

**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

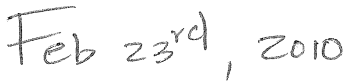
**Study Number:** REG-10-042

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<br>Inspection/Audit | Phase                       | Date Reported to<br>Study Director | Date Reported<br>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**

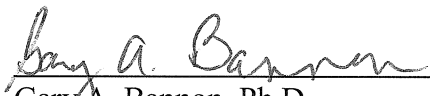
This report is an accurate and complete representation of the study/project activities.

**Signatures of Final Report Approval:**



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Date: 2-23-10



Gary A. Bannon, Ph.D.  
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Date: Feb. 23, 2010

### **Study Information**

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**Study Start Date:** January 22, 2010

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Monsanto-St. Louis.

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### Abbreviations and Definitions

|           |  |
|-----------|--|
| AA        | Amino acid   |
| AD_2010   | Allergen and gliadin protein sequence database (Release date January 22, 2010)   |
| BLOCKS    | A database of amino acid motifs found in protein families  |
| BLOSUM50  | BLOcks SUBstitution Matrix, used to score similarities between pairs of distantly related of protein or nucleotide sequences                 |
| CP4 EPSPS | 5-enolpyruvylshikimate-3-phosphate synthase from <i>Agrobacterium tumefaciens</i> sp. strain CP4   |
| 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).

---

<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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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
WIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSIFIGDASLTKRPMGRVLNPLREMGVQVKSEGDGRL
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 MNCPLVNGQQYDIKYTWNVPKIPNSENVVTVKVLG-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 KCPLVNGQQYDIKYTWNVPKIPNSENVVTVKVLG-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 KCPLVNGQQYDIKYTWNVPKIPNSENVVTVKVLG-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 KCPLVNGQQYDIKYTWNVPKIPNSENVVTVKVLG-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
```

```

      20      30      40      50      60      70
      260      270      280      290      300
CP4_EP AALLVPGSDVTI---LNV-LMNPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRSS
      :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|217 KCPLVNGQQYDIKYTWNVPKIPKSENVVTVKVLG-DNGVLACAIATHAKIQD
      80      90      100      110      120

      310      320      330      340      350      360
CP4_EP TLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGKLKNG

>>gi|21725600|emb|CAD38381.1| unnamed protein product [D (129 aa)
  initn: 35 init1: 35 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-DPSSTAFPLV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|217 PGCHGNEPCIHSGKPFQLEALFEANQNSATAKIEIKASIDGLEVDVPGIDPNACNY--M
      20      30      40      50      60      70

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

      310      320      330      340      350      360
CP4_EP TLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGKLKNG

>>gi|21725592|emb|CAD38377.1| unnamed protein product [D (129 aa)
  initn: 54 init1: 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-DPSSTAFPLV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|217 PGCHGNEPCIHSGKPFQLEALFEANQNSATAKIEIKASIDGLSDVPIDPNACHY--M
      20      30      40      50      60      70

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

      310      320      330      340      350      360
CP4_EP TLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGKLKNG

>>gi|21725590|emb|CAD38376.1| unnamed protein product [D (129 aa)
  initn: 54 init1: 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-DPSSTAFPLV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|217 PGCHGSEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDGLSDVPIDPNACHY--M
      20      30      40      50      60      70

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

      310      320      330      340      350      360
CP4_EP TLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGKLKNG

>>gi|1346568|sp|P49372.1|ALL1_APIGR RecName: Full=Major (154 aa)
  initn: 38 init1: 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 PKTPTPITYRVPMASAQVKSAVLLAGLNTPGITTVEIPIMTRDHTKMLQGF--GANLTV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 MGVTQTHVLELTSSVSAAEKIFQGFVIDVDTVL
      10      20      30

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

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

      340      350      360      370      380      390
CP4_EP AAFAEGATVMNGLEELRVKESDRLSAVANGKLKNGVDCDEGETSLVVRGRPDGKGLGNA

gi|134 ALEAYLIAN
      150

>>gi|21725584|emb|CAD38373.1| unnamed protein product [D (129 aa)
  initn: 54 init1: 54 opt: 74 Z-score: 94.6 bits: 24.9 E(): 2.7
```

```

>>gi|21725590|emb|CAD38376.1| unnamed protein product [D (129 aa)
  initn: 54 init1: 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-DPSSTAFPLV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|217 PGCHGSEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDGLSDVPIDPNACHY--M
      20      30      40      50      60      70

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

      310      320      330      340      350      360
CP4_EP TLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGKLKNG

>>gi|1346568|sp|P49372.1|ALL1_APIGR RecName: Full=Major (154 aa)
  initn: 38 init1: 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 PKTPTPITYRVPMASAQVKSAVLLAGLNTPGITTVEIPIMTRDHTKMLQGF--GANLTV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 MGVTQTHVLELTSSVSAAEKIFQGFVIDVDTVL
      10      20      30

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

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

      340      350      360      370      380      390
CP4_EP AAFAEGATVMNGLEELRVKESDRLSAVANGKLKNGVDCDEGETSLVVRGRPDGKGLGNA

gi|134 ALEAYLIAN
      150

>>gi|21725584|emb|CAD38373.1| unnamed protein product [D (129 aa)
  initn: 54 init1: 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 MGVDQKSEDDGRLPVTLRGPKITPTITYRVPMSAQVKSALLAGLNTPGITTVIEPIMT
gi|219 LLLAAVLVSVFAAAATGPGYCPGMGLPSNPLEGCREYVAQQTGCVGIVGSPVSTPEGNT
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 KHSQNGMGKDDHYLLEFPPTFPDGHDKYKFDKSKNPKEDPGPARVIYTPNKFVFCGIVAHQR
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 CRCEALRYFIALPVPSQPVDPDRSGNVGESGLIDLPGCPREMOWDFVRLLVAPGQCNLATI
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 CRCEALRYFIALPVPSQPVDPDRSGNVGESGLIDLPGCPREMOWDFVRLLVAPGQCNLATI
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 KHSQNGMGKDDHYLLEFPPTFPDGHDKYKFDKSKPKEDPGPARVIYTPNKFVFCGIVAHQRG
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:===== *
 90   4       7:===== *
 92  19      6:===== *
 94   4       4:===== *
 96   2       3:===== *
 98  13       3:===== *

      inset = represents 1 library sequences
```

```

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|AAZ88075.1| 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 AVPLVSARLLSEKVPRLDLPVMHIGDEPYR---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 AVPLVSARLLSEKVPRLDLPVMHIGDEPYR---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 AVPLVSARLLSEKVPRLDLPVMHIGDEPYR---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---VPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGEDVADL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|169 AVPLVSARLLSEKVPDRDLYPVMHIGDEPYR---LLT-----TDMTSV-PATVIGEEVADL
      40      50      60      70      80

      310      320      330      340      350      360
CP4_EP RVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANG
      : : : :
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-TKRP MGRVLNPLREMGVQVKSEGDRLPV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|256 NGAA-----INLFDMSYFGSSSVFQIDANFGTPSAMIEMLVYHRPGLVELLPALPDWSV
      690      700      710      720      730      740

      160      170      180      190      200      210
CP4_EP TLRGPKTPITYRVPMASAVKSAVLLAGLN-TPGITTVEIPIMTRDHEKMLQGFGAN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|256 A--GSVTGVPVRGAMALDMAWGGQVTTATLHGTPGAGTTVK---FGAWSQAVTTIGSGGT
      750      760      770      780      790

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

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

```

      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 EPIMTRDHEKMLQGFGANLTVETDADGVRTIRLEGRGKL---TGQVIDVPGDPSSTAF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|681 MQFKGYTCKRESRYRLFVDVQSDIIDTPG--RRMAV
      10      20      30

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

      310      320      330      340      350      360
CP4_EP RSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGLK
      : : : :
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 GCRLTMGLVGVDYFDSTFIGDASLTKRP MGRVLNPLREMGVQVKSEGDRLPVTLRGPKT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|528 KRTSIFIAGVLIPILLNGCSSGKNKAYLDPKFVPPQVEGGPTVPSPDESGLPLPGPGPAL
      10      20      30      40      50      60

      170      180      190      200      210
CP4_EP PT--PITYRVPMASAVKSAVLLAGLNTPGITTVEIPIMTRDHEKMLQGFGANLTVETD
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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 MQFKVYTYKRESRYRLFDVQSDIIDTPG--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--PITYRVPMASAQVKSAVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD
      ::  ::  ::  ..  :
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--PITYRVPMASAQVKSAVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD
      ::  ::  ::  ..  :
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--PITYRVPMASAQVKSAVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD

```

```

      ::  ::  ::  ..  :
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--PITYRVPMASAQVKSAVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD
      ::  ::  ::  ..  :
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--PITYRVPMASAQVKSAVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD
      ::  ::  ::  ..  :
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--PITYRVPMASAQVKSAVLLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETD

```

```

      ::  ::  ::  ..  :
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--PITYRVPMASQVKSAVLLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETD
      ::  ::  ::  ..  :
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--PITYRVPMASQVKSAVLLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETD
      ::  ::  ::  ..  :
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--PITYRVPMASQVKSAVLLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETD
```

```

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

>>gi|197239660|gb|ACH53456.1| cytolethal distending toxi (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 ILAVQEAGSPPTAVDTGRVIPSPGPVRELINWLSTNSRP--QQVY
      10          20          30          40

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

```
      :      :... :. . . . . :... :. . . : ..... :
gi|197 IYFSAVDALGGRVNLALVSNRRADDEVFLSPVRQGGRRLLGIRIGNDAFFTAHAIAMRNN
      50      60      70      80      90      100

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

>>gi|197239658|gb|ACH53455.1| cytolethal distending toxi (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 KMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSSTAFPLVAALLVPGSDVT
      :.....: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|197 ILAVQEAGSPSTAVDTGRVIPSPGIPVRELIWNLSNRSRPPQVY
      10      20      30      40

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

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

>>gi|218349870|emb|CAQ87274.1| 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; 29.787% identity (57.447% similar) in 94 aa
overlap (223-312:14-100)

      200      210      220      230      240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSST
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|218 MPMRTGTGEMQFKVYTYKRESRYRLFVDVQSDIIDTPG--RRM
      10      20      30      40

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

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPI LAVAAFAEGATVMNGLEELRVKESDRLSAVANGKLKN
      . . :
gi|218 NDIKNAINLMFWGI
      100      110
```

```
CP4_EP STLKGVTVPEDRAPSMIDEYPI LAVAAFAEGATVMNGLEELRVKESDRLSAVANGKLKN
      . . :
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; 29.787% identity (57.447% similar) in 94 aa
overlap (223-312:14-100)

      200      210      220      230      240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSST
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|218 MPMRTGTGEMQFKVYTYKRESRYRLFVDVQSDIIDTPG--RRM
      10      20      30      40

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

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPI LAVAAFAEGATVMNGLEELRVKESDRLSAVANGKLKN
      . . :
gi|218 NDIKNAINLMFWGI
      100      110

>>gi|218359346|emb|CAU95832.1| 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; 29.787% identity (57.447% similar) in 94 aa
overlap (223-312:14-100)

      200      210      220      230      240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSST
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|218 MPMRTGTGEMQFKVYTYKRESRYRLFVDVQSDIIDTPG--RRM
      10      20      30      40

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

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPI LAVAAFAEGATVMNGLEELRVKESDRLSAVANGKLKN
      . . :
gi|218 NDIKNAINLMFWGI
      100      110
```

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>>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 AFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      : : : : : : :
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 AFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      : : : : : : :
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 AFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      : : : : : : :
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 AFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      : : : : : : :
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 AFPLVAALLVPGSDVTILNVLNMPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
.....: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|186 VIPLASARLL--SD-KVSRELYPVVHIGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
      40      50      60      70      80

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSAVANGLKLN
. .:
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 AFPLVAALLVPGSDVTILNVLNMPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
.....: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|186 VIPLASARLL--SD-KVSRELYPVVHIGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
      40      50      60      70      80

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSAVANGLKLN
. .:
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 AFPLVAALLVPGSDVTILNVLNMPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
.....: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|259 VIPLASARLL--SD-KVSRELYPVVHIGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
```

```

      40      50      60      70      80
      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSAVANGLKLN
. .:
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 AFPLVAALLVPGSDVTILNVLNMPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
.....: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|333 VIPLASARLL--SD-KVSRELYPVVHIGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
      40      50      60      70      80

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSAVANGLKLN
. .:
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 AFPLVAALLVPGSDVTILNVLNMPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
.....: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|186 VIPLASARLL--SD-KVSRELYPVVHIGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
      40      50      60      70      80

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

CP4\_EP ILNVL MNPT--RTGLI LTLOEMGADIEVINPRLAGGEDVADLRVRSS---TLKGVTVPED

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```

CP4_EP RAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSAVANGLKLNQDCDEGETSL
      :: ...
gi|541 DAPELVEEVSYFFRDSRPVHQALN
      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 AFPLVAALLVPGSDVTILNVLNMNPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|580 VIPLASARLL--SD-KVSRELYPVVHVGD-ESWRMMTTDMASV-PIFVIGEEVADLSHRE
      40      50      60      70      80      90

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSAVANGLKLN
      . . :
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 AFPLVAALLVPGSDVTILNVLNMNPTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|563 VIPLASARLL--SD-KVSRELYPVVHVGD-ESWRMMTTDMASV-PIFVIGEEVADLSHRE
      40      50      60      70      80      90

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

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>>gi|81248277|gb|ABB68984.1| post-segregation toxin [Shi (108 aa)  
initn: 39 init1: 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|812      MRTGTGEMQFKVYAYKRESRYRLFVDVQSDIIDTPG--RRM
      10      20      30

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|812 VIPLASARLL--SD-KVSRELYPVVHVGD-ESWRMMTTDMASV-PIFVIGEEVADLSHRE
      40      50      60      70      80      90

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGKLKN
      . . :
gi|812 NDIKNAINLMFWGI
      100
```

