0087	gi 136285546 gb EBN13410.1	hypothetical protein G ( 153)	179	46.4	0.014
gi 143317823 gb EBE29836.1	hypothetical protein G ( 176)	183	47.2	0.0088	gi 190688437 gb EBA86115.1	UDP-N-acetylglucosamin ( 420)	185	47.8	0.014
gi 166853016 gb ABY91425.1	UDP-N-acetylglucosamin ( 416)	188	48.4	0.009	gi 139023559 gb ECC87682.1	hypothetical protein G ( 133)	178	46.1	0.014
gi 166857315 gb ABY95723.1	UDP-N-acetylglucosamin ( 416)	188	48.4	0.009	gi 140352867 gb ECL18954.1	hypothetical protein G ( 133)	178	46.1	0.014
gi 140284195 gb ECK74219.1	hypothetical protein G ( 110)	180	46.5	0.009	gi 139883257 gb ECL11584.1	hypothetical protein G ( 137)	178	46.1	0.014
gi 219540331 gb ACL22070.1	UDP-N-acetylglucosamin ( 419)	188	48.4	0.009	gi 162954008 gb ABY23523.1	UDP-N-acetylglucosamin ( 444)	185	47.8	0.015
gi 141432679 gb ECR78915.1	hypothetical protein G ( 67)	177	45.8	0.009	gi 178466894 dbj BAG21414.1	putative UDP-N-acetyl ( 446)	185	47.8	0.015
gi 167283017 gb ABZ35881.1	Sequence 9819 from pat ( 420)	188	48.4	0.009	gi 134374036 gb EBA97727.1	hypothetical protein G ( 122)	177	45.9	0.015
gi 133915492 emb CAM05605.1	3-phosphoshikimate 1- ( 422)	188	48.4	0.0091	gi 142291045 gb ECK01581.1	hypothetical protein G ( 146)	178	46.1	0.015
gi 142955368 gb EDB77607.1	hypothetical protein G ( 95)	179	46.3	0.0091	gi 139501414 gb ECF50392.1	hypothetical protein G ( 285)	182	47.1	0.015
gi 144091022 gb EDI80155.1	hypothetical protein G ( 365)	187	48.2	0.0092	gi 134400389 gb EBB13277.1	hypothetical protein G ( 77)	174	45.2	0.016
gi 141648244 gb ECS65129.1	hypothetical protein G ( 97)	179	46.3	0.0093	gi 144100806 gb EDI87031.1	hypothetical protein G ( 180)	179	46.4	0.016

gi 169803576 gb ACA82194.1	UDP-N-acetylglucosamin ( 428)	184	47.6	0.016	gi 125999056 gb ABN63131.1	UDP-N-acetylglucosamin ( 419)	181	47.0	0.025
gi 141252115 gb ECQ67624.1	hypothetical protein G ( 117)	176	45.7	0.017	gi 160859372 gb ABX47906.1	UDP-N-acetylglucosamin ( 419)	181	47.0	0.025
gi 45775290 gb AAS77246.1	putative 3-phosphoshiki ( 272)	181	46.9	0.017	gi 217497045 gb ACK45238.1	UDP-N-acetylglucosamin ( 419)	181	47.0	0.025
gi 140243474 gb ECK50349.1	hypothetical protein G ( 166)	178	46.2	0.017	gi 71039444 gb AAZ19752.1	UDP-N-acetylglucosamine ( 422)	181	47.0	0.025
gi 136904146 gb EBR14194.1	hypothetical protein G ( 86)	174	45.2	0.017	gi 156224224 gb EDO45052.1	predicted protein [Nem ( 428)	181	47.0	0.025
gi 167831743 dbj BAG08659.1	3-phosphoshikimate 1- ( 401)	183	47.4	0.018	gi 22294501 dbj BAC08331.1	UDP-N-acetylglucosamin ( 439)	181	47.0	0.026
gi 139978480 gb ECI77873.1	hypothetical protein G ( 90)	174	45.2	0.018	gi 137543749 gb EBU66153.1	hypothetical protein G ( 116)	173	45.1	0.026
gi 136287502 gb EBN14730.1	hypothetical protein G ( 411)	183	47.4	0.018	gi 139395280 gb ECE82035.1	hypothetical protein G ( 271)	178	46.3	0.026
gi 212555054 gb ACJ27508.1	UDP-N-acetylglucosamin ( 419)	183	47.4	0.019	gi 139360258 gb ECE62143.1	hypothetical protein G ( 235)	177	46.0	0.027
gi 144219177 gb EDJ73294.1	hypothetical protein G ( 182)	178	46.2	0.019	gi 136799044 gb EBQ48260.1	hypothetical protein G ( 173)	175	45.5	0.027
gi 135323535 gb EBG86796.1	hypothetical protein G ( 357)	182	47.1	0.019	gi 136046461 gb EBL54900.1	hypothetical protein G ( 286)	178	46.3	0.027
gi 219861261 gb ACL41603.1	transcriptional regula ( 507)	184	47.6	0.019	gi 136179199 gb EBM41522.1	hypothetical protein G ( 408)	180	46.8	0.028
gi 269096834 gb ACE221270.1	UDP-N-acetylglucosamin ( 509)	184	47.6	0.019	gi 135420409 gb EBH51870.1	hypothetical protein G ( 127)	173	45.1	0.028
gi 140931170 gb ECO47450.1	hypothetical protein G ( 134)	176	45.7	0.019	gi 228012361 gb ACP48122.1	3-phosphoshikimate 1-c ( 414)	180	46.8	0.028
gi 135441282 gb EBH65877.1	hypothetical protein G ( 136)	176	45.7	0.019	gi 143724011 gb EDG45785.1	hypothetical protein G ( 414)	180	46.8	0.028
gi 134720968 gb EBD02202.1	hypothetical protein G ( 192)	178	46.2	0.019	gi 228020375 gb ACP55782.1	3-phosphoshikimate 1-c ( 414)	180	46.8	0.028
gi 140343210 gb ECL12004.1	hypothetical protein G ( 141)	176	45.7	0.02	gi 227457241 gb ACP35928.1	3-phosphoshikimate 1-c ( 414)	180	46.8	0.028
gi 135487227 gb EBH96246.1	hypothetical protein G ( 283)	180	46.7	0.02	gi 228010404 gb ACP46166.1	3-phosphoshikimate 1-c ( 414)	180	46.8	0.028
gi 138558547 gb ECA42856.1	hypothetical protein G ( 124)	175	45.5	0.02	gi 138081133 gb EBX63740.1	hypothetical protein G ( 130)	173	45.1	0.028
gi 143907330 gb EDH49031.1	hypothetical protein G ( 338)	181	46.9	0.021	gi 143904828 gb EDH47285.1	hypothetical protein G ( 302)	178	46.3	0.029
gi 137616702 gb EBV07380.1	hypothetical protein G ( 147)	176	45.7	0.021	gi 136357609 gb EBN62230.1	hypothetical protein G ( 303)	178	46.3	0.029
gi 143566017 gb EDF66785.1	hypothetical protein G ( 76)	172	44.8	0.021	gi 139601152 gb ECG19101.1	hypothetical protein G ( 308)	178	46.3	0.029
gi 141831273 gb ECT55098.1	hypothetical protein G ( 149)	176	45.7	0.021	gi 46881970 gb AAT05264.1	UDP-N-acetylglucosamine ( 430)	180	46.8	0.029
gi 139190332 gb ECE02882.1	hypothetical protein G ( 108)	174	45.2	0.021	gi 225877536 emb CAS06250.1	Putative UDP-N-acetyl ( 430)	180	46.8	0.029
gi 142857632 gb EDB07334.1	hypothetical protein G ( 128)	175	45.5	0.021	gi 139819050 gb ECH68273.1	hypothetical protein G ( 96)	171	44.6	0.029
gi 13813452 gb AAK40646.1	3-phosphoshikimate 1-ca ( 414)	182	47.2	0.021	gi 177841144 gb ACB75396.1	3-phosphoshikimate 1-c ( 431)	180	46.8	0.029
gi 261601917 gb ACX91520.1	3-phosphoshikimate 1-c ( 414)	182	47.2	0.021	gi 140119616 gb ECJ67272.1	hypothetical protein G ( 222)	176	45.8	0.029
gi 119768707 gb ABM01278.1	UDP-N-acetylglucosamin ( 418)	182	47.2	0.021	gi 140328259 gb ECL01562.1	hypothetical protein G ( 98)	171	44.6	0.03
gi 238549023 dbj BAH65374.1	UDP-N-acetylglucosami ( 419)	182	47.2	0.021	gi 269302841 gb ACZ32941.1	3-phosphoshikimate 1-c ( 445)	180	46.8	0.03
gi 118567546 gb ABL02351.1	UDP-N-acetylglucosamin ( 419)	182	47.2	0.021	gi 4377372 gb AAD19176.1	Phosphoshikimate Vinyltr ( 445)	180	46.8	0.03
gi 150956962 gb ABR78992.1	UDP-N-acetylglucosamin ( 419)	182	47.2	0.021	gi 8163504 gb AAF73706.1	3-phosphoshikimate 1-car ( 445)	180	46.8	0.03
gi 34397864 gb AAQ66925.1	3-phosphoshikimate 1-ca ( 419)	182	47.2	0.021	gi 33236921 gb AAP99008.1	3-phosphoshikimate 1-ca ( 445)	180	46.8	0.03
gi 40111601 gb AAR53881.1	Sequence 13598 from pat ( 423)	182	47.2	0.022	gi 8979412 dbj BAA99246.1	phosphoshikimate vinylt ( 445)	180	46.8	0.03
gi 141223561 gb ECQ47426.1	hypothetical protein G ( 95)	173	45.0	0.022	gi 56660946 gb AAW16305.1	Sequence 1040 from pate ( 449)	180	46.8	0.03
gi 226098022 dbj BAH46464.1	UDP-N-acetylglucosami ( 427)	182	47.2	0.022	gi 140340029 gb ECL09712.1	hypothetical protein G ( 120)	172	44.8	0.031
gi 28410485 emb CAD66871.1	3-phosphoshikimate 1-c ( 443)	182	47.2	0.022	gi 144212288 gb EDJ68348.1	hypothetical protein G ( 331)	178	46.3	0.031
gi 89331472 dbj BAE81065.1	3-phosphoshikimate 1-c ( 445)	182	47.2	0.023	gi 137616572 gb EBV07310.1	hypothetical protein G ( 122)	172	44.9	0.031
gi 136096902 gb EBL89017.1	hypothetical protein G ( 102)	173	45.0	0.023	gi 136907629 gb EBR15450.1	hypothetical protein G ( 281)	177	46.1	0.031
gi 136707484 gb EBP87611.1	hypothetical protein G ( 204)	177	46.0	0.024	gi 142380263 gb ECX65159.1	hypothetical protein G ( 395)	179	46.5	0.031
gi 141686809 gb ECS81156.1	hypothetical protein G ( 124)	174	45.3	0.024	gi 138829636 gb ECC05571.1	hypothetical protein G ( 128)	172	44.9	0.032
gi 141795829 gb ECT33174.1	hypothetical protein G ( 288)	179	46.5	0.024	gi 137192869 gb EBS72151.1	hypothetical protein G ( 128)	172	44.9	0.032
gi 134478916 gb EBB58719.1	hypothetical protein G ( 90)	172	44.8	0.024	gi 211999671 gb EEB05331.1	pentafunctional AROM p (1584)	187	48.5	0.033
gi 137037500 gb EBR85370.1	hypothetical protein G ( 126)	174	45.3	0.024	gi 160429271 gb ABX42834.1	UDP-N-acetylglucosamin ( 418)	179	46.6	0.033
gi 142230728 gb ECW57166.1	hypothetical protein G ( 409)	181	47.0	0.024	gi 142237180 gb ECW61959.1	hypothetical protein G ( 418)	179	46.6	0.033
gi 143314137 gb EDR27504.1	hypothetical protein G ( 210)	177	46.0	0.024	gi 145563522 gb ABP74457.1	UDP-N-acetylglucosamin ( 419)	179	46.6	0.033
gi 28476576 gb AAO44664.1	3-phosphoshikimate 1-ca ( 486)	182	47.2	0.024	gi 120560331 gb ABM26258.1	UDP-N-acetylglucosamin ( 419)	179	46.6	0.033
gi 136031855 gb EBL45103.1	hypothetical protein G ( 414)	181	47.0	0.024	gi 145692283 gb ABP92788.1	UDP-N-acetylglucosamin ( 423)	179	46.6	0.033
gi 247541801 gb ACS98819.1	UDP-N-acetylglucosamin ( 417)	181	47.0	0.025	gi 145690079 gb ABP90585.1	UDP-N-acetylglucosamin ( 423)	179	46.6	0.033
gi 134051246 gb ABO49217.1	UDP-N-acetylglucosamin ( 417)	181	47.0	0.025	gi 55739074 gb AAV62715.1	UDP-N-acetylglucosamine ( 428)	179	46.6	0.034
gi 142013385 gb ECU83405.1	hypothetical protein G ( 418)	181	47.0	0.025	gi 167292185 gb ABZ45049.1	Sequence 18987 from pa ( 373)	178	46.3	0.034
gi 151363855 gb ABS06855.1	UDP-N-acetylglucosamin ( 419)	181	47.0	0.025	gi 140454168 gb ECL86667.1	hypothetical protein G ( 321)	177	46.1	0.035

