ANALYSIS OF THE SEQUENCES OF NEWLY EXPRESSED PROTEINS FOR HOMOLOGY TO TOXINS OR ALLERGENS

Contents (please use bookmarks and hyperlinks for navigation).

1. Introduction

This document provides a complete bioinformatics analysis of all three loci in event FLO-40689-6, using the sequences submitted to the commission in March 2017. The analysis contains results of use of bioinformatics tools to look for homologies to allergens and toxins in the complete sequences of the genes in the T-DNA.

1.1 Overview of bioinformatics methodology and interpretation

The bioinformatic analysis has been carried out using three EFSA guideline documents (EFSA 2010, 2011, 2013).

1. In blastp analysis, a cut-off E-value of less than 1.0 has been used in determining whether similarities are of potential biological significance.
2. In searches for potential allergenic proteins, search for similarity to contiguous amino acids in known allergens has been carried out using an 8 amino acid search window. In recognition of the fact that positive matches obtained with this method are generally regarded to be of low predictive value (Goodman, 2006; Silvanovich et al., 2006; Goodman et al., 2008; Herman et al., 2009; EFSA, 2011; EFSA, 2013) the sliding window (local alignment) method has also been used to screen ORFs.
3. In accordance with guidelines (EFSA, 2010) for analysis for potential allergens, a threshold of 35% sequence identity over a window of at least 80 amino acids has been used in the local alignment method.

2. Bioinformatic analysis to identify whether the newly expressed proteins show similarity with known toxic and /or allergenic proteins

Bioinformatic analysis has been undertaken to provide up-to-date searches of the SwissProt and FARRP databases using the translated sequences of the coding regions contained in the T-

DNA of the transformation vector pCGP1991, the vector used in the generation of FLO-40689-6.

2.1 Methods

The sequences analysed were the (1) selectable marker enzyme tobacco acetolactate synthase (ALS), (2) petunia dihydroflavonol 4-reductase (DFR), derived from 6 exons within the genomic petunia DFR nucleotide sequence contained in pCGP1991 and (3) pansy flavonoid 3’,5’hydroxylase (F3’5’H). The sequences are shown in table 1.

Table 1. Translated nucleotide sequences used in BLAST searches

Code	**Sequence**
*Su*RB (ALS)	MAAAAAAPSPSFSKTLSSSSSKSSTLLPRSTFPFPHHPHKTTPPPLHLTPTHIHSQRRRFTISNVISTTQKVSETQKAETFVSRFAPDEPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVITEGDGRSSY
Petunia DFR	MASEAVHAPSPPVAVPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEHPKADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVSFSSKKLTDMGFQFKYTLEDMYKGAIETCRQKQLLPFSTRSAADNGHNREAIAISAQNYASGKENAPVANHTEMLTNVEV
Pansy F3’5’H	MAILVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMDESFGLALQKAVPLSALVSPRLASNPYAT

2.1.1 Blastp

The sequences shown in table 1 were subjected to a BLAST (blastp) homology search (Appendix 1) used for identifying similar sequences at (http://blast.ncbi.nlm.nih.gov/Blast.cgi; Altschul et al., 1997). Searches were performed against the SwissProt database (protein-protein BLAST of the database UniProtKB/Swiss-Prot (swissprot);

- The translated amino acid sequence (the longest open reading frame with an AUG start codon and a stop codon) derived from the nucleic acid sequence.
- The blastp search program BLAST2.2.27 located within the NCBI (The National Centre for Biotechnology Information) website (http://www.ncbi.nlm.nih.gov ; Altschul et al., 1997).
- The search parameters (indicated in parenthesis) were; word size (3), expected value (10), hit list size (100), Gapcosts (11, 1), matrix (BLOSUM62), Filter string (F), genetic code (1), window size (40), threshold (11).

- The search was carried out with and without the entrez term “toxin”.
- The database was accessed on April 5 2017.

2.1.2 FARRP

The sequences shown in Table 1 were assessed in the FARRP allergen protein database located at http://www.allergenonline.org/databasefasta.shtml. The database was accessed on April 11 2017 (version 17; Jan 18 2017). The amino acid sequences of all ORFs were searched using the full FASTA, sliding 80mer window method and the 8mer exact match method (refer to Appendix 2 for details of how searches were done).

2.2 Results and discussion

2.2.1 Blastp

Appendix 3 provides the outputs of the blastp analysis. The appendix is bookmarked for navigation.

Without the entrez query term “toxin” the highest identities observed with each of the three queries were to homologous genes and functionally related genes from other plant species. The top 100 hits did not reveal any homology to known toxic proteins or allergens.

With the entrez query “toxin” the identity hits obtained were not considered to be biologically significant as E-scores were largely greater than 1.0. E-values less than 1.0 were identified for the newly expressed proteins ALS and DFR. The hits are not considered to be biologically significant because;

- The E-value scores are close to 1.0 (lowest E-value was 0.0002).
- Identity scores were 31% or lower.

2.2.2 FARRP

There were no hits with any of the three query sequences when the FARRP allergen protein database was searched using the sliding 80mer window method or the 8mer exact match method. Similarities to allergenic proteins were identified when sequences of the newly expressed proteins were subjected to full FASTA searches. This output is shown in appendix 4 and is summarised in table 2.

Table 2. Summary of similarities obtained from full FASTA search of the FARRP allergen database. The table shows all hits with an E-value of less than 1.0.

Query sequence	**Allergen**		**Alignment detail**		
	Name	**length (aa)**	**E-value**	**%ID**	**gi Accession ID**
*Su*RB (ALS)	Profilin-like protein [*Ambrosia artemisiifolia*]	131	0.99	36.2	34851180
DFR	No sequences with E < 1.0				
F3’5’H	proteinase inhibitor [*Solanum tuberosum*]	221	0.66	26.9	994779
	Cor a 2 [*Corylus avellana*]	131	0.89	25.0	576017879
	profilin, partial [*Triticum aestivum*]	131	0.89	33.9	548948850
	profilin [*Triticum aestivum*]	131	0.89	33.9	190684061
	profilin, partial [*Triticum aestivum*]	131	0.89	33.9	548948848
	Ana c 1 [*Ananas comosus*]	131	0.89	33.3	75306610

In full FASTA alignments (Table 2) E-values were greater than 0.5 and we do not believe they are likely to represent relevant matches (Hileman, 2002). The three newly expressed proteins are ubiquitous, well-characterized proteins and are not known to be allergens.

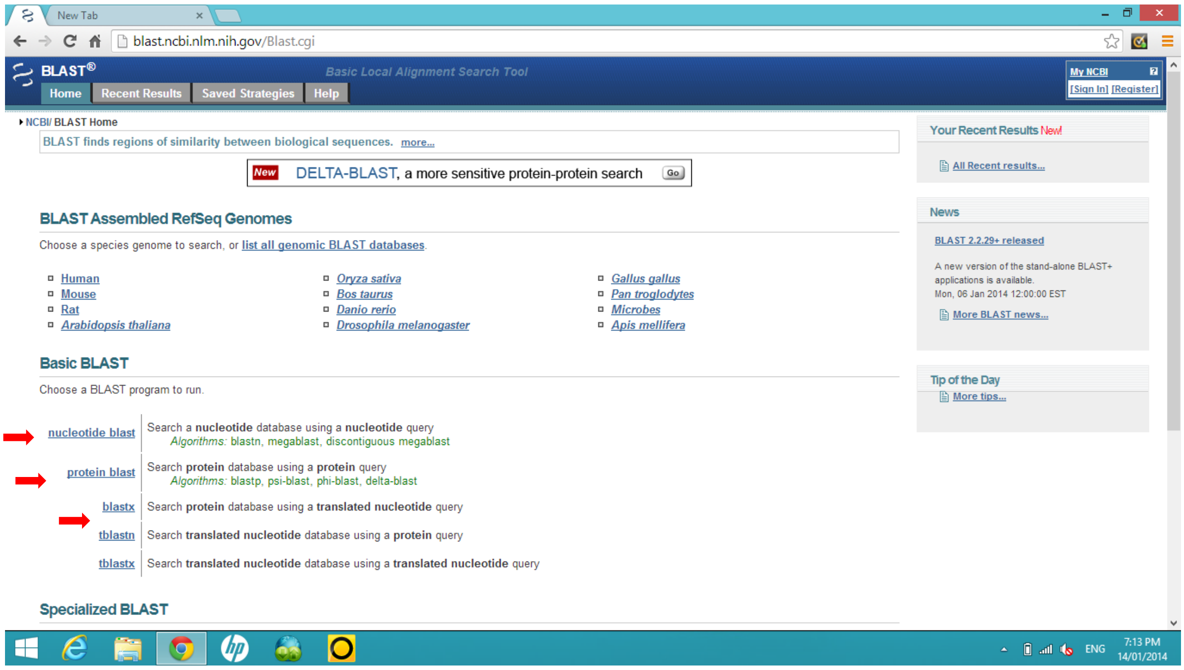
3. Literature cited

1. Altschul SF, Madden TL, Schäffer AA, Zhang J, Zhang Z, Miller W and Lipman DJ, 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Research 25, 3389-3402 Appendix 1.
2. EFSA, 2010. EFSA Panel on Genetically Modified Organisms (GMO); Draft Scientific Opinion on the assessment of allergenicity of GM plants and microorganisms and derived food and feed. EFSA Journal 8(7), 1700.
3. EFSA, 2011. EFSA Panel on Genetically Modified Organisms (GMO); Scientific Opinion on Guidance for risk assessment of food and feed from genetically modified plants. EFSA Journal 9(5), 2150.
4. EFSA, 2013. EFSA Panel on Genetically Modified Organisms (GMO); EFSA guidance on the submission of applications for authorization of genetically modified plants under Regulation (EC) No 1829/2003. EFSA Journal 11(12), 3491.
5. Goodman RE, 2006. Practical and predictive bioinformatics methods for the identification of potentially cross-reactive protein matches. Molecular Nutrition and Food Research 50,655-660.
6. Goodman RE, Vieths S, Sampson HA, Hill D, Ebisawa M, Taylor SL, and vanRee R,2008. Allergenicity assessment of genetically modified crops -- what makes sense? Nature Biotechnology 26, 73-81.
7. Herman RA, Song P and Thirumalaiswamysekhar A, 2009. Value of eight-amino-acid matches in predicting the allergenicity status of proteins: an empirical bioinformatic investigation. Clinical and Molecular Allergy 7, 9 doi: 10.1186/1476-7961-7-9.
8. Hileman RE, Silvanovich A, Goodman RE, Rice EA, Holleschak G, Astwood JD and Hefle S, 2002. Bioinformatic methods for allergenicity assessment using a comprehensive allergen database. International Archives of Allergy and Immunology 128, 280-291.
9. Silvanovich A, Nemeth MA, Song P, Herman R, Tagliani L and Bannon GA, 2006. The value of short amino acid sequence matches for prediction of protein allergenicity.

Appendix 1. Step-by-step explanations of how similarity searches were performed

blastn, blastx and blastp

STEP1. Log in to database search homepage and select BLAST program (i.e. click on options arrowed).



BLAST finds regions of similarity between biological sequences. more...

New DELTA-BLAST, a more sensitive protein-protein search Go

BLAST Assembled RefSeq Genomes

Choose a species genome to search, or list all genomic BLAST databases.

- Human
- Mouse
- Rat
- *Arabidopsis thaliana*
- *Oryza sativa*
- *Bos taurus*
- *Danio rerio*
- *Drosophila melanogaster*
- *Gallus gallus*
- *Pan troglodytes*
- *Microbes*
- *Apis mellifera*

Basic BLAST

Choose a BLAST program to run.

nucleotide blast	Search a **nucleotide** database using a **nucleotide** query *Algorithms:* blastn, megablast, discontiguous megablast
protein blast	Search **protein** database using a **protein** query *Algorithms:* blastp, psi-blast, phi-blast, delta-blast
blastx	Search **protein** database using a **translated nucleotide** query
tblastn	Search **translated nucleotide** database using a **protein** query
tblastx	Search **translated nucleotide** database using a **translated nucleotide** query

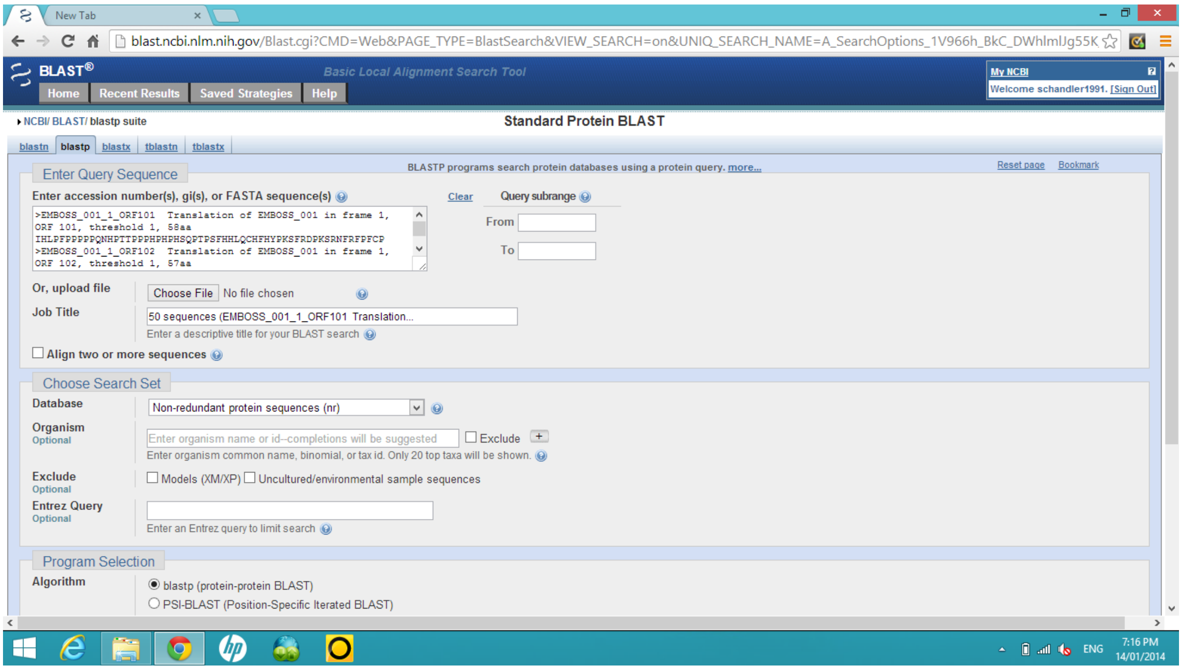
Specialized BLAST

BLAST 2.2.29+ released

A new version of the stand-alone BLAST+ applications is available.
Mon, 06 Jan 2014 12:00:00 EST

More BLAST news...

STEP2. Enter query sequences. The EMBOSS ORF output (Step 6, Appendix 2) was downloaded into word and 50 sequences, in EMBOSS format, were then entered for batch query. Groups of 50 ORF sequences were queried in turn until all ORFs had been analysed. At this step optional Entrez query terms were also entered (i.e. toxin, Dianthus). BLAST was run.



Standard Protein BLAST

BLASTP programs search protein databases using a protein query. more...

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

```
>EMBOSS_001_1_ORF101  Translation of EMBOSS_001 in frame 1,
ORF 101, threshold 1, 58aa
IHLPFPPPPPQNHPTTPPPHPHPHSQPTPSFHHLQCHFHYPKSFRDPKSRNFRFPFCP
>EMBOSS_001_1_ORF102  Translation of EMBOSS_001 in frame 1,
ORF 102, threshold 1, 57aa
```

Query subrange
From
To

Or, upload file: No file chosen

Job Title: 50 sequences (EMBOSS_001_1_ORF101 Translation...
Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Choose Search Set

Database: Non-redundant protein sequences (nr)

Organism Optional: Enter organism name or id--completions will be suggested ☐ Exclude +
Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

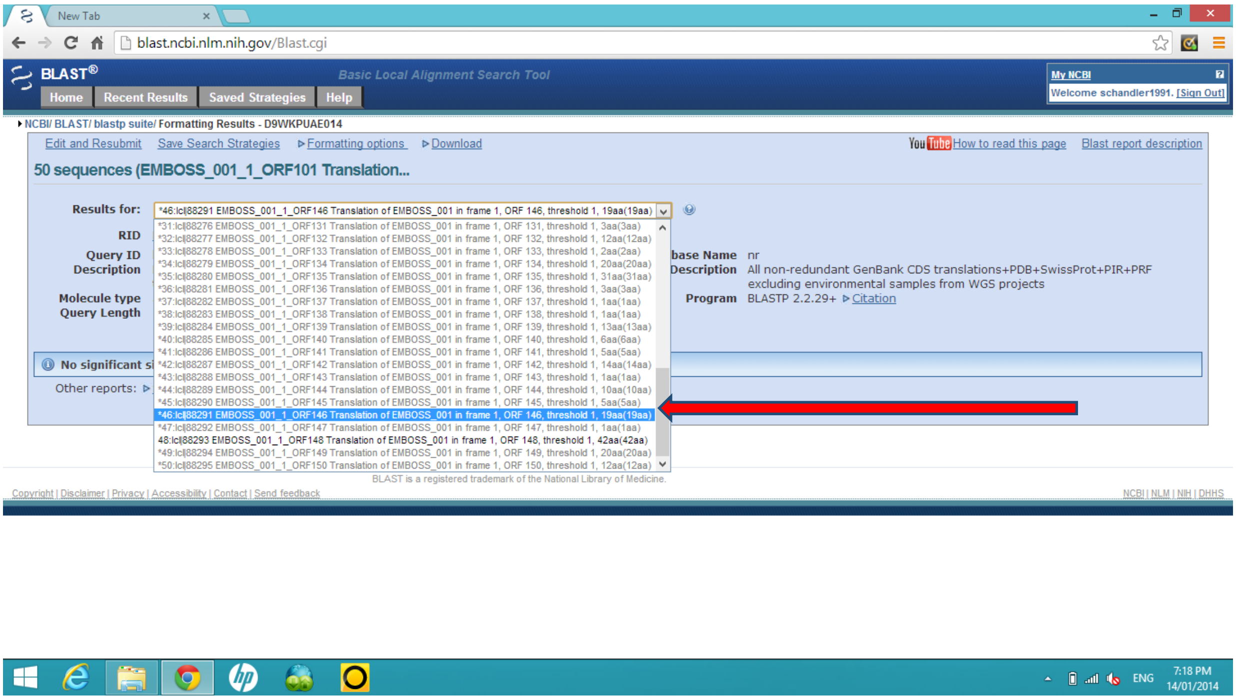
Exclude Optional: ☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

Entrez Query Optional:
Enter an Entrez query to limit search

Program Selection

Algorithm:
● blastp (protein-protein BLAST)
○ PSI-BLAST (Position-Specific Iterated BLAST)

STEP 3. Identify all ORFs within the 50 ORF query batch where a significant homology occurred. The specific ORFs where a significant similarity could be identified are shown in bold font in a drop down menu, as shown in the example of ORF 1.148 in the screen capture below (arrowed).



NCBI/ BLAST/ blastp suite/ Formatting Results - D9WKPUAE014

50 sequences (EMBOSS_001_1_ORF101 Translation...

Results for: *46:lcl|88291 EMBOSS_001_1_ORF146 Translation of EMBOSS_001 in frame 1, ORF 146, threshold 1, 19aa(19aa)

*31:lcl|88276 EMBOSS_001_1_ORF131 Translation of EMBOSS_001 in frame 1, ORF 131, threshold 1, 3aa(3aa)
*32:lcl|88277 EMBOSS_001_1_ORF132 Translation of EMBOSS_001 in frame 1, ORF 132, threshold 1, 12aa(12aa)
*33:lcl|88278 EMBOSS_001_1_ORF133 Translation of EMBOSS_001 in frame 1, ORF 133, threshold 1, 2aa(2aa)
*34:lcl|88279 EMBOSS_001_1_ORF134 Translation of EMBOSS_001 in frame 1, ORF 134, threshold 1, 20aa(20aa)
*35:lcl|88280 EMBOSS_001_1_ORF135 Translation of EMBOSS_001 in frame 1, ORF 135, threshold 1, 31aa(31aa)
*36:lcl|88281 EMBOSS_001_1_ORF136 Translation of EMBOSS_001 in frame 1, ORF 136, threshold 1, 3aa(3aa)
*37:lcl|88282 EMBOSS_001_1_ORF137 Translation of EMBOSS_001 in frame 1, ORF 137, threshold 1, 1aa(1aa)
*38:lcl|88283 EMBOSS_001_1_ORF138 Translation of EMBOSS_001 in frame 1, ORF 138, threshold 1, 1aa(1aa)
*39:lcl|88284 EMBOSS_001_1_ORF139 Translation of EMBOSS_001 in frame 1, ORF 139, threshold 1, 13aa(13aa)
*40:lcl|88285 EMBOSS_001_1_ORF140 Translation of EMBOSS_001 in frame 1, ORF 140, threshold 1, 6aa(6aa)
*41:lcl|88286 EMBOSS_001_1_ORF141 Translation of EMBOSS_001 in frame 1, ORF 141, threshold 1, 5aa(5aa)
*42:lcl|88287 EMBOSS_001_1_ORF142 Translation of EMBOSS_001 in frame 1, ORF 142, threshold 1, 14aa(14aa)
*43:lcl|88288 EMBOSS_001_1_ORF143 Translation of EMBOSS_001 in frame 1, ORF 143, threshold 1, 1aa(1aa)
*44:lcl|88289 EMBOSS_001_1_ORF144 Translation of EMBOSS_001 in frame 1, ORF 144, threshold 1, 10aa(10aa)
*45:lcl|88290 EMBOSS_001_1_ORF145 Translation of EMBOSS_001 in frame 1, ORF 145, threshold 1, 5aa(5aa)
*46:lcl|88291 EMBOSS_001_1_ORF146 Translation of EMBOSS_001 in frame 1, ORF 146, threshold 1, 19aa(19aa)
*47:lcl|88292 EMBOSS_001_1_ORF147 Translation of EMBOSS_001 in frame 1, ORF 147, threshold 1, 1aa(1aa)
48:lcl|88293 EMBOSS_001_1_ORF148 Translation of EMBOSS_001 in frame 1, ORF 148, threshold 1, 42aa(42aa)
*49:lcl|88294 EMBOSS_001_1_ORF149 Translation of EMBOSS_001 in frame 1, ORF 149, threshold 1, 20aa(20aa)
*50:lcl|88295 EMBOSS_001_1_ORF150 Translation of EMBOSS_001 in frame 1, ORF 150, threshold 1, 12aa(12aa)

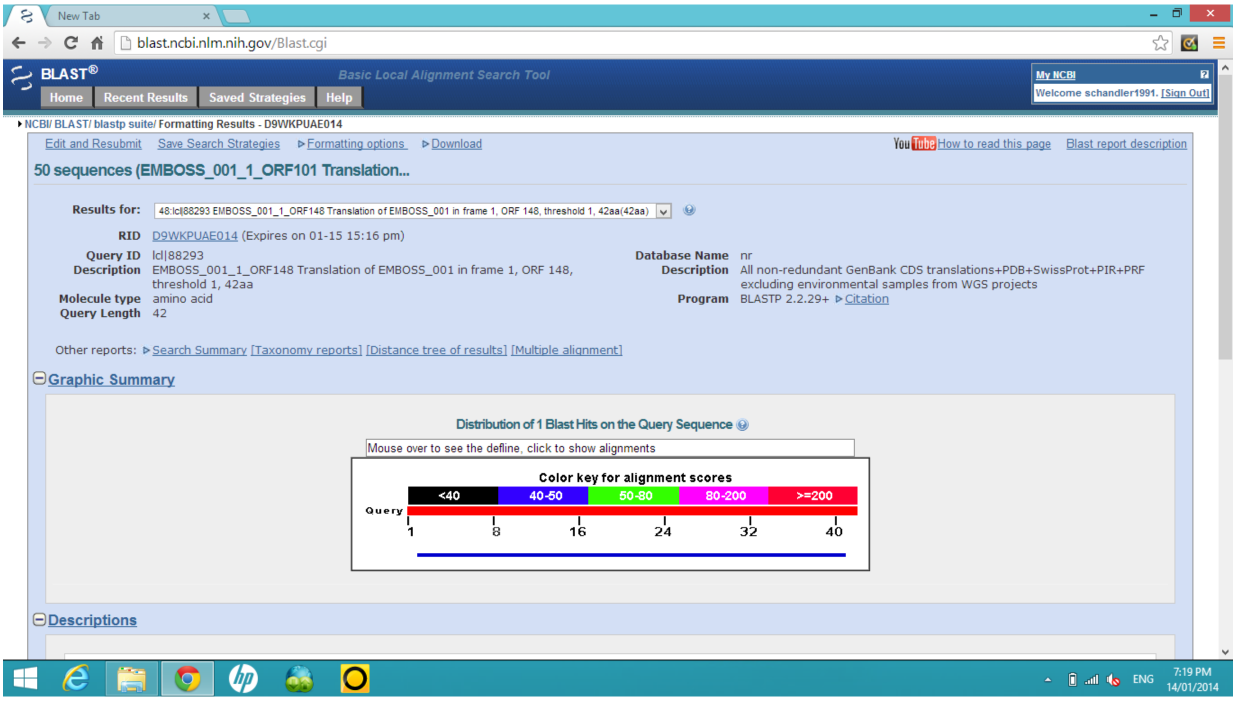
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.29+ Citation

No significant si

Other reports:

BLAST is a registered trademark of the National Library of Medicine.

STEP 4. Open from drop down menu any query ORF with a significant homology, as shown in the example of ORF 1.148 in the screen capture below.



NCBI/ BLAST/ blastp suite/ Formatting Results - D9WKPUAE014

50 sequences (EMBOSS_001_1_ORF101 Translation...

Results for: 48:lcl|88293 EMBOSS_001_1_ORF148 Translation of EMBOSS_001 in frame 1, ORF 148, threshold 1, 42aa(42aa)

RID D9WKPUAE014 (Expires on 01-15 15:16 pm)
Query ID lcl|88293
Description EMBOSS_001_1_ORF148 Translation of EMBOSS_001 in frame 1, ORF 148, threshold 1, 42aa
Molecule type amino acid
Query Length 42

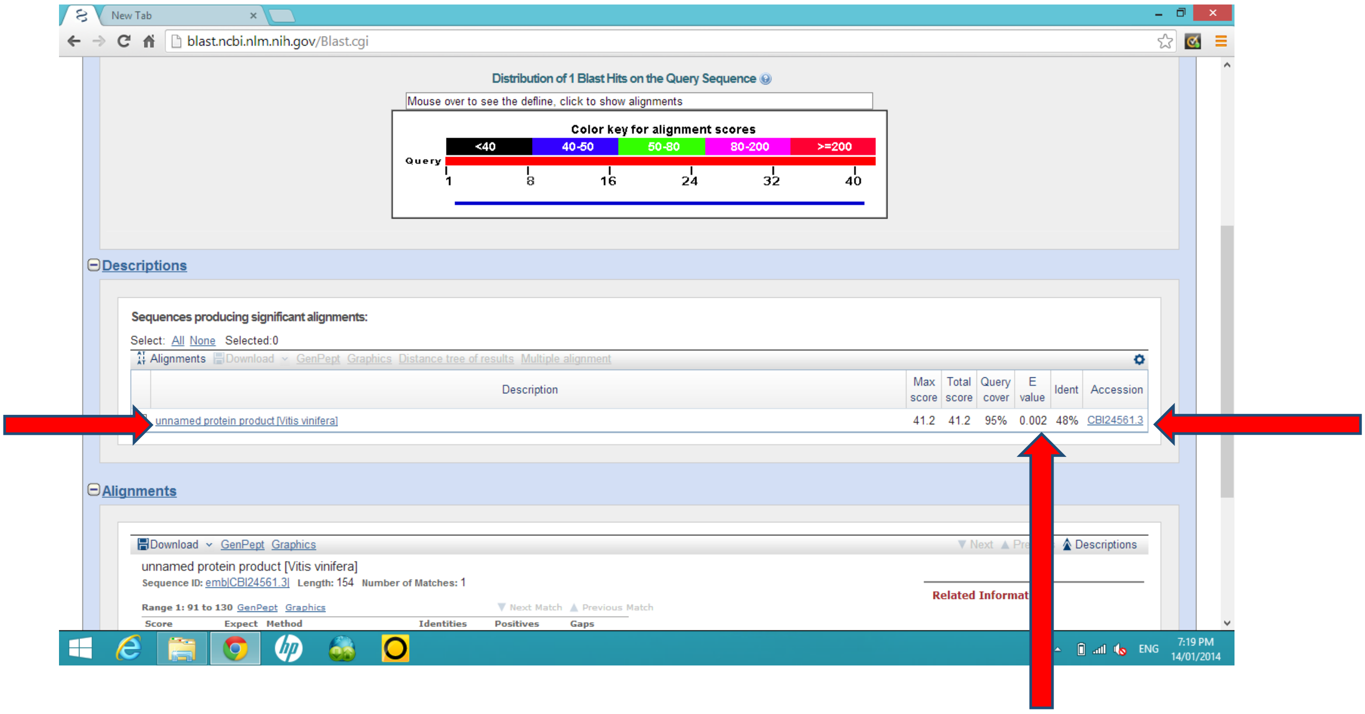
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.29+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Distribution of 1 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments

STEP 5. The E- value, descriptions of homology and details of accession records (arrowed) were noted and tabulated for inclusion in the additional information dossier. As indicated in the additional information, a cut off value of less than 1.0 was used to determine whether similarities were of potential biological significance.



Sequences producing significant alignments:

Select: All None Selected:0

Description	Max score	Total score	Query cover	E value	Ident	Accession
unnamed protein product [Vitis vinifera]	41.2	41.2	95%	0.002	48%	CBI24561.3

unnamed protein product [Vitis vinifera]

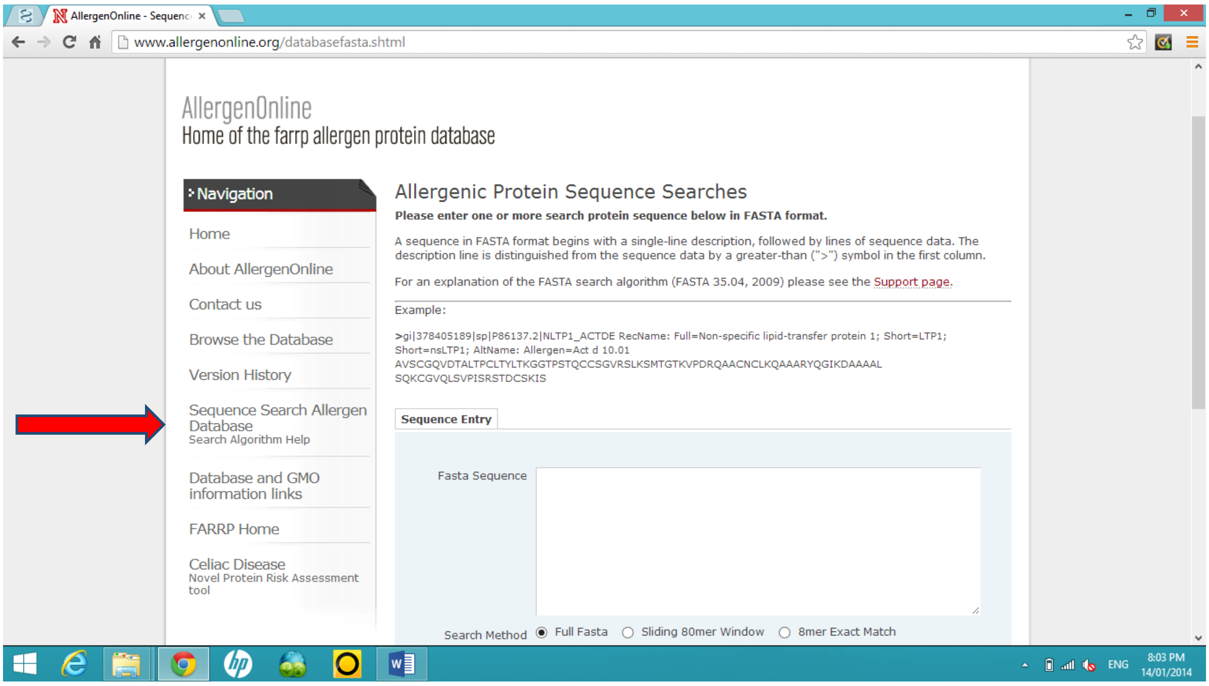
Sequence ID: emb|CBI24561.3| Length: 154 Number of Matches: 1

Range 1: 91 to 130 GenPept Graphics Next Match Previous Match

Score Expect Method Identities Positives Gaps

Appendix 2. Step-by-step explanations of how FARRP allergen protein similarity searches were performed

STEP1. Open website and select ***sequence search allergen database*** page (arrow).



Allergenic Protein Sequence Searches

Please enter one or more search protein sequence below in FASTA format.

A sequence in FASTA format begins with a single-line description, followed by lines of sequence data. The description line is distinguished from the sequence data by a greater-than (">") symbol in the first column.

For an explanation of the FASTA search algorithm (FASTA 35.04, 2009) please see the Support page.

Example:

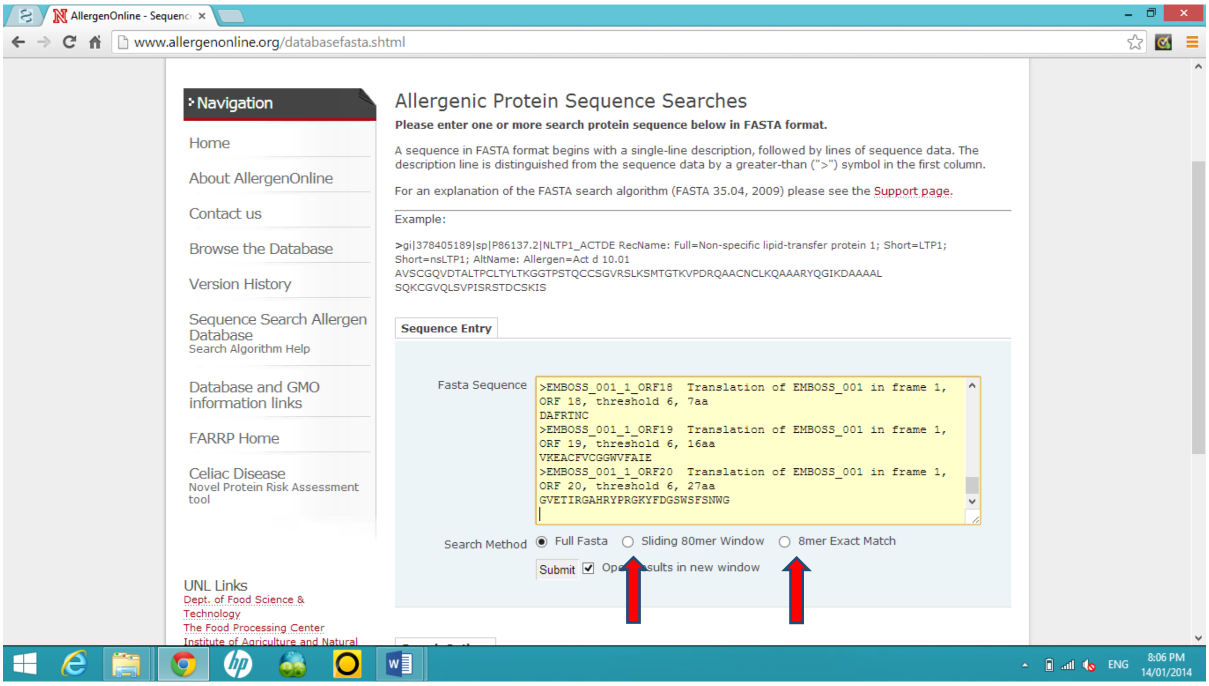
>gi|378405189|sp|P86137.2|NLTP1_ACTDE RecName: Full=Non-specific lipid-transfer protein 1; Short=LTP1;
Short=nsLTP1; AltName: Allergen=Act d 10.01
AVSCGQVDTALTPCLTYLTKGGTPSTQCCSGVRSLKSMTGTKVPDRQAACNCLKQAAARYQGIKDAAAAL
SQKCGVQLSVPISRSTDCSKIS

Sequence Entry

Fasta Sequence

Search Method ● Full Fasta ○ Sliding 80mer Window ○ 8mer Exact Match

STEP 2. Enter query sequences. 20- 30 sequences, in EMBOSS format, were entered for batch query. Groups of ORF sequences were queried in turn until all ORFs generated had been analysed. Each group of ORF were analysed twice; once with the option sliding 80mer window selected and once with the option 8mer exact match method selected (arrows).



Allergenic Protein Sequence Searches

Please enter one or more search protein sequence below in FASTA format.

A sequence in FASTA format begins with a single-line description, followed by lines of sequence data. The description line is distinguished from the sequence data by a greater-than (">") symbol in the first column.

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Example:

>gi|378405189|sp|P86137.2|NLTP1_ACTDE RecName: Full=Non-specific lipid-transfer protein 1; Short=LTP1;
Short=nsLTP1; AltName: Allergen=Act d 10.01
AVSCGQVDTALTPCLTYLTKGGTPSTQCCSGVRSLKSMTGTKVPDRQAACNCLKQAAARYQGIKDAAAAL
SQKCGVQLSVPISRSTDCSKIS

Sequence Entry

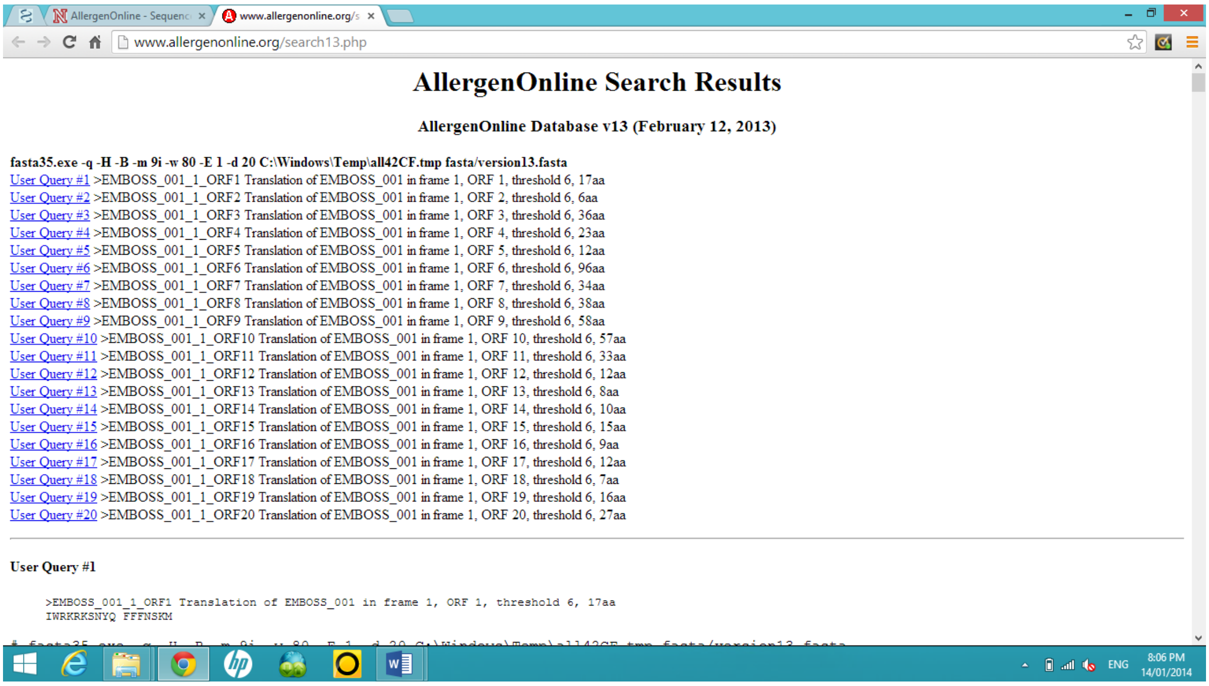
Fasta Sequence

```
>EMBOSS_001_1_ORF18  Translation of EMBOSS_001 in frame 1,
ORF 18, threshold 6, 7aa
DAFRTNC
>EMBOSS_001_1_ORF19  Translation of EMBOSS_001 in frame 1,
ORF 19, threshold 6, 16aa
VKEACFVCGGWVFAIE
>EMBOSS_001_1_ORF20  Translation of EMBOSS_001 in frame 1,
ORF 20, threshold 6, 27aa
GVETIRGAHRYPRGKYFDGSWSFSNWG
```

Search Method ● Full Fasta ○ Sliding 80mer Window ○ 8mer Exact Match

☑ Open results in new window

STEP 3. Review outputs from query sequences.



AllergenOnline Search Results

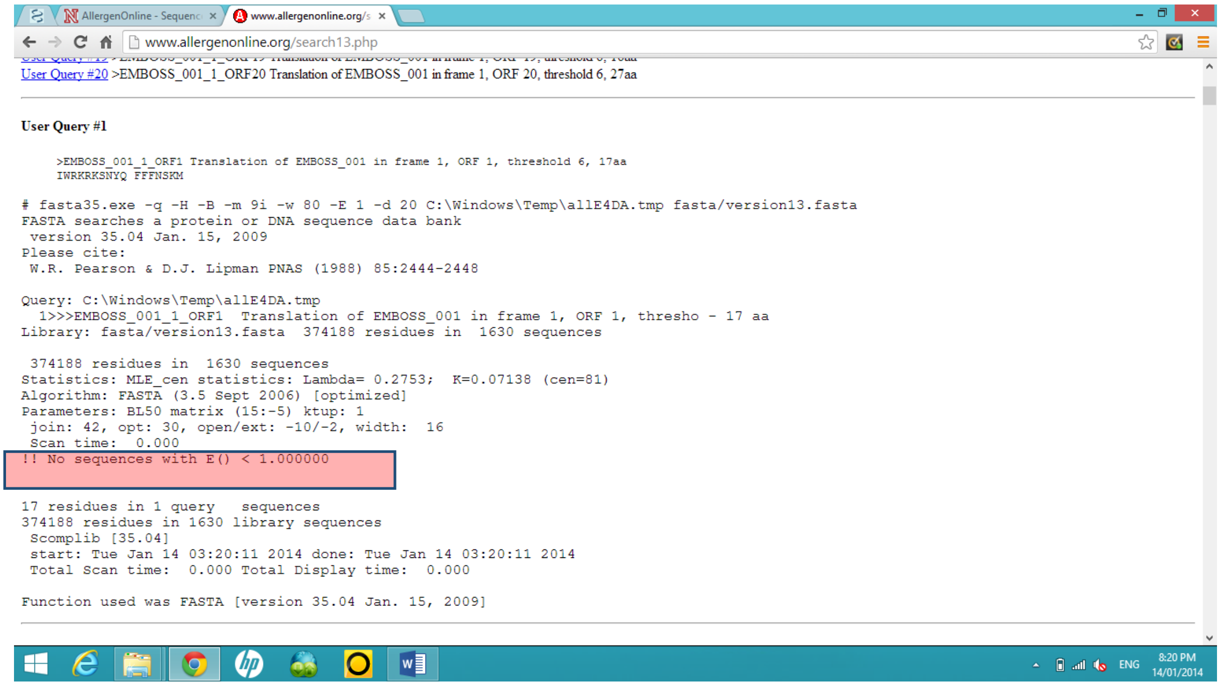
AllergenOnline Database v13 (February 12, 2013)

fasta35.exe -q -H -B -m 9i -w 80 -E 1 -d 20 C:\Windows\Temp\all42CF.tmp fasta/version13.fasta
User Query #1 >EMBOSS_001_1_ORF1 Translation of EMBOSS_001 in frame 1, ORF 1, threshold 6, 17aa
User Query #2 >EMBOSS_001_1_ORF2 Translation of EMBOSS_001 in frame 1, ORF 2, threshold 6, 6aa
User Query #3 >EMBOSS_001_1_ORF3 Translation of EMBOSS_001 in frame 1, ORF 3, threshold 6, 36aa
User Query #4 >EMBOSS_001_1_ORF4 Translation of EMBOSS_001 in frame 1, ORF 4, threshold 6, 23aa
User Query #5 >EMBOSS_001_1_ORF5 Translation of EMBOSS_001 in frame 1, ORF 5, threshold 6, 12aa
User Query #6 >EMBOSS_001_1_ORF6 Translation of EMBOSS_001 in frame 1, ORF 6, threshold 6, 96aa
User Query #7 >EMBOSS_001_1_ORF7 Translation of EMBOSS_001 in frame 1, ORF 7, threshold 6, 34aa
User Query #8 >EMBOSS_001_1_ORF8 Translation of EMBOSS_001 in frame 1, ORF 8, threshold 6, 38aa
User Query #9 >EMBOSS_001_1_ORF9 Translation of EMBOSS_001 in frame 1, ORF 9, threshold 6, 58aa
User Query #10 >EMBOSS_001_1_ORF10 Translation of EMBOSS_001 in frame 1, ORF 10, threshold 6, 57aa
User Query #11 >EMBOSS_001_1_ORF11 Translation of EMBOSS_001 in frame 1, ORF 11, threshold 6, 33aa
User Query #12 >EMBOSS_001_1_ORF12 Translation of EMBOSS_001 in frame 1, ORF 12, threshold 6, 12aa
User Query #13 >EMBOSS_001_1_ORF13 Translation of EMBOSS_001 in frame 1, ORF 13, threshold 6, 8aa
User Query #14 >EMBOSS_001_1_ORF14 Translation of EMBOSS_001 in frame 1, ORF 14, threshold 6, 10aa
User Query #15 >EMBOSS_001_1_ORF15 Translation of EMBOSS_001 in frame 1, ORF 15, threshold 6, 15aa
User Query #16 >EMBOSS_001_1_ORF16 Translation of EMBOSS_001 in frame 1, ORF 16, threshold 6, 9aa
User Query #17 >EMBOSS_001_1_ORF17 Translation of EMBOSS_001 in frame 1, ORF 17, threshold 6, 12aa
User Query #18 >EMBOSS_001_1_ORF18 Translation of EMBOSS_001 in frame 1, ORF 18, threshold 6, 7aa
User Query #19 >EMBOSS_001_1_ORF19 Translation of EMBOSS_001 in frame 1, ORF 19, threshold 6, 16aa
User Query #20 >EMBOSS_001_1_ORF20 Translation of EMBOSS_001 in frame 1, ORF 20, threshold 6, 27aa

User Query #1

```
    >EMBOSS_001_1_ORF1 Translation of EMBOSS_001 in frame 1, ORF 1, threshold 6, 17aa
    IWRKRKSNYQ FFFNSKM
```

STEP 4. Note all ORF sequences in which an E-value of less than 1.0 was not identified (highlighted in screen capture below). These ORF were not analysed further.

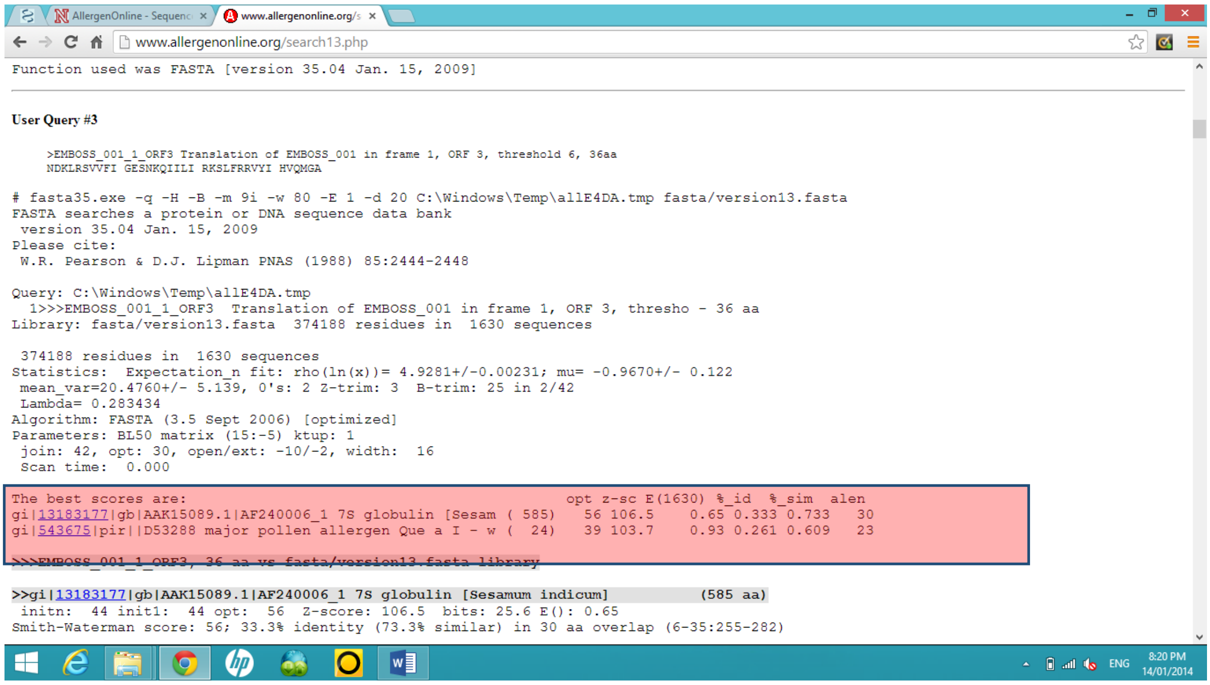


User Query #20 >EMBOSS_001_1_ORF20 Translation of EMBOSS_001 in frame 1, ORF 20, threshold 6, 27aa

User Query #1

```
    >EMBOSS_001_1_ORF1 Translation of EMBOSS_001 in frame 1, ORF 1, threshold 6, 17aa
    IWRKRKSNYQ FFFNSKM

# fasta35.exe -q -H -B -m 9i -w 80 -E 1 -d 20 C:\Windows\Temp\allE4DA.tmp fasta/version13.fasta
FASTA searches a protein or DNA sequence data bank
 version 35.04 Jan. 15, 2009
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

Query: C:\Windows\Temp\allE4DA.tmp
  1>>>EMBOSS_001_1_ORF1  Translation of EMBOSS_001 in frame 1, ORF 1, thresho - 17 aa
Library: fasta/version13.fasta  374188 residues in  1630 sequences

 374188 residues in  1630 sequences
Statistics: MLE_cen statistics: Lambda= 0.2753;  K=0.07138 (cen=81)
Algorithm: FASTA (3.5 Sept 2006) [optimized]
Parameters: BL50 matrix (15:-5) ktup: 1
 join: 42, opt: 30, open/ext: -10/-2, width:  16
 Scan time:  0.000
!! No sequences with E() < 1.000000

17 residues in 1 query   sequences
374188 residues in 1630 library sequences
 Scomplib [35.04]
 start: Tue Jan 14 03:20:11 2014 done: Tue Jan 14 03:20:11 2014
 Total Scan time:  0.000 Total Display time:  0.000

Function used was FASTA [version 35.04 Jan. 15, 2009]
```

STEP 5. Note all ORF sequences in which an E-value of less than 1.0 was identified (highlighted in screen capture below). If sequence identity was greater than 35% these ORF were analysed using the full FASTA option (see step 2). The sequences of the newly introduced proteins were analysed using the full FASTA option.



```
Function used was FASTA [version 35.04 Jan. 15, 2009]
```

User Query #3

```
    >EMBOSS_001_1_ORF3 Translation of EMBOSS_001 in frame 1, ORF 3, threshold 6, 36aa
    NDKLRSVVFI GESNKQIILI RKSLFRRVYI HVQMGA

# fasta35.exe -q -H -B -m 9i -w 80 -E 1 -d 20 C:\Windows\Temp\allE4DA.tmp fasta/version13.fasta
FASTA searches a protein or DNA sequence data bank
 version 35.04 Jan. 15, 2009
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

Query: C:\Windows\Temp\allE4DA.tmp
  1>>>EMBOSS_001_1_ORF3  Translation of EMBOSS_001 in frame 1, ORF 3, thresho - 36 aa
Library: fasta/version13.fasta  374188 residues in  1630 sequences

 374188 residues in  1630 sequences
Statistics:  Expectation_n fit: rho(ln(x))= 4.9281+/-0.00231; mu= -0.9670+/- 0.122
 mean_var=20.4760+/- 5.139, 0's: 2 Z-trim: 3  B-trim: 25 in 2/42
 Lambda= 0.283434
Algorithm: FASTA (3.5 Sept 2006) [optimized]
Parameters: BL50 matrix (15:-5) ktup: 1
 join: 42, opt: 30, open/ext: -10/-2, width:  16
 Scan time:  0.000

The best scores are:                                      opt z-sc E(1630) %_id  %_sim  alen
gi|13183177|gb|AAK15089.1|AF240006_1 7S globulin [Sesam ( 585)   56 106.5    0.65 0.333 0.733   30
gi|543675|pir||D53288 major pollen allergen Que a I - w (  24)   39 103.7    0.93 0.261 0.609   23

>>>EMBOSS_001_1_ORF3, 36 aa vs fasta/version13.fasta library

>>gi|13183177|gb|AAK15089.1|AF240006_1 7S globulin [Sesamum indicum]          (585 aa)
 initn:  44 init1:  44 opt:  56  Z-score: 106.5  bits: 25.6 E(): 0.65
Smith-Waterman score: 56; 33.3% identity (73.3% similar) in 30 aa overlap (6-35:255-282)
```

Appendix 3. Results of blastp analysis

HYPERLINKS

*SuR*B (ALS)

DFR

F3’5’H

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BLAST ® » **blastp suite** » **RID-E930UHE7016**   Home   Recent Results   Saved Strategies   Help

BLAST Results

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Job title: unnamed protein product (664 letters)

RID	E930UHE7016 (Expires on 04-06 14:18 pm)		
Query ID	lcl|Query_16370	**Database Name**	swissprot
Description	unnamed protein product	**Description**	Non-redundant UniProtKB/SwissProt sequences
Molecule type	amino acid	**Program**	BLASTP 2.6.0+ Citation
Query Length	664		

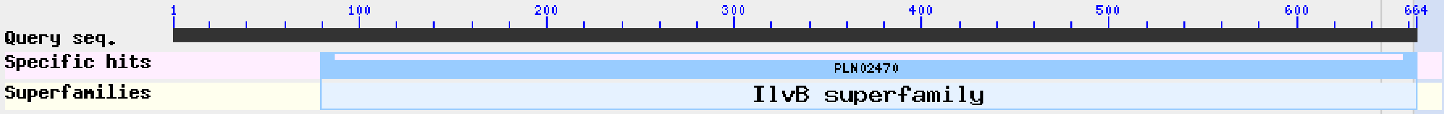
Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment] [MSA viewer]

New Analyze your query with SmartBLAST

Graphic Summary

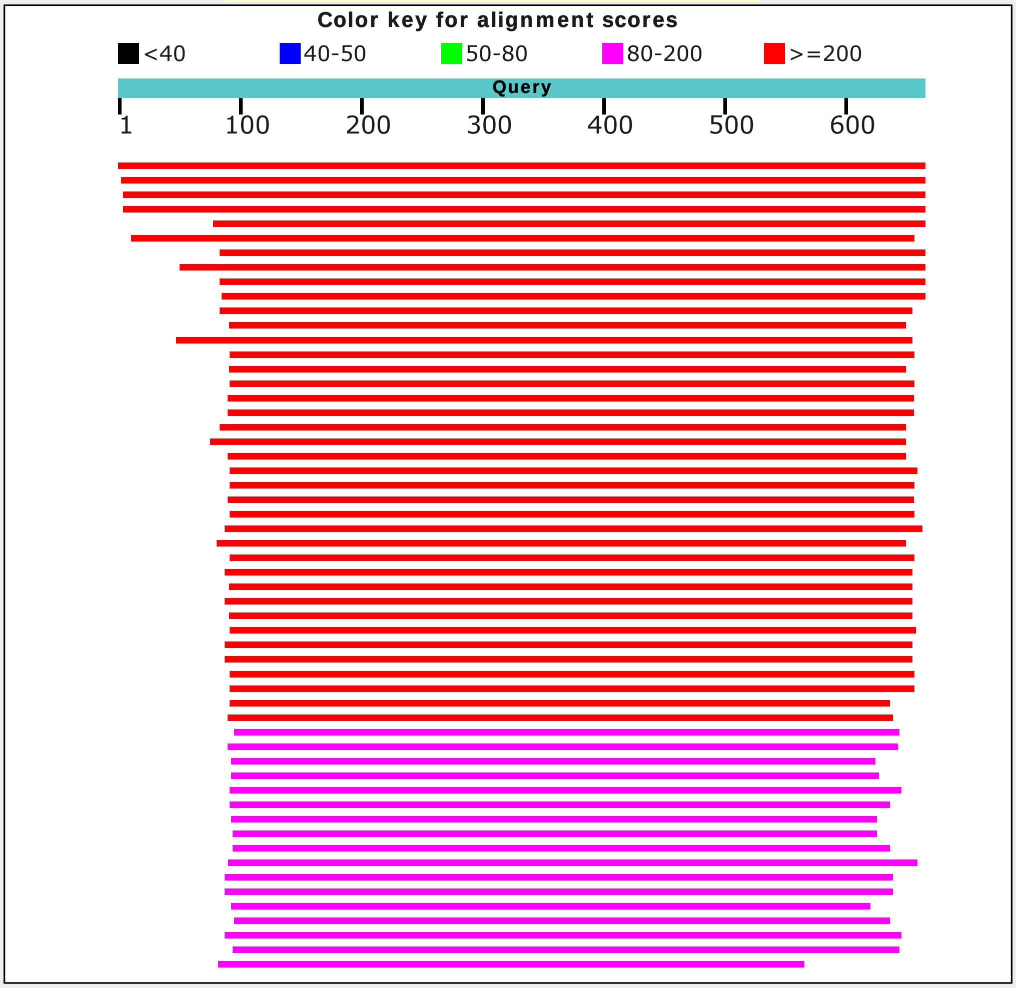
Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of the top 101 Blast Hits on 100 subject sequences

Mouse over to see the title, click to show alignments



Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	RecName: Full=Acetolactate synthase 2, chloroplastic; AltName: Full=ALS II; AltName: Full=Acet	1365	1365	100%	0.0	100%	P09114.1
☐	RecName: Full=Acetolactate synthase 1, chloroplastic; AltName: Full=ALS I; AltName: Full=Acet	1328	1328	99%	0.0	97%	P09342.1
☐	RecName: Full=Acetolactate synthase 3, chloroplastic; AltName: Full=ALS III; AltName: Full=Ace	1063	1063	99%	0.0	78%	P27819.1
☐	RecName: Full=Acetolactate synthase 1, chloroplastic; AltName: Full=ALS I; AltName: Full=Acet	1061	1061	99%	0.0	78%	P27818.1
☐	RecName: Full=Acetolactate synthase, chloroplastic; Short=AtALS; AltName: Full=Acetohydroxy-	1045	1045	88%	0.0	84%	P17597.1
☐	RecName: Full=Acetolactate synthase 2, chloroplastic; AltName: Full=ALS II; AltName: Full=Acet	961	961	97%	0.0	71%	P14874.1
☐	RecName: Full=Acetolactate synthase 1, chloroplastic; AltName: Full=Acetohydroxy-acid synthas	951	951	87%	0.0	77%	Q6K2E8.1
☐	RecName: Full=Acetolactate synthase 1, chloroplastic; AltName: Full=Acetohydroxy-acid synthas	942	942	92%	0.0	73%	Q41768.1
☐	RecName: Full=Acetolactate synthase 2, chloroplastic; AltName: Full=Acetohydroxy-acid synthas	922	922	87%	0.0	76%	Q41769.1
☐	RecName: Full=Probable acetolactate synthase 2, chloroplastic; AltName: Full=Acetohydroxy-aci	901	901	87%	0.0	73%	Q7XKQ8.2
☐	RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-	510	510	85%	4e-173	48%	P42463.1
☐	RecName: Full=Acetolactate synthase; AltName: Full=ALS; AltName: Full=Acetohydroxy-acid syn	502	502	83%	4e-170	48%	P0A623.1
☐	RecName: Full=Acetolactate synthase; AltName: Full=ALS; AltName: Full=Acetohydroxy-acid syn	501	501	91%	1e-169	45%	O33112.1
☐	RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-	498	498	84%	5e-169	46%	P37251.4
☐	RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-	486	486	83%	4e-164	46%	O78518.1
☐	RecName: Full=Acetolactate synthase isozyme 2 large subunit; Short=AHAS-II; AltName: Full=Al	483	483	84%	1e-163	45%	P00892.3
☐	RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-	483	483	85%	4e-163	44%	Q1XDF6.1
☐	RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-	481	481	85%	3e-162	44%	P69683.1
☐	RecName: Full=Acetolactate synthase; AltName: Full=ALS; AltName: Full=Acetohydroxy-acid syn	479	479	85%	8e-161	46%	Q59498.1
☐	RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-	473	473	86%	2e-158	45%	Q7U5G1.1
☐	RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-	470	470	84%	4e-158	46%	O19929.1
☐	RecName: Full=Acetolactate synthase isozyme 1 large subunit; Short=AHAS-I; AltName: Full=Ac	465	465	85%	2e-156	44%	P08142.1
☐	RecName: Full=Probable acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acet	466	466	84%	3e-156	45%	Q57725.1
☐	RecName: Full=Acetolactate synthase, mitochondrial; AltName: Full=AHAS; AltName: Full=ALS;	467	467	85%	1e-155	42%	P36620.2
☐	RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-	456	456	84%	2e-152	41%	P45261.1
☐	RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-	451	451	86%	9e-151	41%	Q9RQ65.1
☐	RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-	450	450	85%	2e-150	44%	Q02137.2
☐	RecName: Full=Acetolactate synthase; AltName: Full=ALS; AltName: Full=Acetohydroxy-acid syn	446	446	84%	2e-148	45%	P27868.1
☐	RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-	445	445	85%	2e-148	41%	O85293.1
☐	RecName: Full=Acetolactate synthase, mitochondrial; AltName: Full=AHAS; AltName: Full=ALS;	450	450	84%	3e-148	41%	Q5KPJ5.1
☐	RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-	444	444	85%	4e-148	41%	P57321.1
☐	RecName: Full=Acetolactate synthase, mitochondrial; AltName: Full=AHAS; AltName: Full=ALS;	449	449	84%	7e-148	41%	Q6SSJ3.1
☐	RecName: Full=Acetolactate synthase catalytic subunit, mitochondrial; AltName: Full=Acetohydro	447	447	84%	1e-147	42%	P07342.1
☐	RecName: Full=Acetolactate synthase isozyme 3 large subunit; AltName: Full=AHAS-III; AltName	440	440	85%	2e-146	41%	P00893.2
☐	RecName: Full=Acetolactate synthase isozyme 3 large subunit; AltName: Full=AHAS-III; AltName	440	440	85%	3e-146	41%	P40811.3
☐	RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-	434	434	84%	4e-144	39%	Q89AP7.1
☐	RecName: Full=Probable acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acet	434	434	84%	1e-143	43%	O08353.1
☐	RecName: Full=Glyoxylate carboligase; AltName: Full=Tartronate-semialdehyde synthase	290	290	81%	2e-88	34%	P0AEP8.2
☐	RecName: Full=Putative thiamine pyrophosphate-containing protein YdaP	213	213	82%	9e-60	28%	P96591.1
☐							

	RecName: Full=Pyruvate dehydrogenase [ubiquinone]; AltName: Full=Pyruvate oxidase; Short=F	198	198	82%	2e-54	29%	P07003.1
☐	RecName: Full=Acetolactate synthase; AltName: Full=ALS; AltName: Full=Acetohydroxy-acid syr	185	185	82%	1e-49	26%	Q04789.3
☐	RecName: Full=Sulfoacetaldehyde acetyltransferase	185	185	79%	1e-49	28%	Q93PS3.1
☐	RecName: Full=Sulfoacetaldehyde acetyltransferase	183	183	80%	1e-48	27%	Q84H44.3
☐	RecName: Full=Acetolactate synthase, catabolic; Short=ALS	178	178	83%	3e-47	27%	P27696.1
☐	RecName: Full=2-hydroxyacyl-CoA lyase; AltName: Full=2-hydroxyphytanoyl-CoA lyase; Short=2	174	174	81%	8e-46	28%	Q9LF46.1
☐	RecName: Full=Sulfoacetaldehyde acetyltransferase	172	172	79%	8e-45	26%	Q84H41.3
☐	RecName: Full=Probable sulfoacetaldehyde acetyltransferase	172	172	79%	9e-45	26%	Q92UW6.1
☐	RecName: Full=Putative acetolactate synthase large subunit IlvB2; Short=ALS; AltName: Full=Ac	169	169	81%	6e-44	27%	O06335.1
☐	RecName: Full=Cyclohexane-1,2-dione hydrolase	169	169	85%	7e-44	26%	P0CH62.1
☐	RecName: Full=2-hydroxyacyl-CoA lyase 1; AltName: Full=2-hydroxyphytanoyl-CoA lyase; Short	162	162	82%	2e-41	26%	Q8CHM7.1
☐	RecName: Full=2-hydroxyacyl-CoA lyase 1; AltName: Full=2-hydroxyphytanoyl-CoA lyase; Short	160	160	82%	1e-40	26%	Q9QXE0.2
☐	RecName: Full=Pyruvate oxidase; AltName: Full=Pyruvic oxidase; Short=POX	160	160	79%	1e-40	27%	Q54970.2
☐	RecName: Full=Pyruvate oxidase; AltName: Full=Pyruvic oxidase; Short=POX	160	160	81%	1e-40	26%	P37063.3
☐	RecName: Full=Acetolactate synthase, catabolic; Short=ALS	157	157	83%	6e-40	27%	Q04524.1
☐	RecName: Full=Uncharacterized protein MJ0663	155	155	82%	9e-40	26%	Q58077.1
☐	RecName: Full=Probable 2-ketoarginine decarboxylase AruI; AltName: Full=2-oxo-5-guanidinope	156	156	72%	1e-39	30%	Q9HUI8.1
☐	RecName: Full=2-hydroxyacyl-CoA lyase 1; AltName: Full=2-hydroxyphytanoyl-CoA lyase; Short	155	155	71%	3e-39	27%	Q9UJ83.2
☐	RecName: Full=Sulfoacetaldehyde acetyltransferase	154	154	79%	2e-38	25%	D5AKX8.1
☐	RecName: Full=N(2)-(2-carboxyethyl)arginine synthase; Short=CEA synthetase; Short=CEAS	149	149	76%	6e-37	27%	Q9LCV9.1
☐	RecName: Full=Probable 2-hydroxyacyl-CoA lyase 1; AltName: Full=2-hydroxyphytanoyl-CoA lya	144	144	64%	4e-35	26%	Q54DA9.1
☐	PUTATIVE PSEUDOGENE: RecName: Full=Putative uncharacterized protein HI_0737	134	176	34%	3e-34	52%	O05031.1
☐	RecName: Full=2-hydroxyacyl-CoA lyase; AltName: Full=2-hydroxyphytanoyl-CoA lyase; Short=2	140	140	76%	5e-34	26%	Q0JMH0.3
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase	140	140	64%	1e-33	26%	Q81QB5.1
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase	139	139	64%	2e-33	26%	B7JPM3.1
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase	139	139	64%	2e-33	26%	Q6HIK2.1
☐	RecName: Full=Acetolactate synthase-like protein; AltName: Full=IlvB-like protein	138	138	70%	5e-33	28%	Q6NV04.1
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase 2; Short=THcHDO hydrola	137	137	77%	9e-33	25%	Q4V1F5.1
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase 1; Short=THcHDO hydrola	137	137	64%	1e-32	26%	Q63B73.1
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase	135	135	75%	3e-32	26%	A4IPB6.1
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase	135	135	64%	6e-32	26%	A0REB6.1
☐	RecName: Full=Probable acetolactate synthase; AltName: Full=ALS; AltName: Full=Acetohydrox	133	133	72%	1e-31	27%	P66947.1
☐	RecName: Full=Acetolactate synthase-like protein; AltName: Full=IlvB-like protein	132	132	70%	3e-31	27%	O61856.2
☐	RecName: Full=Oxalyl-CoA decarboxylase	130	130	70%	1e-30	27%	P0AFI1.1
☐	RecName: Full=Oxalyl-CoA decarboxylase	129	129	75%	3e-30	26%	P40149.1
☐	RecName: Full=Acetolactate synthase-like protein; AltName: Full=IlvB-like protein	127	127	74%	3e-29	27%	Q6DDK5.1
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase	126	126	80%	3e-29	24%	Q5WKY8.1
☐	RecName: Full=Acetolactate synthase-like protein; AltName: Full=IlvB-like protein	126	126	70%	5e-29	26%	A6QQT9.2
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase	125	125	77%	5e-29	25%	P42415.2
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase	123	123	64%	3e-28	24%	Q0TUZ2.1
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase	123	123	64%	3e-28	24%	Q8XP76.1
☐	RecName: Full=Acetolactate synthase-like protein; AltName: Full=IlvB-like protein	123	123	70%	4e-28	25%	A1L0T0.2
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase	122	122	80%	7e-28	24%	Q9KAG9.1
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase	119	119	82%	7e-27	25%	Q8Y9Y1.1
☐	RecName: Full=Benzaldehyde lyase; AltName: Full=Benzoin aldolase; Short=BL; Short=BZL	118	118	64%	8e-27	26%	P51853.1
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase	118	118	77%	1e-26	24%	Q723S8.2

☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolas	118	118	80%	2e-26	24%	Q898E8.2
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolas	117	117	77%	5e-26	25%	Q65D03.1
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolas	115	115	64%	1e-25	25%	Q5KYR0.1
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolas	115	115	75%	2e-25	24%	A5YBJ6.2
☐	RecName: Full=Acetolactate synthase-like protein; AltName: Full=IlvB-like protein	114	114	70%	2e-25	25%	Q8BU33.1
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolas	114	114	64%	3e-25	24%	B2TJ86.1
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolas	112	112	79%	1e-24	22%	B2V4K0.1
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolas	110	110	77%	5e-24	24%	A7ZAH8.1
☐	RecName: Full=Probable pyruvate decarboxylase C186.09	109	109	72%	8e-24	23%	Q9P7P6.1
☐	RecName: Full=Benzoylformate decarboxylase; Short=BFD; Short=BFDC	107	107	80%	3e-23	24%	P20906.2
☐	RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolas	107	107	77%	4e-23	23%	Q92EQ4.1
☐	RecName: Full=Putative 2-hydroxyacyl-CoA lyase	104	104	81%	2e-22	25%	Q9Y7M1.1
☐	RecName: Full=Uncharacterized 42.6 kDa protein in isoamylase 3'region	100	100	51%	3e-21	26%	P10343.1
☐	RecName: Full=Pyruvate decarboxylase; AltName: Full=8-10 nm cytoplasmic filament-associate	97.4	97.4	73%	7e-20	25%	P33287.1
☐	RecName: Full=Benzoylformate decarboxylase; Short=BFD; Short=BFDC	95.9	95.9	80%	1e-19	24%	Q9HUR2.1

Alignments

Download GenPept Graphics Next Previous Descriptions

RecName: Full=Acetolactate synthase 2, chloroplastic; AltName: Full=ALS II; AltName: Full=Acetohydroxy-acid synthase II; AltName: Full=Acetolactate synthase II; Flags: Precursor

Sequence ID: P09114.1 **Length:** 664 **Number of Matches:** 1

Related Information

Range 1: 1 to 664 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
1365 bits(3533)	0.0	Compositional matrix adjust.	664/664(100%)	664/664(100%)	0/664(0%)

```
Query  1    MAAAAAAPSPSFSKTLSSSSSKSSTLLPRSTFPFPHHPHKTTPPPLHLTPTHIHSQRRRF  60
            MAAAAAAPSPSFSKTLSSSSSKSSTLLPRSTFPFPHHPHKTTPPPLHLTPTHIHSQRRRF
Sbjct  1    MAAAAAAPSPSFSKTLSSSSSKSSTLLPRSTFPFPHHPHKTTPPPLHLTPTHIHSQRRRF  60

Query  61   TISNVISTTQKVSETQKAETFVSRFAPDEPRKGSDVLVEALEREGVTDVFAYPGGASMEI  120
            TISNVISTTQKVSETQKAETFVSRFAPDEPRKGSDVLVEALEREGVTDVFAYPGGASMEI
Sbjct  61   TISNVISTTQKVSETQKAETFVSRFAPDEPRKGSDVLVEALEREGVTDVFAYPGGASMEI  120

Query  121  HQALTRSSIIRNVLPRHEQGGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDS  180
            HQALTRSSIIRNVLPRHEQGGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDS
Sbjct  121  HQALTRSSIIRNVLPRHEQGGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDS  180

Query  181  VPIVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGR  240
            VPIVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGR
Sbjct  181  VPIVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGR  240

Query  241  PGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYV  300
            PGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYV
Sbjct  241  PGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYV  300

Query  301  GGGCSQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDL  360
            GGGCSQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDL
Sbjct  301  GGGCSQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDL  360

Query  361  LLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSIL  420
            LLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSIL
Sbjct  361  LLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSIL  420

Query  421  ESKEGKLKLDFSAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVG  480
            ESKEGKLKLDFSAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVG
Sbjct  421  ESKEGKLKLDFSAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVG  480

Query  481  QHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQ  540
            QHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQ
Sbjct  481  QHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQ  540

Query  541  ELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAE  600
            ELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAE
Sbjct  541  ELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAE  600

Query  601  ACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVITEGDG  660
            ACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVITEGDG
Sbjct  601  ACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVITEGDG  660

Query  661  RSSY  664
            RSSY
Sbjct  661  RSSY  664
```

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RecName: Full=Acetolactate synthase 1, chloroplastic; AltName: Full=ALS I; AltName: Full=Acetohydroxy-acid synthase I; AltName: Full=Acetolactate synthase I; Flags: Precursor

Sequence ID: P09342.1 **Length:** 667 **Number of Matches:** 1

Related Information

Range 1: 2 to 667 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
1328 bits(3436)	0.0	Compositional matrix adjust.	649/666(97%)	655/666(98%)	5/666(0%)

```
Query  4      AAAAPSPS---FSKTLSSSSSKSSTLLPRSTFPFPHHPHKTTPPPLHLTPTHIH--SQRR  58
              AAAAPSPS   FSKTLS SSS SSTLLPRSTFPFPHHPHKTTPPPLHLT THIH  SQRR
Sbjct  2      AAAAPSPSSSAFSKTLSPSSSTSSTLLPRSTFPFPHHPHKTTPPPLHLTHTHIHIHSQRR  61

Query  59     RFTISNVISTTQKVSETQKAETFVSRFAPDEPRKGSDVLVEALEREGVTDVFAYPGGASM  118
              RFTISNVIST QKVS+T+K ETFVSRFAPDEPRKGSDVLVEALEREGVTDVFAYPGGASM
Sbjct  62     RFTISNVISTNQKVSQTEKTETFVSRFAPDEPRKGSDVLVEALEREGVTDVFAYPGGASM  121

Query  119    EIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALL  178
              EIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALL
Sbjct  122    EIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALL  181

Query  179    DSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARS  238
              DSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARS
Sbjct  182    DSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARS  241

Query  239    GRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVL  298
              GRPGP+LIDVPKDIQQQLVIPDWDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVL
Sbjct  242    GRPGPILIDVPKDIQQQLVIPDWDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVL  301

Query  299    YVGGGCSQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSS  358
              YVGGGCSQSSE+LRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSS
Sbjct  302    YVGGGCSQSSEDLRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSS  361

Query  359    DLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNS  418
              DLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNS
Sbjct  362    DLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNS  421

Query  419    ILESKEGKLKLDFSAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTG  478
              ILESKEGKLKLDFSAWRQELT QKVK+PLNFKTFGDAIPPQYAIQVLDELTNG+AIISTG
Sbjct  422    ILESKEGKLKLDFSAWRQELTEQKVKHPLNFKTFGDAIPPQYAIQVLDELTNGNAIISTG  481

Query  479    VGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMN  538
              VGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMN
Sbjct  482    VGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMN  541

Query  539    VQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKF  598
              VQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKF
Sbjct  542    VQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKF  601

Query  599    AEACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVITEG  658
              AEACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVITEG
Sbjct  602    AEACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVITEG  661

Query  659    DGRSSY  664
              DGRSSY
Sbjct  662    DGRSSY  667
```

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RecName: Full=Acetolactate synthase 3, chloroplastic; AltName: Full=ALS III; AltName: Full=Acetohydroxy-acid synthase III; AltName: Full=Acetolactate synthase III; Flags: Precursor

Sequence ID: P27819.1 **Length:** 652 **Number of Matches:** 1

Related Information

Range 1: 2 to 652 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
1063 bits(2749)	0.0	Compositional matrix adjust.	516/662(78%)	574/662(86%)	13/662(1%)

```
Query  5      AAAPSPSFSKTLSSSSSKSSTLLPRSTFPFPHHPHKTTPPPLHLTPTHIHSQRRRFTISN  64
              AAA S S     +  SSKS   + R + PF   P K +        + +H   R   IS
Sbjct  2      AAATSSSPISLTAKPSSKSPLPISRFSLPFSLTPQKPS--------SRLH---RPLAISA  50

Query  65     VISTTQKVS--ETQKAETFVSRFAPDEPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQ  122
              V+++   V+  +T K +TF+SR+APDEPRKG+D+LVEALER+GV  VFAYPGGASMEIHQ
Sbjct  51     VLNSPVNVAPEKTDKIKTFISRYAPDEPRKGADILVEALERQGVETVFAYPGGASMEIHQ  110

Query  123    ALTRSSIIRNVLPRHEQGGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVP  182
              ALTRSS IRNVLPRHEQGGVFAAEGYAR++G PG+CIATSGPGATNLVSGLADA+LDSVP
Sbjct  111    ALTRSSTIRNVLPRHEQGGVFAAEGYARSSGKPGICIATSGPGATNLVSGLADAMLDSVP  170

Query  183    IVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPG  242
              +VAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDV+DIPR+V+EAFFLA SGRPG
Sbjct  171    LVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVDDIPRIVQEAFFLATSGRPG  230

Query  243    PVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGG  302
              PVL+DVPKDIQQQL IP+WDQPMRLPGYMSRLP+ P    L QIVRLISESK+PVLYVGG
Sbjct  231    PVLVDVPKDIQQQLAIPNWDQPMRLPGYMSRLPQPPEVSQLGQIVRLISESKRPVLYVGG  290

Query  303    GCSQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLL  362
              G   SSEEL RFVELTGIPVASTLMGLG++P  DELSL MLGMHGTVYANYAV+ SDLLL
```

```
Sbjct  291  GSLNSSEELGRFVELTGIPVASTLMGLGSYPCNDELSLQMLGMHGTVYANYAVEHSDLLL  350

Query  363  AFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILES  422
            AFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNK PHVS+C D+KLALQG+N +LE+
Sbjct  351  AFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVCGDVKLALQGMNKVLEN  410

Query  423  KEGKLKLDFSAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQH  482
            +  +LKLDF  WR EL+ QK K+PL+FKTFG+AIPPQYAIQVLDELT G AIISTGVGQH
Sbjct  411  RAEELKLDFGVWRSELSEQKQKFPLSFKTFGEAIPPQYAIQVLDELTQGKAIISTGVGQH  470

Query  483  QMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQEL  542
            QMWAAQ+YKYRKPRQWL+S GLGAMGFGLPAAIGA+V  PD +VVDIDGDGSFIMNVQEL
Sbjct  471  QMWAAQFYKYRKPRQWLSSSGLGAMGFGLPAAIGASVANPDAIVVDIDGDGSFIMNVQEL  530

Query  543  ATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEAC  602
            ATI+VENLPVKI+LLNNQHLGMV+QWEDRFYKANRAHTYLG+P+ E EIFPNML+FA AC
Sbjct  531  ATIRVENLPVKILLLNNQHLGMVMQWEDRFYKANRAHTYLGDPARENEIFPNMLQFAGAC  590

Query  603  GVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVITEGDGRS  662
            G+PAARVT +++LR AIQ MLDTPGPYLLDVI PHQEHVLPMIPSGG FKDVITEGDGR+
Sbjct  591  GIPAARVTKKEELREAIQTMLDTPGPYLLDVICPHQEHVLPMIPSGGTFKDVITEGDGRT  650

Query  663  SY  664
             Y
Sbjct  651  KY  652
```

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RecName: Full=Acetolactate synthase 1, chloroplastic; AltName: Full=ALS I; AltName: Full=Acetohydroxy-acid synthase I; AltName: Full=Acetolactate synthase I; Flags: Precursor

Sequence ID: P27818.1 **Length:** 655 **Number of Matches:** 1

Related Information

Range 1: 2 to 655 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
1061 bits(2745)	0.0	Compositional matrix adjust.	516/665(78%)	574/665(86%)	16/665(2%)

```
Query  5    AAAPSPSFSKTLSSSSSKSSTLLPRSTFPFPHHPHKTTPPPLHLTPTHIHSQRRRFTISN  64
            AAA S S     +  SSKS   +  R + PF   P K +        + +H   R   IS 
Sbjct  2    AAATSSSPISLTAKPSSKSPLPISRFSLPFSLTPQKDS--------SRLH---RPLAISA  50

Query  65   VISTTQKVS-----ETQKAETFVSRFAPDEPRKGSDVLVEALEREGVTDVFAYPGGASME  119
            V+++   V+     +T K +TFVSR+APDEPRKG+D+LVEALER+GV  VFAYPGGASME
Sbjct  51   VLNSPVNVAPPSPEKTDKNKTFVSRYAPDEPRKGADILVEALERQGVETVFAYPGGASME  110

Query  120  IHQALTRSSIIRNVLPRHEQGGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLD  179
            IHQALTRSS IRNVLPRHEQGGVFAAEGYAR++G PG+CIATSGPGATNLVSGLADA+LD
Sbjct  111  IHQALTRSSTIRNVLPRHEQGGVFAAEGYARSSGKPGICIATSGPGATNLVSGLADAMLD  170

Query  180  SVPIVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSG  239
            SVP+VAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDV+DIPR+V+EAFFLA SG
Sbjct  171  SVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVDDIPRIVQEAFFLATSG  230

Query  240  RPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLY  299
            RPGPVL+DVPKDIQQQL IP+WDQPMRLPGYMSRLP+ P    L QIVRLISESK+PVLY
Sbjct  231  RPGPVLVDVPKDIQQQLAIPNWDQPMRLPGYMSRLPQPPEVSQLGQIVRLISESKRPVLY  290

Query  300  VGGGCSQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSD  359
            VGGG   SSEEL RFVELTGIPVASTLMGLG++P  DELSL MLGMHGTVYANYAV+ SD
Sbjct  291  VGGGSLNSSEELGRFVELTGIPVASTLMGLGSYPCNDELSLQMLGMHGTVYANYAVEHSD  350

Query  360  LLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSI  419
            LLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNK PHVS+C D+KLALQG+N +
Sbjct  351  LLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVCGDVKLALQGMNKV  410

Query  420  LESKEGKLKLDFSAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGV  479
            LE++  +LKLDF  WR EL+ QK K+PL+FKTFG+AIPPQYAIQ+LDELT G AIISTGV
Sbjct  411  LENRAEELKLDFGVWRSELSEQKQKFPLSFKTFGEAIPPQYAIQILDELTEGKAIISTGV  470

Query  480  GQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNV  539
            GQHQMWAAQ+YKYRKPRQWL+S GLGAMGFGLPAAIGA+V  PD +VVDIDGDGSFIMNV
Sbjct  471  GQHQMWAAQFYKYRKPRQWLSSSGLGAMGFGLPAAIGASVANPDAIVVDIDGDGSFIMNV  530

Query  540  QELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFA  599
            QELATI+VENLPVKI+LLNNQHLGMV+QWEDRFYKANRAHTYLG+P+ E EIFPNML+FA
Sbjct  531  QELATIRVENLPVKILLLNNQHLGMVMQWEDRFYKANRAHTYLGDPARENEIFPNMLQFA  590

Query  600  EACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVITEGD  659
             ACG+PAARVT +++LR AIQ MLDTPGPYLLDVI PHQEHVLPMIPSGG FKDVITEGD
Sbjct  591  GACGIPAARVTKKEELREAIQTMLDTPGPYLLDVICPHQEHVLPMIPSGGTFKDVITEGD  650

Query  660  GRSSY  664
            GR+ Y
Sbjct  651  GRTKY  655
```

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RecName: Full=Acetolactate synthase, chloroplastic; Short=AtALS; AltName: Full=Acetohydroxy-acid synthase; AltName: Full=Protein CHLORSULFURON RESISTANT 1; Flags: Precursor

Sequence ID: P17597.1 **Length:** 670 **Number of Matches:** 1

Related Information

Range 1: 85 to 670 GenPept Graphics Next Match Previous Match

Gene - associated gene details

Score	Expect	Method	Identities	Positives	Gaps
1045 bits(2703)	0.0	Compositional matrix adjust.	493/586(84%)	539/586(91%)	0/586(0%)

```
Query  79    ETFVSRFAPDEPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHE  138
             ETF+SRFAPD+PRKG+D+LVEALER+GV  VFAYPGGASMEIHQALTRSS IRNVLPRHE
Sbjct  85    ETFISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHE  144

Query  139   QGGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTD  198
             QGGVFAAEGYAR++G PG+CIATSGPGATNLVSGLADALLDSVP+VAITGQVPRRMIGTD
Sbjct  145   QGGVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTD  204

Query  199   AFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVI  258
             AFQETPIVEVTRSITKHNYLVMDVEDIPR++ EAFFLA SGRPGPVL+DVPKDIQQQL I
Sbjct  205   AFQETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAI  264

Query  259   PDWDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFVELT  318
             P+W+Q MRLPGYMSR+PK P +  LEQIVRLISESKKPVLYVGGGC  SS+EL RFVELT
Sbjct  265   PNWEQAMRLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELT  324

Query  319   GIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEA  378
             GIPVASTLMGLG++P  DELSL MLGMHGTVYANYAV+ SDLLLAFGVRFDDRVTGKLEA
Sbjct  325   GIPVASTLMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTGKLEA  384

Query  379   FASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQEL  438
             FASRAKIVHIDIDSAEIGKNK PHVS+C D+KLALQG+N +LE++  +LKLDF  WR EL
Sbjct  385   FASRAKIVHIDIDSAEIGKNKTPHVSVCGDVKLALQGMNKVLENRAEELKLDFGVWRNEL  444

Query  439   TVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQW  498
              VQK K+PL+FKTFG+AIPPQYAI+VLDELT+G AIISTGVGQHQMWAAQ+Y Y+KPRQW
Sbjct  445   NVQKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQW  504

Query  499   LTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLN  558
             L+SGGLGAMGFGLPAAIGA+V  PD +VVDIDGDGSFIMNVQELATI+VENLPVK++LLN
Sbjct  505   LSSGGLGAMGFGLPAAIGASVANPDAIVVDIDGDGSFIMNVQELATIRVENLPVKVLLLN  564

Query  559   NQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAA  618
             NQHLGMV+QWEDRFYKANRAHT+LG+P+ E EIFPNML FA ACG+PAARVT + DLR A
Sbjct  565   NQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREA  624

Query  619   IQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVITEGDGRSSY  664
             IQ MLDTPGPYLLDVI PHQEHVLPMIPSGG F DVITEGDGR  Y
Sbjct  625   IQTMLDTPGPYLLDVICPHQEHVLPMIPSGGTFNDVITEGDGRIKY  670
```

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RecName: Full=Acetolactate synthase 2, chloroplastic; AltName: Full=ALS II; AltName: Full=Acetohydroxy-acid synthase II; AltName: Full=Acetolactate synthase II; Flags: Precursor

Sequence ID: P14874.1 **Length:** 637 **Number of Matches:** 1

Related Information

Range 1: 5 to 636 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
961 bits(2483)	0.0	Compositional matrix adjust.	462/652(71%)	541/652(82%)	27/652(4%)

```
Query  11    SFSKTLSSSSSKSSTL-LPRSTFPFPHHPHKTTPPPLHLTPTHIHSQRRRFTISNVISTT  69
             SF  T+ SS +K+S   LP S    P  P                  RRR T  +V + +
Sbjct  5     SFFGTIPSSPTKASVFSLPVSVTTLPSFP------------------RRRATRVSVSANS  46

Query  70    QK-----VSETQKAETFVSRFAPDEPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQAL  124
             +K      S  +   TF S++AP+ PR G+D+LVEALER+GV  VFAYPGGASMEIHQAL
Sbjct  47    KKDQDRTASRRENPSTFSSKYAPNVPRSGADILVEALERQGVDVVFAYPGGASMEIHQAL  106

Query  125   TRSSIIRNVLPRHEQGGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIV  184
             TRS+ IRNVLPRHEQGG+FAAEGYAR++G PG+CIATSGPGA NLVSGLADAL DSVP++
Sbjct  107   TRSNTIRNVLPRHEQGGIFAAEGYARSSGKPGICIATSGPGAMNLVSGLADALFDSVPLI  166

Query  185   AITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPV  244
             AITGQVPRRMIGT AFQETP+VEVTR+ITKHNYLVM+V+DIPR+VREAFFLA S RPGPV
Sbjct  167   AITGQVPRRMIGTMAFQETPVVEVTRTITKHNYLVMEVDDIPRIVREAFFLATSVRPGPV  226

Query  245   LIDVPKDIQQQLVIPDWDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC  304
             LIDVPKD+QQQ  IP+W+QPMRLP YMS +PK P    LEQI+RL+SESK+PVLYVGGGC
Sbjct  227   LIDVPKDVQQQFAIPNWEQPMRLPLYMSTMPKPPKVSHLEQILRLVSESKRPVLYVGGGC  286

Query  305   SQSSEELRRFVELTGIPVASTLMGLGAFPTGD-ELSLSMLGMHGTVYANYAVDSSDLLLA  363
               SSEELRRFVELTGIPVAST MGLG++P  D E SL MLGMHGTVYANYAV+ SDLLLA
Sbjct  287   LNSSEELRRFVELTGIPVASTFMGLGSYPCDDEEFSLQMLGMHGTVYANYAVEYSDLLLA  346

Query  364   FGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESK  423
             FGVRFDDRVTGKLEAFASRAKIVHIDIDS EIGKNK PHVS+C D++LALQG+N +LE++
Sbjct  347   FGVRFDDRVTGKLEAFASRAKIVHIDIDSTEIGKNKTPHVSVCCDVQLALQGMNEVLENR  406

Query  424   EGKLKLDFSAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQ  483
               +  LDF  WR EL  Q++K+PL +KTFG+ IPPQYAIQ+LDELT+G AII+TGVGQHQ
Sbjct  407   --RDVLDFGEWRCELNEQRLKFPLRYKTFGEEIPPQYAIQLLDELTDGKAIITTGVGQHQ  464

Query  484   MWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELA  543
             MWAAQ+Y+++KPRQWL+SGGLGAMGFGLPAA+GAA+  P  VVVDIDGDGSFIMN+QELA
Sbjct  465   MWAAQFYRFKKPRQWLSSGGLGAMGFGLPAAMGAAIANPGAVVVDIDGDGSFIMNIQELA  524

Query  544   TIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACG  603
             TI+VENLPVK++L+NNQHLGMV+QWED FY ANRA ++LG+P+N   +FP+ML FA +CG
Sbjct  525   TIRVENLPVKVLLINNQHLGMVLQWEDHFYAANRADSFLGDPANPEAVFPDMLLFAASCG  584

Query  604   VPAARVTHRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVI  655
             +PAARVT R+DLR AIQ MLDTPGP+LLDV+ PHQ+HVLP+IPSGG FKD+I
```

```
Sbjct  585   IPAARVTRREDLREAIQTMLDTPGPFLLDVVCPHQDHVLPLIPSGGTFKDII  636
```

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RecName: Full=Acetolactate synthase 1, chloroplastic; AltName: Full=Acetohydroxy-acid synthase 1; Flags: Precursor

Sequence ID: Q6K2E8.1 **Length:** 644 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 65 to 644 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
951 bits(2457)	0.0	Compositional matrix adjust.	446/580(77%)	508/580(87%)	0/580(0%)

```
Query  85    FAPDEPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFA  144
             + P EPRKG+D+LVEALER GV+DVFAYPGGASMEIHQALTRS +I N L RHEQG  FA
Sbjct  65    WGPAEPRKGADILVEALERCGVSDVFAYPGGASMEIHQALTRSPVITNHLFRHEQGEAFA  124

Query  145   AEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETP  204
             A GYARA+G  GVC+ATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQETP
Sbjct  125   ASGYARASGRVGVCVATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQETP  184

Query  205   IVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQP  264
             IVEVTRSITKHNYLV+DVEDIPRV++EAFFLA SGRPGPVL+D+PKDIQQQ+ +P WD 
Sbjct  185   IVEVTRSITKHNYLVLDVEDIPRVIQEAFFLASSGRPGPVLVDIPKDIQQQMAVPVWDTS  244

Query  265   MRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFVELTGIPVAS  324
             M LPGY++RLPK P   LLEQ++RL+ ES++P+LYVGGGCS S +ELR FVELTGIPV +
Sbjct  245   MNLPGYIARLPKPPATELLEQVLRLVGESRRPILYVGGGCSASGDELRWFVELTGIPVTT  304

Query  325   TLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAK  384
             TLMGLG FP+ D LSL MLGMHGTVYANYAVD +DLLLAFGVRFDDRVTGK+EAFASRAK
Sbjct  305   TLMGLGNFPSDDPLSLRMLGMHGTVYANYAVDKADLLLAFGVRFDDRVTGKIEAFASRAK  364

Query  385   IVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVK  444
             IVHIDID AEIGKNKQPHVSICAD+KLALQGLN++L+    K   DFSAW  EL  QK +
Sbjct  365   IVHIDIDPAEIGKNKQPHVSICADVKLALQGLNALLQQSTTKTSSDFSAWHNELDQQKRE  424

Query  445   YPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGL  504
             +PL +KTFG+ IPPQYAIQVLDELT G AII+TGVGQHQMWAAQYY Y++PRQWL+S GL
Sbjct  425   FPLGYKTFGEEIPPQYAIQVLDELTKGEAIIATGVGQHQMWAAQYYTYKRPRQWLSSAGL  484

Query  505   GAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGM  564
             GAMGFGLPAA GA+V  P   VVDIDGDGSF+MN+QELA I++ENLPVK+M+LNNQHLGM
Sbjct  485   GAMGFGLPAAAGASVANPGVTVVDIDGDGSFLMNIQELALIRIENLPVKVMVLNNQHLGM  544

Query  565   VVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQKMLD  624
             VVQWEDRFYKANRAHTYLGNP  E+EI+P+ +  A+   +PA RVT + ++RAAI+KML+
Sbjct  545   VVQWEDRFYKANRAHTYLGNPECESEIYPDFVTIAKGFNIPAVRVTKKSEVRAAIKKMLE  604

Query  625   TPGPYLLDVIVPHQEHVLPMIPSGGAFKDVITEGDGRSSY  664
             TPGPYLLD+IVPHQEHVLPMIPSGGAFKD+I +GDGR+ Y
Sbjct  605   TPGPYLLDIIVPHQEHVLPMIPSGGAFKDMILDGDGRTVY  644
```

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RecName: Full=Acetolactate synthase 1, chloroplastic; AltName: Full=Acetohydroxy-acid synthase 1; Flags: Precursor

Sequence ID: Q41768.1 **Length:** 638 **Number of Matches:** 1

Related Information

Range 1: 26 to 638 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
942 bits(2435)	0.0	Compositional matrix adjust.	446/613(73%)	513/613(83%)	0/613(0%)

```
Query  52    HIHSQRRRFTISNVISTTQKVSETQKAETFVSRFAPDEPRKGSDVLVEALEREGVTDVFA  111
             H+ + RR        S            T +  + P +PRKG+D+LVE+LER GV DVFA
Sbjct  26    HLLATRRALAAPIRCSAASPAMPMAPPATPLRPWGPTDPRKGADILVESLERCGVRDVFA  85

Query  112   YPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATGFPGVCIATSGPGATNLVS  171
             YPGGASMEIHQALTRS +I N L RHEQG  FAA GYAR++G  GVCIATSGPGATNLVS
Sbjct  86    YPGGASMEIHQALTRSPVIANHLFRHEQGEAFAASGYARSSGRVGVCIATSGPGATNLVS  145

Query  172   GLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVRE  231
              LADALLDSVP+VAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLV+DV+DIPRVV+E
Sbjct  146   ALADALLDSVPMVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVLDVDDIPRVVQE  205

Query  232   AFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRLPKLPNEMLLEQIVRLIS  291
             AFFLA SGRPGPVL+D+PKDIQQQ+ +P WD+PM LPGY++RLPK P   LLEQ++RL+ 
Sbjct  206   AFFLASSGRPGPVLVDIPKDIQQQMAVPVWDKPMSLPGYIARLPKPPATELLEQVLRLVG  265

Query  292   ESKKPVLYVGGGCSQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYA  351
             ES++PVLYVGGGC+ S EELRRFVELTGIPV +TLMGLG FP+ D LSL MLGMHGTVYA
Sbjct  266   ESRRPVLYVGGGCAASGEELRRFVELTGIPVTTTLMGLGNFPSDDPLSLRMLGMHGTVYA  325

Query  352   NYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKL  411
             NYAVD +DLLLA GVRFDDRVTGK+EAFASRAKIVH+DID AEIGKNKQPHVSICAD+KL
Sbjct  326   NYAVDKADLLLALGVRFDDRVTGKIEAFASRAKIVHVDIDPAEIGKNKQPHVSICADVKL  385

Query  412   ALQGLNSILESKEGKLKLDFSAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNG  471
             ALQG+N++LE    K   DF +W  EL  QK ++PL +KT  + I PQYAIQVLDELT G
Sbjct  386   ALQGMNALLEGSTSKKSFDFGSWNDELDQQKREFPLGYKTSNEEIQPQYAIQVLDELTKG  445

Query  472   SAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDG  531
              AII TGVGQHQMWAAQYY Y++PRQWL+S GLGAMGFGLPAA GA+V  P   VVDIDG
Sbjct  446   EAIIGTGVGQHQMWAAQYYTYKRPRQWLSSAGLGAMGFGLPAAAGASVANPGVTVVDIDG  505
```

```
Query  532  DGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEI  591
            DGSF+MNVQELA I++ENLPVK+ +LNNQHLGMVVQWEDRFYKANRAHTYLGNP NE+EI
Sbjct  506  DGSFLMNVQELAMIRIENLPVKVFVLNNQHLGMVVQWEDRFYKANRAHTYLGNPENESEI  565

Query  592  FPNMLKFAEACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAF  651
            +P+ +  A+   +PA RVT ++++RAAI+KML+TPGPYLLD+IVPHQEHVLPMIPSGGAF
Sbjct  566  YPDFVTIAKGFNIPAVRVTKKNEVRAAIKKMLETPGPYLLDIIVPHQEHVLPMIPSGGAF  625

Query  652  KDVITEGDGRSSY  664
            KD+I +GDGR+ Y
Sbjct  626  KDMILDGDGRTVY  638
```

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RecName: Full=Acetolactate synthase 2, chloroplastic; AltName: Full=Acetohydroxy-acid synthase 2; Flags: Precursor

Sequence ID: Q41769.1 **Length:** 638 **Number of Matches:** 1

Related Information

Range 1: 59 to 638 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
922 bits(2384)	0.0	Compositional matrix adjust.	439/580(76%)	500/580(86%)	0/580(0%)

```
Query  85   FAPDEPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFA  144
            + P+EPRKGSD+LVEALER GV DVFAYPGGASMEIHQALTRS +I N L RHEQG  FA
Sbjct  59   WGPNEPRKGSDILVEALERCGVRDVFAYPGGASMEIHQALTRSPVIANHLFRHEQGEAFA  118

Query  145  AEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETP  204
            A  YAR++G  GVCIATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQETP
Sbjct  119  ASAYARSSGRVGVCIATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQETP  178

Query  205  IVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQP  264
            IVEVTRSITKHNYLV+DV+DIPRVV+EAFFLA SGRPGPVL+D+PKDIQQQ+ +P WD P
Sbjct  179  IVEVTRSITKHNYLVLDVDDIPRVVQEAFFLASSGRPGPVLVDIPKDIQQQMAVPAWDTP  238

Query  265  MRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFVELTGIPVAS  324
            M LPGY++RLPK P    LEQ++RL+ ES++PVLYVGGGC+ S EEL RFVELTGIPV +
Sbjct  239  MSLPGYIARLPKPPATEFLEQVLRLVGESRRPVLYVGGGCAASGEELCRFVELTGIPVTT  298

Query  325  TLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAK  384
            TLMGLG FP+ D LSL MLGMHGTVYANYAVD +DLLLAFGVRFDDRVTGK+EAFA RAK
Sbjct  299  TLMGLGNFPSDDPLSLRMLGMHGTVYANYAVDKADLLLAFGVRFDDRVTGKIEAFAGRAK  358

Query  385  IVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVK  444
            IVHIDID AEIGKNKQPHVSICAD+KLALQG+N++LE    K   DF +W  EL  QK +
Sbjct  359  IVHIDIDPAEIGKNKQPHVSICADVKLALQGMNTLLEGSTSKKSFDFGSWHDELDQQKRE  418

Query  445  YPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGL  504
            +PL +K F + I PQYAIQVLDELT G AII+TGVGQHQMWAAQYY Y++PRQWL+S GL
Sbjct  419  FPLGYKIFNEEIQPQYAIQVLDELTKGEAIIATGVGQHQMWAAQYYTYKRPRQWLSSAGL  478

Query  505  GAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGM  564
            GAMGFGLPAA GAAV  P   VVDIDGDGSF+MN+QELA I++ENLPVK+ +LNNQHLGM
Sbjct  479  GAMGFGLPAAAGAAVANPGVTVVDIDGDGSFLMNIQELAMIRIENLPVKVFVLNNQHLGM  538

Query  565  VVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQKMLD  624
            VVQWEDRFYKANRAHT+LGNP NE+EI+P+ +  A+   +PA RVT + ++ AAI+KML+
Sbjct  539  VVQWEDRFYKANRAHTFLGNPENESEIYPDFVAIAKGFNIPAVRVTKKSEVHAAIKKMLE  598

Query  625  TPGPYLLDVIVPHQEHVLPMIPSGGAFKDVITEGDGRSSY  664
             PGPYLLD+IVPHQEHVLPMIPSGGAFKD+I +GDGR+ Y
Sbjct  599  APGPYLLDIIVPHQEHVLPMIPSGGAFKDMILDGDGRTVY  638
```

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RecName: Full=Probable acetolactate synthase 2, chloroplastic; AltName: Full=Acetohydroxy-acid synthase 2; Flags: Precursor

Sequence ID: Q7XKQ8.2 **Length:** 663 **Number of Matches:** 1

Related Information

Range 1: 80 to 663 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
901 bits(2329)	0.0	Compositional matrix adjust.	427/584(73%)	504/584(86%)	5/584(0%)

```
Query  86   APDEPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAA  145
            AP   RKG+D++VEALER GV DVF YPGGASMEIHQALTRS +IRN L RHEQG  FAA
Sbjct  80   APMGQRKGADIVVEALERCGVRDVFEYPGGASMEIHQALTRSPVIRNHLLRHEQGEAFAA  139

Query  146  EGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPI  205
             GYAR++G PGVC+ATSGPGATNLVS LADA LDSVP+VAITGQ PRRMIGTDAFQETPI
Sbjct  140  SGYARSSGRPGVCVATSGPGATNLVSALADAHLDSVPLVAITGQAPRRMIGTDAFQETPI  199

Query  206  VEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPM  265
            VE TRSITKHNYL++DV+DIPRV+ EAFFLA +GRPGPVL+D+PKDIQQQ+ +P WD PM
Sbjct  200  VEFTRSITKHNYLILDVDDIPRVINEAFFLASTGRPGPVLVDIPKDIQQQMAVPSWDAPM  259

Query  266  RLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFVELTGIPVAST  325
            RLPGY+SRLPK P   LL++++RL+ ++++PVLYVGGGCS S  ELRRFVELTGIPV +T
Sbjct  260  RLPGYISRLPKPPANLLDEVIRLVGDAERPVLYVGGGCSASGYELRRFVELTGIPVTTT  319

Query  326  LMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKI  385
            LMG+G FP+ D LSL MLGMHGTVYANYAVD++DLLLA GVRFDDRVTGK+EAFASRAKI
Sbjct  320  LMGIGNFPSDDPLSLRMLGMHGTVYANYAVDNADLLLALGVRFDDRVTGKVEAFASRAKI  379
```

```
Query  386  VHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKE---GKLKLDFSAWRQELTVQK  442
            VH+DID +E+GKNKQPHVSICAD+KLALQG+N++LE +     +  LDFSAWR EL  +K
Sbjct  380  VHVDIDPSELGKNKQPHVSICADVKLALQGMNAMLEEQSAAAARKNLDFSAWRSELEKKK  439

Query  443  VKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSG  502
            V++PL ++TFG+ IPPQYAIQVLDE+TNG AI++TGVGQHQMWA Q+Y YR+PRQWL+S
Sbjct  440  VEFPLGYRTFGEEIPPQYAIQVLDEVTNGEAIVATGVGQHQMWATQHYTYRRPRQWLSSA  499

Query  503  GLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHL  562
            GLGAMGFGLPAA GAAV  P   VVDIDGDGS +MN+QELA ++VE+LPVK+M+LNNQHL
Sbjct  500  GLGAMGFGLPAAAGAAVANPGATVVDIDGDGSLLMNIQELAMVRVEDLPVKVMVLNNQHL  559

Query  563  GMVVQWEDRFYKANRAHTYLGNPSNE--AEIFPNMLKFAEACGVPAARVTHRDDLRAAIQ  620
            GMVVQWEDRFY ANRAHTYLGNP+     E++P+ +  A   G+PAARVT + ++RAA++
Sbjct  560  GMVVQWEDRFYDANRAHTYLGNPAANGGGEVYPDFVTIAGGFGIPAARVTRKGEVRAAVE  619

Query  621  KMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVITEGDGRSSY  664
            +M+  PGPYLLDV+VPHQEHVLPMIPS GAFKD+I +GDGRSSY
Sbjct  620  EMMAAPGPYLLDVVVPHQEHVLPMIPSNGAFKDIIVDGDGRSSY  663
```

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RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-acid synthase large subunit; Short=ALS

Sequence ID: P42463.1 **Length:** 626 **Number of Matches:** 1

Range 1: 19 to 587 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
510 bits(1314)	4e-173	Compositional matrix adjust.	278/575(48%)	360/575(62%)	10/575(1%)

```
Query  84   RFAPDEPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVF  143
            R A  E   G+  +V +LE      VF  PGGA + ++  L  S+ +R+VL RHEQG
Sbjct  19   RSAAPERMTGAKAIVRSLEELNADIVFGIPGGAVLPVYDPLYSSTKVRHVLVRHEQGAGH  78

Query  144  AAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQET  203
            AA GYA+ TG  GVCIATSGPGATNLV+ +ADA LDSVP+VAITGQV   ++GTDAFQE
Sbjct  79   AATGYAQVTGRVGVCIATSGPGATNLVTPIADANLDSVPMVAITGQVGSGLLGTDAFQEA  138

Query  204  PIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQ  263
             I  +T  +TKHN++V +  DIP+ + EAF LA +GRPGPVL+D+PKD+Q   +   W
Sbjct  139  DIRGITMPVTKHNFMVTNPNDIPQALAEAFHLAITGRPGPVLVDIPKDVQNAELDFVWPP  198

Query  264  PMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIP  321
             + LPGY  R    P+   +EQ V+LI E+KKPVLYVGGG   + + EELR F E TGIP
Sbjct  199  KIDLPGY--RPVSTPHARQIEQAVKLIGEAKKPVLYVGGGVIKADAHEELRAFAEYTGIP  256

Query  322  VASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFAS  381
            V +TLM LG FP   EL + M GMHGTV A  A+  SDLL+A G RFDDRVTG ++ FA
Sbjct  257  VVTTLMALGTFPESHELHMGMPGMHGTVSAVGALQRSDLLIAIGSRFDDRVTGDVDTFAP  316

Query  382  RAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQ  441
             AKI+H DID AEIGK KQ  V I  D +  L  L    ++ + + + D S W   L
Sbjct  317  DAKIIHADIDPAEIGKIKQVEVPIVGDAREVLARLLETTKASKAETE-DISEWVDYLKGL  375

Query  442  KVKYPLNF-KTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLT  500
            K ++P   + +  GD + PQ+ I+ L +     AI   GVGQHQMWAAQ+  + KPR WL
Sbjct  376  KARFPRGYDEQPGDLLAPQFVIETLSKEVGPDAIYCAGVGQHQMWAAQFVDFEKPRTWLN  435

Query  501  SGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQ  560
            SGGLG MG+ +PAA+GA  G PD+ V  IDGDG F M  QEL T  VE  P+KI L+NN
Sbjct  436  SGGLGTMGYAVPAALGAKAGAPDKEVWAIDGDGCFQMTNQELTTAAVEGFPIKIALINNG  495

Query  561  HLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQ  620
            +LGMV QW+  FY+   ++T L    N+ E  P+ +  +E  G  A RVT  +++  AIQ
Sbjct  496  NLGMVRQWQTLFYEGRYSNTKL---RNQGEYMPDFVTLSEGLGCVAIRVTKAEEVLPAIQ  552

Query  621  KMLD-TPGPYLLDVIVPHQEHVLPMIPSGGAFKDV  654
            K  +    P ++D IV     V PM+ +G +  D+
Sbjct  553  KAREINDRPVVIDFIVGEDAQVWPMVSAGSSNSDI  587
```

Related Information

Gene - associated gene details

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RecName: Full=Acetolactate synthase; AltName: Full=ALS; AltName: Full=Acetohydroxy-acid synthase

Sequence ID: P0A623.1 **Length:** 618 **Number of Matches:** 1

See 2 more title(s)

Range 1: 40 to 594 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
502 bits(1293)	4e-170	Compositional matrix adjust.	268/560(48%)	348/560(62%)	9/560(1%)

```
Query  93   GSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARAT  152
            G+  ++ +LE  GV  +F  PGGA + ++  L  S  +R+VL RHEQG   AA GYA  T
Sbjct  40   GAQAVIRSLEELGVDVIFGIPGGAVLPVYDPLFDSKKLRHVLVRHEQGAGHAASGYAHVT  99

Query  153  GFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSI  212
            G  GVC+ATSGPGATNLV+ LADA +DS+P+VAITGQV R +IGTDAFQE  I   +T  I
Sbjct  100  GRVGVCMATSGPGATNLVTPLADAQMDSIPVVAITGQVGRGLIGTDAFQEADISGITMPI  159

Query  213  TKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMS  272
            TKHN+LV   +DIPRV+ EAF +A SGRPG VL+D+PKD+ Q      W   M LPGY
Sbjct  160  TKHNFLVRSGDDIPRVLAEAFHIAASGRPGAVLVDIPKDVLQGQCTFSWPPRMELPGYKP  219
```

Related Information

Gene - associated gene details

Identical Proteins - Identical proteins to P0A623.1

```
Query  273  RLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLG  330
                 P+   + +  +LI+ ++KPVLYVGGG    +++E+LR   ELTGIPV +TLM  G
Sbjct  220  NTK--PHSRQVREAAKLIAAARKPVLYVGGGVIRGEATEQLRELAELTGIPVVTTLMARG  277

Query  331  AFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDI  390
            AFP     +L M GMHGTV A  A+  SDLL+A G RFDDRVTGKL++FA  AK++H DI
Sbjct  278  AFPDSHRQNLGMPGMHGTVAAVAALQRSDLLIALGTRFDDRVTGKLDSFAPEAKVIHADI  337

Query  391  DSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVKYPLNFK  450
            D AEIGKN+   V I  D+K  +  L ++L        ++ + W   L   +  YPL++
Sbjct  338  DPAEIGKNRHADVPIVGDVKAVITELIAMLRHHHIPGTIEMADWWAYLNGVRKTYPLSYG  397

Query  451  TFGD-AIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMGF  509
               D ++ P+Y I+ L E+    A+   GVGQHQMWAAQ+ +Y KPR WL SGGLG MGF
Sbjct  398  PQSDGSLSPEYVIEKLGEIAGPDAVFVAGVGQHQMWAAQFIRYEKPRSWLNSGGLGTMGF  457

Query  510  GLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWE  569
             +PAA+GA +  P   V  IDGDG F M  QELAT  VE +PVK+ L+NN +LGMV QW+
Sbjct  458  AIPAAMGAKIALPGTEVWAIDGDGCFQMTNQELATCAVEGIPVKVALINNGNLGMVRQWQ  517

Query  570  DRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAI-QKMLDTPGP  628
              FY    + T L   S+     P+ +K AEA G    R   +D+    I Q       P
Sbjct  518  SLFYAERYSQTDLATHSHR---IPDFVKLAEALGCVGLRCEREEDVVDVINQARAINDCP  574

Query  629  YLLDVIVPHQEHVLPMIPSG  648
             ++D IV     V PM+ +G
Sbjct  575  VVIDFIVGADAQVWPMVAAG  594
```

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RecName: Full=Acetolactate synthase; AltName: Full=ALS; AltName: Full=Acetohydroxy-acid synthase

Sequence ID: O33112.1 **Length:** 625 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 607 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
501 bits(1291)	1e-169	Compositional matrix adjust.	276/610(45%)	368/610(60%)	11/610(1%)

```
Query  49   TPTHIHSQRRRFTISNVISTTQKVSETQKAETFVSRFAPDEPRKGSDVLVEALEREGVTD  108
            T  H   Q    ++ N +    +   ++ A   + R +P++   G+  ++ +LE   V
Sbjct  5    TKPHARPQGAGNSVPNTVKPATQFP-SKPAVAKLERVSPEQ-LTGAQSVIRSLEELDVEV  62

Query  109  VFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATGFPGVCIATSGPGATN  168
            +F  PGGA + ++  L  S  +R+VL RHEQG   AA GYA  TG  GVC+ATSGPGATN
Sbjct  63   IFGIPGGAVLLVYDPLFYSKKLRHVLVRHEQGAGHAASGYAHVTGKVGVCMATSGPGATN  122

Query  169  LVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRV  228
            LV+ LADA +DSVP+VAITGQV R +IGTDAFQE  I  +T  ITKHN+LV   +DIPRV
Sbjct  123  LVTPLADAQMDSVPVVAITGQVGRSLIGTDAFQEADISGITMPITKHNFLVRAGDDIPRV  182

Query  229  VREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRLPKLPNEMLLEQIVR  288
            + EAF +A SGRPG VL+D+PKD+ Q      W   M LPGY       P+   +    +
Sbjct  183  LAEAFHIASSGRPGAVLVDIPKDVLQGQCKFSWPPKMDLPGYKPNTK--PHNRQIRAAAK  240

Query  289  LISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMH  346
            LI++++KPVLYVGGG    +++E+LR   ELTGIPV STLM  GAFP     +L M GMH
Sbjct  241  LIADARKPVLYVGGGVIRGEATEQLRDLAELTGIPVVSTLMARGAFPDSHHQNLGMPGMH  300

Query  347  GTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSIC  406
            GTV A  A+  SDLL+A G RFDDRVTGKL++FA  AK++H DID AEIGKN+   V I
Sbjct  301  GTVAAVAALQRSDLLIALGTRFDDRVTGKLDSFAPDAKVIHADIDPAEIGKNRHADVPIV  360

Query  407  ADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVKYPLNFKTFGDA-IPPQYAIQVL  465
             D+K  +  L ++L   E    ++ + W   L   +  YPL++    D  + P+Y I+ L
Sbjct  361  GDVKAVIVELIAMLRHYEVPGNIEMTDWWSYLDGVRKTYPLSYSPQSDGTLSPEYVIEKL  420

Query  466  DELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEV  525
             E+    A+   GVGQHQMWAAQ+  Y KPR WL SGGLG MGF +PAA+GA + RP+
Sbjct  421  GEIVGPEAVYVAGVGQHQMWAAQFISYEKPRTWLNSGGLGTMGFAIPAAMGAKIARPEAE  480

Query  526  VVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNP  585
            V  IDGDG F M  QELAT  +E  P+K+ L+NN +LGMV QW+  FY+    + T L
Sbjct  481  VWAIDGDGCFQMTNQELATCAIEGAPIKVALINNGNLGMVRQWQALFYQERYSQTDLATH  540

Query  586  SNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAI-QKMLDTPGPYLLDVIVPHQEHVLPM  644
            S+     P+ +K AEA G    R   +D+    I Q       P ++D IV     V PM
Sbjct  541  SHR---IPDFVKLAEALGCVGLRCECEEDVVDVINQARAINNRPVVIDFIVGADAQVWPM  597

Query  645  IPSGGAFKDV  654
            + +G +  ++
Sbjct  598  VAAGASNDEI  607
```

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RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-acid synthase large subunit; Short=ALS; AltName: Full=Vegetative protein 105; Short=VEG105

Sequence ID: P37251.4 **Length:** 574 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 20 to 570 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
498 bits(1282)	5e-169	Compositional matrix adjust.	259/566(46%)	366/566(64%)	18/566(3%)

```
Query  93   GSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARAT  152
            G+ +L+E+L++E V  +F YPGGA + I+  L  S ++ ++LPRHEQG + AAEGYAR +
Sbjct  20   GALMLIESLKKEKVEMIFGYPGGAVLPIYDKLYNSGLV-HILPRHEQGAIHAAEGYARVS  78

Query  153  GFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSI  212
            G PGV IATSGPGATNLV+GLADA++DS+P+V  TGQV   +IG+DAFQE  I+ +T  +
Sbjct  79   GKPGVVIATSGPGATNLVTGLADAMIDSLPLVVFTGQVATSVIGSDAFQEADILGITMPV  138

Query  213  TKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMS  272
            TKH+Y V   ED+PR+++EAF +A +GRPGPVLID+PKD+        +D  M LPGY
Sbjct  139  TKHSYQVRQPEDLPRIIKEAFHIATTGRPGPVLIDIPKDVATIEGEFSYDHEMNLPGYQP  198

Query  273  RLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLG  330
                 PN + + ++V  +S +KKPV+  G G    ++SEEL+ + E   IPVA TL+GLG
Sbjct  199  TTE--PNYLQIRKLVEAVSSAKKPVILAGAGVLHGKASEELKNYAEQQQIPVAHTLLGLG  256

Query  331  AFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDI  390
             FP    L L M GMHGT  AN A+   DLL++ G RFDDRVTG L+ FA  AKI HIDI
Sbjct  257  GFPADHPLFLGMAGMHGTYTANMALHECDLLISIGARFDDRVTGNLKHFARNAKIAHIDI  316

Query  391  DSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVKYPLNF-  449
            D AEIGK  +  + +  D K+ LQ L      ++GK + D S W+++L   K +YPL +
Sbjct  317  DPAEIGKIMKTQIPVVGDSKIVLQELI----KQDGK-QSDSSEWKKQLAEWKEEYPLWYV  371

Query  450  KTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMGF  509
                +   PQ  I+ + + T G AI++T VGQHQMW+AQ+Y ++K  +W+TSGGLG MGF
Sbjct  372  DNEEEGFKPQKLIEYIHQFTKGEAIVATDVGQHQMWSAQFYPFQKADKWVTSGGLGTMGF  431

Query  510  GLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWE  569
            GLPAAIGA +   D  VV + GDG F M +QEL  I+  NLPVK+++LNN  LGMV QW+
Sbjct  432  GLPAAIGAQLAEKDATVVAVVGDGGFQMTLQELDVIRELNLPVKVVILNNACLGMVRQWQ  491

Query  570  DRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQKMLDTPGPY  629
            + FY+   + +   +        P+ +K +EA G+   R++   + +  +++ L +  P
Sbjct  492  EIFYEERYSESKFASQ-------PDFVKLSEAYGIKGIRISSEAEAKEKLEEALTSREPV  544

Query  630  LLDVIVPHQEHVLPMIPSGGAFKDVI  655
            ++DV V  +E V PM+  G    +++
Sbjct  545  VIDVRVASEEKVFPMVAPGKGLHEMV  570
```

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RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-acid synthase large subunit; Short=ALS

Sequence ID: O78518.1 **Length:** 575 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 12 to 564 GenPept Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
486 bits(1250)	4e-164	Compositional matrix adjust.	263/569(46%)	355/569(62%)	29/569(5%)

```
Query  93   GSDVLVEALEREGVTDVFAYPGGASMEIHQAL---TRSSIIRNVLPRHEQGGVFAAEGYA  149
            G+  L+++L R GV  +F YPGGA + I+  L    +   I ++L RHEQG   A++GYA
Sbjct  12   GAFALIDSLVRHGVKHIFGYPGGAILPIYDELYAWEKEGFIEHILVRHEQGAAHASDGYA  71

Query  150  RATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVT  209
            R+TG  GVC ATSGPGATNLV+G+A A +DSVP+V ITGQV R  IGTDAFQE  I  +T
Sbjct  72   RSTGNVGVCFATSGPGATNLVTGIATAHMDSVPMVIITGQVGRSFIGTDAFQEVDIFGIT  131

Query  210  RSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDI-----QQQLVIPDWDQP  264
              I KH+Y+V + +++ ++V E+FF+A+ GRPGPVLID+PKD+       Q+V P+
Sbjct  132  LPIVKHSYVVRETKEMGKIVAESFFIAKYGRPGPVLIDIPKDVGLEKFDYQIVNPN---N  188

Query  265  MRLPGYMSRLPKLPN--EMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGI  320
            + L G     P L N  +  + Q   LI +S +P+LY+GGG   S S  E+   + L  I
Sbjct  189  INLAG----CPVLKNYDQNRISQAANLIKQSSQPLLYIGGGAVTSNSHNEINELINLVKI  244

Query  321  PVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFA  380
            PVA+TLMG G       LSL MLGMHGTVYANYAV   DLL+A G RFDDRVTGKL+ FA
Sbjct  245  PVATTLMGKGIIDESHPLSLGMLGMHGTVYANYAVSECDLLIALGARFDDRVTGKLDEFA  304

Query  381  SRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTV  440
              A+++H+DID AEIGKN+ P + I  +IK  ++ L   L++          AWR  +
Sbjct  305  CHAQVIHVDIDPAEIGKNRTPQIGIVGEIKDFVRDLIECLKNDINFDSEQSQAWRSRIIR  364

Query  441  QKVKYPLNFKTFGDAIPPQYAI-QVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWL  499
             + +YPL      + + PQ  I ++  E TN  A  +T VGQHQMWAAQ+ K  + R W+
Sbjct  365  WRKEYPLLVPKNINNLSPQEVIHEISTEATN--AYFTTDVGQHQMWAAQFIKTSQKR-WI  421

Query  500  TSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNN  559
            TS GLG MG+GLPAAIG  +  P+E V+ I GD SF MN+QEL T+    LP+KI ++NN
Sbjct  422  TSAGLGTMGYGLPAAIGVQIAHPNEQVICISGDASFQMNIQELGTVSQYGLPIKIFIINN  481

Query  560  QHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAI  619
            +  GMV QW+  FY    +H      SN  +  PN  K AEA G+ + ++  R+DL+  I
Sbjct  482  KWQGMVRQWQQAFYGERYSH------SNMEKGAPNFTKVAEAFGLRSLKIKSRNDLKLRI  535

Query  620  QKMLDTPGPYLLDVIVPHQEHVLPMIPSG  648
            ++ LD  GP L+D+ V   E+  PM+  G
Sbjct  536  KEALDYDGPILVDIQVIADENCYPMVAPG  564
```

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RecName: Full=Acetolactate synthase isozyme 2 large subunit; Short=AHAS-II; AltName: Full=ALS-II; AltName:

Full=Acetohydroxy-acid synthase II large subunit

Sequence ID: P00892.3 **Length:** 548 **Number of Matches:** 1

Related Information

Range 1: 2 to 544 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
483 bits(1244)	1e-163	Compositional matrix adjust.	259/571(45%)	361/571(63%)	35/571(6%)

```
Query  92   KGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARA  151
             G+  +V AL  +GV  VF YPGGA M ++ AL    +  ++L RHEQG   AA GYARA
Sbjct  2    NGAQWVVHALRAQGVNTVFGYPGGAIMPVYDALYDGGV-EHLLCRHEQGAAMAAIGYARA  60

Query  152  TGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRS  211
            TG  GVCIATSGPGATNL++GLADALLDS+P+VAITGQV    IGTDAFQE  ++ ++ +
Sbjct  61   TGKTGVCIATSGPGATNLITGLADALLDSIPVVAITGQVSAPFIGTDAFQEVDVLGLSLA  120

Query  212  ITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYM  271
             TKH++LV  +E++PR++ EAF +A SGRPGPVL+D+PKDI  QL   D +     P +
Sbjct  121  CTKHSFLVQSLEELPRIMAEAFDVACSGRPGPVLVDIPKDI--QLASGDLE-----PWFT  173

Query  272  SRLPKLPNEML-----LEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVAS  324
            +    + NE+      +EQ  +++++++KP+LYVGGG   +Q+   LR F+  T +P
Sbjct  174  T----VENEVTFPHAEVEQARQMLAKAQKPMLYVGGGVGMAQAVPALREFLAATKMPATC  229

Query  325  TLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAK  384
            TL GLGA        L MLGMHGT  AN+AV   DLL+A G RFDDRVTGKL  FA  A
Sbjct  230  TLKGLGAVEADYPYYLGMLGMHGTKAANFAVQECDLLIAVGARFDDRVTGKLNTFAPHAS  289

Query  385  IVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVK  444
            ++H+DID AE+ K +Q HV++  D+   L  L   L   +         W+Q     + +
Sbjct  290  VIHMDIDPAEMNKLRQAHVALQGDLNALLPALQQPLNQYD---------WQQHCAQLRDE  340

Query  445  YPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGL  504
            +   +   GDAI     ++ L +      +++T VGQHQMWAAQ+  + +P  ++TS GL
Sbjct  341  HSWRYDHPGDAIYAPLLLKQLSDRKPADCVVTTDVGQHQMWAAQHIAHTRPENFITSSGL  400

Query  505  GAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGM  564
            G MGFGLPAA+GA V RP++ VV I GDGSF+MNVQEL T+K + LP+KI+LL+NQ LGM
Sbjct  401  GTMGFGLPAAVGAQVARPNDTVVCISGDGSFMMNVQELGTVKRKQLPLKIVLLDNQRLGM  460

Query  565  VVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQKMLD  624
            V QW+  F++   + T L +        P+ L  A A G+    +T +D + AA+  ML+
Sbjct  461  VRQWQQLFFQERYSETTLTDN-------PDFLMLASAFGIHGQHITRKDQVEAALDTMLN  513

Query  625  TPGPYLLDVIVPHQEHVLPMIPSGGAFKDVI  655
            + GPYLL V +   E+V P++P G +  +++
Sbjct  514  SDGPYLLHVSIDELENVWPLVPPGASNSEML  544
```

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RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-acid synthase large subunit; Short=ALS

Sequence ID: Q1XDF6.1 **Length:** 590 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 11 to 572 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
483 bits(1244)	4e-163	Compositional matrix adjust.	254/572(44%)	361/572(63%)	17/572(2%)

```
Query  91   RKGSDVLVEALEREGVTDVFAYPGGASMEIHQ---ALTRSSIIRNVLPRHEQGGVFAAEG  147
            + G+  L++++ R GV  +F YPGGA + I+    A   +S+I+++L RHEQG   AA+
Sbjct  11   KTGAFALLDSIVRHGVKHIFGYPGGAILPIYDELYAWEEASLIKHILVRHEQGAAHAADS  70

Query  148  YARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVE  207
            Y+R+TG  GVC ATSGPGATNLVSG+A A +DSVPI+AITGQV R  IGTDAFQE  I
Sbjct  71   YSRSTGEVGVCFATSGPGATNLVSGIATAHIDSVPILAITGQVGRAFIGTDAFQEVDIFG  130

Query  208  VTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQP--M  265
            +T  I KH+Y+V D  D+ R+V EAFF+ + GRPGPVLIDVPKD+  +       +P  +
Sbjct  131  ITLPIVKHSYVVRDPRDMSRIVAEAFFICKHGRPGPVLIDVPKDVGLEKFNYFSVEPGKV  190

Query  266  RLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVA  323
             +PG          ++L+    ++I +S +P+LY+GGG   S S + ++  V+   IPV
Sbjct  191  NIPGCRPITSLKSRQILMA--AKMIQQSSQPLLYIGGGAIISDSHQIIKELVDFYKIPVT  248

Query  324  STLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRA  383
            +TLMG G F    +  L MLGMHGT YAN+AV   DLL+A G RFDDRVTGKL+ FA  A
Sbjct  249  TTLMGKGIFNEDSDYCLGMLGMHGTAYANFAVSECDLLIALGARFDDRVTGKLDEFACNA  308

Query  384  KIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKV  443
            +++H+DID AE+GKN+ P V+I  D+   +  + ++L++          +W++ +   +
Sbjct  309  QVIHVDIDPAEVGKNRIPQVAIVGDVAEVVSEILNLLKTSFPPYPEQIISWQERINRWRQ  368

Query  444  KYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGG  503
            +YPL       +I PQ  +   ++L   +A  +T VGQHQMW+AQ+ K  K + WL+S G
Sbjct  369  QYPLLVPRKSTSISPQVILVATNKLAQ-NAYFTTDVGQHQMWSAQFLKV-KAKHWLSSAG  426

Query  504  LGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLG  563
            LG MG+GLPAAIGA V  P++VV+ I GD SF MN+QEL TI    LPVKI+++NN+  G
Sbjct  427  LGTMGYGLPAAIGAQVAHPNDVVICISGDSSFQMNMQELGTIAQYQLPVKIIIINNRWQG  486

Query  564  MVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQKML  623
            MV QW+  FY    +H+ +       E  P+  K AEA G+ A  + +R ++++A+Q  +
Sbjct  487  MVRQWQQAFYGERYSHSRM------TEGAPDFQKLAEAFGIKAFTINNRQNMQSALQVAI  540
```

```
Query  624  DTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVI  655
            D PGP LLD  V   E+  PM+  G +   +I
Sbjct  541  DYPGPVLLDCQVTENENCYPMVAPGKSNAQMI  572
```

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RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-acid synthase large subunit; Short=ALS

Sequence ID: P69683.1 **Length:** 590 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Identical proteins to P69683.1

Range 1: 11 to 572 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
481 bits(1239)	3e-162	Compositional matrix adjust.	254/572(44%)	358/572(62%)	17/572(2%)

```
Query  91   RKGSDVLVEALEREGVTDVFAYPGGASMEIHQAL---TRSSIIRNVLPRHEQGGVFAAEG  147
            + G   L++++ R GV  +F YPGGA + I+  L      S+I+N+L RHEQG   AA+
Sbjct  11   KTGRFALLDSIVRHGVIHIFGYPGGAILPIYDELYAWEELSLIKNILVRHEQGASHAADA  70

Query  148  YARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVE  207
            Y+R+TG  GVC ATSGPGATNLVSG+A A +DSVPI+AITGQV R  IGTDAFQE  I
Sbjct  71   YSRSTGKVGVCFATSGPGATNLVSGIATAHIDSVPILAITGQVGRPFIGTDAFQEVDIFG  130

Query  208  VTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQP--M  265
            +T  I KH+Y+V D  D+ R+V EAF++ + GRPGPVLIDVPKD+  +       +P  +
Sbjct  131  ITLPIVKHSYVVRDPRDMSRIVAEAFYICKHGRPGPVLIDVPKDVGLEKFNYFSVEPGQV  190

Query  266  RLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVA  323
            ++PG    L  L +  +L    ++I +S +P+LY+GGG   S +   ++  V+L  IPV
Sbjct  191  KIPG-CRPLSNLKSRQIL-MAAKMIQQSSQPLLYIGGGAIISDAHSIIKELVDLYKIPVT  248

Query  324  STLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRA  383
            +TLMG G F    E  L MLGMHGT YAN+AV   DLL+A G RFDDRVTGKL+ FA  A
Sbjct  249  TTLMGKGIFNEDSEFCLGMLGMHGTAYANFAVSECDLLIALGARFDDRVTGKLDEFACNA  308

Query  384  KIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKV  443
            +++H+DID AE+GKN+ P V+I  D+    +  L ++L++          +W++ +   +
Sbjct  309  QVIHVDIDPAEVGKNRIPQVAIVGDVTEVVTSLLNLLKNNFKPYPEQIISWQERIHRWRQ  368

Query  444  KYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGG  503
            +YPL       +I PQ  +   ++L    A  +T VGQHQMW+AQ+ K  K + W++S G
Sbjct  369  QYPLLVPKKSTSISPQEILVTTNQLAQ-DAYFTTDVGQHQMWSAQFLKV-KSKHWISSAG  426

Query  504  LGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLG  563
            LG MG+GLPAAIGA V  P+E+V+ + GD SF MN+QEL TI    LP+KI+++NN+  G
Sbjct  427  LGTMGYGLPAAIGAQVAHPNELVICVSGDSSFQMNMQELGTIAQYKLPIKIVIINNRWQG  486

Query  564  MVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQKML  623
            MV QW+  FY    +H+ +       E  PN  K AEA G+ A  V +R ++ ++++  +
Sbjct  487  MVRQWQQAFYGERYSHSRM------TEGAPNFQKLAEAFGIKAFTVNNRQNMESSLKDAM  540

Query  624  DTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVI  655
              PGP LLD  V   E+  PM+  G +   +I
Sbjct  541  KYPGPVLLDCQVTENENCYPMVAPGKSNAQMI  572
```

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RecName: Full=Acetolactate synthase; AltName: Full=ALS; AltName: Full=Acetohydroxy-acid synthase