>>gi|13310719|gb|AAK18543.1|AF348706\_232 post-segregatio (110 aa)  
initn: 39 init1: 39 opt: 70 Z-score: 98.1 bits: 25.3 E(): 9.9  
Smith-Waterman score: 70; 28.723% identity (58.511% similar) in 94 aa  
overlap (223-312:14-100)

```

      200      210      220      230      240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKL----TGQVIDVPGDPSST
      : . . : : :
gi|133      MPMRTGTGEMQFKVYAYKRESRYRLFVDVQSDIIDTPG--RRM
      10      20      30      40

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|133 VIPLASARLL--SD-KVSRELYPVVHVGD-ESWRMMTTDMASV-PIFVIGEEVADLSHRE
      50      60      70      80      90

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGKLKN
      . . :
gi|133 NDIKNAINLMFWGI
      100      110
```

>>gi|18654301|gb|AAL77581.1|L47837\_1 cytotoxic protein [ (126 aa)  
initn: 39 init1: 39 opt: 71 Z-score: 98.1 bits: 25.5 E(): 10  
Smith-Waterman score: 71; 29.787% identity (56.383% similar) in 94 aa  
overlap (223-312:30-116)

```

      200      210      220      230      240
CP4_EP VIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKL----TGQVIDVPGDPSST
      : : . : : : :
gi|186      MTMITPSLHACRSTLEDPRVPSSNSLQFKVYTYKRESRYRLFVDVQSDIIDTPG--RRM
      10      20      30      40      50

      250      260      270      280      290      300
CP4_EP AFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGEDVADLRVRS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|186 VIPLASARLL--SD-KVSRELYPVVHIGD-ESWRMMTTDMASV-PVSVIGEEVADLSHRE
      60      70      80      90      100      110

      310      320      330      340      350      360
CP4_EP STLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSAVANGKLKN
      . . :
gi|186 NDIKNAINLMFWGI
      120
```

455 residues in 1 query sequences  
2069351 residues in 8448 library sequences  
Scomplib [34t26]  
start: Fri Jan 22 19:50:55 2010 done: Fri Jan 22 19:50:56 2010  
Total Scan time: 0.300 Total Display time: 0.040

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

# fasta34 CP4\_EPSPS.pep /genedata/1/db/PRT\_2010 -Q -E 1 -O  
CP4\_EPSPS.pep\_prt.fasta  
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7,  
2006

Please cite:

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

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

```

      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
gi|240860935|gb|ACS58602.1| 3-phosphoshikimate 1-c ( 452) 2559 541.2 4.4e-151
gi|2484148|gb|AAB72284.1|I49177 Sequence 5 from pa ( 449) 2442 516.9 9.2e-144
gi|2485225|gb|AAB73361.1|I44450 Sequence 5 from pa ( 449) 2442 516.9 9.2e-144
gi|144974728|gb|ABP12439.1| Sequence 7 from patent ( 449) 2442 516.9 9.2e-144
gi|2485226|gb|AAB73362.1|I44451 Sequence 7 from pa ( 449) 2442 516.9 9.2e-144
gi|144974727|gb|ABP12438.1| Sequence 5 from patent ( 449) 2442 516.9 9.2e-144
gi|5957548|gb|AAE08222.1| Sequence 5 from patent U ( 449) 2442 516.9 9.2e-144
gi|5957549|gb|AAE08223.1| Sequence 7 from patent U ( 449) 2442 516.9 9.2e-144
gi|2484149|gb|AAB72285.1|I49178 Sequence 7 from pa ( 449) 2442 516.9 9.2e-144
```

|   |   |
|---|---|
| gi 151559264 gb ABS12762.1  3-phosphoshikimate 1-c ( 450) 2441 516.7 1.1e-143 | gi 260669423 gb EEX56363.1  5-enolpyruvylshikimate ( 450) 2413 510.9 6e-142   |
| gi 221721755 gb ACM24911.1  3-phosphoshikimate 1-c ( 454) 2427 513.8 8.1e-143 | gi 189018862 gb ACD71584.1  3-phosphoshikimate 1-c ( 450) 2413 510.9 6e-142   |
| gi 264661798 gb EEZ32059.1  3-phosphoshikimate 1-c ( 450) 2424 513.1 1.2e-142 | gi 82615053 emb CAJ09979.1  ATP/GTP-binding site m ( 450) 2413 510.9 6e-142   |
| gi 161334826 gb ABX61131.1  3-phosphoshikimate 1-c ( 450) 2423 512.9 1.4e-142 | gi 260096414 gb EEW80290.1  5-enolpyruvyl shikimat ( 461) 2413 510.9 6.1e-142 |
| gi 260156845 gb EEW91925.1  3-phosphoshikimate 1-c ( 450) 2423 512.9 1.4e-142 | gi 148370906 gb ABQ60885.1  3-phosphoshikimate 1-c ( 461) 2409 510.0 1.1e-141 |
| gi 23346795 gb AAN28982.1  3-phosphoshikimate 1-ca ( 450) 2423 512.9 1.4e-142 | gi 260916763 gb EEX83624.1  5-enolpyruvylshikimate ( 450) 2406 509.4 1.7e-141 |
| gi 261745668 gb EEY33594.1  3-phosphoshikimate 1-c ( 450) 2423 512.9 1.4e-142 | gi 62195146 gb AAX73446.1  AroA, 3-phosphoshikimat ( 450) 2404 509.0 2.2e-141 |
| gi 261293812 gb EEX97308.1  3-phosphoshikimate 1-c ( 450) 2419 512.1 2.5e-142 | gi 13487156 gb AAK27445.1 AF326475_1 5-enolpyruvyl ( 480) 2389 505.9 2e-140   |
| gi 262764953 gb EEZ10874.1  3-phosphoshikimate 1-c ( 450) 2419 512.1 2.5e-142 | gi 167285314 gb ABZ38178.1  Sequence 12116 from pa ( 452) 2298 487.0 9.5e-135 |
| gi 264659952 gb EEZ30213.1  3-phosphoshikimate 1-c ( 450) 2419 512.1 2.5e-142 | gi 14025099 dbj BAB51700.1  3-phosphoshikimate 1-c ( 452) 2298 487.0 9.5e-135 |
| gi 261295908 gb EEX99404.1  3-phosphoshikimate 1-c ( 450) 2419 512.1 2.5e-142 | gi 110286919 gb ABG64978.1  3-phosphoshikimate 1-c ( 449) 2253 477.6 6.2e-132 |
| gi 225639934 gb ACN99847.1  3-phosphoshikimate 1-c ( 450) 2419 512.1 2.5e-142 | gi 49239274 emb CAF25595.1  3-phosphoshikimate 1-c ( 442) 1949 414.4 6.3e-113 |
| gi 262551684 gb EEZ07674.1  3-phosphoshikimate 1-c ( 450) 2419 512.1 2.5e-142 | gi 161017021 emb CAK00579.1  3-phosphoshikimate 1- ( 442) 1932 410.9 7.3e-112 |
| gi 261303782 gb EEY07279.1  3-phosphoshikimate 1-c ( 450) 2419 512.1 2.5e-142 | gi 49237722 emb CAF26911.1  3-phosphoshikimate 1-c ( 442) 1918 408.0 5.5e-111 |
| gi 261300126 gb EEY03623.1  3-phosphoshikimate 1-c ( 450) 2419 512.1 2.5e-142 | gi 240266876 gb ACS50464.1  3-phosphoshikimate 1-c ( 442) 1918 408.0 5.5e-111 |
| gi 261741103 gb EEY29029.1  3-phosphoshikimate 1-c ( 450) 2419 512.1 2.5e-142 | gi 120615007 gb ABM45608.1  3-phosphoshikimate 1-c ( 441) 1852 394.3 7.4e-107 |
| gi 261739124 gb EEY27120.1  3-phosphoshikimate 1-c ( 450) 2419 512.1 2.5e-142 | gi 211960244 gb EEA95441.1  3-phosphoshikimate 1-c ( 442) 1820 387.6 7.5e-105 |
| gi 260923117 gb EEX89685.1  3-phosphoshikimate 1-c ( 450) 2419 512.1 2.5e-142 | gi 154154557 gb ABS61774.1  3-phosphoshikimate 1-c ( 451) 1710 364.8 5.8e-98  |
| gi 260919839 gb EEX86492.1  3-phosphoshikimate 1-c ( 450) 2419 512.1 2.5e-142 | gi 179344835 gb ACB80247.1  3-phosphoshikimate 1-c ( 453) 1681 358.7 3.8e-96  |
| gi 163673024 gb ABY37135.1  3-phosphoshikimate 1-c ( 450) 2419 512.1 2.5e-142 | gi 240008687 gb ACS39913.1  3-enolpyruvylshikimate ( 453) 1672 356.9 1.4e-95  |
| gi 255998648 gb ACU47047.1  3-phosphoshikimate 1-c ( 450) 2418 511.9 2.9e-142 | gi 218522663 gb ACK83248.1  3-phosphoshikimate 1-c ( 453) 1666 355.6 3.3e-95  |
| gi 263003296 gb EEZ15589.1  3-phosphoshikimate 1-c ( 450) 2414 511.1 5.2e-142 | gi 154159145 gb ABS66361.1  3-phosphoshikimate 1-c ( 456) 1666 355.6 3.3e-95  |
| gi 260153122 gb EEW88214.1  3-phosphoshikimate 1-c ( 450) 2414 511.1 5.2e-142 | gi 163663156 gb ABY30523.1  3-phosphoshikimate 1-c ( 472) 1654 353.1 1.9e-94  |
| gi 17983963 gb AAL53098.1  3-phosphoshikimate 1-ca ( 480) 2414 511.1 5.5e-142 | gi 91681127 gb ABE37429.1  3-phosphoshikimate 1-ca ( 445) 1653 352.9 2.1e-94  |
| gi 260675989 gb EEX62810.1  5-enolpyruvylshikimate ( 450) 2413 510.9 6e-142   | gi 158332444 dbj BAF89929.1  3-phosphoshikimate 1- ( 471) 1652 352.7 2.6e-94  |
| gi 260874433 gb EEX81502.1  3-phosphoshikimate 1-c ( 450) 2413 510.9 6e-142   | gi 168198858 gb ACA20805.1  3-phosphoshikimate 1-c ( 449) 1642 350.6 1e-93    |
| gi 260671262 gb EEX58083.1  5-enolpyruvylshikimate ( 450) 2413 510.9 6e-142   | gi 209871816 gb ACI91612.1  3-phosphoshikimate 1-c ( 443) 1639 350.0 1.6e-93  |
|   | gi 170658506 gb ACB27561.1  3-phosphoshikimate 1-c ( 449) 1639 350.0 1.6e-93  |
|   | gi 254268596 emb CAX24555.1  3-enolpyruvylshikimat ( 436) 1638 349.8 1.8e-93  |
|   | gi 39652766 emb CAE25505.1  3-phosphoshikimate 1-c ( 445) 1632 348.5 4.3e-93  |
|   | gi 83574549 gb ABC21100.1  3-phosphoshikimate 1-ca ( 451) 1630 348.1 5.8e-93  |
|   | gi 86570797 gb ABD05354.1  3-phosphoshikimate 1-ca ( 445) 1629 347.9 6.7e-93  |
|   | gi 192282246 gb ACE98626.1  3-phosphoshikimate 1-c ( 445) 1628 347.7 7.7e-93  |
|   | gi 115516419 gb ABU04403.1  3-phosphoshikimate 1-c ( 445) 1624 346.9 1.4e-92  |
|   | gi 77390011 gb ABA81195.1  3-phosphoshikimate 1-ca ( 445) 1620 346.0 2.4e-92  |
|   | gi 143260698 gb EDD97066.1  hypothetical protein G ( 451) 1618 345.6 3.3e-92  |
|   | gi 219951457 gb ACL61849.1  3-phosphoshikimate 1-c ( 466) 1614 344.8 6e-92    |
|   | gi 126105843 gb ABN78373.1  3-phosphoshikimate 1-c ( 445) 1613 344.6 6.7e-92  |