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gi 135507526 gb EBI09289.1	hypothetical protein G ( 272)	176	45.8	0.035	gi 140724657 gb ECN08179.1	hypothetical protein G ( 102)	168	44.0	0.047
gi 31710845 gb AAP67810.1	Sequence 1114 from pate ( 449)	179	46.6	0.035	gi 142027336 gb ECU96678.1	hypothetical protein G ( 87)	167	43.7	0.048
gi 281012168 gb ADA07818.1	Sequence 1114 from pat ( 449)	179	46.6	0.035	gi 144079806 gb EDI72256.1	hypothetical protein G ( 87)	167	43.7	0.048
gi 115825398 gb ABJ37297.1	Sequence 1114 from pat ( 449)	179	46.6	0.035	gi 142253022 gb ECW73688.1	hypothetical protein G ( 284)	174	45.4	0.048
gi 139146809 gb ECD72295.1	hypothetical protein G ( 76)	168	43.9	0.037	gi 141310784 gb ECQ97443.1	hypothetical protein G ( 66)	165	43.3	0.05
gi 144974734 gb ABP12445.1	Sequence 18 from paten ( 28)	162	42.5	0.037	gi 136683126 gb EBP71689.1	hypothetical protein G ( 351)	175	45.7	0.05
gi 2484155 gb AAB72291.1	I49184 Sequence 18 from p ( 28)	162	42.5	0.037	gi 166856063 gb ABY94471.1	UDP-N-acetylglucosamin ( 417)	176	45.9	0.051
gi 5957555 gb AAE08229.1	Sequence 18 from patent ( 28)	162	42.5	0.037	gi 50903501 gb AAT87216.1	UDP-N-acetylglucosamine ( 419)	176	45.9	0.051
gi 2485232 gb AAB73368.1	I44457 Sequence 18 from p ( 28)	162	42.5	0.037	gi 22533863 gb AAM99730.1	AE014230_10 UDP-N-acetyl ( 419)	176	45.9	0.051
gi 152206293 gb ABS30603.1	3-phosphoshikimate 1-c ( 413)	178	46.3	0.038	gi 76562914 gb ABA45498.1	UDP-N-acetylglucosamine ( 419)	176	45.9	0.051
gi 227459852 gb ACP38538.1	3-phosphoshikimate 1-c ( 414)	178	46.3	0.038	gi 195974521 gb ACG62047.1	UDP-N-acetylglucosamin ( 419)	176	45.9	0.051
gi 238381356 gb ACR42444.1	3-phosphoshikimate 1-c ( 414)	178	46.3	0.038	gi 19748524 gb AAL97966.1	putative UDP-N-acetylgl ( 419)	176	45.9	0.051
gi 136384109 gb EBN80400.1	hypothetical protein G ( 415)	178	46.3	0.038	gi 158141998 gb ABW20310.1	UDP-N-acetylglucosamin ( 420)	176	45.9	0.051
gi 138671508 gb ECD20179.1	hypothetical protein G ( 130)	171	44.7	0.038	gi 229430270 gb EEO44832.1	UDP-N-acetylglucosamin ( 423)	176	45.9	0.051
gi 206568657 gb ACI10433.1	UDP-N-acetylglucosamin ( 419)	178	46.3	0.038	gi 143182820 gb EDD41234.1	hypothetical protein G ( 133)	169	44.2	0.052
gi 225702160 emb CAW99858.1	UDP-N-acetylglucosami ( 419)	178	46.3	0.038	gi 257804381 gb EEV33203.1	UDP-N-acetylglucosamin ( 429)	176	45.9	0.052
gi 136171835 gb EBM36678.1	hypothetical protein G ( 422)	178	46.3	0.038	gi 142018338 gb ECU88169.1	hypothetical protein G ( 158)	170	44.5	0.052
gi 55737161 gb AAV60803.1	UDP-N-acetylglucosamine ( 428)	178	46.3	0.039	gi 140874660 gb ECO09587.1	hypothetical protein G ( 115)	168	44.0	0.053
gi 140180092 gb ECK06544.1	hypothetical protein G ( 69)	167	43.7	0.039	gi 136049666 gb EBL57068.1	hypothetical protein G ( 314)	174	45.5	0.053
gi 138699474 gb ECB39929.1	hypothetical protein G ( 98)	169	44.2	0.04	gi 143126581 gb EDD00824.1	hypothetical protein G ( 191)	171	44.7	0.053
gi 139143879 gb ECD70262.1	hypothetical protein G ( 192)	173	45.2	0.04	gi 138345862 gb EBZ10558.1	hypothetical protein G ( 83)	166	43.5	0.053
gi 156567059 gb ABU82464.1	3-phosphoshikimate 1-c ( 443)	178	46.4	0.04	gi 136459335 gb EBO30111.1	hypothetical protein G ( 228)	172	45.0	0.053
gi 136634440 gb EBP41579.1	hypothetical protein G ( 86)	168	44.0	0.041	gi 143906341 gb EDH48335.1	hypothetical protein G ( 117)	168	44.0	0.053
gi 136363919 gb EBN66534.1	hypothetical protein G ( 73)	167	43.7	0.041	gi 137151382 gb EBS49008.1	hypothetical protein G ( 164)	170	44.5	0.054
gi 136738289 gb EBQ07820.1	hypothetical protein G ( 124)	170	44.4	0.042	gi 140838038 gb ECN85962.1	hypothetical protein G ( 101)	167	43.8	0.054
gi 1407233067 gb ECN07050.1	hypothetical protein G ( 89)	168	44.0	0.042	gi 270230871 emb CBI20198.1	unnamed protein produ ( 475)	176	46.0	0.057
gi 136476208 gb EBO41023.1	hypothetical protein G ( 243)	174	45.4	0.042	gi 138582552 gb ECA59501.1	hypothetical protein G ( 248)	172	45.0	0.057
gi 137127351 gb EBS35626.1	hypothetical protein G ( 106)	169	44.2	0.042	gi 254044508 gb ACT61301.1	UDP-N-acetylglucosamin ( 426)	175	45.7	0.059
gi 143151259 gb EDD18893.1	hypothetical protein G ( 92)	168	44.0	0.043	gi 28270230 gb CAD63131.1	UDP-N-acetylglucosamin ( 426)	175	45.7	0.059
gi 251818535 emb CAZ56366.1	UDP-N-acetylglucosami ( 419)	177	46.1	0.044	gi 256994553 gb EEU81855.1	UDP-N-acetylglucosamin ( 430)	175	45.7	0.06
gi 251816600 emb CAZ52238.1	UDP-N-acetylglucosami ( 419)	177	46.1	0.044	gi 256952732 gb EEU69364.1	UDP-N-acetylglucosamin ( 430)	175	45.7	0.06
gi 71802859 gb AAX72212.1	UDP-N-acetylglucosamine ( 419)	177	46.1	0.044	gi 256998392 gb EEU84912.1	UDP-N-acetylglucosamin ( 430)	175	45.7	0.06
gi 71853702 gb AAZ51725.1	UDP-N-acetylglucosamine ( 419)	177	46.1	0.044	gi 257160824 gb EEU90784.1	UDP-N-acetylglucosamin ( 430)	175	45.7	0.06
gi 28810988 dbj BAC63922.1	putative UDP-N-acetylgl ( 419)	177	46.1	0.044	gi 256986010 gb EEU73312.1	UDP-N-acetylglucosamin ( 430)	175	45.7	0.06
gi 143565502 gb EDF66515.1	hypothetical protein G ( 419)	177	46.1	0.044	gi 256993601 gb EEU80903.1	UDP-N-acetylglucosamin ( 430)	175	45.7	0.06
gi 94546174 gb ABF36221.1	UDP-N-acetylglucosamine ( 419)	177	46.1	0.044	gi 256598280 gb EEU17456.1	UDP-N-acetylglucosamin ( 430)	175	45.7	0.06
gi 94544194 gb ABF34242.1	UDP-N-acetylglucosamine ( 419)	177	46.1	0.044	gi 29343206 gb AAO80969.1	UDP-N-acetylglucosamine ( 430)	175	45.7	0.06
gi 209540799 gb ACI61375.1	UDP-N-acetylglucosamin ( 419)	177	46.1	0.044	gi 256949162 gb EEU65794.1	UDP-N-acetylglucosamin ( 430)	175	45.7	0.06
gi 13622467 gb AAK34186.1	putative UDP-N-acetylgl ( 419)	177	46.1	0.044	gi 255969024 gb EET99646.1	UDP-N-acetylglucosamin ( 430)	175	45.7	0.06
gi 251820383 emb CAR46971.1	UDP-N-acetylglucosami ( 419)	177	46.1	0.044	gi 255964127 gb EET99603.1	UDP-N-acetylglucosamin ( 430)	175	45.7	0.06
gi 134271847 emb CAM30082.1	UDP-N-acetylglucosami ( 419)	177	46.1	0.044	gi 256683428 gb ECW83000.1	UDP-N-acetylglucosamin ( 430)	175	45.7	0.06
gi 242391406 dbj BAH81865.1	UDP-N-acetylglucosami ( 419)	177	46.1	0.044	gi 257164739 gb EEU94699.1	UDP-N-acetylglucosamin ( 430)	175	45.7	0.06
gi 94542289 gb ABF32338.1	UDP-N-acetylglucosamine ( 419)	177	46.1	0.044	gi 256990899 gb EEU78201.1	UDP-N-acetylglucosamin ( 430)	175	45.7	0.06
gi 142787608 gb EDA58191.1	hypothetical protein G ( 355)	176	45.9	0.044	gi 256955926 gb EEU72558.1	UDP-N-acetylglucosamin ( 430)	175	45.7	0.06
gi 108465795 gb ABF90980.1	UDP-N-acetylglucosamin ( 420)	177	46.1	0.044	gi 257157615 gb EEU87575.1	UDP-N-acetylglucosamin ( 430)	175	45.7	0.06
gi 14517938 gb AAK64441.1	AF377339_2 UDP-GlcNAc 1- ( 420)	177	46.1	0.044	gi 141085359 gb ECP52162.1	hypothetical protein G ( 69)	164	43.1	0.06
gi 116101170 gb ABJ66316.1	UDP-N-acetylglucosamin ( 423)	177	46.1	0.044	gi 142265664 gb ECW83000.1	hypothetical protein G ( 189)	170	44.5	0.061
gi 140152195 gb ECJ87113.1	hypothetical protein G ( 134)	170	44.5	0.045	gi 139799833 gb ECH54842.1	hypothetical protein G ( 84)	165	43.3	0.062
gi 116099232 gb ABJ64381.1	UDP-N-acetylglucosamin ( 435)	177	46.1	0.045	gi 197710518 gb EDY54552.1	UDP-N-acetylglucosamin ( 448)	175	45.7	0.062
gi 136121233 gb EBM05633.1	hypothetical protein G ( 371)	176	45.9	0.046	gi 138633487 gb ECA94615.1	hypothetical protein G ( 119)	167	43.8	0.063
gi 137081208 gb EBS10031.1	hypothetical protein G ( 71)	166	43.5	0.046	gi 143127849 gb EDD01758.1	hypothetical protein G ( 282)	172	45.0	0.064



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gi 143636058 gb EDF98692.1	hypothetical protein G ( 75)	164	43.1	0.065	gi 262261230 gb EEY79929.1	UDP-N-acetylglucosamin ( 420)	171	44.9	0.1
gi 140891397 gb ECO21011.1	hypothetical protein G ( 289)	172	45.0	0.066	gi 135254630 gb EBG45208.1	hypothetical protein G ( 422)	171	44.9	0.1
gi 141883049 gb ECT91469.1	hypothetical protein G ( 77)	164	43.1	0.066	gi 143832894 gb EDG95261.1	hypothetical protein G ( 258)	168	44.2	0.11
gi 136971600 gb EBR48170.1	hypothetical protein G ( 128)	167	43.8	0.067	gi 257473601 gb ACV51720.1	UDP-N-acetylglucosamin ( 427)	171	44.9	0.11
gi 136511372 gb EBO63787.1	hypothetical protein G ( 214)	170	44.5	0.067	gi 138120911 gb EBX85976.1	hypothetical protein G ( 260)	168	44.2	0.11
gi 23095295 emb CAD46505.1	Unknown [Streptococcus ( 419)	174	45.5	0.068	gi 140673198 gb ECM72414.1	hypothetical protein G ( 70)	160	42.2	0.11
gi 188595418 dbj BAG34393.1	putative 3-phosphoshi ( 419)	174	45.5	0.068	gi 142168248 gb ECW09775.1	hypothetical protein G ( 449)	171	44.9	0.11
gi 142134144 gb ECV84003.1	hypothetical protein G ( 215)	170	44.5	0.068	gi 135597220 gb EBI66356.1	hypothetical protein G ( 119)	163	43.0	0.11
gi 135591094 gb EBI62571.1	hypothetical protein G ( 69)	163	42.9	0.07	gi 137253093 gb EBT06079.1	hypothetical protein G ( 119)	163	43.0	0.11
gi 59746623 gb AAW97135.1	Sequence 14698 from pat ( 263)	171	44.8	0.07	gi 135113525 gb EBF57833.1	hypothetical protein G ( 454)	171	44.9	0.11
gi 143298282 gb EDE18600.1	hypothetical protein G ( 268)	171	44.8	0.071	gi 135111290 gb EBF56415.1	hypothetical protein G ( 454)	171	44.9	0.11
gi 137829606 gb EBW23918.1	hypothetical protein G ( 99)	165	43.4	0.071	gi 135096128 gb EBF46697.1	hypothetical protein G ( 454)	171	44.9	0.11
gi 140437930 gb ECL75035.1	hypothetical protein G ( 194)	169	44.3	0.072	gi 139811437 gb ECH63105.1	hypothetical protein G ( 62)	159	42.0	0.11
gi 6911979 emb CAB72195.1	UDP-N-acetylglucosamine ( 448)	174	45.5	0.072	gi 142898535 gb EBB36622.1	hypothetical protein G ( 287)	168	44.2	0.12
gi 140438989 gb ECL75771.1	hypothetical protein G ( 121)	166	43.6	0.073	gi 137104776 gb EBS22894.1	hypothetical protein G ( 250)	167	44.0	0.12
gi 138970500 gb ECC64000.1	hypothetical protein G ( 240)	170	44.6	0.074	gi 166854871 gb ABY93280.1	UDP-N-acetylglucosamin ( 417)	170	44.7	0.12
gi 137693394 gb EBV49130.1	hypothetical protein G ( 125)	166	43.6	0.075	gi 12802942 gb AAK08125.1	UDP-N-acetylglucosamine ( 357)	169	44.4	0.12
gi 139370234 gb ECE65074.1	hypothetical protein G ( 106)	165	43.4	0.076	gi 135046225 gb EBF14853.1	hypothetical protein G ( 257)	167	44.0	0.12
gi 138887694 gb ECC30777.1	hypothetical protein G ( 130)	166	43.6	0.078	gi 212549346 dbj BAG84014.1	3-phosphoshikimate 1- ( 426)	170	44.7	0.12
gi 94548110 gb ABF38156.1	UDP-N-acetylglucosamine ( 419)	173	45.3	0.078	gi 256711277 gb EEU26315.1	UDP-N-acetylglucosamin ( 430)	170	44.7	0.12
gi 139375434 gb ECE68685.1	hypothetical protein G ( 67)	162	42.7	0.078	gi 142973737 gb EDB90282.1	hypothetical protein G ( 96)	161	42.5	0.12
gi 138926726 gb ECC45302.1	hypothetical protein G ( 133)	166	43.6	0.08	gi 142861353 gb EDB10051.1	hypothetical protein G ( 432)	170	44.7	0.12
gi 135734076 gb EBJ51018.1	hypothetical protein G ( 134)	166	43.6	0.08	gi 136573786 gb EBB03634.1	hypothetical protein G ( 222)	166	43.7	0.12
gi 135669959 gb EBJ11406.1	hypothetical protein G ( 159)	167	43.9	0.08	gi 141827987 gb ECT52798.1	hypothetical protein G ( 135)	163	43.0	0.12
gi 139132736 gb ECD62598.1	hypothetical protein G ( 82)	163	42.9	0.081	gi 139819051 gb ECH68274.1	hypothetical protein G ( 70)	159	42.0	0.13
gi 136277271 gb EBN07840.1	hypothetical protein G ( 265)	170	44.6	0.081	gi 142725044 gb EDA12427.1	hypothetical protein G ( 83)	160	42.3	0.13
gi 144009555 gb EDI21805.1	hypothetical protein G ( 316)	171	44.8	0.082	gi 29608787 dbj BAC72840.1	putative UDP-N-acetylgl ( 448)	170	44.7	0.13
gi 134957415 gb EBE55225.1	hypothetical protein G ( 102)	164	43.2	0.084	gi 134464232 gb EBB50113.1	hypothetical protein G ( 118)	162	42.8	0.13
gi 55420321 gb AAV52046.1	AroA [Haemophilus paras ( 329)	171	44.8	0.085	gi 137574225 gb EBU83505.1	hypothetical protein G ( 119)	162	42.8	0.13
gi 134462559 gb EBB49152.1	hypothetical protein G ( 122)	165	43.4	0.085	gi 142158366 gb ECW02190.1	hypothetical protein G ( 454)	170	44.7	0.13
gi 141833611 gb ECT56782.1	hypothetical protein G ( 104)	164	43.2	0.086	gi 55420325 gb AAV52048.1	AroA [Actinobacillus ur ( 338)	168	44.2	0.13
gi 196191655 gb EDX86619.1	UDP-N-acetylglucosamin ( 477)	173	45.3	0.087	gi 140788486 gb ECN51392.1	hypothetical protein G ( 106)	161	42.5	0.13
gi 135188539 gb EBG06001.1	hypothetical protein G ( 342)	171	44.8	0.088	gi 21904770 gb AAM79640.1	putative UDP-N-acetylgl ( 404)	169	44.5	0.13
gi 142718885 gb EDA08059.1	hypothetical protein G ( 417)	172	45.1	0.09	gi 139116258 gb ECD52455.1	hypothetical protein G ( 127)	162	42.8	0.14
gi 135059368 gb EBF23231.1	hypothetical protein G ( 364)	171	44.9	0.092	gi 268625593 gb EEZ57993.1	UDP-N-acetylglucosamin ( 417)	169	44.5	0.14
gi 139434090 gb ECF08739.1	hypothetical protein G ( 96)	163	42.9	0.093	gi 268584379 gb EEZ49055.1	UDP-N-acetylglucosamin ( 417)	169	44.5	0.14
gi 256714009 gb EEU28997.1	UDP-N-acetylglucosamin ( 432)	172	45.1	0.093	gi 268586619 gb EEZ51295.1	UDP-N-acetylglucosamin ( 417)	169	44.5	0.14
gi 256613445 gb EEU18648.1	UDP-N-acetylglucosamin ( 432)	172	45.1	0.093	gi 59719126 gb AAW90531.1	putative UDP-N-acetylgl ( 417)	169	44.5	0.14
gi 144018211 gb EDI27781.1	hypothetical protein G ( 324)	170	44.6	0.096	gi 193935115 gb ACF30939.1	UDP-N-acetylglucosamin ( 417)	169	44.5	0.14
gi 138650547 gb ECB05452.1	hypothetical protein G ( 168)	166	43.7	0.097	gi 226512474 gb EEH61819.1	UDP-N-acetylglucosamin ( 417)	169	44.5	0.14
gi 134737951 gb EBD11912.1	hypothetical protein G ( 235)	168	44.2	0.098	gi 268551781 gb EEZ246800.1	UDP-N-acetylglucosamin ( 417)	169	44.5	0.14
gi 134595715 gb EBC28324.1	hypothetical protein G ( 278)	169	44.4	0.098	gi 228228929 gb ACP86594.1	Sequence 8450 from pat ( 417)	169	44.5	0.14
gi 135179486 gb EBG00241.1	hypothetical protein G ( 330)	170	44.6	0.098	gi 268621293 gb EEZ53693.1	UDP-N-acetylglucosamin ( 417)	169	44.5	0.14
gi 137174025 gb EBS61743.1	hypothetical protein G ( 103)	163	42.9	0.098	gi 268588887 gb EEZ53563.1	UDP-N-acetylglucosamin ( 417)	169	44.5	0.14
gi 141041491 gb ECP22985.1	hypothetical protein G ( 104)	163	43.0	0.099	gi 268549193 gb EEZ44611.1	UDP-N-acetylglucosamin ( 417)	169	44.5	0.14
gi 134600428 gb EBC31021.1	hypothetical protein G ( 242)	168	44.2	0.1	gi 140395645 gb ECL48452.1	hypothetical protein G ( 79)	159	42.1	0.14
gi 142831308 gb EDA91032.1	hypothetical protein G ( 291)	169	44.4	0.1	gi 157075899 gb ABV10582.1	UDP-N-acetylglucosamin ( 420)	169	44.5	0.14
gi 134338116 gb EBA73904.1	hypothetical protein G ( 413)	171	44.9	0.1	gi 198249249 gb ACH84842.1	UDP-N-acetylglucosamin ( 423)	169	44.5	0.14
gi 135167020 gb EBF92253.1	hypothetical protein G ( 352)	170	44.6	0.1	gi 218519485 gb ACK80071.1	UDP-N-acetylglucosamin ( 423)	169	44.5	0.14
gi 137755492 gb EBV82397.1	hypothetical protein G ( 298)	169	44.4	0.1	gi 141040532 gb ECP22321.1	hypothetical protein G ( 96)	160	42.3	0.14
gi 135327958 gb EBG89770.1	hypothetical protein G ( 418)	171	44.9	0.1	gi 143630447 gb EDF95521.1	hypothetical protein G ( 135)	162	42.8	0.14