Sequence ID: Q59498.1 **Length:** 621 **Number of Matches:** 1

Related Information

Range 1: 36 to 597 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
479 bits(1232)	8e-161	Compositional matrix adjust.	263/569(46%)	345/569(60%)	11/569(1%)

```
Query  84   RFAPDEPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVF  143
            R  P++   G+  ++ +LE  GV  +F  PGGA + ++  L  S  +R+VL RHEQG
Sbjct  36   RIGPEQ-VTGAQSVIRSLEELGVEVIFGIPGGAVLPVYDPLFDSKKLRHVLVRHEQGAGH  94

Query  144  AAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQET  203
            AA GYA ATG  GVC+ATSGPGATNLV+ LADA +DS+P+VA+TGQV R +IGTDAFQE
Sbjct  95   AASGYAHATGKVGVCMATSGPGATNLVTALADAQMDSIPVVAVTGQVGRTLIGTDAFQEA  154

Query  204  PIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQ  263
             I  +T  ITKHN+LV+   + P V+ EAF +A SGRP    +D+PKD+ Q      W
Sbjct  155  DISGITMPITKHNFLVVRQRN-PAVLAEAFHIAASGRPARCSVDIPKDVLQGQCTFSWPP  213

Query  264  PMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIP  321
             + LPGY  +    P+    + +  +LI+ ++KPVLYVGGG    ++SE+LR   ELTGIP
Sbjct  214  RIHLPGY--KPTTKPHSRQIRERAKLIAAARKPVLYVGGGVIRGEASEQLRELAELTGIP  271

Query  322  VASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFAS  381
            V +TLM  GAFP      L M GMHGTV A  A+  SDLL+A G RFDDRVTGKL+ FA
Sbjct  272  VVTTLMARGAFPDSHRQHLGMPGMHGTVAAVAALQRSDLLIALGTRFDDRVTGKLDTFAP  331

Query  382  RAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQ  441
             AK++H DID AEIGKN+   V I  D+K  +  L  IL        LD + W   L
Sbjct  332  EAKVIHADIDPAEIGKNRHADVPIVGDVKAVIAELVEILRHDGAPGNLDIADWWAYLDDV  391

Query  442  KVKYPLNFKTFGD-AIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLT  500
            +  YPL++    D ++ P+Y I+ L ++    A+   GVG  QMWAAQ+  Y KPR WL
Sbjct  392  QSTYPLSYGPQSDGSLGPEYVIEKLGQIAGPDALYVAGVGHDQMWAAQFISYEKPRTWLN  451
```

```
Query  501  SGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQ  560
            SGG G MGF +PAA+GA +GRP+  V  IDGDG F M  QELAT  VE +P+K+ L+NN
Sbjct  452  SGGQGTMGFAIPAAMGAKMGRPEAEVWAIDGDGCFQMTNQELATCAVEGIPIKVALINNG  511

Query  561  HLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQ  620
            +LGMV QW+  FY+   + T LG+P       P+ +K AEA G    R    +D+   I
Sbjct  512  NLGMVRQWQTLFYEERYSQTDLGHPLAP---HPDFVKLAEALGCVGLRCEREEDVVDVIN  568

Query  621  KMLD-TPGPYLLDVIVPHQEHVLPMIPSG  648
                    P ++  IV     V PM+ +G
Sbjct  569  AARAINDRPVVIAFIVGADAQVWPMVAAG  597
```

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RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-acid synthase large subunit; Short=ALS

Sequence ID: Q7U5G1.1 **Length:** 617 **Number of Matches:** 1

Related Information

Range 1: 5 to 573 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
473 bits(1216)	2e-158	Compositional matrix adjust.	259/580(45%)	360/580(62%)	19/580(3%)

```
Query  77   KAETFVSRFAPDEPR--KGSDVLVEALEREGVTDVFAYPGGASMEIHQAL---TRSSIIR  131
             A T V     + P+   G+  L++AL R GV  +F YPGGA + I+ AL        ++
Sbjct  5    SASTVVGGLDANAPQTISGAAALMDALRRHGVDTIFGYPGGAILPIYDALHIAESEGWVK  64

Query  132  NVLPRHEQGGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVP  191
            ++L RHEQ G  AA+ YARATG  GVC  TSGPGATNLV+G+A A +DSVP+V ITGQVP
Sbjct  65   HILVRHEQAGTHAADAYARATGKVGVCFGTSGPGATNLVTGIATAQMDSVPMVVITGQVP  124

Query  192  RRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKD  251
            R  IGTDAFQET I  +T  I KH+++V D  D+  +V +AF +A SGRPGPVLID+PKD
Sbjct  125  RPAIGTDAFQETDIFGITLPIVKHSWVVRDPADLGSIVAQAFLIAASGRPGPVLIDIPKD  184

Query  252  I-QQQLVIPDWDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSS  308
            + Q+Q      +    +PG   + P+ P +  +   + LI ++++P+LYVGGG   + +
Sbjct  185  VGQEQFNYVPVEPGSVIPGGFHQ-PEPPLDAAVAAALDLIEQAQRPLLYVGGGAISACAH  243

Query  309  EELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRF  368
            + LR   E   +PV +TLMG GAF   D LS+ MLGMHGT YAN+AV   DLL+A G RF
Sbjct  244  DSLRMLAERYQLPVTTTLMGKGAFDENDALSVGMLGMHGTAYANFAVTECDLLIAVGARF  303

Query  369  DDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLK  428
            DDRVTGKL+ FA RA++VH +ID AEIGKN++  V++  D+ L+L  +  I   +  + +
Sbjct  304  DDRVTGKLDTFAPRARVVHFEIDPAEIGKNRKADVAVLGDLGLSLARMVEISLQRTAEPR  363

Query  429  LDFSAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQ  488
               +AW + +   K +YPL       AI PQ  +  + +L    AI++T VGQHQMWAAQ
Sbjct  364  T--AAWLERINTWKDRYPLTIPPAEGAIYPQEVLLAVRDLAP-DAIVTTDVGQHQMWAAQ  420

Query  489  YYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVE  548
            + +   PR W++S GLG MGFG+PAA+GA V  PD  VV I GD S +MN+QEL T+
Sbjct  421  HLR-NGPRGWISSAGLGTMGFGMPAAMGAQVAMPDRQVVCIAGDASILMNIQELGTLAAY  479

Query  549  NLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAAR  608
             LPVK++++NN   GMV QW++ FY    + + + N        P+ +  A + GV   +
Sbjct  480  GLPVKVVIVNNHWQGMVRQWQESFYDERYSASDMLNG------MPDFIALARSFGVDGVK  533

Query  609  VTHRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSG  648
            +T R+ L   +   L +P P ++DV V   E+  PM+P G
Sbjct  534  ITDRELLHRDLAAALQSPTPTMIDVHVRRGENCYPMVPPG  573
```

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RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-acid synthase large subunit; Short=ALS

Sequence ID: O19929.1 **Length:** 585 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 10 to 567 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
470 bits(1210)	4e-158	Compositional matrix adjust.	259/568(46%)	359/568(63%)	20/568(3%)

```
Query  91   RKGSDVLVEALEREGVTDVFAYPGGASMEIHQAL---TRSSIIRNVLPRHEQGGVFAAEG  147
            + G+  L++ L +  V ++F YPGGA + I+  L    +  +I++ L RHEQ    AA+
Sbjct  10   KTGAFALIDMLVKHKVKNIFGYPGGAILPIYDELYHWEKKKLIKHYLVRHEQSAAHAADA  69

Query  148  YARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVE  207
            YARAT   GVC+ATSGPGATNLV+G+A A +DSVPI+AITGQV R  IGTDAFQE  I
Sbjct  70   YARATNEVGVCLATSGPGATNLVTGIATAQMDSVPIIAITGQVSRAFIGTDAFQEVDIFG  129

Query  208  VTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQ-QQLVIPDWDQPM-  265
            +T  I KH+++V D  DI  +V EAF++++ GRPG VLIDVPKD+  ++    D+D
Sbjct  130  ITLPIVKHSFVVRDPRDISTIVSEAFYISKHGRPGAVLIDVPKDVGLEEFNYHDYDSIRD  189

Query  266  RLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVA  323
              P    R    P+   +E+  +++ ESK+P+LYVGGG   S++  E+        IPV
Sbjct  190  HKPITKYRPIYGPSIRQIEKFKKMLLESKQPILYVGGGAVMSRAQHEIEELASFIKIPVT  249

Query  324  STLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRA  383
            +TLMG G+F   + L L MLGMHGT YAN+AV   DLL+A G RFDDRVTGKL+ FA  A
```

```
Sbjct  250  TTLMGKGSFNEYNPLYLGMLGMHGTAYANFAVSECDLLIALGARFDDRVTGKLDEFACNA  309

Query  384  KIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFS---AWRQELTV  440
            +++H+DID AEIGKN+ P ++I +DIK+ L+ L S +  KEG   +D +   AW   +
Sbjct  310  QVIHVDIDPAEIGKNRIPQLAIISDIKIVLKELLSSM--KEGTNNMDKNQTQAWLHRIHK  367

Query  441  QKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLT  500
             K +YPL+       + PQ  I  + ++    A  +T VGQHQMWAAQ+ K  + + WL+
Sbjct  368  WKKEYPLSIPHDSKLLYPQEVINEISQIAQ-KAFFATDVGQHQMWAAQFLKVEQGK-WLS  425

Query  501  SGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQ  560
            S GLG MG+GLPAAIGA +  P+++++ I GD SF MN+QEL TI    L +KI ++NNQ
Sbjct  426  SSGLGTMGYGLPAAIGAKIANPNDLIICITGDASFQMNLQELGTIAQYELDIKIFIINNQ  485

Query  561  HLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQ  620
              GMV QW+  FY    AH      SN A+  P+ ++ A + G+   RVT   DL++ I+
Sbjct  486  WQGMVRQWQQAFYDQRYAH------SNMAKGQPDFVQLANSYGIRGIRVTTSKDLKSKIE  539

Query  621  KMLDTPGPYLLDVIVPHQEHVLPMIPSG  648
            +++ TPGP L+D IV   E+  PMI  G
Sbjct  540  RIISTPGPLLIDCIVATSENCYPMIAPG  567
```

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RecName: Full=Acetolactate synthase isozyme 1 large subunit; Short=AHAS-I; AltName: Full=Acetohydroxy-acid synthase I large subunit; Short=ALS-I

Sequence ID: P08142.1 **Length:** 562 **Number of Matches:** 1

Related Information

Range 1: 15 to 562 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
465 bits(1197)	2e-156	Compositional matrix adjust.	247/566(44%)	344/566(60%)	19/566(3%)

```
Query  93   GSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARAT  152
            G++ +V  LE++G+  V   PGG+ + ++ AL++S+ IR++L RHEQG  F A+G AR
Sbjct  15   GAEFIVHFLEQQGIKIVTGIPGGSILPVYDALSQSTQIRHILARHEQGAGFIAQGMARTD  74

Query  153  GFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSI  212
            G P VC+A SGPGATNLV+ +ADA LDS+P++ ITGQVP  MIGTDAFQE     ++  I
Sbjct  75   GKPAVCMACSGPGATNLVTAIADARLDSIPLICITGQVPASMIGTDAFQEVDTYGISIPI  134

Query  213  TKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMS  272
            TKHNYLV  +E++P+V+ +AF +A+SGRPGPV ID+PKD+Q   V     QP
Sbjct  135  TKHNYLVRHIEELPQVMSDAFRIAQSGRPGPVWIDIPKDVQTA-VFEIETQPAM---AEK  190

Query  273  RLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFVELTGIPVASTLMGLGAF  332
                  +E  +     +I+ +K+PVLY+GGG   +   +R   E   +P   TLM LG
Sbjct  191  AAAPAFSEESIRDAAAMINAAKRPVLYLGGGVINAPARVRELAEKAQLPTTMTLMALGML  250

Query  333  PTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDS  392
            P    LSL MLGMHG    NY +  +DLL+  G RFDDR  GK E F   AKI+H+DID
Sbjct  251  PKAHPLSLGMLGMHGVRSTNYILQEADLLIVLGARFDDRAIGKTEQFCPNAKIIHVDIDR  310

Query  393  AEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVKYPLNFKTF  452
            AE+GK KQPHV+I AD+   L  L  ++E++        + W Q +   + ++P
Sbjct  311  AELGKIKQPHVAIQADVDDVLAQLIPLVEAQP------RAEWHQLVADLQREFPCPIPKA  364

Query  453  GDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLP  512
             D +     I  +    + +AII+T VGQHQMW AQ Y   +PRQWLTSGGLG MGFGLP
Sbjct  365  CDPLSHYGLINAVAACVDDNAIITTDVGQHQMWTAQAYPLNRPRQWLTSGGLGTMGFGLP  424

Query  513  AAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRF  572
            AAIGAA+  PD  V+   GDGS +MN+QE+AT     L VKI+L+NN+ LG+V Q +  F
Sbjct  425  AAIGAALANPDRKVLCFSGDGSLMMNIQEMATASENQLDVKIILMNNEALGLVHQQQSLF  484

Query  573  YKANR-AHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQKMLDTPGPYLL  631
            Y+    A TY G          N ++ A   G+    + +  D +A++Q++++ PGP L+
Sbjct  485  YEQGVFAATYPGK--------INFMQIAAGFGLETCDLNNEADPQASLQEIINRPGPALI  536

Query  632  DVIVPHQEHVLPMIPSGGAFKDVITE  657
             V +  +E V PM+P G A  +++ E
Sbjct  537  HVRIDAEEKVYPMVPPGAANTEMVGE  562
```

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RecName: Full=Probable acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-acid synthase large subunit; Short=ALS

Sequence ID: Q57725.1 **Length:** 591 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 2 to 562 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
466 bits(1199)	3e-156	Compositional matrix adjust.	257/577(45%)	366/577(63%)	29/577(5%)

```
Query  92   KGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARA  151
            KG++ +++ALE EGV  +F YPGGA +  + AL  S ++ ++L RHEQ    AA+G+ARA
Sbjct  2    KGAEAIIKALEAEGVKIIFGYPGGAMLPFYDALYDSDLV-HILTRHEQAAAHAADGFARA  60

Query  152  TGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRS  211
            +G  GVC++TSGPGATNLV+G+A A  DS P++A+TGQVP ++IG DAFQE   + +
Sbjct  61   SGEAGVCVSTSGPGATNLVTGIATAYADSSPVIALTGQVPTKLIGNDAFQEIDALGLFMP  120

Query  212  ITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQ-QLVIPDWDQPMR--LP  268
```

```
            ITKHN+ +   E+IP   R AF +A +GRPGPV ID+PKD+Q  ++ I  +  P +  LP
Sbjct  121  ITKHNFQIKKPEEIPETFRAAFEIATTGRPGPVHIDLPKDVQDGEIDIEKYPIPAKVDLP  180

Query  269  GYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTL  326
            GY  +    P  + +++  +LI+ES++PV+  GGG   S +SEEL R  E   IPV +TL
Sbjct  181  GYKPKTVGHP--LQIKKAAKLIAESERPVILAGGGVIISGASEELLRLAEFVKIPVCTTL  238

Query  327  MGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIV  386
            MG G FP    L+L M+GMHGT  ANYAV   D+L+A G RF DRVTG +  FA  AKI+
Sbjct  239  MGKGCFPEDHPLALGMVGMHGTKAANYAVTECDVLIAIGCRFSDRVTGDIRYFAPEAKII  298

Query  387  HIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQEL-TVQKVKY  445
            HIDID AEIGKN +  + I  D K  L+ L + L + E K   D   W + +  ++K+
Sbjct  299  HIDIDPAEIGKNVRADIPIVGDAKNVLRDLLAALIALEIK---DKETWLERIYELKKLSI  355

Query  446  PLNFKTFGDA-IPPQYAIQVLDELTN------GSAIISTGVGQHQMWAAQYYKYRKPRQW  498
            P+    F D  I PQ   ++ L E+ N       + II+T VGQ+QMW A ++K + PR +
Sbjct  356  PM--MDFDDKPIKPQRFVKDLMEVLNEIDSKLKNTIITTDVGQNQMWMAHFFKTKMPRSF  413

Query  499  LTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLN  558
            L SGGLG MGFG PAAIGA V +P   V+ I GDG F+MN QELATI   ++PV I + +
Sbjct  414  LASGGLGTMGFGFPAAIGAKVAKPYANVISITGDGGFLMNSQELATISEYDIPVVICIFD  473

Query  559  NQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAA  618
            N+ LGMV QW++ +Y   ++  +LG         P+ +K AE+ GV A R+   D+++
Sbjct  474  NRTLGMVYQWQNLYYGQRQSEVHLGES-------PDFVKLAESYGVKADRIISPDEIKEK  526

Query  619  IQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVI  655
            +++ + +  PYLLD+++   E  LPM+P GG   +++
Sbjct  527  LKEAILSNEPYLLDIVIDPAE-ALPMVPPGGRLTNIV  562
```

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RecName: Full=Acetolactate synthase, mitochondrial; AltName: Full=AHAS; AltName: Full=ALS; AltName: Full=Acetohydroxy-acid synthase; Flags: Precursor

Sequence ID: P36620.2 **Length:** 669 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 87 to 663 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
467 bits(1202)	1e-155	Compositional matrix adjust.	249/588(42%)	357/588(60%)	34/588(5%)

```
Query  91   RKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYAR  150
            + G ++  + + +  V  VF YPGGA + +  A+ RS     +LPRHEQ    AA+ Y+R
Sbjct  87   KTGGEIFHDMMLKHNVKHVFGYPGGAILPVFDAIYRSPHFEFILPRHEQAAGHAAQAYSR  146

Query  151  ATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTR  210
             T  PGV + TSGPGATN+++ +ADAL D  P+V  +GQV    IG+DAFQE  +V ++R
Sbjct  147  VTKKPGVVLVTSGPGATNVITPIADALADGTPLVVFSGQVATSAIGSDAFQEADMVGISR  206

Query  211  SITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGY  270
            S TK N +V DV D+PR + EAF +A SGRPGPVL+D+PKD+   ++         +P
Sbjct  207  SCTKWNVMVKDVADLPRRIDEAFEIATSGRPGPVLVDLPKDVTASVLKEPIPILSSVPSM  266

Query  271  MSRLPKLPNE------MLLEQIVRLISESKKPVLYVGGGCSQSSEE---LRRFVELTGIP  321
              R+ ++  E        ++++  L+  +KKPV++ G G   + E    LR+F E   IP
Sbjct  267  NRRMKEVLEEGSKNVTAKIDRVANLLKLAKKPVIFCGHGVLANPECPTLLRKFSERLQIP  326

Query  322  VASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFAS  381
            V ++L+GLGA     +LSL MLGMHG+ YAN A+  +DL+LA GVRFDDRVTG +  FA
Sbjct  327  VTTSLLGLGAVDERSDLSLHMLGMHGSGYANMAMQEADLILALGVRFDDRVTGNVSLFAP  386

Query  382  RAK---------IVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFS  432
            +A+         I+H DI    IGK  QP  +I  D+  +L+ L+S  ++ +   + D
Sbjct  387  QARLAAAEERGGIIHFDISPKNIGKVVQPTEAIEGDVYESLKLLDSATKNIKIPSRFD--  444

Query  433  AWRQELTVQKVKYPLNFKTF--GDAIPPQYAIQVLDELTN---GSAIISTGVGQHQMWAA  487
             W  ++   K ++P  F     G+ + PQ  IQ LD+ T+       I+TGVG HQMWAA
Sbjct  445  -WLSQIQTWKERFPFTFTRSAPGELVKPQEVIQELDKQTSDIKDKVTITTGVGAHQMWAA  503

Query  488  QYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKV  547
             +Y++ KP   +TSGGLG MGFGLPAAIGA+V  P ++V+DIDGD SF M   ELAT++
Sbjct  504  TFYRWTKPSSLVTSGGLGTMGFGLPAAIGASVAAPKDIVIDIDGDASFSMTGMELATVRQ  563

Query  548  ENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAA  607
             ++PVKI++LNN+  GMV QW++ FY+   +HT+  N        PN +K A+A G+ A
Sbjct  564  FDIPVKILILNNEEQGMVTQWQNLFYEKRYSHTHQKN--------PNFVKLADAMGIKAL  615

Query  608  RVTHRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVI  655
            RV  R+DL   +++ L T GP L++V+V  +EHV P +P G A    I
Sbjct  616  RVEKREDLAKKMKEFLSTKGPVLMEVLVAQKEHVYPFVPGGKALHQFI  663
```

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RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-acid synthase large subunit; Short=ALS

Sequence ID: P45261.1 **Length:** 573 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 6 to 564 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
456 bits(1172)	2e-152	Compositional matrix adjust.	233/570(41%)	346/570(60%)	18/570(3%)

```
Query  93   GSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARAT  152
            G++++V++L  EGV  VF YPGGA ++I+ A+     I ++L RHEQ  V  A+GYAR+T
Sbjct  6    GAEMVVQSLRDEGVEYVFGYPGGAVLDIYDAIHTLGGIEHILVRHEQAAVHMADGYARST  65

Query  153  GFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSI  212
            G  G  + TSGPGATN ++G+  A  DSVP+V I+GQV   +IG+DAFQE  ++ ++R +
Sbjct  66   GKVGCVLVTSGPGATNAITGILTAYTDSVPMVIISGQVMSNLIGSDAFQECDMLGISRPV  125

Query  213  TKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMS  272
             KH+++V   EDIP  +++AF++A +GRPGPV++D+PKD     V P++  P   P Y+
Sbjct  126  VKHSFIVKKAEDIPSTLKKAFYIASTGRPGPVVVDIPKDT----VNPNFKYPYEYPEYVE  181

Query  273  RLPKLP----NEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTL  326
                 P    ++  +++ ++ +  +KKP+L+VGGG   ++ SE+L +F +   +PV S+L
Sbjct  182  LRSYNPTVNGHKGQIKKALKALLVAKKPILFVGGGAITAECSEQLIQFAQRLNLPVTSSL  241

Query  327  MGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIV  386
            MGLGA+P+ D+  L MLGMHGT+ AN A+  SDL+L  GVRFDDR T  LE +   AK++
Sbjct  242  MGLGAYPSTDKQFLGMLGMHGTLEANTAMHESDLILGIGVRFDDRTTNNLEKYCPNAKVI  301

Query  387  HIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVKYP  446
            HIDID   I KN    + I  + K  L+    +L  +  K + D  +W QE+   K K
Sbjct  302  HIDIDPTSISKNVPVAIPIVGNAKNVLEEFLGLLNEEGLKSQTDLESWWQEINQWKAKKC  361

Query  447  LNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGA  506
            L F      I PQ  ++ +  LT G A +++ VGQHQM+AA +Y + +PR W+ SGG G
Sbjct  362  LEFDRTSGVIKPQQVVEAVYRLTKGQAYVASDVGQHQMFAALHYPFDEPRHWINSGGAGT  421

Query  507  MGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVV  566
            MGFG PAA+G  +  P+  VV + GDGS  MN+QEL+T     +PV I+ LNN  LGMV
Sbjct  422  MGFGFPAALGVKLAHPEGTVVCVTGDGSIQMNIQELSTATQYGIPVVIICLNNHFLGMVK  481

Query  567  QWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQKMLDTP  626
            QW+D  Y    + TY+ +        P+  K AE+ G    ++   D+L + +Q+
Sbjct  482  QWQDLIYSGRHSQTYMNS-------LPDFAKLAESYGHVGIKIATPDELESKLQEAFSIK  534

Query  627  GPYL-LDVIVPHQEHVLPMIPSGGAFKDVI  655
               + +D+ V   EHV PM   GGA  ++I
Sbjct  535  NKLVFVDINVDESEHVYPMQIRGGAMNEMI  564
```

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RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-acid synthase large subunit; Short=ALS

Sequence ID: Q9RQ65.1 **Length:** 574 **Number of Matches:** 1

Related Information

Range 1: 2 to 573 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
451 bits(1160)	9e-151	Compositional matrix adjust.	236/582(41%)	344/582(59%)	19/582(3%)

```
Query  89   EPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGY  148
            E   GS++++++L  +G+  +F YPGGA ++I+ +L  +  I+++L RHEQG    A+GY
Sbjct  2    EMLSGSEMIIQSLIDQGIKYIFGYPGGAVLDIYDSLKSTKKIKHILVRHEQGATHMADGY  61

Query  149  ARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEV  208
            ARATG  GV + TSGPGATN ++G+A A +DS+PIV I+GQV   +IG DAFQE  ++ +
Sbjct  62   ARATGKIGVVLVTSGPGATNSITGIATAYMDSIPIVVISGQVSSSLIGYDAFQECDMIGI  121

Query  209  TRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLP  268
            +R I KH++LV   EDIP   ++AF+LA SGRPGP++ID+PKDI        +   P+ +
Sbjct  122  SRPIVKHSFLVKKTEDIPITFKKAFWLASSGRPGPIVIDLPKDILNSYNKKPYIWPIEVN  181

Query  269  GYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTL  326
                      +   +++ + ++  SK+PV+Y GGG   +    EL+   E   IPV ++L
Sbjct  182  IRSYNPITKGHSRQIKKAIDILKLSKQPVIYAGGGVISANCHNELKELAEKLNIPVTTSL  241

Query  327  MGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIV  386
            M LGAFP     +L MLGMHGT  AN A+  +D++LA GVRFDDR T  ++ +   A I+
Sbjct  242  MALGAFPGNHPQNLQMLGMHGTYEANMAMHYADVILAIGVRFDDRTTNNVKKYCPNATII  301

Query  387  HIDIDSAEIGKNKQPHVSICADIKLALQG----LNSILESKEGKLKLDFSAWRQELTVQK  442
            HIDID   I K    H+ I  + K  LQ     +NS +  KE         W  ++   K
Sbjct  302  HIDIDPTSISKTITAHIPIVGNAKNVLQQILVFINSNMFVKEFYC---LKKWWIKIQSWK  358

Query  443  VKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSG  502
             K  LNF T  D I PQ  I+ + +LT G A I++ VGQHQM+AA YY ++KPR+W+ SG
Sbjct  359  NKNSLNFDTNSDNIKPQSVIKTIWKLTKGKAFITSDVGQHQMFAALYYSFQKPRRWINSG  418

Query  503  GLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHL  562
            GLG MGFGLPAA+G  +  P+E V+ + GDGS  MN+QEL+T     LP+ I+ LNN+ L
Sbjct  419  GLGTMGFGLPAALGVKLAFPNETVICVTGDGSIQMNIQELSTAMQYELPILILNLNNKSL  478

Query  563  GMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQ--  620
            GMV QW+D  Y    +H+Y+ +        PN +K AE+ G     +    +L   +Q
Sbjct  479  GMVKQWQDIIYSGRHSHSYMKS-------LPNFIKLAESYGHSGISINTPKELEKKLQLA  531

Query  621  -KMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVITEGDGR  661
             + L       +D+ +   EHV PM    G   +++   +G+
Sbjct  532  LEKLQNGHLVFVDIKIDASEHVYPMQIRDGGMNNMLLRKNGQ  573
```

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RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-acid synthase large subunit; Short=ALS

Sequence ID: Q02137.2 **Length:** 575 **Number of Matches:** 1

Related Information

Range 1: 1 to 554 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
450 bits(1158)	2e-150	Compositional matrix adjust.	251/573(44%)	347/573(60%)	25/573(4%)

```
Query  82   VSRFAPDEPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGG  141
            + +   ++P  GS ++++ L+  GV  +F YPGGA + ++ A+      I+++L RHEQG
Sbjct  1    MKKIKLEKPTSGSQLVLQTLKELGVEIIFGYPGGAMLPLYDAIHNFEGIQHILARHEQGA  60

Query  142  VFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQ  201
               AEGYA+++G  GV + TSGPGATN V+G+ADA LDSVP++  TGQV    IG DAFQ
Sbjct  61   THEAEGYAKSSGKVGVVVVTSGPGATNAVTGIADAYLDSVPLLVFTGQVGPLSIGKDAFQ  120

Query  202  ETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDW  261
            E   V +T  ITK+NY + +  DIPR+V EA++LAR+GRPGPV ID+PKD+    V
Sbjct  121  EADTVGITAPITKYNYQIRETADIPRIVTEAYYLARTGRPGPVEIDLPKDVSTLEVTEIN  180

Query  262  DQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTG  319
            D  + LP Y     K  +E L E +  L S SKKPV+  GGG   S S +  R FVE
Sbjct  181  DPSLNLPHYHES-EKATDEQLQELLTEL-SVSKKPVIIAGGGINYSGSVDIFRAFVEKYQ  238

Query  320  IPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAF  379
            IPV STL+GLG  P   EL L M GMHG+  AN A+  +D ++  G RFDDRV
Sbjct  239  IPVVSTLLGLGTLPISHELQLGMAGMHGSYAANMALVEADYIINLGSRFDDRVVSNPAKV  298

Query  380  ASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELT  439
            A  A + HIDID+AE+GK  +  + I +D+K AL  L  +      K++ DF+ W + +T
Sbjct  299  AKNAVVAHIDIDAAELGKIVKTDIPILSDLKAALSRLLQL-----NKVRTDFNDWIKTVT  353

Query  440  VQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWL  499
              K K P  ++     I PQ  I+++ E T G AII T VGQHQMW AQYY Y+  RQ +
Sbjct  354  KNKEKAPFTYEPQNHDIRPQETIKLIGEYTQGDAIIVTDVGQHQMWVAQYYPYKNARQLI  413

Query  500  TSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNN  559
            TSGG+G MGFG+PAAIGA + +P++ V+   GDG F M  QELA +    + +K++L+NN
Sbjct  414  TSGGMGTMGFGIPAAIGAKLAQPNKNVIVFVGDGGFQMTNQELALLNGYGIAIKVVLINN  473

Query  560  QHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARV----THRDDL  615
              LGMV QW++ FY+  R+ +         ++ PN    AEA G+   ++    T  DDL
Sbjct  474  HSLGMVRQWQESFYEERRSQSVF-------DVEPNFQLLAEAYGIKHVKLDNPKTLADDL  526

Query  616  RAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSG  648
                 K++    P L++V++   EHVLPMIP+G
Sbjct  527  -----KIITEDEPMLIEVLISKSEHVLPMIPAG  554
```

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RecName: Full=Acetolactate synthase; AltName: Full=ALS; AltName: Full=Acetohydroxy-acid synthase

Sequence ID: P27868.1 **Length:** 579 **Number of Matches:** 1

Related Information

Range 1: 13 to 575 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
446 bits(1146)	2e-148	Compositional matrix adjust.	260/573(45%)	338/573(58%)	20/573(3%)

```
Query  93   GSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSI---IRNVLPRHEQGGVFAAEGYA  149
            G+  L+++L R GV  +F YPGG+++ I+  + R+     I++ L RHEQG   AA+GYA
Sbjct  13   GAFALIDSLRRHGVQHIFGYPGGSNLPIYDEIYRAEQAGEIKHYLVRHEQGAAHAADGYA  72

Query  150  RATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVT  209
            R+TG  GVC+ATSGPGATNLV+GLA A LDSVP++AITGQVPR  +GTDAFQE  I  +T
Sbjct  73   RSTGKVGVCLATSGPGATNLVTGLATAYLDSVPVLAITGQVPRSALGTDAFQEIDIFGIT  132

Query  210  RSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLV--IPDWDQPMRL  267
              I KH+YLV +  ++PR+V EAF LA SGRPGPVLID+PKD+    +  IP     +R
Sbjct  133  LPIVKHSYLVREPSELPRIVVEAFHLAMSGRPGPVLIDIPKDVGNAQIDYIPVEPGSVRR  192

Query  268  PGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVAST  325
             GY  R  +  N   + Q ++LISE+ KP+LYVGGG   + +  E+    E   IPV ST
Sbjct  193  VGY--RPTERGNPRQINQALQLISEATKPLLYVGGGAIMAGAHAEIAELSERFQIPVTST  250

Query  326  LMGLGAFPTGDELSL---SMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASR  382
            LMG G F     LSL    MLGMHGT YAN+AV   D ++A GVRFDDRV G  + FA
Sbjct  251  LMGKGRFDENHPLSLGIVGMLGMHGTAYANFAVMELDFVIAVGVRFDDRVAGTGDQFAHS  310

Query  383  AKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQK  442
            AK++HIDID AE+GKN+   V I  D++  L  +       E KL  +      +L   +
Sbjct  311  AKVIHIDIDPAEVGKNRSTDVPIVGDVRQVLGDMLQRTYHWERKLSRNKPRNGTDLNQLR  370

Query  443  VKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSG  502
               PL      D I PQ     L       A  +T VGQHQMWA Q+ +   PR+W+TSG
Sbjct  371  EPIPLTVPHPEDGISPQDGDWELSHQCP-DAFYTTDVGQHQMWAGQFVQ-NGPRRWMTSG  428

Query  503  GLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHL  562
            GLG MG+GLPAA+G  V  P + V  I GDGSF MN+QEL TI    + VK+++LNN  L
Sbjct  429  GLGTMGYGLPAAVGVKVAHPHDTVTCISGDGSFQMNMQELGTIAQYGIGVKVIILNNGWL  488

Query  563  GMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQKM  622
            GMV QW+  FY      T L + +      P   + A+   G+ A  V  R   +  + K
Sbjct  489  GMVRQWQHMFYNDRYEATNLEDGT------PEFARLADVYGLEAMNVRQRKIYQRRLPKA  542

Query  623  LDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVI  655
            L   GP +LDV V   E   PM+  G    D++
```

```
Sbjct  543  LSHKGPMILDVRVTRDEDCYPMVAPGHDNSDMM  575
```

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RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-acid synthase large subunit; Short=ALS

Sequence ID: O85293.1 **Length:** 571 **Number of Matches:** 1

Related Information

Range 1: 2 to 563 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
445 bits(1145)	2e-148	Compositional matrix adjust.	233/573(41%)	345/573(60%)	18/573(3%)

```
Query  89   EPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGY  148
            E   G+++++ +L  +G+  +F YPGGA ++I+ AL     + ++L RHEQ     A+GY
Sbjct  2    EILSGAEMVIRSLINQGIQHIFGYPGGAVLDIYDALKTVGGVEHILVRHEQAATHMADGY  61

Query  149  ARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEV  208
            AR+TG  GV + TSGPGATN ++G+A A +DS+P+V I+GQV   +IG DAFQE  ++ +
Sbjct  62   ARSTGKIGVVLVTSGPGATNAITGIATAYMDSIPMVVISGQVASSLIGYDAFQECDMIGI  121

Query  209  TRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPD--WDQPMR  266
            +R I KH++LV   EDIP + ++AF+LA +GRPGPV+ID+PKDI ++    +  W + +
Sbjct  122  SRPIVKHSFLVKRTEDIPIIFKKAFWLASTGRPGPVVIDLPKDILKKTNKYNFIWPKNIH  181

Query  267  LPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVAS  324
            +  Y         +  +++ +R++ ++KKP++Y GGG   S SSEELR F E    PV +
Sbjct  182  IRSYNPTTKGHQGQ--IKKALRILLKAKKPIIYAGGGIISSNSSEELRIFAEKINCPVTT  239

Query  325  TLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAK  384
            +LMGLGAFP     S+SMLGMHGT  AN A+  SD++ A GVRFDDR T  L+ +   A
Sbjct  240  SLMGLGAFPGNHIQSISMLGMHGTYEANMAMHYSDVIFAIGVRFDDRTTNNLKKYCPNAT  299

Query  385  IVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVK  444
            I+H+DID   I K     + I  D K  L+ +  +++ KE ++      W      +K+K
Sbjct  300  ILHVDIDPTSISKTVSADIPIVGDAKQVLKEMIELIK-KEKQIHSLKEWWSSIGKWKKIK  358

Query  445  YPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGL  504
              L +    + I PQ  IQ L +LT G++ I++ VGQHQM+ A YY++ KPR+W+ SGGL
Sbjct  359  -SLEYNKKSNKIKPQKIIQTLFKLTKGTSYITSDVGQHQMFTALYYQFNKPRRWINSGGL  417

Query  505  GAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGM  564
            G MGFGLPAA+G  +  P   V+ + GDGS  MN+QEL+T +  NL V I+ LNN  LGM
Sbjct  418  GTMGFGLPAALGVKLALPKATVICVTGDGSIQMNIQELSTARQYNLAVLILNLNNSSLGM  477

Query  565  VVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAI---QK  621
            V QW+D  Y    +H+Y+ +        P+ +K  E+ G    +V   ++L   +    K
Sbjct  478  VKQWQDMIYSGRHSHSYMDS-------LPDFVKLVESYGHIGLKVKTNEELEEKLILALK  530

Query  622  MLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDV  654
             L       LD+ +   EHV PM   GG   ++
Sbjct  531  KLSEGNLVFLDIQIDDSEHVYPMQIQGGGMNEM  563
```

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RecName: Full=Acetolactate synthase, mitochondrial; AltName: Full=AHAS; AltName: Full=ALS; AltName: Full=Acetohydroxy-acid synthase; Flags: Precursor

Sequence ID: Q5KPJ5.1 **Length:** 718 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 128 to 706 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
450 bits(1157)	3e-148	Compositional matrix adjust.	246/594(41%)	346/594(58%)	48/594(8%)

```
Query  93   GSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARAT  152
            G  +  E + R  V  VF YPGGA + +  A+  S     VLPRHEQG    AEGYAR +
Sbjct  128  GGQIFQEMMLRHDVKQVFGYPGGAILPVFDAIYNSPHFDFVLPRHEQGAGHMAEGYARVS  187

Query  153  GFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSI  212
            G PGV + TSGPGATN+++ + DAL D VP+V   GQV   +IG+DAFQE  +V ++RS
Sbjct  188  GKPGVVLVTSGPGATNVITPMQDALSDGVPMVVFCGQVATNLIGSDAFQEADVVGISRSC  247

Query  213  TKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMS  272
            TK N +V D+ ++PR + EAF +A +GRPGPVL+D+PKD+   ++          PG+
Sbjct  248  TKWNVMVKDIAELPRRINEAFKIATTGRPGPVLVDLPKDVTAAILRTPIPAKSAQPGHSP  307

Query  273  RLPKLP-------------NEMLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFVELTG  319
             LP  P             +  L+ +  ++I+++K+P+++ G G   S E  +   EL+
Sbjct  308  YLPSNPLNPSSQPSDPLPGDADLITEAAQMINKAKRPIIFAGNGVLSSPEGPKLLKELSD  367

Query  320  ---IPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKL  376
               IPV +TL GLGAF   DE SL M+GMHG+ YAN+A+  +D+L+A GVRFDDRVTGK+
Sbjct  368  KGRIPVTTTLQGLGAFDERDEKSLHMIGMHGSAYANFAMQEADVLIALGVRFDDRVTGKV  427

Query  377  EAFA---------SRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKL  427
            + FA          R  I+H +I    I K  +  + +  D+  +L  L   +E+
Sbjct  428  DTFAPAAKAAAAEGRGGIIHFEIQPKNINKIVEAQIPVLGDVVASLAELVPQIEA-----  482

Query  428  KLDFSAWRQELTVQKVKYPLNF--KTFGDAIPPQYAIQVLDE----LTNGSAIISTGVGQ  481
             +D SAW       K +YP  +     G  + PQ  +Q LD     L     IISTGVGQ
Sbjct  483  -VDRSAWIGRCKATKERYPFTYTPSQEGQKLKPQEVVQELDRQAEALGKEKFIISTGVGQ  541

Query  482  HQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQE  541
```

```
            HQMWA QYY++ +PR W++SGGLG MGFGLP+AIGA V  P++ V+DIDGD SF M   E
Sbjct  542  HQMWACQYYRWTEPRSWVSSGGLGTMGFGLPSAIGAKVAAPEKYVIDIDGDASFSMTAME  601

Query  542  LATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEA  601
            LAT    ++ VK++L NN+  GMV QW+D FY+   +HT + N        P+ +K +E+
Sbjct  602  LATASQYDIGVKVLLFNNEFQGMVEQWQDLFYENRYSHTRMTN--------PDFVKLSES  653

Query  602  CGVPAARVTHRDDLRAAIQKMLDTPG--PYLLDVIVPHQEHVLPMIPSGGAFKD  653
             G    R T  +DL   +++ L+  G  P +L+ +V   EHV PMIP+G A  +
Sbjct  654  MGTKGLRCTKLEDLPRMMKEFLEYDGKRPIVLECLV-SSEHVYPMIPAGKALHE  706
```

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RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-acid synthase large subunit; Short=ALS

Sequence ID: P57321.1 **Length:** 571 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 2 to 563 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
444 bits(1143)	4e-148	Compositional matrix adjust.	234/575(41%)	346/575(60%)	22/575(3%)

```
Query  89   EPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGY  148
            E   G++++V +L  +G+  +F YPGGA ++I+ AL     I ++L RHEQ     A+GY
Sbjct  2    EILSGAEMVVRSLIDQGIQHIFGYPGGAVLDIYDALKTVGGIEHILVRHEQAATHMADGY  61

Query  149  ARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEV  208
            +R+TG  GV + TSGPGATN ++G+A A +DS+P+V I+GQV   +IG DAFQE  ++ +
Sbjct  62   SRSTGKTGVVLVTSGPGATNAITGIATAYMDSIPMVVISGQVASSLIGYDAFQECDMIGI  121

Query  209  TRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDI--QQQLVIPDWDQPMR  266
            +R I KH++LV   EDIP V ++AF+LA SGRPGP++ID+PKDI  +    +  W   +
Sbjct  122  SRPIVKHSFLVKKTEDIPIVFKKAFWLASSGRPGPIVIDLPKDILKKDNKYLYKWPDNIN  181

Query  267  LPGYMSRLPKLPNEM-LLEQIVRLISESKKPVLYVGGG--CSQSSEELRRFVELTGIPVA  323
            +  Y    P     +  +++ +  + ++++PV+Y GGG   S SSEELR F E    PV
Sbjct  182  IRSYN---PTTKGHIGQIKKALHTLLKAQRPVIYAGGGIISSNSSEELRIFAEKINCPVT  238

Query  324  STLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRA  383
            ++LMGLG+FP   + ++SMLGMHGT  AN  +  +D++ A GVRFDDR T  L  +   A
Sbjct  239  TSLMGLGSFPGTHDQNISMLGMHGTYEANMTMHHADVIFAIGVRFDDRTTNNLNKYCPNA  298

Query  384  KIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKV  443
             ++H+DID   I K    ++ I  D K  LQ +  +L+ KE K+ L    W   +   K
Sbjct  299  IVLHVDIDPTSISKTVSANIPIVGDAKHVLQKMIELLK-KEKKISL-LEDWWNTIKKWKK  356

Query  444  KYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGG  503
               L +    + I PQ  I+ L +LT G++ I++ VGQHQM+ A YY + KPR+W+ SGG
Sbjct  357  INSLQYNQLSNKIKPQTVIKTLFKLTKGTSYITSDVGQHQMFTALYYPFNKPRRWINSGG  416

Query  504  LGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLG  563
            LG MGFGLPAA+G  +  P E V+ I GDGS  MN+QEL+T +  NL V I+ LNN  LG
Sbjct  417  LGTMGFGLPAALGVKLALPKETVICITGDGSIQMNIQELSTARQYNLAVLILNLNNSSLG  476

Query  564  MVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTH----RDDLRAAI  619
            MV QW+D  Y    +H+Y+       +  P+ +K +E+ G    ++T      + L  A+
Sbjct  477  MVKQWQDMIYSGRHSHSYM-------DSLPDFVKLSESYGHFGIQITEPIELEEKLMLAL  529

Query  620  QKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDV  654
             K+ D    + +DV + + EHV PM   GG   ++
Sbjct  530  SKLSDGHLVF-VDVQIDNSEHVYPMQIQGGGMNEM  563
```

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RecName: Full=Acetolactate synthase, mitochondrial; AltName: Full=AHAS; AltName: Full=ALS; AltName: Full=Acetohydroxy-acid synthase; Flags: Precursor

Sequence ID: Q6SSJ3.1 **Length:** 718 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 128 to 706 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
449 bits(1154)	7e-148	Compositional matrix adjust.	245/594(41%)	346/594(58%)	48/594(8%)

```
Query  93   GSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARAT  152
            G  +  E + R  V  VF YPGGA + +  A+  S     VLPRHEQG    AEGYAR +
Sbjct  128  GGQIFQEMMLRHDVKQVFGYPGGAILPVFDAIYNSPHFEFVLPRHEQGAGHMAEGYARVS  187

Query  153  GFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSI  212
            G PGV + TSGPGATN+++ + DAL D VP+V   GQV   +IG+DAFQE  +V ++RS
Sbjct  188  GKPGVVLVTSGPGATNVITPMQDALSDGVPMVVFCGQVATNLIGSDAFQEADVVGISRSC  247

Query  213  TKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMS  272
            TK N +V D+ ++PR + EAF +A +GRPGPVL+D+PKD+   ++          PG+
Sbjct  248  TKWNVMVKDIAELPRRINEAFKIATTGRPGPVLVDLPKDVTAAILRTPIPAKSVQPGHSP  307

Query  273  RLPKLP-------------NEMLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFVELTG  319
             LP  P             +  L+ +  ++I+++K+P+++ G G   S E  +   EL+
Sbjct  308  YLPSNPLNPSSQPSDPLPGDADLITEAAQMINKAKRPIIFAGNGVLSSPEGPKLLKELSD  367

Query  320  ---IPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKL  376
               IPV +TL GLGAF   DE SL M+GMHG+ YAN+A+  +D+L+A GVRFDDRVTGK+
Sbjct  368  KGRIPVTTTLQGLGAFDERDEKSLHMIGMHGSAYANFAMQEADVLIALGVRFDDRVTGKV  427
```

```
Query  377  EAFA---------SRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKL  427
            + FA          R  I+H +I    I K  +  + +  D+  +L  L   +E+
Sbjct  428  DTFAPAAKAAAAEGRGGIIHFEIQPKNINKIVEAQIPVLGDVVASLGELVPQIEA-----  482

Query  428  KLDFSAWRQELTVQKVKYPLNF--KTFGDAIPPQYAIQVLDE----LTNGSAIISTGVGQ  481
             +D SAW       K +YP  +     G  + PQ  +Q LD     L     +ISTGVGQ
Sbjct  483  -VDRSAWIGRCKATKERYPFTYTPSQEGQKLKPQEVVQELDRQAEALGKEKFVISTGVGQ  541

Query  482  HQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQE  541
            HQMWA QYY++ +PR W++SGGLG MGFGLP+AIGA V  P++ V+DIDGD SF M   E
Sbjct  542  HQMWACQYYRWTEPRSWVSSGGLGTMGFGLPSAIGAKVAAPEKYVIDIDGDASFSMTAME  601

Query  542  LATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEA  601
            LAT    ++ VK++L NN+  GMV QW+D FY+   +HT + N        P+ +K +E+
Sbjct  602  LATASQYDIGVKVLLFNNEFQGMVEQWQDLFYENRYSHTRMTN--------PDFVKLSES  653

Query  602  CGVPAARVTHRDDLRAAIQKMLDTPG--PYLLDVIVPHQEHVLPMIPSGGAFKD  653
             G    R T  +DL   +++ L+  G  P +L+ +V   EHV PMIP+G A  +
Sbjct  654  MGAKGLRCTKLEDLPRMMKEFLEYDGKRPIVLECLV-SSEHVYPMIPAGKALHE  706
```

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RecName: Full=Acetolactate synthase catalytic subunit, mitochondrial; AltName: Full=Acetohydroxy-acid synthase catalytic subunit; Short=AHAS; Short=ALS; Flags: Precursor

Sequence ID: P07342.1 **Length:** 687 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 94 to 666 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
447 bits(1150)	1e-147	Compositional matrix adjust.	246/587(42%)	351/587(59%)	37/587(6%)

```
Query  93   GSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARAT  152
            G  +  E + R+ V  VF YPGGA + ++ A+  S     VLP+HEQG    AEGYARA+
Sbjct  94   GGQIFNEMMSRQNVDTVFGYPGGAILPVYDAIHNSDKFNFVLPKHEQGAGHMAEGYARAS  153

Query  153  GFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSI  212
            G PGV + TSGPGATN+V+ +ADA  D +P+V  TGQVP   IGTDAFQE  +V ++RS
Sbjct  154  GKPGVVLVTSGPGATNVVTPMADAFADGIPMVVFTGQVPTSAIGTDAFQEADVVGISRSC  213

Query  213  TKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLP-GYM  271
            TK N +V  VE++P  + EAF +A SGRPGPVL+D+PKD+   ++         LP   +
Sbjct  214  TKWNVMVKSVEELPLRINEAFEIATSGRPGPVLVDLPKDVTAAILRNPIPTKTTLPSNAL  273

Query  272  SRL-PKLPNEMLLEQIVR---LISESKKPVLYVGGGCSQSSEELRRFVELTG---IPVAS  324
            ++L  +  +E +++ I +   LI+ +KKPVLYVG G    ++  R   EL+    IPV +
Sbjct  274  NQLTSRAQDEFVMQSINKAADLINLAKKPVLYVGAGILNHADGPRLLKELSDRAQIPVTT  333

Query  325  TLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAF-----  379
            TL GLG+F   D  SL MLGMHG   AN AV ++DL++A G RFDDRVTG +  F
Sbjct  334  TLQGLGSFDQEDPKSLDMLGMHGCATANLAVQNADLIIAVGARFDDRVTGNISKFAPEAR  393

Query  380  ----ASRAKIVHIDIDSAEIGKNKQPHVSICADIKLAL-QGLNSILESKEGKLKLDFSAW  434
                  R  I+H ++    I K  Q  +++  D    L + ++ I   KE       S W
Sbjct  394  RAAAEGRGGIIHFEVSPKNINKVVQTQIAVEGDATTNLGKMMSKIFPVKER------SEW  447

Query  435  RQELTVQKVKYPLNF--KTFGDAIPPQYAIQVLDELTNGSA---IISTGVGQHQMWAAQY  489
              ++   K +YP  +  +T G  I PQ  I+ L ++ N +    I++TGVGQHQMWAAQ+
Sbjct  448  FAQINKWKKEYPYAYMEETPGSKIKPQTVIKKLSKVANDTGRHVIVTTGVGQHQMWAAQH  507

Query  490  YKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVEN  549
            + +R P  ++TSGGLG MG+GLPAAIGA V +P+ +V+DIDGD SF M + EL++
Sbjct  508  WTWRNPHTFITSGGLGTMGYGLPAAIGAQVAKPESLVIDIDGDASFNMTLTELSSAVQAG  567

Query  550  LPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARV  609
             PVKI++LNN+  GMV QW+  FY+   +HT+        ++ P+ +K AEA G+   RV
Sbjct  568  TPVKILILNNEEQGMVTQWQSLFYEHRYSHTH--------QLNPDFIKLAEAMGLKGLRV  619

Query  610  THRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVIT  656
              +++L A +++ + T GP LL+V V  +  VLPM+  G    + I
Sbjct  620  KKQEELDAKLKEFVSTKGPVLLEVEVDKKVPVLPMVAGGSGLDEFIN  666
```

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RecName: Full=Acetolactate synthase isozyme 3 large subunit; AltName: Full=AHAS-III; AltName: Full=ALS-III; AltName: Full=Acetohydroxy-acid synthase III large subunit

Sequence ID: P00893.2 **Length:** 574 **Number of Matches:** 1

Related Information

Range 1: 2 to 566 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
440 bits(1132)	2e-146	Compositional matrix adjust.	235/576(41%)	345/576(59%)	21/576(3%)

```
Query  89   EPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGY  148
            E   G++++V +L  +GV  VF YPGGA ++I+ AL     I +VL RHEQ  V  A+G
Sbjct  2    EMLSGAEMVVRSLIDQGVKQVFGYPGGAVLDIYDALHTVGGIDHVLVRHEQAAVHMADGL  61

Query  149  ARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEV  208
            ARATG  GV + TSGPGATN ++G+A A +DS+P+V ++GQV   +IG DAFQE  +V +
Sbjct  62   ARATGEVGVVLVTSGPGATNAITGIATAYMDSIPLVVLSGQVATSLIGYDAFQECDMVGI  121

Query  209  TRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLP  268
            +R + KH++LV   EDIP+V+++AF+LA SGRPGPV++D+PKDI      P    P   P
Sbjct  122  SRPVVKHSFLVKQTEDIPQVLKKAFWLAASGRPGPVVVDLPKDILN----PANKLPYVWP  177
```

```
Query  269  GYMSRLPKLP----NEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPV  322
              +S     P    ++  +++ ++ +  +KKPV+YVGGG   +    ++L+  VE   +PV
Sbjct  178  ESVSMRSYNPTTTGHKGQIKRALQTLVAAKKPVVYVGGGAITAGCHQQLKETVEALNLPV  237

Query  323  ASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASR  382
              +LMGLGAFP     +L MLGMHGT  AN  + ++D++ A GVRFDDR T  L  +
Sbjct  238  VCSLMGLGAFPATHRQALGMLGMHGTYEANMTMHNADVIFAVGVRFDDRTTNNLAKYCPN  297

Query  383  AKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLD-FSAWRQELTVQ  441
            A ++HIDID   I K     + I  D +  L+ +  +L  +     LD    W Q++
Sbjct  298  ATVLHIDIDPTSISKTVTADIPIVGDARQVLEQMLELLSQESAHQPLDEIRDWWQQIEQW  357

Query  442  KVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTS  501
            + +  L + T  + I PQ  I+ L  LT G A +++ VGQHQM+AA YY + KPR+W+ S
Sbjct  358  RARQCLKYDTHSEKIKPQAVIETLWRLTKGDAYVTSDVGQHQMFAALYYPFDKPRRWINS  417

Query  502  GGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQH  561
            GGLG MGFGLPAA+G   +  P+E VV + GDGS  MN+QEL+T     LPV ++ LNN++
Sbjct  418  GGLGTMGFGLPAALGVKMALPEETVVCVTGDGSIQMNIQELSTALQYELPVLVVNLNNRY  477

Query  562  LGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQK  621
            LGMV QW+D  Y    + +Y+       +  P+ ++ AEA G    +++H  +L + + +
Sbjct  478  LGMVKQWQDMIYSGRHSQSYM-------QSLPDFVRLAEAYGHVGIQISHPHELESKLSE  530

Query  622  MLD---TPGPYLLDVIVPHQEHVLPMIPSGGAFKDV  654
             L+         +DV V   EHV PM   GG   ++
Sbjct  531  ALEQVRNNRLVFVDVTVDGSEHVYPMQIRGGGMDEM  566
```

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RecName: Full=Acetolactate synthase isozyme 3 large subunit; AltName: Full=AHAS-III; AltName: Full=ALS-III; AltName: Full=Acetohydroxy-acid synthase III large subunit

Sequence ID: P40811.3 **Length:** 574 **Number of Matches:** 1

Related Information

Range 1: 2 to 566 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
440 bits(1131)	3e-146	Compositional matrix adjust.	235/576(41%)	346/576(60%)	21/576(3%)

```
Query  89   EPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGY  148
            E   G++++V +L  +GV  VF YPGGA ++I+ AL     I +VL RHEQ  V  A+G
Sbjct  2    EMLSGAEMVVRSLIDQGVKQVFGYPGGAVLDIYDALHTVGGIDHVLVRHEQAAVHMADGL  61

Query  149  ARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEV  208
            ARATG  GV + TSGPGATN ++G+A A +DS+P+V ++GQV   +IG DAFQE  +V +
Sbjct  62   ARATGDVGVVLVTSGPGATNAITGIATAYMDSIPLVILSGQVATSLIGYDAFQECDMVGI  121

Query  209  TRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLP  268
            +R + KH++LV   EDIP V+++AF+LA SGRPGPV++D+PKDI      P    P   P
Sbjct  122  SRPVVKHSFLVKQTEDIPLVLKKAFWLAASGRPGPVVVDLPKDILN----PAKKMPYAWP  177

Query  269  GYMSRLPKLP----NEMLLEQIVRLISESKKPVLYVGGGCSQSS--EELRRFVELTGIPV  322
              +S     P    ++  +++ ++ ++ +KKPV+YVGGG   ++     LR  +E   +PV
Sbjct  178  ETVSMRSYNPTTSGHKGQIKRALQTLASAKKPVVYVGGGAISAACYAPLRHIIETFNLPV  237

Query  323  ASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASR  382
             S+LMGLGAFP     SL MLGMHGT  AN  + ++D++ A GVRFDDR T  L  +
Sbjct  238  VSSLMGLGAFPATHRQSLGMLGMHGTYEANMTMHNADVIFAVGVRFDDRTTNNLAKYCPN  297

Query  383  AKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSIL-ESKEGKLKLDFSAWRQELTVQ  441
            A ++HIDID   I K     + +  D +L L+ +  +L +    + + D    W Q++
Sbjct  298  ATVLHIDIDPTSISKTVNADIPVVGDARLVLEQMLELLAQDAPSQPQDDIRDWWQQIESW  357

Query  442  KVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTS  501
            + +  L +    ++I PQ  I+ L  LT G A +++ VGQHQM+AA YY + KPR+W+ S
Sbjct  358  RARQCLKYDAESESIKPQAVIETLWRLTKGDAYVTSDVGQHQMFAALYYPFDKPRRWINS  417

Query  502  GGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQH  561
            GGLG MGFGLPAA+G   +  P E+VV + GDGS  MN+QEL+T     LPV ++ LNN++
Sbjct  418  GGLGTMGFGLPAALGVKMALPKEMVVCVTGDGSIQMNIQELSTALQYELPVLVLNLNNRY  477

Query  562  LGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQK  621
            LGMV QW+D  Y    + +Y+       +  P+ ++ AEA G    ++   D+L + + +
Sbjct  478  LGMVKQWQDMIYSGRHSQSYM-------QSLPDFVRLAEAYGHVGLQINRPDELESKLSE  530

Query  622  MLD---TPGPYLLDVIVPHQEHVLPMIPSGGAFKDV  654
             L+         +DV V   EHV PM   GG   ++
Sbjct  531  ALEHVRNNRLVFVDVTVDGSEHVYPMQIRGGGMDEM  566
```

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RecName: Full=Acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-acid synthase large subunit; Short=ALS

Sequence ID: Q89AP7.1 **Length:** 576 **Number of Matches:** 1

Related Information

Range 1: 6 to 567 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
434 bits(1116)	4e-144	Compositional matrix adjust.	225/570(39%)	345/570(60%)	15/570(2%)

```
Query  93   GSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARAT  152
            GSD+++ +L  +G+  +F YPGGA ++I+ +L +   I+++L RHEQ     A+GYARAT
```

```
Sbjct  6    GSDMVIRSLIDQGIKYIFGYPGGAVLDIYDSLKQMHGIKHILVRHEQSATHMADGYARAT  65

Query  153  GFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSI  212
            G  GV + TSGPGATN ++G+A A +DS+P+V I+GQV   +IG DAFQE  ++ ++R I
Sbjct  66   GKIGVVLVTSGPGATNSITGIATAYMDSIPLVVISGQVASSLIGYDAFQECDMIGISRPI  125

Query  213  TKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMS  272
             KH++LV + EDIP++ ++AF+LA SGRPGP++ID+PKDI   L+   +  P +L    S
Sbjct  126  VKHSFLVKNTEDIPKIFKKAFWLASSGRPGPIVIDLPKDILNPLIKKPYIWP-KLISIRS  184

Query  273  RLPKLP-NEMLLEQIVRLISESKKP--VLYVGGGCSQSSEELRRFVELTGIPVASTLMGL  329
              P L  ++  +++ + ++ ++K+P   +  G   S S +EL+   E   IPV ++LM L
Sbjct  185  YSPVLQGHQGQIKKALHILIKAKQPIIYIGGGIITSNSHKELKLLAETLNIPVTTSLMAL  244

Query  330  GAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHID  389
            GA P     +L MLGMHGT  AN A+ ++D++LA GVRFDDR T  ++ +   A I+HID
Sbjct  245  GALPQNHPQNLKMLGMHGTYEANMAIHNADVILAIGVRFDDRTTNNVDKYCPNATIIHID  304

Query  390  IDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKL-DFSAWRQELTVQKVKYPLN  448
            ID   I K    H+ I    +  L+ + ++L+++  K  + +   W +++   K K  L
Sbjct  305  IDPTSISKTISAHIPIVGHARNVLKQILNLLKNQFSKKNIYNLEHWWKQINCWKSKNSLE  364

Query  449  FKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMG  508
            +      I PQ  I+++  LTNG+A +++ VGQHQM+ A YY + KPR+W+ SGGLG MG
Sbjct  365  YDRKSKKIKPQNVIEIISALTNGNAFVTSDVGQHQMFTALYYSFNKPRRWVNSGGLGTMG  424

Query  509  FGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQW  568
            +GLPAA+G  +  P E V+ I GDGS  MN+QEL+T     L + I+ LNN+ LGMV QW
Sbjct  425  YGLPAALGVKLALPKETVLCITGDGSIQMNIQELSTAMQYKLSILILNLNNRSLGMVKQW  484

Query  569  EDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDD---LRAAIQKMLDT  625
            +D  Y    +H+Y+ +        PN +K AE+ G     + + +D           LD
Sbjct  485  QDIIYSGRHSHSYMKS-------LPNFIKLAESYGHIGISIHNPEDLEKKLKLALLKLDQ  537

Query  626  PGPYLLDVIVPHQEHVLPMIPSGGAFKDVI  655
                 +D+ +  +EHV PM    G   ++I
Sbjct  538  GNLVFVDITIDPEEHVYPMQIRSGGMNEMI  567
```

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RecName: Full=Probable acetolactate synthase large subunit; Short=AHAS; AltName: Full=Acetohydroxy-acid synthase large subunit; Short=ALS

Sequence ID: O08353.1 **Length:** 599 **Number of Matches:** 1

Related Information

Range 1: 2 to 570 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
434 bits(1115)	1e-143	Compositional matrix adjust.	252/581(43%)	360/581(61%)	29/581(4%)

```
Query  92   KGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARA  151
             G++ +++ALE E V  +F YPGGA +  + AL  S +I ++L RHEQ    AA+GYARA
Sbjct  2    NGAEAMIKALEAEKVEILFGYPGGALLPFYDALHHSDLI-HLLTRHEQAAAHAADGYARA  60

Query  152  TGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRS  211
            +G  GVCI TSGPGATNLV+G+A A  DS P+VA+TGQVP ++IG DAFQE   + +
Sbjct  61   SGKVGVCIGTSGPGATNLVTGVATAHSDSSPMVALTGQVPTKLIGNDAFQEIDALGLFMP  120

Query  212  ITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQ-QLVIPDWDQP--MRLP  268
            I KHN+ +     IP + R AF +A++GRPGPV ID+PKD+Q+ +L I     P  ++L
Sbjct  121  IVKHNFQIQKTCQIPEIFRSAFEIAQTGRPGPVHIDLPKDVQELELDIDKHPIPSKVKLI  180

Query  269  GYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTL  326
            GY       P +  +++ ++LI+ +K+P++  GGG   S ++EEL + VEL  IPV +TL
Sbjct  181  GYNPTTIGHPRQ--IKKAIKLIASAKRPIILAGGGVLLSGANEELLKLVELLNIPVCTTL  238

Query  327  MGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIV  386
            MG G       L+L M+GMHGT  ANY +  SD+L++ G RF DR+TG +++FA+ AKI+
Sbjct  239  MGKGCISENHPLALGMVGMHGTKPANYCLSESDVLISIGCRFSDRITGDIKSFATNAKII  298

Query  387  HIDIDSAEIGKNKQPHVSICADIKLAL----QGLNSIL--ESKEGKLKLDFSAWRQELTV  440
            HIDID AEIGKN    V I  D KL L    + L+ I+  +SKE   K + S W + +
Sbjct  299  HIDIDPAEIGKNVNVDVPIVGDAKLILKEVIKQLDYIINKDSKENNDKENISQWIENVNS  358

Query  441  QKVKYPLNFKTFGDA-IPPQYAIQ----VLDELT-NGSAIISTGVGQHQMWAAQYYKYRK  494
             K K  +    + D  I PQ  ++    V+D+L  N + II+T VGQ+QMW A Y+K +
Sbjct  359  LK-KSSIPVMDYDDIPIKPQKIVKELMAVIDDLNINKNTIITTDVGQNQMWMAHYFKTQT  417

Query  495  PRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKI  554
            PR +L+SGGLG MGFG P+AIGA V +PD  V+ I GDG F+MN QEL TI   N+PV I
Sbjct  418  PRSFLSSGGLGTMGFGFPSAIGAKVAKPDSKVICITGDGGFMMNCQELGTIAEYNIPVVI  477

Query  555  MLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDD  614
             + +N+ LGMV QW++ FY   +     G          P+ +K AE+ G+ A R+   ++
Sbjct  478  CIFDNRTLGMVYQWQNLFYGKRQCSVNFGGA-------PDFIKLAESYGIKARRIESPNE  530

Query  615  LRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVI  655
            +  A+++ ++   PYLLD  +      L M+P G    ++I
Sbjct  531  INEALKEAINCDEPYLLDFAI-DPSSALSMVPPGAKLTNII  570
```

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RecName: Full=Glyoxylate carboligase; AltName: Full=Tartronate-semialdehyde synthase

Sequence ID: P0AEP8.2 **Length:** 593 **Number of Matches:** 1

See 1 more title(s)

Range 1: 5 to 551 GenPept Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
290 bits(743)	2e-88	Compositional matrix adjust.	190/555(34%)	287/555(51%)	19/555(3%)

```
Query  92   KGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARA  151
            +  D  +  LE+EG+T  F  PG A    + A+ +   IR++L RH +G    AEGY RA
Sbjct  5    RAVDAAMYVLEKEGITTAFGVPGAAINPFYSAMRKHGGIRHILARHVEGASHMAEGYTRA  64

Query  152  T-GFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTR  210
            T G  GVC+ TSGP  T++++ L  A  DS+PI+ ITGQ PR  +  + FQ   I  + +
Sbjct  65   TAGNIGVCLGTSGPAGTDMITALYSASADSIPILCITGQAPRARLHKEDFQAVDIEAIAK  124

Query  211  SITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGY  270
             ++K    V +   +PRV+++AF L RSGRPGPVL+D+P D+Q   +  D D    LP Y
Sbjct  125  PVSKMAVTVREAALVPRVLQQAFHLMRSGRPGPVLVDLPFDVQVAEIEFDPDMYEPLPVY  184

Query  271  MSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMG  328
                    + M +E+ V ++ ++++PV+  GGG   + ++  L++F ELT +PV  TLMG
Sbjct  185  ----KPAASRMQIEKAVEMLIQAERPVIVAGGGVINADAAALLQQFAELTSVPVIPTLMG  240

Query  329  LGAFPTGDELSLSMLGMH-GTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVH  387
             G  P   EL   M+G+     Y N  + +SD++   G RF +R TG +E +    KIVH
Sbjct  241  WGCIPDDHELMAGMVGLQTAHRYGNATLLASDMVFGIGNRFANRHTGSVEKYTEGRKIVH  300

Query  388  IDIDSAEIGKNKQPHVSICADIKLALQGLNSILES--KEGKLKLDFSAWRQELTVQKVKY  445
            IDI+  +IG+   P + I +D K AL  L  + +   K G+L      W  +   Q+ K
Sbjct  301  IDIEPTQIGRVLCPDLGIVSDAKAALTLLVEVAQEMQKAGRLPCR-KEWVAD--CQQRKR  357

Query  446  PLNFKTFGDAIP--PQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGG  503
             L  KT  D +P  PQ   +  +++         T +G  Q+ AAQ     K R W+  G
Sbjct  358  TLLRKTHFDNVPVKPQRVYEEMNKAFGRDVCYVTTIGLSQIAAAQMLHVFKDRHWINCGQ  417

Query  504  LGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLG  563
             G +G+ +PAA+G     P   VV I GD  F   ++ELA     N+P   +L+NN +LG
Sbjct  418  AGPLGWTIPAALGVCAADPKRNVVAISGDFDFQFLIEELAVGAQFNIPYIHVLVNNAYLG  477

Query  564  MVVQWEDRF---YKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQ  620
            ++ Q +  F   Y    A   + N S       + +K AE  G  A RV   +D+  A +
Sbjct  478  LIRQSQRAFDMDYCVQLAFENI-NSSEVNGYGVDHVKVAEGLGCKAIRVFKPEDIAPAFE  536

Query  621  KMLDTPGPYLLDVIV  635
            +       Y + V+V
Sbjct  537  QAKALMAQYRVPVVV  551
```