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|                             |                         |        |      |       |         |                             |                         |        |      |       |         |
|-----------------------------|-------------------------|--------|------|-------|---------|-----------------------------|-------------------------|--------|------|-------|---------|
| gi 119374725 gb ABL70318.1  | 3-phosphoshikimate 1-c  | ( 443) | 1608 | 343.5 | 1.4e-91 | gi 167291237 gb ABZ44101.1  | Sequence 18039 from pa  | ( 420) | 1494 | 319.8 | 1.8e-84 |
| gi 167293964 gb ABZ46828.1  | Sequence 20766 from pa  | ( 430) | 1606 | 343.1 | 1.8e-91 | gi 254040135 gb ACT56931.1  | 3-phosphoshikimate 1-c  | ( 449) | 1479 | 316.7 | 1.6e-83 |
| gi 91798691 gb ABE61066.1   | 3-phosphoshikimate 1-ca | ( 449) | 1605 | 342.9 | 2.1e-91 | gi 13425333 gb AAK25551.1   | 3-phosphoshikimate 1-ca | ( 443) | 1477 | 316.3 | 2.2e-83 |
| gi 98977055 gb ABF53206.1   | 3-phosphoshikimate 1-ca | ( 446) | 1601 | 342.1 | 3.8e-91 | gi 220965813 gb ACL97169.1  | 3-phosphoshikimate 1-c  | ( 443) | 1477 | 316.3 | 2.2e-83 |
| gi 148500563 gb ABQ68817.1  | 3-phosphoshikimate 1-c  | ( 479) | 1599 | 341.7 | 5.4e-91 | gi 167290272 gb ABZ43136.1  | Sequence 17074 from pa  | ( 443) | 1477 | 316.3 | 2.2e-83 |
| gi 221162652 gb ACM03623.1  | 3-phosphoshikimate 1-c  | ( 436) | 1597 | 341.3 | 6.6e-91 | gi 144160862 gb EDJ30885.1  | hypothetical protein G  | ( 457) | 1476 | 316.1 | 2.6e-83 |
| gi 27348987 dbj BAC46003.1  | aroA [Bradyrhizobium j  | ( 469) | 1597 | 341.3 | 7e-91   | gi 136767257 gb EBQ27100.1  | hypothetical protein G  | ( 439) | 1475 | 315.9 | 2.8e-83 |
| gi 90103938 gb ABD85975.1   | 3-phosphoshikimate 1-ca | ( 467) | 1595 | 340.9 | 9.3e-91 | gi 196187174 gb EDX82150.1  | 3-phosphoshikimate 1-c  | ( 436) | 1465 | 313.8 | 1.2e-82 |
| gi 144898829 emb CAM75693.1 | 3-phosphoshikimate 1-   | ( 446) | 1591 | 340.0 | 1.6e-90 | gi 144127406 gb EDJ06257.1  | hypothetical protein G  | ( 412) | 1462 | 313.2 | 1.8e-82 |
| gi 74419278 gb ABA03477.1   | 3-phosphoshikimate 1-ca | ( 449) | 1591 | 340.0 | 1.6e-90 | gi 142444644 gb ECY12567.1  | hypothetical protein G  | ( 459) | 1458 | 312.4 | 3.4e-82 |
| gi 145558123 gb ABP72735.1  | 3-phosphoshikimate 1-c  | ( 445) | 1590 | 339.8 | 1.8e-90 | gi 114316863 gb ABI62923.1  | 3-phosphoshikimate 1-c  | ( 454) | 1456 | 312.0 | 4.5e-82 |
| gi 87135028 gb ABD25770.1   | 3-phosphoshikimate 1-ca | ( 441) | 1589 | 339.6 | 2.1e-90 | gi 167346504 gb ABZ69239.1  | 3-phosphoshikimate 1-c  | ( 439) | 1453 | 311.3 | 6.8e-82 |
| gi 209959239 gb ACI99875.1  | 3-phosphoshikimate 1-c  | ( 448) | 1589 | 339.6 | 2.1e-90 | gi 134334509 gb EBA71436.1  | hypothetical protein G  | ( 478) | 1453 | 311.4 | 7.3e-82 |
| gi 258553029 gb ACV75975.1  | 3-phosphoshikimate 1-c  | ( 453) | 1585 | 338.8 | 3.8e-90 | gi 209532709 gb ACI52646.1  | 3-phosphoshikimate 1-c  | ( 449) | 1452 | 311.1 | 8e-82   |
| gi 56544266 gb AAV90420.1   | 5-enolpyruvylshikimate- | ( 453) | 1584 | 338.6 | 4.4e-90 | gi 161787807 emb CAP57405.1 | 3-phosphoshikimate 1-   | ( 449) | 1452 | 311.1 | 8e-82   |
| gi 88862748 gb ABD53625.1   | 3-phosphoshikimate 1-ca | ( 450) | 1583 | 338.4 | 5.1e-90 | gi 142778383 gb EDA51368.1  | hypothetical protein G  | ( 450) | 1449 | 310.5 | 1.2e-81 |
| gi 260421386 gb EEX14637.1  | 3-phosphoshikimate 1-c  | ( 442) | 1582 | 338.1 | 5.8e-90 | gi 143036643 gb EDC35022.1  | hypothetical protein G  | ( 423) | 1447 | 310.1 | 1.6e-81 |
| gi 167283674 gb ABZ36538.1  | Sequence 10476 from pa  | ( 432) | 1581 | 337.9 | 6.6e-90 | gi 143821962 gb EDG87373.1  | hypothetical protein G  | ( 451) | 1444 | 309.5 | 2.5e-81 |
| gi 109457166 gb ABG33371.1  | 3-phosphoshikimate 1-c  | ( 450) | 1580 | 337.7 | 7.8e-90 | gi 196477074 gb ACG76602.1  | 3-phosphoshikimate 1-c  | ( 452) | 1439 | 308.4 | 5.2e-81 |
| gi 135091817 gb EBF43950.1  | hypothetical protein G  | ( 451) | 1575 | 336.7 | 1.6e-89 | gi 142210143 gb ECW41740.1  | hypothetical protein G  | ( 492) | 1438 | 308.2 | 6.5e-81 |
| gi 146190077 emb CAL74069.1 | 3-phosphoshikimate 1-   | ( 445) | 1573 | 336.3 | 2.1e-89 | gi 114339116 gb ABI64396.1  | 3-phosphoshikimate 1-c  | ( 447) | 1421 | 304.7 | 6.9e-80 |
| gi 82948203 dbj BAE53067.1  | 5-enolpyruvylshikimate  | ( 446) | 1573 | 336.3 | 2.1e-89 | gi 142140539 gb ECV88729.1  | hypothetical protein G  | ( 672) | 1423 | 305.2 | 7.4e-80 |
| gi 214030157 gb EEB70992.1  | 3-phosphoshikimate 1-c  | ( 449) | 1572 | 336.1 | 2.5e-89 | gi 143831861 gb EBG94516.1  | hypothetical protein G  | ( 451) | 1414 | 303.2 | 1.9e-79 |
| gi 146403899 gb ABQ32405.1  | 3-phosphoshikimate 1-c  | ( 445) | 1569 | 335.4 | 3.8e-89 | gi 136701932 gb EBP83990.1  | hypothetical protein G  | ( 463) | 1410 | 302.4 | 3.5e-79 |
| gi 142198284 gb ECW32705.1  | hypothetical protein G  | ( 456) | 1565 | 334.6 | 6.9e-89 | gi 136594870 gb EBP17072.1  | hypothetical protein G  | ( 452) | 1404 | 301.2 | 8.1e-79 |
| gi 255105080 gb EET47754.1  | 3-phosphoshikimate 1-c  | ( 496) | 1565 | 334.6 | 7.4e-89 | gi 114740446 gb ABI78571.1  | 3-phosphoshikimate 1-c  | ( 439) | 1376 | 295.3 | 4.4e-77 |
| gi 217502178 gb ACK49587.1  | 3-phosphoshikimate 1-c  | ( 443) | 1564 | 334.4 | 7.8e-89 | gi 142227889 gb ECW55072.1  | hypothetical protein G  | ( 420) | 1369 | 293.9 | 1.2e-76 |
| gi 56680491 gb AAV97156.1   | 3-phosphoshikimate 1-ca | ( 448) | 1564 | 334.4 | 7.8e-89 | gi 135799022 gb EBJ91601.1  | hypothetical protein G  | ( 412) | 1362 | 292.4 | 3.2e-76 |
| gi 99036320 gb ABF62932.1   | 3-phosphoshikimate 1-ca | ( 450) | 1562 | 334.0 | 1e-88   | gi 136155475 gb EBM26016.1  | hypothetical protein G  | ( 373) | 1355 | 290.9 | 8e-76   |
| gi 259348589 gb EEW60351.1  | 3-phosphoshikimate 1-c  | ( 450) | 1561 | 333.8 | 1.2e-88 | gi 136746874 gb EBQ13460.1  | hypothetical protein G  | ( 391) | 1354 | 290.7 | 9.6e-76 |
| gi 167281012 gb ABZ33876.1  | Sequence 7814 from pat  | ( 418) | 1549 | 331.3 | 6.4e-88 | gi 136765878 gb EBQ26143.1  | hypothetical protein G  | ( 423) | 1351 | 290.1 | 1.6e-75 |
| gi 260414998 gb EEX08257.1  | 3-phosphoshikimate 1-c  | ( 448) | 1548 | 331.1 | 7.8e-88 | gi 142122134 gb ECV75183.1  | hypothetical protein G  | ( 406) | 1339 | 287.6 | 8.6e-75 |
| gi 256635297 dbj BAI01266.1 | 3-phosphoshikimate 1-   | ( 466) | 1538 | 329.0 | 3.4e-87 | gi 135334376 gb EBG94098.1  | hypothetical protein G  | ( 446) | 1331 | 286.0 | 2.9e-74 |
| gi 256632240 dbj BAH98215.1 | 3-phosphoshikimate 1-   | ( 466) | 1538 | 329.0 | 3.4e-87 | gi 143470309 gb EDF15730.1  | hypothetical protein G  | ( 362) | 1325 | 284.7 | 5.8e-74 |
| gi 256644461 dbj BAI10409.1 | 3-phosphoshikimate 1-   | ( 466) | 1538 | 329.0 | 3.4e-87 | gi 143106897 gb EDC86357.1  | hypothetical protein G  | ( 449) | 1326 | 284.9 | 6.1e-74 |
| gi 256647516 dbj BAI13457.1 | 3-phosphoshikimate 1-   | ( 466) | 1538 | 329.0 | 3.4e-87 | gi 120323802 gb ABM18117.1  | 3-phosphoshikimate 1-c  | ( 742) | 1320 | 283.8 | 2.2e-73 |
| gi 256650569 dbj BAI16503.1 | 3-phosphoshikimate 1-   | ( 466) | 1538 | 329.0 | 3.4e-87 | gi 117607246 gb ABK42701.1  | 3-phosphoshikimate 1-c  | ( 445) | 1312 | 282.0 | 4.5e-73 |
| gi 256638352 dbj BAI04314.1 | 3-phosphoshikimate 1-   | ( 466) | 1538 | 329.0 | 3.4e-87 | gi 134806831 gb EBD56326.1  | hypothetical protein G  | ( 435) | 1311 | 281.8 | 5.1e-73 |
| gi 256641406 dbj BAI07361.1 | 3-phosphoshikimate 1-   | ( 466) | 1538 | 329.0 | 3.4e-87 | gi 143147782 gb EDD16387.1  | hypothetical protein G  | ( 416) | 1308 | 281.2 | 7.6e-73 |
| gi 256653560 dbj BAI19487.1 | 3-phosphoshikimate 1-   | ( 466) | 1538 | 329.0 | 3.4e-87 | gi 134969061 gb EBE63039.1  | hypothetical protein G  | ( 421) | 1300 | 279.5 | 2.4e-72 |
| gi 212536211 gb EEE39199.1  | 3-phosphoshikimate 1-c  | ( 448) | 1537 | 328.8 | 3.8e-87 | gi 198263265 gb EDY87543.1  | 3-phosphoshikimate 1-c  | ( 442) | 1297 | 278.9 | 3.9e-72 |
| gi 157911331 gb ABV92764.1  | 3-phosphoshikimate 1-c  | ( 450) | 1536 | 328.6 | 4.4e-87 | gi 114226484 gb ABI56283.1  | 3-phosphoshikimate 1-c  | ( 446) | 1294 | 278.3 | 6.1e-72 |
| gi 206686690 gb EDZ47172.1  | 3-phosphoshikimate 1-c  | ( 448) | 1534 | 328.2 | 5.9e-87 | gi 144019737 gb EDI28838.1  | hypothetical protein G  | ( 748) | 1296 | 278.8 | 7.1e-72 |
| gi 198253480 gb EDY77794.1  | 3-phosphoshikimate 1-c  | ( 469) | 1530 | 327.3 | 1.1e-86 | gi 144221151 gb EDJ74707.1  | hypothetical protein G  | ( 439) | 1291 | 277.7 | 9.2e-72 |
| gi 144125505 gb EDJ04872.1  | hypothetical protein G  | ( 515) | 1530 | 327.4 | 1.2e-86 | gi 77384298 gb ABA75811.1   | putative bifunctional p | ( 735) | 1292 | 278.0 | 1.2e-71 |
| gi 206679873 gb EDZ44360.1  | 3-phosphoshikimate 1-c  | ( 441) | 1525 | 326.3 | 2.1e-86 | gi 150959179 gb ABR81204.1  | prephenate dehydrogena  | ( 746) | 1292 | 278.0 | 1.3e-71 |
| gi 198269136 gb EDY93406.1  | 3-phosphoshikimate 1-c  | ( 450) | 1521 | 325.5 | 3.9e-86 | gi 143774157 gb EDG71670.1  | hypothetical protein G  | ( 477) | 1288 | 277.1 | 1.5e-71 |
| gi 214045586 gb EEB86224.1  | 3-phosphoshikimate 1-c  | ( 450) | 1520 | 325.3 | 4.4e-86 | gi 142247445 gb ECW69575.1  | hypothetical protein G  | ( 400) | 1283 | 276.0 | 2.7e-71 |
| gi 58001482 gb AAW60376.1   | 3-Phosphoshikimate 1-ca | ( 442) | 1515 | 324.2 | 9e-86   | gi 136201992 gb EBM56643.1  | hypothetical protein G  | ( 477) | 1283 | 276.0 | 3.1e-71 |
| gi 146400733 gb ABQ29260.1  | 3-phosphoshikimate 1-c  | ( 445) | 1514 | 324.0 | 1e-85   | gi 84787408 gb ABC63590.1   | 5-enolpyruvylshikimate- | ( 463) | 1280 | 275.4 | 4.7e-71 |
| gi 136727461 gb EBQ00749.1  | hypothetical protein G  | ( 459) | 1498 | 320.7 | 1.1e-84 | gi 228385087 gb ACQ29040.1  | Sequence 21554 from pa  | ( 782) | 1283 | 276.1 | 4.8e-71 |