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gi 141775381 gb ECT22687.1	hypothetical protein G ( 135)	162	42.8	0.14	gi 140152257 gb ECJ87157.1	hypothetical protein G ( 97)	157	41.7	0.22
gi 137848322 gb EBW34669.1	hypothetical protein G ( 83)	159	42.1	0.15	gi 165931440 emb CAP07015.1	3-phosphoshikimate 1- ( 440)	166	43.9	0.22
gi 138467471 gb EBZ87871.1	hypothetical protein G ( 269)	166	43.8	0.15	gi 111957970 gb ABH73822.1	Sequence 59 from paten ( 440)	166	43.9	0.22
gi 142903519 gb EDB40319.1	hypothetical protein G ( 319)	167	44.0	0.15	gi 259306889 gb ACW37700.1	Sequence 59 from paten ( 440)	166	43.9	0.22
gi 6063409 dbj BAA85335.1	UDP-N-acetylglucosamine ( 446)	169	44.5	0.15	gi 165930565 emb CAP04061.1	3-phosphoshikimate 1- ( 440)	166	43.9	0.22
gi 143528632 gb EDF47496.1	hypothetical protein G ( 379)	168	44.2	0.15	gi 136637968 gb EBP43697.1	hypothetical protein G ( 326)	164	43.4	0.23
gi 73912408 dbj BAE20403.1	5-enolpyruvylshikimate ( 231)	165	43.5	0.15	gi 134893000 gb EBE12404.1	hypothetical protein G ( 86)	156	41.5	0.23
gi 141468301 gb ECR99942.1	hypothetical protein G ( 275)	166	43.8	0.15	gi 136491502 gb EBO50898.1	hypothetical protein G ( 169)	160	42.4	0.23
gi 143091256 gb EDC75017.1	hypothetical protein G ( 73)	158	41.8	0.15	gi 135044669 gb EBF13863.1	hypothetical protein G ( 170)	160	42.4	0.23
gi 136612405 gb EBP28570.1	hypothetical protein G ( 174)	163	43.1	0.15	gi 134521141 gb EBB83682.1	hypothetical protein G ( 104)	157	41.7	0.24
gi 137764462 gb EBV87009.1	hypothetical protein G ( 107)	160	42.3	0.16	gi 137172829 gb EBS61062.1	hypothetical protein G ( 89)	156	41.5	0.24
gi 25166285 dbj BAC24475.1	murA [Wigglesworthia g ( 418)	168	44.3	0.16	gi 135135012 gb EBF71681.1	hypothetical protein G ( 402)	165	43.6	0.24
gi 125498222 gb ABN44888.1	Conserved uncharacteri ( 419)	168	44.3	0.16	gi 140369628 gb ECL30304.1	hypothetical protein G ( 294)	163	43.2	0.24
gi 136440761 gb EBO18088.1	hypothetical protein G ( 111)	160	42.3	0.16	gi 214034673 gb EBB75413.1	UDP-N-acetylglucosamin ( 415)	165	43.6	0.25
gi 143736357 gb EDG51926.1	hypothetical protein G ( 155)	162	42.8	0.16	gi 151280568 gb ABR88978.1	UDP-N-acetylglucosamin ( 416)	165	43.6	0.25
gi 16412040 emb CAD00630.1	murZ [Listeria monocyt ( 423)	168	44.3	0.16	gi 142423151 gb ECX96538.1	hypothetical protein G ( 417)	165	43.6	0.25
gi 135591110 gb EBI62581.1	hypothetical protein G ( 132)	161	42.6	0.16	gi 135561634 gb EBI43929.1	hypothetical protein G ( 418)	165	43.6	0.25
gi 160347816 gb ABX26490.1	UDP-N-acetylglucosamin ( 431)	168	44.3	0.16	gi 167591717 gb ABZ83465.1	udp-n-acetylglucosamin ( 420)	165	43.6	0.25
gi 137036035 gb EBR84572.1	hypothetical protein G ( 70)	157	41.6	0.17	gi 135513173 gb EBI12931.1	hypothetical protein G ( 94)	156	41.5	0.25
gi 197720926 gb EDY64834.1	UDP-N-acetylglucosamin ( 446)	168	44.3	0.17	gi 78037096 emb CAJ24841.1	UDP-N-acetylglucosamin ( 424)	165	43.6	0.25
gi 137233843 gb EBS95366.1	hypothetical protein G ( 102)	159	42.1	0.17	gi 256583776 gb ACU94910.1	UDP-N-acetylglucosamin ( 425)	165	43.6	0.25
gi 137935986 gb EBW84686.1	hypothetical protein G ( 201)	163	43.1	0.18	gi 138619891 gb ECA85573.1	hypothetical protein G ( 158)	159	42.2	0.25
gi 228227429 gb ACP85094.1	Sequence 5450 from pat ( 282)	165	43.6	0.18	gi 137520362 gb EBU53503.1	hypothetical protein G ( 69)	154	41.0	0.25
gi 171851474 emb CAQ04450.1	3-phosphoshikimate 1- ( 467)	168	44.3	0.18	gi 143591526 gb EDF75600.1	hypothetical protein G ( 226)	161	42.7	0.26
gi 134410709 gb EBB19029.1	hypothetical protein G ( 285)	165	43.6	0.18	gi 134891434 gb EBE11362.1	hypothetical protein G ( 138)	158	42.0	0.26
gi 135629141 gb EBI86117.1	hypothetical protein G ( 89)	158	41.9	0.18	gi 134767538 gb EBD29426.1	hypothetical protein G ( 120)	157	41.7	0.27
gi 137233043 gb EBS94913.1	hypothetical protein G ( 249)	164	43.3	0.18	gi 141041104 gb ECP22722.1	hypothetical protein G ( 102)	156	41.5	0.27
gi 137560711 gb EBU75797.1	hypothetical protein G ( 109)	159	42.1	0.18	gi 142900460 gb EDB38056.1	hypothetical protein G ( 332)	163	43.2	0.27
gi 142900568 gb EDB38135.1	hypothetical protein G ( 352)	166	43.8	0.18	gi 136086971 gb EBL82277.1	hypothetical protein G ( 145)	158	42.0	0.27
gi 139812606 gb ECH63945.1	hypothetical protein G ( 130)	160	42.4	0.19	gi 239911204 gb ACS34095.1	3-phosphoshikimate 1-c ( 398)	164	43.4	0.27
gi 225699514 emb CAW93074.1	UDP-N-acetylglucosami ( 419)	167	44.1	0.19	gi 138345237 gb EBZ10125.1	hypothetical protein G ( 106)	156	41.5	0.28
gi 167732521 emb CAP50715.1	UDP-N-acetylglucosami ( 424)	167	44.1	0.19	gi 142433170 gb ECY04151.1	hypothetical protein G ( 91)	155	41.3	0.28
gi 137259628 gb EBT09802.1	hypothetical protein G ( 261)	164	43.3	0.19	gi 138967682 gb ECC62769.1	hypothetical protein G ( 66)	153	40.8	0.28
gi 137867122 gb EBW45478.1	hypothetical protein G ( 262)	164	43.3	0.19	gi 229380775 gb EEO30866.1	UDP-N-acetylglucosamin ( 417)	164	43.4	0.28
gi 231274025 emb CAX10818.1	3-phosphoshikimate 1- ( 440)	167	44.1	0.19	gi 137945478 gb EBW90050.1	hypothetical protein G ( 300)	162	43.0	0.29
gi 231273013 emb CAX09925.1	3-phosphoshikimate 1- ( 440)	167	44.1	0.19	gi 143014918 gb EDC19274.1	hypothetical protein G ( 154)	158	42.0	0.29
gi 76167624 gb AA50632.1	3-phosphoshikimate 1-ca ( 440)	167	44.1	0.19	gi 135550325 gb EBI36633.1	hypothetical protein G ( 307)	162	43.0	0.29
gi 141200123 gb ECQ31132.1	hypothetical protein G ( 237)	163	43.1	0.2	gi 137859016 gb EBW40859.1	hypothetical protein G ( 69)	153	40.8	0.29
gi 140339709 gb ECL09481.1	hypothetical protein G ( 88)	157	41.7	0.2	gi 139795572 gb ECH51845.1	hypothetical protein G ( 136)	157	41.8	0.3
gi 142888082 gb EDB29077.1	hypothetical protein G ( 341)	165	43.6	0.21	gi 3328790 gb AAC67962.1	Phosphoshikimate 1-carbo ( 440)	164	43.4	0.3
gi 141756443 gb ECT12702.1	hypothetical protein G ( 208)	162	42.9	0.21	gi 140777409 gb ECN43706.1	hypothetical protein G ( 71)	153	40.8	0.3
gi 143875110 gb EDH25993.1	hypothetical protein G ( 152)	160	42.4	0.21	gi 136905237 gb EBR14604.1	hypothetical protein G ( 287)	161	42.7	0.32
gi 20515136 gb AAM23459.1	UDP-N-acetylglucosamine ( 415)	166	43.8	0.21	gi 141741379 gb ECT05533.1	hypothetical protein G ( 151)	157	41.8	0.32
gi 161594583 gb ABX72243.1	UDP-N-acetylglucosamin ( 417)	166	43.8	0.21	gi 143435502 gb EDE94103.1	hypothetical protein G ( 295)	161	42.7	0.33
gi 254671262 emb CBA08549.1	UDP-N-acetylglucosami ( 417)	166	43.8	0.21	gi 133740129 emb CAL63180.1	UDP-N-acetylglucosami ( 416)	163	43.2	0.33
gi 219679913 gb EED36262.1	UDP-N-acetylglucosamin ( 420)	166	43.8	0.21	gi 167283169 gb ABZ36033.1	Sequence 9971 from pat ( 417)	163	43.2	0.33
gi 140421466 gb ECL64457.1	hypothetical protein G ( 111)	158	41.9	0.22	gi 141800948 gb ECT35640.1	hypothetical protein G ( 93)	154	41.1	0.33
gi 144188789 gb EDJ51600.1	hypothetical protein G ( 94)	157	41.7	0.22	gi 117608277 gb ABK43732.1	UDP-N-acetylglucosamin ( 419)	163	43.2	0.33
gi 21109273 gb AAM37810.1	UDP-N-acetylglucosamine ( 424)	166	43.9	0.22	gi 57638265 gb AAW55053.1	UDP-N-acetylglucosamine ( 419)	163	43.2	0.33
gi 137052829 gb EBR94060.1	hypothetical protein G ( 112)	158	41.9	0.22	gi 262298484 gb EEY86397.1	UDP-N-acetylglucosamin ( 419)	163	43.2	0.33
gi 260572493 gb EEX29055.1	UDP-N-acetylglucosamin ( 431)	166	43.9	0.22	gi 143193365 gb EDD48952.1	hypothetical protein G ( 421)	163	43.2	0.33

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gi 167289411 gb ABZ42275.1	Sequence 16213 from pa ( 423)	163	43.2	0.33	gi 138737511 gb ECB66481.1	hypothetical protein G ( 118)	154	41.1	0.4
gi 167288662 gb ABZ41526.1	Sequence 15464 from pa ( 423)	163	43.2	0.33	gi 142767344 gb EDA43135.1	hypothetical protein G ( 119)	154	41.1	0.41
gi 116103448 gb ABJ68591.1	UDP-N-acetylglucosamin ( 423)	163	43.2	0.33	gi 140241779 gb ECK49161.1	hypothetical protein G ( 142)	155	41.3	0.41
gi 167289031 gb ABZ41895.1	Sequence 15833 from pa ( 423)	163	43.2	0.33	gi 142693403 gb ECZ89811.1	hypothetical protein G ( 102)	153	40.9	0.41
gi 21113985 gb AAM42067.1	UDP-N-acetylglucosamine ( 424)	163	43.2	0.33	gi 138212658 gb EBY44975.1	hypothetical protein G ( 169)	156	41.6	0.41
gi 66572977 gb AAY48387.1	UDP-N-acetylglucosamine ( 424)	163	43.2	0.33	gi 136884865 gb EBR04394.1	hypothetical protein G ( 87)	152	40.6	0.41
gi 138016246 gb EBX28950.1	hypothetical protein G ( 156)	157	41.8	0.33	gi 40134109 gb AAR60243.1	Sequence 6777 from pate ( 237)	158	42.1	0.41
gi 134708780 gb EBC95330.1	hypothetical protein G ( 158)	157	41.8	0.34	gi 138764059 gb ECB78674.1	hypothetical protein G ( 201)	157	41.8	0.42
gi 281044951 gb ADA23679.1	Sequence 4217 from pat ( 431)	163	43.2	0.34	gi 136430523 gb EB011467.1	hypothetical protein G ( 249)	158	42.1	0.43
gi 259270370 gb ACW30183.1	Sequence 4217 from pat ( 431)	163	43.2	0.34	gi 140728797 gb ECN11186.1	hypothetical protein G ( 300)	159	42.3	0.44
gi 259365177 gb ACW59123.1	Sequence 3841 from pat ( 431)	163	43.2	0.34	gi 142007843 gb ECU78491.1	hypothetical protein G ( 79)	151	40.4	0.44
gi 217110295 gb ACJ94175.1	Sequence 4217 from pat ( 431)	163	43.2	0.34	gi 139167173 gb ECD86616.1	hypothetical protein G ( 302)	159	42.3	0.44
gi 144970267 gb ABP08557.1	Sequence 3841 from pat ( 431)	163	43.2	0.34	gi 218323683 emb CAV20010.1	UDP-N-acetylglucosami ( 422)	161	42.8	0.44
gi 112037166 gb ABH88468.1	Sequence 3841 from pat ( 431)	163	43.2	0.34	gi 140010510 gb ECI98634.1	hypothetical protein G ( 132)	154	41.1	0.45
gi 140811098 gb ECN67441.1	hypothetical protein G ( 262)	160	42.5	0.34	gi 134333526 gb EBA70769.1	hypothetical protein G ( 219)	157	41.9	0.45
gi 135393658 gb EBH33888.1	hypothetical protein G ( 82)	153	40.8	0.34	gi 144169455 gb EDJ37230.1	hypothetical protein G ( 437)	161	42.8	0.46
gi 136512696 gb EBC64623.1	hypothetical protein G ( 369)	162	43.0	0.34	gi 183224458 dbj BAG24975.1	UDP-N-acetylglucosami ( 438)	161	42.8	0.46
gi 136628582 gb EBP38113.1	hypothetical protein G ( 115)	155	41.3	0.34	gi 148530739 gb ABQ82738.1	UDP-N-acetylglucosamin ( 438)	161	42.8	0.46
gi 136764602 gb EBQ25258.1	hypothetical protein G ( 437)	163	43.2	0.34	gi 141974299 gb ECU55148.1	hypothetical protein G ( 83)	151	40.4	0.46
gi 139046784 gb ECD04192.1	hypothetical protein G ( 191)	158	42.0	0.34	gi 75701382 gb ABA21058.1	UDP-N-acetylglucosamine ( 447)	161	42.8	0.47
gi 112802798 gb EAU00142.1	UDP-N-acetylglucosamin ( 442)	163	43.2	0.35	gi 136442255 gb EB019063.1	hypothetical protein G ( 272)	158	42.1	0.47
gi 142812888 gb EDA77094.1	hypothetical protein G ( 444)	163	43.2	0.35	gi 141228028 gb ECQ50671.1	hypothetical protein G ( 85)	151	40.4	0.47
gi 140434033 gb ECL72356.1	hypothetical protein G ( 60)	151	40.3	0.35	gi 140977470 gb EC079842.1	hypothetical protein G ( 276)	158	42.1	0.47
gi 139391915 gb ECE79642.1	hypothetical protein G ( 117)	155	41.3	0.35	gi 135459070 gb EBH77757.1	hypothetical protein G ( 86)	151	40.4	0.47
gi 140887232 gb ECO18192.1	hypothetical protein G ( 273)	160	42.5	0.35	gi 135078388 gb EBF35366.1	hypothetical protein G ( 388)	160	42.6	0.48
gi 142664031 gb ECZ68739.1	hypothetical protein G ( 72)	152	40.6	0.35	gi 135139598 gb EBF74601.1	hypothetical protein G ( 396)	160	42.6	0.48
gi 138945420 gb ECC53340.1	hypothetical protein G ( 73)	152	40.6	0.36	gi 135058427 gb EBF22632.1	hypothetical protein G ( 396)	160	42.6	0.48
gi 142003655 gb ECU75567.1	hypothetical protein G ( 235)	159	42.3	0.36	gi 142204617 gb ECW37535.1	hypothetical protein G ( 396)	160	42.6	0.48
gi 140462588 gb ECL90454.1	hypothetical protein G ( 170)	157	41.8	0.36	gi 138911545 gb ECC39122.1	hypothetical protein G ( 105)	152	40.7	0.49
gi 141399980 gb ECR56139.1	hypothetical protein G ( 122)	155	41.3	0.36	gi 136868207 gb EBQ94410.1	hypothetical protein G ( 338)	159	42.4	0.49
gi 135863805 gb EBK32366.1	hypothetical protein G ( 335)	161	42.8	0.36	gi 134532404 gb EBB90389.1	hypothetical protein G ( 64)	149	39.9	0.49
gi 135174336 gb EBF96923.1	hypothetical protein G ( 284)	160	42.5	0.36	gi 135188364 gb EBG05889.1	hypothetical protein G ( 177)	155	41.4	0.5
gi 136556862 gb EBO92852.1	hypothetical protein G ( 339)	161	42.8	0.37	gi 254951509 gb ACT96209.1	3-phosphoshikimate 1-c ( 411)	160	42.6	0.5
gi 913618 gb AAB32920.1	enolpyruvylshikimate-3-ph ( 108)	154	41.1	0.37	gi 138296296 gb EBY85354.1	hypothetical protein G ( 78)	150	40.2	0.5
gi 138201102 gb EBY37054.1	hypothetical protein G ( 108)	154	41.1	0.37	gi 143230676 gb EDD76083.1	hypothetical protein G ( 110)	152	40.7	0.51
gi 1049100 gb AAA97400.1	encodes EPSP synthase do ( 108)	154	41.1	0.37	gi 140674676 gb ECM73477.1	hypothetical protein G ( 110)	152	40.7	0.51
gi 140266572 gb ECK66197.1	hypothetical protein G ( 179)	157	41.8	0.38	gi 262316857 gb EEY97895.1	UDP-N-acetylglucosamin ( 419)	160	42.6	0.51
gi 143558889 gb EDF62870.1	hypothetical protein G ( 78)	152	40.6	0.38	gi 116094484 gb ABJ59636.1	UDP-N-acetylglucosamin ( 421)	160	42.6	0.51
gi 143569979 gb EDF68808.1	hypothetical protein G ( 417)	162	43.0	0.38	gi 55739449 gb AAV63090.1	UDP-N-acetylglucosamine ( 423)	160	42.6	0.51
gi 268625775 gb EEZ58175.1	UDP-N-acetylglucosamin ( 417)	162	43.0	0.38	gi 55737521 gb AAV61163.1	UDP-N-acetylglucosamine ( 423)	160	42.6	0.51
gi 138381113 gb EBZ27633.1	hypothetical protein G ( 110)	154	41.1	0.38	gi 137662455 gb EBV31632.1	hypothetical protein G ( 112)	152	40.7	0.52
gi 134904511 gb EBE20045.1	hypothetical protein G ( 79)	152	40.6	0.38	gi 58253892 gb AAV42129.1	udp-n-acetylglucosamine ( 431)	160	42.6	0.52
gi 27316187 gb AAO05321.1	AE016749_267 UDP-N-acety ( 419)	162	43.0	0.38	gi 139341795 gb ECE56379.1	hypothetical protein G ( 114)	152	40.7	0.52
gi 135671323 gb EBJ12248.1	hypothetical protein G ( 301)	160	42.5	0.38	gi 139444518 gb ECL14274.1	hypothetical protein G ( 160)	154	41.2	0.53
gi 165970311 gb ABY76172.1	chloroplast CTP/EPSPS ( 41)	148	39.7	0.39	gi 182996761 gb ACC31203.1	Sequence 120 from pate ( 441)	160	42.6	0.53
gi 84366787 dbj BAE67945.1	UDP-N-acetylglucosamin ( 424)	162	43.0	0.39	gi 239678519 gb ACS07433.1	Sequence 120 from pate ( 441)	160	42.6	0.53
gi 58425507 gb AAW74544.1	UDP-N-acetylglucosamine ( 424)	162	43.0	0.39	gi 239684576 gb ACS09904.1	Sequence 120 from pate ( 441)	160	42.6	0.53
gi 188522559 gb ACD60504.1	UDP-N-acetylglucosamin ( 424)	162	43.0	0.39	gi 139904103 gb ECT26001.1	hypothetical protein G ( 316)	158	42.1	0.53
gi 138672413 gb ECB20843.1	hypothetical protein G ( 309)	160	42.5	0.39	gi 143330349 gb EDE37054.1	hypothetical protein G ( 376)	159	42.4	0.54
gi 143080046 gb EDC66841.1	hypothetical protein G ( 69)	151	40.4	0.39	gi 134366442 gb EBA92583.1	hypothetical protein G ( 194)	155	41.4	0.54
gi 194345478 gb EDX26444.1	UDP-N-acetylglucosamin ( 448)	162	43.0	0.4	gi 134973646 gb EBE66138.1	hypothetical protein G ( 321)	158	42.1	0.54