Related Information

Identical Proteins - Identical proteins to P0AEP8.2

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RecName: Full=Putative thiamine pyrophosphate-containing protein YdaP

Sequence ID: P96591.1 **Length:** 574 **Number of Matches:** 1

Range 1: 4 to 532 GenPept Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
213 bits(542)	9e-60	Compositional matrix adjust.	157/556(28%)	260/556(46%)	35/556(6%)

```
Query  91   RKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRS-SIIRNVLPRHEQGGVFAAEGYA  149
            +     + E LE+ GV  V+  PG +  E  + L    + ++ +  RHE+    AA   A
Sbjct  4    KTAGQAMTELLEQWGVDHVYGIPGDSINEFIEELRHERNQLKFIQTRHEEVAALAAAAEA  63

Query  150  RATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVT  209
            + TG  GVC++ +GPGA +L++GL DA  D  P++AI GQV    +G D FQE  + ++
Sbjct  64   KLTGKIGVCLSIAGPGAVHLLNGLYDAKADGAPVLAIAGQVSSGEVGRDYFQEIKLEQMF  123

Query  210  RSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVI--PDWDQPMRL  267
              +   N  V   E +P ++ +A   A S + G  ++ V  D+  + +   P +  P+ +
Sbjct  124  EDVAVFNREVHSAESLPDLLNQAIRTAYS-KKGVAVLSVSDDLFAEKIKREPVYTSPVYI  182

Query  268  PGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFVELTGIPVASTLM  327
             G +      P +  L    + I+ +KKP++  G G  ++  EL  F +    P+  TL
Sbjct  183  EGNLE-----PKKEQLVTCAQYINNAKKPIILAGQGMKKAKRELLEFADKAAAPIVVTLP  237

Query  328  GLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVH  387
              G  P      L  LG  GT  A  A++  DLL+  G  F  R     +        +
Sbjct  238  AKGVVPDKHPHFLGNLGQIGTKPAYEAMEECDLLIMLGTSFPYR-----DYLPDDTPAIQ  292

Query  388  IDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLD-----FSAWRQELTVQK  442
            +D D A+IGK       +  D  L L+ L   +E KE +  L+        W  E+   +
Sbjct  293  LDSDPAKIGKRYPVTAGLVCDSALGLRELTEYIERKEDRRFLNACTEHMQHWWNEIEKDE  352

Query  443  VKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSG  502
             +     K       PQ  +  L E     A++S  VG   +W A+++K    + ++ S
Sbjct  353  TEATTPLK-------PQQVVARLQEAAADDAVLSVDVGTVTVWMARHFKMNANQDFIVSS  405

Query  503  GLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHL  562
             L  MG GLP AI A++  P+   + + GDG F M +Q+L T     LP+ +++LNN++L
Sbjct  406  WLATMGCGLPGAIAASLSEPERQAIAVCGDGGFSMVMQDLPTAVKYKLPITVVILNNENL  465

Query  563  GMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQKM  622
            GM +++E +        T L N    A        FAE+CG    +VT  ++L  A  +
Sbjct  466  GM-IEYEQQVKGNIDYVTKLQNVDYAA--------FAESCGAKGIKVTKAEELAPAFHEA  516

Query  623  LDTPGPYLLDVIVPHQ  638
            L +  P ++DV++ ++
Sbjct  517  LHSDQPVVVDVMIGNE  532
```

Related Information

Gene - associated gene details

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RecName: Full=Pyruvate dehydrogenase [ubiquinone]; AltName: Full=Pyruvate oxidase; Short=POX; Contains: RecName: Full=Alpha-peptide

Sequence ID: P07003.1 **Length:** 572 **Number of Matches:** 1

Related Information

Range 1: 9 to 535 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
198 bits(504)	2e-54	Compositional matrix adjust.	160/548(29%)	255/548(46%)	22/548(4%)

```
Query  97   LVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATGFPG  156
            + + LE  GV  ++   G +   +  +L R   I  +  RHE+   FAA   A+ +G
Sbjct  9    IAKTLESAGVKRIWGVTGDSLNGLSDSLNRMGTIEWMSTRHEEVAAFAAGAEAQLSGELA  68

Query  157  VCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSITKHN  216
            VC  + GPG  +L++GL D   + VP++AI   +P   IG+  FQET   E+ R  + +
Sbjct  69   VCAGSCGPGNLHLINGLFDCHRNHVPVLAIAAHIPSSEIGSGYFQETHPQELFRECSHYC  128

Query  217  YLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRLPK  276
             LV   E IP+V+  A   A   R G  ++ +P D+     +    +   +  Y +  P
Sbjct  129  ELVSSPEQIPQVLAIAMRKAVLNR-GVSVVVLPGDV----ALKPAPEGATMHWYHAPQPV  183

Query  277  L-PNEMLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFVELTGIPVASTLMGLGAFPTG  335
            + P E  L ++ +L+  S    L  G GC+ + +EL  F      P+   L G
Sbjct  184  VTPEEEELRKLAQLLRYSSNIALMCGSGCAGAHKELVEFAGKIKAPIVHALRGKEHVEYD  243

Query  336  DELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEI  395
            +   + M G+ G     + + ++D L+  G +F  R       + + AKI+ IDI+ A I
Sbjct  244  NPYDVGMTGLIGFSSGFHTMMNADTLVLLGTQFPYRAF-----YPTDAKIIQIDINPASI  298

Query  396  GKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVKYPLNFKTFGDA  455
            G + +  +++  DIK  L+ L  ++E K  +  LD  A       +K    L  K    A
Sbjct  299  GAHSKVDMALVGDIKSTLRALLPLVEEKADRKFLD-KALEDYRDARKGLDDLA-KPSEKA  356

Query  456  IPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAI  515
            I PQY  Q +       AI +  VG   +WAA+Y K    R+ L S   G+M   +P A+
Sbjct  357  IHPQYLAQQISHFAADDAIFTCDVGTPTVWAARYLKMNGKRRLLGSFNHGSMANAMPQAL  416

Query  516  GAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKA  575
            GA    P+  VV + GDG F M + +  ++    LPVKI++ NN  LG V
Sbjct  417  GAQATEPERQVVAMCGDGGFSMLMGDFLSVVQMKLPVKIVVFNNSVLGFVAM-------E  469

Query  576  NRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIV  635
             +A  YL + +   +   N  + AEACG+   RV    ++  A+Q+     GP L+DV+V
Sbjct  470  MKAGGYLTDGTELHDT--NFARIAEACGITGIRVEKASEVDEALQRAFSIDGPVLVDVVV  527

Query  636  PHQEHVLP  643
              +E  +P
Sbjct  528  AKEELAIP  535
```

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RecName: Full=Acetolactate synthase; AltName: Full=ALS; AltName: Full=Acetohydroxy-acid synthase

Sequence ID: Q04789.3 **Length:** 570 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 14 to 550 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
185 bits(470)	1e-49	Compositional matrix adjust.	144/564(26%)	266/564(47%)	40/564(7%)

```
Query  91   RKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYAR  150
             +G++++V+ L  +GVT VF  PG     +  AL        ++ RHEQ   F A+   R
Sbjct  14   NRGAELVVDCLVEQGVTHVFGIPGAKIDAVFDALQDKGP-EIIVARHEQNAAFMAQAVGR  72

Query  151  ATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTR  210
             TG PGV + TSGPGA+NL +GL  A  +  P+VA+ G V R        Q      + +
Sbjct  73   LTGKPGVVLVTSGPGASNLATGLLTANTEGDPVVALAGNVIRADRLKRTHQSLDNAALFQ  132

Query  211  SITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGY  270
             ITK++  V DV++IP  V  AF +A +G+ G   +  P+D+  ++      + +  P
Sbjct  133  PITKYSVEVQDVKNIPEAVTNAFRIASAGQAGAAFVSFPQDVVNEVTNTKNVRAVAAP--  190

Query  271  MSRLPKLPNEMLLEQIVRLISESKKPVLYVG--GGCSQSSEELRRFVELTGIPVASTLMG  328
              +L    ++ +   I + I  +K PV+ VG  GG  ++ + +R+ ++   +P   T
Sbjct  191  --KLGPAADDAISAAIAK-IQTAKLPVVLVGMKGGRPEAIKAVRKLLKKVQLPFVETYQA  247

Query  329  LGAFPTG-DELSLSMLGMHGTVYANYAVDSSDLLLAFG---VRFDDRVTGKLEAFASRAK  384
             G      ++     +G+      +  ++ +D++L  G   + +D     K
Sbjct  248  AGTLSRDLEDQYFGRIGLFRNQPGDLLLEQADVVLTIGYDPIEYDP----KFWNINGDRT  303

Query  385  IVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVK  444
            I+H+D   A+I    QP + +  DI       ++I   +   +K++F+   Q++     +
Sbjct  304  IIHLDEIIADIDHAYQPDLELIGDIP------STINHIEHDAVKVEFAEREQKILSDLKQ  357

Query  445  Y-------PLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQ  497
            Y       P ++K+  D   P   ++ L    +    ++  +G H +W ++Y++  +P
Sbjct  358  YMHEGEQVPADWKS--DRAHPLEIVKELRNAVDDHVTVTCDIGSHAIWMSRYFRSYEPLT  415

Query  498  WLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLL  557
             + S G+  +G  LP AIGA++ +P E VV + GDG F+ +  EL T      P+  ++
Sbjct  416  LMISNGMQTLGVALPWAIGASLVKPGEKVVSVSGDGGFLFSAMELETAVRLKAPIVHIVW  475
```

```
Query  558  NNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRA  617
            N+    MV   + + Y    A  + GN         +++K+AE+ G    RV   D L
Sbjct  476  NDSTYDMVAFQQLKKYNRTSAVDF-GN--------IDIVKYAESFGATGLRVESPDQLAD  526

Query  618  AIQKMLDTPGPYLLDVIVPHQEHV  641
             +++ ++  GP ++DV V + +++
Sbjct  527  VLRQGMNAEGPVIIDVPVDYSDNI  550
```

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RecName: Full=Sulfoacetaldehyde acetyltransferase

Sequence ID: Q93PS3.1 **Length:** 584 **Number of Matches:** 1

Related Information

Range 1: 9 to 534 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
185 bits(470)	1e-49	Compositional matrix adjust.	155/551(28%)	253/551(45%)	46/551(8%)

```
Query  94   SDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATG  153
            S+ + E L  EGVT V    G A M++   L  ++ I  +  RHEQ      + Y R TG
Sbjct  9    SEAMTEVLVNEGVTHVTGILGSAFMDMLD-LWPTAGIEFIAVRHEQTAGHMQDAYCRITG  67

Query  154  FPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSIT  213
               VCI  +GPG TNLV+ +A A     P+V +        +G D FQE   V + RSIT
Sbjct  68   KASVCIGQNGPGVTNLVTCVAAANQAHTPMVVLGPSAGTPTVGWDGFQECDQVSIFRSIT  127

Query  214  KHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKD-----IQQQLVIPDWDQPMRLP  268
            K    V        V+R AF +A + R GPV +D+P++     + ++++ PD  + M +
Sbjct  128  KQVLQVPHPSRAGDVLRTAFRIAYAER-GPVYVDIPRNYFYGEVYEEILRPDQYRAMNVR  186

Query  269  GYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTL  326
            G         +   L +   +++ +K PV+  G G   + +  E++    +   PVA +
Sbjct  187  G-------AGDATELARATEILAAAKNPVIISGRGVVDADAFAEVKEIAHMLTAPVAMSY  239

Query  327  MGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKL-----EAFAS  381
            +    +P  DEL +  +G  G   A Y++  +D++LA G R    V G L       F
Sbjct  240  LHNDTYPADDELWVGPIGYMGAKSAMYSLQDADVILAIGSRLS--VFGTLPQYDINYFPE  297

Query  382  RAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKE---------GKLKLDFS  432
             AKI+ I+++  +IG+     V I  D KLA   L  +L++K           K++    +
Sbjct  298  NAKIIQIEVNPKQIGRRHPVTVPIIGDAKLATAELIKLLKAKGDVKPNAERLAKIQERRN  357

Query  433  AWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKY  492
             W +E+  +    P      G+ I P+  +  + +L    AI++T +G     A  Y+K+
Sbjct  358  DWFKEIE-EMAMMP------GNPINPRRVLFEVAKLMPEDAILTTDIGNVASTANSYFKF  410

Query  493  RKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPV  552
             KP++ + +   G  GF   A +GA +  PD  VV I GDG++  ++ E++T     LPV
Sbjct  411  TKPKKHIAALTFGNTGFAYQAGLGAQMAEPDSPVVAIVGDGAWGQSLHEISTAVQYKLPV  470

Query  553  KIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHR  612
               +  N       + +  FY      T + NP        + +  AEA G    RV
Sbjct  471  IACVFRNMAWCAEKKNQIDFYNNRFVGTEIPNPI-------SFIPAAEAFGAKGIRVEKP  523

Query  613  DDLRAAIQKML  623
            +D+  A ++ L
Sbjct  524  EDIADAFKQGL  534
```

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RecName: Full=Sulfoacetaldehyde acetyltransferase

Sequence ID: Q84H44.3 **Length:** 598 **Number of Matches:** 1

Related Information

Range 1: 18 to 557 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
183 bits(464)	1e-48	Compositional matrix adjust.	150/563(27%)	257/563(45%)	54/563(9%)

```
Query  94   SDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPR-HEQGGVFAAEGYARAT  152
            S+  VE +   GVT++F   G A M+       + I   ++P  HEQG    A+G+AR +
Sbjct  18   SEAFVETMVANGVTEIFGIMGSAFMDAMDIFAPAGI--KLIPVVHEQGAAHMADGFARVS  75

Query  153  GFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSI  212
            G  GV I  +GPG +N V+ +A A     P+V +T +     IG   FQE   + + +
Sbjct  76   GRTGVVIGQNGPGISNCVTAIAAAYWAHTPVVIVTPEAGTTGIGLGGFQEARQLPMFQEF  135

Query  213  TKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKD-----IQQQLVIPDWDQPM-R  266
            TK+   V     +       F  AR    GP  +++P+D     I+ ++ +P   QP+ R
Sbjct  136  TKYQGHVTHPARMAEYTARCFARARD-EMGPAQLNIPRDYFYGKIKCEIPLP---QPLDR  191

Query  267  LPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVAS  324
             PG             L+   RL++E+K PV+  GGG     + EE +   E  G PV +
Sbjct  192  GPG---------GAQSLDAAARLLAEAKFPVIISGGGVVMGDAVEECKALAERLGAPVVN  242

Query  325  TLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVR---FDDRVTGKLEAFAS  381
            + +   +FP    L    LG  G+  A   +  +D++LA G R   F       L+ +
Sbjct  243  SYLHNDSFPASHPLWCGPLGYQGSKAAMKLLADADVVLALGTRLGPFGTLPQHGLDYWPK  302

Query  382  RAKIVHIDIDSAEIGKNKQPHVSICADIKLA-------LQGLNSILES----KEGKLKLD  430
             A+I+ +D DS  +G  K+  V +C D K +       + G+    ++    +  +++ +
Sbjct  303  NARIIQVDADSKMLGLVKKITVGVCGDAKASAAEISRRIDGMKLACDANKAERAARIQAE  362

Query  431  FSAWRQELTV---QKVKYPLNF-----KTFGDAIPPQYAIQVLDELTNGSAIISTGVGQH  482
              AW QELT    ++  + L+      K  G+ + P+  ++ L++      ++ST +G
```

```
Sbjct  363  KDAWEQELTDWTHERDPFSLDMIEEQSKEEGNWLHPRQVLRELEKAMPEDVMVSTDIGNI  422

Query  483  QMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQEL  542
               A  Y ++ KPR +  +   G  G+  P  IGA V  P    V   GDG++ M++ E+
Sbjct  423  NSVANSYLRFEKPRSFFAAMSWGNCGYAFPTIIGAKVAAPHRPAVSYAGDGAWGMSMSEI  482

Query  543  ATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEAC  602
             T    ++PV  ++ +N+  G   + +  FY        L     E+E F  + +   A
Sbjct  483  MTCVRHDIPVTAVVFHNRQWGAEKKNQVDFYNRRFVAGEL-----ESESFAGIARAMGAE  537

Query  603  GVPAARVTHRDDLRAAIQKMLDT  625
            GV   R+   +D+  A++K +D
Sbjct  538  GVVVDRI---EDVGPALKKAIDA  557
```

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RecName: Full=Acetolactate synthase, catabolic; Short=ALS

Sequence ID: P27696.1 **Length:** 559 **Number of Matches:** 1

Related Information

Range 1: 13 to 550 GenPept Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
178 bits(452)	3e-47	Compositional matrix adjust.	157/575(27%)	270/575(46%)	60/575(10%)

```
Query  93   GSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARAT  152
            G+D++V  LE +GV  VF  PG    ++  +L  SSI R +  RHE    F A    R T
Sbjct  13   GADLVVSQLEAQGVRQVFGIPGAKIDKVFDSLLDSSI-RIIPVRHEANAAFMAAAVGRIT  71

Query  153  GFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSI  212
            G  GV + TSGPG +NL++G+A A  +  P+VA+ G V R        Q    V +   +
Sbjct  72   GKAGVALVTSGPGCSNLITGMATANSEGDPVVALGGAVKRADKAKQVHQSMDTVAMFSPV  131

Query  213  TKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMR---LPG  269
            TK+   V   + +  VV  AF  A  GRPG   + +P+D+         D P+    LP
Sbjct  132  TKYAIEVTAPDALAEVVSNAFRAAEQGRPGSAFVSLPQDVV--------DGPVSGKVLPA  183

Query  270  YMSRLPKL---PNEMLLEQIVRLISESKKPVLYVGGGCSQ--SSEELRRFVELTGIPVAS  324
              S  P++   P++  ++Q+ +LI+++K P+  +G   SQ  +S+ LRR +E + IPV S
Sbjct  184  --SGAPQMGAAPDDA-IDQVAKLIAQAKNPIFLLGLMASQPENSKALRRLLETSHIPVTS  240

Query  325  TLMGLGAFPTGDELSLSMLGMHGTVYANYAVDS----SDLLLAFG---VRFDDRVTGKLE  377
            T    GA    ++ + S       ++ N A D     +DL++  G   V ++   +
Sbjct  241  TYQAAGAV---NQDNFSRFAGRVGLFNNQAGDRLLQLADLVICIGYSPVEYEPAMWN---  294

Query  378  AFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNS------ILESKEGKLKLDF  431
              +  A +VHID+  A   +N  P V +  DI   L  L        +L  +  ++  D
Sbjct  295  --SGNATLVHIDVLPAYEERNYTPDVELVGDIAGTLNKLAQNIDHRLVLSPQAAEILRDR  352

Query  432  SAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYK  491
               R+ L  +  +       F  A+ P   ++ + ++ N    ++  +G   +W A+Y
Sbjct  353  QHQRELLDRRGAQ----LNQF--ALHPLRIVRAMQDIVNSDVTLTVDMGSFHIWIARYLY  406

Query  492  YRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELAT-IKVENL  550
              + RQ + S G   MG  LP AIGA +  P+  VV + GDG F+ +  EL T ++++
Sbjct  407  TFRARQVMISNGQQTMGVALPWAIGAWLVNPERKVVSVSGDGGFLQSSMELETAVRLKAN  466

Query  551  PVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLK-FAEACGVPAARV  609
             + ++ ++N +  + +Q E ++ +            +  E  P   K +AE+ G     V
Sbjct  467  VLHLIWVDNGYNMVAIQEEKKYQRL-----------SGVEFGPMDFKAYAESFGAKGFAV  515

Query  610  THRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPM  644
               + L   ++  +D  GP ++ + V ++++ L M
Sbjct  516  ESAEALEPTLRAAMDVDGPAVVAIPVDYRDNPLLM  550
```

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RecName: Full=2-hydroxyacyl-CoA lyase; AltName: Full=2-hydroxyphytanoyl-CoA lyase; Short=2-HPCL; AltName: Full=Oxalyl-CoA decarboxylase

Sequence ID: Q9LF46.1 **Length:** 572 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 14 to 557 GenPept Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
174 bits(442)	8e-46	Compositional matrix adjust.	161/576(28%)	261/576(45%)	65/576(11%)

```
Query  93   GSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSI--IRNVLPRHEQGGVFAAEGYAR  150
            G+ ++ ++L   GVT +F   G   + +    +R+    IR +   +EQ   +AA  Y
Sbjct  14   GNVLVAKSLSHLGVTHMFGVVG---IPVTSLASRAMALGIRFIAFHNEQSAGYAASAYGY  70

Query  151  ATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTR  210
             TG PG+ +  SGPG  + ++GL++A +++ P+V I+G   +R +G   FQE   +E  +
Sbjct  71   LTGKPGILLTVSGPGCVHGLAGLSNAWVNTWPMVMISGSCDQRDVGRGDFQELDQIEAVK  130

Query  211  SITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGY  270
            + +K +    DV +IP  V      A SGRPG   +D+P D+ +Q +     +  +L
Sbjct  131  AFSKLSEKAKDVREIPDCVSRVLDRAVSGRPGGCYLDIPTDVLRQKI--SESEADKLVDE  188

Query  271  MSRLPK-------LPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIP  321
            + R  K       L +E  +E  V L+ ++++P++  G G   S++ +EL++ VE+TGIP
Sbjct  189  VERSRKEEPIRGSLRSE--IESAVSLLRKAERPLIVFGKGAAYSRAEDELKKLVEITGIP  246

Query  322  VASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVT-GKLEAFA  380
               T MG G  P   E S        T   + A+   D+ L  G R +  + G+   +
```

```
Sbjct  247  FLPTPMGKGLLPDTHEFS-------ATAARSLAIGKCDVALVVGARLNWLLHFGESPKWD  299

Query  381  SRAKIVHIDIDSAEIGKNKQPHVSICADIK--------------LALQGLNSILESKEGK  426
               K + +D+   EI + ++PH+ I  D K                L   NS +ES   K
Sbjct  300  KDVKFILVDVSEEEI-ELRKPHLGIVGDAKTVIGLLNREIKDDPFCLGKSNSWVESISKK  358

Query  427  LKLDFSAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWA  486
             K +    + E+ + K   P NF T      P   I+       G + +    G + M
Sbjct  359  AKEN--GEKMEIQLAKDVVPFNFLT------PMRIIRDAILAVEGPSPVVVSEGANTMDV  410

Query  487  AQYYKYRK-PRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATI  545
             +    +K PR  L +G  G MG GL   I AAV  PD +VV ++GD  F  +  E+ T+
Sbjct  411  GRSVLVQKEPRTRLDAGTWGTMGVGLGYCIAAAVASPDRLVVAVEGDSGFGFSAMEVETL  470

Query  546  KVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNE----AEIFPN--MLKFA  599
               NL V I++ NN      V   DR     R    +  P  E        PN    K
Sbjct  471  VRYNLAVVIIVFNNGG----VYGGDR-----RGPEEISGPHKEDPAPTSFVPNAGYHKLI  521

Query  600  EACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIV  635
            EA G     V   D+L++A+ +      P +++VI+
Sbjct  522  EAFGGKGYIVETPDELKSALAESFAARKPAVVNVII  557
```

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RecName: Full=Sulfoacetaldehyde acetyltransferase

Sequence ID: Q84H41.3 **Length:** 603 **Number of Matches:** 1

Related Information

Range 1: 19 to 561 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
172 bits(436)	8e-45	Compositional matrix adjust.	148/560(26%)	250/560(44%)	46/560(8%)

```
Query  94   SDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATG  153
            S+  VE     GV+++F   G A M+       + I R +   HEQG    A+GYAR +G
Sbjct  19   SEAFVETCVANGVSEMFGIMGSAFMDAMDIFAPAGI-RLIPVVHEQGAAHMADGYARVSG  77

Query  154  FPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSIT  213
              GV I  +GPG +N V+G+A A     P+V +T +     +G   FQE   + + +  T
Sbjct  78   RHGVVIGQNGPGISNCVTGIAAAYWAHSPVVIVTPETGTMGMGLGGFQEANQLPMFQEFT  137

Query  214  KHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLP-GYMS  272
            K+   V + + +       F  A S   GP  +++P+D     +  +  +PMR+  G+
Sbjct  138  KYQGHVCNPKRMAEFTGRVFDRAMS-EMGPTQLNIPRDYFYGEIECEIPKPMRVDRGH--  194

Query  273  RLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLG  330
                   E  L+  V L+  +K PV+  GGG     + EE ++  E  G PVA+  +
Sbjct  195  -----GGEASLQAAVELLKTAKFPVILAGGGVVMGDAVEEAKQLAERLGAPVATGYLRND  249

Query  331  AFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVR---FDDRVTGKLEAFASRAKIVH  387
            AFP    L    LG  G+  A   +  +D+++A G R   F       ++ +   AKI+
Sbjct  250  AFPAKHPLWAGPLGYQGSKAAMKLIAQADVVIALGSRMGPFGTLPQHGMDYWPKAAKIIQ  309

Query  388  IDIDSAEIGKNKQPHVSICADIKLALQ-----------GLNSILESKEGKLKLDFSAWRQ  436
            I+ D   +G  K+  V I  D K               G ++   ++   +  + +AW +
Sbjct  310  IEADHTNLGLVKKIAVGINGDAKAVAAELSRRLADVTLGCDATKAARADTIATEKAAWEK  369

Query  437  EL---TVQKVKYPLNF---------KTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQM  484
            EL   T ++  Y L+           T G  + P+  ++ L++      ++ST +G
Sbjct  370  ELDGWTHERDPYSLDMIEEAKGERTPTGGSYLHPRQVLRELEKAMPARVMVSTDIGNINS  429

Query  485  WAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELAT  544
             A  Y ++ +PR +      G  G+ LP  IGA    PD   +   GDG++ M++ E+ T
Sbjct  430  VANSYLRFDEPRSFFAPMSFGNCGYALPTIIGAKCAAPDRPAIAYAGDGAWGMSMMEIMT  489

Query  545  IKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGV  604
                ++PV  ++ +N+  G   + +  FY        L     E+E F ++   A+A G
Sbjct  490  AVRHDIPVTAVVFHNRQWGAEKKNQVDFYNRRFVAGEL-----ESESFSDI---AKAMGA  541

Query  605  PAARVTHRDDLRAAIQKMLD  624
                V H +D+  A+QK +D
Sbjct  542  EGIVVDHIEDVGPALQKAID  561
```

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RecName: Full=Probable sulfoacetaldehyde acetyltransferase

Sequence ID: Q92UW6.1 **Length:** 591 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 7 to 544 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
172 bits(435)	9e-45	Compositional matrix adjust.	146/556(26%)	243/556(43%)	44/556(7%)

```
Query  95   DVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATGF  154
            +  V+ L+  G+   F   G A M +     ++ I R     HE      A+G++RATG
Sbjct  7    EAFVKVLQMHGIEHAFGIIGSAMMPVSDLFPKAGI-RFWDCAHETNAGMMADGFSRATGT  65

Query  155  PGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSITK  214
              + I  +GPG T  ++ +  A  +  P++ +T Q   + IG   FQE   + +   +
Sbjct  66   MSMAIGQNGPGVTGFITAMKTAYWNHTPLLMVTPQAANKTIGQGGFQEVDQMAMFEEMVC  125

Query  215  HNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRL  274
            +   V D   IP V+      A  G   P  I++P+D   Q++  D  + +R      R
Sbjct  126  YQEEVRDPSRIPEVLNRVIEKAWRG-CAPAQINIPRDFWTQVIDVDLPRIVRF----ERP  180
```

```
Query  275  PKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLGAF  332
               P    + Q  RL+SE+K PV+  G G     + +E     E    PV        AF
Sbjct  181  AGGP--AAIAQAARLLSEAKFPVILNGAGVVIGNAIQESMALAEKLDAPVCCGYQHNDAF  238

Query  333  PTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVT---GKLEAFASRAKIVHID  389
            P    LS+  LG +G+  A   +  +D++LA G R +   T     ++ +   A I+ +D
Sbjct  239  PGSHRLSVGPLGYNGSKAAMELISKADVVLALGTRLNPFSTLPGYGIDYWPKDAAIIQVD  298

Query  390  IDSAEIGKNKQPHVSICADIKLALQGL---------NSILESKEGKLKLDFSAWRQELTV  440
            I++  IG  K+  V IC D K   Q +         ++  E ++  +    SAW Q+L+
Sbjct  299  INADRIGLTKKVTVGICGDAKQVAQQILQQLAPAAGDASREERKALVHQTRSAWLQQLSS  358

Query  441  --QKVKYPLNFKTFG------DAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKY  492
               +   P      G      D + P+   + +  +    AIIST +G +      Y  +
Sbjct  359  MDHEDDDPGTEWNVGARQREPDRMSPRQVWRAIQAVLPKEAIISTDIGNNCAIGNAYPSF  418

Query  493  RKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPV  552
             + R++L  G  G  G+G P+ +GA +G PD  VV   GDG+F +++ E+ +I  E  P
Sbjct  419  EQGRKYLAPGMFGPCGYGFPSIVGAKIGCPDVPVVGFAGDGAFGISMNEMTSIGREGWPA  478

Query  553  KIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSN--EAEIFPNM--LKFAEACGVPAAR  608
              M++   +     QW      A + +T L   +N    E+ PN+   K A+ CG+
Sbjct  479  ITMVIFRNY-----QW-----GAEKRNTTLWYDNNFVGTELNPNLSYAKVADGCGLKGVT  528

Query  609  VTHRDDLRAAIQKMLD  624
            V     L  A+ K ++
Sbjct  529  VDTPAALTEALAKAIE  544
```

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RecName: Full=Putative acetolactate synthase large subunit IlvB2; Short=ALS; AltName: Full=Acetohydroxy-acid synthase large subunit; Short=AHAS

Sequence ID: O06335.1 **Length:** 552 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 539 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
169 bits(427)	6e-44	Compositional matrix adjust.	154/561(27%)	256/561(45%)	46/561(8%)

```
Query  95   DVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATGF  154
            D LV  +   G++ V   P      +   L+R +  + VL RHE G  + A+G+ARA+G
Sbjct  5    DHLVARMRAAGISVVCGLPTSRLDSLLVRLSRDAGFQIVLARHEGGAGYLADGFARASG-  63

Query  155  PGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETP-----IVEVT  209
                +  +GPGATN++S +A+A ++ VP++ +TG+V     G  + Q+T      +
Sbjct  64   KSAAVFVAGPGATNVISAVANASVNQVPMLILTGEVAVGEFGLHSQQDTSDDGLGLGATF  123

Query  210  RSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPD--WDQPMRL  267
            R   + +  +  + +    +  AF    S   GPV I +P+D+  + +           L
Sbjct  124  RRFCRCSVSIESIANARSKIDSAFRALASIPRGPVHIALPRDLVDERLPAHQLGTAAAGL  183

Query  268  PGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQS--SEELRRFVELTGIPVAST  325
             G  +  P  P+  + ++++  +  S+ P+L +G GC      E++  F E  G+P A+T
Sbjct  184  GGLRTLAPCGPD--VADEVIGRLDRSRAPMLVLGNGCRLDGIGEQIVAFCEKAGLPFATT  241

Query  326  LMGLGAFPTGDELSLSMLGMHGTVYAN-YAVDS-SDLLLAFGVRFDDRVTGKLEAFASR-  382
              G G       LSL +LG+ G   A+ Y  D+  DLL+A GV F   VT    +F+ R
Sbjct  242  PNGRGIVAETHPLSLGVLGIFGDGRADEYLFDTPCDLLIAVGVSFGGLVT---RSFSPRW  298

Query  383  ----AKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQEL  438
                A +VH+D D + +G+     + I    +  +  LN     +          + + +
Sbjct  299  RGLKADVVHVDPDPSAVGRFVATSLGITTSGRAFVNALNCGRPPR----------FCRRV  348

Query  439  TVQ---KVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKP  495
             V+       P   +  G++I P   +  LD     +A I   VG    W  +    R+P
Sbjct  349  GVRPPAPAALPGTPQARGESIHPLELMHELDRELAPNATICADVGTCISWTFRGIPVRRP  408

Query  496  RQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIM  555
             ++  +     MG G+  AIG A+ RP+E V+ I GDG+F+M+  E++T     + V
Sbjct  409  GRFFATVDFSPMGCGIAGAIGVALARPEEHVICIAGDGAFLMHGTEISTAVAHGIRVTWA  468

Query  556  LLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNML-KFAEACGVPAARVTHRDD  614
            +LN+  +            A      + +PS  A I  N L   A A G    RV  R +
Sbjct  469  VLNDGQMS---------ASAGPVSGRM-DPSPVARIGANDLAAMARALGAEGIRVDTRCE  518

Query  615  LRAAIQKMLDTPGPYLLDVIV  635
            LRA +QK L   GP +LD+ +
Sbjct  519  LRAGVQKALAATGPCVLDIAI  539
```

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RecName: Full=Cyclohexane-1,2-dione hydrolase

Sequence ID: P0CH62.1 **Length:** 589 **Number of Matches:** 1

Related Information

Range 1: 4 to 567 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
169 bits(428)	7e-44	Compositional matrix adjust.	149/584(26%)	258/584(44%)	36/584(6%)

```
Query  91   RKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVL-PRHEQGGVFAAEGYA  149
            ++G+D++VEALE  G   V  + G  S  +  A ++S + + V+ P  E GG +   GY
Sbjct  4    KRGADLIVEALEEYGTEQVVGFIGHTSHFVADAFSKSHLGKRVINPATELGGAWMVNGYN  63
```

```
Query  150  RATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIG-TDAFQETPIVEV  208
                      A    G   L + + +A    +P V I      R+ G ++A Q+ P
Sbjct  64   YVKDRSAAVGAWHCVGNLLLHAAMQEARTGRIPAVHIGLNSDGRLAGRSEAAQQVPWQSF  123

Query  209  TRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLP  268
            T  I +    V  ++ +   + EAF +A     GP  +D+P D+    +    D    +P
Sbjct  124  T-PIARSTQRVERLDKVGEAIHEAFRVAEGHPAGPAYVDIPFDLTADQI----DDKALVP  178

Query  269  GYMSRLPKL---PNEMLLEQIVRLISESKKPVLYVGGGCSQS--SEELRRFVELTGIPVA  323
               +R   +   PNE + E   +L++ +K PV+  GGG ++S  SE L +  E+ G+PV
Sbjct  179  RGATRAKSVLHAPNEDVREAAAQLVA-AKNPVILAGGGVARSGGSEALLKLAEMVGVPVV  237

Query  324  STLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRA  383
            +T  G G FP    L++   G  G   AN  + ++D +L  G R  D   G  + + ++
Sbjct  238  TTSTGAGVFPETHALAMGSAGFCGWKSANDMMAAADFVLVLGSRLSD--WGIAQGYITKM  295

Query  384  -KIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQK  442
             K VH+D D A +G    P +S+ AD K  ++ L  +L    G   + +    +E   Q
Sbjct  296  PKFVHVDTDPAVLGTFYFPLLSVVADAKTFMEQLIEVLPGTSGFKAVRYQ--ERENFRQA  353

Query  443  VKYPLNFKTF------GDAIPPQY--AIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRK  494
             ++   +  +      GD +P     A+  + ++     II T +G H +        ++
Sbjct  354  TEFRAAWDGWVREQESGDGMPASMFRAMAEVRKVQRPEDIIVTDIGNHTLPMFGGAILQR  413

Query  495  PRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKI  554
            PR+ +TS   G +G G P A+GA +  P+  V    GDG+   +  E        LPV
Sbjct  414  PRRLVTSMAEGILGCGFPMALGAQLAEPNSRVFLGTGDGALYYHFNEFRVAVEHKLPVIT  473

Query  555  MLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDD  614
            M+  N+  G      +  +  N    ++          P+ +  A+A G     V    D
Sbjct  474  MVFTNESYGANWTLMNHQFGQNNWTEFMN---------PDWVGIAKAFGAYGESVRETGD  524

Query  615  LRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSGGAFKDVITEG  658
            +  A+Q+ +D+  P L+++ V   +  L   P GG   +++ +G
Sbjct  525  IAGALQRAIDSGKPALIEIPVSKTQG-LASDPVGGVGPNLLLKG  567
```

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RecName: Full=2-hydroxyacyl-CoA lyase 1; AltName: Full=2-hydroxyphytanoyl-CoA lyase; Short=2-HPCL; AltName: Full=Phytanoyl-CoA 2-hydroxylase 2

Sequence ID: Q8CHM7.1 **Length:** 581 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 14 to 565 GenPept Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
162 bits(410)	2e-41	Compositional matrix adjust.	155/585(26%)	257/585(43%)	67/585(11%)

```
Query  88   DEPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSI-IRNVLPRHEQGGVFAAE  146
            +E   G+ V+ +AL+ + V  +F   G    EI  AL    + I+ + R+EQ    +AA
Sbjct  14   EEQVSGAKVIAQALKTQDVEYMFGVVGIPVTEI--ALAAQELGIKYIGMRNEQAACYAAS  71

Query  147  GYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIV  206
                 TG PGVC+  SGPG  + + G+A+A ++  P++ I G   R      AFQE P V
Sbjct  72   AVGYLTGRPGVCLVVSGPGLIHALGGMANANMNCWPLIVIGGSSERNQEAMGAFQEFPQV  131

Query  207  EVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDI--QQQLVIPDWDQP  264
            E  R  +K +     ++ IP V+ +A   +  GRPG   IDVP D+   Q+       +
Sbjct  132  EACRLYSKFSARPSSIQHIPFVIEKAVRSSIYGRPGACYIDVPADLVTLQESTTSIKYKE  191

Query  265  MRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSSEE--LRRFVELTGIPV  322
              +P  +S    L     +     ++  +K+P+L +G G + S  E  +R+ VEL  +P
Sbjct  192  CCMPPPLS----LAETSAVRAAASVLRSAKQPLLIIGKGAAYSHAEDSIRKLVELCNLPF  247

Query  323  ASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKL-EAFAS  381
              T MG G  P      +           + A+  +D+++ FG R +  +   L   + +
Sbjct  248  LPTPMGKGVVPDNHPNCVG-------AARSRALQFADVIVLFGARLNWILHFGLPPRYQA  300

Query  382  RAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWR------  435
              K + IDI + E+G N +P V++  D+    + L         +   D   W
Sbjct  301  DVKFIQIDICAEELGNNVRPSVTLLGDVNAVSKQLLEQFVKNPWQYPTDSKWWETLREKR  360

Query  436  -------QELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQ  488
                   +EL  +K   P+N+ T        Y +Q  ++L     I+S G     +
Sbjct  361  KNNEAVSKELASKK-SLPMNYYTVF------YHVQ--EQLPRNCFIVSEGANTMDIGRTV  411

Query  489  YYKYRKPRQWLTSGGLGAMGFGLPAAIGAAV----GRPDEVVVDIDGDGSFIMNVQELAT  544
               Y  PR  L +G  G MG GL  AI AAV      P + V+ ++GD +F  +  E+ T
Sbjct  412  LQNYL-PRHRLDAGSFGTMGVGLGFAIAAAVVAKERSPGQRVICVEGDSAFGFSGMEVET  470

Query  545  IKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTY--LGNPSNEAEIFPNML------  596
            I   NLP+ I+++NN  +          Y+   A T+  + N    A   P M
Sbjct  471  ICRYNLPIIILVVNNNGI----------YQGFDADTWGKILNFQGTATTIPPMCLLPNSH  520

Query  597  --KFAEACGVPAARVTHRDDLRAAIQKML-DTPGPYLLDVIVPHQ  638
              +   A G     V   ++L+ ++++ L DT  P L+++++  Q
Sbjct  521  YEQVMTAFGGKGYFVQTPEELQDSLRQALKDTSKPCLINIMIEPQ  565
```

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RecName: Full=2-hydroxyacyl-CoA lyase 1; AltName: Full=2-hydroxyphytanoyl-CoA lyase; Short=2-HPCL; AltName: Full=Phytanoyl-CoA 2-hydroxylase 2

Sequence ID: Q9QXE0.2 **Length:** 581 **Number of Matches:** 1

Related Information

Range 1: 14 to 565 GenPept Graphics Next Match Previous Match

Gene - associated gene details

Score	Expect	Method	Identities	Positives	Gaps
160 bits(404)	1e-40	Compositional matrix adjust.	153/581(26%)	256/581(44%)	59/581(10%)

```
Query  88   DEPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSI-IRNVLPRHEQGGVFAAE  146
            +E   G+ V+ +AL+ + V  +F   G    EI  AL    + I+ +  R+EQ   +AA
Sbjct  14   EEQVSGAKVIAQALKTQDVEYMFGVVGIPVTEI--ALAAQELGIKYIGMRNEQAACYAAS  71

Query  147  GYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIV  206
                 TG PGVC+  SGPG  + + G+A+A ++  P++ I G   R      AFQE P V
Sbjct  72   AVGYLTGRPGVCLVVSGPGLIHALGGMANANMNCWPLIVIGGSSERNQEAMGAFQEFPQV  131

Query  207  EVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKD---IQQQLVIPDWDQ  263
            E  R  TK +     +E IP ++ +A   +  GRPG   ID+P D   +Q  +    + +
Sbjct  132  EACRLYTKFSARPSTIELIPFIIEKAVRSSIYGRPGACYIDIPADFVTLQANVTSIKYKE  191

Query  264  PMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSSEE--LRRFVELTGIP  321
                P        +     +     ++ ++K+P+L +G G + S  E  +R+ VE   +P
Sbjct  192  CCMPPPV-----SMAETSAVCAAASVLRDAKQPLLIIGKGAAYSHAEDSIRKLVEQCSLP  246

Query  322  VASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVT-GKLEAFA  380
               T MG G  P      +           + A+ S+D+++ FG R +  +  G    +
Sbjct  247  FLPTPMGKGVVPDNHPNCVG-------AARSRALQSADVIVLFGARLNWILHFGLPPRYQ  299

Query  381  SRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWR-----  435
            +  K + IDI + E+G N +P V +  DI    + L    +    +   D   W+
Sbjct  300  ADVKFIQIDICAEELGNNVRPSVILLGDIDAVSKQLLEQFDKTPWQCPPDSQWWKTLREK  359

Query  436  --------QELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAA  487
                    +EL  QK   P+N+ T        Y +Q  ++L   S I+S G     +
Sbjct  360  MKSNEAISKELASQK-SLPMNYYTVF------YHVQ--EQLPRDSFIVSEGANTMDI-GR  409

Query  488  QYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAV----GRPDEVVVDIDGDGSFIMNVQELA  543
               +   PR  L +G  G MG GL  AI AA+      P + V+ ++GD +F  +  E+
Sbjct  410  TMLQNCLPRHRLDAGSFGTMGVGLGFAIAAALVAKDRSPGQRVICVEGDSAFGFSGMEVE  469

Query  544  TIKVENLPVKIMLLNNQHLGMVVQ---WEDRFYKANRAHTYLGNPSNEAEIFPN--MLKF  598
            TI   NLP+ ++++NN  +        WE   +    A T          + PN    +
Sbjct  470  TICRYNLPIILLVVNNNGIYQGFDADTWEKMLHFQEAATTV-----PPMCLLPNSHYEQV  524

Query  599  AEACGVPAARVTHRDDLRAAIQKML-DTPGPYLLDVIVPHQ  638
              A G     V   ++L+ ++++ L DT  P LL++++  Q
Sbjct  525  MTAFGGKGYFVRTPEELQHSLRQALQDTSKPCLLNIMIEPQ  565
```

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RecName: Full=Pyruvate oxidase; AltName: Full=Pyruvic oxidase; Short=POX

Sequence ID: Q54970.2 **Length:** 591 **Number of Matches:** 1

Related Information

Range 1: 9 to 519 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
160 bits(404)	1e-40	Compositional matrix adjust.	143/539(27%)	236/539(43%)	41/539(7%)

```
Query  94   SDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATG  153
            S  ++  L+  GV  ++  P G    +  AL     IR +  RHE+ G  AA   A+  G
Sbjct  9    SAAMLNVLKTWGVDTIYGIPSGTLSSLMDALAEDKDIRFLQVRHEETGALAAVMQAKFGG  68

Query  154  FPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSIT  213
              GV + + GPGAT+L++G+ DA +D+ P +AI G  P   +  DAFQE     +   I
Sbjct  69   SIGVAVGSGGPGATHLINGVYDAAMDNTPFLAILGSRPVNELNMDAFQELNQNPMYNGIA  128

Query  214  KHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSR  273
             +N  V   E +P+V+ EA   A S + GP ++++P +   Q +    +      G   R
Sbjct  129  VYNKRVAYAEQLPKVIDEACRAAVS-KKGPAVVEIPVNFGFQEID---ENSYYGSGSYER  184

Query  274  LPKLP--NEMLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFVELTGIPVASTLMGLGA  331
                P  NE+ +++ V +++ +++PV+Y G G  ++ E +         P+ +T     A
Sbjct  185  SFIAPALNEVEIDKAVEILNNAERPVIYAGFGGVKAGEVITELSRKIKAPIITTGKNFEA  244

Query  332  FPTGDELSLSMLGMHGTVY------ANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKI  385
            F    E      G+ G+ Y      AN  V  +D +L  G  F        EAF +  K
Sbjct  245  FEWNYE------GLTGSAYRVGWKPANEVVFEADTVLFLGSNFP--FAEVYEAFKNTEKF  296

Query  386  VHIDIDSAEIGKNKQPHVSICAD----IKLALQGLNSILESKEGKLKL-DFSAWRQELTV  440
            + +DID  ++GK      SI  D     K  L  +N +  +   +  + +   WR  +
Sbjct  297  IQVDIDPYKLGKRHALDASILGDAGQAAKAILDKVNPVESTPWWRANVKNNQNWRDYMN-  355

Query  441  QKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLT  500
                  L  KT G+    Q     +++  +  AI S  VG     + ++        W T
Sbjct  356  -----KLEGKTEGELQLYQ-VYNAINKHADQDAIYSIDVGNTTQTSTRHLHMTPKNMWRT  409

Query  501  SGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQ  560
            S     MG  LP  I A    PD  V +I GDG+F M   ++ T    +LPV  ++ +N
Sbjct  410  SPLFATMGIALPGGIAAKKDNPDRQVWNIMGDGAFNMCYPDVITNVQYDLPVINLVFSNA  469

Query  561  HLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAI  619
              G +   ++++   N+ H +  + +N      +  K AEA G     V   +D+ A +
Sbjct  470  EYGFI---KNKYEDTNK-HLFGVDFTN-----ADYAKIAEAQGAVGFTVDRIEDIDAVV  519
```

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RecName: Full=Pyruvate oxidase; AltName: Full=Pyruvic oxidase; Short=POX

Sequence ID: P37063.3 **Length:** 603 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 17 to 544 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
160 bits(404)	1e-40	Compositional matrix adjust.	143/547(26%)	249/547(45%)	27/547(4%)

```
Query  97    LVEALEREGVTDVFAYPGGASMEIHQALT-RSSIIRNVLPRHEQGGVFAAEGYARATGFP  155
             +++ LE  GV  ++  PGG+   I  AL+     I  +  RHE+ G  AA   A+ TG
Sbjct  17    VIKVLEAWGVDHLYGIPGGSINSIMDALSAERDRIHYIQVRHEEVGAMAAAADAKLTGKI  76

Query  156   GVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSITKH  215
             GVC  ++GPG T+L++GL DA  D VP++A+ GQ     +  D FQE     +   +  +
Sbjct  77    GVCFGSAGPGGTHLMNGLYDAREDHVPVLALIGQFGTTGMNMDTFQEMNENPIYADVADY  136

Query  216   NYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDI-QQQLVIPDWDQPMRLPGYMSRL  274
             N   ++   +P V+ EA   A + + G  ++ +P D+  QQ+   DW        Y + L
Sbjct  137   NVTAVNAATLPHVIDEAIRRAYAHQ-GVAVVQIPVDLPWQQIPAEDWYASAN--SYQTPL  193

Query  275   PKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFVELTGIPVASTLMGLGAFPT  334
                P+   + ++ + +  +++P++Y G G  ++ +EL +  +   IP+ ST    G
Sbjct  194   LPEPDVQAVTRLTQTLLAAERPLIYYGIGARKAGKELEQLSKTLKIPLMSTYPAKGIVAD  253

Query  335   GDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAE  394
                  L          AN A+  +D++L  G  +      K  AF +    + IDID A+
Sbjct  254   RYPAYLGSANRVAQKPANEALAQADVVLFVGNNYPFAEVSK--AFKNTRYFLQIDIDPAK  311

Query  395   IGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVKYPLNFKTFGD  454
             +GK  +  +++ AD +  L  + + +  +E       + W Q        +     +  D
Sbjct  312   LGKRHKTDIAVLADAQKTLAAILAQVSERES------TPWWQANLANVKNWRAYLASLED  365

Query  455   AIP-PQYAIQVL---DELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFG  510
                 P  A QVL   +++    AI S  VG   + A ++ K     + +TS     MG G
Sbjct  366   KQEGPLQAYQVLRAVNKIAEPDAIYSIDVGDINLNANRHLKLTPSNRHITSNLFATMGVG  425

Query  511   LPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWED  570
             +P AI A +  P+  V ++ GDG   M +Q+LAT    +LPV  ++  N   G +   +D
Sbjct  426   IPGAIAAKLNYPERQVFNLAGDGGASMTMQDLATQVQYHLPVINVVFTNCQYGFI---KD  482

Query  571   RFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQ--KMLDTPGP  628
                  N+ + ++G   N+ +      K A+   + A RV   + L    +  K +    P
Sbjct  483   EQEDTNQ-NDFIGVEFNDID----FSKIADGVHMQAFRVNKIEQLPDVFEQAKAIAQHEP  537

Query  629   YLLDVIV  635
              L+D ++
Sbjct  538   VLIDAVI  544
```

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RecName: Full=Acetolactate synthase, catabolic; Short=ALS

Sequence ID: Q04524.1 **Length:** 559 **Number of Matches:** 1

Related Information

Range 1: 2 to 550 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
157 bits(397)	6e-40	Compositional matrix adjust.	154/581(27%)	257/581(44%)	56/581(9%)

```
Query  88    DEPRK------GSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGG  141
             D+PR       G+D++V  LE +GV  VF  PG    ++  +L  SSI R +  RHE
Sbjct  2     DKPRHERQWAHGADLIVSQLEAQGVRQVFGIPGAKIDKVFDSLLDSSI-RIIPVRHEANA  60

Query  142   VFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQ  201
              F A    R TG  GV + TSGPG +NL++G+A A  +  P+VA+ G V R        Q
Sbjct  61    AFMAAAVGRITGKAGVALVTSGPGCSNLITGMATANSEGDPVVALGGAVKRADKAKLVHQ  120

Query  202   ETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDW  261
                 V +   +TK+   V   + +  VV   AF  A  GRPG   + +P+DI
Sbjct  121   SMDTVAMFSPVTKYAVEVTASDALAEVVSNAFRAAEQGRPGSAFVSLPQDIV--------  172

Query  262   DQPMR---LPGYMSRLPKLPN--EMLLEQIVRLISESKKPVLYVGGGCSQ--SSEELRRF  314
             D P     LP   SR P++    +  ++ + + I+ +K P+  +G   SQ  +S  L R
Sbjct  173   DGPASGSTLPA--SRAPQMGAAPDGAVDSVAQAIAAKNPIFLLGLMASQPENSRALHRH  230

Query  315   VELTGIPVASTLMGLGAFPTGDELSLS-MLGMHGTVYANYAVDSSDLLLAFG---VRFDD  370
                        L G GA    +    +  +G+      +  +  +DL++  G   V ++
Sbjct  231   AGKKPYSGHQHLSGAGAVNQDNFARFAGRVGLFNNQAGDRLLRQADLIICIGYSPVEYEP  290

Query  371   RVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKL-  429
              +       +  A +VHID+  A   +N  P + +  DI   L+ L   +E    +L L
Sbjct  291   AMWN-----SGTATLVHIDVLPAYEERNYVPDIELVGDIAATLEKLAQRIEH---RLVLT  342

Query  430   ----DFSAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMW  485
                 D  A RQ       +       F  A+ P   ++ + ++ N    ++  +G   +W
Sbjct  343   PQAADILADRQRQRELLDRRGAQLNQF--ALHPLRIVRAMQDIVNSDVTLTVDMGSFHIW  400

Query  486   AAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELAT-  544
              A+Y    + RQ + S G   MG  LP AIGA +  P   VV + GDG F+ +  EL T
Sbjct  401   IARYLYSFRARQVMISNGQQTMGVALPWAIGAWLVNPQRKVVSVSGDGGFLQSSMELETA  460

Query  545   IKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLK-FAEACG  603
             +++    + I+ ++N +  + +Q + ++ +            +  E  P   K +AEA G
Sbjct  461   VRLHANILHIIWVDNGYNMVAIQEQKKYQRL-----------SGVEFGPVDFKVYAEAFG  509

Query  604   VPAARVTHRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPM  644
                  V   + L   ++  +D  GP ++ + V ++++ L M
Sbjct  510   ACGFAVESAEALEPTLRAAMDVDGPAVVAIPVDYRDNPLLM  550
```

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RecName: Full=Uncharacterized protein MJ0663

Sequence ID: Q58077.1 **Length:** 494 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 9 to 490 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
155 bits(393)	9e-40	Compositional matrix adjust.	147/564(26%)	252/564(44%)	97/564(17%)

```
Query  95   DVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATGF  154
            + +V+ LER  V  +F+YPG   + ++  +  SSI +N++ R E+G  F A+GYAR T +
Sbjct  9    EAMVDFLER-NVKTIFSYPGEQILPLYNEIEGSSI-KNIMVRDERGAGFMADGYARITNY  66

Query  155  PGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSITK  214
             GVC+AT+GPGATNL + +A A  D+  ++AITG+  R+ IG + FQE   V +
Sbjct  67   IGVCLATAGPGATNLTTPIATAYKDNSSVLAITGRCQRKYIGKNYFQE---VNMDFLNFY  123

Query  215  HNYLV--MDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGY--  270
              Y V   +V  I +   +  F  +     PV +++P D+ ++       + + +  Y
Sbjct  124  KGYFVDKAEVSYIAKAFADCLFNKK-----PVQLNIPVDLYKEEA-----KDINITTYTD  173

Query  271  MSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEE---LRRFVELTGIPVAST  325
            + +  + P+  + E  V      KKP+  +G G   + S +E   + + +E    P+A+T
Sbjct  174  IYKDDETPSNNIKEIDV------KKPLFLIGQGIFGTLSYKEIVKISKILEKINCPIATT  227

Query  326  LMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKI  385
                G      E  + ++G  G        D   LL A      D++     + +    +
Sbjct  228  FPARGVINEKLENCIGLVGRRG--------DLKSLLEA------DKIINIGSSLSYNTYV  273

Query  386  VHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVKY  445
              +          ++  +S   +I+L  + +  + E  E  L +  S+W         K
Sbjct  274  ESV----------REKLLSKTENIQLKPKSIKELKEFFEN-LDVKNSSWIY-------KN  315

Query  446  PLNFKTFGDAIPPQYAIQVLDELTN--GSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGG  503
               F+  GD     Y+ ++ + + N    AII T  G+H ++         PR  ++S
Sbjct  316  SNKFQPSGD-----YSNKIYEIIKNIPEDAIIVTDAGKHTVFTCLLKTCVIPRNIISSHS  370

Query  504  LGAMGFGLPAAIGAAVG----RPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNN  559
             G MGFGLPA+IG   G      D  VV I GDG F+MNV+EL  +   NL + ++++ N
Sbjct  371  FGTMGFGLPASIGVKFGTIDFNIDREVVLISGDGGFLMNVEELQVVAENNLKILMVVMKN  430

Query  560  QHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAI  619
              L    + ++                      PN  K A+A  +    + + D++ + I
Sbjct  431  NSLAEFCKIKN----------------------PNFNKIADAFEIDNCYIENVDEIGSEI  468

Query  620  QKMLDTPGPYLLDVIVPHQEHVLP  643
            +  L    P L  V+V  +   LP
Sbjct  469  KGYLKKNKPLL--VVVETENEPLP  490
```

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RecName: Full=Probable 2-ketoarginine decarboxylase AruI; AltName: Full=2-oxo-5-guanidinopentanoate decarboxylase; AltName: Full=5-guanidino-2-oxopentanoate decarboxylase

Sequence ID: Q9HUI8.1 **Length:** 559 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 19 to 494 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
156 bits(395)	1e-39	Compositional matrix adjust.	147/496(30%)	222/496(44%)	33/496(6%)

```
Query  83   SRFAPDEPRK---GSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQ  139
            +R  P +P+K       LV  L   GV  VF  PG  ++E+++ L  S I R+VL RHEQ
Sbjct  19   TRILPMQPQKTLTAGQALVRLLANYGVDTVFGIPGVHTLELYRGLPGSGI-RHVLTRHEQ  77

Query  140  GGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTD-  198
            G  F A+GYAR +G PGVC   +GPG TN+ + +  A  DSVP++ I+       +G
Sbjct  78   GAGFMADGYARVSGKPGVCFVITGPGVTNVATAIGQAYADSVPLLVISSVNHSASLGKGW  137

Query  199  -AFQETPIVE-VTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQL  256
                ET     +T  IT  + L +  E +P ++  A+ +  S RP PV I +P D+
Sbjct  138  GCLHETQDQRAMTAPITAFSALALSPEQLPELIARAYAVFDSERPRPVHISIPLDVLAAP  197

Query  257  VIPDWDQPM-RLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFV  315
            V  DW   + R PG       +P    L      ++ +++P+L  GGG   + E L
Sbjct  198  VAHDWSAAVARRPGR-----GVPCSEALRAAAERLAAARRPMLIAGGGALAAGEALAALS  252

Query  316  ELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYA-VDSSDLLLAFGVRFDDRVTG  374
            E    P+ +++ G G  P    L+    G    V   +  +  +DL+LA G    D
Sbjct  253  ERLAAPLFTSVAGKGLLPPDAPLNA---GASLCVAPGWEMIAEADLVLAVGTEMADTDFW  309

Query  375  KLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAW  434
            + E      +++ +DID  +        V++  D +  L+ L   L  +
Sbjct  310  R-ERLPLSGELIRVDIDPRKFNDFYPSAVALRGDARQTLEALLVRLPQEA----------  358

Query  435  RQELTVQKVKYPLNFKTFGDAIPPQYAIQ-VLDELTNG---SAIISTGVGQHQMWAAQYY  490
            R           L  +      P Q   Q +LD +       A +ST + Q        +
Sbjct  359  RDSAPAAARVARLRAEIRAAHAPLQALHQAILDRIAAALPADAFVSTDMTQLAYTGNYAF  418

Query  491  KYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVE-N  549
              R PR WL   G G +G+GLPA IGA +G P    + + GDG F+   QELAT   E +
Sbjct  419  ASRAPRSWLHPTGYGTLGYGLPAGIGAKLGAPQRPGLVLVGDGGFLYTAQELATASEELD  478
```

```
Query  550  LPVKIMLLNNQHLGMV  565
             P+ ++L NN  LG +
Sbjct  479  SPLVVLLWNNDALGQI  494
```

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RecName: Full=2-hydroxyacyl-CoA lyase 1; AltName: Full=2-hydroxyphytanoyl-CoA lyase; Short=2-HPCL; AltName: Full=Phytanoyl-CoA 2-hydroxylase 2

Sequence ID: Q9UJ83.2 **Length:** 578 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 4 to 483 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
155 bits(393)	3e-39	Compositional matrix adjust.	136/504(27%)	223/504(44%)	50/504(9%)

```
Query  83   SRFA--PDEPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQG  140
            S FA   +E   G+ V+ +AL+ + V  +F   G    EI  A  +  I + +  R+EQ
Sbjct  4    SNFAERSEEQVSGAKVIAQALKTQDVEYIFGIVGIPVTEIAIAAQQLGI-KYIGMRNEQA  62

Query  141  GVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAF  200
              +AA      T  PGVC+  SGPG  + + G+A+A ++  P++ I G   R      AF
Sbjct  63   ACYAASAIGYLTSRPGVCLVVSGPGLIHALGGMANANMNCWPLLVIGGSSERNQETMGAF  122

Query  201  QETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPD  260
            QE P VE  R  TK +     +E IP V+ +A   +  GRPG   +D+P D     V
Sbjct  123  QEFPQVEACRLYTKFSARPSSIEAIPFVIEKAVRSSIYGRPGACYVDIPADFVNLQV---  179

Query  261  WDQPMRLPGYMSRLPKLPNEMLLEQIV----RLISESKKPVLYVGGGC--SQSSEELRRF  314
                +    YM R    P  M     V     +I  +K+P+L +G G   + + E +++
Sbjct  180  ---NVNSIKYMERCMSPPISMAETSAVCTAASVIRNAKQPLLIIGKGAAYAHAEESIKKL  236

Query  315  VELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTG  374
            VE   +P   T MG G  P      +           + A+  +D+++ FG R +  +
Sbjct  237  VEQYKLPFLPTPMGKGVVPDNHPYCVG-------AARSRALQFADVIVLFGARLNWILHF  289

Query  375  KL-EAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSA  433
             L   +    K + +DI + E+G N +P V++  +I    + L   L+    +   +
Sbjct  290  GLPPRYQPDVKFIQVDICAEELGNNVKPAVTLLGNIHAVTKQLLEELDKTPWQYPPESKW  349

Query  434  WR-------------QELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVG  480
            W+             +EL  +K   P+N+ T        Y +Q  ++L     ++S G
Sbjct  350  WKTLREKMKSNEAASKELASKK-SLPMNYYTVF------YHVQ--EQLPRDCFVVSEGAN  400

Query  481  QHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAV----GRPDEVVVDIDGDGSFI  536
               +       Y  PR  L +G  G MG GL  AI AAV      P + ++ ++GD +F
Sbjct  401  TMDIGRTVLQNYL-PRHRLDAGTFGTMGVGLGFAIAAAVVAKDRSPGQWIICVEGDSAFG  459

Query  537  MNVQELATIKVENLPVKIMLLNNQ  560
             +  E+ TI   NLP+ ++++NN
Sbjct  460  FSGMEVETICRYNLPIILLVVNNN  483
```

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RecName: Full=Sulfoacetaldehyde acetyltransferase

Sequence ID: D5AKX8.1 **Length:** 590 **Number of Matches:** 1

Related Information

Range 1: 7 to 543 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
154 bits(388)	2e-38	Compositional matrix adjust.	138/552(25%)	238/552(43%)	38/552(6%)

```
Query  95   DVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATGF  154
            +  V+ L+R G+   F   G A M I     R+ I R     HE  G   A+G+ RA+G
Sbjct  7    EAFVKVLQRHGIDTAFGIIGSAFMPISDLFPRAGI-RFFDCAHEGSGGMMADGFTRASGR  65

Query  155  PGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSITK  214
              + IA +GPG TN V+ +  A  +  P++ +T Q   R IG   FQE   + + R +
Sbjct  66   MAMIIAQNGPGVTNFVTAVKTAYWNHTPMLVVTPQAANRTIGQGGFQEVEQMALFRDMVC  125

Query  215  HNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRL  274
                + D   I  V+      AR      P  I++P+D+  +++  +  Q + LP
Sbjct  126  WQEELRDPARIAEVLDRVIRKARRAS-APAQINLPRDMFTKIIDIELPQGVDLP------  178

Query  275  PKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLGAF  332
               P+   L++   L+S ++ PV+  G G   +++  +     E    PV +      AF
Sbjct  179  RPAPDAQALDRAAALLSSARFPVILNGAGVVLAEAIPDTVALAERLEAPVCTGYQHNDAF  238

Query  333  PTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVT---GKLEAFASRAKIVHID  389
            P    L    LG +G+  A   +  +D++L  G R +   T     ++ +   A ++ +D
Sbjct  239  PGSHPLFAGPLGYNGSKAAMQLMSQADVVLCLGTRLNPFSTLPGYGIDYWPKAAAVIQVD  298

Query  390  IDSAEIGKNKQPHVSICADIKLALQGLNSILESKEG---------KLKLDFSAWRQELTV  440
            I+   IG  +   + I AD     +G+ + L ++ G         ++    S W QEL
Sbjct  299  INPDRIGLTRPVTLGIAADAGAVARGILARLGAQAGDQDRAERAARIATTKSRWAQELAS  358

Query  441  QKVKYPLNFKTFGDA--------IPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKY  492
               +      ++ +         + P+ A + +       AI+S+ +G +      Y  +
Sbjct  359  MDHEEDDPGTSWNERARAAKPGWMSPRMAWRAITAALPPEAILSSDIGNNCAIGNAYPSF  418

Query  493  RKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLP-  551
               R++L  G  G  G+GLPA IGA +  P+  VV   GDG+F ++V EL  I   + P
Sbjct  419  AAGRKYLAPGLFGPCGYGLPAIIGAKIACPETPVVGFAGDGAFGISVTELTAIGRADWPA  478
```

```
Query  552  VKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTH  611
            + +++  N   G   +    +Y  N   T L    + A I       A+ACG+
Sbjct  479  ITMVVFRNYQWGAEKRNSTLWYDDNFVGTELDLQVSYAGI-------AQACGLQGVVART  531

Query  612  RDDLRAAIQKML  623
             ++L  A++K L
Sbjct  532  MEELTEALRKAL  543
```

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RecName: Full=N(2)-(2-carboxyethyl)arginine synthase; Short=CEA synthetase; Short=CEAS