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|   |   |
|---|---|
| gi 218770867 emb CAW26632.1  still frameshift 3-PH ( 746) 1282 275.9 5.3e-71  | gi 194349115 gb ACF52238.1  3-phosphoshikimate 1-c ( 435) 1235 266.0 2.9e-68  |
| gi 167283172 gb ABZ36036.1  Sequence 9974 from pat ( 411) 1278 275.0 5.7e-71  | gi 142142726 gb ECV90367.1  hypothetical protein G ( 524) 1235 266.1 3.4e-68  |
| gi 237685422 gb ACR12686.1  response regulator rec ( 742) 1281 275.7 6.1e-71  | gi 83635703 gb ABC31670.1  3-phosphoshikimate 1-ca ( 738) 1237 266.5 3.5e-68  |
| gi 126195230 gb EAS59293.1  3-phosphoshikimate 1-c ( 746) 1281 275.7 6.2e-71  | gi 190012912 emb CAQ46544.1  putative 3-phosphoshi ( 435) 1232 265.4 4.5e-68  |
| gi 254043237 gb ACT60032.1  3-phosphoshikimate 1-c ( 438) 1276 274.5 8e-71    | gi 142215066 gb ECW45518.1  hypothetical protein G ( 602) 1233 265.7 5.2e-68  |
| gi 145575084 gb ABP84616.1  3-phosphoshikimate 1-c ( 746) 1279 275.3 8.2e-71  | gi 142454573 gb ECY19775.1  hypothetical protein G ( 736) 1234 265.9 5.3e-68  |
| gi 262315671 gb EEY96710.1  3-phosphoshikimate 1-c ( 749) 1278 275.1 9.5e-71  | gi 224463889 gb EEF80156.1  3-phosphoshikimate 1-c ( 439) 1230 265.0 6.1e-68  |
| gi 260406041 gb EEW99527.1  5-enolpyruvylshikimate ( 756) 1278 275.1 9.6e-71  | gi 50404063 gb AAT76791.1  5-enolpyruvylshikimate- ( 449) 1227 264.4 9.5e-68  |
| gi 115586374 gb ABJ12389.1  EPSP synthase/prephena ( 746) 1277 274.9 1.1e-70  | gi 219718621 gb EED37146.1  3-phosphoshikimate 1-c ( 435) 1224 263.7 1.4e-67  |
| gi 135021201 gb EBE98359.1  hypothetical protein G ( 431) 1273 273.9 1.2e-70  | gi 143927391 gb EDH63433.1  hypothetical protein G ( 433) 1219 262.7 2.9e-67  |
| gi 143034105 gb EDC33172.1  hypothetical protein G ( 433) 1273 273.9 1.2e-70  | gi 167288581 gb ABZ41445.1  Sequence 15383 from pa ( 442) 1219 262.7 3e-67    |
| gi 169151779 emb CAP00598.1  bifunctional protein ( 748) 1274 274.2 1.7e-70   | gi 167733824 emb CAP52030.1  3-phosphoshikimate 1- ( 438) 1218 262.5 3.4e-67  |
| gi 262309719 gb EEY90849.1  3-phosphoshikimate 1-c ( 748) 1274 274.2 1.7e-70  | gi 136454660 gb EBO27076.1  hypothetical protein G ( 440) 1216 262.1 4.6e-67  |
| gi 169148265 emb CAM86130.1  bifunctional protein ( 748) 1274 274.2 1.7e-70   | gi 182632076 gb ABE92852.1  3-phosphoshikimate 1-c ( 442) 1216 262.1 4.6e-67  |
| gi 261836400 gb ACX96167.1  3-phosphoshikimate 1-c ( 456) 1271 273.5 1.7e-70  | gi 28057346 gb AAO29203.1  3-phosphoshikimate 1-ca ( 454) 1216 262.1 4.7e-67  |
| gi 213985849 gb ACJ56148.1  3-phosphoshikimate 1-c ( 756) 1274 274.2 1.7e-70  | gi 142716963 gb EDA06672.1  hypothetical protein G ( 467) 1215 261.9 5.5e-67  |
| gi 213057836 gb ACJ42738.1  hypothetical protein A ( 756) 1274 274.2 1.7e-70  | gi 110647719 emb CAL17195.1  prephenate dehydrogen ( 760) 1216 262.2 7.3e-67  |
| gi 262258779 gb EEY77512.1  3-phosphoshikimate 1-c ( 756) 1274 274.2 1.7e-70  | gi 167965401 gb ACA12411.1  3-phosphoshikimate 1-c ( 442) 1208 260.4 1.4e-66  |
| gi 193077824 gb ABO12699.2  hypothetical protein A ( 756) 1274 274.2 1.7e-70  | gi 126168057 gb EAS23568.1  3-phosphoshikimate 1-c ( 747) 1210 260.9 1.7e-66  |
| gi 260410993 gb EEEX04290.1  3-phosphoshikimate 1-c ( 756) 1274 274.2 1.7e-70 | gi 66574282 gb AAY49692.1  3-phosphoshikimate 1-ca ( 438) 1204 259.6 2.6e-66  |
| gi 143454605 gb EDF05664.1  hypothetical protein G ( 437) 1270 273.3 1.9e-70  | gi 21112672 gb AAM40886.1  3-phosphoshikimate 1-ca ( 438) 1204 259.6 2.6e-66  |
| 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    |
| gi 160878077 gb ABX52003.1  G6 [synthetic construc ( 507) 1269 273.1 2.5e-70  | gi 218517584 gb ACK78170.1  3-phosphoshikimate 1-c ( 433) 1196 257.9 8e-66    |
| 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    |
| gi 142617034 gb EC235624.1  hypothetical protein G ( 402) 1243 267.7 8.6e-69  | gi 53754137 emb CAH15610.1  3-phosphoshikimate 1-c ( 433) 1180 254.6 8e-65    |
| 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  |
| gi 229361034 emb CAY47896.1  putative bifunctional ( 748) 1240 267.2 2.3e-68  | gi 166086651 dbj BAG01359.1  3-phosphoshikimate 1- ( 446) 1160 250.4 1.5e-63  |
| 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 |
| gi 169884470 gb ACA98183.1  3-phosphoshikimate 1-c ( 446) 1157 249.8 2.3e-63 | gi 142097015 gb ECV56446.1  hypothetical protein G ( 434) 1105 239.0 4e-60   |
| gi 159028618 emb CAO90621.1  aroA [Microcystis aer ( 446) 1157 249.8 2.3e-63 | gi 146326549 dbj BAF61692.1  3-phosphoshikimate 1- ( 435) 1105 239.0 4e-60   |
| gi 144149402 gb EDJ22378.1  hypothetical protein G ( 451) 1155 249.4 3.1e-63 | gi 167294115 gb ABZ46979.1  Sequence 20917 from pa ( 424) 1094 236.7 1.9e-59 |
| gi 78197121 gb ABB34886.1  3-phosphoshikimate 1-ca ( 441) 1154 249.2 3.5e-63 | gi 161762125 gb ABX77767.1  3-phosphoshikimate 1-c ( 438) 1093 236.5 2.3e-59 |
| 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   |
| gi 142376209 gb ECX62405.1  hypothetical protein G ( 456) 1154 249.2 3.6e-63 | gi 219863318 gb ACL43657.1  3-phosphoshikimate 1-c ( 451) 1090 235.9 3.6e-59 |
| 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 |
| gi 515936 emb CAA53074.1  3-phosphoshikimate 1-car ( 447) 1149 248.2 7.2e-63 | gi 169638186 gb ACA59692.1  3-phosphoshikimate 1-c ( 429) 1081 234.0 1.2e-58 |
| gi 2485261 gb AAB73397.1 I44486 Sequence 67 from p ( 447) 1149 248.2 7.2e-63 | gi 143958022 gb EBH85453.1  hypothetical protein G ( 441) 1080 233.8 1.5e-58 |
| gi 144974763 gb ABP12474.1  Sequence 67 from paten ( 447) 1149 248.2 7.2e-63 | gi 143018092 gb EDC21594.1  hypothetical protein G ( 322) 1077 233.1 1.7e-58 |
| 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   |
| gi 78169193 gb ABB26290.1  3-phosphoshikimate 1-ca ( 437) 1142 246.7 1.9e-62 | gi 143847787 gb EDH06009.1  hypothetical protein G ( 446) 1075 232.8 3.1e-58 |
| gi 167287132 gb ABZ39996.1  Sequence 13934 from pa ( 675) 1143 247.0 2.4e-62 | gi 166854307 gb ABY92716.1  3-phosphoshikimate 1-c ( 423) 1074 232.6 3.4e-58 |
| gi 260414082 gb EEK07378.1  3-phosphoshikimate 1-c ( 441) 1139 246.1 3e-62   | gi 166856233 gb ABY94641.1  3-phosphoshikimate 1-c ( 423) 1074 232.6 3.4e-58 |
| 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 |
| gi 171698150 gb ACB51131.1  3-phosphoshikimate 1-c ( 451) 1136 245.5 4.7e-62 | gi 118567567 gb ABL02372.1  3-phosphoshikimate 1-c ( 435) 1071 231.9 5.3e-58 |
| 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  |
| gi 144061985 gb EDL59285.1  hypothetical protein G ( 451) 1131 244.4 9.7e-62 | gi 260865161 gb ACX52267.1  3-phosphoshikimate 1-c ( 434) 1070 231.7 6.1e-58 |
| 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 |
| gi 225645909 gb ACO04095.1  3-phosphoshikimate 1-c ( 432) 1127 243.6 1.7e-61 | gi 142941726 gb EDB67886.1  hypothetical protein G ( 446) 1067 231.1 9.7e-58 |
| 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 |
| gi 218166375 gb ACK65112.1  3-phosphoshikimate 1-c ( 448) 1123 242.8 3e-61   | gi 223698186 gb ACN18694.1  3-phosphoshikimate 1-c ( 428) 1065 230.7 1.2e-57 |
| gi 188931025 gb ACD65655.1  3-phosphoshikimate 1-c ( 431) 1122 242.5 3.4e-61 | gi 223697750 gb ACN18367.1  3-phosphoshikimate 1-c ( 428) 1065 230.7 1.2e-57 |
| 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 |
| gi 33632708 emb BAF07520.1  EPSP synthase (3-phosp ( 441) 1113 240.7 1.3e-60 | gi 144974764 gb ABP12475.1  Sequence 69 from paten ( 443) 1065 230.7 1.3e-57 |
| gi 29541129 gb AAO90072.1  3-phosphoshikimate 1-ca ( 438) 1111 240.3 1.7e-60 | gi 152026654 gb ABS24422.1  3-phosphoshikimate 1-c ( 430) 1064 230.5 1.4e-57 |
| 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 |
| gi 226718629 gb ACO77880.1  3-phosphoshikimate 1-c ( 752) 1111 240.4 2.7e-60 | gi 143254111 gb EDD92278.1  hypothetical protein G ( 446) 1060 229.7 2.7e-57 |
| 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 144049341 gb EDI49929.1  | hypothetical protein G  | ( 434) | 1057 | 229.0 | 4e-57   |
| gi 135675261 gb EBJ14661.1  | hypothetical protein G  | ( 312) | 1055 | 228.6 | 4e-57   |
| gi 139614992 gb ECG28587.1  | hypothetical protein G  | ( 296) | 1053 | 228.1 | 5.1e-57 |
| gi 144022190 gb EDI30532.1  | hypothetical protein G  | ( 355) | 1054 | 228.4 | 5.2e-57 |
| gi 143998481 gb EDI13750.1  | hypothetical protein G  | ( 434) | 1055 | 228.6 | 5.3e-57 |
| gi 72001739 gb AAZ57541.1   | 3-phosphoshikimate 1-ca | ( 444) | 1055 | 228.6 | 5.4e-57 |
| gi 56380573 dbj BAD76481.1  | 3-phosphoshikimate 1-c  | ( 427) | 1054 | 228.4 | 6.1e-57 |
| gi 83573093 gb ABC19645.1   | 3-phosphoshikimate 1-ca | ( 435) | 1054 | 228.4 | 6.2e-57 |
| gi 196170465 gb ACG71438.1  | 3-phosphoshikimate 1-c  | ( 440) | 1053 | 228.2 | 7.2e-57 |
| gi 197627301 gb EDY39860.1  | 3-phosphoshikimate 1-c  | ( 441) | 1053 | 228.2 | 7.2e-57 |
| gi 142180162 gb ECW18900.1  | hypothetical protein G  | ( 665) | 1055 | 228.7 | 7.7e-57 |
| gi 136364387 gb EBN66848.1  | hypothetical protein G  | ( 346) | 1051 | 227.7 | 7.8e-57 |
| gi 143140739 gb EDD11230.1  | hypothetical protein G  | ( 437) | 1051 | 227.8 | 9.5e-57 |
| gi 135394319 gb EBH34333.1  | hypothetical protein G  | ( 446) | 1051 | 227.8 | 9.7e-57 |
| gi 77545564 gb ABA89126.1   | 3-phosphoshikimate 1-ca | ( 431) | 1050 | 227.6 | 1.1e-56 |
| gi 146232268 gb ABD13246.1  | 3-phosphoshikimate 1-c  | ( 442) | 1050 | 227.6 | 1.1e-56 |
| gi 33238026 gb AAQ00093.1   | 5-enolpyruvylshikimate- | ( 444) | 1050 | 227.6 | 1.1e-56 |
| gi 116097111 gb ABJ62262.1  | 3-phosphoshikimate 1-c  | ( 434) | 1048 | 227.2 | 1.5e-56 |
| gi 123198314 gb ABM69955.1  | EPSP synthase (3-phosp  | ( 436) | 1048 | 227.2 | 1.5e-56 |
| gi 143346942 gb EDE47625.1  | hypothetical protein G  | ( 452) | 1048 | 227.2 | 1.5e-56 |
| gi 55771839 dbj BAD70280.1  | 3-phosphoshikimate 1-c  | ( 427) | 1047 | 226.9 | 1.7e-56 |
| gi 46196018 gb AAS80436.1   | 3-phosphoshikimate 1-ca | ( 427) | 1046 | 226.7 | 1.9e-56 |
| gi 39984592 gb AAR35978.1   | 3-phosphoshikimate 1-ca | ( 429) | 1046 | 226.7 | 1.9e-56 |
| gi 143061916 gb EDC53506.1  | hypothetical protein G  | ( 432) | 1045 | 226.5 | 2.2e-56 |
| gi 159888754 gb ABX08968.1  | EPSP synthase (3-phosp  | ( 445) | 1045 | 226.5 | 2.3e-56 |
| gi 140139249 gb ECJ80061.1  | hypothetical protein G  | ( 293) | 1042 | 225.8 | 2.5e-56 |
| gi 226095016 dbj BAH43458.1 | 3-phosphoshikimate 1-   | ( 426) | 1044 | 226.3 | 2.6e-56 |
| gi 256791333 gb ACV22003.1  | 3-phosphoshikimate 1-c  | ( 439) | 1044 | 226.3 | 2.6e-56 |
| gi 146397030 gb ABQ25663.1  | 3-phosphoshikimate 1-c  | ( 428) | 1042 | 225.9 | 3.4e-56 |
| gi 138838604 gb ECC09871.1  | hypothetical protein G  | ( 340) | 1038 | 225.0 | 5e-56   |
| gi 206602804 gb EDZ39285.1  | 3-phosphoshikimate 1-c  | ( 454) | 1039 | 225.3 | 5.5e-56 |
| gi 135494224 gb EBI00757.1  | hypothetical protein G  | ( 385) | 1038 | 225.1 | 5.6e-56 |
| gi 123960447 gb ABM75230.1  | EPSP synthase (3-phosp  | ( 422) | 1038 | 225.1 | 6e-56   |
| gi 207088576 gb EDZ65848.1  | 3-phosphoshikimate 1-c  | ( 444) | 1038 | 225.1 | 6.3e-56 |
| gi 76882029 gb ABA56710.1   | 3-phosphoshikimate 1-ca | ( 444) | 1038 | 225.1 | 6.3e-56 |
| gi 143333051 gb EDE38631.1  | hypothetical protein G  | ( 428) | 1037 | 224.9 | 7e-56   |
| gi 134267287 gb ABO67482.1  | 3-phosphoshikimate 1-c  | ( 432) | 1037 | 224.9 | 7.1e-56 |
| gi 143926783 gb EDH62981.1  | hypothetical protein G  | ( 436) | 1037 | 224.9 | 7.1e-56 |
| gi 251774476 gb ACT17057.1  | 3-phosphoshikimate 1-c  | ( 429) | 1036 | 224.7 | 8.1e-56 |
| gi 136170720 gb EBM35960.1  | hypothetical protein G  | ( 435) | 1036 | 224.7 | 8.2e-56 |
| gi 123200279 gb ABM71887.1  | EPSP synthase (3-phosp  | ( 438) | 1036 | 224.7 | 8.3e-56 |
| gi 135777024 gb EBJ77664.1  | hypothetical protein G  | ( 414) | 1035 | 224.4 | 9.1e-56 |
| gi 141174096 gb ECQ14403.1  | hypothetical protein G  | ( 315) | 1032 | 223.8 | 1.1e-55 |
| gi 167282168 gb ABZ35032.1  | Sequence 8970 from pat  | ( 424) | 1033 | 224.0 | 1.2e-55 |
| gi 167290440 gb ABZ43304.1  | Sequence 17242 from pa  | ( 431) | 1033 | 224.0 | 1.3e-55 |
| gi 10174284 dbj BAB05386.1  | 5-enolpyruvoylshikimat  | ( 431) | 1033 | 224.0 | 1.3e-55 |
| gi 222447240 gb ACM51506.1  | 3-phosphoshikimate 1-c  | ( 435) | 1033 | 224.0 | 1.3e-55 |
| gi 163666945 gb ABY33311.1  | 3-phosphoshikimate 1-c  | ( 435) | 1033 | 224.0 | 1.3e-55 |
| gi 142953087 gb EDB75980.1  | hypothetical protein G  | ( 446) | 1032 | 223.8 | 1.5e-55 |
| gi 143633398 gb EDF97125.1  | hypothetical protein G  | ( 452) | 1032 | 223.8 | 1.5e-55 |
| gi 187426429 gb ACD05708.1  | 3-phosphoshikimate 1-c  | ( 435) | 1031 | 223.6 | 1.7e-55 |
| gi 144053315 gb EDI52883.1  | hypothetical protein G  | ( 435) | 1030 | 223.4 | 2e-55   |
| gi 143212092 gb EDD62650.1  | hypothetical protein G  | ( 440) | 1030 | 223.4 | 2e-55   |
| gi 124514310 gb EAY55824.1  | 3-phosphoshikimate 1-c  | ( 454) | 1030 | 223.4 | 2e-55   |
| gi 142267869 gb ECW84629.1  | hypothetical protein G  | ( 424) | 1029 | 223.2 | 2.2e-55 |
| gi 136251086 gb EBM89813.1  | hypothetical protein G  | ( 439) | 1029 | 223.2 | 2.3e-55 |
| gi 91070245 gb ABE11164.1   | EPSP synthase [uncultur | ( 436) | 1028 | 223.0 | 2.6e-55 |
| gi 143440288 gb EDE96880.1  | hypothetical protein G  | ( 450) | 1027 | 222.8 | 3.1e-55 |
| gi 257820270 gb EEV47418.1  | 3-phosphoshikimate 1-c  | ( 431) | 1026 | 222.6 | 3.5e-55 |
| gi 257836234 gb EEV61308.1  | 3-phosphoshikimate 1-c  | ( 431) | 1026 | 222.6 | 3.5e-55 |
| gi 257832317 gb EEV58738.1  | 3-phosphoshikimate 1-c  | ( 431) | 1026 | 222.6 | 3.5e-55 |
| gi 142796331 gb EDA64709.1  | hypothetical protein G  | ( 436) | 1026 | 222.6 | 3.5e-55 |
| gi 142700747 gb ECZ95072.1  | hypothetical protein G  | ( 438) | 1026 | 222.6 | 3.5e-55 |
| gi 142089244 gb ECV49966.1  | hypothetical protein G  | ( 447) | 1026 | 222.6 | 3.6e-55 |
| gi 134284387 gb ABO69382.1  | 5-enolpyruvylshikimate  | ( 429) | 1025 | 222.4 | 4e-55   |
| gi 142343370 gb ECX40386.1  | hypothetical protein G  | ( 437) | 1025 | 222.4 | 4e-55   |
| gi 91070157 gb ABE11079.1   | EPSP synthase 3-p [uncu | ( 449) | 1025 | 222.4 | 4.1e-55 |
| gi 137453563 gb EBU18911.1  | hypothetical protein G  | ( 299) | 1022 | 221.7 | 4.5e-55 |
| gi 242391389 dbj BAH81848.1 | 3-phosphoshikimate 1-   | ( 430) | 1024 | 222.2 | 4.6e-55 |
| gi 257823269 gb EEV50201.1  | 3-phosphoshikimate 1-c  | ( 431) | 1024 | 222.2 | 4.6e-55 |
| gi 142552593 gb ECY90600.1  | hypothetical protein G  | ( 432) | 1024 | 222.2 | 4.6e-55 |
| gi 142400398 gb ECX79396.1  | hypothetical protein G  | ( 449) | 1024 | 222.2 | 4.8e-55 |
| gi 135374189 gb EBV20771.1  | hypothetical protein G  | ( 414) | 1023 | 222.0 | 5.1e-55 |
| gi 142076285 gb ECV39284.1  | hypothetical protein G  | ( 430) | 1023 | 222.0 | 5.3e-55 |
| gi 146426078 emb CAM89510.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426070 emb CAM89501.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426954 emb CAM89870.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426038 emb CAM89465.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426994 emb CAM89915.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426086 emb CAM89519.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426094 emb CAM89528.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426962 emb CAM89879.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426978 emb CAM89897.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426938 emb CAM89852.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426102 emb CAM89537.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426046 emb CAM89474.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426350 emb CAM89816.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146427026 emb CAM89951.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426062 emb CAM89492.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426030 emb CAM89456.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146427002 emb CAM89924.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146427034 emb CAM89960.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426946 emb CAM89861.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146427018 emb CAM89942.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426054 emb CAM89483.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426358 emb CAM89825.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426986 emb CAM89906.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426022 emb CAM89447.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146427010 emb CAM89933.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-55 |
| gi 146426930 emb CAM89843.1 | 3-phosphoshikimate-1-   | ( 188) | 1018 | 220.8 | 5.3e-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- ( 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 EDX87686.1            | 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 ABN44858.1            | 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 EDB88665.1            | 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 amyloli  | (     | 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 ECR81908.1  | 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 EB286300.1 | 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 ECQ97441.1 | 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 ECP85624.1 | 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 EC570196.1  | 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 |