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gi 135489195 gb EBH97504.1	hypothetical protein G ( 119)	152	40.7	0.54	gi 270281718 gb EFA27550.1	UDP-N-acetylglucosamin ( 423)	157	42.0	0.79
gi 141068175 gb ECP40329.1	hypothetical protein G ( 101)	151	40.5	0.54	gi 139540894 gb ECF77125.1	hypothetical protein G ( 156)	151	40.5	0.79
gi 135127298 gb EBF66688.1	hypothetical protein G ( 276)	157	41.9	0.55	gi 142115059 gb ECV70074.1	hypothetical protein G ( 437)	157	42.0	0.81
gi 139579622 gb ECG03906.1	hypothetical protein G ( 120)	152	40.7	0.55	gi 143351054 gb EDE49890.1	hypothetical protein G ( 228)	153	41.0	0.82
gi 142185192 gb ECW22719.1	hypothetical protein G ( 278)	157	41.9	0.55	gi 73912410 dbj BAE20404.1	5-enolpyruvylshikimate ( 231)	153	41.0	0.83
gi 137667452 gb EBV34442.1	hypothetical protein G ( 169)	154	41.2	0.55	gi 140854433 gb ECN95237.1	hypothetical protein G ( 276)	154	41.3	0.84
gi 134698699 gb EBC89437.1	hypothetical protein G ( 282)	157	41.9	0.56	gi 142593676 gb ECZ19246.1	hypothetical protein G ( 392)	156	41.8	0.85
gi 136360997 gb EBN64555.1	hypothetical protein G ( 394)	159	42.4	0.56	gi 140108185 gb ECJ59176.1	hypothetical protein G ( 63)	145	39.1	0.86
gi 140383936 gb ECL40504.1	hypothetical protein G ( 123)	152	40.7	0.56	gi 254672604 emb CBA06320.1	UDP-N-acetylglucosami ( 398)	156	41.8	0.87
gi 135136907 gb EBF72904.1	hypothetical protein G ( 396)	159	42.4	0.56	gi 142197920 gb ECW32422.1	hypothetical protein G ( 400)	156	41.8	0.87
gi 135138671 gb EBF74016.1	hypothetical protein G ( 396)	159	42.4	0.56	gi 142908315 gb EDB43847.1	hypothetical protein G ( 90)	147	39.6	0.88
gi 135104860 gb EBF52299.1	hypothetical protein G ( 288)	157	41.9	0.57	gi 137370618 gb EBT71981.1	hypothetical protein G ( 292)	154	41.3	0.88
gi 137615022 gb EBV06424.1	hypothetical protein G ( 293)	157	41.9	0.58	gi 134656392 gb EBC64520.1	hypothetical protein G ( 91)	147	39.6	0.89
gi 142169325 gb ECW10606.1	hypothetical protein G ( 419)	159	42.4	0.59	gi 149938155 gb ABR44852.1	3-phosphoshikimate 1-c ( 411)	156	41.8	0.89
gi 135359014 gb EBH10607.1	hypothetical protein G ( 419)	159	42.4	0.59	gi 7225236 gb AAF40490.1	UDP-N-acetylglucosamine ( 417)	156	41.8	0.9
gi 13638978 gb AAF86297.2	UDP-N-acetylglucosamine ( 423)	159	42.4	0.59	gi 149950500 gb ABR49028.1	UDP-N-acetylglucosamin ( 417)	156	41.8	0.9
gi 46881995 gb AAT05289.1	UDP-N-acetylglucosamine ( 423)	159	42.4	0.59	gi 261391570 emb CAX49003.1	UDP-N-acetylglucosami ( 417)	156	41.8	0.9
gi 225877561 emb CAS06275.1	Putative UDP-N-acetyl ( 423)	159	42.4	0.59	gi 135835202 gb EBK14373.1	hypothetical protein G ( 214)	152	40.8	0.9
gi 16415233 emb CAG97923.1	murZ [Listeria innocua ( 423)	159	42.4	0.59	gi 139577870 gb ECG02772.1	hypothetical protein G ( 299)	154	41.3	0.9
gi 143380233 gb EDB67130.1	hypothetical protein G ( 430)	159	42.4	0.6	gi 260404638 gb EEW98154.1	UDP-N-acetylglucosamin ( 418)	156	41.8	0.9
gi 117648040 gb ABK52142.1	UDP-N-acetylglucosamin ( 432)	159	42.4	0.6	gi 142171308 gb ECW12107.1	hypothetical protein G ( 419)	156	41.8	0.91
gi 139586669 gb ECG08967.1	hypothetical protein G ( 117)	151	40.5	0.62	gi 142302812 gb ECX10225.1	hypothetical protein G ( 419)	156	41.8	0.91
gi 197703480 gb EDY49292.1	UDP-N-acetylglucosamin ( 445)	159	42.4	0.62	gi 262313451 gb EEY94536.1	UDP-N-acetylglucosamin ( 419)	156	41.8	0.91
gi 33748212 gb AAQ45218.1	Sequence 5776 from pate ( 446)	159	42.4	0.62	gi 135223693 gb EBG26997.1	hypothetical protein G ( 421)	156	41.8	0.91
gi 138264746 gb EBY66748.1	hypothetical protein G ( 61)	147	39.5	0.63	gi 158140612 gb ABW18924.1	UDP-N-acetylglucosamin ( 421)	156	41.8	0.91
gi 135176976 gb EBF98626.1	hypothetical protein G ( 324)	157	41.9	0.63	gi 239506969 gb ACR80456.1	UDP-N-acetylglucosamin ( 421)	156	41.8	0.91
gi 162688145 gb EDQ74524.1	predicted protein [Phy ( 454)	159	42.4	0.63	gi 139398701 gb ECE84261.1	hypothetical protein G ( 94)	147	39.6	0.91
gi 141825909 gb ECT51361.1	hypothetical protein G ( 122)	151	40.5	0.64	gi 167293014 gb ABZ45878.1	Sequence 19816 from pa ( 425)	156	41.8	0.92
gi 142094653 gb ECV54445.1	hypothetical protein G ( 282)	156	41.7	0.64	gi 237506170 gb ACQ98488.1	gramicidin S biosynthe (1372)	163	43.5	0.92
gi 135611902 gb EBI75428.1	hypothetical protein G ( 125)	151	40.5	0.65	gi 126241755 gb ABO04848.1	conserved hypothetical (1372)	163	43.5	0.92
gi 141048527 gb ECP27825.1	hypothetical protein G ( 125)	151	40.5	0.65	gi 121230412 gb ABM52930.1	conserved hypothetical (1372)	163	43.5	0.92
gi 136659917 gb EBP56687.1	hypothetical protein G ( 126)	151	40.5	0.66	gi 148026983 gb EDK85004.1	conserved hypothetical (1372)	163	43.5	0.92
gi 141350070 gb ECR21239.1	hypothetical protein G ( 65)	147	39.5	0.66	gi 169653498 gb EDS86191.1	conserved hypothetical (1372)	163	43.5	0.92
gi 142642921 gb ECZ53921.1	hypothetical protein G ( 91)	149	40.0	0.66	gi 52209051 emb CAH34991.1	putative membrane prot (1372)	163	43.5	0.92
gi 136457490 gb EBQ28915.1	hypothetical protein G ( 248)	155	41.5	0.66	gi 124292891 gb ABN02160.1	conserved hypothetical (1372)	163	43.5	0.92
gi 140159165 gb ECJ91878.1	hypothetical protein G ( 300)	156	41.7	0.68	gi 126226851 gb ABN90391.1	conserved hypothetical (1372)	163	43.5	0.92
gi 137997686 gb EBX19252.1	hypothetical protein G ( 94)	149	40.0	0.68	gi 242141152 gb EES27554.1	conserved hypothetical (1372)	163	43.5	0.92
gi 140885888 gb ECO17231.1	hypothetical protein G ( 68)	147	39.5	0.69	gi 217502985 gb ACK50394.1	UDP-N-acetylglucosamin ( 429)	156	41.8	0.92
gi 217332615 gb ACK38409.1	UDP-N-acetylglucosamin ( 439)	158	42.2	0.71	gi 140037262 gb ECJ16748.1	hypothetical protein G ( 309)	154	41.3	0.93
gi 142610502 gb ECZ31048.1	hypothetical protein G ( 440)	158	42.2	0.71	gi 138012622 gb EBX27133.1	hypothetical protein G ( 188)	151	40.6	0.93
gi 138263743 gb EBY66096.1	hypothetical protein G ( 162)	152	40.8	0.71	gi 136266331 gb EBN00256.1	hypothetical protein G ( 263)	153	41.1	0.93
gi 124515207 gb EAY56718.1	UDP-N-acetylglucosamin ( 442)	158	42.2	0.71	gi 186468218 gb ACC84019.1	UDP-N-acetylglucosamin ( 435)	156	41.8	0.94
gi 17135152 dbj BAB77698.1	UDP-N-acetylglucosamin ( 447)	158	42.2	0.72	gi 141298287 gb ECQ92990.1	hypothetical protein G ( 100)	147	39.6	0.96
gi 135625189 gb EBI83682.1	hypothetical protein G ( 101)	149	40.0	0.73	gi 141594479 gb ECS50739.1	hypothetical protein G ( 85)	146	39.4	0.96
gi 141429393 gb ECR76551.1	hypothetical protein G ( 121)	150	40.3	0.74	gi 141941218 gb ECU32154.1	hypothetical protein G ( 102)	147	39.6	0.98
gi 137217195 gb EBS85944.1	hypothetical protein G ( 104)	149	40.0	0.74	gi 134327061 gb EBA66421.1	hypothetical protein G ( 74)	145	39.1	0.99
gi 140528342 gb ECM11325.1	hypothetical protein G ( 75)	147	39.6	0.75	gi 138900786 gb ECC34331.1	hypothetical protein G ( 123)	148	39.9	0.99
gi 137182770 gb EBS66594.1	hypothetical protein G ( 75)	147	39.6	0.75	gi 228229599 gb ACP87264.1	Sequence 9206 from pat ( 397)	155	41.6	1
gi 135372780 gb EBH19824.1	hypothetical protein G ( 93)	148	39.8	0.78					
gi 142185596 gb ECW23027.1	hypothetical protein G ( 419)	157	42.0	0.78					
gi 77995958 gb ABBI4857.1	UDP-N-acetylglucosamine ( 420)	157	42.0	0.79	>>gi 27549260 gb AAO17037.1	CP4EPSPS protein [synthetic (455 aa)			

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Regulatory Product Characterization Center

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initn: 2917 initl: 2917 opt: 2917 Z-score: 3277.0 bits: 615.6 E(): 1.8e-173  
Smith-Waterman score: 2917; 100.000% identity (100.000% similar) in 455 aa overlap (1-455:1-455)

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CP4_EP MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      .....
gi|275 MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      10      20      30      40      50      60

      70      80      90     100     110     120
CP4_EP KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
      .....
gi|275 KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
      70      80      90     100     110     120

      130     140     150     160     170     180
CP4_EP GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMASQVKSASV
      .....
gi|275 GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMASQVKSASV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP LLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      .....
gi|275 LLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      190     200     210     220     230     240

      250     260     270     280     290     300
CP4_EP VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNPRTGLILTLQEMGADIEVINPRLAGGED
      .....
gi|275 VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNPRTGLILTLQEMGADIEVINPRLAGGED
      250     260     270     280     290     300

      310     320     330     340     350     360
CP4_EP VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
      .....
gi|275 VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
      310     320     330     340     350     360

      370     380     390     400     410     420
CP4_EP VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
      .....
gi|275 VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
      370     380     390     400     410     420

      430     440     450
CP4_EP VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      .....
gi|275 VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
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      430      440      450
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      initn: 2917 initl: 2917 opt: 2917 Z-score: 3277.0 bits: 615.6 E(): 1.8e-
      173
      Smith-Waterman score: 2917; 100.000% identity (100.000% similar) in 455 aa
      overlap (1-455:1-455)

      10      20      30      40      50      60
CP4_EP MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      .....
gi|182 MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      10      20      30      40      50      60

      70      80      90     100     110     120
CP4_EP KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
      .....
gi|182 KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
      70      80      90     100     110     120

      130     140     150     160     170     180
CP4_EP GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMASQVKSASV
      .....
gi|182 GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMASQVKSASV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP LLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      .....
gi|182 LLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      190     200     210     220     230     240

      250     260     270     280     290     300
CP4_EP VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNPRTGLILTLQEMGADIEVINPRLAGGED
      .....
gi|182 VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNPRTGLILTLQEMGADIEVINPRLAGGED
      250     260     270     280     290     300

      310     320     330     340     350     360
CP4_EP VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
      .....
gi|182 VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
      310     320     330     340     350     360

      370     380     390     400     410     420
CP4_EP VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
      .....
gi|182 VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
      370     380     390     400     410     420

      430      440      450
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CP4_EP VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      10      20      30      40      50      60
      .....
gi|182 VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      430      440      450

>>gi|144974765|gb|ABP12476.1| Sequence 70 from patent US (455 aa)
      initn: 2917 initl: 2917 opt: 2917 Z-score: 3277.0 bits: 615.6 E(): 1.8e-
      173
      Smith-Waterman score: 2917; 100.000% identity (100.000% similar) in 455 aa
      overlap (1-455:1-455)

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CP4_EP MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      .....
gi|144 MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      10      20      30      40      50      60

      70      80      90      100     110     120
CP4_EP KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
      .....
gi|144 KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
      70      80      90      100     110     120

      130     140     150     160     170     180
CP4_EP GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMSAQVKSASV
      .....
gi|144 GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMSAQVKSASV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP LLAGLNTPGITTVIEPIMTRDHEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      .....
gi|144 LLAGLNTPGITTVIEPIMTRDHEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      190     200     210     220     230     240

      250     260     270     280     290     300
CP4_EP VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
      .....
gi|144 VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
      250     260     270     280     290     300

      310     320     330     340     350     360
CP4_EP VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
      .....
gi|144 VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
      310     320     330     340     350     360

      370     380     390     400     410     420
CP4_EP VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
      .....
gi|144 VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
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      370      380      390      400      410      420

      430      440      450
CP4_EP VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      .....
gi|144 VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      430      440      450

>>gi|281079467|gb|ADA36175.1| Sequence 15 from patent US (455 aa)
      initn: 2917 initl: 2917 opt: 2917 Z-score: 3277.0 bits: 615.6 E(): 1.8e-
      173
      Smith-Waterman score: 2917; 100.000% identity (100.000% similar) in 455 aa
      overlap (1-455:1-455)

      10      20      30      40      50      60
CP4_EP MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      .....
gi|281 MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
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      70      80      90      100     110     120
CP4_EP KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
      .....
gi|281 KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
      70      80      90      100     110     120

      130     140     150     160     170     180
CP4_EP GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMSAQVKSASV
      .....
gi|281 GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMSAQVKSASV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP LLAGLNTPGITTVIEPIMTRDHEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      .....
gi|281 LLAGLNTPGITTVIEPIMTRDHEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      190     200     210     220     230     240

      250     260     270     280     290     300
CP4_EP VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
      .....
gi|281 VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
      250     260     270     280     290     300

      310     320     330     340     350     360
CP4_EP VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
      .....
gi|281 VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
      310     320     330     340     350     360

      370      380      390      400      410      420
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              310           320           330           340           350           360
              370           380           390           400           410           420
CP4_EP  VANGLKLNQVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSEN
gi|197  VANGLKLNQVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSEN
              370           380           390           400           410           420
              430           440           450
CP4_EP  VIVDDATMIATSPFPEFMDLMAGLGAKIELSDTKAA
gi|197  VIVDDATMIATSPFPEFMDLMAGLGAKIELSDTKAA
              430           440           450

>>gi|2484147|gb|AAB72283.1|I49176 Sequence 3 from patent (455 aa)
initn: 2909 initl: 2909 opt: 2909 Z-score: 3268.1 bits: 613.9 E(): 5.7e-
173
Smith-Waterman score: 2909; 99.780% identity (99.780% similar) in 455 aa
overlap (1-455:1-455)