Sequence ID: Q9LCV9.1 **Length:** 573 **Number of Matches:** 1

Related Information

Range 1: 49 to 559 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
149 bits(375)	6e-37	Compositional matrix adjust.	140/526(27%)	235/526(44%)	35/526(6%)

```
Query  130  IRNVLPRHEQGGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQ  189
            I  VL RHE     AA+  AR TG P  C AT GPG TNL +G+A ++LD  P++A+  Q
Sbjct  49   IDFVLTRHEFTAGVAADVLARITGRPQACWATLGPGMTNLSTGIATSVLDRSPVIALAAQ  108

Query  190  VPRR-MIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDV  248
                 +   D  Q    V +   ++K+   +    +I  +V  A   A +   GP  I +
Sbjct  109  SESHDIFPNDTHQCLDSVAIVAPMSKYAVELQRPHEITDLVDSAVNAAMTEPVGPSFISL  168

Query  249  PKDIQQQLVIPDWDQPMRLPGYMSRLPKLPNEMLLE-------QIVRLISESKKPVLYVG  301
            P D+       D      +P   +  P  P  ++ +       Q   L++E+K PVL VG
Sbjct  169  PVDLLGSSEGID----TTVPNPPANTPAKPVGVVADGWQKAADQAAALLAEAKHPVLVVG  224

Query  302  GGCSQSSE--ELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSS-  358
                +S     +R   E   IPV +T +  G  P G EL+   +  +     N+    +
Sbjct  225  AAAIRSGAVPAIRALAERLNIPVITTYIAKGVLPVGHELNYGAVTGYMDGILNFPALQTM  284

Query  359  ----DLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQ  414
                DL+L  G  + + +   +       K V I      I +  +P V +  D+   ++
Sbjct  285  FAPVDLVLTVGYDYAEDLRPSMWQKGIEKKTVRISPTVNPIPRVYRPDVDVVTDVLAFVE  344

Query  415  GLNSILESKEGKLKLDFSAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTN----  470
               +   S   K + D    R  +     ++  + +T+ D +     I  ++ +
Sbjct  345  HFETATASFGAKQRHDIEPLRARIA----EFLADPETYEDGMRVHQVIDSMNTVMEEAAE  400

Query  471  -GSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDI  529
             G   I + +G  + +   + +  +P  +LTS G  + G+G+PAAIGA + RPD+    I
Sbjct  401  PGEGTIVSDIGFFRHYGVLFARADQPFGFLTSAGCSSFGYGIPAAIGAQMARPDQPTFLI  460

Query  530  DGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEA  589
             GDG F  N  +L TI   NLP+  +++NN   G++  ++      N  H    +P+ +
Sbjct  461  AGDGGFHSNSSDLETIARLNLPIVTVVVNNDTNGLIELYQ------NIGHHRSHDPAVKF  514

Query  590  EIFPNMLKFAEACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIV  635
                + +  AEA GV A R T+R++L AA++K  +   P+L++V V
Sbjct  515  GGV-DFVALAEANGVDATRATNREELLAALRKGAELGRPFLIEVPV  559
```

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RecName: Full=Probable 2-hydroxyacyl-CoA lyase 1; AltName: Full=2-hydroxyphytanoyl-CoA lyase; Short=2-HPCL

Sequence ID: Q54DA9.1 **Length:** 580 **Number of Matches:** 1

Related Information

Range 1: 45 to 491 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
144 bits(362)	4e-35	Compositional matrix adjust.	118/456(26%)	209/456(45%)	40/456(8%)

```
Query  136  RHEQGGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMI  195
            R+EQ   +AA      TG PG+C+  SGPG  + ++G+ +A  +  P++ ++  + + ++
Sbjct  45   RNEQSCSYAASIVGYLTGLPGLCMTVSGPGVVHALAGVLNAQSNGWPMILLSSSIDQSLV  104

Query  196  GTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQ  255
            G   FQE    E      K  Y + +++  P ++++A   + S RPGPV I +P D+ +
Sbjct  105  GKGGFQECKQFESAELYCKKCYYLTEIDHFPEILKDAIETSLSNRPGPVYIQIPADLIKS  164

Query  256  LVIPDWDQPMRLPGYMSRLPK--LPNEMLLEQIVRLISESKKPVLYVGGGCS--QSSEEL  311
                +        GY +   K  +P+  L++  V+L+SE+K+P++  G G +  +S  EL
Sbjct  165  KC-KESPNIREAAGYGTIAIKSVVPDMKLIKDAVQLLSEAKRPLVIGGKGAAYCRSENEL  223

Query  312  RRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDR  371
              F+E T IP   + MG G       L +           +YA+ ++D++L  G R +
Sbjct  224  LEFIEATKIPFLPSPMGKGLLRDDHPLVVG-------AARSYALKNADVVLVLGARLNWM  276

Query  372  VT-GKLEAFASRAKIVHIDIDSAEIGKNKQPHV----SICADIKLALQGLNSIL--ESKE  424
               GK   F++  K + +D+D  +  K K P+V    +I  D +L++  +  +   E+ E
Sbjct  277  FNFGKAPTFSTDVKFIIVDVDENQASKTKNPNVVPEIAIVGDARLSIAEMRKLFIGETDE  336

Query  425  ----------GKLKLDFSAW---RQELTVQKVKYPLNFKTFGDAIPPQYAI--QVLDELT  469
                        +K++ S W    Q++ V K K      +       +Y    +V + L
Sbjct  337  QPQPPQDSLIKSMKMEESWWSNLNQDIQV-KTKSLATLMSEPQNNDQEYLTYHKVFNALR  395

Query  470  NGSAI----ISTGVGQHQMWAAQYYKYRK-PRQWLTSGGLGAMGFGLPAAIGAAVGRPDE  524
             G       I    G + M   +    +  PR  L +G L  MG G+  ++ A +  PD
Sbjct  396  VGGLFQEDTIFVNEGANTMDIGRLCIPQTLPRSRLDAGTLATMGVGVGYSVAAQICFPDR  455

Query  525  VVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQ  560
             VV I GD +F  +  E+       LP+  ++LNN
```

```
Sbjct  456   SVVCIQGDSAFGFSAMEMEVAVRYKLPIVFIVLNNN  491
```

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PUTATIVE PSEUDOGENE: RecName: Full=Putative uncharacterized protein HI_0737

Sequence ID: O05031.1 **Length:** 265 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 3 to 128 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
134 bits(337)	3e-34	Compositional matrix adjust.	66/127(52%)	92/127(72%)	1/127(0%)

```
Query  93    GSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARAT  152
             G+ +++  L+   VT +F YPGGA M  + AL  + +  ++L R+EQG   AA GYAR+T
Sbjct  3     GAQLIMACLKAHHVTTLFGYPGGAIMPTYDALYDAGL-DHLLCRNEQGTAMAAIGYARST  61

Query  153   GFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSI  212
             G  GVCIATSGPGATNLV GL DA++DS+P+V ITGQV   +IGTDAFQE  ++ ++ +
Sbjct  62    GKVGVCIATSGPGATNLVIGLGDAMMDSIPVVTITGQVASPLIGTDAFQEADVLGLSLAC  121

Query  213   TKHNYLV  219
             TKH+++V
Sbjct  122   TKHSFIV  128
```

Range 2: 113 to 212 GenPept Graphics Next Match Previous Match First Match

Score	Expect	Method	Identities	Positives	Gaps
42.0 bits(97)	0.009	Compositional matrix adjust.	31/108(29%)	47/108(43%)	15/108(13%)

```
Query  389   DIDSAEIGKNKQPHVSICADIKLA---LQGLNSILESKEGKLKLDFSAWRQELTVQKVKY  445
             D+    +   K   +   AD+ L    +Q LN++      K  LD   WR++  ++  K
Sbjct  113   DVLGLSLACTKHSFIVQSADVALQGDLIQALNAL------KQDLDIEPWREQ--IRNFKA  164

Query  446   PLNFKTFGDA----IPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQY  489
              L+F    +     I P   +  L      +AII T VGQHQMW  Q+
Sbjct  165   KLDFTYVENQGNRPIDPWALLNSLSNRKPNNAIICTDVGQHQMWLVQH  212
```

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RecName: Full=2-hydroxyacyl-CoA lyase; AltName: Full=2-hydroxyphytanoyl-CoA lyase; Short=2-HPCL; AltName: Full=Oxalyl-CoA decarboxylase

Sequence ID: Q0JMH0.3 **Length:** 577 **Number of Matches:** 1

Related Information

Range 1: 51 to 562 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
140 bits(353)	5e-34	Compositional matrix adjust.	137/531(26%)	232/531(43%)	44/531(8%)

```
Query  130   IRNVLPRHEQGGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQ  189
             +R +  R+EQ   +AA  Y   TG PG+ +  SGPG  + ++GL+ A  ++ P++ ++G
Sbjct  51    VRFLAFRNEQSAGYAAAAYGFLTGSPGLLLTVSGPGCVHGLAGLSHATANAWPLLMVSGS  110

Query  190   VPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVP  249
               +   G   FQE   +  T+   K       + DIPR+V +A     SGRPG   +D+P
Sbjct  111   CSQPDAGRGDFQELDQIAATKPFIKIAVKATTIADIPRLVFQALAATVSGRPGGCYLDIP  170

Query  250   KDIQQQLVIPDWDQPMRLPGYMSRL------PKLPN-EMLLEQIVRLISESKKPVLYVGG  302
              D+  Q +       +               PK  + +  +E+   L+  +++P++  G
Sbjct  171   SDVLHQTLTESEAAALIDAAAADSAKSDSSPPKHKSLDEGIEKAAELLRRAERPLVVFGK  230

Query  303   GCSQSSEE--LRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDL  360
             G + S  E  + + V+ TGIP   T MG G  P    LS        T   + A+   D+
Sbjct  231   GAAYSRAEDAIWKLVDTTGIPFLPTPMGKGVVPDTHPLS-------ATAARSLAIGQCDV  283

Query  361   LLAFGVRFDDRVT-GKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSI  419
              L  G R +  +  G+   ++   K + +D+   EI + ++PHV I  D K  ++ +N
Sbjct  284   ALVVGARLNWLLHFGEPPKWSKDVKFILVDVCEEEI-ELRKPHVGIVGDAKRVVELINRE  342

Query  420   LESKEGKL------------KLDFSAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQ--VL  465
             ++ +   L            K   +  + E  + K   P NF T      P   I+  +L
Sbjct  343   IKDQPFCLAPSHPWVEAITKKARDNVLKMEAQLAKDVVPFNFLT------PLRIIRDAIL  396

Query  466   DELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEV  525
              E      ++S G     +  A   +  +PR  L +G  G MG GL   +AAV  PD +
Sbjct  397   AEGNPAPVVVSEGANTMDVGRAVLVQ-NEPRTRLDAGTWGTMGVGLGFCVAAAVAEPDRL  455

Query  526   VVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNP  585
             VV ++GD  F  +  E+ T+    LPV +++ NN      V   DR         Y  +P
Sbjct  456   VVAVEGDSGFGFSAMEVETLVRYQLPVVVIVFNNNG----VYGGDRRSPDEITGPYKDDP  511

Query  586   SNEAEI-FPNMLKFAEACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIV  635
             +  + +      K  EA G     V   D+L++A+ +      P +++VI+
Sbjct  512   APTSFVPAAGYHKMMEAFGGKGYLVETPDELKSALSESFRARKPAVINVII  562
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: Q81QB5.1 **Length:** 644 **Number of Matches:** 1

See 2 more title(s)

Related Information

Identical Proteins - Identical proteins to Q81QB5.1

Range 1: 63 to 526 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
140 bits(352)	1e-33	Compositional matrix adjust.	127/489(26%)	211/489(43%)	84/489(17%)

```
Query  136  RHEQGGVFAAEGYARATGFPGV--CIATSGPGATNLVSGLADALLDSVPIVAITGQVPRR  193
            R+EQG   AA  +A+      +  C ++ GPG+ N+++  A A  +++P++ + G
Sbjct  63   RNEQGMANAAMAFAKQKHRKQIMACTSSVGPGSANMITSAATASANNIPVLLLPG-----  117

Query  194  MIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRP------------  241
                D F       V + I + + L +   D  R V +  +  R  RP
Sbjct  118  ----DVFATRQPDPVLQQIEQTHDLSISTNDAFRAVSK--YWDRINRPEQLMTAMIQAMR  171

Query  242  --------GPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRL----PKLPNEMLLEQIVRL  289
                    G V I +P+D+Q +     WD P     +  R+     +LP +  L   V +
Sbjct  172  VLTNPADTGAVTICLPQDVQGEA----WDFPSYF--FQKRVHRIERRLPTKASLADAVEM  225

Query  290  ISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHG  347
            I   KKPV+  GGG   ++++EEL++F E   IP   T  G  A  +    +L  +G+ G
Sbjct  226  IKRKKKPVMICGGGVRYAEAAEELKQFAETFHIPFGETQAGKSAIESSHPYNLGGIGVTG  285

Query  348  TVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICA  407
             V AN     +DL++  G RF D  T   + F +  ++  ++I+ +E   NK   + + A
Sbjct  286  NVAANTIAKEADLVIGIGTRFTDFTTASKQLFQNE-EVEFLNINISEFHANKLDALKVIA  344

Query  408  DIKLALQGLNSILESKEGKLKLDFS--------AWRQELT-VQKVKYPL-----------  447
            D K AL  L  I E +E   +  ++        AW  EL+ +  +++
Sbjct  345  DAKEALLAL--IDELQEIDYQSSYTVEIADAKDAWETELSRLHNIRFTCQDFTPEVEGHF  402

Query  448  --NFKTFGDAIPPQYA----IQVLDELTNGSAIISTGVGQ-----HQMWAAQYYKYRKPR  496
              N   + DA+  Q      I  ++ L +  AII    G       +MWA+     RKP
Sbjct  403  NENLNEYVDALGTQLTQTAVIGQINTLLDKDAIIVGAAGSLPGDLQRMWAS-----RKPN  457

Query  497  QWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIML  556
             +    G   MG+ +  A+GA +  P + V  + GDGS+ M   EL T   EN  + ++L
Sbjct  458  TYHMEYGYSCMGYEVAGALGAKLAEPSKEVYAMVGDGSYQMLHSELVTSLQENKKINVLL  517

Query  557  LNNQHLGMV  565
             +N   G +
Sbjct  518  FDNSGFGCI  526
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: B7JPM3.1 **Length:** 644 **Number of Matches:** 1

Related Information

Range 1: 63 to 526 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
139 bits(351)	2e-33	Compositional matrix adjust.	127/489(26%)	211/489(43%)	84/489(17%)

```
Query  136  RHEQGGVFAAEGYARATGFPGV--CIATSGPGATNLVSGLADALLDSVPIVAITGQVPRR  193
            R+EQG   AA  +A+      +  C ++ GPG+ N+++  A A  +++P++ + G
Sbjct  63   RNEQGMANAAMAFAKQKHRKQIMACTSSVGPGSANMITSAATASANNIPVLLLPG-----  117

Query  194  MIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRP------------  241
                D F       V + I + + L +   D  R V +  +  R  RP
Sbjct  118  ----DVFATRQPDPVLQQIEQTHDLSISTNDAFRAVSK--YWDRINRPEQLMTAMIQAMR  171

Query  242  --------GPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRL----PKLPNEMLLEQIVRL  289
                    G V I +P+D+Q +     WD P     +  R+     +LP +  L   V +
Sbjct  172  VLTNPADTGAVTICLPQDVQGEA----WDFPSYF--FQKRVHRIERRLPTKASLADAVEM  225

Query  290  ISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHG  347
            I   KKPV+  GGG   ++++EEL++F E   IP   T  G  A  +    +L  +G+ G
Sbjct  226  IKRKKKPVMICGGGVRYAEAAEELKQFAETFHIPFGETQAGKSAIESSHPYNLGGIGVTG  285

Query  348  TVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICA  407
             V AN     +DL++  G RF D  T   + F +  ++  ++I+ +E   NK   + + A
Sbjct  286  NVAANTIAKEADLVIGIGTRFTDFTTASKQLFQNE-EVEFLNINISEFHANKLDALKVIA  344

Query  408  DIKLALQGLNSILESKEGKLKLDFS--------AWRQELT-VQKVKYPL-----------  447
            D K AL  L  I E +E   +  ++        AW  EL+ +  +++
Sbjct  345  DAKEALLAL--IDELQEIDYQSSYTVEIADAKDAWETELSRLHNIRFTCQDFTPEVEGHF  402

Query  448  --NFKTFGDAIPPQYA----IQVLDELTNGSAIISTGVGQ-----HQMWAAQYYKYRKPR  496
              N   + DA+  Q      I  ++ L +  AII    G       +MWA+     RKP
Sbjct  403  DENLNEYVDALGTQLTQTAVIGQINTLLDEDAIIVGAAGSLPGDLQRMWAS-----RKPN  457

Query  497  QWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIML  556
             +    G   MG+ +  A+GA +  P + V  + GDGS+ M   EL T   EN  + ++L
Sbjct  458  TYHMEYGYSCMGYEVAGALGAKLAEPSKEVYAMVGDGSYQMLHSELVTSLQENKKINVLL  517

Query  557  LNNQHLGMV  565
             +N   G +
Sbjct  518  FDNSGFGCI  526
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: Q6HIK2.1 **Length:** 644 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 63 to 526 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
139 bits(351)	2e-33	Compositional matrix adjust.	127/489(26%)	211/489(43%)	84/489(17%)

```
Query  136  RHEQGGVFAAEGYARATGFPGV--CIATSGPGATNLVSGLADALLDSVPIVAITGQVPRR  193
            R+EQG   AA  +A+      +  C ++ GPG+ N+++  A A  +++P++ + G
Sbjct  63   RNEQGMANAAMAFAKQKHRKQIMACTSSVGPGSANMITSAATASANNIPVLLLPG-----  117

Query  194  MIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRP------------  241
                D F       V + I + + L +   D  R V +  +  R  RP
Sbjct  118  ----DVFATRQPDPVLQQIEQTHDLSISTNDAFRAVSK--YWDRINRPEQLMTAMIQAMR  171

Query  242  --------GPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRL----PKLPNEMLLEQIVRL  289
                    G V I +P+D+Q +     WD P     +  R+     +LP +  L   V +
Sbjct  172  VLTNPADTGAVTICLPQDVQGEA----WDFPSYF--FQKRVHRIERRLPTKASLADAVEM  225

Query  290  ISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHG  347
            I   KKPV+  GGG   ++++EEL++F E   IP   T  G  A  +    +L  +G+ G
Sbjct  226  IKRKKKPVMICGGGVRYAEAAEELKQFAETFHIPFGETQAGKSAIESSHPYNLGGIGVTG  285

Query  348  TVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICA  407
             V AN     +DL++  G RF D  T   + F +  ++  ++I+ +E   NK   + + A
Sbjct  286  NVAANTIAKEADLVIGIGTRFTDFTTASKQLFQNE-EVEFLNINISEFHANKLDALKVIA  344

Query  408  DIKLALQGLNSILESKEGKLKLDFS--------AWRQELT-VQKVKYPL-----------  447
            D K AL  L  I E +E   +  ++        AW  EL+ +  +++
Sbjct  345  DAKEALLAL--IDELQEIDYQSSYTVEIADAKDAWETELSRLHNIRFTCQDFTPEVEGHF  402

Query  448  --NFKTFGDAIPPQYA----IQVLDELTNGSAIISTGVGQ-----HQMWAAQYYKYRKPR  496
              N   + DA+  Q      I  ++ L +  AII    G       +MWA+     RKP
Sbjct  403  NENLNEYVDALGTQLTQTAVIGQINTLLDKDAIIVGAAGSLPGDLQRMWAS-----RKPN  457

Query  497  QWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIML  556
             +    G   MG+ +  A+GA +  P + V  + GDGS+ M   EL T   EN  + ++L
Sbjct  458  TYHMEYGYSCMGYEVAGALGAKLAEPSKEVYAMVGDGSYQMLHSELVTSLQENKKINVLL  517

Query  557  LNNQHLGMV  565
             +N   G +
Sbjct  518  FDNSGFGCI  526
```

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RecName: Full=Acetolactate synthase-like protein; AltName: Full=IlvB-like protein

Sequence ID: Q6NV04.1 **Length:** 621 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 40 to 537 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
138 bits(347)	5e-33	Compositional matrix adjust.	145/517(28%)	223/517(43%)	66/517(12%)

```
Query  90   PRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYA  149
            PR G + + E L   GV  VF   GG    I  A  +  I R V  RHE   VFAA+  A
Sbjct  40   PRHGGESVAEVLRSHGVKFVFTLVGGHISPILVACEKLGI-RIVDTRHEATAVFAADAVA  98

Query  150  RATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVT  209
            R +G  GV   T+GPG TN V+ + +A +   P++ I G     + G  A Q+   + +
Sbjct  99   RLSGTVGVAAVTAGPGLTNTVTAVKNAQMAESPLLLIGGAAATLLQGRGALQDIDQMSLF  158

Query  210  RSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKD-IQQQLVIPDWDQPMRLP  268
            + + K    V  V +I   VR+A  +A+SG PGPV I+ P D +    V+     P   P
Sbjct  159  KPLCKFCASVRTVREIVPTVRKALAIAQSGTPGPVFIEFPIDTLYPYHVVEKEFAPKNTP  218

Query  269  -GYMSR----------------------LPKLP------NEMLLEQIVRLISESKKPVLY  299
             G M +                      L  LP       +  +++ V L+S +KKPV+
Sbjct  219  KGLMGKIIAWYLKNHLSNLFAGAWESRDLSPLPVHIPHATDDQVQRCVELVSRAKKPVIL  278

Query  300  VGGGCS---QSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANY---  353
            +G   +     ++++R+ +E  GIP          F  G  +S  +LG +  ++
Sbjct  279  LGSQATLPPTPADDIRKALESLGIP---------CFLGG--MSRGLLGKNSPLHIRQNRR  327

Query  354  -AVDSSDLLLAFGVRFDDRVT-GKLEAFASRAKIVHIDIDSAEIGKNK----QPHVSICA  407
             A+  +DL+L  G   D R++ G++     R+KI+ ++ D +++ KN     +P V+I
Sbjct  328  DALKDADLVLLAGTVCDFRLSYGRV--LNRRSKIIAVNRDKSQLLKNSDMFWKPTVAIQG  385

Query  408  DIKLALQGLNSILESKEGKLKLDFSAWRQELTV-QKVKYPLNFKTFGDA----IPPQYAI  462
            D    L  L+  L+            W Q L     VK   N     +     + P   +
Sbjct  386  DAGSFLLNLSKALKGHRCP-----EEWPQSLKEGDNVKEKANRAKADEKTERHLNPLSVL  440

Query  463  QVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRP  522
              +DEL    +II    G     AA   + R P  WL  G  G +G G   A+GA + RP
Sbjct  441  HRVDELLAEDSIIVADGGDFVGSAAYIMRPRGPLCWLDPGAFGTLGVGGGFALGAKLCRP  500

Query  523  DEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNN  559
            +  V  + GDGS    V E  T      PV  ++ N+
Sbjct  501  ESEVWIVYGDGSLGYTVAEFDTFTRHKTPVIALVGND  537
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase 2; Short=THcHDO hydrolase 2

Sequence ID: Q4V1F5.1 **Length:** 644 **Number of Matches:** 1

Related Information

Range 1: 63 to 609 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
137 bits(345)	9e-33	Compositional matrix adjust.	145/574(25%)	238/574(41%)	87/574(15%)

```
Query  136  RHEQGGVFAAEGYARATGFPGV--CIATSGPGATNLVSGLADALLDSVPIVAITGQVPRR  193
            R+EQG   AA  +A+      +  C ++ GPG+ N+++  A A  +++P++ + G
Sbjct  63   RNEQGMANAAMAFAKQKHRKQIMACTSSVGPGSANMITSAATASANNIPVLLLPG-----  117

Query  194  MIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRP------------  241
                D F       V + I + + L +   D  R V +  +  R  RP
Sbjct  118  ----DVFATRQPDPVLQQIEQTHDLSISTNDAFRAVSK--YWDRINRPEQLMTAMIQAMR  171

Query  242  --------GPVLIDVPKDIQQQLVIPDWDQPMRL-PGYMSRLPK-LPNEMLLEQIVRLIS  291
                    G V I +P+D+Q +     WD P       + R+ + LP    L   V +I
Sbjct  172  VLTNPADTGAVTICLPQDVQGEA----WDFPSYFFQKCVHRIERRLPTRASLADAVEMIK  227

Query  292  ESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTV  349
              KKPV+  GGG   ++++EEL++F E   IP   T  G  A  +    +L  +G+ G +
Sbjct  228  RKKKPVMICGGGVRYAEAAEELKQFAEAFRIPFGETQAGKSAIESSHPYNLGGIGVTGNL  287

Query  350  YANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADI  409
             AN     +DL++  G RF D  T   + F +  ++  ++I+ +E   NK   + + AD
Sbjct  288  AANTIAKEADLVIGIGTRFTDFTTASKQLFQNE-EVEFVNINISEFHANKLDALKVIADA  346

Query  410  KLALQGLNSILESKEGK--LKLDFSA----WRQEL--------TVQKVK------YPLNF  449
            K AL  L + L++ E +    ++ +A    W  EL        T Q  K      +  N
Sbjct  347  KEALLALINELQAIEYRSSYTVEIAAAKEFWETELARLHNIRFTGQDFKPEVEGHFDDNL  406

Query  450  KTFGDAIPPQYA----IQVLDELTNGSAIISTGVGQ-----HQMWAAQYYKYRKPRQWLT  500
              + DA+  Q      I  ++ L +  AII    G       +MW +     RKP  +
Sbjct  407  NEYVDALGTQLTQTAVIGEMNTLLDEDAIIVGAAGSLPGDLQRMWTS-----RKPNTYHM  461

Query  501  SGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQ  560
              G   MG+ +  A+GA +  P + V  + GDGS+ M   EL T   EN  + ++L +N
Sbjct  462  EYGYSCMGYEVAGALGAKLAEPSKEVYAMVGDGSYQMLHSELVTSLQENKKINVLLFDNS  521

Query  561  HLGMVVQWE-----DRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDL  615
              G +   +       F    R         N A +  +    A   GV   RVT  + L
Sbjct  522  GFGCINNLQMGNGMGSFGTEFRYRNEETRKLNGAIMKIDFAASAAGYGVKTYRVTSVEQL  581

Query  616  RAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSGG  649
            + A++         L+D+       VLP   + G
Sbjct  582  QEALKDAKKQTVSTLIDI------KVLPKTMTNG  609
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase 1; Short=THcHDO hydrolase 1

Sequence ID: Q63B73.1 **Length:** 644 **Number of Matches:** 1

Related Information

Range 1: 63 to 526 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
137 bits(344)	1e-32	Compositional matrix adjust.	125/487(26%)	209/487(42%)	80/487(16%)

```
Query  136  RHEQGGVFAAEGYARATGFPGV--CIATSGPGATNLVSGLADALLDSVPIVAITGQVPRR  193
            R+EQG   AA  +A+      +  C ++ GPG+ N+++  A A  +++P++ + G
Sbjct  63   RNEQGMANAAMAFAKQKHRKQIMACTSSVGPGSANMITSAATASANNIPVLLLPG-----  117

Query  194  MIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRP------------  241
                D F       V + I + + L +   D  R V +  +  R  RP
Sbjct  118  ----DVFATRQPDPVLQQIEQTHDLSISTNDAFRAVSK--YWDRINRPEQLMTAMIQAMR  171

Query  242  --------GPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRL----PKLPNEMLLEQIVRL  289
                    G V I +P+D+Q +     WD P     +   R+    +LP +  L   V +
Sbjct  172  VLTNPADTGAVTICLPQDVQGEA----WDFPSYF--FQKRVHRIERRLPTKASLADAVEM  225

Query  290  ISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHG  347
            I   KKPV+  GGG   ++++EEL++F E   IP   T  G  A  +    +L  +G+ G
Sbjct  226  IKRKKKPVMICGGGVRYAEAAEELKQFAETFHIPFGETQAGKSAIESSHPYNLGGIGVTG  285

Query  348  TVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICA  407
             + AN     +DL++  G RF D  T   + F +  ++  ++I+ +E   NK   + + A
Sbjct  286  NIAANTIAKEADLVIGIGTRFTDFTTASKQLFQNE-EVEFVNINISEFHANKLDALKVIA  344

Query  408  DIKLALQGLNSILE------SKEGKLKLDFSAWRQELT-VQKVKYPL-------------  447
            D K AL  L   L+      S    ++     AW  EL+ +  +++
Sbjct  345  DAKEALLTLIDELQVIDYRSSYTVEIADAKEAWETELSRLHNIRFTGQDFTPEVEGHFDG  404

Query  448  NFKTFGDAIPPQYA----IQVLDELTNGSAIISTGVGQ-----HQMWAAQYYKYRKPRQW  498
            N   + DA+  Q      I  ++ L +  AII    G       +MWA+     RKP  +
Sbjct  405  NLNEYVDALGSQLTQTAVIGQINTLLDEDAIIVGAAGSLPGDLQRMWAS-----RKPNTY  459

Query  499  LTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLN  558
                G   MG+ +  A+GA +  P + V  + GDGS+ M   EL T   EN  + ++L +
Sbjct  460  HMEYGYSCMGYEVAGALGAKIAEPSKEVYAMVGDGSYQMLHSELVTSLQENKKINVLLFD  519

Query  559  NQHLGMV  565
            N   G +
Sbjct  520  NSGFGCI  526
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: A4IPB6.1 **Length:** 639 **Number of Matches:** 1

Related Information

Range 1: 63 to 596 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
135 bits(341)	3e-32	Compositional matrix adjust.	146/561(26%)	233/561(41%)	88/561(15%)

```
Query  136  RHEQGGVFAAEGYARATGFPGVCIATS--GPGATNLVSGLADALLDSVPIVAITGQVPRR  193
            R+EQG   AA  +A+      +  ATS  GPGA N+V+  A A  +++P++ + G V
Sbjct  63   RNEQGMANAAIAFAKQKNRKQIMAATSSVGPGAANMVTSAATATANNIPVLLLPGDVFAT  122

Query  194  MIGTDAFQET--------PIVEVTRSITKHNYLVMDVEDIPRVVREAF-FLARSGRPGPV  244
                   Q+            +  R+++K+   V   E +   +  A   L      G V
Sbjct  123  RQPDPVLQQIEHTHDLSISTNDAFRAVSKYWDRVCRPEQLMSAMLNAMRVLTNPADTGAV  182

Query  245  LIDVPKDIQQQLVIPDWDQP-----MRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLY  299
             I +P+D+Q +     WD P      R+     R P L +   +   V+LI   KKP+L
Sbjct  183  TIALPQDVQGEA----WDFPESFFAKRVHRIERRQPSLES---VRDAVKLIRSKKKPLLV  235

Query  300  VGGGC--SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDS  357
            +GGG   S++++   +F E   IP A T  G G   +   L+L  +G+ G + AN
Sbjct  236  LGGGVRYSEAADAFVKFAEKFNIPFAETQAGKGTIESSHPLNLGGIGVTGNLAANTIAKQ  295

Query  358  SDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGL-  416
            +DL++  G RF D  T   + F+S A+I+ I++  +E   +K   V + AD K  L+ +
Sbjct  296  ADLIIGVGTRFTDFTTASKQLFSS-AEILTINV--SEFHASKLDAVKVVADAKAGLEAIA  352

Query  417  -----------NSILESKEGKLKLDFSAWRQELT-VQKVKYPLNF---------------  449
                       N I E+K+        AW +EL  +  V Y  NF
Sbjct  353  EALGDYVSAYGNEISEAKQ--------AWNRELERLCSVAYGENFTPEIAGHLDEKLPEY  404

Query  450  -KTFGDAIPPQYAIQVLDELTNGSAIISTGVGQ-----HQMWAAQYYKYRKPRQWLTSGG  503
             + FG  +     I  ++EL +  A+I    G       +MW       +    +    G
Sbjct  405  REAFGSELTQTGVIGKVNELIDDDAVIVGASGSLPGDLQRMWVC-----KDRNTYHMEYG  459

Query  504  LGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLG  563
               MG+ +  A G  +  PD+ V  + GDGSF+M   EL T   E   + I+L +N   G
Sbjct  460  YSCMGYEIAGAFGVKLAEPDKEVYAMVGDGSFLMLHSELVTSLQEGQKINIILFDNSGFG  519

Query  564  MV--VQWED-------RFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDD  614
             +  +Q E+        F K N     L  P     +  +  K AE  G+    V   ++
Sbjct  520  CINNLQMENGMGSFVTEFRKRNLETGQLDGPI----MTIDYAKVAEGYGLKTYSVRTMEE  575

Query  615  LRAAIQKMLDTPGPYLLDVIV  635
            L  A+          L+D+ V
Sbjct  576  LETALIDSKKQSISTLIDIKV  596
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: A0REB6.1 **Length:** 644 **Number of Matches:** 1

See 1 more title(s)

Related Information

Identical Proteins - Identical proteins to A0REB6.1

Range 1: 63 to 526 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
135 bits(339)	6e-32	Compositional matrix adjust.	124/485(26%)	208/485(42%)	76/485(15%)

```
Query  136  RHEQGGVFAAEGYARATGFPGV--CIATSGPGATNLVSGLADALLDSVPIVAITGQVPRR  193
            R+EQG   AA  +A+      +  C ++ GPG+ N+++  A A  +++P++ + G
Sbjct  63   RNEQGMANAAMAFAKQKHRKQIMACTSSVGPGSANMITSAATASANNIPVLLLPG-----  117

Query  194  MIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRP------------  241
                D F       V + I + + L +   D  R V +   +  R  RP
Sbjct  118  ----DVFATRQSDPVLQQIEQTHDLSISTNDAFRAVSK--YWDRINRPEQLMTAMIQAMR  171

Query  242  --------GPVLIDVPKDIQQQLVIPDWDQP-MRLPGYMSRLPK-LPNEMLLEQIVRLIS  291
                    G V I +P+D+Q +     WD P       + R+ + LP +  L   V +I
Sbjct  172  VLTNPADTGAVTICLPQDVQGEA----WDFPDYFFQKRVHRIERRLPTKASLADAVEMIK  227

Query  292  ESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTV  349
              KKPV+  GGG   ++++EEL++F E   IP   T  G  A  +    +L  +G+ G +
Sbjct  228  RKKKPVMICGGGVRYAEAAEELKQFAETFHIPFGETQAGKSAIESSHPYNLGGIGVTGNI  287

Query  350  YANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADI  409
             AN     +DL++  G RF D  T   + F +  ++  ++I+ +E   NK   + + AD
Sbjct  288  AANTIAKEADLVIGIGTRFTDFTTASKQLFQNE-EVEFLNINISEFHANKLDALKVIADA  346

Query  410  KLALQGLNSILESKEGKLKLDFS------AWRQELT-VQKVKYPL-------------NF  449
            K AL  L   L+  + +            AW  EL+ +  +++               N
Sbjct  347  KEALLVLIDELQVMDYRSSYTVEIADAKEAWETELSRLHNIRFTGQDFTPEVEGHFDGNL  406

Query  450  KTFGDAIPPQYA----IQVLDELTNGSAIISTGVGQ-----HQMWAAQYYKYRKPRQWLT  500
              + DA+  Q      I  ++ L +  AII    G       +MWA+     RKP  +
Sbjct  407  NEYVDALGSQLTQTAVIGQINTLLDEDAIIVGAAGSLPGDLQRMWAS-----RKPNTYHM  461

Query  501  SGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQ  560
              G   MG+ +  A+GA +  P + V  + GDGS+ M   EL T   EN  + ++L +N
Sbjct  462  EYGYSCMGYEVAGALGAKLAEPSKEVYAMVGDGSYQMLHSELVTSLQENKKINVLLFDNS  521

Query  561  HLGMV  565
              G +
Sbjct  522  GFGCI  526
```

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RecName: Full=Probable acetolactate synthase; AltName: Full=ALS; AltName: Full=Acetohydroxy-acid synthase

Sequence ID: P66947.1 **Length:** 547 **Number of Matches:** 1

See 2 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Identical proteins to P66947.1

Range 1: 6 to 471 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
133 bits(334)	1e-31	Compositional matrix adjust.	130/488(27%)	199/488(40%)	31/488(6%)

```
Query  86   APDEPRKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAA  145
            AP +      ++   L+  G+  VF   GG    I+    R   IR +  RHEQ   FAA
Sbjct  6    APAQTMHAGRLIARRLKASGIDTVFTLSGGHLFSIYDG-CREEGIRLIDTRHEQTAAFAA  64

Query  146  EGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPI  205
            EG+++ T  PGV   T+GPG TN +S +A A  +  P+V + G+ P    G  + QE
Sbjct  65   EGWSKVTRVPGVAALTAGPGITNGMSAMAAAQQNQSPLVVLGGRAPALRWGMGSLQEIDH  124

Query  206  VEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPM  265
            V     + +        E+   +V +A   A S   G   +D P D    +
Sbjct  125  VPFVAPVARFAATAQSAENAGLLVDQALQAAVSAPSGVAFVDFPMDHAFSM-----SSDN  179

Query  266  RLPGYMSRLPKLPNEM--LLEQIVRLISESKKPVLYVGGGCSQSSEE--LRRFVELTGIP  321
              PG ++ LP  P      L++   L+S +++PV+  G        E  L R VE   IP
Sbjct  180  GRPGALTELPAGPTPAGDALDRAAGLLSTAQRPVIMAGTNVWWGHAEAALLRLVEERHIP  239

Query  322  VASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFAS  381
            V    M  G  P    L+ S          + A+  +D+ L  GV  D R+ G    F S
Sbjct  240  VLMNGMARGVVPADHRLAFSR-------ARSKALGEADVALIVGVPMDFRL-GFGGVFGS  291

Query  382  RAKIVHIDIDSAEIGKNKQPHVSICADIKLALQG-LNSILESKEGKLKLDFSAWRQEL-T  439
              +++        +    +P       +   L G L + L +  G    D   W +EL T
Sbjct  292  TTQLI--------VADRVEPAREHPRPVAAGLYGDLTATLSALAGSGGTDHQGWIEELAT  343

Query  440  VQKVKYPLNFKTFGDAIPPQYAIQVLDELT---NGSAIISTGVGQHQMWAAQYYKYRKPR  496
             + +   L      D   P + ++V  EL       A++    G    +A +      P
Sbjct  344  AETMARDLEKAELVDDRIPLHPMRVYAELAALLERDALVVIDAGDFGSYAGRMIDSYLPG  403

Query  497  QWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIML  556
             WL SG  G +G G   A+ A + RP   VV + GDG+F  +  E  T+   N+ V  ++
Sbjct  404  CWLDSGPFGCLGSGPGYALAAKLARPQRQVVLLQGDGAFGFSGMEWDTLVRHNVAVVSVI  463

Query  557  LNNQHLGM  564
             NN   G+
Sbjct  464  GNNGIWGL  471
```

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RecName: Full=Acetolactate synthase-like protein; AltName: Full=IlvB-like protein

Sequence ID: O61856.2 **Length:** 640 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 48 to 548 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
132 bits(333)	3e-31	Compositional matrix adjust.	144/527(27%)	228/527(43%)	85/527(16%)

```
Query  85   FAPDEP--RKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGV  142
            F  DE   R G +++   L+   V ++F   GG    I  A  +  I + V  RHE   V
Sbjct  48   FQVDEKSKRHGGELVASVLKAHDVEEIFVLCGGHISPILVAAEKLGI-KIVDTRHEVTAV  106

Query  143  FAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQE  202
            FAA+  AR     GV   T+GPG TN ++ + +A +   P++ I G  P  + G  A Q+
Sbjct  107  FAADAVARLRQSIGVAAVTAGPGLTNTITAVKNAQMAESPLLLIGGAAPTLLKGRGALQD  166

Query  203  TPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQ--QQLVIPD  260
               + + R + K+   V  + DI   VREA   A+SG PGPV ++ P D+    +LV+ +
Sbjct  167  IDQMVLFRPLCKYVARVERLRDIVPTVREAIKAAKSGCPGPVFVEFPVDVLYPYELVVKE  226

Query  261  WDQPMRLPGYMSR-------------------------LPK---LPNEMLLEQIVRLISE  292
                    G++ R                         LP    +P    +++IV+L+
Sbjct  227  IGFNPNAKGFIQRALNFYLRCHVSRQFGNAWAPQTITPLPTNIPMPKSEKIQEIVQLVKS  286

Query  293  SKKPVLYVGGGCSQSS------EELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMH  346
            +K+PVL +G   SQ++       +L + VE  G PV   L G+     G +  L M  +
Sbjct  287  AKRPVLLIG---SQATLPPVKPADLVKAVEALGCPV--FLGGMARGLLGKDHPLQMRQVR  341

Query  347  GTVYANYAVDSSDLLLAFGVRFDDRVT-GKLEAFASRAKIVHIDIDSAEIGKNKQP----  401
                   A+  +DL +  G   D R++ G+    + ++KIV ++ +S+++ KN++
Sbjct  342  -----RDALKDADLTILAGTVCDFRLSYGR--TLSKKSKIVALNRNSSQLTKNEKAFWNS  394

Query  402  HVSICADIKLAL----------------QGLNSILESKEGKLKLDFSAWRQELTVQKVKY  445
             VS+ AD+  +L                + + S+ E  + K   +     Q+LT
Sbjct  395  DVSVQADVATSLVQVANALGANHTTTPTEWVKSLREKDDEKESANAKKMEQKLT-NGFLN  453

Query  446  PLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLG  505
            PLNF            ++ LD+     AI+    G     AA   + R P QWL  G  G
Sbjct  454  PLNF------------LRTLDQSLPDDAILVADGGDFVGSAAYIVRPRGPLQWLDPGAFG  501

Query  506  AMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPV  552
             +G G   A+GA    P   V  I GDGS   ++ E  T     LPV
Sbjct  502  TLGVGGGFALGAKTVYPKRPVYIIWGDGSCGYSLMEYDTFARHKLPV  548
```

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RecName: Full=Oxalyl-CoA decarboxylase

Sequence ID: P0AFI1.1 **Length:** 564 **Number of Matches:** 1

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Related Information

Identical Proteins - Identical proteins to P0AFI1.1

Range 1: 10 to 474 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
130 bits(327)	1e-30	Compositional matrix adjust.	127/479(27%)	219/479(45%)	26/479(5%)

```
Query  93    GSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARAT  152
             G  ++VEAL++  +   ++  G    ++ +   ++  IR +  RHEQ   +AA      T
Sbjct  10    GMHIIVEALKQNNIDTIYGVVGIPVTDMARH-AQAEGIRYIGFRHEQSAGYAAAASGFLT  68

Query  153   GFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDA--FQETPIVEVTR  210
               PG+C+  S PG  N ++ LA+A ++  P++ I+G   R ++      ++E   +   +
Sbjct  69    QKPGICLTVSAPGFLNGLTALANATVNGFPMIMISGSSDRAIVDLQQGDYEELDQMNAAK  128

Query  211   SITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGY  270
                K  + V   +D+   +  A  ++ SGRPG V +D+P ++    +  D      +
Sbjct  129   PYAKAAFRVNQPQDLGIALARAIRVSVSGRPGGVYLDLPANVLAATMEKDEALTTIVKVE  188

Query  271   MSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMG  328
                   LP    +   + L++++++P++ +G G   SQ+ E+LR F+E   IP     M
Sbjct  189   NPSPALLPCPKSVTSAISLLAKAERPLIILGKGAAYSQADEQLREFIESAQIPFLPMSMA  248

Query  329   LGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHI  388
              G     D   LS         AN     +D+++  G R +  +    + +A+  + + +
Sbjct  249   KGILE--DTHPLSAAAARSFALAN-----ADVVMLVGARLNWLLAHGKKGWAADTQFIQL  301

Query  389   DIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVK--YP  446
             DI+  EI  N+   V +  DI  ++QG+ + L+       L    WR  L + K +
Sbjct  302   DIEPQEIDSNRPIAVPVVGDIASSMQGMLAELKQNTFTTPL---VWRDILNIHKQQNAQK  358

Query  447   LNFKTFGDAIPPQY---AIQVLDELTNGSAIISTGVGQHQMWAAQ-YYKYRKPRQWLTSG  502
             ++ K   D  P  Y      V D L     I     G + +  A+      KPR+ L  G
Sbjct  359   MHEKLSTDTQPLNYFNALSAVRDVLRENQDIYLVNEGANTLDNARNIIDMYKPRRRLDCG  418

Query  503   GLGAMGFGLPAAIGAAV--GRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNN  559
               G MG G+  AIGA+V  G P   VV I+GD +F  +  E+ TI   NLPV I++ NN
Sbjct  419   TWGVMGIGMGYAIGASVTSGSP---VVAIEGDSAFGFSGMEIETICRYNLPVTIVIFNN  474
```

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RecName: Full=Oxalyl-CoA decarboxylase

Sequence ID: P40149.1 **Length:** 568 **Number of Matches:** 1

Related Information

Range 1: 54 to 545 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
129 bits(324)	3e-30	Compositional matrix adjust.	134/523(26%)	220/523(42%)	54/523(10%)

```
Query  136   RHEQGGVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMI  195
             RHEQ   +AA       G PGVC+  S PG  N V+ LA A  +  P++ ++G   R ++
Sbjct  54    RHEQHAGYAASIAGYIEGKPGVCLTVSAPGFLNGVTSLAHATTNCFPMILLSGSSEREIV  113

Query  196   GTDA--FQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQ  253
                   ++E   + V R   K ++ +  ++DIP  +  A   A SGRPG V +D+P  +
Sbjct  114   DLQQGDYEEMDQMNVARPHCKASFRINSIKDIPIGIARAVRTAVSGRPGGVYVDLPAKLF  173

Query  254   QQLVIPDWDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEEL  311
              Q +  +    +          ++P E  + +   LI  +K+PV+ +G G   +Q  +E+
Sbjct  174   GQTISVEEANKLLFKPIDPAPAQIPAEDAIARAADLIKNAKRPVIMLGKGAAYAQCDDEI  233

Query  312   RRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDR  371
             R  VE TGIP     M  G  P     S             +A+   D+ +  G R +
Sbjct  234   RALVEETGIPFLPMGMAKGLLPDNHPQSA-------AATRAFALAQCDVCVLIGARLNWL  286

Query  372   VT-GKLEAFASR-AKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESK------  423
             +  GK + +     K V IDI + E+  N+     +  DIK A+  L   L+
Sbjct  287   MQHGKGKTWGDELKKYVQIDIQANEMDSNQPIAAPVVGDIKSAVSLLRKALKGAPKADAE  346

Query  424   -EGKLKLDFSAWRQELTVQ--------KVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAI  474
               G LK      + +L  +         + Y  +     D +     I +++E  N  A+
Sbjct  347   WTGALKAKVDGNKAKLAGKMTAETPSGMMNYSNSLGVVRDFMLANPDISLVNEGAN--AL  404

Query  475   ISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAA--VGRPDEVVVDIDGD  532
              +T                KPR+ L SG  G MG G+   + AA   G+P   V+ ++GD
Sbjct  405   DNT---------RMIVDMLKPRKRLDSGTWGVMGIGMGYCVAAAAVTGKP---VIAVEGD  452

Query  533   GSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIF  592
              +F  +  EL TI   NLPV ++++NN  +          YK N A    G  S
Sbjct  453   SAFGFSGMELETICRYNLPVTVIIMNNGGI----------YKGNEADPQPGVISCTRLTR  502

Query  593   PNMLKFAEACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIV  635
                    EA G          +L+AA+++ + +  P L++ ++
Sbjct  503   GRYDMMMEAFGGKGYVANTPAELKAALEEAVASGKPCLINAMI  545
```

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RecName: Full=Acetolactate synthase-like protein; AltName: Full=IlvB-like protein

Sequence ID: Q6DDK5.1 **Length:** 649 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 30 to 571 GenPept Graphics

Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
127 bits(318)	3e-29	Compositional matrix adjust.	152/561(27%)	248/561(44%)	86/561(15%)

```
Query  85   FAPDEPRK--GSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGV  142
            F  D+  K  G +++ + L+   V  +F   GG    I  A  R +I R +  RHE   V
Sbjct  30   FELDQNSKHFGGELVADVLKAHDVRFLFTLCGGHISPILVAAERQNI-RVIDVRHEASAV  88

Query  143  FAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQE  202
            FAA+  +R +G  GV   T+GPG TN V+ + +A +   PIV + G     + G  + Q+
Sbjct  89   FAADAVSRLSGTVGVAAVTAGPGLTNTVTAVKNAQMAESPIVLLAGAAAGLLRGRGSLQD  148

Query  203  TPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKD-------IQQQ  255
               + + R + K +  V  V+DI  ++ +AF+LARSG PGPVL++ P D       ++Q
Sbjct  149  IDQLSLFRPLCKWSGRVNCVKDIVPMLCKAFYLARSGTPGPVLVEFPIDTLYPYSLVRQH  208

Query  256  LVIPDWDQPMR-------LPGYMSRL--------PKLPNEM-----------------LL  283
            L I D  Q  R       L  Y+ RL        P LP ++                  +
Sbjct  209  LRISDNPQSWRQRFTNWYLRFYLFRLFANGFRIQPCLPGQVPTQIPVEIPSIPWPSTKSI  268

Query  284  EQIVRLISESKKPVLYVGGG-------CSQSSEELRRFVELTGIPVASTLMGLGAFPTGD  336
            +Q+V L+S++K+PV+ V           +Q++E ++       IPV  T M  G
Sbjct  269  DQLVWLLSQAKRPVIVVSSQALLPPVPATQTAEHVKSL----RIPVYLTGMARG------  318

Query  337  ELSLSMLGMHGTVYANY----AVDSSDLLLAFGVRFDDRVT-GKLEAFASRAKIVHIDID  391
                 +LG H      +    A+  +DL++  G   D R+  G++     +AKIV I+ D
Sbjct  319  -----LLGRHHPCVFRHARRAALRVADLIILAGSVCDFRMDYGRV--LNRKAKIVIINRD  371

Query  392  SAEIGKNK----QPHVSICADIKLALQGLNSILESKEGKLKLDF---SAWRQELTVQKVK  444
              ++  N     +P+++I  D+  AL+ L+  L  +   L  DF   + W  EL  ++
Sbjct  372  KKQLYLNSDIFWRPYLAIRGDVGTALKELSISLNDRFPCLS-DFRCPTEWVGELLAREHH  430

Query  445  YPLNFKTF-----GDAIPPQYAIQVLDE--LTNGSAIISTGVGQHQMWAAQYYKYRKPRQ  497
                 +        + I P   +  L+   LT+  +II    G     AA   + R P
Sbjct  431  RDEEIRQSSLTQPAERINPLSVLWQLEHNGLTDQESIIVADGGDFVGSAAYILRPRGPLS  490

Query  498  WLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLL  557
            WL  G  G +G G   A+GA + RP   V  + GDGS   ++ E  T+     P   ++
Sbjct  491  WLDPGPFGTLGVGGGFALGAKLCRPQAHVWVVYGDGSAGYSLAEWDTMARHKAPAIGVIG  550

Query  558  NNQHLGMVVQWEDRFYKANRA  578
            N+     + + +   + +N A
Sbjct  551  NDACWSQIARDQLGLFGSNVA  571
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: Q5WKY8.1 **Length:** 637 **Number of Matches:** 1

Related Information

Range 1: 33 to 594 GenPept Graphics

Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
126 bits(317)	3e-29	Compositional matrix adjust.	140/583(24%)	242/583(41%)	72/583(12%)

```
Query  104  EGVTDVFAYPGGASMEIHQALTRSSIIRNVLP-RHEQGGVFAAEGYARATGFPGVCIATS  162
            EG+  +F +  G  + I QAL + +   NV   ++EQG   AA  +++      +   T+
Sbjct  33   EGIFTIFGH--GNVLGIGQALEQDAGRLNVWQGKNEQGMAHAAMAFSKQMLRKKIYAVTT  90

Query  163  --GPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAF---QETPIV-----EVTRSI  212
              GPGA NLV+    AL +++P++         ++  D F   Q  P++     E ++++
Sbjct  91   SVGPGAANLVAAAGTALANNIPVL---------LLPADTFATRQPDPVLQQFEQEYSQAV  141

Query  213  TKHNYLVMDVEDIPRVVR---------EAF-FLARSGRPGPVLIDVPKDIQQQLVIPDWD  262
            T ++ L        R+ R          AF  +   G+ GP  I + +D++ +      +
Sbjct  142  TTNDALKPVSRYWDRITRPEQLMSSLIRAFEVMTDPGKAGPATICIAQDVEGEAYEYPEE  201

Query  263  QPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGI  320
               +   Y+ R  + P E  +E+ +  I  SK+P+L VGGG   S++ EEL    E  GI
Sbjct  202  FFRKRIHYLER--RKPTEREIEEALERIRRSKRPLLVVGGGAKYSEAKEELVALSEQCGI  259

Query  321  PVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFA  380
            P+  T  G          +L  LG+ GT+ AN A   +DL++  G R+ D  T    AF
Sbjct  260  PLVETQAGKATVAADFANNLGGLGVTGTLAANKAAREADLVIGVGTRYTDFATSSKTAF-  318

Query  381  SRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTV  440
                   ++I+ + +   K     + AD K  L  L S L++         +A ++E
Sbjct  319  DFEHTTFLNINVSRMQTYKLDAYQVVADAKETLSLLISRLKTYRSAFGDRIAALKEEWLA  378

Query  441  QKVKYP---LNFKTF--------------------GDAIPPQYAIQVLDELTNGSAIIST  477
            ++ +      N KTF                    G  +P   A+  ++E  +  + I
Sbjct  379  ERNRLKSVVFNRKTFVPEVKEHFSQEKLNEYADALGTELPQTTALLAINETIDEDSTIIC  438

Query  478  GVGQ-----HQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGD  532
              G       ++W A      +P  +    G   MG+ +  A+G  +  P+  V  I GD
Sbjct  439  SSGSLPGDLQRLWHAN-----EPNTYHLEYGYSCMGYEISGALGIKLAEPEREVYSIVGD  493

Query  533  GSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIF  592
            GSF+M   EL T    N  + I+L +N   G +   +      +    +L   +    I
Sbjct  494  GSFLMLHSELITAIQYNKKINILLFDNAGFGCISNLQMDHGGGSYYCEFLTADNQVMNI-  552

Query  593  PNMLKFAEACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIV  635
             +  K AE  G    R    + L+AA++         L+++ V
Sbjct  553  -DYAKVAEGYGAKTYRANTVEQLKAALKDAKKQETSTLIEMKV  594
```

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RecName: Full=Acetolactate synthase-like protein; AltName: Full=IlvB-like protein

Sequence ID: A6QQT9.2 **Length:** 632 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 52 to 548 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
126 bits(316)	5e-29	Compositional matrix adjust.	133/518(26%)	223/518(43%)	70/518(13%)

```
Query  91    RKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYAR  150
            R G + +   L+  GV  +F   GG    +  A  +  I R V  RHE   VFAA+  AR
Sbjct  52    RHGGENVAAVLKAHGVRFLFTLVGGHISPLLVACEKLGI-RVVDTRHEVTAVFAADAVAR  110

Query  151   ATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTR  210
             TG  GV   T+GPG TN V+ + +A +   P++ + G     +    A Q    + + R
Sbjct  111   LTGTVGVAAVTAGPGLTNTVTAVKNAQIAQSPVLLLGGAASTLLQNRGALQAIDQIALFR  170

Query  211   SITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKD-------IQQQLVIPDWDQ  263
             + K    V  V DI   +R A   A+SG PGPV +++P D       +Q+++V
Sbjct  171   PLCKFCASVRRVRDIIPTLRAAMAAAQSGTPGPVFVELPLDVLYPYFMVQKEMV------  224

Query  264   PMRLP-GYMSRLPK--LPNEML--------------------------LEQIVRLISESK  294
            P + P G MSR     L N +                           +++ V ++S +K
Sbjct  225   PAKPPKGLMSRAVHWYLANSLANLFAGAWEPQPEGPLPLDIPQASPQQVQRCVEILSRAK  284

Query  295   KPVLYVGGGC---SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYA  351
            KP++ +G        SS++LR  VE  GIP     M  G       L       H
Sbjct  285   KPLMLIGSQALLPPTSSDKLRVAVETLGIPCFLAGMARGLLGRNHPL-------HFRQNR  337

Query  352   NYAVDSSDLLLAFGVRFDDRVT-GKLEAFASRAKIVHIDIDSAEIGKNK----QPHVSIC  406
              A+  +D+++  G   D R++ G++   +  +KI+ ++ D  E+  N     +P  ++
Sbjct  338   RAALKKADVVVLAGAVCDFRLSYGRV--LSRSSKIIVVNRDRKEMLINSDIFWKPQEAVQ  395

Query  407   ADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVKYPLNFKT-----FGDAIPPQYA  461
             D+      +  ++E   G++    S W +EL     +    F+          + P
Sbjct  396   GDVG---SFVVKLVEGLRGQMWA--SDWAEELRQADQQKEQAFREKALMPVAQHLNPVRV  450

Query  462   IQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGR  521
            +Q++++    ++I+    G     AA   + R P +WL  G  G +G G   A+GA + R
Sbjct  451   LQLVEDTLPDNSILVVDGGDFVGTAAYLVQPRGPLRWLDPGAFGTLGVGAGFALGAKLCR  510

Query  522   PDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNN  559
            PD  V  + GDG+F  ++ E  T     +PV  ++ N+
Sbjct  511   PDAEVWCLFGDGAFGYSLIEFDTFVRHKIPVMALIGND  548
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: P42415.2 **Length:** 637 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 33 to 579 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
125 bits(315)	5e-29	Compositional matrix adjust.	143/570(25%)	244/570(42%)	76/570(13%)

```
Query  104   EGVTDVFAYPGGASMEIHQALTRSSIIRNVLP-RHEQGGVFAAEGYARATGFPGV-CIAT  161
            EG+  +F +  G  + I QAL + +    V   ++EQG   AA  Y++      +  ++T
Sbjct  33    EGIFTIFGH--GNVLGIGQALEQDAGHLKVYQGKNEQGMAHAAMAYSKQMLRRKIYAVST  90

Query  162   S-GPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAF---QETPIV-----EVTRSI  212
            S GPGA NLV+    AL +++P++         +I  D F   Q  P++     E + +I
Sbjct  91    SVGPGAANLVAAAGTALANNIPVL---------LIPADTFATRQPDPVLQQMEQEYSAAI  141

Query  213   TKHNYLVMDVEDIPRVVR---------EAF-FLARSGRPGPVLIDVPKDIQQQLVIPDWD  262
            T ++ L        R+ R          AF  +    + GP  I + +D++ +    D
Sbjct  142   TTNDALKPVSRYWDRITRPEQLMSSLLRAFEVMTDPAKAGPATICISQDVEGEAYDFDES  201

Query  263   QPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSS--EELRRFVELTGI  320
              ++   Y+ R+   P+E  L+    LI  SKKPV+ VGGG   S   +EL    E   I
Sbjct  202   FFVKRVHYIDRMQ--PSERELQGAAELIKSSKKPVILVGGGAKYSGARDELVAISEAYNI  259

Query  321   PVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFA  380
            P+  T  G          +L  +G+ GT+ AN A   +DL++  G R+ D  T    AF
Sbjct  260   PLVETQAGKSTVEADFANNLGGMGITGTLAANKAARQADLIIGIGTRYTDFATSSKTAFD  319

Query  381   -SRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGK-------LKLDFS  432
              +AK ++I++  + +   K     + AD K+ L  L+ +LE  E +       LK ++
Sbjct  320   FDKAKFLNINV--SRMQAYKLDAFQVVADAKVTLGKLHGLLEGYESEFGTTIRELKDEWL  377

Query  433   AWRQEL---TVQKVKYPLNFKT---------FGDAI----PPQYAIQVLDELTNGSAIIS  476
            A R+ L   T ++  +    K          + DA+    P   A+  ++E     ++I
Sbjct  378   AERERLSKVTFKREAFDPEIKNHFSQEVLNEYADALNTELPQTTALLTINETIPEDSVII  437

Query  477   TGVGQ-----HQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDG  531
               G       ++W +       P  +    G   MG+ +   +G  +  PD  V  I G
Sbjct  438   CSAGSLPGDLQRLWHSNV-----PNTYHLEYGYSCMGYEVSGTLGLKLAHPDREVYSIVG  492

Query  532   DGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEI  591
            DGSF+M   EL T    N  + ++L +N   G +   +           Y    +++ +I
Sbjct  493   DGSFLMLHSELITAIQYNKKINVLLFDNSGFGCINNLQ---MDHGSGSYYCEFRTDDNQI  549

Query  592   FP-NMLKFAEACGVPAARVTHRDDLRAAIQ  620
               +  K AE  G    R    ++L+AA++
```

```
Sbjct  550  LNVDYAKVAEGYGAKTYRANTVEELKAALE  579
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: Q0TUZ2.1 **Length:** 639 **Number of Matches:** 1

Related Information

Range 1: 60 to 522 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
123 bits(309)	3e-28	Compositional matrix adjust.	115/481(24%)	206/481(42%)	69/481(14%)

```
Query  136  RHEQGGVFAAEGYARATGFPGV--CIATSGPGATNLVSGLADALLDSVPIVAITG-----  188
            R+EQG    +  +A+      +  C ++ GPGA N+V+  A A ++++P++ + G
Sbjct  60   RNEQGMAHVSTAFAKQNNRRKIIACSSSVGPGAANMVTAAATATVNNIPLLLLPGDSFAT  119

Query  189  --------QVPRR----MIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLA  236
                    Q+ +     +   DAF+  P+ +    I +   L+  + +  RV      L
Sbjct  120  RQPDPVLQQIEQSYNLGITTNDAFK--PVCKYWDRINRPEQLMSAMINAMRV------LT  171

Query  237  RSGRPGPVLIDVPKDIQQQLV-IPDWDQPMRLPGYMSRLPK-LPNEMLLEQIVRLISESK  294
                 G V I +P+D+Q +    P++    R+     R+ + L  +   E+ + +I   K
Sbjct  172  DPAETGAVCIALPQDVQGEAYDFPEYFFKKRV----HRITRPLAVQEEFEEALDIIMNKK  227

Query  295  KPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYAN  352
            KP++  GGG   S++ E L  F E   IP+  T  G  A  +   L+L  +G+ G + AN
Sbjct  228  KPIIICGGGVRYSEAGEALVDFAEEFNIPICETQAGKSAIKSSHPLNLGGIGVTGNLAAN  287

Query  353  YAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLA  412
                 +DL++  G RF D  T     F +  ++  I ++ ++    K     I  D K+
Sbjct  288  MIAKDADLVIGVGTRFSDFTTSSKSLFKN-PEVDFITVNVSKFHGEKMDAHKIIGDAKVC  346

Query  413  LQGLNSILE------SKEGKLKLDFSAWRQELT-VQKVKYPLNFKTF-------------  452
            ++ L ++LE      S E ++     AW++E+  +  +KY  NF+
Sbjct  347  IEELQAMLEANNYESSYEDEIVNAKKAWKEEMKRLTNIKYDENFEALIKPKREGCIEEFS  406

Query  453  ---GDAIPPQYAIQVLDELTNGSAIISTGVGQ-----HQMWAAQYYKYRKPRQWLTSGGL  504
               G  I    A+ V+ E  +  AI+    G       +MW            +    G
Sbjct  407  VLTGGLITQTAALGVIRETIDDDAIVVGAAGSLPGDLQRMWETDVRD-----SYHMEYGY  461

Query  505  GAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGM  564
              MG+ + A +GA +  P+  V  + GDGS++M   E+ T   E   + I+L +N   G
Sbjct  462  SCMGYEIAATLGAKLAEPEREVYSMVGDGSYLMLHSEMVTAMQEQKKINILLFDNCGFGC  521

Query  565  V  565
            +
Sbjct  522  I  522
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: Q8XP76.1 **Length:** 639 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 60 to 522 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
123 bits(309)	3e-28	Compositional matrix adjust.	115/481(24%)	206/481(42%)	69/481(14%)

```
Query  136  RHEQGGVFAAEGYARATGFPGV--CIATSGPGATNLVSGLADALLDSVPIVAITG-----  188
            R+EQG    +  +A+      +  C ++ GPGA N+V+  A A ++++P++ + G
Sbjct  60   RNEQGMAHVSTAFAKQNNRRKIIACSSSVGPGAANMVTAAATATVNNIPLLLLPGDSFAT  119

Query  189  --------QVPRR----MIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLA  236
                    Q+ +     +   DAF+  P+ +    I +   L+  + +  RV      L
Sbjct  120  RQPDPVLQQIEQSYNLGITTNDAFK--PVCKYWDRINRPEQLMSAMINAMRV------LT  171

Query  237  RSGRPGPVLIDVPKDIQQQLV-IPDWDQPMRLPGYMSRLPK-LPNEMLLEQIVRLISESK  294
                 G V I +P+D+Q +    P++    R+     R+ + L  +   E+ + +I   K
Sbjct  172  DPAETGAVCIALPQDVQGEAYDFPEYFFKKRV----HRITRPLAVQEEFEEALDIIMNKK  227

Query  295  KPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYAN  352
            KP++  GGG   S++ E L  F E   IP+  T  G  A  +   L+L  +G+ G + AN
Sbjct  228  KPIIICGGGVRYSEAGEALVDFAEEFNIPICETQAGKSAIKSSHPLNLGGIGVTGNLAAN  287

Query  353  YAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLA  412
                 +DL++  G RF D  T     F +  ++  I ++ ++    K     I  D K+
Sbjct  288  MIAKDTDLVIGVGTRFSDFTTSSKSLFKN-PEVDFITVNVSKFHGGKMDAHKIIGDAKVC  346

Query  413  LQGLNSILE------SKEGKLKLDFSAWRQELT-VQKVKYPLNFKTF-------------  452
            ++ L ++LE      S E ++     AW++E+  +  +KY  NF+
Sbjct  347  IEELQAMLEANNYESSYEDEIVNAKKAWKEEMKRLTNIKYDENFEALIKPKREGCIEEFS  406

Query  453  ---GDAIPPQYAIQVLDELTNGSAIISTGVGQ-----HQMWAAQYYKYRKPRQWLTSGGL  504
               G  I    A+ V+ E  +  AI+    G       +MW            +    G
Sbjct  407  VLTGGLITQTAALGVIRETIDDDAIVVGAAGSLPGDLQRMWETD-----ARDSYHMEYGY  461

Query  505  GAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGM  564
              MG+ + A +GA +  P+  V  + GDGS++M   E+ T   E   + I+L +N   G
Sbjct  462  SCMGYEIAATLGAKLAEPEREVYSMVGDGSYLMLHSEMVTAMQEQKKINILLFDNCGFGC  521

Query  565  V  565
            +
Sbjct  522  I  522
```

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RecName: Full=Acetolactate synthase-like protein; AltName: Full=IlvB-like protein

Sequence ID: A1L0T0.2 **Length:** 632 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 52 to 548 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
123 bits(308)	4e-28	Compositional matrix adjust.	131/521(25%)	229/521(43%)	76/521(14%)

```
Query  91   RKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYAR  150
            R G + +   L   GV  +F   GG    +  A  +  I R V  RHE   VFAA+  AR
Sbjct  52   RHGGENVAAVLRAHGVRFIFTLVGGHISPLLVACEKLGI-RVVDTRHEVTAVFAADAMAR  110