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|----------------------------|--------------------------------|-----|-------|---------|-----------------------------|---------------------------------|-----|-------|---------|
| 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 AAA21529.1     | 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 AAA24943.1     | 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 ECI11482.1  | 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 262365043 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 EC546281.1  | 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 |

|                            |                          |        |     |      |         |                             |                          |        |     |      |         |
|----------------------------|--------------------------|--------|-----|------|---------|-----------------------------|--------------------------|--------|-----|------|---------|
| 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 AAx45945.1   | 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 ACE65036.1  | 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 EEO24774.1  | 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 EAZ35730.1  | 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 ECJ83031.1  | 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 ECB88544.1  | 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 EEQ33118.1  | 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 EDE52319.1  | 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 EBH16215.1  | 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 ACZ21056.1  | 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 |

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|-----------------------------|--------------------------------|-----|------|---------|-----------------------------|----------------------------------|-----|------|---------|
| 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-c ( 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 CAP19468.1  | 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 AAAY06820.1  | 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 EBI61823.1  | 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 G ( 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 EAJ22487.1 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 pat (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 cer (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 EE87996.1   | 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 EBZ25287.1  | 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 ACL29768.1  | 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 EQ47426.1   | 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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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 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 | VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED  |       |       |       |       |       |
|        | .....   | ..... | ..... | ..... | ..... | ..... |
| gi 275 | VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED  |       |       |       |       |       |
|        | 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 | VANGLKLVGDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP   |       |       |       |       |       |
|        | .....   | ..... | ..... | ..... | ..... | ..... |
| gi 275 | VANGLKLVGDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP   |       |       |       |       |       |
|        | 370   | 380   | 390   | 400   | 410   | 420   |
|        | 430   | 440   | 450   |       |       |       |
| CP4_EP | VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA                           |       |       |       |       |       |
|        | .....   | ..... | ..... | ..... | ..... | ..... |
| gi 275 | VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA                           |       |       |       |       |       |

430 440 450  
>>gi|18266432|gb|AAL67577.1|AF464188\_1 CP4EPS [Glycine (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 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 | VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED  |       |       |       |       |       |
|        | .....   | ..... | ..... | ..... | ..... | ..... |
| gi 182 | VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED  |       |       |       |       |       |
|        | 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 | VANGLKLVGDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP   |       |       |       |       |       |
|        | .....   | ..... | ..... | ..... | ..... | ..... |
| gi 182 | VANGLKLVGDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP   |       |       |       |       |       |
|        | 370   | 380   | 390   | 400   | 410   | 420   |
|        | 430   | 440   | 450   |       |       |       |

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CP4_EP VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      .....
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)

      10      20      30      40      50      60
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
```

```
      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
      10      20      30      40      50      60

      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)

```

|        | 10   | 20  | 30  | 40  | 50  | 60  |
|--------|--|-----|-----|-----|-----|-----|
| CP4_EP | MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSMFGGLASGETRITGLLEGEDVINTG  |     |     |     |     |     |
| gi 248 | MSHGASSRPATARKSSGLSGTVRIPGDKSISHRSMFGGLASGETRITGLLEGEDVINTG  |     |     |     |     |     |
|        | 10   | 20  | 30  | 40  | 50  | 60  |
| CP4_EP | KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI |     |     |     |     |     |
| gi 248 | KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI |     |     |     |     |     |
|        | 70   | 80  | 90  | 100 | 110 | 120 |
| CP4_EP | GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTILRGPKTPTPIYRVPMSAQVKS     |     |     |     |     |     |
| gi 248 | GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTILRGPKTPTPIYRVPMSAQVKS     |     |     |     |     |     |
|        | 130  | 140 | 150 | 160 | 170 | 180 |
| CP4_EP | LLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID  |     |     |     |     |     |
| gi 248 | LLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID  |     |     |     |     |     |
|        | 190  | 200 | 210 | 220 | 230 | 240 |
| CP4_EP | VPGDPSSTAFLVAALLVPGSDVTILNVLNMPNTRTGLILTLQEMGADIEVINPRLAGGED |     |     |     |     |     |
| gi 248 | VPGDPSSTAFLVAALLVPGSDVTILNVLNMPNTRTGLILTLQEMGADIEVINPRLAGGED |     |     |     |     |     |
|        | 250  | 260 | 270 | 280 | 290 | 300 |
| CP4_EP | VPGDPSSTAFLVAALLVPGSDVTILNVLNMPNTRTGLILTLQEMGADIEVINPRLAGGED |     |     |     |     |     |
| gi 248 | VPGDPSSTAFLVAALLVPGSDVTILNVLNMPNTRTGLILTLQEMGADIEVINPRLAGGED |     |     |     |     |     |
|        | 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|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)

```

|        |  |     |     |     |     |     |
|--------|--|-----|-----|-----|-----|-----|
|        | 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 | GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPI TYRVPMSAQVKS AV             |     |     |     |     |     |
| gi 595 | GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPI TYRVPMSAQVKS AV             |     |     |     |     |     |
|        | 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 |



CP4\_EP LLAGLNTPGITTVIEPIINTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID  
gi|144 LLAGLNTPGITTVIEPIINTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID

190            200            210            220            230            240

```
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
```

```
      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 LLAGLNTPGITTVIEPIIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
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 VADLRVRSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
gi|150 VADLRVRHSELKGVTVPEDRAPSMIDEYPVLAVAAAFAGATTVMNGLEELRVKESDRLSA
      310     320     330     340     350     360

      370     380     390     400     410     420
CP4_EP VANGKLKLVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
gi|150 VADGLKLVDCDEGEASLVVRGRPGGKGLGKISGGQVKTHLDHRIAMSFLVMGLASEHP
      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 MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGLASGETRITGLLEGEDVINTG
gi|227 MSHGLSPRPATAKKSADLKGTVRIPGDKSISHRSFMFGLASGETRITGLLEGEDVINTG
      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 LLAGLNTPGITTVIEPIIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
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 VADLRVRSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
gi|227 VADLRVRYSELKGVTVPEERAPSMIDEYPVLAVAAAFAGATVMNGLEELRVKESDRLSA
      310     320     330     340     350     360

      370     380     390     400     410     420
CP4_EP VANGKLKLVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
gi|227 VADGLKLVDCDEGEASLVVRGRPGGKGLGNAAGGQVKTHLDHRIAMSFLVLGLASEHP
      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 MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGLASGETRITGLLEGEDVINTG
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MSL0022522  
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CP4_EP      10      20      30      40      50      60
MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGLLASGETRITGLLEGEDVINTG
gi|115      10      20      30      40      50      60
MLNGSASKPATARKSAGLTGSGVRIPGDKSISHRSFMFGLLASGETRITGLLEGEDVINTG

CP4_EP      70      80      90      100     110     120
KAMQAMGARIRKEGDWTIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
gi|115      70      80      90      100     110     120
RAMQAMGARIRKEGAQWVIEGTGNGALLAPDAPLDFGNAGTGVRLTMGLVGTYDFHSTFI

CP4_EP      130     140     150     160     170     180
GDASLTKRPMGRVLNPLREMGVQVKSIEDGRLPVTLRGPKTPTPITYRVPMASAVQVKS
gi|115      130     140     150     160     170     180
GDASLSKRPMPGRVLNPLREMGVQVSASEGDRLPVTLRGPGTPSPIRYRVPMASAVQVKS

CP4_EP      190     200     210     220     230     240
LLAGLNTPGITTVIEPIIMTRDHEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
gi|115      190     200     210     220     230     240
LLAGLNTPGVTTVIEFVMTDRDHEKMLQGFGAALSVETDGDGVRTIRLEGRGKLAGQVID

CP4_EP      250     260     270     280     290     300
VPGDPSSSTAFLVAALLVPGSDVTILNVLNMPNTRTGLILTLQEMGADIEVINPRLAGGED
gi|115      250     260     270     280     290     300
VPGDPSSSTAFLVAALIVPGSDITIVNVLNMPNTRTGLILTLQEMGADIEVVNARLAGGED

CP4_EP      310     320     330     340     350     360
VADLRVRSSTLKGVTVPEDRAPSMIDEYPI LAVAAAFAGATVMNGLEELRVKESDRLSA
gi|115      310     320     330     340     350     360
VADLRVRHSGLKGVTVPEDRAPSMIDEYPI LAVAACFAGATVMKGLEELRVKESDRLSA

CP4_EP      370     380     390     400     410     420
VANGKLKNGVDCDEGETSLVVVRGPRDGKGLGNASGAAVATHLDHRIAMSFVLVGLVSEN
gi|115      370     380     390     400     410     420
VADGLKNGVDCDEGEDFLIVRGRPDGKGLGNAADGRVSTHLDHRIAMSFVLGLASEHA

CP4_EP      430     440     450
VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
gi|115      430     440     450
VTIDDAAMIATSFPEFMQLMTGLGAKIELVAE

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

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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 GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMSAQVKSASV
      .....
gi|240 GDASLSKRPMGRVLNPLREMGVQVSASEGDRLPVTLRGPGTSPPIRYRVPMSAQVKSASV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP LLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      .....
gi|240 LLAGLNTPGITTVIEPVMTRDHTEKMLQGFGAALSVDSEGVRTIRLEGRGKLQAGQVID
      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 MSHSASPKPATARRSEALTGEIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
      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 GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMSAQVKSASV
      .....
gi|248 GDASLSKRPMGRVLNPLREMGVQVEAADGDRMPLTLIGPKTANPITYRVPMSAQVKSASV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP LLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      .....
gi|248 LLAGLNTPGVTTTIEPVMTRDHTEKMLQGFGADLTVDKDGVRHIRITGQGLVGTQID
      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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CP4_EP VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
: :::::
gi|248 VTVDDSNMIATSFPEFMDMMPGLGAKIELSIL
420 430 440

>>gi|2485225|gb|AAB73361.1|I44450 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 MSHSASPKPATARRSEALTGEIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
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 LLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
: :::::
gi|248 LLAGLNTPGVTTVIEPVMTRDHTKMLQGFGADLTVETDKDGVRRHIRITGQKLVGQTID
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 VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSEN
: :::::
gi|248 VARGLEANGVDCTEGEMSLTVRGRPDGKGLG---GGTVATHLDHRIAMSFLVMGLAAEKP
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370 380 390 400 410
430 440 450
CP4_EP VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
: :::::
gi|248 VTVDDSNMIATSFPEFMDMMPGLGAKIELSIL
420 430 440

>>gi|144974728|gb|ABP12439.1| Sequence 7 from patent US (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|144 MSHSASPKPATARRSEALTGEIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG
10 20 30 40 50 60

70 80 90 100 110 120
CP4_EP KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFSTFI
: :::::
gi|144 RAMQAMGAKIRKEGDVWIINGVNGCLLQPEAALDFGNAGTGARLTMGLVGTYDMKTSFI
70 80 90 100 110 120

130 140 150 160 170 180
CP4_EP GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMASAVQKSAV
: :::::
gi|144 GDASLSKRPMGRVLNPLREMGVQVEAADGDRMPLTLIGPKTANPITYRVPMASAVQKSAV
130 140 150 160 170 180

190 200 210 220 230 240
CP4_EP LLAGLNTPGITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
: :::::
gi|144 LLAGLNTPGVTTVIEPVMTRDHTKMLQGFGADLTVETDKDGVRRHIRITGQKLVGQTID
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
CP4_EP VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAGATVMNGLEELRVKESDRLSA
: :::::
gi|144 VADLRVRASKLKGVVVPPERAPSMIDEYPVLAIAASFAGETVMDGLDELRVKESDRLAA
310 320 330 340 350 360

370 380 390 400 410 420
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CP4_EP  VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
:: ... ::::: :: ::::::::::::::: ::::::::::::::::::::
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  GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMSAQVKSASV
: ::::: ::::: ::: ::::::::::::::: ::::::::::::::::::::
gi|248  GDASLSKRPMGRVLNPLREMGVQVEAADGDRMPLTLIGPKTANPITYRVPMSAQVKSASV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP  LLAGLNTPGITTVIEPIMTRDHEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
: ::::: ::::: ::: ::::::::::::::: ::::::::::::::::::::
gi|248  LLAGLNTPGVTTVIEPVMTRDHEKMLQGFGADLTVEDDKDGVRRHIRITGQKLVGQTID
      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
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      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
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  GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMSAQVKSASV
: ::::: ::::: ::: ::::::::::::::: ::::::::::::::::::::
gi|144  GDASLSKRPMGRVLNPLREMGVQVEAADGDRMPLTLIGPKTANPITYRVPMSAQVKSASV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP  LLAGLNTPGITTVIEPIMTRDHEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
: ::::: ::::: ::: ::::::::::::::: ::::::::::::::::::::
gi|144  LLAGLNTPGVTTVIEPVMTRDHEKMLQGFGADLTVEDDKDGVRRHIRITGQKLVGQTID
      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  VADLRVRASKLKGVVPPERAPSMIDEYPVLATAASFAEGETVM DGLDELRVKESDRLAA
              310           320           330           340           350           360

              370           380           390           400           410           420
CP4_EP  VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAATHLDHRIAMSFLVMGLVSEN
       :. :. :..... :..... :..... :..... :..... :..... :..... :.....
gi|595  VARGLEANGVDCETEGMSLTVRGRPDGKGLG---GGTVATHLDHRIAMSFLVMGLAAEKP
              370           380           390           400           410

              430           440           450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
       ..... :..... :..... :..... :..... :..... :..... :.....
gi|595  VTVDDSNMIATSFPEFMDMMPGLGAKIELSIL
       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)

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|        |  |     |     |     |     |     |
|--------|--|-----|-----|-----|-----|-----|
|        | 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 |



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190          200          210          220          230          240
      250      260      270      280      290      300
CP4_EP VPGDPSSTAFPLVAALLVPGSDVTILNVLNMPTRTGLILTLQEMGADIEVINPRLAGGED
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::
gi|248 VPGDPSSTAFPLVAALLVEGSDVTIRNVLNMPTRTGLILTLQEMGADIEVLNARLAGGED
      250      260      270      280      290      300
      310      320      330      340      350      360
CP4_EP VADLRVRSSTILKGVTPEDRAPSMIDEYPI LAVAAAFAGATVMNGLEELRVKESDRLSA
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::
gi|248 VADLRVRASKLKGVVPPERAPSMIDEYPIVLAIAASFAEGETVMGDGLDELRVKESDRLAA
      310      320      330      340      350      360
      370      380      390      400      410      420
CP4_EP VANGKLKNGVDCDEGETSLVVVRGPDGKGLGNASGAAVATHLDHRIAMSFVLMGLVSENP
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::
gi|248 VARGLEANGVDCTEGEMSLTVRGRPDGKGLG---GGTVATHLDHRIAMSFVLMGLAAEKP
      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 init1: 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)

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|        |   |     |     |     |     |     |
|--------|---|-----|-----|-----|-----|-----|
|        | 10  | 20  | 30  | 40  | 50  | 60  |
| CP4_EP | MLHGASSRPATARKSSGLSGTVRIPGDKISHSRFMFGGLASGETRITGLLEGEDVINTG   |     |     |     |     |     |
| :      | :   | :   | :   | :   | :   | :   |
| gi 151 | MSHSAPPKPATARRSEALTGEIRIPGDKISHSRFMFGGLASGETRITGLLEGEDVINTG   |     |     |     |     |     |
|        | 10  | 20  | 30  | 40  | 50  | 60  |
|        | 70  | 80  | 90  | 100 | 110 | 120 |
| CP4_EP | KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNAGTGCRLTMGLVGVDYDSTFI    |     |     |     |     |     |
| :      | :   | :   | :   | :   | :   | :   |
| gi 151 | RAMQAMGARIKRKDGDAWIIIVNGVNGCLLPQAALDFGNAGTGARLTMGLVGTYDMRTSFI |     |     |     |     |     |
|        | 70  | 80  | 90  | 100 | 110 | 120 |
|        | 130   | 140 | 150 | 160 | 170 | 180 |
| CP4_EP | GDASLTKRPMGRVLNPLREMGVQVKSEDDRLPVTLRGPKTPTPITYRVPMASAQVKSAY   |     |     |     |     |     |
| :      | :   | :   | :   | :   | :   | :   |
| gi 151 | GDASLSKRPMPGRVLNPLREMGVQEAAEGDRMPLTLIGPKTANPITYRVPMASAQVKSAY  |     |     |     |     |     |
|        | 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  VTVDDATMIATSFPEFMDLMAGLGAKEILSDTKAA
      : .....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|221  VKVDDSAMIAATSFPEFFDLMAELGADMDEGSISP
      420          430          440          450

>>gi|264661798|gb|EEZ32059.1| 3-phosphoshikimate 1-carbo (450 aa)
  initn: 2453 init1: 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 | MSHSACPATARHQSQALTGEIRIPGDKSISHSRFMGGLASGETRITGLLEGEDVINTG   |           |           |           |           |           |
|        | 10   | 20        | 30        | 40        | 50        | 60        |
|        | 70   | 80        | 90        | 100       | 110       | 120       |
| CP4_EP | KAMQAMGARIRKEGDTWIIDGVNGNGLLAPEAPLDFGNAAATGCRLTMGLVGVDFTSFIF |           |           |           |           |           |
|        | . . . . .  | . . . . . | . . . . . | . . . . . | . . . . . | . . . . . |
| gi 264 | RAMQAMGARIRKEGDWIIINGVNGNCLQPEAPLDFGNAGTGARLTMGVLGYDMDKTSFIF |           |           |           |           |           |
|        | 70   | 80        | 90        | 100       | 110       | 120       |
|        | 130  | 140       | 150       | 160       | 170       | 180       |

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              200          300          400          500          600          700          800
CP4_EP      GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPTITYRVPMSAQVKS
gi|161      GDASLSKRPMPGRVLNPLREMGVQVEAAEGDRMPLTLIGPTANPTAYRVPMSAQVKS
              130          140          150          160          170          180
CP4_EP      LLAGNLTPGIITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
gi|161      LLAGNLTPGVTTVIEPVMTRDHTKMLQGFGADLTVETDKDGVRRHIRVGGGKLTGQTID
              190          200          210          220          230          240
CP4_EP      LLAGNLTPGIITTVIEPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
gi|161      LLAGNLTPGVTTVIEPVMTRDHTKMLQGFGADLTVETDKDGVRRHIRVGGGKLTGQTID
              190          200          210          220          230          240
CP4_EP      VPGDPSSSTAFPLVAALLVPGSDVTILNVLNMNPTRTGLILTLQEMGADIEVINPRLAGGED
gi|161      VPGDPSSSTAFPLVAALLVEGSDVTIRNVLNMNPTRTGLILTLQEMGADIEIIDPRLAGGED
              250          260          270          280          290          300
CP4_EP      VPGDPSSSTAFPLVAALLVPGSDVTILNVLNMNPTRTGLILTLQEMGADIEVINPRLAGGED
gi|161      VPGDPSSSTAFPLVAALLVEGSDVTIRNVLNMNPTRTGLILTLQEMGADIEIIDPRLAGGED
              250          260          270          280          290          300
CP4_EP      VADLRVRSSTLKGVTVPEDRAPSMIDEYPI LavAAAFAEGATVMNGLEELRVKESDRLSA
gi|161      VADLRVRASKLKGVVPPPERAPSMIDEYYPVLAIAASFAEGETVMDGLDELRVKESDRLAA
              310          320          330          340          350          360
CP4_EP      VADLRVRSSTLKGVTVPEDRAPSMIDEYPI LavAAAFAEGATVMNGLEELRVKESDRLSA
gi|161      VADLRVRASKLKGVVPPPERAPSMIDEYYPVLAIAASFAEGETVMDGLDELRVKESDRLAA
              310          320          330          340          350          360
CP4_EP      VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAATHLDHRIAMSFLVMGLVSEN
gi|161      VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFLVMGLASEKP
              370          380          390          400          410          420
CP4_EP      VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAATHLDHRIAMSFLVMGLVSEN
gi|161      VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFLVMGLASEKP
              370          380          390          400          410
CP4_EP      VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
gi|161      VTVDDSTMIATSFPEFMGMAGLGAKIAESGAE
              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 | MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG |     |     |     |     |     |
|        | : :  | : : | : : | : : | : : | : : |
| gi 260 | MSHSACPKPATARHSQALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTG |     |     |     |     |     |
|        | 10   | 20  | 30  | 40  | 50  | 60  |
|        | 70   | 80  | 90  | 100 | 110 | 120 |