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	10	20	30	40	50	60
CP4_EP	MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG					
gi 248	MSHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG					
	10	20	30	40	50	60
CP4_EP	KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI					
gi 248	KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI					
	70	80	90	100	110	120
CP4_EP	GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPIITYRVPMAASAQVKS					
gi 248	GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPIITYRVPMAASAQVKS					
	130	140	150	160	170	180
CP4_EP	GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPIITYRVPMAASAQVKS					
gi 248	GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPIITYRVPMAASAQVKS					
	190	200	210	220	230	240
CP4_EP	LLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID					
gi 248	LLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID					
	190	200	210	220	230	240
CP4_EP	VPGDPSSTAFLVAALLVPGSDVTILNVLNMPNPTRTGLILTLQEMGADIEVINPRLAGED					
gi 248	VPGDPSSTAFLVAALLVPGSDVTILNVLNMPNPTRTGLILTLQEMGADIEVINPRLAGED					
	250	260	270	280	290	300
CP4_EP	VPGDPSSTAFLVAALLVPGSDVTILNVLNMPNPTRTGLILTLQEMGADIEVINPRLAGED					
gi 248	VPGDPSSTAFLVAALLVPGSDVTILNVLNMPNPTRTGLILTLQEMGADIEVINPRLAGED					
	310	320	330	340	350	360

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                250          260          270          280          290          300
              310          320          330          340          350          360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|248  VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSA
              310          320          330          340          350          360

              370          380          390          400          410          420
CP4_EP  VANGLKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSEN
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|248  VANGLKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSEN
              370          380          390          400          410          420

              430          440          450
CP4_EP  VIVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|248  VIVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
              430          440          450

>>gi|5957547|gb|AAE08221.1| Sequence 3 from patent US 58 (455 aa)
  initn: 2909 initl: 2909 opt: 2909 Z-score: 3268.1 bits: 613.9 E(): 5.7e-
173
Smith-Waterman score: 2909; 99.780% identity (99.780% similar) in 455 aa
overlap (1-455:1-455)

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	10	20	30	40	50	60
CP4_EP	MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG					
gi 595	MSHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG					
	10	20	30	40	50	60
	70	80	90	100	110	120
CP4_EP	KAMQAMGARIRKEGDTWIIDGVGNGLLAPEAPLDFGNAATGCRLTMLGVGYDFDSTFI					
gi 595	::					
	70	80	90	100	110	120
	130	140	150	160	170	180
CP4_EP	GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPIITYRVPMSAQVKS					
gi 595	GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPIITYRVPMSAQVKS					
	130	140	150	160	170	180
	190	200	210	220	230	240
CP4_EP	LLAGLNTPGITTVIEPIIMTRDHTKMLQGFGGANLTVETDADGVRTIRLEGRGKLTGQVID					
gi 595	LLAGLNTPGITTVIEPIIMTRDHTKMLQGFGGANLTVETDADGVRTIRLEGRGKLTGQVID					
	190	200	210	220	230	240
	250	260	270	280	290	300



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190      200      210      220      230      240
      250      260      270      280      290      300
CP4_EP  VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNPTRTGLILTLQEMGADIEVINPRLAGGED
      .....
gi|144  VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNPTRTGLILTLQEMGADIEVINPRLAGGED
      250      260      270      280      290      300
      310      320      330      340      350      360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDEYPLAVAAAAFAEGATVMNGLEELRVKESDRLSA
      .....
gi|144  VADLRVRSSTLKGVTVPEDRAPSMIDEYPLAVAAAAFAEGATVMNGLEELRVKESDRLSA
      310      320      330      340      350      360
      370      380      390      400      410      420
CP4_EP  VANGKLKNGVDCDEGETSLVVVRGPRDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSEN
      .....
gi|144  VANGKLKNGVDCDEGETSLVVVRGPRDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSEN
      370      380      390      400      410      420
      430      440      450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      .....
gi|144  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      430      440      450

>>gi|217243929|gb|ACK18296.1| Sequence 1 from patent US (455 aa)
  initn: 2909 initil: 2909 opt: 2909 Z-score: 3268.1 bits: 613.9 E(): 5.7e-
  173
  Smith-Waterman score: 2909; 99.780% identity (99.780% similar) in 455 aa
  overlap (1-455:1-455)

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		10	20	30	40	50	60
CP4_EP	MLHGASSRPATARKSSGLSGTVRIPGDKISHSRSMF	GGLASGETRITG	LLGEDVINTG				
	:	:	:	:	:	:	:
gi 217	MSHGASSRPATARKSSGLSGTVRIPGDKISHSRSMF	GGLASGETRITG	LLGEDVINTG				
	:	:	:	:	:	:	:
		10	20	30	40	50	60
		70	80	90	100	110	120
CP4_EP	KAMQAMGARIRKEGDTWIIDGVGNGLLAPEAPLDF	GNAATGCRLT	MGVLGVYDF	DSFTFI			
	:	:	:	:	:	:	:
gi 217	KAMQAMGARIRKEGDTWIIDGVGNGLLAPEAPLDF	GNAATGCRLT	MGVLGVYDF	DSFTFI			
	:	:	:	:	:	:	:
		70	80	90	100	110	120

	130	140	150	160	170	180
CP4_EP	GDASLTKRPMGRVLNPLREMGGVQVKS	EDGDRLPVTLRGPKTPTPI	TYRVPMAS	QVKS	SAV	
	.....	.....	.....	.....	.....	.....
gi 217	GDASLTKRPMGRVLNPLREMGGVQVKS	EDGDRLPVTLRGPKTPTPI	TYRVPMAS	QVKS	SAV	
	.....	.....	.....	.....	.....	.....
	130	140	150	160	170	180
	190	200	210	220	230	240

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CP4_EP  LLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
:
gi|217  LLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      190      200      210      220      230      240

      250      260      270      280      290      300
CP4_EP  VPGDPSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLILTLQEMGADIEVINPRLAGGED
:
gi|217  VPGDPSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLILTLQEMGADIEVINPRLAGGED
      250      260      270      280      290      300

      310      320      330      340      350      360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
:
gi|217  VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
      310      320      330      340      350      360

      370      380      390      400      410      420
CP4_EP  VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
:
gi|217  VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
      370      380      390      400      410      420

      430      440      450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
:
gi|217  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      430      440      450

>>gi|62318479|dbj|BAD94823.1| 5-enol-pyruvylshikimate-3- (527 aa)
  initn: 2886 initl: 2886 opt: 2886  Z-score: 3241.2  bits: 609.2 E(): 1.8e-
  171
Smith-Waterman score: 2886; 99.341% identity (99.341% similar) in 455 aa
overlap (1-455:73-527)

      10      20      30
CP4_EP  MLHGASSRPATARKSSGLSGTVRIPGDKSI
:
gi|623  ANSMLVLKKDSIFMQKFCFSFRISASVATACMLHGASSRPATARKSSGLSGTVRIPGDKSI
      50      60      70      80      90      100

      40      50      60      70      80      90
CP4_EP  SHRSFMFGGLASGETRITGLLEGEDVINTGKAMQAMGARIRKEGDTWIIDGVGNGGLLAP
:
gi|623  SHRSFMFGGLASGETRITGLLEGEDVINTGKAMQAMGARIRKEGDTWIIDGVGNGGLLAP
      110      120      130      140      150      160

      100      110      120      130      140      150
CP4_EP  EAPLDFGNAATGCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEDGD
:
gi|623  EAPLDFGNAATGCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEDGD
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      170      180      190      200      210      220

      160      170      180      190      200      210
CP4_EP  RLPVTLRGPKTPTPITYRVPMASAVKSAVLLAGLNTPGITTVIEPIMTRDHTKMLQGF
:
gi|623  RLPVTLRGPKTPTPITYRVPMASAVKSAVLLAGLNTPGITTVIEPIMTRDHTKMLQGF
      230      240      250      260      270      280

      220      230      240      250      260      270
CP4_EP  GANLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSSTAFPLVAALLVPGSDVTILNVLM
:
gi|623  GANLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSSTAFPLVAALLVPGSDVTILNVLM
      290      300      310      320      330      340

      280      290      300      310      320      330
CP4_EP  NPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRSSTLKGVTVPEDRAPSMIDEYPI
:
gi|623  NPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRSSTLKGVTVPEDRAPSMIDEYPI
      350      360      370      380      390      400

      340      350      360      370      380      390
CP4_EP  LAVAAAFAGATVMNGLEELRVKESDRLSAVANGKLKNGVDCDEGETSLVVRGRPDGKGL
:
gi|623  LAVAAAFAGATVMNGLEELRVKESDRLSAVANGKLKNGVDCDEGETSLVVRGRPDGKGL
      410      420      430      440      450      460

      400      410      420      430      440      450
CP4_EP  GNASGAAVATHLDHRIAMSFLVMGLVSENPVTVDDATMIATSFPEFMDLMAGLGAKIELS
:
gi|623  GNASGAAVATHLDHRIAMSFLVMGLVSENPVTVDDATMIATSFPEFMDLMAGLGAKIELS
      470      480      490      500      510      520

CP4_EP  DTKAA
:
gi|623  DTKAA

>>gi|15073182|emb|CAC41690.1| Putative 3-phosphoshikimat (455 aa)
  initn: 2685 initl: 2685 opt: 2685  Z-score: 3016.5  bits: 567.4 E(): 5.8e-
  159
Smith-Waterman score: 2685; 90.549% identity (97.143% similar) in 455 aa
overlap (1-455:1-455)

      10      20      30      40      50      60
CP4_EP  MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
:
gi|150  MSHGSNPRPATARKSSDLKGTLRIPGDKSISHRSFMFGGLAAGETRITGLLEGEDVINTG
      10      20      30      40      50      60

      70      80      90      100      110      120
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CP4_EP KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
gi|150 KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
      70      80      90      100     110     120

      130     140     150     160     170     180
CP4_EP GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMASAVQKSAV
gi|150 GDASLTKRPMGRVLDPLREMGVQVKSAGDRLPVTLRGPKTPNPITYRVPMASAVQKSAV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP LLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
gi|150 LLAGLNTPGITTVIEPVMTRDHTKMLQGFGANLTVETDAEGVRTIRLEGRGKLTGQVID
      190     200     210     220     230     240

      250     260     270     280     290     300
CP4_EP VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
gi|150 VPGDPSSTAFPLVAGLIVPGSDITILNVLNPNTRTGLILTLQEMGANIEVMNKRLAGGED
      250     260     270     280     290     300

      310     320     330     340     350     360
CP4_EP VADLRVRSTLKGVTVPEDRAPSMIDEYPI LAVAAAF AEGATVMNGLEELRVKESDRLSA
gi|150 VADLRVRHSELKGVTVPEDRAPSMIDEY PVLAVAAAF AEGTVMNGLEELRVKESDRLSA
      310     320     330     340     350     360

      370     380     390     400     410     420
CP4_EP VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGA AVATHLDHRIAMSFLVMGLVSENP
gi|150 VADGLKLNVDCEGEASLVVRGRPGGKGLGKISGGQVKTHLDHRIAMSFLVMGLASEHP
      370     380     390     400     410     420

      430     440     450
CP4_EP VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
gi|150 VTVDDATMIATSFPEFMGLMTGLGAKIEEAENKAA
      430     440     450

>>gi|227343087|gb|ACP27305.1| 3-phosphoshikimate 1-carbo (448 aa)
  initn: 2670 initl: 2670 opt: 2670 Z-score: 2999.7 bits: 564.3 E(): 5e-158
Smith-Waterman score: 2670; 91.518% identity (97.321% similar) in 448 aa
overlap (1-448:1-448)

      10      20      30      40      50      60
CP4_EP MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
gi|227 MSHGLSPRPATAKKSADLKGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      10      20      30      40      50      60
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      70      80      90      100     110     120
CP4_EP KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
gi|227 KAMQAMGARIRKEGDTWIINGVNGALLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
      70      80      90      100     110     120

      130     140     150     160     170     180
CP4_EP GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMASAVQKSAV
gi|227 GDASLTKRPMGRVLDPLREMGVQVKSAGDRLPVTLRGPKTPNPITYRVPMASAVQKSAV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP LLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
gi|227 LLAGLNTPGITTVIEPVMTRDHTKMLQGFGANLSVETDTAGVRTIRLEGRGKLTGQVID
      190     200     210     220     230     240

      250     260     270     280     290     300
CP4_EP VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
gi|227 VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGANIEVMNKRLAGGED
      250     260     270     280     290     300

      310     320     330     340     350     360
CP4_EP VADLRVRSTLKGVTVPEDRAPSMIDEYPI LAVAAAF AEGATVMNGLEELRVKESDRLSA
gi|227 VADLRVRYSELKGVTVPEERAPSMIDEY PVLAVAAAF AEGATVMNGLEELRVKESDRLSA
      310     320     330     340     350     360

      370     380     390     400     410     420
CP4_EP VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGA AVATHLDHRIAMSFLVMGLVSENP
gi|227 VADGLKLNVDCEGEASLVVRGRPGGKGLGNAAGGQVKTHLDHRIAMSFLVLGLASEHP
      370     380     390     400     410     420

      430     440     450
CP4_EP VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
gi|227 VTVDDATMIATSFPEFMDLMTGLGATIE
      430     440

>>gi|150030157|gb|ABR62274.1| 3-phosphoshikimate 1-carbo (456 aa)
  initn: 2660 initl: 2660 opt: 2660 Z-score: 2988.4 bits: 562.2 E(): 2.1e-
  157
Smith-Waterman score: 2660; 89.890% identity (96.264% similar) in 455 aa
overlap (1-455:1-455)

      10      20      30      40      50      60
CP4_EP MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
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	10	20	30	40	50	60
CP4_EP	MLHGASSRPATARKSSGLSGTVRI	PGDKSISHR	SFMFGLASGETRITGLLEGEDVINTG			
gi 115	MLNGSASKPATARKSAGLTG	SVRI	PGDKSISHR	SFMFGLASGETRITGLLEGEDVINTG		
	10	20	30	40	50	60
CP4_EP	70	80	90	100	110	120
CP4_EP	KAMQAMGARIRKEGD	TWIIDGVNGGLLAPEAPLDFGNAATGCRLT	MGLVG	YDFDSTF		
gi 115	RAMQAMGARIRKEGAQ	WVIEGTGNGALLAPDAPLDFGNAGTGVRLT	MGLVG	YDFHSTFI		
	70	80	90	100	110	120
CP4_EP	130	140	150	160	170	180
CP4_EP	GDASLTKRPMGRVLNPLREMGVQV	KSE	GDRLPVT	LRGPKTPTPITYRV	PMASAQVKS	SAV
gi 115	GDASLSKRP	MGRVLNPLREMGVQVSASEG	DRLPVT	LRGPGT	PSPIRYRV	PMASAQVKS
	130	140	150	160	170	180
CP4_EP	190	200	210	220	230	240
CP4_EP	LLAGLNTPGITTVIEP	IMTRDHT	EKMLQGFGANLTVETDADGVRTIR	LEGR	KG	L
gi 115	LLAGLNTPGVTTVIEP	VMTRDHT	EKMLQFGAALSVETDGDGVRTIR	LEGR	KG	L
	190	200	210	220	230	240
CP4_EP	250	260	270	280	290	300
CP4_EP	VPGDPSSTAFPLVAALLVPGSDVT	ILNVL	MNP	TRTGLIL	TLQEMGADIEVIN	PR
gi 115	VPGDPSSTAFPLVAALIVPGSDIT	IVNVL	MNP	TRTGLIL	TLQEMGADIEVV	N
	250	260	270	280	290	300
CP4_EP	310	320	330	340	350	360
CP4_EP	VADLRVRSSTLKGVTVPEDRAPSM	ID	YPI	LAVAAAF	AEGATVMNGLEELRV	KES
gi 115	VADLRVRHSELKGVTVPEDRAPSM	ID	YPI	LAVAAACF	AEGATVMKGLEELRV	KES
	310	320	330	340	350	360
CP4_EP	370	380	390	400	410	420
CP4_EP	VANGLK	LVGDCDEGETSLVV	RRPDKGLGNASGA	VATHLDHRIAMSFLVMGLV	SEN	P
gi 115	VADGLK	LVGDCDEGEDFLIV	RRPDKGLGNAA	DGRVSTHLDHRIAMSFLVL	GLAS	EH
	370	380	390	400	410	420
CP4_EP	430	440	450			
CP4_EP	VTVDDATMIATSFPEFMDL	MAGL	GAKIELSDTKAA			
gi 115	VTIDDAAMIATSFPEFM	QLMTGL	GAKIELVAE			
	430	440	450			

>>gi|240860935|gb|ACS58602.1| 3-phosphoshikimate 1-carbo (452 aa)

initn: 2559 initl: 2559 opt: 2559 Z-score: 2875.0 bits: 541.2 E(): 4.4e-151  
Smith-Waterman score: 2559; 86.801% identity (95.973% similar) in 447 aa overlap (1-447:1-447)

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      10      20      30      40      50      60
CP4_EP MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      .....
gi|240 MLNGSAPKPATARKSAGLTGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      10      20      30      40      50      60

      70      80      90     100     110     120
CP4_EP KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFSTFI
      .....
gi|240 RAMQAMGARIRKEGEQWVIDGTGNGALLAPDAPLDFGNAGTVRLTMGLVGTYDFRSTFT
      70      80      90     100     110     120

      130     140     150     160     170     180
CP4_EP GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMASAVQKSAV
      .....
gi|240 GDASLSKRPMGRVLNPLREMGVQVSASEGDRLPVTLRGPGTSPPIRYRVPMASAVQKSAV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP LLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      .....
gi|240 LLAGLNTPGITTVIEPVMTRDHTEKMLQGFGAALSVETDSEGVRTIRLEGRGKLAGQVID
      190     200     210     220     230     240

      250     260     270     280     290     300
CP4_EP VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
      .....
gi|240 VPGDPSSTAFPLVAALLVPGSDITIVNVLNPNTRTGLILTLQEMGADIEVANARLAGGED
      250     260     270     280     290     300

      310     320     330     340     350     360
CP4_EP VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
      .....
gi|240 VADLRVRHSELKGVTVPEERAPSMIDEYPILAVAAAFAGATIMKGLEELRVKESDRLSA
      310     320     330     340     350     360