Query  151  ATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTR  210
             +G  GV   T+GPG TN V+ + +A +   PI+ + G     +    A Q    + + R
Sbjct  111  LSGTVGVAAVTAGPGLTNTVTAVKNAQMAQSPILLLGGAASTLLQNRGALQAVDQLSLFR  170

Query  211  SITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKD-------IQQQLV------  257
             + K    V  V DI   +R A   A+SG PGPV +++P D       +Q+++V
Sbjct  171  PLCKFCVSVRRVRDIVPTLRAAMAAAQSGTPGPVFVELPVDVLYPYFMVQKEMVPAKPPK  230

Query  258  -----IPDWDQPMRLPGYMSRL--------PKLP--------NEMLLEQIVRLISESKKP  296
                 +  W     L  Y++ L        P+ P        +   +++ V ++S +K+P
Sbjct  231  GLVGRVVSW----YLENYLANLFAGAWEPQPEGPLPLDIPQASPQQVQRCVEILSRAKRP  286

Query  297  VLYVGGGC---SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLG----MHGTV  349
            ++ +G        S+++LR  VE  G+P       LG    G      +LG    +H
Sbjct  287  LMVLGSQALLTPTSADKLRAAVETLGVPCF-----LGGMARG------LLGRNHPLHIRE  335

Query  350  YANYAVDSSDLLLAFGVRFDDRVT-GKLEAFASRAKIVHIDIDSAEIGKNK----QPHVS  404
              + A+  +D+++  G   D R++ G++ + +S  KI+ ++ +  E+  N     +P  +
Sbjct  336  NRSAALKKADVIVLAGTVCDFRLSYGRVLSHSS--KIIIVNRNREEMLLNSDIFWKPQEA  393

Query  405  ICADIKLALQGLNSILESKEGKLKLDFSA-WRQELTVQKVKYPLNFKT-----FGDAIPP  458
            +  D+       + +L+  EG     ++  W +EL     +    F+          + P
Sbjct  394  VQGDVG------SFVLKLVEGLQGQTWAPDWVEELREADRQKEQTFREKAAMPVAQHLNP  447

Query  459  QYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAA  518
               +Q+++E    ++I+    G     AA   + R P +WL  G  G +G G   A+GA
Sbjct  448  VQVLQLVEETLPDNSILVVDGGDFVGTAAHLVQPRGPLRWLDPGAFGTLGVGAGFALGAK  507

Query  519  VGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNN  559
            + RPD  V  + GDG+F  ++ E  T     +PV  ++ N+
Sbjct  508  LCRPDAEVWCLFGDGAFGYSLIEFDTFVRHKIPVMALVGND  548
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: Q9KAG9.1 **Length:** 637 **Number of Matches:** 1

Related Information

Range 1: 32 to 593 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
122 bits(306)	7e-28	Compositional matrix adjust.	138/578(24%)	254/578(43%)	62/578(10%)

```
Query  104  EGVTDVFAYPGGASMEIHQALTRS-SIIRNVLPRHEQGGVFAAEGYARATGFPGVCIAT-  161
            EG+ ++F +  G  + I  AL +    ++    ++EQG    A  Y++      +   T
Sbjct  32   EGIFNIFGH--GNVLGIGHALEQDPGHLKVYQGKNEQGMAHTAIAYSKQMLRKKIYAITT  89

Query  162  -SGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGT-------DAFQETPIVEVTRS--  211
             SGPG+ NLV+  A AL + +PI+ +    P     T         F++   + +T +
Sbjct  90   SSGPGSANLVTAAATALANQIPILLL----PADTYATRQPDPVLQQFEQEQSIAITTNDA  145

Query  212  ---ITKHNYLVMDVEDIPRVVREAF-FLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRL  267
               ++++   +   E +   +  AF  +    + GP  I + +D++ +    D     +
Sbjct  146  LQPVSRYWDRITRPEQLMSSLIRAFEVMTDPAKAGPATICISQDVEGEAFDYDVRFFEKR  205

Query  268  PGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVAST  325
              Y+ R  KLP+E  L+    LI +SK+P+L VGGG   S++ E L  F E   +P+  T
Sbjct  206  VHYIDR--KLPSERELKGAADLIKKSKRPLLVVGGGAKYSEAREALIAFSETFNVPLTET  263

Query  326  LMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKI  385
              G  A     + +L  LG+ GT+ AN A   +DL++  G RF D  T     F    K+
Sbjct  264  QAGKSAVEASFKNNLGGLGITGTLAANKAAQQADLVIGIGTRFTDFATSSKTLF-DFEKV  322

Query  386  VHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKE-------GKLKLDFSAWRQEL  438
              ++I+ + +   K     + AD K  L+ L  +LE  +       G+LK ++   R+ L
Sbjct  323  KFVNINVSRMQAYKLDAFPVVADAKRTLEALVPMLEGYKSEYGDDIGQLKAEWLKERERL  382

Query  439  ---TVQKVKYPLNFK---------TFGDAIPPQY----AIQVLDELTNGSAIISTGVGQ-  481
               T  + ++    K          + DA+  ++    A+  ++E  +  ++I    G
Sbjct  383  GKVTFDRERFEPEIKGHFTQEVMNEYADALQTEFAQTTALLTINETIDPDSVIICAAGSL  442

Query  482  ----HQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIM  537
                 ++W A+       P  +    G   MG+ +   +G  +  P++ V  I GDGSF+M
Sbjct  443  PGDLQRLWHAEV-----PNTYHLEYGYSCMGYEVSGTLGLKLAEPNKEVYAIVGDGSFLM  497

Query  538  NVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLK  597
               EL T    +  + ++L +N   G +   +  F   +    +    ++E  +  +  K
Sbjct  498  LHSELVTAIQYHKKINVLLFDNSGYGCINNLQMDFGGGSYFCEF--RTADEKILHVDYAK  555

Query  598  FAEACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIV  635
             AE  G  + RV+  ++L+AA++         L+D+ V
```

```
Sbjct  556  VAEGYGAKSYRVSTVEELKAALEDAKKQECSTLIDIKV  593
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: Q8Y9Y1.1 **Length:** 638 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 34 to 603 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
119 bits(298)	7e-27	Compositional matrix adjust.	149/601(25%)	248/601(41%)	86/601(14%)

```
Query  104  EGVTDVFAYPGGASMEIHQALTRSSIIRNVLP-RHEQGGVFAAEGYARATGFPGV--CIA  160
            +G+  VF +  G  + I QAL       NV   ++EQG   AA  YA+      +  C A
Sbjct  34   DGIFTVFGH--GNVVGIGQALEEDPGHLNVYQGKNEQGMAHAAIAYAKQKNRKRIYACSA  91

Query  161  TSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIV-----EVTRSITKH  215
            ++GPG+ NL++  + AL +++P++ +    P     T   Q  P++     E + +IT +
Sbjct  92   SAGPGSANLITAASTALANNLPVLFL----PADTFATR--QPDPVLQQLEHESSAAITTN  145

Query  216  NYLVMDVEDIPRVVR---------EAF-FLARSGRPGPVLIDVPKDIQQQLVIPDWDQPM  265
            +          RV R          AF  +      GP  I + +D + +     +D P+
Sbjct  146  DGFQAVSRYFDRVQRPEQLMSALIRAFEVMTNPASAGPATICIAQDTEGEA----FDYPV  201

Query  266  RL----PGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVELTG  319
                    Y++R  ++P +  L +  RLI  SK PV+ VGGG   S + EEL    E +
Sbjct  202  EFFQKRIHYLNR--QIPTKRELTEAARLIQASKTPVIIVGGGARYSDAREELIALSEQSN  259

Query  320  IPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAF  379
            IP+  T  G        + +L   G+ GT+ AN A+  +DL++  G R+ D  T    AF
Sbjct  260  IPLVETHAGKSTVEFDFKNNLGGTGILGTLAANKAIRDADLVIGIGTRYTDFTTSSKTAF  319

Query  380  ASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKE----GKLKLDFSAWR  435
                K ++I++  + +   K     +  D K  L  L  +L+  +     ++ +  + W
Sbjct  320  GPATKFININV--SRMQTYKLDAFQVVGDAKATLAELAPLLKGYQTQFGDRIAVYKAEWL  377

Query  436  QELT-VQKVKY------PLNFKTFGDAIPPQYAIQVLDELTNGSAIIS------------  476
             E T +Q  K+      P     F  A   +YA  +  E T   A+I+
Sbjct  378  AERTRLQNTKFNREAFTPEIKDQFDQATLNEYADSLQTEFTQTEALITINDTVAPDSIVV  437

Query  477  TGVGQ-----HQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRP-DEVVVDID  530
               G       ++W         P  +    G   MG+ +  A+GA +    ++ V  I
Sbjct  438  CSAGSLPGDLQRLWNPAV-----PNTYHLEYGYSCMGYEINGALGAKMAAANNQEVYSIV  492

Query  531  GDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGN--PSNE  588
            GDGSF M+  EL T       + IML +N   G +    +    AN + ++      S+
Sbjct  493  GDGSFCMSHSELLTSLQYGKKINIMLFDNSGFGCI----NNLQMANGSDSFFCEFRDSDN  548

Query  589  AEIFPNMLKFAEACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIVPHQEHVLPMIPSG  648
              +  + K AE  G    R   ++DL +A++         L+D+       VLP   S
Sbjct  549  QIMQVDYAKIAEGYGAKVYRANTKEDLISALEDAKKQTKTTLIDM------KVLPKTMSE  602

Query  649  G  649
            G
Sbjct  603  G  603
```

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RecName: Full=Benzaldehyde lyase; AltName: Full=Benzoin aldolase; Short=BL; Short=BZL

Sequence ID: P51853.1 **Length:** 563 **Number of Matches:** 1

Related Information

Range 1: 119 to 544 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
118 bits(296)	8e-27	Compositional matrix adjust.	115/445(26%)	203/445(45%)	34/445(7%)

```
Query  206  VEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDI------QQQLVIP  259
            V +   ITK  + VM  E IPR+V +A   A S   GPVL+D+P DI      +  ++IP
Sbjct  119  VAMAAPITKWAHRVMATEHIPRLVMQAIRAALSAPRGPVLLDLPWDILMNQIDEDSVIIP  178

Query  260  DWDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSSEE--LRRFVEL  317
            D    + L  + +R    P+   L+Q + L+ ++++PV+ +G   S+++ +  L  FV
Sbjct  179  D----LVLSAHGAR----PDPADLDQALALLRKAERPVIVLGSEASRTARKTALSAFVAA  230

Query  318  TGIPVASTLMGLGAFPTGDELSLSML-GMHGTVYANYAVDSS-DLLLAFGVRFD-DRVTG  374
            TG+PV +   GL        L  +M  G+   +Y+    D++ DL+L  G RF  +   G
Sbjct  231  TGVPVFADYEGLSML---SGLPDAMRGGLVQNLYSFAKADAAPDLVLMLGARFGLNTGHG  287

Query  375  KLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGL-NSILESKEGKLKLDFSA  433
              +     A+++ +D D+ E+G+ +   + I AD+   ++ L  +  +      + D+ A
Sbjct  288  SGQLIPHSAQVIQVDPDACELGRLQGIALGIVADVGGTIEALAQATAQDAAWPDRGDWCA  347

Query  434  WRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYR  493
               +L  ++        +   A+ P +A QV+ +  +    +        +W ++
Sbjct  348  KVTDLAQERYASIAAKSSSEHALHPFHASQVIAKHVDAGVTVVADGALTYLWLSEVMSRV  407

Query  494  KPRQWLTSGGLGAMGFGLPAAIGAAVG--RPDEVVVDIDGDGSFIMNVQELATIKVENLP  551
            KP  +L  G LG+MG G   A+GA V         + + GDGS   ++ E  T+  + LP
Sbjct  408  KPGGFLCHGYLGSMGVGFGTALGAQVADLEAGRRTILVTGDGSVGYSIGEFDTLVRKQLP  467

Query  552  VKIMLLNNQHLGMVVQWEDRFYKANR-AHTYLGNPSNEAEIFPNMLKFAEACGVPAARVT  610
            + ++++NNQ  G  + ++      NR   T L N S            A A G     V
Sbjct  468  LIVIIMNNQSWGATLHFQQLAVGPNRVTGTRLENGSYHG--------VAAAFGADGYHVD  519
```

```
Query  611  HRDDLRAAIQKMLDTPGPYLLDVIV  635
              +   AA+ + L    P  ++V V
Sbjct  520  SVESFSAALAQALAHNRPACINVAV  544
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: Q723S8.2 **Length:** 638 **Number of Matches:** 1

Related Information

Range 1: 65 to 603 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
118 bits(296)	1e-26	Compositional matrix adjust.	139/569(24%)	235/569(41%)	85/569(14%)

```
Query  136  RHEQGGVFAAEGYARATGFPGV--CIATSGPGATNLVSGLADALLDSVPIVAITGQVPRR  193
            ++EQG   AA  YA+      +  C  ++GPG+ NL++    AL +++P++ +    P
Sbjct  65   KNEQGMAHAAIAYAKQKNRQRIYACSTSAGPGSANLITAAGTALANNLPVLFL----PAD  120

Query  194  MIGTDAFQETPIV-----EVTRSITKHNYLVMDVEDIPRVVR---------EAF-FLARS  238
               T   Q  P++     E + +IT ++          RV R          AF  +
Sbjct  121  TFATR--QPDPVLQQLEHESSTAITTNDGFQAVSRYFDRVQRPEQLMSALIRAFEVMTNP  178

Query  239  GRPGPVLIDVPKDIQQQLVIPDWDQPMRL----PGYMSRLPKLPNEMLLEQIVRLISESK  294
               GP  I + +D + +     +D P+        Y++R  ++P +  L +  RLI  SK
Sbjct  179  ASAGPATICIAQDTEGEA----FDYPVEFFQKRIHYLNR--QIPTKRELTEAARLIKASK  232

Query  295  KPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYAN  352
             PV+ VGGG   S++ EEL    E T IP+  T  G        + +L   G+ GT+ AN
Sbjct  233  TPVIIVGGGARYSRAREELIALSEQTNIPLVETHAGKSTLEFDFKNNLGGTGILGTLAAN  292

Query  353  YAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLA  412
             A+  +DL++  G R+ D  T    AF    K ++I++  + +   K     +  D K
Sbjct  293  KAIRDADLVIGIGTRYTDFTTSSKTAFDPTTKFININV--SRMQTYKLDAFQVVGDAKAT  350

Query  413  LQGLNSILESKEGKLKLDFSAWRQELTVQKVKY---PLNFKT--------FGDAIPPQYA  461
            L  L  +L+  + +     +A++ E   ++ +      N +T        F  AI  +YA
Sbjct  351  LAELAPLLKGYQTQFGNKIAAYKTEWLDERARLQTTKFNRETFTPEIKDQFDQAILNEYA  410

Query  462  IQVLDELTNGSAIIS------------TGVGQ-----HQMWAAQYYKYRKPRQWLTSGGL  504
             ++  E T   A+I+               G       ++W         P  +    G
Sbjct  411  DRLQTEFTQTEALITINDNVAPDSIVVCSAGSLPGDLQRLWNPAV-----PDTYHLEYGY  465

Query  505  GAMGFGLPAAIGA--AVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHL  562
              MG+ +  A+GA  A  +  EV   I GDGSF M+  EL T       + IML +N
Sbjct  466  SCMGYEINGALGAKMAAAKKQEVYA-IVGDGSFCMSHSELLTSLQYGKKINIMLFDNSGF  524

Query  563  GMVVQWEDRFYKANRAHTYLGN--PSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQ  620
            G +    +    AN + ++      S+   +  +  K AE  G    R   ++DL +A++
Sbjct  525  GCI----NNLQMANGSDSFFCEFRDSDNQIMQVDYAKIAEGYGAKVYRANTKEDLISALE  580

Query  621  KMLDTPGPYLLDVIVPHQEHVLPMIPSGG  649
                     L+++       VLP   S G
Sbjct  581  DAKTQSKTTLIEM------KVLPKTMSEG  603
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: Q898E8.2 **Length:** 644 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 32 to 603 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
118 bits(295)	2e-26	Compositional matrix adjust.	142/594(24%)	247/594(41%)	83/594(13%)

```
Query  104  EGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRH-EQGGVFAAEGYARATGFPGV--CIA  160
            +G+  +F +  G  + I QAL        V   H EQG   +A  +A+ +    +  C +
Sbjct  32   QGIFTIFGH--GNVLGIGQALEEDPGHLEVYQGHNEQGMAQSAIAFAKQSNRKQIYACTS  89

Query  161  TSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVM  220
            + GPGA N+V+  A A  +++P++ + G         D F       V + + +   L +
Sbjct  90   SVGPGAANMVTAAATATANNIPVLLLPG---------DTFSTRQPDPVLQQVEQTYNLSI  140

Query  221  DVEDIPRVVREAFFLARSGRP--------------------GPVLIDVPKDIQQQLV-IP  259
               D  + V +  +  R  RP                    G V I +P+D+Q ++   P
Sbjct  141  TTNDAFKAVSK--YWDRVNRPEQLMTAMINAMRVLTDPANTGAVTIALPQDVQGEIYDFP  198

Query  260  DWDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGC--SQSSEELRRFVEL  317
            ++    R+   + R P  P++  +E  V LI   KKP++  GGG   S+++E L+RF E
Sbjct  199  EYFFKKRVH-RIERTP--PSKQAIEDAVELIKRKKKPLIICGGGVRYSEAAESLKRFSEK  255

Query  318  TGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLE  377
              IP   T  G  A      L+L  +G+ G   AN     +DL++  G RF D  T
Sbjct  256  FNIPFGETQAGKSAIEWSYGLNLGGIGVTGNSAANSIAKDADLIIGVGTRFTDFTTCSKF  315

Query  378  AFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESK------EGKLKLDF  431
             F +   +  + I+ +    NK   + + +D K+ L  + + LE +      E ++K
Sbjct  316  LFQND-DVEFLTINISSFHANKLDALKVISDAKVGLDTIANELERQGYSSDYEDEIKKAK  374

Query  432  SAWRQELT-VQKVKYPLN-----------------FKTFGDAIPPQYAIQVLDELTNGSA  473
            + W +EL  +  ++Y                    +K F   +     +  L+EL +  A
Sbjct  375  NEWEKELNRLFNIEYTEKEFVPEIAGHCDKVVEEFYKEFDSCLTQTKVLGELNELLDDDA  434

Query  474  IISTGVGQ-----HQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVD  528
            I+    G      H++W        ++   +    G   MG+ + AA+G  +   D+ V
```

```
Sbjct  435  IVIGASGSLPGDLHKVWCP-----KRSNTYHMEYGYSCMGYEVSAALGVKLAEEDKEVYS  489

Query  529  IDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNE  588
            + GDG+++M   EL T   E   + I+L +N   G +   +      + A  +    S
Sbjct  490  LVGDGAYLMLHSELITSIKEGKKINILLFDNAGFGCINNLQMSNGMGSFATEFRHRNSET  549

Query  589  AEIFPNMLKF-----AEACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDV-IVP  636
             ++   +LK      AE  GV   +V   D LR AI+         L+D+ I+P
Sbjct  550  GKLDGKLLKIDFAKSAEGYGVKTYKVNTIDKLRYAIEDSKKQKISTLIDIKILP  603
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: Q65D03.1 **Length:** 637 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 33 to 579 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
117 bits(292)	5e-26	Compositional matrix adjust.	143/580(25%)	242/580(41%)	96/580(16%)

```
Query  104  EGVTDVFAYPGGASMEIHQALTRSSIIRNVLP-RHEQGGVFAAEGYARATGFPGV-CIAT  161
            EG+  +F +  G  + I QAL + +    V   ++EQG   AA  Y++      +  ++T
Sbjct  33   EGIFTIFGH--GNVVGIGQALEQDAGHLKVFQGKNEQGMAHAAMAYSKQMLRRKIYAVST  90

Query  162  S-GPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAF---QETPIV-----EVTRSI  212
            S GPGA NLV+    AL +++P++         +I  D F   Q  P++     E + +I
Sbjct  91   SVGPGAANLVAAAGTALANNIPVL---------LIPADTFATRQPDPVLQQVEQEYSAAI  141

Query  213  TKHNYLVMDVEDIPRVVR---------EAF-FLARSGRPGPVLIDVPKDIQQQLVIPDWD  262
            T ++ L        R+ R          AF  +    + GP  I + +D++ +    D+D
Sbjct  142  TTNDALKPVSRYWDRITRPEQLMSSLIRAFEVMTDPAKAGPATICISQDVEGEAY--DFD  199

Query  263  QPM--RLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSS--EELRRFVELT  318
            +    +   Y+ R  K P+E  L+    LI  SKKP++ VGGG   S   +EL    E
Sbjct  200  ESFFEKRVHYVDR--KEPSERELKGAAELIKSSKKPLILVGGGAKYSGARDELIAMSEAY  257

Query  319  GIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEA  378
             IP+  T  G          +L  +G+ GT+ AN A   +DL++  G R+ D  T    A
Sbjct  258  NIPLVETQAGKSTVEADFANNLGGMGITGTLAANKAARGADLIIGIGTRYTDFATSSKTA  317

Query  379  FA-SRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGK-------LKLD  430
            F    AK ++I++  + +   K     + AD K+ L  L+ +LE  + +       LK +
Sbjct  318  FDFDNAKFLNINV--SRMQAYKLDAFQVVADAKVTLGKLHGLLEGYKSEFGSTIKELKDE  375

Query  431  FSAWRQELTVQKVKYPLNF-------------KTFGDAI----PPQYAIQVLDELTNGSA  473
            + A R  L+    K   NF               + D +    P   A+  ++E  +  +
Sbjct  376  WLAERDRLSKVTFKRE-NFTPEIKDHFSQDILNEYADVLQTELPQTTALLAINETVDPDS  434

Query  474  IISTGVGQ-----HQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVD  528
            ++    G       ++W +       P  +    G   MG+ +   +G  +  PD  V
Sbjct  435  VVICSAGSLPGDLQRLWHSNV-----PNTYHLEYGYSCMGYEVSGTLGLKLAHPDREVYS  489

Query  529  IDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNE  588
            + GDGSF+M   EL T    N  + ++L +N   G +          N      GN S
Sbjct  490  LVGDGSFLMLHSELITAIQYNKKINVLLFDNSGFGCI----------NNLQMDHGNGSYY  539

Query  589  AE--------IFPNMLKFAEACGVPAARVTHRDDLRAAIQ  620
             E        +  +  K AE  G    +    ++L+AA++
Sbjct  540  CEFRTADNQILNVDYAKVAEGYGAKTYKANTIEELKAALE  579
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: Q5KYR0.1 **Length:** 644 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 63 to 526 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
115 bits(288)	1e-25	Compositional matrix adjust.	123/487(25%)	203/487(41%)	80/487(16%)

```
Query  136  RHEQGGVFAAEGYARATGFPGV--CIATSGPGATNLVSGLADALLDSVPIVAITGQVPRR  193
            R+EQG   AA  +A+      +  C ++ GPGA N+V+  A A  + +P++ + G
Sbjct  63   RNEQGMAHAAIAFAKQKHRRQIMACTSSVGPGAANMVTAAATASANHIPVLLLPG-----  117

Query  194  MIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRP------------  241
                D F       V + I   + L +   D  R V +  +  R  RP
Sbjct  118  ----DTFATRQPDPVLQQIEHWHDLTVSTNDAFRAVSK--YWDRISRPEQLMSAMIQAMR  171

Query  242  --------GPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRLPKL----PNEMLLEQIVRL  289
                    G V I +P+D+Q +     +D P     +  R+ ++    P +  + + V L
Sbjct  172  VLTDPANTGAVTIALPQDVQGEA----YDFPESF--FQKRIHRIERRVPAKAAIHEAVEL  225

Query  290  ISESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHG  347
            I   KKP++  GGG   S+++EEL++F E   IP   T  G  A  +    +L  +G+ G
Sbjct  226  IRRKKKPIIICGGGVRYSEAAEELKQFAEKFHIPYGETQAGKSAVESAHPYNLGGIGVTG  285

Query  348  TVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICA  407
             + AN     +DL++  G R+ D  TG  + F    ++  + I+ +     K   V + A
Sbjct  286  NLAANIIAKEADLVIGIGTRYTDFTTGSKQLF-QHPEVEFLTINVSVFDACKLDAVRVVA  344

Query  408  DIKLALQGLNSIL------ESKEGKLKLDFSAWRQELT-VQKVKYP-------------  446
            D KLAL  L   L           ++ +   AW +EL  +  V+Y
Sbjct  345  DAKLALLALTEELEKIGYRSGYTNEIDIAKKAWEEELNRLHHVRYRQSGFQPEVAGHLDE  404
```

```
Query  447  --LNFKTFGDAIPPQY-AIQVLDELTNGSAIISTGVGQ-----HQMWAAQYYKYRKPRQW  498
                +  F D+   Q   I  ++E  +  AII    G       +MW A     R+P  +
Sbjct  405  VLTEYSEFFDSSLTQTEVIGAINEWIDDDAIIIGAAGSLPGDLQRMWVA-----RRPNTY  459

Query  499  LTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLN  558
                G   MG+ +  A+G  +  PD+ V  + GDGS++M   EL T   E   + ++L +
Sbjct  460  HMEYGYSCMGYEIAGALGVKMAEPDKEVYAMVGDGSYLMLHSELVTSIQEKKKINVLLFD  519

Query  559  NQHLGMV  565
            N   G +
Sbjct  520  NGGFGCI  526
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: A5YBJ6.2 **Length:** 642 **Number of Matches:** 1

Related Information

Range 1: 70 to 598 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
115 bits(287)	2e-25	Compositional matrix adjust.	129/539(24%)	224/539(41%)	50/539(9%)

```
Query  137  HEQGGVFAAEGYARATGFPGV--CIATSGPGATNLVSGLADALLDSVPIVAITGQV----  190
            +EQG    A  Y+R      +    A++GPG+ N V+   +A ++S+PI+ +
Sbjct  70   NEQGMASTAIAYSRQLYRHKIFAVTASAGPGSANFVTAAGNAYVNSIPILFLPADTFATR  129

Query  191  ----PRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAF-FLARSGRPGPVL  245
                  + I  D   +T   +V + ++K+   +   E +   + +AF  L      GPV
Sbjct  130  QPDPVLQQIEVDYSADTTTNDVLKPVSKYWDRIERPEQLMSALLKAFEVLTNPATAGPVT  189

Query  246  IDVPKDIQQQLVIPDWDQPMRLPGYMSRLPK--LPNEMLLEQIVRLISESKKPVLYVGGG  303
            I +P+D++ Q     +D P+        + K   P+   L   V LI  S+ PVL VGGG
Sbjct  190  IALPQDVEGQA----YDYPLSFFKKRVHVVKRVQPSSAELAGAVELIQASQTPVLIVGGG  245

Query  304  C--SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLL  361
               S +   +  F E   IP+  T  G  A  +    ++   G+ GT  AN  +  +DL+
Sbjct  246  AKFSDAGAAIETFSERFNIPIVETPTGKSAISSDFPNNMGGTGILGTAAANAVITKADLI  305

Query  362  LAFGVRFDDRVTGKLEAFA-SRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSIL  420
            +  G R+ D  T    A    + ++++I+++  +    K     I AD++  L  L   L
Sbjct  306  IGAGTRYTDFTTASKTAIHPGKTQLININLNRMQ--SYKFDAFPIVADVRDTLSQLTESL  363

Query  421  ---ESKEGKLKLDFSAWRQE------------LTVQKVKYPLNFKTFG-------DAIPP  458
                S+   L     AW++E              V +VK   + KT           +
Sbjct  364  SDYRSQFTDLATIKEAWQKERQRLAHTNYDAPAYVPEVKNQFDAKTMAAYAEKLQTHLTQ  423

Query  459  QYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAA  518
              A+  ++   + ++II    G       + +    P  +    G   MG+ +PAA+G
Sbjct  424  TEAVIAVNNTIDPTSIIVAAAGSLPGDVQRIWDPVVPNTYHMEYGYSMMGYEVPAALGIK  483

Query  519  VGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRA  578
            + +PD+    + GDGSF+M   EL T    +  + I++ +N     +    +    A  +
Sbjct  484  LAQPDQESYALVGDGSFMMLHSELVTALQYHKKINILVFDNSGFASI----NNLQMAQGS  539

Query  579  HTYLGN--PSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIV  635
            ++YL     S+   +  +  K AE  G  A R   R  L AAI+         L+D+ V
Sbjct  540  NSYLTEFRTSDNDIMKTDFAKIAEGYGAKAYRANDRKSLIAAIEDAKKQTVSTLIDIKV  598
```

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RecName: Full=Acetolactate synthase-like protein; AltName: Full=IlvB-like protein

Sequence ID: Q8BU33.1 **Length:** 632 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 52 to 548 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
114 bits(286)	2e-25	Compositional matrix adjust.	130/517(25%)	228/517(44%)	68/517(13%)

```
Query  91   RKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYAR  150
            R G + +   L   GV  VF   GG    +  A  +  I R V  RHE   VFAA+  AR
Sbjct  52   RHGGESVAAVLRAHGVRFVFTLVGGHISPLLVACEKLGI-RVVDTRHEVTAVFAADAVAR  110

Query  151  ATGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTR  210
             TG  GV   T+GPG TN V+ + +A +   P++ + G     +    A Q    + + R
Sbjct  111  LTGTVGVAAVTAGPGLTNTVTAVKNAQVAQSPVLLLGGAASTLLQKRGALQAIDQMSLFR  170

Query  211  SITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQ-PMRLPG  269
             + K    V  V DI   +R A   A+SG PGPV +++P D+     + + +  P +LP
Sbjct  171  PLCKFCASVRRVRDIVPTLRTAIAAAQSGTPGPVFVELPLDVLYPYFMVEKEMIPTKLPN  230

Query  270  -YMSRL------------------PK----LPNEM------LLEQIVRLISESKKPVLYV  300
              M R+                  P+    LP ++       +++ V ++S +K+P+L +
Sbjct  231  SLMGRVVVWYLQNCLANLFVGAWEPRPEGPLPLDIPQASPQQVQRCVEILSRAKRPLLVL  290

Query  301  GGGCSQS------SEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLG----MHGTVY  350
            G   SQ+      + +LR  VE  G+P          F  G  +S  +LG    +H
Sbjct  291  G---SQALLPPTPANKLRAAVETLGVP---------CFLGG--MSRGLLGRNHPLHIRQN  336

Query  351  ANYAVDSSDLLLAFGVRFDDRVT-GKLEAFASRAKIVHIDIDSAEIGKN--KQPHVSICA  407
             + A+  +D+++  G   D R++ G++    S   IV+ + D   +  +   +P  ++
Sbjct  337  RSAALKKADVVVLAGAVCDFRLSYGRVLNRKSSIIIVNRNRDDLLLNSDIFWKPQEAVQG  396

Query  408  DIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVKYPLNFKTFG-----DAIPPQYAI  462
            D+      +  ++E  +G++    S W +EL     +    ++          + P + +
```

```
Sbjct  397  DVG---SFMIKLVEGLQGQMW--SSDWAEELRKADQQKEQTYRDKALMPVLQHLNPVWVL  451

Query  463  QVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRP  522
            Q ++E    +A++    G     AA   + R P +WL  G  G +G G   A+GA + +P
Sbjct  452  QQVEETLPDNALLVVDGGDFVATAAYLVQPRGPLRWLDPGAFGTLGVGAGFALGAKLCQP  511

Query  523  DEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNN  559
            +  V  + GDG+F  ++ E  T     +PV  ++ N+
Sbjct  512  EAEVWCLFGDGAFGYSLIEFDTFVRHKVPVIALVGND  548
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: B2TJ86.1 **Length:** 643 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 63 to 525 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
114 bits(286)	3e-25	Compositional matrix adjust.	115/485(24%)	206/485(42%)	77/485(15%)

```
Query  136  RHEQGGVFAAEGYARATGFPGV--CIATSGPGATNLVSGLADALLDSVPIVAITG-----  188
            R+EQG   AA  +A+      +  C ++ GPGA N+V+  A A ++++P++ + G
Sbjct  63   RNEQGMAHAATAFAKQNNRRKIIACSSSIGPGAANMVTAAATATVNNIPLLLLPGDSFAT  122

Query  189  --------QVPRR----MIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLA  236
                    Q+ +     +   D F+  P+ +    + +   L+  + +  RV      L
Sbjct  123  RQPDPVLQQIEQSYNLGITTNDVFK--PVCKYWDRVNRPEQLMSAMINAMRV------LT  174

Query  237  RSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYM--SRLPKLPNEMLLEQ----IVRLI  290
                 G V I +P+D+Q         +    P Y    R+ K+   + +E+     + +I
Sbjct  175  DPAETGAVCIALPQDVQ--------GESFEFPEYFFKKRVHKITRPLAVEEEFYECLNII  226

Query  291  SESKKPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGT  348
               KKP++  GGG   S++ + L +F     IP+  T  G  +  + D ++L  +G+ G
Sbjct  227  KNKKKPIIICGGGVRYSEAGDTLSKFANRFNIPIGETQAGKSSIKSSDLMNLGGIGVTGN  286

Query  349  VYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICAD  408
            + AN     +DL++  G RF D  T     F +   +  + I+ ++   +K     +  D
Sbjct  287  LAANIIAKDADLVIGVGTRFSDFTTASKSLFEN-PDVEFVTINLSKFHASKLDSCKMVGD  345

Query  409  IKLALQGLNSILE------SKEGKLKLDFSAWRQELT-VQKVKYPLNF------------  449
            +K  L+ L  +LE      S + ++K    AW++E+  +  +KY  NF
Sbjct  346  VKECLEYLYKLLEKENYISSYKDEIKDAKMAWKEEMKKLTNIKYEENFDPIIKFRNKESL  405

Query  450  ----KTFGDAIPPQYAIQVLDELTNGSAIISTGVGQ-----HQMWAAQYYKYRKPRQWLT  500
                K     I    A+ ++ E  +  AII    G       +MW  +         +
Sbjct  406  EEFKKLTDTTITQTSALGLIRECIDNDAIIVGASGSLPGDLQRMWETE-----SLNSYHM  460

Query  501  SGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQ  560
              G   MG+ + A  GA +  P++ V  I GDGS++M   EL T   EN  V ++L +N
Sbjct  461  EYGYSCMGYEIAAGFGAKLAEPEKEVYSILGDGSYLMLHSELITSIQENKKVNVLLFDNC  520

Query  561  HLGMV  565
              G +
Sbjct  521  GFGCI  525
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: B2V4K0.1 **Length:** 643 **Number of Matches:** 1

Related Information

Range 1: 33 to 600 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
112 bits(280)	1e-24	Compositional matrix adjust.	133/592(22%)	249/592(42%)	85/592(14%)

```
Query  105  GVTDVFAYPGGASMEIHQALTRSSIIRNVLP-RHEQGGVFAAEGYARATGFPGV--CIAT  161
            G+  +F +  G  + + QAL  ++    V   R+EQG   AA  +A+      +  C ++
Sbjct  33   GIFTIFGH--GIVVGLGQALDENTRDLKVYQGRNEQGMAHAATAFAKQNNRRKIIACSSS  90

Query  162  SGPGATNLVSGLADALLDSVPIVAITG-------------QVPRR----MIGTDAFQETP  204
             GPGA N+V+  A A ++++P++ + G             Q+ +     +   D F+  P
Sbjct  91   IGPGAANMVTAAATATVNNIPLLLLPGDSFATRQPDPVLQQIEQSYNLGITTNDVFK--P  148

Query  205  IVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQP  264
            + +    + +   L+  + +  RV      L      G V I +P+D+Q         +
Sbjct  149  VCKYWDRVNRPEQLMSAMINAMRV------LTDPAETGAVCISLPQDVQ--------GES  194

Query  265  MRLPGYM--SRLPKLPNEMLLEQ----IVRLISESKKPVLYVGGGC--SQSSEELRRFVE  316
               P Y    R+ K+   + +E+     + +I   KKP++  GGG   S++ + L +F
Sbjct  195  FEFPEYFFKKRVHKITRPLAVEEEFYECLNIIKNKKKPIIICGGGVRYSEAGDALSKFAN  254

Query  317  LTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKL  376
               IP+  T  G  +  + D ++L  +G+ G + +N     +DL++  G RF D  T
Sbjct  255  KFNIPIGETQAGKSSIKSSDPMNLGGIGVTGNLASNIIAKDADLVIGVGTRFSDFTTASK  314

Query  377  EAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILE------SKEGKLKLD  430
              F +   +  + I+ ++   +K     +  D K  L+ L+ +LE      S + ++K
Sbjct  315  SLFKN-PDVEFVTINLSKFHASKLDSCKMVGDAKECLEYLHKLLEKENYISSYKDEIKDA  373

Query  431  FSAWRQELT-VQKVKYPLNF----------------KTFGDAIPPQYAIQVLDELTNGSA  473
              AW++E+  +  +KY  NF                K     I    A+ ++ E  +  +
Sbjct  374  KIAWKEEMKRLTNIKYEENFEPIIKFRNKESLEEFKKLTDTTITQTSALGLIRECIDDDS  433
```

```
Query  474  IISTGVGQ-----HQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVD  528
            II    G       +MW  +         +    G   MG+ + A  GA +  P++ V
Sbjct  434  IIVGASGSLPGDLQRMWETE-----SLNSYHMEYGYSCMGYEIAAGFGAKLADPEKEVYS  488

Query  529  IDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMV--VQWEDRFYKANRAHTYLGNPS  586
            I GDGS++M   EL T   EN  V ++L +N   G +  +Q  +          Y  + +
Sbjct  489  ILGDGSYLMLHSELITSIQENKKVNVLLFDNCGFGCINNLQMSNGIGNLATEFRYRNSET  548

Query  587  NE--AEIFP-NMLKFAEACGVPAARVTHRDDLRAAIQKMLDTPGPYLLDVIV  635
            N+   ++ P +  K AE  G+      + ++L+ A+          L+D+ V
Sbjct  549  NKLNGKLIPIDFAKAAEGYGLKTYTAKNLEELKNALIDAKKQKVSTLIDIKV  600
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: A7ZAH8.1 **Length:** 637 **Number of Matches:** 1

Related Information

Range 1: 33 to 579 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
110 bits(275)	5e-24	Compositional matrix adjust.	138/575(24%)	242/575(42%)	86/575(14%)

```
Query  104  EGVTDVFAYPGGASMEIHQALTRSSIIRNVLP-RHEQGGVFAAEGYARATGFPGV-CIAT  161
            EG+  +F +  G  + I QAL + +    V   ++EQG   AA  Y++      +  ++T
Sbjct  33   EGIFTIFGH--GNVLGIGQALEQDAGHLKVYQGKNEQGMAHAAMAYSKQMLRRKIYAVST  90

Query  162  S-GPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAF---QETPIV-----EVTRSI  212
            S GPGA NL +    AL + +P++         ++  D F   Q  P++     E + ++
Sbjct  91   SVGPGAANLTAAAGTALANHIPVL---------LLPADTFATRQPDPVLQQVEQEYSAAV  141

Query  213  TKHNYLVMDVEDIPRVVR---------EAF-FLARSGRPGPVLIDVPKDIQQQLVIPDWD  262
            T ++ L        R+ R          AF  +    + GP  I + +D++ +    D+D
Sbjct  142  TTNDALKPVSRYWDRITRPEQLMSSLIRAFEVMTDPAKAGPATICISQDVEGEAF--DFD  199

Query  263  QPM--RLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSS--EELRRFVELT  318
            +    +   Y+ R+   P+E  L+     I +S +PV+ VGGG   S   EEL    E
Sbjct  200  ESFFEKRVHYIDRMQ--PSERELKGAAERIKQSSRPVILVGGGAKYSGAREELIALSETY  257

Query  319  GIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEA  378
            GIP+  T  G          +L  +G+ GT+ AN A   +DL++  G R+ D  T    A
Sbjct  258  GIPLVETQAGKSTVEADFANNLGGMGITGTLAANKAARQADLIIGVGTRYTDFATSSKTA  317

Query  379  FA-SRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQE  437
            F   +AK ++I++  + +   K     + AD K+ L  L+ +L+  +         W+ E
Sbjct  318  FDFDKAKFLNINV--SRMQAYKLDAFQVVADAKVTLGRLHGLLDGYKSAFGTAIKDWKDE  375

Query  438  LTVQKVKYPLNFKTFG-DAIPPQ----YAIQVLDELTNG---------------------  471
               ++ +  L   TF  DA  P+    ++  VL+E  +
Sbjct  376  WQAERDR--LGKVTFTRDAFEPEIKNHFSQDVLNEYADALGTELPQTTALLTINDTIPED  433

Query  472  SAIISTGVGQ----HQMWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVV  527
            S +IS+         ++W +       P  +    G   MG+ +   +G  +  PD+ V
Sbjct  434  SVVISSAGSLPGDLQRLWHSNV-----PNTYHLEYGYSCMGYEVSGTLGLKLAHPDKEVY  488

Query  528  DIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSN  587
             + GDGSF+M   EL T    N  + ++L +N   G +    +     + + +Y
Sbjct  489  SLVGDGSFLMLHSELITALQYNKKINVLLFDNSGFGCI----NNLQMDHGSGSYFCEFRT  544

Query  588  EAEIFPNM--LKFAEACGVPAARVTHRDDLRAAIQ  620
            E     N+   K AE  G    R    ++L+AA++
Sbjct  545  EDNQILNVDYAKVAEGYGAKTYRANTVEELKAALE  579
```

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RecName: Full=Probable pyruvate decarboxylase C186.09

Sequence ID: Q9P7P6.1 **Length:** 572 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 24 to 499 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
109 bits(273)	8e-24	Compositional matrix adjust.	118/504(23%)	207/504(41%)	51/504(10%)

```
Query  101  LEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATGFPGVCIA  160
            L + GV   F  PG  ++ +   L  ++ +  V   +E    FAAEGYARA G    C+
Sbjct  24   LAQAGVKHHFVVPGDYNLGLLDKLQYNNYLEEVNCANELNCAFAAEGYARANGI-AACVV  82

Query  161  TSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPI--------VEVTRSI  212
            T   GA     G+  A  + +P++ I+G      IG+       +         E+ + I
Sbjct  83   TYSVGAFTAFDGIGGAYAEDLPVILISGSPNTNDIGSSHLLHHTLGTHDFSYQYEMAKKI  142

Query  213  TKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMS  272
            T     +    + PR++  A  +A   +  PV I+VP ++          QP   PG  S
Sbjct  143  TCAAVSIQRPTEAPRLIDYAIKMALLKKK-PVYIEVPTNVA--------SQPCAAPGPAS  193

Query  273  RL--PKLPNEMLLEQIV----RLISESKKPVLYVGGGCSQSSEELRRFVELTG---IPVA  323
             +  P+  N+  L+  V    ++++  +KPVL  G        E   F+EL       VA
Sbjct  194  LITEPETSNQEYLQMAVDISAKIVNGKQKPVLLAGPKLRSFKAE-SAFLELANSLNCSVA  252

Query  324  STLMGLGAFPTGD-ELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASR  382
                    FP      +    G   T+ A   ++ SD ++  G  F D  +    +   +
Sbjct  253  VMPNAKSFFPESHPNYAGIYWGQASTLGAESIINWSDCIICAGTTFTDYSSNGWTSLPPK  312

Query  383  AKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQK  442
            A ++H+D+D   +           +D +     L   L     K+K + ++  +   ++
```

```
Sbjct  313  ANVLHVDVDRVTV-----------SDAEFGGVLLRDFLHELAKKVKANNASVVEYKRIRP  361

Query  443  VKYPLNFKTFGDAIPPQYAIQVLDELTN--GSAIISTG---VGQHQMWAAQYYKYRKPRQ  497
                +  +    A+  +  I+ +  L N   +  + TG    G  ++   +  ++    Q
Sbjct  362  ESLEIPMENPKAALNRKEIIRQVQNLVNQETTLFVDTGDSWFGGMRITLPEKARFEIEMQ  421

Query  498  WLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLL  557
            W      G +G+ +P+A G A+G P   VV   GDGSF   VQE++ +   NLP+ + L+
Sbjct  422  W------GHIGWSVPSAFGYAIGAPKRNVVVFVGDGSFQETVQEVSQMVRLNLPIIMFLI  475

Query  558  NNQHLGMVVQWEDRFYKANRAHTY  581
            NN+   + V+  D  Y   +   Y
Sbjct  476  NNRGYTIEVEIHDGPYNRIKNWDY  499
```

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RecName: Full=Benzoylformate decarboxylase; Short=BFD; Short=BFDC

Sequence ID: P20906.2 **Length:** 528 **Number of Matches:** 1

Related Information

PubChem BioAssay - bioactivity screening

Range 1: 10 to 521 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
107 bits(267)	3e-23	Compositional matrix adjust.	138/569(24%)	228/569(40%)	91/569(15%)

```
Query  99   EALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATGFPGVC  158
            E L R+G+  VF  PG   +   +        R +L   E   V  A+GYA+A+  P
Sbjct  10   ELLRRQGIDTVFGNPGSNELPFLKDFPED--FRYILALQEACVVGIADGYAQASRKPAFI  67

Query  159  IATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAF-QETPIVEVTRSITKHNY  217
               S  G  N +  L++A     P++   GQ  R MIG +A         + R + K +Y
Sbjct  68   NLHSAAGTGNAMGALSNAWNSHSPLIVTAGQQTRAMIGVEALLTNVDAANLPRPLVKWSY  127

Query  218  LVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMR------LPGYM  271
                  ++P  +  A  +A     GPV + VP D        DWD+            ++
Sbjct  128  EPASAAEVPHAMSRAIHMASMAPQGPVYLSVPYD--------DWDKDADPQSHHLFDRHV  179

Query  272  SRLPKLPNEMLLEQIVRLISESKKPVLYVG---------GGCSQSSEELRRFVELTGIPV  322
            S   +L N+  L+ +V+ ++ +  P + +G           C   +E L+  V +   P
Sbjct  180  SSSVRL-NDQDLDILVKALNSASNPAIVLGPDVDAANANADCVMLAERLKAPVWVA--PS  236

Query  323  ASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGV---RFDDRVTGKLEAF  379
            A        FPT       ++   G    +  ++  D++L  G    R+     G+
Sbjct  237  APRC----PFPTRHPCFRGLMPA-GIAAISQLLEGHDVVLVIGAPVFRYHQYDPGQYLKP  291

Query  380  ASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKL--------KLDF  431
             +R  ++ +  D  E  +      +I ADI      L +++E    +L        K+D
Sbjct  292  GTR--LISVTCDPLEAARAPMGD-AIVADIGAMASALANLVEESSRQLPTAAPEPAKVDQ  348

Query  432  SAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYK  491
             A R  L  + V     F T  D + P+ AI  L+E T+ +A         QMW  Q
Sbjct  349  DAGR--LHPETV-----FDTLND-MAPENAI-YLNESTSTTA---------QMW--QRLN  388

Query  492  YRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLP  551
             R P  +      G +GF LPAAIG  +  P+  V+ + GDGS   ++  L T    N+P
Sbjct  389  MRNPGSYYFCAA-GGLGFALPAAIGVQLAEPERQVIAVIGDGSANYSISALWTAAQYNIP  447

Query  552  VKIMLLNNQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNM-------LKFAEACGV  604
               +++NN   G +     R++              EAE  P +          A+  GV
Sbjct  448  TIFVIMNNGTYGAL-----RWFAGVL----------EAENVPGLDVPGIDFRALAKGYGV  492

Query  605  PAARVTHRDDLRAAIQKMLDTPGPYLLDV  633
             A +  + + L+ ++Q+ L   GP L++V
Sbjct  493  QALKADNLEQLKGSLQEALSAKGPVLIEV  521
```

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RecName: Full=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase; Short=THcHDO hydrolase

Sequence ID: Q92EQ4.1 **Length:** 638 **Number of Matches:** 1

Related Information

Range 1: 65 to 603 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
107 bits(268)	4e-23	Compositional matrix adjust.	130/568(23%)	228/568(40%)	83/568(14%)

```
Query  136  RHEQGGVFAAEGYARATGFPGV--CIATSGPGATNLVSGLADALLDSVPIVAITGQVPRR  193
            ++EQG   AA  YA+      +  C  ++GPG+ NL++    A  +++P++ +    P
Sbjct  65   KNEQGMAHAAIAYAKQKNRKRIYACSTSAGPGSANLITAAGTAFANNLPVLFL----PAD  120

Query  194  MIGTDAFQETPIV-----EVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRP-------  241
               T   Q  P++     E + +IT ++      +   RV R    ++   R
Sbjct  121  TFATR--QPDPVLQQLEHESSTAITTNDGFQAVSKYFDRVQRPEQLMSALIRAFEVMTNP  178

Query  242  ---GPVLIDVPKDIQQQLVIPDWDQPM----RLPGYMSRLPKLPNEMLLEQIVRLISESK  294
               GP  I + +D + +     +D P+    +   Y++R  ++P +  L + +LI   S+
Sbjct  179  VSAGPATICIAQDTEGEA----FDYPVTFFQKRIHYLNR--QIPTKRELTEAAKLIKASQ  232

Query  295  KPVLYVGGGC--SQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYAN  352
             PV+ VGGG   S + +EL    E   IP+  T  G        + +L   G+ GT+ AN
Sbjct  233  TPVIIVGGGARYSDARKELIALSEQNDIPLVETHAGKSTVEFSFKNNLGGTGILGTLAAN  292

Query  353  YAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIKLA  412
              +  +DL++  G R+ D  T    AF    K ++I++  + +   K     +  D K
Sbjct  293  KIIHEADLVIGIGTRYTDFTTSSKTAFNPATKFININV--SRMQTYKLDAFQVVGDAKAT  350
```

```
Query  413  LQGLNSILESKEGKLKLDFSAWRQELTVQKVKY---PLNFKTFGDAIPPQ--------YA  461
            L  L  +L+  + +     S +++E   ++ +      N   F   I  Q        YA
Sbjct  351  LIELTPLLKGYKTQFGDKISTYKKEWLKERTRLQHTKFNRDNFAPEIKNQFDQTTLNEYA  410

Query  462  IQVLDELTNGSAIIS------------TGVGQ-----HQMWAAQYYKYRKPRQWLTSGGL  504
              +  E T   A+I+               G       ++W         P  +    G
Sbjct  411  DSLQTEFTQTEALITINDTVAPDSIVVCSAGSLPGDLQRLWNPAV-----PNTYHLEYGY  465

Query  505  GAMGFGLPAAIGAAVGRPD-EVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQHLG  563
              MG+ +  A+GA +   D + V  I GDGSF M+  EL T       + IML +N   G
Sbjct  466  SCMGYEINGALGAKMAASDNQEVYSIVGDGSFCMSHSELLTSLQYGKKINIMLFDNSGFG  525

Query  564  MVVQWEDRFYKANRAHTYLGN--PSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQK  621
             +    +    AN + ++      +N   +  +  K AE  G    +   ++DL  A++
Sbjct  526  CI----NNLQMANGSDSFFCEFRDNNNQIMQVDYAKIAEGYGAKVYKANTKEDLVNALED  581

Query  622  MLDTPGPYLLDVIVPHQEHVLPMIPSGG  649
                    L+D+       VLP   S G
Sbjct  582  AKKQTKTTLIDM------KVLPKTMSEG  603
```

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RecName: Full=Putative 2-hydroxyacyl-CoA lyase

Sequence ID: Q9Y7M1.1 **Length:** 568 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 6 to 546 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
104 bits(260)	2e-22	Compositional matrix adjust.	140/555(25%)	248/555(44%)	27/555(4%)

```
Query  94   SDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATG  153
            S+++ + L    V  VF   G   +EI +A+ ++S IR V  R+EQ   +AA  Y   T
Sbjct  6    SELVAKTLLDLEVKVVFGIVGIPVIEICEAI-QASGIRFVGFRNEQSAAYAATAYGYLTQ  64

Query  154  FPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRSIT  213
             PGVC+   GPG  + ++G+ ++  +  P++ + G          AFQE   V      T
Sbjct  65   RPGVCVVVGGPGVVHAMAGVFNSKTNRWPLLLLAGSSETFQQNCGAFQELDQVSYLSPHT  124

Query  214  KHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSR  273
            K        + +   +R A+ ++ +G PG   +D+P +  +  V      P  LP   S
Sbjct  125  KLAVRPPSPKMVVDSIRRAYRVSMTGTPGTCYVDLPANYIESTVDDFPKDP--LPPIPSS  182

Query  274  LPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSSEE--LRRFVELTGIPVASTLMGLGA  331
                P+   L++    +  +K P+L VG G + +  E  L  FVE TGIP   + MG G
Sbjct  183  PKCAPDPTQLQKAAYYLKNAKAPLLVVGKGAAYACAEKQLLEFVEHTGIPFLPSPMGKGL  242

Query  332  FPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKL-EAFASRAKIVHIDI  390
             P    L++S          + A+ ++D++L  G R +      L   ++  AK + ID
Sbjct  243  LPESHPLNVSSA-------RSAALRNADVVLLAGARLNWIFQYGLPPKWSPNAKFIQIDT  295

Query  391  DSAEIGKNKQP-HVSICADIKLALQGLNSILESKEGKLKLDFSAWRQELTVQKVKYPLNF  449
            ++  +G N     ++I AD+ L +  L  ++++ +  + +     R     +
Sbjct  296  NAETLGNNAADLDLAIWADVGLTIDCLFKLVQTWKYSVGISTPYLRTLNETRSKNEKKAL  355

Query  450  KTFGDAIPPQ--YAIQVLDE------LTNGSAIISTGVGQHQM-WAAQYYKYRKPRQWLT  500
            ++   +IP Q  YA+ V++E      L +   I     G + M    Q  +   PR  L
Sbjct  356  ESRKSSIPLQMNYALYVVNEELQSLSLKSKRNITWVSEGANTMDRGRQLLEVTHPRGRLD  415

Query  501  SGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNNQ  560
            +G +  MG G+  AI +A     + +V ++GD +F  +  EL T     L + ++++NN
Sbjct  416  AGTMSTMGVGMGYAIASAFAHSSDKIVVVEGDSAFGFSAMELETAIRNQLDLLVIVINNN  475

Query  561  HLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQ  620
              G+    +   Y+  R +  L  P+          +  EACG     V + +DLR++++
Sbjct  476  --GVYHGLDTDAYETLRDNHQL--PTTALGTSIRYDQICEACGGKGFFVKNEEDLRSSLR  531

Query  621  KMLDTPGPYLLDVIV  635
            K   T    L++V+V
Sbjct  532  KAWQTSSVSLINVMV  546
```

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RecName: Full=Uncharacterized 42.6 kDa protein in isoamylase 3'region

Sequence ID: P10343.1 **Length:** 396 **Number of Matches:** 1

Related Information

Range 1: 5 to 335 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
100 bits(248)	3e-21	Compositional matrix adjust.	90/342(26%)	152/342(44%)	14/342(4%)

```
Query  92   KGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARA  151
            K +DV+ E L   GV  ++   G +   I  +L R   I  +  RHE+   FAA   A
Sbjct  5    KVADVVTETLHVAGVKRIYGVVGDSLNGITDSLRRRGDIDWIHVRHEESAAFAAGAEAHL  64

Query  152  TGFPGVCIATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDAFQETPIVEVTRS  211
            TG   VC  + GPG  +L++GL D     VP++AI   +P   IG   FQET    + R
Sbjct  65   TGELAVCAGSCGPGNLHLINGLFDCHRSRVPVLAIAAHIPSAEIGRGYFQETHPESLFRE  124

Query  212  ITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDI--QQQLVIPDWDQPMRLPG  269
             + +  LV   E +P V+ E+   A  G  G  ++ +P D+  ++    P     M L
Sbjct  125  CSHYCELVSSPEQLPGVL-ESAIRAAVGLRGVAVVIIPGDVALRESNAKPAAGASMAL--  181

Query  270  YMSRLPKL-PNEMLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFVELTGIPVASTLMG  328
               R P + P    ++ + +L+++S K  L  G GC+ + + L +  E    P+     G
```

```
Sbjct  182  ---RPPVVQPAAADVDALAQLLNDSGKVTLLCGRGCAGAHDPLVKLAEALKAPIVHAFGG  238

Query  329  LGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGVRFDDRVTGKLEAFASRAKIVHI  388
                   +   + M G+ G     +A+ + D LL  G  F  R     + + + AKI  +
Sbjct  239  KEYVEYDNPYDVGMTGLIGFSSGYHAMLNCDTLLMLGTDFPYR-----QFYPADAKIAQV  293

Query  389  DIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLD  430
            D+    +G+  +  + +  D+   +  L   L+++  +  LD
Sbjct  294  DVRPENLGRRARLDLGMVGDVSATIGALLPKLKARTDRAYLD  335
```

Download GenPept Graphics Next Previous Descriptions

RecName: Full=Pyruvate decarboxylase; AltName: Full=8-10 nm cytoplasmic filament-associated protein; AltName: Full=P59NC; Flags: Precursor

Sequence ID: P33287.1 **Length:** 570 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 13 to 493 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
97.4 bits(241)	7e-20	Compositional matrix adjust.	130/518(25%)	216/518(41%)	68/518(13%)

```
Query  95   DVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATGF  154
            D L E L + GV   F  PG  ++ +   L     ++ V   +E     AAEGYARA G
Sbjct  13   DYLAERLAQVGVRHHFVVPGDYNLILLDKLQAHPDLKEVGCANELNCSLAAEGYARANGI  72

Query  155  PGVCIATSGPGATNLVSGLADALLDSVPIVAITG----------QVPRRMIGTDAFQETP  204
               C+ T   GA +  +G   A  +++P+V I+G           +    +G   +  T
Sbjct  73   -SACVVTYSVGALSAFNGTGSAYAENLPLVLISGSPNTNDPSQYHILHHTLGHPDY--TY  129

Query  205  IVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQP  264
              E+ + IT     +    D PR++  A   A   R  P  I++P ++     +
Sbjct  130  QYEMAKKITCCAVAIPRAIDAPRLIDRALRAAILARK-PCYIEIPTNLAGATCV------  182

Query  265  MRLPGYMSRLP------KLPNEMLLEQIVRLISESKKPVLYVG--GGCSQSSEELRRFVE  316
               PG +S +       K   E   +     +    KPV+ VG   G + S +EL  F E
Sbjct  183  --RPGPISAITDPITSDKSALEAAAKCAAEYLDGKLKPVILVGPKAGRAGSEKELIEFAE  240

Query  317  LTGIPVASTLMGLGAFPTGDELSLSML-GMHGTVYANYAVDSSDLLLAFGVRFDDRVTGK  375
              G  VA      G FP   +  + +  G   +  A+  V  +D ++  G  F+D  T
Sbjct  241  AMGCAVALQPAAKGMFPEDHKQFVGIFWGQVSSDAADAMVHWADAMICVGAVFNDYSTVG  300

Query  376  LEAFASRAKIVHIDIDSAEIGKNKQPHVSICADIK-LALQ---GLNSILESKEGKLKLD-  430
              A  +   ++ +D+D           V +C   +  LA Q     ++++E K  +LK D
Sbjct  301  WTAVPN-IPLMTVDMDHVTFPGAHFSRVRMCEFLSHLATQVTFNDSTMIEYK--RLKPDP  357

Query  431  ---FSAWRQELTVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAI-ISTGVGQH---Q  483
                +A R+E        PL+ K        + + QV + LT+ +++ + TG       Q
Sbjct  358  PHVHTAEREE--------PLSRK--------EISRQVQEMLTDKTSLFVDTGDSWFNGIQ  401

Query  484  MWAAQYYKYRKPRQWLTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELA  543
            +      K+    QW      G +G+ +PAA G A+  PD   + + GDGSF +  QE++
Sbjct  402  LKLPPGAKFEIEMQW------GHIGWSIPAAFGYALRHPDRHTIVLVGDGSFQVTAQEVS  455

Query  544  TIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHTY  581
             +    +P+ IML+NN+   + V+  D  Y   +   Y
Sbjct  456  QMVRFKVPITIMLINNRGYTIEVEIHDGSYNKIKNWDY  493
```

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RecName: Full=Benzoylformate decarboxylase; Short=BFD; Short=BFDC

Sequence ID: Q9HUR2.1 **Length:** 528 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 10 to 521 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
95.9 bits(237)	1e-19	Compositional matrix adjust.	135/557(24%)	212/557(38%)	67/557(12%)

```
Query  99   EALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAEGYARATGFPGVC  158
            E L R G+T VF  PG   +   +        R +L  HE   V  A+G+A A+G P
Sbjct  10   EILRRHGLTTVFGNPGSNELPFLKDFPED--FRYILGLHEGAVVGMADGFALASGRPAFV  67

Query  159  IATSGPGATNLVSGLADALLDSVPIVAITGQVPRRMIGTDA-FQETPIVEVTRSITKHNY  217
               +  G  N +  L +A     P+V   GQ  R MIG +A        ++ + + K ++
Sbjct  68   NLHAAAGTGNGMGALTNAWYSHSPLVITAGQQVRSMIGVEAMLANVDAGQLPKPLVKWSH  127

Query  218  LVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRLPK-  276
                 +D+PR + +A   A      PV + +P D        DW QP   P  +  L
Sbjct  128  EPACAQDVPRALSQAIQTASLPPRAPVYLSIPYD--------DWAQPA--PAGVEHLAAR  177

Query  277  ------LPNEMLLEQIVRLISESKKPVLYVG---------GGCSQSSEELRRFVELTGIP  321
                  LP   LL ++   +S S+ PVL +G         G   + +E+LR    +   P
Sbjct  178  QVSGAALPAPALLAELGERLSRSRNPVLVLGPDVDGANANGLAVELAEKLRMPAWVA--P  235

Query  322  VASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSSDLLLAFGV---RFDDRVTGKLEA  378
             AS       FPT       +L        +  +D  DL+L  G    R+     G  +
Sbjct  236  SASRC----PFPTRHACFRGVLPA-AIAGISRLLDGHDLILVVGAPVFRYHQFAPG--DY  288

Query  379  FASRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDFSAWRQEL  438
              + A++V +  D  E  +      ++   DI L L+ L   +      L
Sbjct  289  LPAGAELVQVTCDPGEAARAPMGD-ALVGDIALTLEALLEQVRPSARPLP----------  337

Query  439  TVQKVKYPLNFKTFGDAIPPQYAIQVLDELTNGSAIISTGVGQHQMWAAQYYKYRKPRQW  498
              + +  P      G  + P+    V+D L    AI             Q  + R+P  +
```

```
Sbjct  338  --EALPRPPALAEEGGPLRPETVFDVIDALAPRDAIFVKESTSTVTAFWQRVEMREPGSY  395

Query  499  LTSGGLGAMGFGLPAAIGAAVGRPDEVVVDIDGDGSFIMNVQELATIKVENLPVKIMLLN  558
                  G +GFGLPAA+GA + +P   V+ I GDGS    +  L +     +P   ++L
Sbjct  396  FFPAA-GGLGFGLPAAVGAQLAQPRRQVIGIIGDGSANYGITALWSAAQYRVPAVFIILK  454

Query  559  NQHLGMVVQWEDRFYKANRAHTYLGNPSNEAEIFPNM--LKFAEACGVPAARVTHRDDLR  616
            N   G +      R++        L  P       P +     A   GV A     R++L
Sbjct  455  NGTYGAL-----RWFAG-----VLEVPDAPGLDVPGLDFCAIARGYGVEALHAATREELE  504

Query  617  AAIQKMLDTPGPYLLDV  633
             A++  L    P L++V
Sbjct  505  GALKHALAADRPVLIEV  521
```

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RID E937W995016 (Expires on 04-06 14:21 pm)

Query ID lcl|Query_69668
Description unnamed protein product
Molecule type amino acid
Query Length 664

Database Name swissprot
Description Non-redundant UniProtKB/SwissProt sequences
Program BLASTP 2.6.0+ Citation

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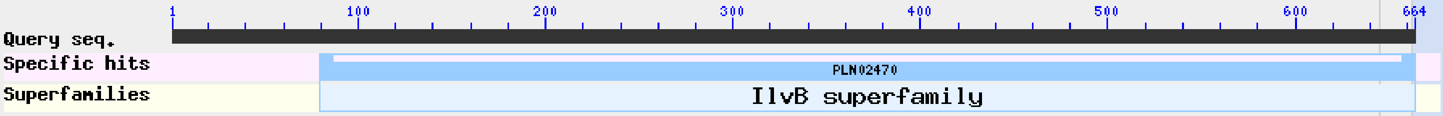

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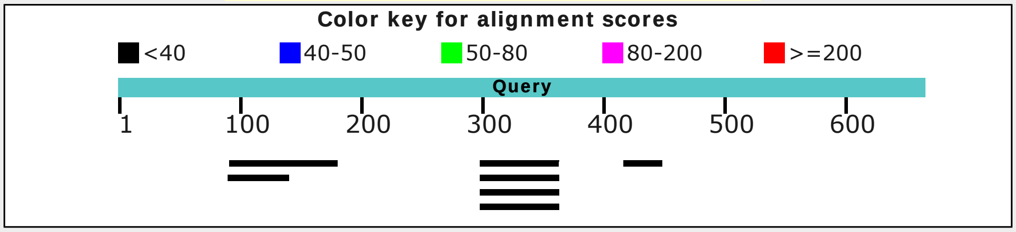

Descriptions

Sequences producing significant alignments:

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Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	RecName: Full=Pesticidal crystal protein Cry1Ag; AltName: Full=134 kDa crystal protein; AltName: F	30.8	30.8	9%	0.43	31%	Q9S515.1
☐	RecName: Full=Serine protease sat autotransporter; Contains: RecName: Full=Serine protease sat;	29.6	29.6	13%	0.95	29%	Q8FDW4.2
☐	RecName: Full=Leukotoxin; Short=Lkt	26.9	26.9	4%	7.1	44%	Q9EV30.1
☐	RecName: Full=Pesticidal crystal protein Cry10Aa; AltName: Full=78 kDa crystal protein; AltName: F	26.6	26.6	7%	8.0	25%	P09662.1
☐	RecName: Full=Pesticidal crystal protein Cry1Gb; AltName: Full=133 kDa crystal protein; AltName:	26.6	26.6	9%	8.1	28%	Q9ZAZ6.1
☐	RecName: Full=Pesticidal crystal protein Cry1Aa; AltName: Full=133 kDa crystal protein; AltName: F	26.2	26.2	9%	10.0	30%	P0A367.1
☐	RecName: Full=Pesticidal crystal protein Cry1Ad; AltName: Full=133 kDa crystal protein; AltName: F	26.2	26.2	9%	10.0	28%	Q03744.1

Alignments

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RecName: Full=Pesticidal crystal protein Cry1Ag; AltName: Full=134 kDa crystal protein; AltName: Full=Crystaline entomocidal protoxin; AltName: Full=Insecticidal delta-endotoxin CryIA(g)

Sequence ID: Q9S515.1 **Length:** 1176 **Number of Matches:** 1

Related Information

Range 1: 1114 to 1173 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
30.8 bits(68)	0.43	Compositional matrix adjust.	20/64(31%)	29/64(45%)	4/64(6%)