```
CP4_EP KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
.....
gi|260 RAMQAMGARIRKEGDVWIINGVNGCLLQPEAPLDFGNAGTGARLTMGVLGTYDMKTSFI
      70      80      90      100     110     120

      130     140     150     160     170     180
CP4_EP GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMASAVKSAV
.....
gi|260 GDASLSKRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPIAYRVPMASAVKSAV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP LLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
.....
gi|260 LLAGLNTPGVTTVIEPVMTRDHTEKMLQGFGADLTIVETDKDGVRRHIVGQKLTGQTID
      190     200     210     220     230     240

      250     260     270     280     290     300
CP4_EP VPGDPSSTAFLPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
.....
gi|260 VPGDPSSTAFLPLVAALLVEGSDVTIRNVLNPNTRTGLILTLQEMGADIEIIDPRLAGGED
      250     260     270     280     290     300

      310     320     330     340     350     360
CP4_EP VADLRVRSTLKGVTVPEDRAPSMIDEYPI LAVAAFAEGATVMNGLEELRVKESDRLSA
.....
gi|260 VADLRVRASKLKGVVVPPERAPSMIDEYPVLAIAASFAEGETVM DGLDEL RVKESDRLAA
      310     320     330     340     350     360

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

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

>>gi|23346795|gb|AAN28982.1| 3-phosphoshikimate 1-carbox (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 MLHGASSRPATARKSSGLSGTVRIPGDKSISHSFMFGGLASGETRITGLLEGEDVINTG
: :: .....
gi|233 MSHSACPKPATARHSQALTGEIRIPGDKSISHSFMFGGLASGKTRITGLLEGEDVINTG
```

```
      10      20      30      40      50      60

      70      80      90     100     110     120
CP4_EP KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFDSTFI
.....
gi|233 RAMQAMGARIRKEGDVWIINGVNGCLLQPEAPLDFGNAGTGARLTMGVLGTYDMKTSFI
      70      80      90     100     110     120

      130     140     150     160     170     180
CP4_EP GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMASAVKSAV
.....
gi|233 GDASLSKRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPIAYRVPMASAVKSAV
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP LLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
.....
gi|233 LLAGLNTPGVTTVIEPVMTRDHTEKMLQGFGADLTIVETDKDGVRRHIVGQKLTGQTID
      190     200     210     220     230     240

      250     260     270     280     290     300
CP4_EP VPGDPSSTAFLPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
.....
gi|233 VPGDPSSTAFLPLVAALLVEGSDVTIRNVLNPNTRTGLILTLQEMGADIEIIDPRLAGGED
      250     260     270     280     290     300

      310     320     330     340     350     360
CP4_EP VADLRVRSTLKGVTVPEDRAPSMIDEYPI LAVAAFAEGATVMNGLEELRVKESDRLSA
.....
gi|233 VADLRVRASKLKGVVVPPERAPSMIDEYPVLAIAASFAEGETVM DGLDEL RVKESDRLAA
      310     320     330     340     350     360

      370     380     390     400     410     420
CP4_EP VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGA AVATHLDHRIAMSFLVMGLVSENP
:: :: .....
gi|233 VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFLVMGLASEKP
      370     380     390     400     410

      430     440     450
CP4_EP VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
.....
gi|233 VTVDDSTMIATSFPEFMGMAGLGAKIAESGAE
      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(): 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
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CP4_EP MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGLASGETRITGLLEGEDVINTG
: .:. :..... :..... :..... :..... :..... :.....
gi|261 MSHSACPKPATARHSQALTGEIRIPGDKSISHRSFMFGLASGKTRITGLLEGEDVINTG
      10      20      30      40      50      60

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

      130     140     150     160     170     180
CP4_EP GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPITPYRVPMSAQVKSAY
:..... :..... :..... :..... :..... :..... :.....
gi|261 GDASLSKRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPIAYRVPMSAQVKSAY
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP LLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRKLTGQVID
:..... :..... :..... :..... :..... :..... :.....
gi|261 LLAGLNTPGVTTVIEPVMTRDHTEKMLQGFGADLTVDKDGVRHIRIVGQKLTGQTID
      190     200     210     220     230     240

      250     260     270     280     290     300
CP4_EP VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
:..... :..... :..... :..... :..... :..... :.....
gi|261 VPGDPSSTAFPLVAALLVEGSDVTIRNVLMNPNTRTGLILTLQEMGADIEIIDPRLAGGED
      250     260     270     280     290     300

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

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

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

>>gi|261293812|gb|EEX97308.1| 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 MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGLASGETRITGLLEGEDVINTG
: .:. :..... :..... :..... :..... :..... :.....
gi|261 MSHSACPKPATARHSQALTGEIRIPGDKSISHRSFMFGLASGKTRITGLLEGEDVINTG
      10      20      30      40      50      60

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

      130     140     150     160     170     180
CP4_EP GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPITPYRVPMSAQVKSAY
:..... :..... :..... :..... :..... :..... :.....
gi|261 GDASLSKRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPIAYRVPMSAQVKSAY
      130     140     150     160     170     180

      190     200     210     220     230     240
CP4_EP LLAGLNTPGITTVIEPIIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRKLTGQVID
:..... :..... :..... :..... :..... :..... :.....
gi|261 LLAGLNTPGVTTVIEPVMTRDHTEKMLQGFGADLTVDKDGVRHIRIVGQKLTGQTID
      190     200     210     220     230     240

      250     260     270     280     290     300
CP4_EP VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
:..... :..... :..... :..... :..... :..... :.....
gi|261 VPGDPSSTAFPLVAALLVEGSDVTIRNVLMNPNTRTGLILTLQEMGADIEIIDPRLAGGED
      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 VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
: .:. :..... :..... :..... :..... :..... :.....
gi|261 VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFLVMGLASEKP
      370     380     390     400     410

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

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```
gi|262 VTVDDSTMIATSFPEFMGMMAGLGAKIAESGAE
      420      430      440      450
>>gi|264659952|gb|EEZ30213.1| 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|264  MSHSACPKPATARHSQALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTG
          10          20          30          40          50          60

```

```

              70          80          90          100          110          120
CP4_EP  KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFNGAATGCRLTMGLVGVDYDFSTFI
        .....:.....:.....:.....:.....:.....:.....:.....:.....:.....
gi|264  RAMQAMGARIRKEGDVWIINGVNGGCLLQPEAPLDFNGAGTGARLTMGLVGTYDMKTSFI
              70          80          90          100          110          120

```

```

      130      140      150      160      170      180
CP4_EP  GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVLTLRGPKTPTPIYRVPMASAQVKSAV
      .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....
gi|264  GDASLSKRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPIAYRVPMASAQVKSAV
      130      140      150      160      170      180

```

```

          190      200      210      220      230      240
CP4_EP  LLALNLTGPGITTVIEPIMTRDHTKMLQGFGANLTVETADGVRTIRLEGRGKLTGQVID
          ::::::::::::::::::::::::::::::::::::::::::::::: :: :: :: :: :: :: ::
gi|264  LLALNLTGPGITTVIEPVMTRDHTKMLQGFGADLTVETDKDGVRRIRIVGQGKLTGQTID
          190      200      210      220      230      240

```

```

                250          260          270          280          290          300
CP4_EP  VPGDPSSSTAFPLVAALLVPGSDVTILNVLMPNTRTGLILTLQEMGADIEVINPRLAGGED
          :::::::::::::::::::: ::::: ::::::::::::::::::::::::::::::::::::::::::::
gi|264  VPGDPSSSTAFPLVAALLVEGSDVTIRNVLMPNTRTGLILTLQEMGADIEIIDPRLAGGED
          250          260          270          280          290          300

```

```

          310          320          330          340          350          360
CP4_EP  VADLRVRSSTLKGTVPEDRAPSMIDVYPILAVAAAFAGATVMNGLEELRVKESDRLSA
          :::::::::: :::::::::: :::::::::::::::::::::::::: ::::::::::::::::::
gi|264  VADLRVKASKLKGTVVPPERAPSMIDVYPVLAIAASFAGETVMGDLDELRVKESDRLAA
          310          320          330          340          350          360

```

```

          370          380          390          400          410          420
CP4_EP  VANGKLKLVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFVLMGLVSENP
      :: :: ::::: :: ::::: ::::: ::::: ::::::::::::::::::::::::::::::
gi|264  VARGLEANGVCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFVLMGLASEKP
          370          380          390          400          410

```

CP4\_EP VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP

|        |  |       |       |       |       |       |
|--------|--|-------|-------|-------|-------|-------|
|        | 250  | 260   | 270   | 280   | 290   | 300   |
| CP4_EF | VPGDPSSSTAFPLVAALLVPGSDVTILNVLNMNPTRTGLILTLQEMGADIEVINPRLAGGED |       |       |       |       |       |
| gi 225 | VPGDPSSSTAFPLVAALLVEGSDVTIRNVLNMNPTRTGLILTLQEMGADIEIIDPRLAGGED |       |       |       |       |       |
|        | 250  | 260   | 270   | 280   | 290   | 300   |
|        |  |       |       |       |       |       |
|        | 310  | 320   | 330   | 340   | 350   | 360   |
| CP4_EF | VADLRVRSSTLKGVTVPEDRAPSMIDEYPI LAVAAAF AEGATVMNGLEELRVKESDRLSA |       |       |       |       |       |
|        | .....  | ..... | ..... | ..... | ..... | ..... |
| gi 225 | VADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAEGETVMNGDLELRVKESDRLAA    |       |       |       |       |       |
|        | 310  | 320   | 330   | 340   | 350   | 360   |

```

          370      380      390      400      410      420
CP4_EP  VANGKLKLVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|225  VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFLVMGLASEKP
          370      380      390      400      410

          430      440      450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|225  VTVDDSTMIATSFPEFMGMAGLGAKIAESGAE
          420      430      440      450
```

>>gi|262551684|gb|EEZ07674.1| 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|262  MSHSACPKPATARHSQALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTG
          10      20      30      40      50      60

          70      80      90      100     110     120
CP4_EP  KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFSTFI
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|262  RAMQAMGARIRKEGDVWIINGVNGCGLLQPEAPLDFGNAGTGARLTMGLVGTYDMKTSFI
          70      80      90      100     110     120
```

```

          130     140     150     160     170     180
CP4_EP  GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMSAQVKS AV
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|262  GDASLSKRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPIAYRVPMSAQVKS AV
          130     140     150     160     170     180
```

```

          190     200     210     220     230     240
CP4_EP  LLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|262  LLAGLNTPGVTTVIEPVMTRDHTEKMLQGFADLTVETDKDGVRHIRIVGQGKLTGQTID
          190     200     210     220     230     240
```

```

          250     260     270     280     290     300
CP4_EP  VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|262  VPGDPSSTAFPLVAALLVEGSDVTIRNVLNPNTRTGLILTLQEMGADIEIIDPRLAGGED
          250     260     270     280     290     300
```

```

          310     320     330     340     350     360
CP4_EP  VADLRVRSTLKGVTVPEDRAPSMIDEYPILAVAAAFEGATVMNGLEELRVKESDRLSA
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
```

```

          310     320     330     340     350     360
gi|262  VADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAGETVMDGLDELRVKESDRLAA
          370     380     390     400     410     420
CP4_EP  VANGKLKLVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|262  VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFLVMGLASEKP
          370     380     390     400     410
```

```

          430     440     450
CP4_EP  VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|262  VTVDDSTMIATSFPEFMGMAGLGAKIAESGAE
          420     430     440     450
```

>>gi|261303782|gb|EEY07279.1| 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  KAMQAMGARIRKEGDTWIIDGVNGGGLLAPEAPLDFGNAATGCRLTMGLVGVDYDFSTFI
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|261  RAMQAMGARIRKEGDVWIINGVNGCGLLQPEAPLDFGNAGTGARLTMGLVGTYDMKTSFI
          70      80      90      100     110     120
```

```

          130     140     150     160     170     180
CP4_EP  GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTPITYRVPMSAQVKS AV
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|261  GDASLSKRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPIAYRVPMSAQVKS AV
          130     140     150     160     170     180
```

```

          190     200     210     220     230     240
CP4_EP  LLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|261  LLAGLNTPGVTTVIEPVMTRDHTEKMLQGFADLTVETDKDGVRHIRIVGQGKLTGQTID
          190     200     210     220     230     240
```