      370     380     390     400     410     420
CP4_EP VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
      .....
gi|240 VADGLKLNVDCEDEGDFLIVRGRPDGKGLGNAADGRVSTHLDHRIAMSFLVMGLASEHP
      370     380     390     400     410     420

      430     440     450
CP4_EP VTDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      .....
gi|240 VTIDDAAMIATSFPEFMQLMTGLGAKIAEVPE
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      430      440      450
>>gi|2484148|gb|AAB72284.1|I49177 Sequence 5 from patent (449 aa)
initn: 2139 initl: 2139 opt: 2442 Z-score: 2743.6 bits: 516.9 E(): 9.2e-144
Smith-Waterman score: 2442; 82.889% identity (93.556% similar) in 450 aa overlap (1-450:1-447)

      10      20      30      40      50      60
CP4_EP MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      : : : : :
gi|248 MSHSAPKPATARRSEALTGEIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      10      20      30      40      50      60

      70      80      90     100     110     120
CP4_EP KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFSTFI
      .....
gi|248 RAMQAMGAKIRKEGDVWIINGVNGCLLQPEAALDFGNAGTGARLTMGLVGTYDMKTSFI
      70      80      90     100     110     120

      130     140     150     160     170     180
CP4_EP GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMASAVQKSAV
      .....
gi|248 GDASLSKRPMGRVLNPLREMGVQVEAADGDRMPLTLIGPKTANPITYRVPMASAVQKSAV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP LLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      .....
gi|248 LLAGLNTPGVTTTIEPVMTRDHTEKMLQGFGADLTVDKDGVRHIRTGQGLVGTQID
      190     200     210     220     230     240

      250     260     270     280     290     300
CP4_EP VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
      .....
gi|248 VPGDPSSTAFPLVAALLVEGSDVTIRNVLNPNTRTGLILTLQEMGADIEVLNARLAGGED
      250     260     270     280     290     300

      310     320     330     340     350     360
CP4_EP VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
      .....
gi|248 VADLRVRASKLKGVVVPPERAPSMIDEYPVLAIAASFAGETVMDGLDELRVKESDRLAA
      310     320     330     340     350     360

      370     380     390     400     410     420
CP4_EP VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
      : : : : :
gi|248 VARGLEANGVDCTEGEMSLTVRGRPDGKGLG---GGTVATHLDHRIAMSFLVMGLAAEKP
      370     380     390     400     410

      430      440      450
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          370          380          390          400          410
      430      440      450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKEIELSDTKAA
      .....
gi|248  VTVDDSLNMIATSFPEFMDMMPLGLGAKEIELSIL
      420      430      440

>>gi|144974728|gb|ABP12439.1| Sequence 7 from patent US (449 aa)
      initn: 2139 init1: 2139 opt: 2442 Z-score: 2743.6 bits: 516.9 E(): 9.2e-
144
Smith-Waterman score: 2442; 82.889% identity (93.556% similar) in 450 aa
overlap (1-450:1-447)

```

```

              10          20          30          40          50          60
CP4_EP MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|144 MSHSASPKPATARRSEALTGEIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
              10          20          30          40          50          60

```

```

              70          80          90          100          110          120
CP4_EF KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 RAMQAMGAKIRKEGDVWIINGVNGCLLQPEAALDFGNAGTGARLTMGLVGTYDMKTSFI
              70          80          90          100          110          120

```

```

      130      140      150      160      170      180
CP4_EP  GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVLTRGPKTPTPITYRVPMASAQVKS AV
      .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....
gi|144  GDASLSKRPMGRVLNPLREMGVQVEAADGRMPLTLIGPKTANPITYRVPMASAQVKS AV
      130      140      150      160      170      180

```

```

          190          200          210          220          230          240
CP4_EP  LLAGLNTPGITTVIEPIMRDHTKEMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
        :::::::::::::::::::::::::::::::::::::::::::::: :: :: ::::::::::
gi|144  LLAGLNTPGVTTVIEPVMTRDHTKEMLQGFGADLTVETDKDGVRHIRITGQKLVGQTID
          190          200          210          220          230          240

```

```

                250          260          270          280          290          300
CP4_EP  VPGDPSSSTAFPLVAALLVPGSDVTILNVLNMPNTRTGLILLTQEMGADIEVINPRLAGED
          :::::::::::::::::::: ::::: ::::::::::::::::::::::::::::::: :::::
gi|144  VPGDPSSSTAFPLVAALLVPGSDVTIRNVLNMPNTRTGLILLTQEMGADIEVLNARLAGED
          250          260          270          280          290          300

```

```

          310      320      330      340      350      360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDVEYPI LAVA AAF AEGATVMNGLEELRVKESDRLSA
          :::::  :::::  :::::  :::::  :::::  :::::
gi|144  VADLRVRASKLKGVVPPERAPSMIDVEYPLVLAIAASFAEGETVMDGLDLRVKESDRLLAA
          310      320      330      340      350      360

```

370                      380                      390                      400                      410                      420

```
CP4_EP  VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
:: ... ::::: :: ::::::::::::::: ::::::::::::::::::::
gi|144  VARGLEANGVDCTEGEMSLTVRGRPDGKGLG---GGTVATHLDHRIAMSFLVMGLAAEKP
      370      380      390      400      410

      430      440      450
CP4_EP  VTVDATMIATSFPEFMDLMAGLGAKIELSDTKAA
::::::::::::::::::: :::::::::::
gi|144  VTVDSDNMIATSFPEFMDMMPGLGAKIELSIL
      420      430      440

>>gi|2485226|gb|AAB73362.1|I44451 Sequence 7 from patent (449 aa)
  initn: 2139 init1: 2139 opt: 2442 Z-score: 2743.6 bits: 516.9 E(): 9.2e-
  144
Smith-Waterman score: 2442; 82.889% identity (93.556% similar) in 450 aa
overlap (1-450:1-447)

      10      20      30      40      50      60
CP4_EP  MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
: ... ::::: ::: ::::::::::::::: ::::::::::::::::::::
gi|248  MSHSASPKPATARRSEALTGEIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      10      20      30      40      50      60

      70      80      90      100     110     120
CP4_EP  KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
::::::::::::::::::: ::::::::::: ::: :::::::::::::::
gi|248  RAMQAMGAKIRKEGDVWIINGVNGCCLLQPEAALDFGNAGTGARLTMGLVGTYDMKTSFI
      70      80      90      100     110     120

      130     140     150     160     170     180
CP4_EP  GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPITPYRVPMSAQVKSASV
::::::::::::::::::: ::::::::::: ::: :::::::::::::::
gi|248  GDASLSKRPMGRVLNPLREMGVQVEAADGDRMPLTLIGPKTANPITYRVPMSAQVKSASV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP  LLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
::::::::::::::::::: ::::::::::: ::: :::::::::::::::
gi|248  LLAGLNTPGVTTVIEPVMTRDHTKMLQGFGADLTVETDKDGVRHIRITGQKLVGQTID
      190     200     210     220     230     240

      250     260     270     280     290     300
CP4_EP  VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
::::::::::::::::::: ::::::::::: ::: :::::::::::::::
gi|248  VPGDPSSTAFPLVAALLVEGSDVTIRNVLNPNTRTGLILTLQEMGADIEVLNARLAGGED
      250     260     270     280     290     300

      310     320     330     340     350     360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAAFAEGATVMNGLEELRVKESDRLSA
::::::::::::::::::: ::::::::::: ::: :::::::::::::::
gi|248  VADLRVRASKLKGVVPPERAPSMIDEYPVLAIAASFAEGETVMDGLDELRVKESDRLAA
```

```
      310      320      330      340      350      360

      370      380      390      400      410      420
CP4_EP  VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
:: ... ::::: ::: ::::::::::::::: ::::::::::::::::::::
gi|248  VARGLEANGVDCTEGEMSLTVRGRPDGKGLG---GGTVATHLDHRIAMSFLVMGLAAEKP
      370      380      390      400      410

      430      440      450
CP4_EP  VTVDATMIATSFPEFMDLMAGLGAKIELSDTKAA
::::::::::::::::::: :::::::::::
gi|248  VTVDSDNMIATSFPEFMDMMPGLGAKIELSIL
      420      430      440

>>gi|144974727|gb|ABP12438.1| Sequence 5 from patent US (449 aa)
  initn: 2139 init1: 2139 opt: 2442 Z-score: 2743.6 bits: 516.9 E(): 9.2e-
  144
Smith-Waterman score: 2442; 82.889% identity (93.556% similar) in 450 aa
overlap (1-450:1-447)

      10      20      30      40      50      60
CP4_EP  MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
: ... ::::: ::: ::::::::::::::: ::::::::::::::::::::
gi|144  MSHSASPKPATARRSEALTGEIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      10      20      30      40      50      60

      70      80      90      100     110     120
CP4_EP  KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
::::::::::::::::::: ::::::::::: ::: :::::::::::::::
gi|144  RAMQAMGAKIRKEGDVWIINGVNGCCLLQPEAALDFGNAGTGARLTMGLVGTYDMKTSFI
      70      80      90      100     110     120

      130     140     150     160     170     180
CP4_EP  GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPITPYRVPMSAQVKSASV
::::::::::::::::::: ::::::::::: ::: :::::::::::::::
gi|144  GDASLSKRPMGRVLNPLREMGVQVEAADGDRMPLTLIGPKTANPITYRVPMSAQVKSASV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP  LLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
::::::::::::::::::: ::::::::::: ::: :::::::::::::::
gi|144  LLAGLNTPGVTTVIEPVMTRDHTKMLQGFGADLTVETDKDGVRHIRITGQKLVGQTID
      190     200     210     220     230     240

      250     260     270     280     290     300
CP4_EP  VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
::::::::::::::::::: ::::::::::: ::: :::::::::::::::
gi|144  VPGDPSSTAFPLVAALLVEGSDVTIRNVLNPNTRTGLILTLQEMGADIEVLNARLAGGED
      250     260     270     280     290     300

      310      320      330      340      350      360
```

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```

                250          260          270          280          290          300
              310          320          330          340          350          360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSA
       :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
gi|595  VADLRVRASKLKGVVPPERAPSMIDEYPVLAIAASFAGEGTVM DGLDELRVKESDRLAA
              310          320          330          340          350          360

              370          380          390          400          410          420
CP4_EP  VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSEN
       :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|595  VARGLEANGVDCTEGEMSLTVRGRPDGKGLG---GGTVATHLDHRIAMSFLVMGLAAEKP
              370          380          390          400          410

              430          440          450
CP4_EP  VIVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
       ::::::::::::::::::::::::::::::::::
gi|595  VIVDDSNMIATSFPEFMDMMPGLGAKIELSIL
       420          430          440

>>gi|5957549|gb|AAE08223.1| Sequence 7 from patent US 58 (449 aa)
  initn: 2139 initl: 2139 opt: 2442 Z-score: 2743.6 bits: 516.9 E(): 9.2e-
144
Smith-Waterman score: 2442; 82.889% identity (93.556% similar) in 450 aa
overlap (1-450:1-447)

```

	10	20	30	40	50	60
CP4_EP	MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSMFGGLASGETRITGLLEGEDVINTG					
gi 595	MSHSASPKPATARRSEALTGEIRIPGDKSISHRSMFGGLASGETRITGLLEGEDVINTG					
	10	20	30	40	50	60
	70	80	90	100	110	120
CP4_EP	KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRLTMGLVGVDSTFI					
gi 595	RAMQAMGARIRKEGDVWIINGVNGCLLQPEAALDFGNAAGTGARLTMGLVGTYDMKTSFI					
	70	80	90	100	110	120
	130	140	150	160	170	180
CP4_EP	GDASLTKRPMGRVLNPLREMGVQVKSSEDGRPLVTLRGPKTPTPIYRVPMAAQVKS					
gi 595	GDASLSKRPMPGRVLNPLREMGVQVEAADGRMPLTLIGPKTANPIYRVPMAAQVKS					
	130	140	150	160	170	180
	190	200	210	220	230	240
CP4_EP	LLAGLNTPGITTVIEPIIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID					
gi 595	LLAGLNTPGVTTVIEPVMTRDHTKMLQGFAGDLTVETDKDGVRRHIRTGQGLVGTID					
	190	200	210	220	230	240
	250	260	270	280	290	300



```

190      200      210      220      230      240
      250      260      270      280      290      300
CP4_EP  VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNPRTGLILTLQEMGADIEVINPRLAGGED
      :::::::::::::::::::: :::::::::::::::::::: :::::::::::::::::::: ::::::::::::::::::::
gi|248  VPGDPSSTAFPLVAALLVEGSDVTIRNVLNPNPRTGLILTLQEMGADIEVLNARLAGGED
      250      260      270      280      290      300
      310      320      330      340      350      360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDEYPI LAVAAAFAGATVMNGLEELRVKESDRLSA
      :::::::::::::::::::: :::::::::::::::::::: :::::::::::::::::::: ::::::::::::::::::::
gi|248  VADLRVRASKLKGVVPPERAPSMIDEYPI LAIAAFAEGETVMNGLDLRLVKESDRLAA
      310      320      330      340      350      360
      370      380      390      400      410      420
CP4_EP  VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSEN
      :::::::::::::::::::: :::::::::::::::::::: :::::::::::::::::::: ::::::::::::::::::::
gi|248  VARGLEANGVDCTEGEMSLTVRGRPDGKGLG---GGTVATHLDHRIAMSFLVMGLAAEKP
      370      380      390      400      410
      430      440      450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      :::::::::::::::::::: ::::::::::::::::::::
gi|248  VTVDDSNMIATSFPEFMDMMPGLGAKIELSIL
      420      430      440

>>gi|151559264|gb|ABS12762.1| 3-phosphoshikimate 1-carbo (450 aa)
initn: 2443 initl: 2112 opt: 2441 Z-score: 2742.5 bits: 516.7 E(): 1.1e-
143
Smith-Waterman score: 2441; 82.119% identity (93.157% similar) in 453 aa
overlap (1-453;1-450)

```

	10	20	30	40	50	60
CP4_EP	MLHGASSRPATARKSSGLSGTVIRIPGDKSISHRSMFMGGLASGETRITGLLEGEDVINTG					
gi 151	MSHSAPPKPATARRSEALTGEIRIPGDKSISHRSMFMGGLASGETRITGLLEGEDVINTG					
	10	20	30	40	50	60
	70	80	90	100	110	120
CP4_EP	KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAGTGCRLTMGLVGVDYDFDSTFI					
gi 151	RAMQAMGARIRKRDGDAWIINGVNGCLLOPEAALDFGNAGTGARLTMGLVGTYDMRTSFI					
	70	80	90	100	110	120
	130	140	150	160	170	180
CP4_EP	GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMASAVQVKS					
gi 151	GDASLSKRPMPGRVLNPLREMGVQVEAAEGDRMPLTLIGPKTANPITYRVPMASAVQVKS					
	130	140	150	160	170	180
	190	200	210	220	230	240

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```

130          140          150          160          170          180
      190          200          210          220          230          240
CP4_EP  LLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|221  LLAGLNAPGITSVIEPVMTRDHTKMLAGFGAELSVETDRDGVRIIRLQGQKLFQGQTID
      190          200          210          220          230          240
      250          260          270          280          290          300
CP4_EP  VPGDPSSSTAFPLVAALLVPGSDVTIINVLNMNPTRTGLILTLQEMGADIEVINPRLAGGED
      .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|221  VPGDPSSSTAFPLVAALLVAGSDITIRNVLNMNPTRTGLILTLQEMGADIEILDKRLAGGED
      250          260          270          280          290          300
      310          320          330          340          350          360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDEYPI LavAAAAFAEGATVMNGLEELRVKESDRLSA
      .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|221  VADLRVRSSALKGVTVPAERAPSMIDEYPIVLAVAAAAFAEGTVMGLGLEELRVKESDRLSA
      310          320          330          340          350          360
      370          380          390          400          410          420
CP4_EP  VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENIP
      .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|221  VAEGTLKNGVDCTEGEASLTVRGRPDGKGLGNAGGE-VKTHLDHRIAMSFLVMGLASEHP
      370          380          390          400          410
      430          440          450
CP4_EP  VTVDDATMIATSPFEFFMDLMAGLGAKEILSDTKAA
      : .....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|221  VKVDDSAMIAATSPFEFFDLMAELGADMDEGSISP
      420          430          440          450