```
Query  299   YVGGGCSQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSS  358
             Y  G      E  R + + TG+PV      L  FP  D++ + +    GT    + VDS
Sbjct  1114  YTDGRRENPCEFNRGYRDYTGLPVGYVTKALEYFPETDKVWIEIGETEGT----FIVDSV  1169

Query  359   DLLL  362
             +LLL
Sbjct  1170  ELLL  1173
```

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RecName: Full=Serine protease sat autotransporter; Contains: RecName: Full=Serine protease sat; AltName: Full=Secreted autotransporter toxin sat; Contains: RecName: Full=Serine protease sat translocator; Flags: Precursor

Sequence ID: Q8FDW4.2 **Length:** 1295 **Number of Matches:** 1

Related Information

Range 1: 924 to 1017 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
29.6 bits(65)	0.95	Compositional matrix adjust.	29/99(29%)	47/99(47%)	14/99(14%)

```
Query  92    KGSDVLVEALEREGVT-----DVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGGVFAAE  146
             K + +LV+ +E+ G +     D+ + P G ++++ +A TRS    +V P  EQ
Sbjct  924   KNNLLLVDFIEKNGNSNGLNIDLVSAPKGTAVDVFKATTRSIGFSDVTPVIEQ-----KN  978

Query  147   GYARAT----GFPGVCIATSGPGATNLVSGLADALLDSV  181
                +AT    G+  V  A +   AT L+SG   A L  V
Sbjct  979   DTDKATWTLIGYKSVANADAAKKATLLMSGGYKAFLAEV  1017
```

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RecName: Full=Leukotoxin; Short=Lkt

Sequence ID: Q9EV30.1 **Length:** 953 **Number of Matches:** 1

Related Information

Range 1: 794 to 825 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
26.9 bits(58)	7.1	Compositional matrix adjust.	14/32(44%)	19/32(59%)	1/32(3%)

```
Query  417  NSILESKEGKLKLDFSAWR-QELTVQKVKYPL  447
            N I+   +G  KL FS    ++LT +KVKY L
Sbjct  794  NDIISDSDGNDKLSFSDSNLKDLTFEKVKYNL  825
```

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RecName: Full=Pesticidal crystal protein Cry10Aa; AltName: Full=78 kDa crystal protein; AltName: Full=Crystaline entomocidal protoxin; AltName: Full=Insecticidal delta-endotoxin CryXA(a)

Sequence ID: P09662.1 **Length:** 675 **Number of Matches:** 1

Related Information

Range 1: 418 to 468 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
26.6 bits(57)	8.0	Compositional matrix adjust.	13/51(25%)	27/51(52%)	0/51(0%)

```
Query  91   RKGSDVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPRHEQGG  141
            R+ SD++ E +     ++VF Y   +++E +   T S +I     ++E+ G
Sbjct  418  REYSDIIYEMIFFSNSSEVFRYSSNSTIENNYKRTDSYMIPKQTWKNEEYG  468
```

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RecName: Full=Pesticidal crystal protein Cry1Gb; AltName: Full=133 kDa crystal protein; AltName: Full=Crystaline entomocidal protoxin; AltName: Full=Insecticidal delta-endotoxin CryIG(b)

Sequence ID: Q9ZAZ6.1 **Length:** 1169 **Number of Matches:** 1

Related Information

Range 1: 1107 to 1166 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
26.6 bits(57)	8.1	Compositional matrix adjust.	18/64(28%)	28/64(43%)	4/64(6%)

```
Query  299   YVGGGCSQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSS  358
             Y  G    + E  R + + T +P       L  FP  D++ + +    GT    + VDS
Sbjct  1107  YTDGRRDNTCESNRGYGDYTPLPAGYVTKELEYFPETDKVWIEIGETEGT----FIVDSV  1162

Query  359   DLLL  362
```

```
             +LLL
Sbjct  1163  ELLL  1166
```

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RecName: Full=Pesticidal crystal protein Cry1Aa; AltName: Full=133 kDa crystal protein; AltName: Full=Crystaline entomocidal protoxin; AltName: Full=Insecticidal delta-endotoxin CryIA(a)

Sequence ID: P0A367.1 **Length:** 1176 **Number of Matches:** 1

Related Information

Range 1: 1114 to 1173 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
26.2 bits(56)	10.0	Compositional matrix adjust.	19/64(30%)	28/64(43%)	4/64(6%)

```
Query  299   YVGGGCSQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSS  358
             Y  G      E  R + + T +PV      L  FP  D++ + +    GT    + VDS
Sbjct  1114  YTDGRRENPCEFNRGYRDYTPLPVGYVTKELEYFPETDKVWIEIGETEGT----FIVDSV  1169

Query  359   DLLL  362
             +LLL
Sbjct  1170  ELLL  1173
```

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RecName: Full=Pesticidal crystal protein Cry1Ad; AltName: Full=133 kDa crystal protein; AltName: Full=Crystaline entomocidal protoxin; AltName: Full=Insecticidal delta-endotoxin CryIA(d)

Sequence ID: Q03744.1 **Length:** 1179 **Number of Matches:** 1

Related Information

Range 1: 1117 to 1176 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
26.2 bits(56)	10.0	Compositional matrix adjust.	18/64(28%)	28/64(43%)	4/64(6%)

```
Query  299   YVGGGCSQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSS  358
             Y+ G      E  R + + T +P      L  FP  D++ + +    GT    + VDS
Sbjct  1117  YIDGRKENPCESNRGYGDYTPLPAGYVTKELEYFPETDKVWIEIGETEGT----FIVDSV  1172

Query  359   DLLL  362
             +LLL
Sbjct  1173  ELLL  1176
```

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Molecule type	amino acid	**Program**	BLASTP 2.6.0+ Citation
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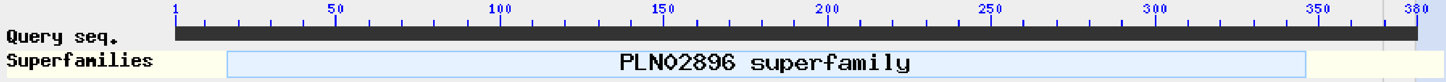
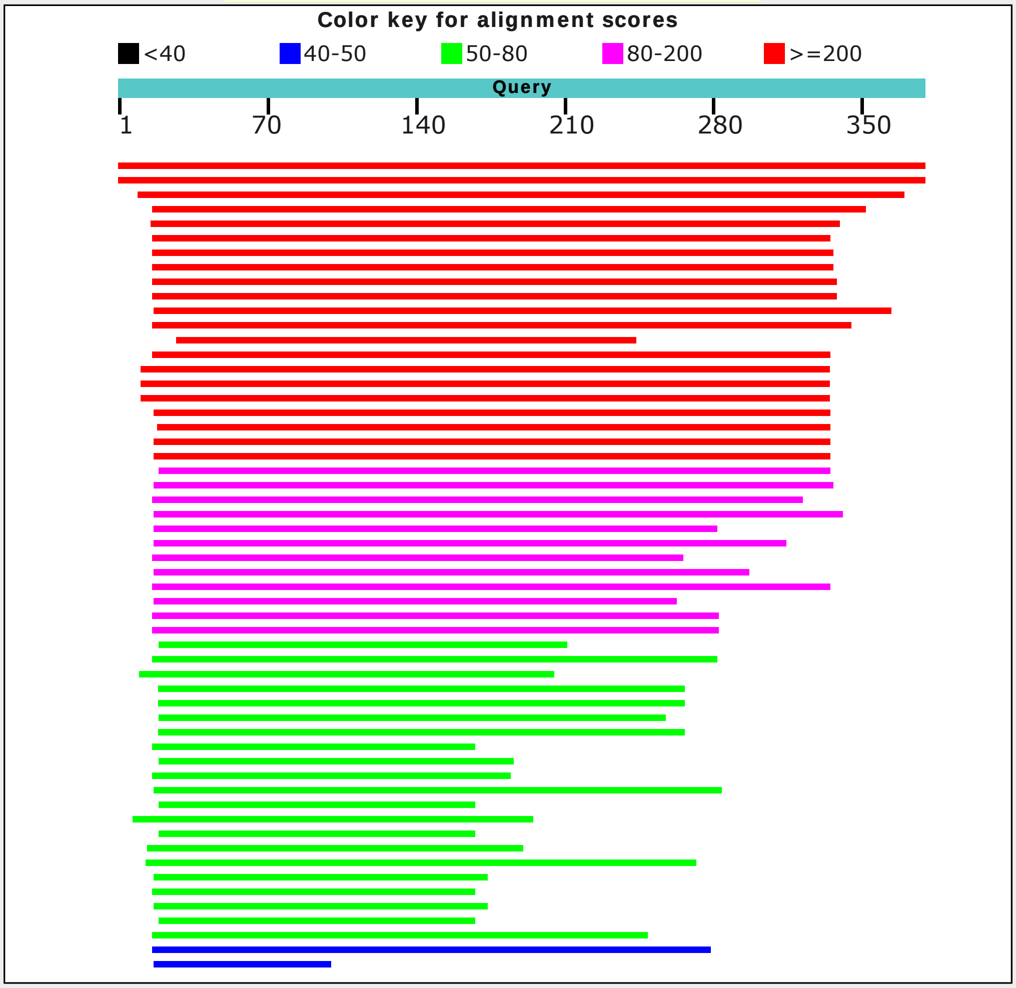


Distribution of the top 100 Blast Hits on 100 subject sequences

Mouse over to see the title, click to show alignments



Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-red	786	786	100%	0.0	98%	P14720.2
☐	RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-red	687	687	100%	0.0	88%	P51107.1
☐	RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-red	555	555	95%	0.0	70%	P14721.1
☐	RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-red	544	544	88%	0.0	76%	P51105.1
☐	RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-red	526	526	85%	0.0	77%	P51103.1
☐	RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-red	504	504	83%	2e-179	73%	P51110.1
☐	RecName: Full=Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase; AltName: Full=Dil	493	493	84%	9e-175	70%	Q9XES5.1
☐	RecName: Full=Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase; AltName: Full=Dil	491	491	84%	4e-174	69%	Q84KP0.1
☐	RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-red	491	491	84%	2e-173	71%	P51102.2
☐	RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-red	480	480	84%	2e-169	70%	P51104.1
☐	RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-red	450	450	91%	6e-158	61%	P51106.1
☐	RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-red	426	426	86%	4e-148	61%	P51108.1
☐	RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-red	326	326	57%	4e-111	71%	P51109.1
☐	RecName: Full=Putative anthocyanidin reductase; Short=GbANR	320	320	83%	6e-107	50%	Q5XLY0.1
☐	RecName: Full=Anthocyanidin reductase ((2S)-flavan-3-ol-forming); Short=VvANR	274	274	85%	8e-89	43%	D7U6G6.1
☐	RecName: Full=Anthocyanidin reductase ((2S)-flavan-3-ol-forming); Short=VvANR; AltName: Full=	274	274	85%	8e-89	42%	Q7PCC4.1
☐	RecName: Full=Anthocyanidin reductase ((2S)-flavan-3-ol-forming); Short=VvANR	273	273	85%	2e-88	42%	Q5FB34.1
☐	RecName: Full=Vestitone reductase	264	264	83%	4e-85	42%	Q40316.1
☐	RecName: Full=Anthocyanidin reductase; Short=AtANR; AltName: Full=Anthocyanin spotted testa	249	249	83%	3e-79	39%	Q9SEV0.2
☐	RecName: Full=Protein BRI1-5 ENHANCED 1	250	250	83%	3e-79	41%	O22133.1
☐	RecName: Full=Tetraketide alpha-pyrone reductase 1; AltName: Full=Protein DIHYDROFLAVONC	234	234	83%	2e-73	38%	Q500U8.1
☐	RecName: Full=Tetraketide alpha-pyrone reductase 2; AltName: Full=Protein CINNAMOYL-COA I	196	196	83%	1e-58	35%	Q9CA28.1
☐	RecName: Full=Cinnamoyl-CoA reductase 1; Short=OsCCR1	192	192	84%	6e-57	36%	Q6K9A2.1
☐	RecName: Full=Cinnamoyl-CoA reductase 1; Short=AtCCR1; AltName: Full=Protein IRREGULAR	189	189	80%	1e-55	39%	Q9S9N9.1
☐	RecName: Full=Cinnamoyl-CoA reductase 2; Short=AtCCR2	186	186	85%	1e-54	38%	Q9SAH9.1
☐	RecName: Full=Putative uncharacterized oxidoreductase C513.07	114	114	69%	2e-27	29%	Q9UT59.1
☐	RecName: Full=Ketoreductase azaE; AltName: Full=Azaphilone biosynthesis cluster protein azaE	111	111	78%	2e-26	30%	G3XMB9.1
☐	RecName: Full=Cinnamoyl-CoA reductase-like SNL6; AltName: Full=Protein SUPPRESSOR OF N	93.6	93.6	65%	6e-20	27%	Q0JKZ0.1
☐	RecName: Full=Aldehyde reductase 2; AltName: Full=Aldehyde reductase II; Short=ARII	91.7	91.7	73%	2e-19	26%	Q9UUN9.3
☐	RecName: Full=Putative uncharacterized oxidoreductase YDR541C	89.7	89.7	83%	8e-19	26%	Q03049.2
☐	RecName: Full=Putative uncharacterized oxidoreductase YGL039W	85.5	85.5	64%	3e-17	29%	P53183.1
☐	RecName: Full=Putative NADPH-dependent methylglyoxal reductase GRP2; AltName: Full=Cytop	84.7	84.7	70%	4e-17	28%	P83775.2
☐	RecName: Full=NADPH-dependent aldehyde reductase ARI1	83.6	83.6	70%	1e-16	28%	P53111.1
☐	RecName: Full=Putative dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempfe	78.6	78.6	50%	6e-15	31%	P73212.1
☐	RecName: Full=NADPH-dependent methylglyoxal reductase GRE2; AltName: Full=3-methylbutana	74.3	74.3	70%	1e-13	27%	Q12068.1
☐	RecName: Full=NAD-dependent epimerase/dehydratase terH; AltName: Full=Terrein biosynthesis	72.4	72.4	51%	7e-13	29%	Q0D1P7.1
☐	RecName: Full=Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	62.4	62.4	65%	1e-09	25%	Q9R1J0.1
☐	RecName: Full=Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	62.4	62.4	65%	2e-09	26%	Q5PPL3.1
☐	RecName: Full=Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	60.1	60.1	62%	8e-09	26%	Q3ZBE9.1
☐	RecName: Full=Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating; AltName: Full=Prot	55.8	55.8	65%	2e-07	24%	Q15738.2
☐	RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 1; AltName: Fu	55.5	55.5	40%	3e-07	27%	Q60555.3

☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase; Short=3-beta-HSD;	53.9	53.9	43%	8e-07	28%	Q9N119.4
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 2; AltName: Fu	53.1	53.1	44%	1e-06	26%	Q64421.3
☐ RecName: Full=Putative uncharacterized oxidoreductase C1773.04; Flags: Precursor	52.8	52.8	70%	2e-06	24%	O94563.1
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 1; AltName: Fu	52.8	52.8	39%	2e-06	25%	P24815.3
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase type 7; AltName: Full=3 beta-hydroxysteroi	52.4	52.4	49%	2e-06	26%	O35048.1
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase; Short=3-beta-HSD;	52.0	52.0	39%	3e-06	26%	P14893.2
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase type 7; AltName: Full=3 beta-hydroxysteroi	51.2	51.2	46%	6e-06	27%	Q9EQC1.1
☐ RecName: Full=Short-chain dehydrogenase/reductase family 42E member 1	51.2	51.2	68%	6e-06	25%	Q0IH73.1
☐ RecName: Full=ADP-L-glycero-D-manno-heptose-6-epimerase; AltName: Full=ADP-L-glycero-bet	50.1	50.1	41%	1e-05	29%	Q12CM2.1
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 6; AltName: Fu	50.1	50.1	40%	1e-05	25%	O35469.4
☐ RecName: Full=ADP-L-glycero-D-manno-heptose-6-epimerase; AltName: Full=ADP-L-glycero-bet	50.1	50.1	41%	1e-05	29%	A1VR25.1
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 2; AltName: Fu	50.1	50.1	39%	1e-05	24%	P26149.4
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase; Short=3-beta-HSD;	50.1	50.1	61%	2e-05	22%	O46516.3
☐ RecName: Full=UDP-glucose 4-epimerase; AltName: Full=Galactowaldenase; AltName: Full=UDP	49.7	49.7	69%	2e-05	25%	Q56623.1
☐ RecName: Full=Uncharacterized protein C2A9.02	49.3	49.3	21%	2e-05	39%	Q9Y7K4.1
☐ RecName: Full=Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	49.3	49.3	33%	2e-05	26%	Q54L85.1
☐ RecName: Full=UDP-D-apiose/UDP-D-xylose synthase 1	49.3	49.3	79%	3e-05	22%	Q9ZUY6.1
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase type 5; AltName: Full=3 beta-hydroxysteroi	48.9	48.9	40%	3e-05	25%	P27364.3
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 1; AltName: Fu	48.9	48.9	39%	3e-05	23%	P22071.3
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 4; AltName: Fu	48.5	48.5	39%	4e-05	23%	Q62878.4
☐ RecName: Full=ADP-L-glycero-D-manno-heptose-6-epimerase; AltName: Full=ADP-L-glycero-bet	48.5	48.5	68%	4e-05	25%	Q46Y59.1
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase type 3; AltName: Full=3 beta-hydroxysteroi	48.1	48.1	40%	6e-05	27%	O35296.3
☐ RecName: Full=Putative sugar dehydratase/epimerase YfnG	47.8	47.8	36%	7e-05	30%	O06485.2
☐ RecName: Full=UDP-D-apiose/UDP-D-xylose synthase 2	47.8	47.8	79%	9e-05	21%	Q9SGE0.1
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 3; AltName: Fu	47.4	47.4	39%	9e-05	24%	P26150.3
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase type 4; AltName: Full=3 beta-hydroxysteroi	47.4	47.4	39%	1e-04	27%	Q61767.3
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase; Short=3-beta-HSD;	47.0	47.0	31%	1e-04	27%	P21097.1
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase; Short=3-beta-HSD;	47.0	47.0	31%	1e-04	27%	P26670.1
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase; Short=3-beta-HSD;	47.0	47.0	31%	2e-04	27%	O57245.1
☐ RecName: Full=ADP-L-glycero-D-manno-heptose-6-epimerase; AltName: Full=ADP-L-glycero-bet	46.6	46.6	68%	2e-04	24%	B3R3C0.1
☐ RecName: Full=UDP-glucose 4-epimerase uge1; AltName: Full=Galactowaldenase	46.6	46.6	32%	2e-04	33%	Q9Y7X5.1
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase; AltName: Full=Chol	46.6	46.6	70%	2e-04	23%	P9WQP6.1
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase; Short=3-beta-HSD;	46.2	46.2	32%	3e-04	25%	Q5IFP1.3
☐ RecName: Full=Bifunctional polymyxin resistance protein ArnA; Includes: RecName: Full=UDP-4-a	46.2	46.2	49%	3e-04	27%	A8FRR2.1
☐ RecName: Full=ADP-L-glycero-D-manno-heptose-6-epimerase; AltName: Full=ADP-L-glycero-bet	45.4	45.4	68%	4e-04	24%	Q2L2R8.1
☐ RecName: Full=GDP-mannose 4,6 dehydratase; AltName: Full=GDP-D-mannose dehydratase; Sh	45.4	45.4	33%	5e-04	30%	Q8K3X3.1
☐ RecName: Full=GDP-mannose 4,6 dehydratase; AltName: Full=GDP-D-mannose dehydratase; Sh	45.4	45.4	33%	5e-04	30%	Q8K0C9.1
☐ RecName: Full=dTDP-4-oxo-6-deoxy-D-allose reductase; AltName: Full=dTDP-4-dehydro-6-deoxy	45.1	45.1	68%	5e-04	25%	Q5SFA6.1
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 2; AltName: Fu	45.4	45.4	40%	5e-04	23%	P22072.3
☐ RecName: Full=UDP-D-apiose/UDP-D-xylose synthase	45.4	45.4	79%	5e-04	21%	Q8S9Z2.1
☐ RecName: Full=GDP-mannose 4,6 dehydratase; AltName: Full=GDP-D-mannose dehydratase; Sh	44.7	44.7	33%	8e-04	30%	O60547.1
☐ RecName: Full=UDP-glucose 4-epimerase; AltName: Full=Galactowaldenase; AltName: Full=UDP	44.3	44.3	32%	8e-04	32%	Q8R059.1
☐ RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 1; AltName: Fu	44.7	44.7	32%	9e-04	25%	P27365.2
☐ RecName: Full=UDP-glucose 4-epimerase 2; Short=OsUGE-2; AltName: Full=UDP-galactose 4-ep	44.3	44.3	33%	0.001	33%	Q6ZDJ7.1
☐ RecName: Full=ADP-L-glycero-D-manno-heptose-6-epimerase; AltName: Full=ADP-L-glycero-bet	43.9	43.9	32%	0.001	32%	Q0KDH0.1
☐ RecName: Full=ADP-L-glycero-D-manno-heptose-6-epimerase; AltName: Full=ADP-L-glycero-bet	43.9	43.9	41%	0.001	27%	Q1LQG2.1

☐	RecName: Full=ADP-L-glycero-D-manno-heptose-6-epimerase; AltName: Full=ADP-L-glycero-bet	43.5	43.5	36%	0.002	26%	Q21Y60.1
☐	RecName: Full=UDP-glucose 4-epimerase; AltName: Full=Galactowaldenase; AltName: Full=UDF	42.7	42.7	32%	0.003	32%	Q3T105.2
☐	RecName: Full=UDP-glucose 4-epimerase; AltName: Full=Galactowaldenase; AltName: Full=UDF	42.7	42.7	32%	0.003	30%	Q14376.2
☐	RecName: Full=UDP-glucose 4-epimerase; AltName: Full=Galactowaldenase; AltName: Full=UDF	42.7	42.7	32%	0.003	30%	Q5R8D0.1
☐	RecName: Full=UDP-glucose 4-epimerase; AltName: Full=Galactowaldenase; AltName: Full=UDF	42.4	42.4	32%	0.004	31%	P18645.1
☐	RecName: Full=UDP-glucose 4-epimerase; AltName: Full=Galactowaldenase; AltName: Full=UDF	42.4	42.4	32%	0.004	31%	Q45291.2
☐	RecName: Full=Bifunctional polymyxin resistance protein ArnA; Includes: RecName: Full=UDP-4-a	42.7	42.7	54%	0.004	26%	B5XTK9.1
☐	RecName: Full=GDP-mannose 4,6-dehydratase; AltName: Full=GDP-D-mannose dehydratase	41.6	41.6	15%	0.007	41%	Q06952.1
☐	RecName: Full=Bifunctional polymyxin resistance protein ArnA; Includes: RecName: Full=UDP-4-a	42.0	42.0	54%	0.007	26%	A6TF98.1
☐	RecName: Full=dTDP-4-oxo-6-deoxy-D-allose reductase; AltName: Full=dTDP-4-dehydro-6-deoxy	41.6	41.6	68%	0.007	25%	Q331Q7.1
☐	RecName: Full=UDP-glucose 4-epimerase; AltName: Full=Galactowaldenase; AltName: Full=UDF	39.7	39.7	32%	0.008	29%	P45602.1
☐	RecName: Full=UDP-glucose 4-epimerase 4; Short=OsUGE-4; AltName: Full=UDP-galactose 4-ep	41.6	41.6	32%	0.008	32%	Q6K2E1.1
☐	RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 1; AltName: Fu	41.6	41.6	32%	0.009	24%	P14060.2

Alignments

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RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-reductase; AltName: Full=Flavanone 4-reductase; Short=FNR

Sequence ID: P14720.2 **Length:** 380 **Number of Matches:** 1

Related Information

Range 1: 1 to 380 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
786 bits(2030)	0.0	Compositional matrix adjust.	374/380(98%)	377/380(99%)	0/380(0%)

```
Query  1    MASEAVHAPSPPVAVPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLE  60
            MASEAVHAPSPPVAVPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLE
Sbjct  1    MASEAVHAPSPPVAVPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLE  60

Query  61   LPKADTNLTLWKADLTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSI  120
            LPKADTNLTLWKADLTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSI
Sbjct  61   LPKADTNLTLWKADLTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSI  120

Query  121  IESCAKANTVKRLVFTSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILA  180
            IESCAKANTVKRLVFTSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYF SKILA
Sbjct  121  IESCAKANTVKRLVFTSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFASKILA  180

Query  181  EKSAMEETKKKNIDFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVH  240
            EK+AMEE KKKNIDFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVH
Sbjct  181  EKAAMEEAKKKNIDFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVH  240

Query  241  LDDLCEAHIFLYEHPKADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVV  300
            LDDLCEAHIFLYEHPKADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVV
Sbjct  241  LDDLCEAHIFLYEHPKADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVV  300

Query  301  SFSSKKLTDMGFQFKYTLEDMYKGAIETCRQKQLLPFSTRSAADNGHNREAIAISAQNYA  360
            SFSSKKLTDMGFQFKYTLEDMYKGAI+TCRQKQLLPFSTRSA DNGHNREAIAISAQNYA
Sbjct  301  SFSSKKLTDMGFQFKYTLEDMYKGAIDTCRQKQLLPFSTRSAEDNGHNREAIAISAQNYA  360

Query  361  SGKENAPVANHTEMLTNVEV  380
            SGKENAPVANHTEML+NVEV
Sbjct  361  SGKENAPVANHTEMLSNVEV  380
```

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RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-reductase; AltName: Full=Flavanone 4-reductase; Short=FNR

Sequence ID: P51107.1 **Length:** 379 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 1 to 379 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
687 bits(1773)	0.0	Compositional matrix adjust.	337/383(88%)	351/383(91%)	7/383(1%)

```
Query  1    MASEA---VHAPSPPVAVPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKH  57
            MASEA   V A SPP    TV VTG AGFIGSWLVMRLLERGYNVHATVRDPEN+KKVKH
Sbjct  1    MASEAHAVVDAHSPP-KTTTVWVTGGAGFIGSWLVMRLLERGYNVHATVRDPENQKKVKH  59

Query  58   LLELPKADTNLTLWKADLTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGM  117
            LLELPKADTNLTLWKADL VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGM
Sbjct  60   LLELPKADTNLTLWKADLAVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGM  119
```

```
Query  118  LSIIESCAKANTVKRLVFTSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSK  177
            LSIIESCAKANTVKRLVFTSSAGTLDVQE QKLFYD+TSWSDLDFIYAKKMTGWMYFVSK
Sbjct  120  LSIIESCAKANTVKRLVFTSSAGTLDVQEDQKLFYDETSWSDLDFIYAKKMTGWMYFVSK  179

Query  178  ILAEKSAMEETKKKNIDFISIIPPLVVGPFITPTFFPPSLITALSLITGNEAHYCIIKQGQ  237
            ILAEK+AMEE +K NIDFISIIPPLVVGPFIT TFFPPSLITALSLIT   AHY IIKQGQ
Sbjct  180  ILAEKAAMEEARKNNIDFISIIPPLVVGPFITSTFFPPSLITALSLIT---AHYGIIKQGQ  236

Query  238  YVHLDDLCEAHIFLYEHPKADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDL  297
            YVHLDDLCEAHIFLYEHPKA+GRFICSSHHAIIYDVAKMVR+KWPEYYVPTEFKGIDKDL
Sbjct  237  YVHLDDLCEAHIFLYEHPKAEGRFICSSHHAIIYDVAKMVRQKWPEYYVPTEFKGIDKDL  296

Query  298  PVVSFSSKKLTDMGFQFKYTLEDMYKGAIETCRQKQLLPFSTRSAADNGHNREAIAISAQ  357
             +VSFSSKKL D+ FQFK+TLEDMYKGAIETCRQKQLLPFSTRS ADNG ++EAI IS +
Sbjct  297  ALVSFSSKKLMDIKFQFKHTLEDMYKGAIETCRQKQLLPFSTRSTADNGKDKEAIPISTE  356

Query  358  NYASGKENAPVANHTEMLTNVEV  380
            NY+SGKENAPVAN T   TN E+
Sbjct  357  NYSSGKENAPVANCTGKFTNGEI  379
```

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RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-reductase; AltName: Full=Flavanone 4-reductase; Short=FNR

Sequence ID: P14721.1 **Length:** 446 **Number of Matches:** 1

Related Information

Range 1: 13 to 386 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
555 bits(1429)	0.0	Compositional matrix adjust.	261/375(70%)	313/375(83%)	15/375(4%)

```
Query  10   SPPVAVPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLT  69
            +PP +  TVCVTGAAGFIGSWLVMRLLERGY V ATVRDP N KKVKHL+ELPKADTNLT
Sbjct  13   APPSST-TVCVTGAAGFIGSWLVMRLLERGYTVRATVRDPGNMKKVKHLIELPKADTNLT  71

Query  70   LWKADLTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANT  129
            LWKAD+TVEGSFDEAIQGC+GVFH+AT M+F+S DPENEVIKPT+ GML+II+SC +A T
Sbjct  72   LWKADMTVEGSFDEAIQGCEGVFHLATSMEFDSVDPENEVIKPTIDGMLNIIKSCVQAKT  131

Query  130  VKRLVFTSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETK  189
            VK+ +FT+S GT++V+E QK  YD+T  SD+DFI +KKMTGWMYFVSKILAEK+ ME  K
Sbjct  132  VKKFIFTTSGGTVNVEEHQKPVYDETDSSDMDFINSKKMTGWMYFVSKILAEKAGMEAAK  191

Query  190  KKNIDFISIIPPLVVGPFITPTFFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHI  249
            + NIDFISIIPPLVVGPFI PTFFPPSLITALS ITGNEAHY IIKQ QYVHLDDLCE HI
Sbjct  192  ENNIDFISIIPPLVVGPFIMPTFFPPSLITALSPITGNEAHYSIIKQCQYVHLDDLCEGHI  251

Query  250  FLYEHPKADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVSFSSKKLTD  309
            FL+E+PKA+GR+ICSSH A IYD+AK++ E WPEY++P EF+GIDKD+PVVSFSSKK+
Sbjct  252  FLFEYPKAEGRYICSSHDATIYDIAKLITENWPEYHIPDEFEGIDKDIPVVSFSSKKMIG  311

Query  310  MGFQFKYTLEDMYKGAIETCRQKQLLPFSTR-----------SAADNGHN---REAIAIS  355
            MGF FKYTLEDM +GAI+TCR+K +LP+ST+           ++ +N +N   +E   IS
Sbjct  312  MGFIFKYTLEDMVRGAIDTCREKGMLPYSTKNNKGDEKEPILNSLENNYNIQDKELFPIS  371

Query  356  AQNYASGKENAPVAN  370
             + + +G+ENA ++N
Sbjct  372  EEKHINGQENALLSN  386
```

Download GenPept Graphics Next Previous Descriptions

RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-reductase; AltName: Full=Flavanone 4-reductase; Short=FNR

Sequence ID: P51105.1 **Length:** 366 **Number of Matches:** 1

Related Information

Range 1: 8 to 343 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
544 bits(1402)	0.0	Compositional matrix adjust.	255/336(76%)	292/336(86%)	0/336(0%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            TVCVTGAAGFIGSWLVMRLLERGY VHATVRDP + KKVKHLLELPKA TNL LWKADLT
Sbjct  8    TVCVTGAAGFIGSWLVMRLLERGYVVHATVRDPGDLKKVKHLLELPKAQTNLKLWKADLT  67

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
             EGSFDEAIQGC GVFH+ATPMDFESKDPENE+IKPT+ G+LSII SC KA TVK+LVFT
Sbjct  68   QEGSFDEAIQGCHGVFHLATPMDFESKDPENEIIKPTIEGVLSIIRSCVKAKTVKKLVFT  127

Query  137  SSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDFI  196
            SSAGT++ QE+Q   YD++ WSDLDFIY+KKMT WMYFVSK LAEK+A + TK  NI FI
Sbjct  128  SSAGTVNGQEKQLHVYDESHWSDLDFIYSKKMTAWMYFVSKTLAEKAAWDATKGNNISFI  187

Query  197  SIIPPLVVGPFITPTFFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEHPK  256
            SIIP LVVGPFIT TFFPPSL+TALSLITGNEAHY IIKQGQYVHLDDLCE HI+LYE+PK
Sbjct  188  SIIPTLVVGPFITSTFFPPSLVTALSLITGNEAHYSIIKQGQYVHLDDLCECHIYLYENPK  247

Query  257  ADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVSFSSKKLTDMGFQFKY  316
            A GR+ICSSH A I+ +AK++++KWPEYY+PT+F GID++LP+VSFSSKKL D GF+FKY
Sbjct  248  AKGRYICSSHDATIHQLAKIIKDKWPEYYIPTKFPGIDEELPIVSFSSKKLIDTGFEFKY  307

Query  317  TLEDMYKGAIETCRQKQLLPFSTRSAADNGHNREAI  352
             LEDM+KGAI+TCR+K LLP+ST     NG++   +
Sbjct  308  NLEDMFKGAIDTCREKGLLPYSTIKNHINGNHVNGV  343
```

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RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-reductase; AltName: Full=Flavanone 4-reductase; Short=FNR

Sequence ID: P51103.1 **Length:** 364 **Number of Matches:** 1

Related Information

Range 1: 7 to 331 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
526 bits(1355)	0.0	Compositional matrix adjust.	250/325(77%)	288/325(88%)	0/325(0%)

```
Query  16   PTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADL  75
            PTVCVTGAAGFIGSWLVMRLLERGY V ATVR+P + KKVKHLLELPKA+TNLTLWKADL
Sbjct  7    PTVCVTGAAGFIGSWLVMRLLERGYIVRATVRNPGDMKKVKHLLELPKAETNLTLWKADL  66

Query  76   TVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVF  135
            T EGSFDEAI+GC GVFHVATPMDFESKDPENE+IKPT+ G+LSII SCAKA TVK+LV+
Sbjct  67   TQEGSFDEAIEGCHGVFHVATPMDFESKDPENEIIKPTIEGILSIIRSCAKAKTVKKLVY  126

Query  136  TSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDF  195
            TSSAGT++VQE Q   YD++ WSDLDFIY+KKMT WMYFVSK LAEK+AME  K+ NIDF
Sbjct  127  TSSAGTVNVQETQLPVYDESHWSDLDFIYSKKMTAWMYFVSKTLAEKAAMEAAKENNIDF  186

Query  196  ISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEHP  255
            +SIIPPLVVGPFI PTFPPSLITALSLI G E+HY IIKQGQYVHLDDLCE HIFLYE+P
Sbjct  187  VSIIPPLVVGPFINPTFPPSLITALSLINGAESHYSIIKQGQYVHLDDLCECHIFLYENP  246

Query  256  KADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVSFSSKKLTDMGFQFK  315
            +A GR+ICS   A I+ +A+M+++KWPEY+VPT+F GID++LP VSFSSKKL DMGF+FK
Sbjct  247  EAKGRYICSKQDATIHQLARMIKQKWPEYHVPTQFAGIDEELPTVSFSSKKLIDMGFKFK  306

Query  316  YTLEDMYKGAIETCRQKQLLPFSTR  340
            Y LEDM+KGAI++C++K  LP+ST
Sbjct  307  YDLEDMFKGAIDSCKEKGFLPYSTN  331
```

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RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-reductase; AltName: Full=Flavanone 4-reductase; Short=FNR

Sequence ID: P51110.1 **Length:** 337 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 7 to 325 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
504 bits(1298)	2e-179	Compositional matrix adjust.	234/319(73%)	276/319(86%)	0/319(0%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            TVCVTGA+GFIGSWLVMRLLER   V ATVRDP N KKVKHLL+LPKA+T+LTLWKADL
Sbjct  7    TVCVTGASGFIGSWLVMRLLERRLTVRATVRDPTNVKKVKHLLDLPKAETHLTLWKADLA  66

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
             EGSFDEAI+GC GVFHVATPMDFESKDPENEVIKPT+ GML I++SCA A TV+RLVFT
Sbjct  67   DEGSFDEAIKGCTGVFHVATPMDFESKDPENEVIKPTIEGMLGIMKSCAAAKTVRRLVFT  126

Query  137  SSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDFI  196
            SSAGT+++QE Q   YD++ WSD++F  AKKMT WMYFVSK LAE++A +  K+ NIDFI
Sbjct  127  SSAGTVNIQEHQLPVYDESCWSDMEFCRAKKMTAWMYFVSKTLAEQAAWKYAKENNIDFI  186

Query  197  SIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEHPK  256
            +IIP LVVGPFI  + PPSLITALS ITGNEAHY II+QGQ+VHLDDLC AHI+L+E+PK
Sbjct  187  TIIPTLVVGPFIMSSMPPSLITALSPITGNEAHYSIIRQGQFVHLDDLCNAHIYLFENPK  246

Query  257  ADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVSFSSKKLTDMGFQFKY  316
            A+GR+ICSSH  II D+AKM+REK+PEY +PTEFKG+D++L  V FSSKKLTD+GF+FKY
Sbjct  247  AEGRYICSSHDCIILDLAKMLREKYPEYNIPTEFKGVDENLKSVCFSSKKLTDLGFEFKY  306

Query  317  TLEDMYKGAIETCRQKQLL  335
            +LEDM+ GA++TCR K LL
Sbjct  307  SLEDMFTGAVDTCRAKGLL  325
```

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RecName: Full=Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase; AltName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-reductase; AltName: Full=Flavanone 4-reductase; Short=FNR

Sequence ID: Q9XES5.1 **Length:** 348 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 7 to 327 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
493 bits(1268)	9e-175	Compositional matrix adjust.	225/321(70%)	276/321(85%)	0/321(0%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            +VCVTGA+GFIGSWLVMRLLE GY V ATVRDP N+KKVKHLL+LPKA+T+LTLWKADL
Sbjct  7    SVCVTGASGFIGSWLVMRLLEHGYTVRATVRDPTNQKKVKHLLDLPKAETHLTLWKADLA  66

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
             EGSFDEAIQGC GVFHVATPMDFESKDPENEVIKPT+ G+L I+++C KA TV++LVFT
Sbjct  67   DEGSFDEAIQGCSGVFHVATPMDFESKDPENEVIKPTINGLLDILKACQKAKTVRKLVFT  126
```

```
Query  137  SSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDFI  196
            SSAGT++V+E QK  YD+++WSD++F  + KMTGWMYFVSK LAE++A +  K+ NIDFI
Sbjct  127  SSAGTVNVEEHQKPVYDESNWSDVEFCRSVKMTGWMYFVSKTLAEQAAWKYAKENNIDFI  186

Query  197  SIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEHPK  256
            +IIP LV+GPF+ P+ PPSLIT LS I  NE+HY IIKQGQYVHLDDLC +HI+LYEHPK
Sbjct  187  TIIPTLVIGPFLMPSMPPSLITGLSPILRNESHYGIIKQGQYVHLDDLCLSHIYLYEHPK  246

Query  257  ADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVSFSSKKLTDMGFQFKY  316
            A+GR+ICSSH A I+++ KM+REK+PEY +PT+FKGID +L  V FSSKKL ++GF+FKY
Sbjct  247  AEGRYICSSHDATIHELVKMLREKYPEYNIPTKFKGIDDNLEPVHFSSKKLREIGFEFKY  306

Query  317  TLEDMYKGAIETCRQKQLLPF  337
            +LEDM+ GA++ CR K L+P
Sbjct  307  SLEDMFVGAVDACRAKGLIPI  327
```

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RecName: Full=Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase; AltName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Flavanone 4-reductase; Short=FNR

Sequence ID: Q84KP0.1 **Length:** 347 **Number of Matches:** 1

Related Information

Range 1: 7 to 327 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
491 bits(1264)	4e-174	Compositional matrix adjust.	223/321(69%)	276/321(85%)	0/321(0%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            +VCVTGA+GFIGSWLVMRLLE GY V ATVRDP N+KKVKHLL+LPKA+T+LTLWKADL
Sbjct  7    SVCVTGASGFIGSWLVMRLLEHGYTVRATVRDPTNQKKVKHLLDLPKAETHLTLWKADLA  66

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
             EGSFDEAIQGC GVFHVATPMDFES+DPENEVIKPT+ G+L I+++C KA TV++LVFT
Sbjct  67   DEGSFDEAIQGCSGVFHVATPMDFESRDPENEVIKPTINGLLDILKACQKAKTVRKLVFT  126

Query  137  SSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDFI  196
            SSAGT++V+E QK  YD+++WSD++F  + KMTGWMYFVSK LAE++A +  K+ NIDFI
Sbjct  127  SSAGTVNVEEHQKPVYDESNWSDVEFCRSVKMTGWMYFVSKTLAEQAAWKYAKENNIDFI  186

Query  197  SIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEHPK  256
            +IIP LV+GPF+ P+ PPSLIT LS I  NE+HY IIKQGQYVHLDDLC +HI+LY+HPK
Sbjct  187  TIIPTLVIGPFLMPSMPPSLITGLSPILRNESHYGIIKQGQYVHLDDLCLSHIYLYKHPK  246

Query  257  ADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVSFSSKKLTDMGFQFKY  316
            A+GR+ICSSH A I+++ KM+REK+PEY +PT+FKGID +L  V FSSKKL ++GF+FKY
Sbjct  247  AEGRYICSSHDATIHELVKMLREKYPEYNIPTKFKGIDDNLEPVHFSSKKLREIGFEFKY  306

Query  317  TLEDMYKGAIETCRQKQLLPF  337
            +LEDM+ GA++ CR K L+P
Sbjct  307  SLEDMFVGAVDACRAKGLIPI  327
```

Download GenPept Graphics Next Previous Descriptions

RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-reductase; AltName: Full=Flavanone 4-reductase; Short=FNR; AltName: Full=Protein TRANSPARENT TESTA 3

Sequence ID: P51102.2 **Length:** 382 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 7 to 328 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
491 bits(1263)	2e-173	Compositional matrix adjust.	230/322(71%)	268/322(83%)	0/322(0%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            TVCVTGA+GFIGSWLVMRLLERGY V ATVRDP N KKV+HLL+LP A T LTLWKADL+
Sbjct  7    TVCVTGASGFIGSWLVMRLLERGYFVRATVRDPGNLKKVQHLLDLPNAKTLLTLWKADLS  66

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
             EGS+D+AI GC GVFHVATPMDFESKDPENEVIKPTV GML I+++C KA TV+R VFT
Sbjct  67   EEGSYDDAINGCDGVFHVATPMDFESKDPENEVIKPTVNGMLGIMKACVKAKTVRRFVFT  126

Query  137  SSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDFI  196
            SSAGT++V+E QK  YD+  WSDL+FI +KKMTGWMYFVSK LAEK+A +  ++K +DFI
Sbjct  127  SSAGTVNVEEHQKNVYDENDWSDLEFIMSKKMTGWMYFVSKTLAEKAAWDFAEEKGLDFI  186

Query  197  SIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEHPK  256
            SIIP LVVGPFIT + PPSLITALS IT NEAHY II+QGQYVHLDDLC AHIFLYE
Sbjct  187  SIIPTLVVGPFITTSMPPSLITALSPITRNEAHYSIIRQGQYVHLDDLCNAHIFLYEQAA  246

Query  257  ADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVSFSSKKLTDMGFQFKY  316
            A GR+ICSSH A I  ++K +R K+PEY VP+ F+G+D++L  + FSSKKLTDMGF FKY
Sbjct  247  AKGRYICSSHDATILTISKFLRPKYPEYNVPSTFEGVDENLKSIEFSSKKLTDMGFNFKY  306

Query  317  TLEDMYKGAIETCRQKQLLPFS  338
            +LE+M+  +IETCRQK  LP S
Sbjct  307  SLEEMFIESIETCRQKGFLPVS  328
```

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RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-reductase; AltName:

Full=Flavanone 4-reductase; Short=FNR

Sequence ID: P51104.1 **Length:** 360 **Number of Matches:** 1

Related Information

Range 1: 24 to 344 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
480 bits(1235)	2e-169	Compositional matrix adjust.	224/322(70%)	269/322(83%)	1/322(0%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            TVCVTGA+GFIGSWL+MRLLERGY V ATVRDP+N KKV+HLL+LP A TNLTLWKADL
Sbjct  24   TVCVTGASGFIGSWLIMRLLERGYTVRATVRDPDNTKKVQHLLDLPNAKTNLTLWKADLH  83

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
             EGSFD A+ GC GVFH+ATPMDFESKDPENE+IKPT+ GML I++SC KA  ++R+VFT
Sbjct  84   EEGSFDAAVDGCTGVFHIATPMDFESKDPENEMIKPTINGMLDILKSCVKAK-LRRVVFT  142

Query  137  SSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDFI  196
            SS GT++V+  QK  YD+T WS LDFI + KMTGWMYFVSKILAE++A +   + N++FI
Sbjct  143  SSGGTVNVEATQKPVYDETCWSALDFIRSVKMTGWMYFVSKILAEQAAWKYAAENNLEFI  202

Query  197  SIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEHPK  256
            SIIPPLVVGPFI P+ PPSLITALS IT  E+HY IIKQGQ+VHLDDLC +HIFLYE+PK
Sbjct  203  SIIPPLVVGPFIMPSMPPSLITALSPITRTESHYTIIKQGQFVHLDDLCMSHIFLYENPK  262

Query  257  ADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVSFSSKKLTDMGFQFKY  316
            A+GR+I S+  A IYD+AKM+RE++PEY VPT+FK   +D+  V FSSKKLTD+GF+FKY
Sbjct  263  ANGRYIASACAATIYDIAKMLREEYPEYNVPTKFKDYKEDMGQVQFSSKKLTDLGFEFKY  322

Query  317  TLEDMYKGAIETCRQKQLLPFS  338
             L+DMY  A+E+CR K LLP S
Sbjct  323  GLKDMYTAAVESCRAKGLLPLS  344
```

Download GenPept Graphics Next Previous Descriptions

RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-reductase; AltName: Full=Flavanone 4-reductase; Short=FNR

Sequence ID: P51106.1 **Length:** 354 **Number of Matches:** 1

Related Information

Range 1: 8 to 353 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
450 bits(1158)	6e-158	Compositional matrix adjust.	210/347(61%)	268/347(77%)	1/347(0%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTV  77
            V VTGA+GF+GSWLVM+LL+ GY V ATVRDP N +K K LLELP A   L++WKADL+
Sbjct  8    VVVTGASGFVGSWLVMKLLQAGYTVRATVRDPANVEKTKPLLELPGAKERLSIWKADLSE  67

Query  78   EGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTS  137
            +GSF+EAI GC GVFHVATPMDF+S+DPENEVIKPTV GMLSI+ +C +A TVKR+VFTS
Sbjct  68   DGSFNEAIAGCTGVFHVATPMDFDSQDPENEVIKPTVEGMLSIMRACKEAGTVKRIVFTS  127

Query  138  SAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDFIS  197
            SAG+++++E+ +  YDQ +WSD+D+    KMTGWMYFVSK LAEK+AME   +  +DFIS
Sbjct  128  SAGSVNIEERPRPAYDQDNWSDIDYCRRVKMTGWMYFVSKALAEKAAMEYASENGLDFIS  187

Query  198  IIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEHPKA  257
            IIP LVVGPF++   PPSL+TAL+LITGNEAHY I+KQ Q VHLDDLC+A  FL+EHP+A
Sbjct  188  IIPTLVVGPFLSAGMPPSLVTALALITGNEAHYSILKQVQLVHLDDLCDAMTFLFEHPEA  247

Query  258  DGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVSFSSKKLTDMGFQFKYT  317
            +GR+ICSSH A I+ +A+M+++++PEY +P +F G+D +L  + FSSKKL D GF F+YT
Sbjct  248  NGRYICSSHDATIHGLARMLQDRFPEYDIPQKFAGVDDNLQPIHFSSKKLLDHGFSFRYT  307

Query  318  LEDMYKGAIETCRQKQLLPFSTRSAADNGHNREAIAISAQNYASGKE  364
             EDM+  AI TCR K L+P     A   G    A+A + +  A G E
Sbjct  308  TEDMFDAAIHTCRDKGLIPLGDVPAPAAGGKLGALA-AGEGQAIGAE  353
```

Download GenPept Graphics Next Previous Descriptions

RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-reductase; AltName: Full=Flavanone 4-reductase; Short=FNR

Sequence ID: P51108.1 **Length:** 357 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 12 to 341 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
426 bits(1094)	4e-148	Compositional matrix adjust.	201/330(61%)	256/330(77%)	1/330(0%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            TV VTGA+GF+GSWLVM+LL+ GY V ATVRDP N  K K L++LP A   L++WKADL
Sbjct  12   TVLVTGASGFVGSWLVMKLLQAGYTVRATVRDPANVGKTKPLMDLPGATERLSIWKADLA  71

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
             EGSF +AI+GC GVFHVATPMDF SKDPENEVIKPTV GM+SI+ +C +A TV+R+VFT
Sbjct  72   EEGSFHDAIRGCTGVFHVATPMDFLSKDPENEVIKPTVEGMISIMRACKEAGTVRRIVFT  131

Query  137  SSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDFI  196
            SSAGT++++E+Q+  YD+ SW+D+DF    KMTGWMYFVSK LAEK+A+    +  +D +
Sbjct  132  SSAGTVNLEERQRPVYDEESWTDVDFCRRVKMTGWMYFVSKTLAEKAALAYAAEHGLDLV  191

Query  197  SIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEHPK  256
            +IIP LVVGPFI+ + PPSLITAL+LITGN  HY I+KQ Q +HLDDLC+A IFL+E+P
```

```
Sbjct  192  TIIPTLVVGPFISASMPPSLITALALITGNAPHYSILKQVQLIHLDDLCDAEIFLFENPA  251

Query  257  ADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVSFSSKKLTDMGFQFKY  316
            A GR++CSSH   I+ +A M+R+++PEY VP  F GI  DL  V FSSKKL D+GF F+Y
Sbjct  252  AAGRYVCSSHDVTIHGLAAMLRDRYPEYDVPQRFPGIQDDLQPVRFSSKKLQDLGFTFRY  311

Query  317  -TLEDMYKGAIETCRQKQLLPFSTRSAADN  345
             TLEDM+  AI TC++K L+P +T +  D
Sbjct  312  KTLEDMFDAAIRTCQEKGLIPLATAAGGDG  341
```

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RecName: Full=Dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-reductase; AltName: Full=Flavanone 4-reductase; Short=FNR

Sequence ID: P51109.1 **Length:** 217 **Number of Matches:** 1

Related Information

Range 1: 1 to 217 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
326 bits(836)	4e-111	Compositional matrix adjust.	154/217(71%)	181/217(83%)	0/217(0%)

```
Query  28   GSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTVEGSFDEAIQG  87
            GSWLVMRL+E GY V ATVRDPEN KKV  LLELP A + L++WKADL  EGSFDEAI+G
Sbjct  1    GSWLVMRLMEPGYMVRATVRDPENLKKVSPLLELPGAKSKLSIWKADLGEEGSFDEAIKG  60

Query  88   CQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTSSAGTLDVQEQ  147
            C GVFHVATPMDFESKDPENE+IKPT++G+L I+++C KA TV+RL++TSSAGTL+V E
Sbjct  61   CTGVFHVATPMDFESKDPENEMIKPTIKGVLDIMKACLKAKTVRRLIYTSSAGTLNVTED  120

Query  148  QKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDFISIIPPLVVGPF  207
            QK  +D++ WSD++F    KMTGWMYFVSK LAE+ A +  K+  +D I+IIPPLVVGPF
Sbjct  121  QKPLWDESCWSDVEFCRRVKMTGWMYFVSKTLAEQEAWKFAKEHKMDVITIIPPLVVGPF  180

Query  208  ITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDL  244
            + PT PPSLITALS ITGNEAHY IIKQGQYVHLDDL
Sbjct  181  LIPTMPPSLITALSPITGNEAHYSIIKQGQYVHLDDL  217
```

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RecName: Full=Putative anthocyanidin reductase; Short=GbANR

Sequence ID: Q5XLY0.1 **Length:** 342 **Number of Matches:** 1

Related Information

Range 1: 14 to 340 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
320 bits(821)	6e-107	Compositional matrix adjust.	163/328(50%)	229/328(69%)	10/328(3%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            TVCVTGAAGF+ SWLV RLLE+GY VHATVRDPENK KV HLL LP A   L L++A+L
Sbjct  14   TVCVTGAAGFMASWLVKRLLEKGYIVHATVRDPENKAKVSHLLNLPGATDRLKLFRAELC  73

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
             +GSFD A+ GC GVFHVATP +F  KDPEN++IKP + G L++++SC K +++KR+V T
Sbjct  74   EDGSFDAAVAGCNGVFHVATPTEFMPKDPENDLIKPAIEGTLNVLKSCTKVDSIKRVVVT  133

Query  137  SSAGTLDVQE--QQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNID  194
            SSA T+ +    +Q  + D++ W+D++F+ ++K  GW Y VSK LAE++A++  ++ ++D
Sbjct  134  SSAATVSINNSSEQNQYIDESCWTDVNFLTSQKPPGWAYPVSKTLAEQAALKYAEEHSLD  193

Query  195  FISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQY-------VHLDDLCEA  247
             +++IP LVVGP +TPT P S+  ALSLITG+E     +K  Q+       VH+DD+C A
Sbjct  194  VVTVIPVLVVGPAVTPTVPSSVELALSLITGDEFKMGALKGMQFVSGSISLVHIDDVCSA  253

Query  248  HIFLYEHPKADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVSFSSKKL  307
             IFL E P A GR+IC   +  I  +A+ + +++P+Y VPT+F  +    P ++ SS+KL
Sbjct  254  QIFLMEKPSAQGRYICFPVNTGIPQLAEFLSKRYPQYKVPTKFDDVPAT-PKLTISSQKL  312

Query  308  TDMGFQFKYTLEDMYKGAIETCRQKQLL  335
             D GF FKY +ED+Y  AIE  + K LL
Sbjct  313  LDCGFSFKYGIEDIYDQAIEYMKTKGLL  340
```

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RecName: Full=Anthocyanidin reductase ((2S)-flavan-3-ol-forming); Short=VvANR

Sequence ID: D7U6G6.1 **Length:** 338 **Number of Matches:** 1

Related Information

Range 1: 6 to 336 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
274 bits(700)	8e-89	Compositional matrix adjust.	143/336(43%)	216/336(64%)	17/336(5%)

```
Query  12   PVAVPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLW  71
            P+   T CV G  GF+ S LV  LL++GY V+ TVRDP+N+KKV HLLEL +   +L ++
Sbjct  6    PIGKKTACVVGGTGFVASLLVKLLLQKGYAVNTTVRDPDNQKKVSHLLELQELG-DLKIF  64

Query  72   KADLTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVK  131
            +ADLT E SF+  I GC  VFHVATP+ F S+DPEN++IKP V+G+++++++C +A +VK
Sbjct  65   RADLTDELSFEAPIAGCDFVFHVATPVHFASEDPENDMIKPAVQGVVNVMKACTRAKSVK  124

Query  132  RLVFTSSAG--TLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETK  189
```

```
             R++ TSSA   T++  +   L  D+ +W+D++F+ + K   W Y  SK LAEK+A +  +
Sbjct  125   RVILTSSAAAVTINQLDGTGLVVDEKNWTDIEFLTSAKPPTWGYPASKTLAEKAAWKFAE  184

Query  190   KKNIDFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYV-------HLD  242
             + NID I++IP L+ G  +T   P S+  A+SLITGNE     +K  Q +       H++
Sbjct  185   ENNIDLITVIPTLMAGSSLTSDVPSSIGLAMSLITGNEFLINGMKGMQMLSGSVSIAHVE  244

Query  243   DLCEAHIFLYEHPKADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVS-  301
             D+C AHIF+ E   A GR+IC + +  + ++AK + +++P+Y VPT+F     D P  S
Sbjct  245   DVCRAHIFVAEKESASGRYICCAANTSVPELAKFLSKRYPQYKVPTDF----GDFPSKSK  300

Query  302   --FSSKKLTDMGFQFKYTLEDMYKGAIETCRQKQLL  335
                SS KL   GF FKY +E++Y  ++E  + K LL
Sbjct  301   LIISSDKLVKEGFSFKYGIEEIYDESVEYFKAKGLL  336
```

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RecName: Full=Anthocyanidin reductase ((2S)-flavan-3-ol-forming); Short=VvANR; AltName: Full=Protein BANYULS; Short=VvBAN

Sequence ID: Q7PCC4.1 **Length:** 338 **Number of Matches:** 1

Related Information

Range 1: 6 to 336 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
274 bits(700)	8e-89	Compositional matrix adjust.	142/336(42%)	218/336(64%)	17/336(5%)

```
Query  12    PVAVPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLW  71
             P+   T CV G  GF+ S LV  LL++GY V+ TVRDP+N+KKV HLLEL +   +L ++
Sbjct  6     PIGKKTACVVGGTGFVASLLVKLLLQKGYAVNTTVRDPDNQKKVSHLLELQELG-DLKIF  64

Query  72    KADLTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVK  131
             +ADLT E SF+  I GC  VFHVATP+ F S+DPEN++IKP ++G+++++++C +A +VK
Sbjct  65    RADLTDELSFEAPIAGCDFVFHVATPVHFASEDPENDMIKPAIQGVVNVMKACTRAKSVK  124

Query  132   RLVFTSSAG--TLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETK  189
             R++ TSSA   T++  +   L  D+ +W+D++F+ + K   W Y  SK LAEK+A +  +
Sbjct  125   RVILTSSAAAVTINQLDGTGLVVDEKNWTDIEFLTSAKPPTWGYPASKTLAEKAAWKFAE  184

Query  190   KKNIDFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYV-------HLD  242
             + NID I++IP L+ G  +T   P S+  A+SLITGNE     +K  Q +       H++
Sbjct  185   ENNIDLITVIPTLMAGSSLTSDVPSSIGLAMSLITGNEFLINGMKGMQMLSGSVSIAHVE  244

Query  243   DLCEAHIFLYEHPKADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVS-  301
             D+C+AHIF+ E   A GR+IC + +  + ++AK + +++P+Y VPT+F     D P  S
Sbjct  245   DVCQAHIFVAEKESASGRYICCAANTSVPELAKFLSKRYPQYKVPTDF----GDFPPKSK  300

Query  302   --FSSKKLTDMGFQFKYTLEDMYKGAIETCRQKQLL  335
                SS+KL   GF FKY +E++Y  ++E  + K LL
Sbjct  301   LIISSEKLVKEGFSFKYGIEEIYDESVEYFKAKGLL  336
```

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RecName: Full=Anthocyanidin reductase ((2S)-flavan-3-ol-forming); Short=VvANR

Sequence ID: Q5FB34.1 **Length:** 338 **Number of Matches:** 1

Related Information

Range 1: 6 to 336 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
273 bits(698)	2e-88	Compositional matrix adjust.	142/336(42%)	217/336(64%)	17/336(5%)

```
Query  12    PVAVPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLW  71
             P+   T CV G  GF+ S LV  LL++GY V+ TVRDP+N+KKV HLLEL +   +L ++
Sbjct  6     PIGKKTACVVGGTGFVASLLVKLLLQKGYAVNTTVRDPDNQKKVSHLLELQELG-DLKIF  64

Query  72    KADLTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVK  131
             +ADLT E SF+  I GC  VFHVATP+ F S+DPEN++IKP ++G+++++++C +A +VK
Sbjct  65    RADLTDELSFEAPIAGCDFVFHVATPVHFASEDPENDMIKPAIQGVVNVMKACTRAKSVK  124

Query  132   RLVFTSSAG--TLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETK  189
             R++ TSSA   T++  +   L  D+ +W+D++F+ + K   W Y  SK LAEK+A +  +
Sbjct  125   RVILTSSAAAVTINQLDGTGLVVDEKNWTDIEFLTSAKPPTWGYPASKTLAEKAAWKFAE  184

Query  190   KKNIDFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYV-------HLD  242
             + NID I++IP L+ G  +T   P S+  A+SLITGNE     +K  Q +       H++
Sbjct  185   ENNIDLITVIPTLMAGSSLTSDVPSSIGLAMSLITGNEFLINGMKGMQMLSGSVSIAHVE  244

Query  243   DLCEAHIFLYEHPKADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVS-  301
             D+C AHIF+ E   A GR+IC + +  + ++AK + +++P+Y VPT+F     D P  S
Sbjct  245   DVCRAHIFVAEKESASGRYICCAANTSVPELAKFLSKRYPQYKVPTDF----GDFPPKSK  300

Query  302   --FSSKKLTDMGFQFKYTLEDMYKGAIETCRQKQLL  335
                SS+KL   GF FKY +E++Y  ++E  + K LL
Sbjct  301   LIISSEKLVKEGFSFKYGIEEIYDESVEYFKAKGLL  336
```

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RecName: Full=Vestitone reductase

Sequence ID: Q40316.1 **Length:** 326 **Number of Matches:** 1

Related Information

Range 1: 8 to 326 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
264 bits(675)	4e-85	Compositional matrix adjust.	134/321(42%)	196/321(61%)	5/321(1%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGYNVHATVR-DPENKKKVKHLLELPKADTNLTLWKADLT  76
            VCVTG  GF+GSW++  LLE GY+V+ T+R DPE K+ V  L  LP A   L  + ADL+
Sbjct  8    VCVTGGTGFLGSWIIKSLLENGYSVNTTIRADPERKRDVSFLTNLPGASEKLHFFNADLS  67

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
               SF  AI+GC G+FH A+P+DF   +PE  V K TV G L I+++C  + TVKR ++T
Sbjct  68   NPDSFAAAIEGCVGIFHTASPIDFAVSEPEEIVTKRTVDGALGILKACVNSKTVKRFIYT  127

Query  137  SSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDFI  196
            SS   +    + K   D++ WSD+D + + K  GW Y VSK LAEK+ +E  ++  ID +
Sbjct  128  SSGSAVSFNGKDKDVLDESDWSDVDLLRSVKPFGWNYAVSKTLAEKAVLEFGEQNGIDVV  187

Query  197  SIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEHPK  256
            ++I P +VG F+ P  P S+  AL L+ G +    + +    VH+DD+  AHI+L E+
Sbjct  188  TLILPFIVGRFVCPKLPDSIEKALVLVLGKKEQIGVTRF-HMVHVDDVARAHIYLLENSV  246

Query  257  ADGRFICSSHHAIIYDVAKMVREKWPEYYVPT--EFKGIDKDLPVVSFSSKKLTDMGFQF  314
              GR+ CS     I ++++++  K+PEY + T  E K I K   +   ++KKL D GF F
Sbjct  247  PGGRYNCSPFIVPIEEMSQLLSAKYPEYQILTVDELKEI-KGARLPDLNTKKLVDAGFDF  305

Query  315  KYTLEDMYKGAIETCRQKQLL  335
            KYT+EDM+  AI+ C++K  L
Sbjct  306  KYTIEDMFDDAIQCCKEKGYL  326
```

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RecName: Full=Anthocyanidin reductase; Short=AtANR; AltName: Full=Anthocyanin spotted testa; Short=ast; AltName: Full=Protein BANYULS

Sequence ID: Q9SEV0.2 **Length:** 340 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 14 to 337 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
249 bits(637)	3e-79	Compositional matrix adjust.	127/327(39%)	214/327(65%)	13/327(3%)

```
Query  19   CVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTVE  78
            CV G  G + S L+  LL+ GY V+ TVRDPEN+KK+ HL +L +   +L ++KADLT E
Sbjct  14   CVIGGTGNLASILIKHLLQSGYKVNTTVRDPENEKKIAHLRKLQELG-DLKIFKADLTDE  72

Query  79   GSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTSS  138
             SF+ +  GC+ +FHVATP++F+S+DPE ++IKP ++G++++++SC K+ +VKR+++TSS
Sbjct  73   DSFESSFSGCEYIFHVATPINFKSEDPEKDMIKPAIQGVINVLKSCLKSKSVKRVIYTSS  132

Query  139  AGTLDVQEQQ--KLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDFI  196
            A  + +       +  ++ +W+D++F+  +K   W Y +SK+LAEK+A E  K+  I+ +
Sbjct  133  AAAVSINNLSGTGIVMNEENWTDVEFLTEEKPFNWGYPISKVLAEKTAWEFAKENKINLV  192

Query  197  SIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQ-------YVHLDDLCEAHI  249
            ++IP L+ G  +    P SL  ++S ITG E H   +K+ Q       +VH+DDL  AH+
Sbjct  193  TVIPALIAGNSLLSDPPSSLSLSMSFITGKEMHVTGLKEMQKLSGSISFVHVDDLARAHL  252

Query  250  FLYEHPKADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEF-KGIDKDLPVVSFSSKKLT  308
            FL E   A GR+IC +++  + ++A  + +++P+Y V +EF +G+   +P ++ SS+KL
Sbjct  253  FLAEKETASGRYICCAYNTSVPEIADFLIQRYPKYNVLSEFEEGL--SIPKLTLSSQKLI  310

Query  309  DMGFQFKYTLEDMYKGAIETCRQKQLL  335
            + GF+F+Y + +MY   IE    K L+
Sbjct  311  NEGFRFEYGINEMYDQMIEYFESKGLI  337
```

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RecName: Full=Protein BRI1-5 ENHANCED 1

Sequence ID: O22133.1 **Length:** 364 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 40 to 364 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
250 bits(639)	3e-79	Compositional matrix adjust.	134/325(41%)	194/325(59%)	7/325(2%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGYNVHATVRDPE--NKKKVKHLLELPKADTNLTLWKADL  75
            VCVTG +GF+ SWL+MRLL+RGY+V ATVR     NKK + +L ELP A   L ++ ADL
Sbjct  40   VCVTGGSGFVASWLIMRLLQRGYSVRATVRTNSEGNKKDISYLTELPFASERLQIFTADL  99

Query  76   TVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVF  135
                SF  AI+GC+ VFHVA PMD  S + E  V K TV+G++ I++SC  A TVKR  +
Sbjct  100  NEPESFKPAIEGCKAVFHVAHPMDPNSNETEETVTKRTVQGLMGILKSCLDAKTVKRFFY  159

Query  136  TSSAGTLDVQEQQKLF---YDQTSWSDLDFIYAK--KMTGWMYFVSKILAEKSAMEETKK  190
            TSSA T+              D++ WSD++    +  K     Y VSK+ AE +A+E   K
Sbjct  160  TSSAVTVFYSGGNGGGGGEVDESVWSDVEVFRNQKEKRVSSSYVVSKMAAETAALEFGGK  219

Query  191  KNIDFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIF  250
              ++ ++++ PLVVGPFI+ + P S+  +L+++ GN     +      VH+DD+  A IF
Sbjct  220  NGLEVVTLVIPLVVGPFISSSLPSSVFISLAMLFGNYKEKYLFDTYNMVHIDDVARAMIF  279

Query  251  LYEHPKADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVSFSSKKLTDM  310
            L E P A GR+ICSS    I +V + +  K+P++ +P+      K    +  SSKKL
Sbjct  280  LLEKPVAKGRYICSSVEMKIDEVFEFLSTKFPQFQLPSIDLNKYKVEKRMGLSSKKLKSA  339

Query  311  GFQFKYTLEDMYKGAIETCRQKQLL  335
```

```
            GF+FKY  E+++ GAI +C+ +  L
Sbjct  340  GFEFKYGAEEIFSGAIRSCQARGFL  364
```