```

          250     260     270     280     290     300
CP4_EP  VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|261  VPGDPSSTAFPLVAALLVEGSDVTIRNVLNPNTRTGLILTLQEMGADIEIIDPRLAGGED
          250     260     270     280     290     300
```



```

          310      320      330      340      350      360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSA
          ..... : ..... : ..... : ..... : ..... : ..... :
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  LLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
          ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  LLAGLNTPGVTTVIEPVMTRDHTEKMLQGFGADLTVETDKDGVRHIRIVGQKLTGQTID
          190     200     210     220     230     240

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

```

```

gi|261  VPGDPSSTAFPLVAALLVEGSDVTIRNVLNPNTRTGLILTLQEMGADIEIIDPRLAGGED
          250     260     270     280     290     300

          310     320     330     340     350     360
CP4_EP  VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEELRVKESDRLSA
          ..... : ..... : ..... : ..... : ..... : ..... :
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  LLAGLNTPGITTVIEPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
          ..... : ..... : ..... : ..... : ..... : ..... :
gi|261  LLAGLNTPGVTTVIEPVMTRDHTEKMLQGFGADLTVETDKDGVRHIRIVGQKLTGQTID
          190     200     210     220     230     240

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gi|261 LLAGLNTPGVITVIEPVMTDRHTEKMLQGADLTVETDKDGVRRHRIVGQKLTGQTID
      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 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIlavAAAFaEGATVMNGLEELRVKESDRLSA
      :::::::::::::::::::: :::::::::::::::::::: ::::::::::::::::::::
gi|261 VADLRVKASKLKGVVVPPERAPSMIDEYPLVlaAASFaEGETVMdGLDELrvKESDRlaA
      310      320      330      340      350      360

      370      380      390      400      410      420
CP4_EP VANGLKLNGVDCDEGETSLVVRGRPDGKGLGNASGAaVATHLDHRIaMSFLVMGLVSENp
      :: :: :::::::::::::: :::::::::::::::::::: ::::::::::::::::::::
gi|261 VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIaMSFLVMGLaSEKp
      370      380      390      400      410

      430      440      450
CP4_EP VTVDDATMIATSFPEFMDLMAGLgAKIeLSDTKAA
      :::::::::::::::::::: :::::::::::::: ::
gi|261 VTVDDSTMIATSFPEFMGMmAGLgAKIaESGAe
      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)

```

|        |                                       |                          |           |     |     |     |
|--------|---------------------------------------|--------------------------|-----------|-----|-----|-----|
|        | 10                                    | 20                       | 30        | 40  | 50  | 60  |
| CP4_EP | MLHGASSRPATARKSSGLSGTVRIPGDKSISHRSMF  | GGLASGETRITGLLEGEDVINTG  | :         | :   | :   | :   |
| gi 260 | MSHSACPKPATARHSQALTGEIRIPGDKSISHRSMF  | GGLASGKTRITGLLEGEDVINTG  | :         | :   | :   | :   |
|        | 10                                    | 20                       | 30        | 40  | 50  | 60  |
|        | 70                                    | 80                       | 90        | 100 | 110 | 120 |
| CP4_EP | KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFG  | NAATGCRLTMGLVGVD         | FDSTFI    | :   | :   | :   |
| gi 260 | RAMQAMGARIRKEGDVWIINGVNGGCLLQPEAPLDFG | NAAGTGARLTMGLVGTYDMKTSFI | :         | :   | :   | :   |
|        | 70                                    | 80                       | 90        | 100 | 110 | 120 |
|        | 130                                   | 140                      | 150       | 160 | 170 | 180 |
| CP4_EP | GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLR  | GPKTPTPIYRVP             | MASAVQVKS | AV  | :   | :   |
| gi 260 | GDASLSKRPMPGRVLNPLREMGVQVEAAEGDRMPLTL | IGRPTANPIAYRVPM          | ASAVQVKS  | AV  | :   | :   |
|        | 130                                   | 140                      | 150       | 160 | 170 | 180 |

```

      190      200      210      220      230      240
CP4_EP  LLAGLNTPGITTVEIPIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      .....
gi|260  LLAGLNTPGVTTVIEPVMTRDHTKMLQGFGADLTVDKDGVRHIRIVGQKLTGQTID
      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  LLAGLNTPGVTTVIEPVMTRDHTKMLQGFGADLTVDKDGVRHIRIVGQKLTGQTID
      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 RAMQAMGARIRKEGDVWIINGVGNGLLQPEAPLDFGNAGTGARLTMGLVGTYDMKTSFI
      70          80          90          100          110          120
      130          140          150          160          170          180
CP4_EP GDASLTKRPMGRVLNPLNPLREMGVQVKSEDDRLPVTLRGPKTPTPITYRVPMASQVKSAAV
      .....
gi|255 GDASLSKRPMPGRVLNPLNPLREMGVQVEAAEGDRMPLTLIGPRTANPIAYRVPMASQVKSAAI
      130          140          150          160          170          180
      190          200          210          220          230          240
CP4_EP LLAGLNTPGIITTVIEPIIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
      .....
gi|255 LLAGLNTPGVTTTVEPVMTRDHTKMLQGFADLTVETDKDGVRHRIHVQGGKLTGQTID
      190          200          210          220          230          240
      250          260          270          280          290          300
CP4_EP VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNPRTGLILTLQEMGADIEVINPRLAGGED
      .....
gi|255 VPGDPSSTAFPLVAALLVEGSDVTIRNVLNPNPRTGLILTLQEMGADIEIIDPRLAGGED
      250          260          270          280          290          300
      310          320          330          340          350          360
CP4_EP VADLRVRSSTLKGVTVPEDRAPSMIDEYPI LAVAAAFAGATVMNGLEELRVKESDRLSA
      .....
gi|255 VADLRVKASKLKGVVPPERAPSMIDEYVPLAIAASFAEGETVMGDGLDLRVKESDRLAA
      310          320          330          340          350          360
      370          380          390          400          410          420
CP4_EP VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFVMGLVSENP
      :: :: .....
gi|255 VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVATHLDHRIAMSFVMGLASEKP
      370          380          390          400          410
      430          440          450
CP4_EP VTVDDATMIATSFPEFMDLMAGLGAKIELSDTKAA
      .....
gi|255 VTVDDSTMIATSFPEFMGMAGLGAKIAESGAE
      420          430          440          450

>>gi|263003296|gb|EEZ15589.1| 3-phosphoshikimate 1-carbo (450 aa)
  initn: 2437 init1: 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

```

```

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 GDASLTKRPMGRVLNPLREMGVQVKSEDDRLPVTLRGPKTPTPITYRVPMASQVKSAAV
      .....
gi|260 GDASLSKRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPERTANPIAYRVPMASQVKSAAV
      130         140         150         160         170         180
      190         200         210         220         230         240
CP4_EP LLAGLNTPGITTVIEPIIMTRDHTKMLQGGFANLTVETDADGVRTIRLEGRGKLTGQVID
      .....
gi|260 LLAGLNTPGVTTVIEFVMTDRDHTKMLQGGFADLTVETDKDGVRRHIRIVGQKLTGTID
      190         200         210         220         230         240
      250         260         270         280         290         300
CP4_EP VPGDPSSTAFPLVAALLVPGSDVTILNVLNPNTRTGLILTLQEMGADIEVINPRLAGGED
      .....
gi|260 VPGDPSSTAFPLVAALLVEGSDVTIRNVLNPNTRTGLILTLQEMGADIEIIDPRLAGGED
      250         260         270         280         290         300
      310         320         330         340         350         360
CP4_EP VADLRVRSSTLKGVTVPEDRAPSMIDEYPI LAVAAAFAGATVMNGLEELRVKESDRLSA
      .....
gi|260 VADLRVKASKLKGVVPPERAPSMIDEYVPLAIAASFAEGETVMGDLDEL RVKESDRLAA
      310         320         330         340         350         360
      370         380         390         400         410         420
CP4_EP VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVSENP
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|260 VARGLEANGVDCTEGEMSLTVRGRPGGKGLG---GGTVGTHLDHRIAMSFLVMGLASEKP
      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 init1: 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|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 | MLHGASSR  | PATARKSS | GLSGTVR | IPGDKS  | ISHR    | SFMFGGLASGETRITGLLEGEDVINTG       |
|        | :         | ..:      | .....   | .....   | .....   | .....                             |
| gi 260 | MSHSACPK  | PATARHSQ | ALTGEIR | IPGDKS  | ISHR    | SFMFGGLASGKTRITGLLEGEDVINTG       |
|        | 10        | 20       | 30      | 40      | 50      | 60                                |
|        | 70        | 80       | 90      | 100     | 110     | 120                               |
| CP4_EP | KAMQAMGAR | IRKEGDTW | IIDGVGN | GGLLAPE | APLDFG  | NAATGCRLTMGLVGVDFTSTFI            |
|        | .....     | .....    | .....   | .....   | .....   | .....                             |
| gi 260 | RAMQAMGAR | IRKEGDTV | IINGVGN | GCLLQPE | APLDFG  | NAGTGARLTMGLVGTYDMKTSFI           |
|        | 70        | 80       | 90      | 100     | 110     | 120                               |
|        | 130       | 140      | 150     | 160     | 170     | 180                               |
| CP4_EP | GDASLTKR  | PMGRVLN  | NPLREMG | VQVKSE  | DGDRLP  | VTILRGPKTPITIRVPMASAVQVKS         |
|        | .....     | .....    | .....   | .....   | .....   | .....                             |
| gi 260 | GDASLTKR  | PMGRVLN  | NPLREMG | VQVEAEG | DRMPLTL | IGPRTANPIAYRVPMASAVQVKS           |
|        | 130       | 140      | 150     | 160     | 170     | 180                               |
|        | 190       | 200      | 210     | 220     | 230     | 240                               |
| CP4_EP | LLAGLNT   | PGITTVI  | EPIMTRD | HTEKML  | QGFGAN  | LTVETDADGVRTIRLEGRGKLTGQVID       |
|        | .....     | .....    | .....   | .....   | .....   | .....                             |
| gi 260 | LLAGLNT   | PGVTTVI  | EPVMT   | RDHTEK  | MLQGFAD | LTVETDKDQVGRHIRVGGQKLTGQTID       |
|        | 190       | 200      | 210     | 220     | 230     | 240                               |
|        | 250       | 260      | 270     | 280     | 290     | 300                               |
| CP4_EP | VPGDPSST  | AFPLVA   | ALLVPG  | SDVTIL  | NVLNMN  | PTRTGLLITLQEMGADIEVINPRLAGGED     |
|        | .....     | .....    | .....   | .....   | .....   | .....                             |
| gi 260 | VPGDPSST  | AFPLVA   | ALLVEG  | SEVTRN  | VLMNP   | TRTGLLITLQEMGADIEIIDPRLAGGED      |
|        | 250       | 260      | 270     | 280     | 290     | 300                               |
|        | 310       | 320      | 330     | 340     | 350     | 360                               |
| CP4_EP | VADLRVRS  | STLKGVT  | VPEDRAP | SIMIDE  | YPI     | LAVAAAFNEGATVMNGLEELRVKESDRLSA    |
|        | .....     | .....    | .....   | .....   | .....   | .....                             |
| gi 260 | VADLRVK   | SKSLKGV  | VVPPER  | APSMID  | EYFVL   | AIASFAEGETVMDGLDELRVKESDRLAA      |
|        | 310       | 320      | 330     | 340     | 350     | 360                               |
|        | 370       | 380      | 390     | 400     | 410     | 420                               |
| CP4_EP | VANGLKL   | NGVDC    | DEGETS  | LSLVVR  | GRPDG   | KGLGNASGAAVATHLDHRIAMSFVLMGLVSEN  |
|        | ..:       | ..:      | .....   | .....   | .....   | .....                             |
| gi 260 | VARGLE    | ANGVDC   | TEGEM   | SLTVR   | GRPGG   | KGLG---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
```

```

              70          80          90          100          110          120
CP4_EP  KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFNGAATGCRLTMGLVGVDFTSFI
        .....:.....:.....:.....:.....:.....:.....:.....:.....
gi|260   RAMQAMGARIRKEGDVWIINGVNGCLLQPEAPLDFNGAGTGARLTMGLVGTYDMKTSFI
              70          80          90          100          110          120

```

```

              130          140          150          160          170          180
CP4_EP   GDASLTKRPMGRVLNPLREMGVQVKSEGDRLPVTLRGPKTPTIPITYRVPMASAQVKS AV
         .....::.....:.....:.....:.....:.....:.....:.....:.....:.....:.....
gi|260    GDASLSKRPMGRVLNPLREMGVQEAAEGDRMPLTLIGPERTANPIAYRVVPMSAQVKS AV
              130          140          150          160          170          180

```

```

          190      200      210      220      230      240
CP4_EP  LLAGLNTPGITTVEIPIMTRDHTEKMLQGFGANLTVETDADGVRTIRLEGRGKLTGQVID
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260  LLAGLNTPGVTTVEIPVMTRDHTEKMLQGFGADLTVETDKDGVRRHIVGQGKLTGQTID
          190      200      210      220      230      240

```

```

                250      260      270      280      290      300
CP4_EP  VPGDPSSTAFLVAALLVPGSDVTILNLMNPTRTGLILTLQEMGADIEVINPRLAGGED
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|260  VPGDPSSTAFLVAALLVEGSEVTIRNLMNPTRTGLILTLQEMGADIEIIDPRLAGGED
                250      260      270      280      290      300

```

```

          310          320          330          340          350          360
CP4_EP  VADLRVRSS TLKGVTV PEDRAPSM IDEYPI LAAVAA FAEAGAT VMNGLE ELRVKE SDRLSA
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|260  VADLRVKASK LKGVVPP ERAPSM IDEYPV LAIAA SFAEGET VM DGLDEL RVKE SDRLAA
          310          320          330          340          350          360

```

```

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

```