>>gi|264661798|gb|EEZ32059.1| 3-phosphoshikimate 1-carbo (450 aa)
  initn: 2453 initl: 2124 opt: 2424  Z-score: 2723.4  bits: 513.1 E(): 1.2e-
  142
Smith-Waterman score: 2424; 82.444% identity (93.111% similar) in 450 aa
overlap (1-450:1-447)

```

	10	20	30	40	50	60
CP4_EP	MLHGASSRPATARKSSGLSGTVRIPGDKSISHSRFMGGLASGETRITGLLEGEDVINTG					
	: : :	. . . . .	. . . . .	. . . . .	. . . . .	. . . . .
gi 264	MSHSACPAPATARHSQLTGEIRIPGDKSISHSRFMGGLASGETRITGLLEGEDVINTG					
	10	20	30	40	50	60
<hr/>						
	70	80	90	100	110	120
CP4_EP	KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAAATGCRLTMGLVGVDFTSFII					
	. . . . .	. . . . .	. . . . .	. . . . .	. . . . .	. . . . .
gi 264	RAMQAMGARIRKEGDWIIINGVNGCLLQPEAPLDFGNAGTGARLTMGVLGYDMDKTSFI					
	70	80	90	100	110	120
<hr/>						
	130	140	150	160	170	180

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```

              70          80          90          100         110         120
               130          140          150          160          170          180
CP4_EP GDASLTKRPMGRVLNPLREMGVQVKSEDDGRLPVTLRGPKTPTPIYRVPMASAQVKS AV
      :::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : : :
gi|161 GDASLSKRPMPGRVLNPLREMGVQVEAAGDRMPLTLIGPTANPIAYRVPMASAQVKS AV
               130          140          150          160          170          180
               190          200          210          220          230          240
CP4_EP LLAGLNTPGIITTVIEPIMTRDHTKEMLQGFGANLTVETDADGVRTIRLEGRGKLTGGVID
      :::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : : :
gi|161 LLAGLNTPGVTTVIEPVMTRDHTKEMLQGFGADLTVETDKDVRHIRIVGGGKLTGGQTID
               190          200          210          220          230          240
               250          260          270          280          290          300
CP4_EP VPGDPSSSTAFPLVAALLVPGSDVTILNVLMNPTRTGILILTLOEMGADIIEVINPRLAGGED
      :::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : : :
gi|161 VPGDPSSSTAFPLVAALLVEGSDVTIRNVLMNPTRTGILILTLOEMGADIIEIIDPRLAGGED
               250          260          270          280          290          300
               310          320          330          340          350          360
CP4_EP VADLRVRSSTLKGVTPEDRAPSMIDEYPILAVAAAFAGATVMNGLEE LR VKES D RL SA
      :::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : : :
gi|161 VADLRVRASKLGKVVPPE RAPSMIDEY PVLAI AASF AEGET VM DGLDEL RV KES D RL AA
               310          320          330          340          350          360
               370          380          390          400          410          420
CP4_EP VANGLKLVGDCDEGETSLVVRGRP DGK GLGN SGA AVATHLDHRIAMSFVLMGLVSEN P
      :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|161 VARGLEANGVDCTEGEMS LTVR GR PG GKL G ---GGTVATHLDHRIAMSFVLMGLASEKP
               370          380          390          400          410
               430          440          450
CP4_EP VTVDDATMIATSFP EFMDLMAGLGAKIELSDTKAA
      :::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : : :
gi|161 VTVDDSTMIATSFP EFMGM MAGLGAKIAESGAE
               420          430          440          450

>>gi|260156845|gb|EEW91925.1| 3-phosphoshikimate 1-carbo (450 aa)
initn: 2452 initl: 2123 opt: 2423 Z-score: 2722.3 bits: 512.9 E(): 1.4e-
142
Smith-Waterman score: 2423; 82.222% identity (93.333% similar) in 450 aa
overlap (1-450:1-447)

```

	10	20	30	40	50	60
CP4_EP	MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSMFMGGLASGETRITGLLEGEDVINTG					
	:	:	:	:	:	:
gi 260	MSHSACPKPATARHSQALTGEIRIPGDKSISHRSMFMGGLASGKTRITGLLEGEDVINTG					
	10	20	30	40	50	60
	70	80	90	100	110	120

CP4\_EP MLHGASSRPPATARKSSGLSGTVIRPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG  
gi|233 MSHSACPAPATARHSQALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTG

	10	20	30	40	50	60
CP4_EP	70	80	90	100	110	120
	KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDFTSTFI					
gi 233	RAMQAMGARIRKEGDVWIIINGVNGCCLLQPEAPLDFGNAGTGARLTMGLVGTYDMKTSFI					
	70	80	90	100	110	120
CP4_EP	130	140	150	160	170	180
	GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVLTRGPKTPTPTITYRVPMASAQVKSAV					
gi 233	GDASLSKRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPIAYRVPMASAQVKSAV					
	130	140	150	160	170	180
CP4_EP	190	200	210	220	230	240
	LLAGLNTPGITTVEIPIMTRDHTEKMLQGFGGANLTVETDADGVRTIRLEGRGKLTGQVID					
gi 233	LLAGLNTPGVTTVEIPVMTRDHTEKMLQGFGADLTVETDKDGVRHRIHVQGKLTGQTID					
	190	200	210	220	230	240
CP4_EP	250	260	270	280	290	300
	VPGDPSSTAFPLVAALLVPGSDVTILNVLNMPNTRTGLILTLQEMGADIEVINPRLAGGED					
gi 233	VPGDPSSTAFPLVAALLVEGSDVTIRNVLNMPNTRTGLILTLQEMGADIEIIDPRLAGGED					
	250	260	270	280	290	300
CP4_EP	310	320	330	340	350	360
	VADLRVRSSTLKGVTVPEDRAPSMIDEYPI LavAAFAEGATVMNGLEELRVKESDRLSA					
gi 233	VADLRVRASKLKGVVVPPERAPSMIDEYPVLAIAAASFAGETVMNGLDELRVKESDRLAA					
	310	320	330	340	350	360
CP4_EP	370	380	390	400	410	420
	VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP					
gi 233	VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFLVMGLASEKP					
	370	380	390	400	410	
CP4_EP	430	440	450			
	VTVDDATMIATSFPEFMDMLMAGLGAKIELSDTKAA					
gi 233	VTVDDSTMIATSFPEFMMAGLGAKIAESGAE					
	420	430	440	450		
>>gi 261745668 gb EEY33594.1  3-phosphoshikimate 1-carbo (450 aa)						
initn: 2452 initl: 2123 opt: 2423 Z-score: 2722.3 bits: 512.9 E(142						
Smith-Waterman score: 2423; 82.222% identity (93.333% similar) in overlap (1-450:1-447)						
	10	20	30	40	50	60

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Smith-Waterman score: 2419; 82.000% identity (93.333% similar) in 450 aa overlap (1-450:1-447)

```

      10      20      30      40      50      60
CP4_EP  MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|261  MSHSACPKPATARHSQALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTG
      10      20      30      40      50      60

      70      80      90     100     110     120
CP4_EP  KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFSTFI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|261  RAMQAMGARIRKEGDVWIINGVNGCLLQPEAPLDFGNAGTGARLTMGLVGTYDMKTSFI
      70      80      90     100     110     120

      130     140     150     160     170     180
CP4_EP  GDASLTKRPMGRVLNPLREMGVQVKSEDDGRLPVTLRGPKTPTPTITYRVPMSAQVKSASV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|261  GDASLSKREPMGRVLNPLREMGVQVEAEGDRMPLTLIGPRTANPIAYRVPMSAQVKSASV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP  LLAGLNTPGITTVEIPIIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|261  LLAGLNTPGVTTVEIPEVMTRDHTEKMLQGFGADLTVETDKDGVRRHIRIVGQGKLTGQTID
      190     200     210     220     230     240

      250     260     270     280     290     300
CP4_EP  VPGDPSSTAFPLVAALLVPGSDVTILNVLNMPNTRTGLILTLQEMGADIEVINPRLAGGED
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|261  VPGDPSSTAFPLVAALLVEGSDVTIRNVLNMPNTRTGLILTLQEMGADIEIIDPRLAGGED
      250     260     270     280     290     300

      310     320     330     340     350     360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|261  VADLRVKASKLKGVVPPERAPSMIDEYPVLIAAASFAEGETVMDGLDELRVKESDRLAAS
      310     320     330     340     350     360

      370     380     390     400     410     420
CP4_EP  VANGKLNGVDCDEGETSLVVRGPRDGKGLGNASGAAVATHLDHRIAMSLVMGLVSENP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|261  VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSLVMGLLASEKP
      370     380     390     400     410

      430     440     450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|261  VTVDDSTMIATSFPEFGMMLAGLGAKIAESGAE
      420     430     440     450
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gi|262 VIVDDSTMIATSFPEFMGMMAGLGAKIAESGAE
      420      430      440      450
>>gi|264659952|gb|EEZ30213.1| 3-phosphoshikimate 1-carbo (450 aa)
      inin: 2448 init1: 2119 opt: 2419 Z-score: 2717.8 bits: 512.1 E(): 2.5e-
      142
Smith-Waterman score: 2419; 82.000% identity (93.333% similar) in 450 aa
overlap (1-450:1-447)
```

	10	20	30	40	50	60
CP4_EP	MLHGASSRPATARKSSGLSGTVIRIPGDKS	ISHRFSFMFGGLASGETRITGLLEGEDVINTG				
gi 264	MSHSACPKPATARHSQALTGEIRIPGDKS	ISHRFSFMFGGLASGKTRITGLLEGEDVINTG				
	10	20	30	40	50	60
CP4_EP	KAMQAMGARIRKEGDTWI	IDGVGNGGLLAPEAPLDFGNAATGCRLTMGLVG	VYDFDSTFI			
gi 264	RAMQAMGARIRKEGDVWI	IVGVGNGCLLQPEAPLDFGNAATGARLTMGLVG	TYDMKTSFI			
	70	80	90	100	110	120
CP4_EP						
gi 264						
	70	80	90	100	110	120

	130	140	150	160	170	180
CP4_EP	GDASLTKRPMGRVLNPLREMGVQVKSEPDGDRPLVTLRGPKTPTPTITYRVPMASAQVKSAV					
	.....	.....	.....	.....	.....	.....
gi 264	GDASLSKRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPIAYRVPMASAQVKSAV					
	.....	.....	.....	.....	.....	.....
	190	200	210	220	230	240
CP4_EP	LLAGLNTPGITTVEIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID					
	.....	.....	.....	.....	.....	.....
gi 264	LLAGLNTPGVTTTVEIEPMVTRDHTEKMLQGFADLTVETDGDGVRHIRIVGQKLTGQTID					
	.....	.....	.....	.....	.....	.....

	250	260	270	280	290	300
CP4_EP	VPGDPSSTAFPLVAALLVPGSDVTILNVLNMNPTRTGLIITLQEMGADIEVINPRLAGGED					
gi 264	VPGDPSSTAFPLVAALLVEGSDVTIRNVLNMNPTRTGLIITLQEMGADIEIIDPRLAGGED					
	250	260	270	280	290	300
CP4_EP	VADLRVRSTLKGVTVPEDRAPSMIDEPYILAVAAAFAGATVMNGLEELRVKESDRLSA					
gi 264	VADLRVKASKLKGVVPPERAPSMIDEPYVPLAIAASFAGETVMGDLDELRVKESDRLAA					
	310	320	330	340	350	360
CP4_EP	VADLRVRSTLKGVTVPEDRAPSMIDEPYILAVAAAFAGATVMNGLEELRVKESDRLSA					
gi 264	VADLRVKASKLKGVVPPERAPSMIDEPYVPLAIAASFAGETVMGDLDELRVKESDRLAA					

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          370          380          390          400          410          420
CP4_EP  VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
      :: :: ::::: :: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|264  VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFLVMGLASEKP
          370          380          390          400          410

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          430      440      450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
          ..... :
gi|261  VTVDDSTMIATSFPEFMGMAGLGAKIAESGAE
          420      430      440      450

>>gi|261295908|gb|EEX99404.1| 3-phosphoshikimate 1-carbo (450 aa)
  initn: 2448 initl: 2119 opt: 2419 Z-score: 2717.8 bits: 512.1 E(): 2.5e-
  142
Smith-Waterman score: 2419; 82.000% identity (93.333% similar) in 450 aa
overlap (1-450:1-447)

          10      20      30      40      50      60
CP4_EP  MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
          : .. : ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  MSHSACPKPATARHSQALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTG
          10      20      30      40      50      60

          70      80      90      100     110     120
CP4_EP  KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRITMGLVGVDYDFDSTFI
          ..... : ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  RAMQAMGARIRKEGDVWIINGVNGCLLQPEAPLDFGNAGTGARLTMGLVGTYDMKTSFI
          70      80      90      100     110     120

          130     140     150     160     170     180
CP4_EP  GDASLTKRPMGRVLNPLREMGVQVKSSEDGDRLPVTLRGPKTPTPIYRVPMASAQVKSASV
          ..... : ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  GDASLSKRPMGRVLNPLREMGVQVEAEGDRMPLTLIGPRTANPIAYRVPMASAQVKSASV
          130     140     150     160     170     180

          190     200     210     220     230     240
CP4_EP  LLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
          ..... : ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  LLAGLNTPGVTTVIEPVMTRDHTEKMLQGFADLTVETDKDGVRHIRIVGQGKLTGQTID
          190     200     210     220     230     240

          250     260     270     280     290     300
CP4_EP  VPGDPSSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
          ..... : ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  VPGDPSSSTAFPLVAALLVEGSDVTIRNVLNPNTRTGLILTLQEMGADIEIIDPRLAGGED
          250     260     270     280     290     300

          310     320     330     340     350     360
CP4_EP  VADLRVRSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
          ..... : ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  VADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAEGETVMMDGLDELRVKESDRLAA
          310     320     330     340     350     360

          370     380     390     400     410     420
CP4_EP  VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
          : .. : ..... : ..... : ..... : ..... : ..... : ..... :

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gi|261  VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFLVMGLASEKP
          370      380      390      400      410

          430      440      450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
          ..... :
gi|261  VTVDDSTMIATSFPEFMGMAGLGAKIAESGAE
          420      430      440      450

>>gi|225639934|gb|ACN99847.1| 3-phosphoshikimate 1-carbo (450 aa)
  initn: 2448 initl: 2119 opt: 2419 Z-score: 2717.8 bits: 512.1 E(): 2.5e-
  142
Smith-Waterman score: 2419; 82.000% identity (93.333% similar) in 450 aa
overlap (1-450:1-447)

          10      20      30      40      50      60
CP4_EP  MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
          : .. : ..... : ..... : ..... : ..... : ..... : ..... :
gi|225  MSHSACPKPATARHSQALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTG
          10      20      30      40      50      60

          70      80      90      100     110     120
CP4_EP  KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRITMGLVGVDYDFDSTFI
          ..... : ..... : ..... : ..... : ..... : ..... : ..... :
gi|225  RAMQAMGARIRKEGDVWIINGVNGCLLQPEAPLDFGNAGTGARLTMGLVGTYDMKTSFI
          70      80      90      100     110     120

          130     140     150     160     170     180
CP4_EP  GDASLTKRPMGRVLNPLREMGVQVKSSEDGDRLPVTLRGPKTPTPIYRVPMASAQVKSASV
          ..... : ..... : ..... : ..... : ..... : ..... : ..... :
gi|225  GDASLSKRPMGRVLNPLREMGVQVEAEGDRMPLTLIGPRTANPIAYRVPMASAQVKSASV
          130     140     150     160     170     180

          190     200     210     220     230     240
CP4_EP  LLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
          ..... : ..... : ..... : ..... : ..... : ..... : ..... :
gi|225  LLAGLNTPGVTTVIEPVMTRDHTEKMLQGFADLTVETDKDGVRHIRIVGQGKLTGQTID
          190     200     210     220     230     240

          250     260     270     280     290     300
CP4_EP  VPGDPSSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
          ..... : ..... : ..... : ..... : ..... : ..... : ..... :
gi|225  VPGDPSSSTAFPLVAALLVEGSDVTIRNVLNPNTRTGLILTLQEMGADIEIIDPRLAGGED
          250     260     270     280     290     300

          310     320     330     340     350     360
CP4_EP  VADLRVRSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
          ..... : ..... : ..... : ..... : ..... : ..... : ..... :
gi|225  VADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAEGETVMMDGLDELRVKESDRLAA
          310     320     330     340     350     360

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gi|262 VADLRVKASKLKGVVVPPERAPSMIDEYPLVAIAASFAEGETVMDGLDELRVKESDRLAA
      310      320      330      340      350      360
      370      380      390      400      410      420
CP4_EP VANGCLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSEN
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|262 VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFLVMGLASEKP
      370      380      390      400      410
      430      440      450
CP4_EP VTVDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      :::::::::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|262 VTVDSDTIATSFPEFMGMAGLGAKIAESGAE
      420      430      440      450

>>gi|261303782|gb|EEY07279.1| 3-phosphoshikimate 1-carbo (450 aa)
  initn: 2448 init1: 2119 opt: 2419 Z-score: 2717.8 bits: 512.1 E(): 2.5e-
  142
  Smith-Waterman score: 2419; 82.000% identity (93.333% similar) in 450 aa
  overlap (1-450:1-447)

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[illegible]

	190	200	210	220	230	240
CP4_EP	LLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID					
	.....					
gi 261	LLAGLNTPGVTTVIEPVMTRDHTEKMLQGFGADLTVETDKDGVRRHIRVVGQKLTGQTID					
	.....					
	190	200	210	220	230	240
	250	260	270	280	290	300
CP4_EP	VPGDPSSTAFPLVAALLVPGSDVTILNVLNMPNTRTGLILTLQEMGADIEVINPRLAGGED					
	.....					
gi 261	VPGDPSSTAFPLVAALLVPGSDVTIRNVLNMPNTRTGLILTLQEMGADIEIIDPRLAGGED					
	.....					
	250	260	270	280	290	300

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                250      260      270      280      290      300
CP4_EP  VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNPRTGLILTLQEMGADIEVINPRLAGGED
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|261  VPGDPSSTAFPLVAALLVEGSDVTIRNVLNPNPRTGLILTLQEMGADIEIIDPRLAGGED
                250      260      270      280      290      300

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          310      320      330      340      350      360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
          ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  VADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAGETVMDGLDELRVKESDRLAA
          310      320      330      340      350      360

          370      380      390      400      410      420
CP4_EP  VANGKLKLVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
          :: :: : ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFLVMGLASEKP
          370      380      390      400      410

          430      440      450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
          ..... : ..... :
gi|261  VTVDDSTMIATSFPEFMGMAGLGAKIAESGAE
          420      430      440      450

>>gi|261300126|gb|EEY03623.1| 3-phosphoshikimate 1-carbo (450 aa)
  initn: 2448 initl: 2119 opt: 2419 Z-score: 2717.8 bits: 512.1 E(): 2.5e-
  142
Smith-Waterman score: 2419; 82.000% identity (93.333% similar) in 450 aa
overlap (1-450:1-447)

          10      20      30      40      50      60
CP4_EP  MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
          : :: : ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  MSHSACPKPATARHSQALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTG
          10      20      30      40      50      60

          70      80      90      100     110     120
CP4_EP  KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
          ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  RAMQAMGARIRKEGDVWIINGVNGCCLLQPEAPLDFGNAGTGARLTMGLVGYDMKTSFI
          70      80      90      100     110     120

          130     140     150     160     170     180
CP4_EP  GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMASAVQKSAV
          ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  GDASLSKRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPIAYRVPMASAVQKSAV
          130     140     150     160     170     180

          190     200     210     220     230     240
CP4_EP  LLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
          ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  LLAGLNTPGVTTVIEPVMTRDHTEKMLQGFGADLTVETDKDGVRHIRIVGQGKLTGQTID
          190     200     210     220     230     240

          250     260     270     280     290     300
CP4_EP  VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
          ..... : ..... : ..... : ..... : ..... : ..... :

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gi|261  VPGDPSSTAFPLVAALLVEGSDVTIRNVLNPNTRTGLILTLQEMGADIEIIDPRLAGGED
          250     260     270     280     290     300

          310     320     330     340     350     360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
          ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  VADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAGETVMDGLDELRVKESDRLAA
          310     320     330     340     350     360

          370     380     390     400     410     420
CP4_EP  VANGKLKLVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
          :: :: : ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFLVMGLASEKP
          370     380     390     400     410

          430     440     450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
          ..... : ..... :
gi|261  VTVDDSTMIATSFPEFMGMAGLGAKIAESGAE
          420     430     440     450

>>gi|261741103|gb|EEY29029.1| 3-phosphoshikimate 1-carbo (450 aa)
  initn: 2448 initl: 2119 opt: 2419 Z-score: 2717.8 bits: 512.1 E(): 2.5e-
  142
Smith-Waterman score: 2419; 82.000% identity (93.333% similar) in 450 aa
overlap (1-450:1-447)

          10      20      30      40      50      60
CP4_EP  MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
          : :: : ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  MSHSACPKPATARHSQALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTG
          10      20      30      40      50      60

          70      80      90      100     110     120
CP4_EP  KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
          ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  RAMQAMGARIRKEGDVWIINGVNGCCLLQPEAPLDFGNAGTGARLTMGLVGYDMKTSFI
          70      80      90      100     110     120

          130     140     150     160     170     180
CP4_EP  GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMASAVQKSAV
          ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  GDASLSKRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPIAYRVPMASAVQKSAV
          130     140     150     160     170     180

          190     200     210     220     230     240
CP4_EP  LLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
          ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  LLAGLNTPGVTTVIEPVMTRDHTEKMLQGFGADLTVETDKDGVRHIRIVGQGKLTGQTID
          190     200     210     220     230     240

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gi|261 LLAGLNTPGVITVIEPVMTDRHTEKMLQGADLTVDKDGVRHRIVGQGKLTGQTID
      190      200      210      220      230      240
      250      260      270      280      290      300
CP4_EP VPGDPSSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLILTLQEMGADIEVINPRLAGGED
      :::::::::::::::::::: :::::::::::::::::::: ::::::::::::::::::::
gi|261 VPGDPSSSTAFPLVAALLVEGSDVTIRNVLMNPTRTGLILTLQEMGADIEIIDPRLAGGED
      250      260      270      280      290      300
      310      320      330      340      350      360
CP4_EP VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
      :::::::::::::::::::: :::::::::::::::::::: ::::::::::::::::::::
gi|261 VADLRVKASKLKGVVVPPERAPSMIDEYPVLAIAASFAEGETVMDGLDELRVKESDRLAA
      310      320      330      340      350      360
      370      380      390      400      410      420
CP4_EP VANGLKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFVLMGLVSEN
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|261 VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFVLMGLASEKP
      370      380      390      400      410
      430      440      450
CP4_EP VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      :::::::::::::::::::: :::::::::::::: ::
gi|261 VTVDDSTMIATSFPEFMGMAGLGAKIAESGAE
      420      430      440      450

>>gi|260923117|gb|EEX89685.1| 3-phosphoshikimate 1-carbo (450 aa)
      initn: 2448 initl: 2119 opt: 2419 Z-score: 2717.8 bits: 512.1 E(): 2.5e-
      142
Smith-Waterman score: 2419; 82.000% identity (93.333% similar) in 450 aa
      overlap (1-450:1-447)

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	10	20	30	40	50	60
CP4_EP	MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSMF	GGLASGETRITGLLEGEDVINTG	:	:	:	:
gi 260	MHSACPKPATARHSQALTEIRIPGDKSISHRSMF	GGLASGKTRITGLLEGEDVINTG	:	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
CP4_EP	KAMQAMGARIRKEGDTWIIDVGNGGLLAPEAPLDF	GNAGTGCRLTMGLVGVD	FDSTFI	:	:	:
gi 260	RAMQAMGARIRKEGDVWIINGVNGGCLLQPEAPLDF	GNAGTGARLTMGLVGTYDMKTSFI	:	:	:	:
	70	80	90	100	110	120
	130	140	150	160	170	180
CP4_EP	GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPV	TLRGPKTPITIRVPMASAV	:	:	:	:
gi 260	GDASLSKRPMPGRVLNPLREMGVQVEAAGDRMPL	TLIGRTPANP IAYRVPMA	SAV	:	:	:
	130	140	150	160	170	180

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      190      200      210      220      230      240
CP4_EP  LLAGLNTPGITTVEIPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      .....
gi|260  LLAGLNTPGVTTVIEPVMTRDHTKMLQGFGADLTVDKDGVRHIRIVGQGKLTGQTID
      190      200      210      220      230      240

      250      260      270      280      290      300
CP4_EP  VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLLITLQEMGADIEVINPRLAGGED
      .....
gi|260  VPGDPSSTAFPLVAALLVEGSDVTIRNVLNPNTRTGLLITLQEMGADIEIIDPRLAGGED
      250      260      270      280      290      300

      310      320      330      340      350      360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSA
      .....
gi|260  VADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAEGETVMDGLDELRVKESDRLAA
      310      320      330      340      350      360

      370      380      390      400      410      420
CP4_EP  VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
      :: .. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260  VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFLVMGLASEKP
      370      380      390      400      410

      430      440      450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      .....
gi|260  VTVDDSTMIATSFPEFMGMAGLGAKIAESGAE
      420      430      440      450

>>gi|260919839|gb|EEX86492.1| 3-phosphoshikimate 1-carbo (450 aa)
      initn: 2448 initl: 2119 opt: 2419 Z-score: 2717.8 bits: 512.1 E(): 2.5e-
      142
      Smith-Waterman score: 2419; 82.000% identity (93.333% similar) in 450 aa
      overlap (1-450:1-447)

      10      20      30      40      50      60
CP4_EP  MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      : .. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260  MSHSACPKPATARHSQALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTG
      10      20      30      40      50      60

      70      80      90      100     110     120
CP4_EP  KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
      .....
gi|260  RAMQAMGARIRKEGDVWIINGVNGCLLQPEAPLDFGNAGTGARLTMGLVGTYDMKTSFI
      70      80      90      100     110     120

      130     140     150     160     170     180
CP4_EP  GDASLTKRPMGRVLNPLREMGVQVKSSEDGDRLPVTLRGPKPTPTITYRVPMSAQVKSASV
      .....

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```

gi|260  GDASLSKRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPIAYRVPMSAQVKSASV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP  LLAGLNTPGITTVEIPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      .....
gi|260  LLAGLNTPGVTTVIEPVMTRDHTKMLQGFGADLTVDKDGVRHIRIVGQGKLTGQTID
      190     200     210     220     230     240

      250     260     270     280     290     300
CP4_EP  VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLLITLQEMGADIEVINPRLAGGED
      .....
gi|260  VPGDPSSTAFPLVAALLVEGSDVTIRNVLNPNTRTGLLITLQEMGADIEIIDPRLAGGED
      250     260     270     280     290     300

      310     320     330     340     350     360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSA
      .....
gi|260  VADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAEGETVMDGLDELRVKESDRLAA
      310     320     330     340     350     360

      370     380     390     400     410     420
CP4_EP  VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
      :: .. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260  VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFLVMGLASEKP
      370     380     390           400     410

      430     440     450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      .....
gi|260  VTVDDSTMIATSFPEFMGMAGLGAKIAESGAE
      420     430     440     450

>>gi|163673024|gb|ABY37135.1| 3-phosphoshikimate 1-carbo (450 aa)
      initn: 2448 initl: 2119 opt: 2419 Z-score: 2717.8 bits: 512.1 E(): 2.5e-
      142
      Smith-Waterman score: 2419; 82.000% identity (93.333% similar) in 450 aa
      overlap (1-450:1-447)

      10      20      30      40      50      60
CP4_EP  MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      : .. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|163  MSHSACPKPATARHSQALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTG
      10      20      30      40      50      60

      70      80      90      100     110     120
CP4_EP  KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
      .....
gi|163  RAMQAMGARIRKEGDVWIINGVNGCLLQPEAPLDFGNAGTGARLTMGLVGTYDMKTSFI
      70      80      90      100     110     120

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```
gi|255 RAMQAMGARIRKEGDVWIINGVGNCLLQPEAPLDFGNAGTGARLTMTGLVTGYDMKTSFI
      70          80          90         100         110         120
      130          140          150         160         170         180
CP4_EP GDASLTKRPMGRVLNPLREMGVVQVKSEDDRLPVTLRGPKTPPTITYRVPMASAVQKSVA
.....
gi|255 GDASLSKRPMGRVLNPLREMGVVQEAAEGDRMPLTLIGPRTANPIAYRVPMASAVQKSAI
      130          140          150         160         170         180
      190          200          210         220         230         240
CP4_EP LLAGLNTPGITTVIEPIIMTRDHTTEKMLQGFGGANLTVETDADGVRTIRLEGRGKLTGGVID
.....
gi|255 LLAGLNTPGVTTVIEPVMTDRDHTTEKMLQGFGADLTVETDKDGVRHRIHVQQGLTGQTID
      190          200          210         220         230         240
      250          260          270         280         290         300
CP4_EP VPGDPSSSTAFPLVAALLVPGSVDVTILNVLMNPTRTGLILTQEMGADIEVINPRLAGGED
.....
gi|255 VPGDPSSSTAFPLVAALLVEGSDVTIRNVLMNPTRTGLILTQEMGADIEIIDPRLAGGED
      250          260          270         280         290         300
      310          320          330         340         350         360
CP4_EP VADLRVRSSSTLKGVTVPEDRAPSMIDEYPI LAVAAAFAEGATVMNGLEELRVKESDRLSA
.....
gi|255 VADLRVKASKLKGVVPPERAPSMDIEYVPLAIAASFAGETVMGDGLDLRVKESDRLA
      310          320          330         340         350         360
      370          380          390         400         410         420
CP4_EP VANGLKLNGVDCDEGETSLVVRGRPDKGLGNASGA AVATHLDHRIAMSFLVMGLVSEN
:: :: .....
gi|255 VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFLVMGLASEKP
      370          380          390         400         410
      430          440          450
CP4_EP VTVDDATMIATSFPFMDLMAGLGAKIELSDTKAA
.....
gi|255 VTVDDSTMIATSFPFMMGMAGLGAKIAESGAE
      420          430          440          450

>>gi|263003296|gb|EEZ15589.1| 3-phosphoshikimate 1-carbo (450 aa)
initn: 2437 initl: 2118 opt: 2414 Z-score: 2712.2 bits: 511.1 E(): 5.2e-
142
Smith-Waterman score: 2414; 81.778% identity (93.333% similar) in 450 aa
overlap (1-450:1-447)

      10          20          30          40          50          60
CP4_EP MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
: : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|263 MSHSACPKPATARHSQALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTG
      10          20          30          40          50          60
```

```

      70      80      90      100      110      120
CP4_EP  KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVYDFDSTFI
      ..... : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|263  RAMQAMGARIRKEGDVWIINGVNGCCLLQPEAPLDFGNAGTGARLTMGLVGTYDMKTSFI
      70      80      90      100      110      120

      130      140      150      160      170      180
CP4_EP  GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPITIRVPMASAVKSAV
      ..... : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|263  GDASLSKRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPIAYRVPMSAVKSAV
      130      140      150      160      170      180

      190      200      210      220      230      240
CP4_EP  LLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      ..... : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|263  LLAGLNTPGVTTVIEPVMTRDHTKMLQGFGADLTVDKDGVRHIRIVGQKLTGTID
      190      200      210      220      230      240

      250      260      270      280      290      300
CP4_EP  VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLLTLQEMGADIEVINPRLAGGED
      ..... : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|263  VPGDPSSTAFPLVAALLVEGSDVTIRNVLNPNTRTGLLTLQEMGADIEIIDPRLAGGED
      250      260      270      280      290      300

      310      320      330      340      350      360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSA
      ..... : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|263  VADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAEGETVMDGLDELRVKESDRLAA
      310      320      330      340      350      360

      370      380      390      400      410      420
CP4_EP  VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLHRIAMSFLVMGLVSENP
      :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|263  VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVGTHLHRIAMSFLVMGLASEKP
      370      380      390      400      410

      430      440      450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      ..... : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|263  VTVDDSTMIATSFPEFMGMAGLGAKIAESGAE
      420      430      440      450

>>gi|260153122|gb|EEW88214.1| 3-phosphoshikimate 1-carbo (450 aa)
  initn: 2437 initl: 2118 opt: 2414 Z-score: 2712.2 bits: 511.1 E(): 5.2e-
  142
Smith-Waterman score: 2414; 81.778% identity (93.333% similar) in 450 aa
overlap (1-450:1-447)

      10      20      30      40      50      60
CP4_EP  MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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gi|260  MSHSACPKPATARHSQALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTG
      10      20      30      40      50      60

      70      80      90      100      110      120
CP4_EP  KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVYDFDSTFI
      ..... : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260  RAMQAMGARIRKEGDVWIINGVNGCCLLQPEAPLDFGNAGTGARLTMGLVGTYDMKTSFI
      70      80      90      100      110      120

      130      140      150      160      170      180
CP4_EP  GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPITIRVPMASAVKSAV
      ..... : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260  GDASLSKRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPIAYRVPMSAVKSAV
      130      140      150      160      170      180

      190      200      210      220      230      240
CP4_EP  LLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      ..... : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260  LLAGLNTPGVTTVIEPVMTRDHTKMLQGFGADLTVDKDGVRHIRIVGQKLTGTID
      190      200      210      220      230      240

      250      260      270      280      290      300
CP4_EP  VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLLTLQEMGADIEVINPRLAGGED
      ..... : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260  VPGDPSSTAFPLVAALLVEGSDVTIRNVLNPNTRTGLLTLQEMGADIEIIDPRLAGGED
      250      260      270      280      290      300

      310      320      330      340      350      360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSA
      ..... : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260  VADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAEGETVMDGLDELRVKESDRLAA
      310      320      330      340      350      360

      370      380      390      400      410      420
CP4_EP  VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLHRIAMSFLVMGLVSENP
      :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260  VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVGTHLHRIAMSFLVMGLASEKP
      370      380      390      400      410

      430      440      450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      ..... : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260  VTVDDSTMIATSFPEFMGMAGLGAKIAESGAE
      420      430      440      450

>>gi|17983963|gb|AAL53098.1| 3-phosphoshikimate 1-carbox (480 aa)
  initn: 2437 initl: 2118 opt: 2414 Z-score: 2711.7 bits: 511.1 E(): 5.5e-
  142
Smith-Waterman score: 2414; 81.778% identity (93.333% similar) in 450 aa
overlap (1-450:31-477)

```

```
>>gi|179 GAE
480
>>gi|260675989|gb|EEX62810.1| 5-enolpyruvylshikimate-3-p (450 aa)
initn: 2442 initl: 2113 opt: 2413 Z-score: 2711.0 bits: 510.9 E(): 6e-142
Smith-Waterman score: 2413; 81.778% identity (93.333% similar) in 450 aa
overlap (1-450:1-447)

      10          20          30          40          50          60
CP4_EP MLHGASSRPPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      : . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260 MSHSACPKPATARHSQALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTG
      10          20          30          40          50          60

      70          80          90          100         110         120
CP4_EP KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRLTMGLVGVDSTFI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260 RAMQAMGARIRKEGDVWIINGVNGCLLQPEAPLDFGNAGTGARLTMGLVGTYDMKTSFI
      70          80          90          100         110         120

      130         140         150         160         170         180
CP4_EP GDASLTKRPMGRVLNPLREMGVQVKSEDDGRLPVLTRGPKTPTPITYRVPMSAQVKSAV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260 GDASLSKRPMGRVLNPLREMGVQVEAAGDRMPLTLIGPRTANPIAYRVPMSAQVKSAV
      130         140         150         160         170         180

      190         200         210         220         230         240
CP4_EP LLAGLNTPGITTVEIPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260 LLAGLNTPGVTTVEIPVMTRDHTKMLQGFGADLTVETDKDGVRHIRIVGGGKLTGQTID
      190         200         210         220         230         240

      250         260         270         280         290         300
CP4_EP VPGDPSSTAFPLVAALLVPGSDVTILNVLNMNPTRTGLLTLQEMGADIEVINPRLAGGED
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260 VPGDPSSTAFPLVAALLVEGSEVTRNVLNMNPTRTGLLTLQEMGADIEIIDPRLAGGED
      250         260         270         280         290         300

      310         320         330         340         350         360
CP4_EP VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFNEGATVMNGLEELRVKESDRLSA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260 VADLRVKASKLKGVVPPERAPSMIDEYPVLIAAASFAEGETVMDGLDELRVKESDRLAA
      310         320         330         340         350         360

      370         380         390         400         410         420
CP4_EP VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFVLMGLVSENP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260 VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFVLMGLASEKP
      370         380         390         400         410

      430         440         450
```

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              430          440          450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
        .....:.....:
gi|260   VTVDDSTMIATSFPEFMGMAGLGAKIAESGAE
              420          430          440          450

```

```
455 residues in 1 query sequences
4761287459 residues in 17815538 library sequences
Scomplib [34t26]
start: Fri Jan 22 19:56:10 2010 done: Fri Jan 22 20:10:35 2010
Total Scan time: 691.790 Total Display time: 16.320
```

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

Database checksum values:

```
Fri Jan 22 19:50:56 GMT 2010      17c3a19148dfb0163e270cf41e2aa437
/genedata/1/db/TOX_2010
```

```

                250      260      270      280      290      300
CP4_EP  VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
        ::::::::::::::::::::: ::::::::::::::::::::::::::::::::::::::::::::
gi|260  VPGDPSSTAFPLVAALLVEGSEVTIRNVLNPNTRTGLILTLQEMGADIEIIDPRLAGGED
                250      260      270      280      290      300

```

```

          370          380          390          400          410          420
CP4_EP  VANG LKLNGVDCDEGETSLVVRGPRDGKGLGNASGAAVATHLDHRIAMSLVMGLVSEN
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|260  VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSLVMGLASEKP
          370          380          390          400          410

```