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RecName: Full=Tetraketide alpha-pyrone reductase 1; AltName: Full=Protein DIHYDROFLAVONOL 4-REDUCTASE-LIKE 1

Sequence ID: Q500U8.1 **Length:** 326 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 8 to 321 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
234 bits(596)	2e-73	Compositional matrix adjust.	120/320(38%)	194/320(60%)	8/320(2%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTV  77
            VCVTGA+GF+ SWLV RLL  GY V  TVRDP N+KK+ HL +L  A   L L KADL
Sbjct  8    VCVTGASGFLASWLVKRLLLEGYEVIGTVRDPGNEKKLAHLWKLEGAKERLRLVKADLME  67

Query  78   EGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTS  137
            EGSFD AI GCQGVFH A+P+   + +PE E+++P + G L+++ SC K  ++KR+V TS
Sbjct  68   EGSFDNAIMGCQGVFHTASPVLKPTSNPEEEILRPAIEGTLNVLRSCRKNPSLKRVVLTS  127

Query  138  SAGTLDVQE--QQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDF  195
            S+ T+ +++    K+  D++ W+ ++    K+   W Y +SK LAE++A + +++  ID
Sbjct  128  SSSTVRIRDDFDPKIPLDESIWTSVEL--CKRFQVW-YALSKTLAEQAAWKFSEENGIDL  184

Query  196  ISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEHP  255
            ++++P  +VGP + P    +    L L+ G    +    Q  YVH+DD+   HI ++EH
Sbjct  185  VTVLPSFLVGPSLPPDLCSTASDVLGLLKGETEKFQWHGQMGYVHIDDVARTHIVVFEHE  244

Query  256  KADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVSFSSKKLTDMGFQFK  315
             A GR+ICSS+   + ++   +  ++P   +P  F+ +++      F + K+  +G +FK
Sbjct  245  AAQGRYICSSNVISLEELVSFLSARYPSLPIPKRFEKLNR--LHYDFDTSKIQSLGLKFK  302

Query  316  YTLEDMYKGAIETCRQKQLL  335
             +LE+M+   I +  ++  L
Sbjct  303  -SLEEMFDDCIASLVEQGYL  321
```

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RecName: Full=Tetraketide alpha-pyrone reductase 2; AltName: Full=Protein CINNAMOYL-COA REDUCTASE-LIKE 6

Sequence ID: Q9CA28.1 **Length:** 321 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 6 to 321 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
196 bits(497)	1e-58	Compositional matrix adjust.	113/322(35%)	181/322(56%)	12/322(3%)

```
Query  20   VTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTVEG  79
            VTG  GFI S+++  LLE G+ V  TVR+P +++KV  L E   A   L + +ADLTVEG
Sbjct  6    VTGGTGFIASYIIKSLLELGHTVRTTVRNPRDEEKVGFLWEFQGAKQRLKILQADLTVEG  65

Query  80   SFDEAIQGCQGVFHVATPMDF-ESKDPENEVIKPTVRGMLSIIESCAKAN-TVKRLVFTS  137
            SFDEA+ G  GVFH A+P+   +  + +  ++ P ++G  +++ SCAK+  T+KR+V TS
Sbjct  66   SFDEAVNGVDGVFHTASPVLVPQDHNIQETLVDPIIKGTTNVMSSCAKSKATLKRIVLTS  125

Query  138  SAGTL----DVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNI  193
            S  ++    D  E   L  +++ WSD +  Y K+   W Y  +K L E+ A    ++K +
Sbjct  126  SCSSIRYRFDATEASPL--NESHWSDPE--YCKRFNLW-YGYAKTLGEREAWRIAEEKGL  180

Query  194  DFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYE  253
            D + + P  VVGP + P    +L+  L++  G    Y     G +VH+DD+  AH+   E
Sbjct  181  DLVVVNPSFVVGPLLGPKPTSTLLMILAIAKGLAGEYPNFTVG-FVHIDDVVAAHVLAME  239

Query  254  HPKADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVVSFSSKKLTDMGFQ  313
             PKA GR ICSS  A   ++ +++R K+P Y    +    + D    S  ++K+ ++GF
Sbjct  240  EPKASGRIICSSSVAHWSEIIELMRNKYPNYPFENKCSNKEGDNSPHSMDTRKIHELGFG  299

Query  314  FKYTLEDMYKGAIETCRQKQLL  335
               +L +M+   I + ++K LL
Sbjct  300  SFKSLPEMFDDCIISFQKKGLL  321
```

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RecName: Full=Cinnamoyl-CoA reductase 1; Short=OsCCR1

Sequence ID: Q6K9A2.1 **Length:** 338 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 18 to 328 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
192 bits(487)	6e-57	Compositional matrix adjust.	117/325(36%)	173/325(53%)	19/325(5%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTV  77
            VCVTGA GFIGSW+V  LL RGY+V  T RDP + K   HLLEL  AD  L+L +AD+
Sbjct  18   VCVTGAGGFIGSWVVKELLIRGYHVRGTARDPADSKNA-HLLELEGADERLSLCRADVLD  76

Query  78   EGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTS  137
              S   A  GC GVFHVA+P+   S DP  +++   V G  ++I + A    V+R+VFTS
Sbjct  77   AASLRAAFSGCHGVFHVASPV---SNDP--DLVPVAVEGTRNVINAAADMG-VRRVVFTS  130
```

```
Query  138  SAGTLDVQEQQK--LFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDF  195
            S G + +   +      D+T WSD +F    K T  +Y  +K++AE +A EE  K+ ++
Sbjct  131  SYGAVHMNPNRSPDAVLDETCWSDYEFC---KQTDNLYCCAKMMAEMTATEEAAKRGLEL  187

Query  196  ISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEHP  255
              ++P + +GP +  T   S       + G +  Y       YV + D+  AH+ +YE P
Sbjct  188  AVVVPSMTMGPMLQQTLNFSTNHVARYLMGTKKSY-PNAVAAYVDVRDVARAHVLVYERP  246

Query  256  KADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVV---SFSSKKLTDMGF  312
            +A GR++C        ++ +M+RE +P Y  P   K  D   P+     FS+++L D+G
Sbjct  247  EARGRYLCIGTVLHRAELLRMLRELFPRY--PATAKCEDDGKPMAKPYKFSNQRLKDLGL  304

Query  313  QFKYTLEDMYKGAIETCRQKQLLPF  337
            +F   L      A+   +QK  LP
Sbjct  305  EFT-PLRKSLNEAVLCMQQKGHLPL  328
```

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RecName: Full=Cinnamoyl-CoA reductase 1; Short=AtCCR1; AltName: Full=Protein IRREGULAR XYLEM 4

Sequence ID: Q9S9N9.1 **Length:** 344 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 12 to 310 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
189 bits(479)	1e-55	Compositional matrix adjust.	121/311(39%)	179/311(57%)	17/311(5%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            TVCVTGA G+I SW+V  LLERGY V  TVR+P++ K   HL EL      L L KADL
Sbjct  12   TVCVTGAGGYIASWIVKILLERGYTVKGTVRNPDDPKNT-HLRELEGGKERLILCKADLQ  70

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
               +   AI GC GVFH A+P+   + DPE ++++P V G   +I + A+A  VKR+V T
Sbjct  71   DYEALKAAIDGCDGVFHTASPV---TDDPE-QMVEPAVNGAKFVINAAAEAK-VKRVVIT  125

Query  137  SSAGT--LDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNID  194
            SS G   +D     +   D++ WSDLDF   K    W Y   K++AE++A E  K+K +D
Sbjct  126  SSIGAVYMDPNRDPEAVVDESCWSDLDF--CKNTKNW-YCYGKMVAEQAAWETAKEKGVD  182

Query  195  FISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEH  254
             + + P LV+GP + PT   SL   L  +TG+   Y  + Q  YV + D+  AH+ +YE
Sbjct  183  LVVLNPVLVLGPPLQPTINASLYHVLKYLTGSAKTYANLTQA-YVDVRDVALAHVLVYEA  241

Query  255  PKADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVV---SFSSKKLTDMG  311
            P A GR++ +       +V +++ + +PEY +PT+ K  D+  P      F+++K+ D+G
Sbjct  242  PSASGRYLLAESARHRGEVVEILAKLFPEYPLPTKCK--DEKNPRAKPYKFTNQKIKDLG  299

Query  312  FQFKYTLEDMY  322
             +F  T + +Y
Sbjct  300  LEFTSTKQSLY  310
```

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RecName: Full=Cinnamoyl-CoA reductase 2; Short=AtCCR2

Sequence ID: Q9SAH9.1 **Length:** 332 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 8 to 323 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
186 bits(471)	1e-54	Compositional matrix adjust.	126/329(38%)	184/329(55%)	18/329(5%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTV  77
            VCVTGA G+I SW+V  LLERGY V  TVR+P + K   HL EL  A   LTL  ADL
Sbjct  8    VCVTGAGGYIASWIVKLLLERGYTVRGTVRNPTDPKN-NHLRELQGAKERLTLHSADLLD  66

Query  78   EGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTS  137
              +    I GC GVFH A+PM   + DPE  +++P V G   +I++ AKA  VKR+VFTS
Sbjct  67   YEALCATIDGCDGVFHTASPM---TDDPET-MLEPAVNGAKFVIDAAAKAK-VKRVVFTS  121

Query  138  SAGT--LDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDF  195
            S G   ++     +   D+  WSDLDF   K    W Y   K+LAE+SA E  K K +D
Sbjct  122  SIGAVYMNPNRDTQAIVDENCWSDLDF--CKNTKNW-YCYGKMLAEQSAWETAKAKGVDL  178

Query  196  ISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEHP  255
            + + P LV+GP +      SL+  L  +TG+   Y  + Q  YV + D+   H+ +YE P
Sbjct  179  VVLNPVLVLGPPLQSAINASLVHILKYLTGSAKTYANLTQ-VYVDVRDVALGHVLVYEAP  237

Query  256  KADGRFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDKDLPVV---SFSSKKLTDMGF  312
             A GR+I +       +V +++ + +PEY +PT  K  D+  P      F+++K+ D+G
Sbjct  238  SASGRYILAETALHRGEVVEILAKFFPEYPLPT--KCSDEKNPRAKPYKFTTQKIKDLGL  295

Query  313  QFKYTLEDMYKGAIETCRQKQLLPFSTRS  341
            +FK   + +Y+ ++++ ++K  LP    S
Sbjct  296  EFKPIKQSLYE-SVKSLQEKGHLPLPQDS  323
```

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RecName: Full=Putative uncharacterized oxidoreductase C513.07

Sequence ID: Q9UT59.1 **Length:** 336 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 6 to 281 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
114 bits(284)	2e-27	Compositional matrix adjust.	83/282(29%)	140/282(49%)	23/282(8%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTV  77
            V VTG  GFIG+ +  +LL+ GY V  TVR  E   ++  L    K      + K D++
Sbjct  6    VLVTGVTGFIGAHVAEQLLQAGYRVRGTVRSMEKADELIRLNPGLKDKIEFVIVK-DVSA  64

Query  78   EGSFDEAIQGCQGVFHVATPMDFES-KDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
              +FD  ++  + + H+A+P   E+  D +++++ P V+G L I+E+      ++KR+V T
Sbjct  65   SNAFDGVLKDVELICHIASPFFVENVTDNKSQLLDPAVKGTLGILEAAQGVKSIKRIVIT  124

Query  137  SS---AGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWM--YFVSKILAEKSAMEETKKK  191
            SS    G   +       Y +  W+ + +  A      +  Y  SK LAE++A E  K+K
Sbjct  125  SSFAAVGNFQIDPHNNKVYTEKDWNPITYEEALTTDNGIVAYCASKKLAEEAAREYVKEK  184

Query  192  --NIDFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQ--------YVHL  241
              + D  +I PP V GP I P     +    SL T N+  + +I   +        YV +
Sbjct  185  KPSYDICTINPPYVYGPPIHP-----MKNMDSLNTSNQIFWKLIDGSKEATPFYYYYVDV  239

Query  242  DDLCEAHIFLYEHPK-ADGRFICSSHHAIIYDVAKMVREKWP  282
             D+  AH+F  E+ K ++GR + S       D+ K++R+++P
Sbjct  240  RDVAAAHVFALENAKLSNGRMLVSKGVFTTGDICKVLRKEFP  281
```

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RecName: Full=Ketoreductase azaE; AltName: Full=Azaphilone biosynthesis cluster protein azaE

Sequence ID: G3XMB9.1 **Length:** 338 **Number of Matches:** 1

Related Information

Range 1: 8 to 321 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
111 bits(277)	2e-26	Compositional matrix adjust.	96/323(30%)	148/323(45%)	34/323(10%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTV  77
            V +TG  GFI S ++  LL+ GY V  TVR  +  +++   L          +   D+
Sbjct  8    VLLTGGTGFIASHILTELLDAGYQVVVTVRTHDKGRQLLESLSNTGDKAASYVVVEDIAK  67

Query  78   EGSFDEAIQGCQG---VFHVATPMDFESKDPENEVIKPTVRGMLSIIESC-AKANTVKRL  133
            +G++DEAIQ       V H A+P  F   DP+ + + P ++G   ++ S  A A TVKR+
Sbjct  68   DGAYDEAIQSISDLDLVVHTASPYHFNYTDPKTDFLDPAIKGTAGLLASIKAYAPTVKRV  127

Query  134  VFTSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAME--ETKKK  191
            V TSS+ T+         YD+TS+  + +  A  +    Y  SKI AE++A +  E  K
Sbjct  128  VLTSSSATIVTPPNHPEVYDETSYGSVTWEEA-MVPQVTYRASKIFAERAAFDFIENDKP  186

Query  192  NIDFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCII-------KQG--------  236
            N D ++I PPLV GP       P  +T L  +  N +++ I        K G
Sbjct  187  NFDLVTINPPLVFGP------KPRHVTDLKAL--NTSNHIIRDTMLGKWKDGGAPIAIPF  238

Query  237  QYVHLDDLCEAHIFLYEHPKADG-RFICSSHHAIIYDVAKMVREKWPEYYVPTEFKGIDK  295
             +V + D+  AH    E P+  G RF   + H     +A+ +R   PE         +
Sbjct  239  TWVDVRDVAFAHRQALELPEVSGQRFFTVAGHFSNKRIAEAIRATHPELADRLPPSDVPD  298

Query  296  DLP--VVSF-SSKKLTDMGFQFK  315
            DLP  +  F +SK    +G  F+
Sbjct  299  DLPEGIYGFDNSKSRKVLGMTFR  321
```

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RecName: Full=Cinnamoyl-CoA reductase-like SNL6; AltName: Full=Protein SUPPRESSOR OF NH1-MEDIATED LESION 6

Sequence ID: Q0JKZ0.1 **Length:** 379 **Number of Matches:** 1

Related Information

Range 1: 61 to 314 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
93.6 bits(231)	6e-20	Compositional matrix adjust.	72/264(27%)	121/264(45%)	24/264(9%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWK--AD  74
            TVCVTG   F+G  +V RLL  GY V   +   E+  K++  +E+   D    +W   A+
Sbjct  61   TVCVTGGISFVGFAVVDRLLRHGYTVRLALETQEDLDKLRE-MEMFGEDGRDGVWTVMAN  119

Query  75   LTVEGSFDEAIQGCQGVFHVATPMDFESKDP-ENEVIKPTVRGMLSIIESCAKANTVKRL  133
            +T   S   A  GC GVFH +  +D          +     +    +IE+C +  +V++
Sbjct  120  VTDPESLHRAFDGCAGVFHTSAFVDPGGMSGYTKHMASLEAKAAEQVIEACVRTESVRKC  179

Query  134  VFTSSAGTLDVQE---QQKLF---YDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEE  187
            VFTSS      ++     + F    D+  WSD  F    K+  W + + K  AEK+A
Sbjct  180  VFTSSLLACVWRQNYPHDRRFPTIIDENCWSDESFCRDNKL--W-FALGKTAAEKTAWRA  236

Query  188  TKKKNIDFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQG--QYVHLDDLC  245
             + +++  +++ P LV GP        +   +++ + G  A   ++  G      ++ +
Sbjct  237  ARGRDLKLVTVCPALVTGPGFRRR---NSTASIAYLKGARA---MLADGLLATASVETVA  290

Query  246  EAHIFLYE---HPKADGRFICSSH  266
            EAH+ +YE      A GR+IC  H
Sbjct  291  EAHVRVYEAMGDNTAGGRYICYDH  314
```

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RecName: Full=Aldehyde reductase 2; AltName: Full=Aldehyde reductase II; Short=ARII

Sequence ID: Q9UUN9.3 **Length:** 343 **Number of Matches:** 1

Related Information

Range 1: 15 to 307 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
91.7 bits(226)	2e-19	Compositional matrix adjust.	76/295(26%)	132/295(44%)	17/295(5%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTV  77
            V VTGA GF+ S +V +LLE GY V  T R       ++   +        T    D+
Sbjct  15   VLVTGANGFVASHVVEQLLEHGYKVRGTARSASKLANLQKRWDAKYPGRFETAVVEDMLK  74

Query  78   EGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTS  137
            +G++DE I+G  GV H+A+ + F +K   +EV+ P + G L+ + + A   +VKR V TS
Sbjct  75   QGAYDEVIKGAAGVAHIASVVSFSNK--YDEVVTPAIGGTLNALRAAAATPSVKRFVLTS  132

Query  138  S--AGTLDVQEQQKLFYDQTSWSDLDFIYAKKM-------TGWMYFVSKILAEKSAME--  186
            S  +  +     + ++ D+ SW+      AK +       + W+Y  SK  AE +A +
Sbjct  133  STVSALIPKPNVEGIYLDEKSWNLESIDKAKTLPESDPQKSLWVYAASKTEAELAAWKFM  192

Query  187  ETKKKNIDFISIIPPLVVGPFITPTFPPSLITA--LSLITGNEAHYCIIKQGQ-YVHLDD  243
            +  K +    +++P   +G    P       +   +SL  G  +    +   Q YV   D
Sbjct  193  DENKPHFTLNAVLPNYTIGTIFDPETQSGSTSGWMMSLFNGEVSPALALMPPQYYVSAVD  252

Query  244  LCEAHIFLYEHPKADGRFICSSHHAIIYD-VAKMVREKWPEYYVPTEFKGIDKDL  297
            +   H+     P+ + R +  +     ++ V    R+ +P    P +F    +DL
Sbjct  253  IGLLHLGCLVLPQIERRRVYGTAGTFDWNTVLATFRKLYPSKTFPADFPDQGQDL  307
```

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RecName: Full=Putative uncharacterized oxidoreductase YDR541C

Sequence ID: Q03049.2 **Length:** 344 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 4 to 344 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
89.7 bits(221)	8e-19	Compositional matrix adjust.	91/348(26%)	169/348(48%)	36/348(10%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKA-DL  75
            TV V+GA+GFI   ++ +LL++ Y V  TVR  E + K   LL   + + NLTL    D+
Sbjct  4    TVLVSGASGFIALHILSQLLKQDYKVIGTVRSHEKEAK---LLRQFQHNPNLTLEIVPDI  60

Query  76   TVEGSFDEAIQG----CQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAK--ANT  129
            +   +FD+ +Q      + V H A+P  +++ + E +++ P + G  +I+ S  K  A+T
Sbjct  61   SHPNAFDKVLQKRGREIRYVLHTASPFHYDTTEYEKDLLIPALEGTKNILNSIKKYAADT  120

Query  130  VKRLVFTSSAG---TLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAME  186
            V+R+V TSS     TL   +   + + + SW++  +   +      YF SK  AEK+A E
Sbjct  121  VERVVVTSSCTAIITLAKMDDPSVVFTEESWNEATWESCQIDGINAYFASKKFAEKAAWE  180

Query  187  ETKKKNIDFI-----SIIPPLVVGP-FITPTFPPSLITALSLITGNEAHYCIIK-----Q  235
             T K+N D I     ++ P L+ GP          L T+  +I G   H  +
Sbjct  181  FT-KENEDHIKFKLTTVNPSLLFGPQLFDEDVHGHLNTSCEMING-LIHTPVNASVPDFH  238

Query  236  GQYVHLDDLCEAHIFLYEHPKADG-RFICSSHHAIIYDVAKMVREKWPEY--YVPTEFKG  292
              ++ + D+  AH++ ++     G R + ++      D+  ++ E +P+    +P   G
Sbjct  239  SIFIDVRDVALAHLYAFQKENTAGKRLVVTNGKFGNQDILDILNEDFPQLRGLIPLGKPG  298

Query  293  -----IDKDLPVVSFSSKKLTDMGFQFKYTLEDMYKGAIETCRQKQLL  335
                 ID+     + +++K+  +GF+F+   E ++  A +  +++  L
Sbjct  299  TGDQVIDRGSTTDNSATRKI--LGFEFRSLHESVHDTAAQILKKQNRL  344
```

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RecName: Full=Putative uncharacterized oxidoreductase YGL039W

Sequence ID: P53183.1 **Length:** 348 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 8 to 271 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
85.5 bits(210)	3e-17	Compositional matrix adjust.	78/268(29%)	131/268(48%)	26/268(9%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKA-DLT  76
            V V+GA GFI   +V  LL+ GY V  + R  E   K   LL+  K++ NL++    D+
Sbjct  8    VFVSGATGFIALHVVDDLLKTGYKVIGSGRSQE---KNDGLLKKFKSNPNLSMEIVEDIA  64

Query  77   VEGSFDEAIQG----CQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAK--ANTV  130
               +FD+  Q      + V H+A+P+ F + D E +++ P V G  SI+E+     A+TV
Sbjct  65   APNAFDKVFQKHGKEIKVVLHIASPVHFNTTDFEKDLLIPAVNGTKSILEAIKNYAADTV  124

Query  131  KRLVFTSSAGTL----DVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAME  186
            +++V TSS   L    D+++      ++ SW+   +   +      Y  SK  AEK+A +
Sbjct  125  EKVVITSSVAALASPGDMKDTS-FVVNEESWNKDTWESCQANAVSAYCGSKKFAEKTAWD  183

Query  187  --ETKKKNIDFI--SIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQ-----GQ  237
              E  + +I F   +I P  V GP +      + I + S I  N   Y +        G
Sbjct  184  FLEENQSSIKFTLSTINPGFVFGPQLFADSLRNGINSSSAIIANLVSYKLGDNFYNYSGP  243

Query  238  YVHLDDLCEAHIFLYEHPKADGR--FIC  263
            ++ + D+ +AH+  +E P+  G+  F+C
Sbjct  244  FIDVRDVSKAHLLAFEKPECAGQRLFLC  271
```

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RecName: Full=Putative NADPH-dependent methylglyoxal reductase GRP2; AltName: Full=Cytoplasmic antigenic protein 2

Sequence ID: P83775.2 **Length:** 341 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 6 to 289 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
84.7 bits(208)	4e-17	Compositional matrix adjust.	79/285(28%)	137/285(48%)	19/285(6%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWK--AD  74
            TV V+GA+GFI   LV +L+E+GY V  TVR  E    +K  L+  K  +    ++   D
Sbjct  6    TVFVSGASGFIAQTLVKQLIEKGYKVVGTVRSNEKGDSLKENLKAAKLQSENFTYEIVKD  65

Query  75   LTVEGSFDEAIQGCQGV---FHVATPMDFESKDPENEVIKPTVRGMLSIIESC-AKANTV  130
            + V+G+FD+A++    V    H A+P  F   D E E++ P V G  + +++       +
Sbjct  66   IAVKGAFDDALKKHPEVTVFLHTASPFHFNVTDIEKELLTPAVEGTNNALQAIKTHGPQI  125

Query  131  KRLVFTSS---AGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEE  187
            KR+V TSS    G         +   + SW+ + +  +       Y  SK  AEK+A +
Sbjct  126  KRVVVTSSYAAVGRFADLADPSIPATEESWNPITWEQSLSNPLAGYVGSKKFAEKAAWDF  185

Query  188  TKKKNIDF-ISIIPPL-VVGPFITPTFPPS-LITALSLITG-----NEAHYCIIKQGQYV  239
             +K+  +F +S+I P+ V GP        S L T+  +I G      ++ +  +  G ++
Sbjct  186  VEKEKPNFTLSVINPVYVFGPQAFEIKNKSQLNTSSEIINGLLNSKPDSKFDNL-TGYFI  244

Query  240  HLDDLCEAHIFLYEHPKADG-RFICSSHHAIIYDVAKMVREKWPE  283
             + D+ +AHI  +E     G R I +        +  ++R+ +P+
Sbjct  245  DVRDVAKAHIVAFEKDSIQGQRLILAESPFSTQSILDLIRKDFPQ  289
```

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RecName: Full=NADPH-dependent aldehyde reductase ARI1

Sequence ID: P53111.1 **Length:** 347 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 6 to 289 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
83.6 bits(205)	1e-16	Compositional matrix adjust.	81/294(28%)	132/294(44%)	37/294(12%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPE-NKKKVKHLLELPKADTNLTLWKADL  75
            TV V+GA GFI   ++  LL+ GY V  + R  E N   +K     PK    +     D+
Sbjct  6    TVFVSGATGFIALHIMNDLLKAGYTVIGSGRSQEKNDGLLKKFNNNPKLSMEIV---EDI  62

Query  76   TVEGSFDEAIQG----CQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAK--ANT  129
                +FDE  +      + V H A+P  FE+ + E +++ P V G  SI+E+  K  A+T
Sbjct  63   AAPNAFDEVFKKHGKEIKIVLHTASPFHFETTNFEKDLLTPAVNGTKSILEAIKKYAADT  122

Query  130  VKRLVFTSSAGTLDV---QEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAME  186
            V++++ TSS   L       +  L   + SW+   +   +      Y  SK  AEK+A E
Sbjct  123  VEKVIVTSSTAALVTPTDMNKGDLVITEESWNKDTWDSCQANAVAAYCGSKKFAEKTAWE  182

Query  187  ETK--KKNIDFI--SIIPPLVVGPFITPTFPPSLITAL------------SLITGNEAHY  230
              K  K ++ F   +I P  V GP     F  SL   +            S + G   +Y
Sbjct  183  FLKENKSSVKFTLSTINPGFVFGP---QMFADSLKHGINTSSGIVSELIHSKVGGEFYNY  239

Query  231  CIIKQGQYVHLDDLCEAHIFLYEHPKADG-RFICSSHHAIIYDVAKMVREKWPE  283
            C    G ++ + D+ +AH+   E P+  G R + S       ++  ++ E++P+
Sbjct  240  C----GPFIDVRDVSKAHLVAIEKPECTGQRLVLSEGLFCCQEIVDILNEEFPQ  289
```

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RecName: Full=Putative dihydroflavonol 4-reductase; Short=DFR; AltName: Full=Dihydrokaempferol 4-reductase

Sequence ID: P73212.1 **Length:** 343 **Number of Matches:** 1

Related Information

Range 1: 15 to 188 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
78.6 bits(192)	6e-15	Compositional matrix adjust.	61/194(31%)	98/194(50%)	22/194(11%)

```
Query  20   VTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHL-LELPKADTNLTLWKADLTVE  78
            VTG  GF+G+ LV  LLE+GY V A VR       +++L ++    D N          +
Sbjct  15   VTGGTGFVGANLVRHLLEQGYQVRALVRASSRPDNLQNLPIDWVVGDLN----------D  64

Query  79   GSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTSS  138
            G   + +QGCQG+FHVA       KD E  + +  V G  +I+ +CA+   ++R V+TSS
Sbjct  65   GDLHQQMQGCQGLFHVAAHYSLWQKDRE-ALYRSNVLGTRNIL-ACAQKAGIERTVYTSS  122

Query  139  AGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDFISI  198
               + V+   +   D++  S ++     K+ G  Y  SK  AE+ A+   ++   D + +
Sbjct  123  VAAIGVKGDGQRA-DESYQSPVE-----KLIG-AYKQSKYWAEQEALTAAQQGQ-DIVIV  174

Query  199  IPPLVVGPF-ITPT  211
             P   +GP+ I PT
Sbjct  175  NPSTPIGPWDIKPT  188
```

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RecName: Full=NADPH-dependent methylglyoxal reductase GRE2; AltName: Full=3-methylbutanal reductase; AltName:

Full=Genes de respuesta a estres protein 2; AltName: Full=Isovaleraldehyde reductase

Sequence ID: Q12068.1 **Length:** 342 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 2 to 284 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
74.3 bits(181)	1e-13	Compositional matrix adjust.	77/287(27%)	133/287(46%)	25/287(8%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKA-DL  75
            +V V+GA GFI   +V  LL+  Y V  + R  E   K ++L E    +   ++    D+
Sbjct  2    SVFVSGANGFIAQHIVDLLLKEDYKVIGSARSQE---KAENLTEAFGNNPKFSMEVVPDI  58

Query  76   TVEGSFDEAIQ----GCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAK--ANT  129
            +   +FD   Q      + V H A+P  F+  D E +++ P V G+  I+ S  K  A++
Sbjct  59   SKLDAFDHVFQKHGKDIKIVLHTASPFCFDITDSERDLLIPAVNGVKGILHSIKKYAADS  118

Query  130  VKRLVFTSS-AGTLDV--QEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAME  186
            V+R+V TSS A   D+  +  + L +++ SW+   +   +      Y  SK  AEK+A E
Sbjct  119  VERVVLTSSYAAVFDMAKENDKSLTFNEESWNPATWESCQSDPVNAYCGSKKFAEKAAWE  178

Query  187  --ETKKKNIDF--ISIIPPLVVGP-FITPTFPPSLITALSLITGNEAHYCIIKQ-----G  236
              E  + ++ F   ++ P  V GP          L T+  L+  +  H     +     G
Sbjct  179  FLEENRDSVKFELTAVNPVYVFGPQMFDKDVKKHLNTSCELVN-SLMHLSPEDKIPELFG  237

Query  237  QYVHLDDLCEAHIFLYEHPKADG-RFICSSHHAIIYDVAKMVREKWP  282
             Y+ + D+ +AH+  ++  +  G R I S     + DV  ++ E +P
Sbjct  238  GYIDVRDVAKAHLVAFQKRETIGQRLIVSEARFTMQDVLDILNEDFP  284
```

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RecName: Full=NAD-dependent epimerase/dehydratase terH; AltName: Full=Terrein biosynthesis cluster protein terH

Sequence ID: Q0D1P7.1 **Length:** 340 **Number of Matches:** 1

Related Information

Range 1: 9 to 210 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
72.4 bits(176)	7e-13	Compositional matrix adjust.	59/206(29%)	95/206(46%)	15/206(7%)

```
Query  11   PPVAVPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNL-T  69
            PP  +  V VTG  GFIGS++   LLE GY V  TVR  E    V   L       N
Sbjct  9    PPGGL--VLVTGVTGFIGSYIANGLLELGYRVRGTVRSSEKATWVTKALTKRNPSANFEA  66

Query  70   LWKADLTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANT  129
            +   D    G ++  ++   G+ HVA  + F   DP  +VI P+V  +  ++E+  K  +
Sbjct  67   VIVPDQNAPGVWEAVLKDVDGIAHVAGDVSF-GPDP-TKVITPSVEALRRLLEAAKKEPS  124

Query  130  VKRLVFTSS-AGTLDVQEQQKLFYDQTSWSDLDFIYAKK------MTGW-MYFVSKILAE  181
            VKR VFTSS     +    +++  ++ +W++     A +        GW +Y   K   E
Sbjct  125  VKRFVFTSSDQAASNRSTTREILINEDTWNEEAIEAAWRPPPYEAERGWDVYSALKAQVE  184

Query  182  KSAMEETKKKNIDFI--SIIPPLVVG  205
            K     ++++   F+  S++P   +G
Sbjct  185  KEMWRFSREEKPSFVVNSVLPTYTIG  210
```

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RecName: Full=Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating

Sequence ID: Q9R1J0.1 **Length:** 362 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 31 to 255 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
62.4 bits(150)	1e-09	Compositional matrix adjust.	65/258(25%)	110/258(42%)	43/258(16%)

```
Query  20   VTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTVEG  79
            V G +GF+G  +V +LLERGY V        N   +    + P+    +  +  DL  +
Sbjct  31   VIGGSGFLGQHMVEQLLERGYTV--------NVFDIHQGFDNPR----VQFFIGDLCNQQ  78

Query  80   SFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTSSA  139
                A++G   VFH A+P  + +   +    +    G  ++IE+C +A  V++L+ TSSA
Sbjct  79   DLYPALKGVSTVFHCASPPPYSNN--KELFYRVNFIGTKTVIETCREAG-VQKLILTSSA  135

Query  140  GT----LDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETK-KKNID  194
                  +D++   +           D  YA K   + Y  +KIL E++ ++    KKN
Sbjct  136  SVVFEGVDIKNGTE-----------DLPYAMKPIDY-YTETKILQERAVLDANDPKKNFL  183

Query  195  FISIIPPLVVGPFITPTFPPSLITA-----LSLITGNEAHYCIIKQGQYVHLDDLCEAHI  249
              +I P  + GP   P   P LI A     +  + GN  +        +  ++++   HI
Sbjct  184  TAAIRPHGIFGP-RDPQLVPILIDAARKGKMKFMIGNGENLV-----DFTFVENVVHGHI  237

Query  250  FLYEHPKADGRFICSSHH  267
               EH   D      + H
Sbjct  238  LAAEHLSQDAALGGKAFH  255
```

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RecName: Full=Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating

Sequence ID: Q5PPL3.1 **Length:** 362 **Number of Matches:** 1

Related Information

Range 1: 31 to 255 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
62.4 bits(150)	2e-09	Compositional matrix adjust.	67/259(26%)	110/259(42%)	45/259(17%)

Gene - associated gene details

```
Query  20   VTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTVEG  79
            V G +GF+G  +V +LL RGY V        N   V+   + P+    +  +  DL  +
Sbjct  31   VIGGSGFLGQHMVEQLLSRGYAV--------NVFDVRQGFDNPR----VQFFIGDLCNQQ  78

Query  80   SFDEAIQGCQGVFHVATPMDFESKDPENEVI-KPTVRGMLSIIESCAKANTVKRLVFTSS  138
                A++G   VFH A+P    S     E+  +    G  ++IE+C +A  V++L+ TSS
Sbjct  79   DLYPALKGVSTVFHCASP---PSNSNNKELFYRVNSTGTKTVIETCKEAG-VQKLILTSS  134

Query  139  AGT----LDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETK-KKNI  193
            A      +D++   +           D  YA K   + Y  +KIL E++ ++    KKN
Sbjct  135  ASVVFEGVDIKNGTE-----------DLPYAMKPIDY-YTETKILQERAVLDANDPKKNF  182

Query  194  DFISIIPPLVVGPFITPTFPPSLITA-----LSLITGNEAHYCIIKQGQYVHLDDLCEAH  248
               +I P  + GP   P   P LI A     +  + GN  +        +  ++++   H
Sbjct  183  LTAAIRPHGIFGP-RDPQLVPVLIDAARKGKMKFMIGNGKNLV-----DFTFVENVVHGH  236

Query  249  IFLYEHPKADGRFICSSHH  267
            I   EH   D      + H
Sbjct  237  ILAAEHLSRDAGLGGKAFH  255
```

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RecName: Full=Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating

Sequence ID: Q3ZBE9.1 **Length:** 356 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 25 to 240 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
60.1 bits(144)	8e-09	Compositional matrix adjust.	64/250(26%)	106/250(42%)	45/250(18%)

```
Query  20   VTGAAGFIGSWLVMRLLERGYNVHA-TVRDPENKKKVKHLLELPKADTNLTLWKADLTVE  78
            V G  GF+G  +V +LL RGY V+   +R   +  +V+  L              DL  +
Sbjct  25   VIGGCGFLGQHMVEQLLARGYAVNVFDIRQGFDNPRVQFFL-------------GDLCSQ  71

Query  79   GSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTSS  138
                 A++G   VFH A+P  F +   +    +    G  ++IE+C +A  V++L+ TSS
Sbjct  72   QDLYPALKGVSTVFHCASPPPFNNN--KELFYRVNYIGTKNVIETCKEAG-VQKLILTSS  128

Query  139  AGTL----DVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAM-EETKKKNI  193
            A  +    D++   +           D  YA K   + Y  +KIL E++ +     +KN
Sbjct  129  ASVIFEGVDIKNGTE-----------DLPYATKPIDY-YTETKILQERAVLGAHDPEKNF  176

Query  194  DFISIIPPLVVGPFITPTFPPSLITA-----LSLITGNEAHYCIIKQGQYVHLDDLCEAH  248
               +I P  + GP   P   P LI A     +  + GN  +        +  ++++   H
Sbjct  177  LTTAIRPHGIFGP-RDPQLVPILIEAAKKGKMKFMIGNGKNLV-----DFTFVENVVHGH  230

Query  249  IFLYEHPKAD  258
            I   EH   D
Sbjct  231  ILAAEHLSQD  240
```

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RecName: Full=Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating; AltName: Full=Protein H105e3

Sequence ID: Q15738.2 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 42 to 266 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
55.8 bits(133)	2e-07	Compositional matrix adjust.	63/258(24%)	107/258(41%)	43/258(16%)

```
Query  20   VTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTVEG  79
            V G +GF+G  +V +LL RGY V        N   ++   + P+    +  +  DL
Sbjct  42   VIGGSGFLGQHMVEQLLARGYAV--------NVFDIQQGFDNPQ----VRFFLGDLCSRQ  89

Query  80   SFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTSSA  139
                A++G   VFH A+P    S +  +    +    G  ++IE+C +A  V++L+ TSSA
Sbjct  90   DLYPALKGVNTVFHCASPP--PSSNNKELFYRVNYIGTKNVIETCKEAG-VQKLILTSSA  146

Query  140  GTL----DVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETK-KKNID  194
              +    D++   +           D  YA K   + Y  +KIL E++ +     +KN
Sbjct  147  SVIFEGVDIKNGTE-----------DLPYAMKPIDY-YTETKILQERAVLGANDPEKNFL  194

Query  195  FISIIPPLVVGPFITPTFPPSLITA-----LSLITGNEAHYCIIKQGQYVHLDDLCEAHI  249
              +I P  + GP   P   P LI A     +  + GN  +        +  ++++   HI
Sbjct  195  TTAIRPHGIFGPR-DPQLVPILIEAARNGKMKFVIGNGKNLV-----DFTFVENVVHGHI  248

Query  250  FLYEHPKADGRFICSSHH  267
               E    D      + H
Sbjct  249  LAAEQLSRDSTLGGKAFH  266
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 1; AltName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type I; Short=3-beta-HSD I; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone

reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: Q60555.3 **Length:** 373 **Number of Matches:** 1

Related Information

Range 1: 5 to 161 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
55.5 bits(132)	3e-07	Compositional matrix adjust.	45/166(27%)	79/166(47%)	23/166(13%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRD----PENKKKVKHLLELPKADTNLTLWK  72
            +  VTGA GF+G  ++  L++          D    PE +++   L    +  T +T+ +
Sbjct  5    SCLVTGAGGFLGQRIIRMLVQEKELQEVRALDKVFRPETREEFCKL----QTKTKVTVLE  60

Query  73   ADLTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKR  132
             D+        A QG   V H A  +D     P   +I   ++G L+++E+C +A +V
Sbjct  61   GDILDAQCLRRACQGISVVIHTAAAIDVFGAIPRQTIIDINLKGTLNLLEACVQA-SVPA  119

Query  133  LVFTSS---AG-------TLDVQEQQKLFYDQTSWSDLDFIYAKKM  168
             ++TSS   AG         L+  E+Q+    +++WSD  + Y+KKM
Sbjct  120  FIYTSSIDVAGPNSYKEIVLNGHEEQQ---HESTWSD-PYPYSKKM  161
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase; Short=3-beta-HSD; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: Q9N119.4 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 8 to 168 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
53.9 bits(128)	8e-07	Compositional matrix adjust.	47/169(28%)	75/169(44%)	10/169(5%)

```
Query  20   VTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTVEG  79
            VTG  GF+G  +V  LLE        V D   K +V+      ++   LT+ + D+  E
Sbjct  8    VTGGGGFLGQRIVHLLLEEKDLQEIRVLDKVFKPEVREEFSKLQSKIKLTMLEGDILDEQ  67

Query  80   SFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTSSA  139
                A QG   V H A+ +D  +      V+K  V+G   ++E+C +A +V   + TSS
Sbjct  68   CLKGACQGASVVIHTASIIDVVNAVGRETVMKVNVKGTQLLLEACVQA-SVPVFIHTSSI  126

Query  140  GTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWM--YFVSKILAEKSAME  186
                    +++  +      L+       T W   Y +SK LAEK+ +E
Sbjct  127  EVAGPNSYREVIQNACEEDRLE-------TAWSAPYPLSKKLAEKAVLE  168
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 2; AltName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type II; Short=3-beta-HSD II; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: Q64421.3 **Length:** 373 **Number of Matches:** 1

Related Information

Range 1: 5 to 167 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
53.1 bits(126)	1e-06	Compositional matrix adjust.	48/183(26%)	84/183(45%)	34/183(18%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRD----PENKKKVKHLLELPKADTNLTLWK  72
            +  VTGA GF+G  ++  L++        + D    PE +++   L    +  T +T+ +
Sbjct  5    SCLVTGAGGFLGQRIIHLLVQEKDLEEVRLLDKVFRPETREEFFKL----QTKTKVTVLE  60

Query  73   ADLTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKR  132
             D+        A QG   V H A  +D     P   +I   V+G L+++E+C +A +V
Sbjct  61   GDILDAQCLRRACQGISVVIHTAAAIDVWGIIPRQTIIDINVKGTLNLLEACVQA-SVPA  119

Query  133  LVFTSS---AG-------TLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEK  182
             ++TSS   AG         L+  E+Q+    +++WSD             Y  SK++AEK
Sbjct  120  FIYTSSIDVAGPNSYKEIVLNGHEEQQ---HESTWSD------------PYPYSKMMAEK  164

Query  183  SAM  185
            + +
Sbjct  165  AVL  167
```

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RecName: Full=Putative uncharacterized oxidoreductase C1773.04; Flags: Precursor

Sequence ID: O94563.1 **Length:** 336 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 284 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
52.8 bits(125)	2e-06	Compositional matrix adjust.	72/295(24%)	117/295(39%)	43/295(14%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGYNVHATVR-----------DPENKKKVKHLLELPKADT  66
            V +TG  GF+ S     LL +GY V  T R            PE +KKV+  +++P
Sbjct  5    VLITGITGFVASHSAEALLSQGYRVRGTYRFQEKLDGLLKNRPEWEKKVE-FVQVP----  59
```

```
Query  67   NLTLWKADLTVEGSFDEAIQGCQGVFHVATP----MDFESKDPENEVIKPTVRGMLSIIE  122
                   D     ++ EA +G   V H AT     ++   KDP +E++   ++G  + +
Sbjct  60   -------DCRAPNAYVEAAKGVDYVIHAATEVHSNLEPPRKDP-HELLHIAIQGCENALI  111

Query  123  SCAKANTVKRLVFTSSAGTLDVQEQQKLFYD-----QTSWSDLDFIYAKKMTGWM--YFV  175
            + A+   VKR V+ SS   L  +     F D     +  W+      A++    +  Y V
Sbjct  112  AAAQEPKVKRFVYISSEAAL--KGPVNYFGDGHVFTEKDWNPKTLREAEESDDELLNYTV  169

Query  176  SKILAEKSAMEETKKKNIDF--ISIIPPLVVGPFI----TPTFPPSLITALSLITGNEAH  229
             K L E++      +    F  I++ PPL++GP            S      LI G
Sbjct  170  CKKLGERAMHAFVARNTPRFQAIALNPPLILGPVFHLQSVDNLNFSTWFFWQLIKGRYEV  229

Query  230  YCIIKQGQYVHLDDLCEAHIFLYEHPKADGRFICSSHHAIIYDVAKMVREKWPEY  284
                K   YV + DL EA +          RF+ S       D+  +  + +P++
Sbjct  230  APESKFFNYVDVRDLAEAQVKALTAKTDKDRFVISGGAFKNDDIVNVALKYFPQF  284
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 1; AltName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type I; Short=3-beta-HSD I; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: P24815.3 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 8 to 161 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
52.8 bits(125)	2e-06	Compositional matrix adjust.	40/160(25%)	72/160(45%)	17/160(10%)

```
Query  20   VTGAAGFIGSWLVMRLLERGYNVHATVRD----PENKKKVKHLLELPKADTNLTLWKADL  75
            VTGA GF+G  ++  L++          D    PE K++   L    +  T +T+ + D+
Sbjct  8    VTGAGGFVGQRIIKMLVQEKELQEVRALDKVFRPETKEEFSKL----QTKTKVTVLEGDI  63

Query  76   TVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVF  135
                    A QG   V H A  +D     P   ++   ++G  +++E+C +A +V   +F
Sbjct  64   LDAQCLRRACQGISVVIHTAAVIDVTGVIPRQTILDVNLKGTQNLLEACVQA-SVPAFIF  122

Query  136  TSSAGTLDVQEQQKLFYD-------QTSWSDLDFIYAKKM  168
             SS         +K+  +       +++WSD  + Y+KKM
Sbjct  123  CSSVDVAGPNSYKKIVLNGHEEQNHESTWSD-PYPYSKKM  161
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase type 7; AltName: Full=3 beta-hydroxysteroid dehydrogenase type VII; Short=3-beta-HSD VII; AltName: Full=3-beta-hydroxy-Delta(5)-C27 steroid oxidoreductase; Short=C(27) 3-beta-HSD; AltName: Full=Cholest-5-ene-3-beta,7-alpha-diol 3-beta-dehydrogenase; AltName: Full=Confluent 3Y1 cell-associated 2

Sequence ID: O35048.1 **Length:** 338 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 2 to 181 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
52.4 bits(124)	2e-06	Compositional matrix adjust.	51/196(26%)	80/196(40%)	24/196(12%)

```
Query  8    APSPPVAVPTVCVTGAAGFIGSWLVMRLLE--------RGYNVHATVRDPENKKKVKHLL  59
            A S  V      VTG  GF+G  +V  LLE        R +++H +            L
Sbjct  2    ADSAQVPALVYLVTGGCGFLGEHIVRMLLEWEPRLRELRVFDLHLS----------SWLE  51

Query  60   ELPKADTNLTLWKADLTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLS  119
            EL      +T  + D+T       A+ G   V H A  +D   K     + K  V+G  +
Sbjct  52   ELKTGPVQVTAIQGDVTQAHEVAAAMAGSHVVIHTAGLVDVFGKASPETIHKVNVQGTQN  111

Query  120  IIESCAKANTVKRLVFTSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKIL  179
            +I++C +  T + LV+TSS   +    +   FY     +  + I+        Y  SK L
Sbjct  112  VIDACVQTGT-RLLVYTSSMEVVGPNVKGHPFYRGNEDTPYEAIHRHP-----YPCSKAL  165

Query  180  AEKSAMEETKKKNIDF  195
            AE+  +E   +K + F
Sbjct  166  AEQLVLEANGRKGLRF  181
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase; Short=3-beta-HSD; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: P14893.2 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 8 to 161 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
52.0 bits(123)	3e-06	Compositional matrix adjust.	40/156(26%)	75/156(48%)	9/156(5%)

```
Query  20   VTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTVEG  79
            VTG  GF+G  ++  L+E        V D   + +V+      ++   LTL + D+  E
Sbjct  8    VTGGGGFLGQRIICLLVEEKDLQEIRVLDKVFRPEVREEFSKLQSKIKLTLLEGDILDEQ  67
```

```
Query  80   SFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTSS-  138
                A QG   V H A+ +D  +  P   ++   V+G   ++E+C +A +V   + TS+
Sbjct  68   CLKGACQGTSVVIHTASVIDVRNAVPRETIMNVNVKGTQLLLEACVQA-SVPVFIHTSTI  126

Query  139  --AGTLD----VQEQQKLFYDQTSWSDLDFIYAKKM  168
              AG       +Q+ ++  + +++WS   + Y+KK+
Sbjct  127  EVAGPNSYREIIQDGREEEHHESAWSS-PYPYSKKL  161
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase type 7; AltName: Full=3 beta-hydroxysteroid dehydrogenase type VII; Short=3-beta-HSD VII; AltName: Full=3-beta-hydroxy-Delta(5)-C27 steroid oxidoreductase; Short=C(27) 3-beta-HSD; AltName: Full=Cholest-5-ene-3-beta,7-alpha-diol 3-beta-dehydrogenase

Sequence ID: Q9EQC1.1 **Length:** 369 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 7 to 177 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
51.2 bits(121)	6e-06	Compositional matrix adjust.	49/181(27%)	79/181(43%)	14/181(7%)

```
Query  15   VPTVC--VTGAAGFIGSWLVMRLLERGYNVHATVRDPE--NKKKVKHLLELPKADTNLTL  70
            VPT+   VTG  GF+G  +V  LLER       +R+    +      L EL      +T
Sbjct  7    VPTLVYLVTGGCGFLGEHIVRMLLER----EPRLRELRVFDLHLSSWLEELKAGPVQVTA  62

Query  71   WKADLTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTV  130
             + D+T       A+ G   V H A  +D   K     + K  V+G  ++I++C +  T
Sbjct  63   IQGDVTQAHEVAAAMSGSHVVIHTAGLVDVFGKASPKTIHKVNVQGTQNVIDACVQTGT-  121

Query  131  KRLVFTSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKK  190
            + LV+TSS   +    +   FY      +  + +++       Y  SK LAE+  +E   +
Sbjct  122  QYLVYTSSMEVVGPNIKGHPFYRGNEDTPYEAVHSHP-----YPCSKALAEQLVLEANGR  176

Query  191  K  191
            K
Sbjct  177  K  177
```

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RecName: Full=Short-chain dehydrogenase/reductase family 42E member 1

Sequence ID: Q0IH73.1 **Length:** 386 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 7 to 253 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
51.2 bits(121)	6e-06	Compositional matrix adjust.	69/274(25%)	115/274(41%)	42/274(15%)

```
Query  14   AVPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKA  73
            A  TV +TG  G+ G  L   L E+G  VH  + D     +     ELP+    +   +
Sbjct  7    AKETVVITGGGGYFGHRLGCTLHEKG--VHVILFDIRKPDQ-----ELPEG---IHFVQG  56

Query  74   DLTVEGSFDEAIQGCQGVFHVAT-PMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKR  132
            D+      ++ + G   VFH A+  M  + +    ++    VRG  +II+C   N V R
Sbjct  57   DVRSLSQLEDVVAGASCVFHTASYGMSGKEQLHRQKIEAINVRGTENIIQACINTN-VPR  115

Query  133  LVFTSS------AGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAME  186
            LV+TS+        T+   ++   +  Q ++ D    Y++  T    FV K+
Sbjct  116  LVYTSTFNVIFGGQTIRDGDESLPYLPQDAFVD---NYSRTKTVAEMFVLKM------NN  166

Query  187  ETKKKNIDFI---SIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQG-----QY  238
            +  K N  F+   S+    + GP       P +I+AL      E    +   G     Q+
Sbjct  167  QELKNNSGFLRTCSLRAAGIYGP-GEQRHLPRIISAL------EKGMFLFVYGDNPLVQF  219

Query  239  VHLDDLCEAHIFLYEHPKADGRFICSSHHAIIYD  272
            VH+D+L  AHI   E   ++ ++I +     I D
Sbjct  220  VHVDNLISAHILAAEALTSEKKYIAAGQPYFISD  253
```

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RecName: Full=ADP-L-glycero-D-manno-heptose-6-epimerase; AltName: Full=ADP-L-glycero-beta-D-manno-heptose-6-epimerase; Short=ADP-glyceromanno-heptose 6-epimerase; Short=ADP-hep 6-epimerase; Short=AGME

Sequence ID: Q12CM2.1 **Length:** 335 **Number of Matches:** 1

Related Information

Range 1: 3 to 171 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
50.1 bits(118)	1e-05	Compositional matrix adjust.	51/176(29%)	76/176(43%)	26/176(14%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTV  77
            + VTGAAGFIGS LV  L +RG +    V D  +  K ++L +L  AD        DL
Sbjct  3    IVVTGAAGFIGSNLVKGLNDRGIDDIIAVDDLTHGDKFRNLADLQIADYIDADDFYDLFA  62

Query  78   EGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTS  137
            EG+F +     + VFH     D    D +  ++         +  +C +  T  RL++ S
Sbjct  63   EGAFGQ----VEAVFHEGACSDTMELDGK-YMMDNNYTLSCELFHACQEQGT--RLLYAS  115

Query  138  SAGT----------------LDVQEQQKLFYDQTSWSDLDFIY---AKKMTGWMYF  174
            SA T                L+V    KL +DQ    +L   +   A ++ G+ YF
Sbjct  116  SAATYGGSDTFSESPEFERPLNVYGYSKLLFDQRMRRELGARFENAATQVAGFRYF  171
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 6; AltName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type VI; Short=3-beta-HSD VI; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: O35469.4 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 161 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
50.1 bits(118)	1e-05	Compositional matrix adjust.	42/165(25%)	77/165(46%)	21/165(12%)

```
Query  17    TVCVTGAAGFIGSWLVMRLLERGYNVHATVRD----PENKKKVKHLLELPKADTNL--TL  70
             +  VTGA GF+G  +V  L++        V D    PE +++  +L      DTN+  T+
Sbjct  5     SCLVTGAGGFLGQRIVQLLMQEKDLEEIRVLDKFFRPETREQFFNL------DTNIKVTV  58

Query  71    WKADLTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTV  130
              + D+       +A QG   V H A  +D     P   ++   ++G  +++E+C +A +V
Sbjct  59    LEGDILDTQYLRKACQGISVVIHTAAVIDVTGVIPRQTILDVNLKGTQNLLEACIQA-SV  117

Query  131   KRLVFTSSAGTLDVQEQQKLFYD-------QTSWSDLDFIYAKKM  168
                +F+SS         +++  +       ++ WSD  + Y+KKM
Sbjct  118   PAFIFSSSVDVAGPNSYKEIILNGNEEEHHESIWSD-PYPYSKKM  161
```

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RecName: Full=ADP-L-glycero-D-manno-heptose-6-epimerase; AltName: Full=ADP-L-glycero-beta-D-manno-heptose-6-epimerase; Short=ADP-glyceromanno-heptose 6-epimerase; Short=ADP-hep 6-epimerase; Short=AGME

Sequence ID: A1VR25.1 **Length:** 335 **Number of Matches:** 1

Related Information

Range 1: 3 to 171 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
50.1 bits(118)	1e-05	Compositional matrix adjust.	51/177(29%)	74/177(41%)	28/177(15%)

```
Query  18    VCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTV  77
             + VTGAAGFIGS LV  L  RG +    V D     K ++L +L  AD        D
Sbjct  3     IVVTGAAGFIGSNLVKGLNARGIDDIIAVDDLTQGDKFRNLADLRIADYMDAGDFYDRFA  62

Query  78    EGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGM-LSIIESCAKANTVKRLVFT  136
             EG+F       + VFH     D  + +P+ + +      +  ++  +C   NT  RL++
Sbjct  63    EGAFGH----VEAVFHEGACSD--TMEPDGKYMMANNYTLSCNLFRACQNQNT--RLLYA  114

Query  137   SSAGT----------------LDVQEQQKLFYDQTSWSDLDFIYAKKMT---GWMYF  174
             SSA T                L+V    KL +DQ    +L   +    T   G+ YF
Sbjct  115   SSAATYGGSDTFSESPEFEKPLNVYGYSKLLFDQHMRRELGMRFENAQTQVAGFRYF  171
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 2; AltName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type II; Short=3-beta-HSD II; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: P26149.4 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 8 to 161 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
50.1 bits(118)	1e-05	Compositional matrix adjust.	39/160(24%)	74/160(46%)	17/160(10%)

```
Query  20    VTGAAGFIGSWLVMRLLERG----YNVHATVRDPENKKKVKHLLELPKADTNLTLWKADL  75
             VTGA GF+G  ++  L++        V   V  PE +K+  +L    +    +T+ + D+
Sbjct  8     VTGAGGFLGQRIIQLLVQEEDLEEIRVLDKVFRPETRKEFFNL----ETSIKVTVLEGDI  63

Query  76    TVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVF  135
                     A QG   V H A  +D     P   ++   ++G  +++E+C +A +V   +F
Sbjct  64    LDTQYLRRACQGISVVIHTAAIIDVTGVIPRQTILDVNLKGTQNLLEACIQA-SVPAFIF  122

Query  136   TSSAGTLDVQEQQKLFYD-------QTSWSDLDFIYAKKM  168
             +SS         +++  +       +++WSD  + Y+KKM
Sbjct  123   SSSVDVAGPNSYKEIVLNGHEEECHESTWSD-PYPYSKKM  161
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase; Short=3-beta-HSD; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: O46516.3 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 234 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
50.1 bits(118)	2e-05	Compositional matrix adjust.	53/239(22%)	98/239(41%)	15/239(6%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            +  VTGA GF+G  +V  L+E          D   + +++      ++   LT+ + D+
Sbjct  5    SCLVTGAGGFLGQRIVRLLVEEKEVQEIRALDKVFRPELREEFSKLQSKVKLTVLEGDIL  64

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
             E     A QG   V H A+ +D  +       +   V G   ++E+C++A +V   ++T
Sbjct  65   DEQFLKRACQGASAVIHTASIIDVTNLFNPQVTMNVNVEGTQLLLEACSQA-SVPIFIYT  123

Query  137  SSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWM--YFVSKILAEKSAMEET----KK  190
            SS         +++  +    + L+       T W   Y  SK LAEK+ +       K
Sbjct  124  SSVAVAGPNSYREIIQNGHEEAHLE-------TKWSSPYPYSKKLAEKAVLAANGLPLKN  176

Query  191  KNIDFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAHI  249
                +   + P+ +    +PT    +   L+   G   H C   +   V++ ++  AHI
Sbjct  177  GGTLYTCALRPMFIYGEGSPTLYYLMHEGLN-NNGILTHNCKFSRANPVYVGNIAWAHI  234
```

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RecName: Full=UDP-glucose 4-epimerase; AltName: Full=Galactowaldenase; AltName: Full=UDP-galactose 4-epimerase

Sequence ID: Q56623.1 **Length:** 328 **Number of Matches:** 1

Related Information

Range 1: 11 to 253 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
49.7 bits(117)	2e-05	Compositional matrix adjust.	69/274(25%)	117/274(42%)	42/274(15%)

```
Query  17   TVCVTGAAGFIGSWLVMRL-LERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADL  75
            ++ +TG+ GF+G+ LV  L L+  Y V + VR   NK            D  L     D+
Sbjct  11   SILLTGSTGFVGTNLVKSLTLKSDYIVKSAVRHAVNK------------DDGLLFEVGDI  58

Query  76   TVEGSFDEAIQGCQGVFHVATP---MDFESKDPENEVIKPTVRGMLSIIESCAKANTVKR  132
                 F+  ++    V H A     MD +  +P     +    G +++ +    +  VKR
Sbjct  59   NASTDFELPLKNTTVVVHCAARAHVMDDKEAEPLTLYREVNTAGTVNLAKQAIDSG-VKR  117

Query  133  LVFTSSAGTLDVQEQQKL----FYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEET  188
             +F SS    + V  +  L    F  + + +  D           Y +SK  AEK  +
Sbjct  118  FIFISS---IKVNGEGTLVGCPFKTEDNHAPED----------DYGLSKSEAEKQLVALA  164

Query  189  KKKNIDFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQ--YVHLDDLCE  246
            K  +++ + I P +V GP +   F  SL+  +S   G    +  I Q +   V +++L +
Sbjct  165  KDSSMEVVIIRPTIVYGPGVKANF-ASLMRLVS--KGIPLPFGSITQNKRSLVSINNLVD  221

Query  247  AHIFLYEHPKADGR-FICSSHHAIIYDVAKMVRE  279
              +   +HPKA  + F+ S  H +    A+MVRE
Sbjct  222  LIVTCIDHPKAANQVFLVSDGHDV--STAEMVRE  253
```

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RecName: Full=Uncharacterized protein C2A9.02

Sequence ID: Q9Y7K4.1 **Length:** 295 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 3 to 77 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
49.3 bits(116)	2e-05	Compositional matrix adjust.	32/83(39%)	41/83(49%)	8/83(9%)

```
Query  18  VCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTV  77
           + VTGAAGFIGS +V +LLE G+ V   VR  EN  K++     P      TL   D
Sbjct  3   IFVTGAAGFIGSEIVRQLLEAGHEVVGLVRSEENAAKLRAAGGTPYIG---TLEDLD---  56

Query  78  EGSFDEAIQGCQGVFHVATPMDF  100
             +  + +  C GV H A   DF
Sbjct  57  --TLKKGVAQCDGVIHTAFVHDF  77
```

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RecName: Full=Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating

Sequence ID: Q54L85.1 **Length:** 328 **Number of Matches:** 1

Related Information

Range 1: 1 to 121 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
49.3 bits(116)	2e-05	Compositional matrix adjust.	34/130(26%)	58/130(44%)	11/130(8%)

```
Query  15   VPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKAD  74
            +  V +TG +GF+G +++  L+  GY V A  R   + K +  +   P          +
Sbjct  1    MKNVFLTGGSGFLGKYIIEELISNGYKVFALSRSETSNKVLSQMGATPVM--------SS  52

Query  75   LTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANT--VKR  132
            L  E    EAI+GC  V H A  ++  S+  + E+ K  +     +   C +++T  V
Sbjct  53   LHDEQGLTEAIKGCDIVIHCAAKLETNSESVQ-ELYKDNIDATELLFNICNQSSTSSVSV  111

Query  133  LVFTSSAGTL  142
              F SS G +
Sbjct  112  FCFISSEGVI  121
```

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RecName: Full=UDP-D-apiose/UDP-D-xylose synthase 1

Sequence ID: Q9ZUY6.1 **Length:** 389 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 14 to 335 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
49.3 bits(116)	3e-05	Compositional matrix adjust.	73/335(22%)	128/335(38%)	47/335(14%)

```
Query  12   PVAVPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKAD--TNLT  69
            P+   T+C+ GA GFIGS L  +LL      H  +       K+KHLLE    +    +
Sbjct  14   PIQPLTICMIGAGGFIGSHLCEKLLTE--TPHKVLALDVYNDKIKHLLEPDTVEWSGRIQ  71

Query  70   LWKADLTVEGSFDEAIQGCQGVFHVA---TPMDFESKDPENEVIKPTVRGMLSIIESCAK  126
              + ++  +   +  ++    + ++A   TP D+ ++    + I       L +++ C++
Sbjct  72   FHRINIKHDSRLEGLVKMADLIINLAAICTPADYNTR--PLDTIYSNFIDALPVVKYCSE  129

Query  127  ANTVKRLVFTSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTG-----------WMYFV  175
             N  KRL+  S+           L  D     D  F   K+              W Y
Sbjct  130  NN--KRLIHFSTCEVYGKTIGSFLPKDHPLRDDPAFYVLKEDISPCIFGSIEKQRWSYAC  187

Query  176  SKILAEKSAMEETKKKNIDFISIIPPLVVGP---FITPTFPPS---------------LI  217
            +K L E+    E  +  ++F  + P   +GP   FI     PS
Sbjct  188  AKQLIERLVYAEGAENGLEFTIVRPFNWIGPRMDFIPGIDGPSEGVPRVLACFSNNLLRR  247

Query  218  TALSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEHPKADGRFICSSHHAIIYDVAKMV  277
              L L+ G E+      Q  +V+++D  EA + + E+P+     I +  +       + +
Sbjct  248  EPLKLVDGGES------QRTFVYINDAIEAVLLMIENPERANGHIFNVGNPNNEVTVRQL  301

Query  278  REKWPEYYVPTEFKGIDKDLPVVSFSSKKLTDMGF  312
             E   E Y     +G  +  P V  SSK+    G+
Sbjct  302  AEMMTEVYAKVSGEGAIES-PTVDVSSKEFYGEGY  335
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase type 5; AltName: Full=3 beta-hydroxysteroid dehydrogenase type V; Short=3-beta-HSD V; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=NADPH-dependent 3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=Progesterone reductase

Sequence ID: P27364.3 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 161 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
48.9 bits(115)	3e-05	Compositional matrix adjust.	41/164(25%)	76/164(46%)	19/164(11%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTN--LTLWKAD  74
            +  VTGA GF+G  +V  L++        VR        KH  EL K  T   +T+ + D
Sbjct  5    SCLVTGAGGFLGQRIVQMLVQE--KELQEVRVLYRTFSPKHKEELSKLQTKAKVTVLRGD  62

Query  75   LTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLV  134
            +        A QG   + H A  +D     P   ++   V+G   ++++C +A +V   +
Sbjct  63   IVDAQFLRRACQGMSVIIHTAAALDIAGFLPRQTILDVNVKGTQLLLDACVEA-SVPAFI  121

Query  135  FTSSAGT----------LDVQEQQKLFYDQTSWSDLDFIYAKKM  168
            ++SS G           L+ +E++   + +++WS+  + Y+K+M
Sbjct  122  YSSSTGVAGPNSYKETILNDREEE---HRESTWSN-PYPYSKRM  161
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 1; AltName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type I; Short=3-beta-HSD I; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: P22071.3 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 8 to 161 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
48.9 bits(115)	3e-05	Compositional matrix adjust.	37/160(23%)	71/160(44%)	17/160(10%)

```
Query  20   VTGAAGFIGSWLVMRLLERGYNVHATVRD----PENKKKVKHLLELPKADTNLTLWKADL  75
            VTGA GF+G  ++  L++          D    PE K++   L    +    +T+ + D+
Sbjct  8    VTGAGGFVGQRIIRMLVQEKELQEVRALDKVFRPETKEEFSKL----QTKAKVTMLEGDI  63

Query  76   TVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVF  135
                    A QG   V H A  +D     P   ++   ++G  +I+E+C +A +V   ++
Sbjct  64   LDAQYLRRACQGISVVIHTAAVIDVSHVLPRQTILDVNLKGTQNILEACVEA-SVPAFIY  122

Query  136  TSSAGTLDVQEQQKLFYD-------QTSWSDLDFIYAKKM  168
             S+         +K+  +       +++WSD  + Y+K+M
Sbjct  123  CSTVDVAGPNSYKKIILNGHEEEHHESTWSD-AYPYSKRM  161
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 4; AltName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type IV; Short=3-beta-HSD IV; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: Q62878.4 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 8 to 161 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
48.5 bits(114)	4e-05	Compositional matrix adjust.	37/160(23%)	74/160(46%)	17/160(10%)

```
Query  20   VTGAAGFIGSWLVMRLLE----RGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADL  75
            VTGA GF+G  +V  L++    +   V   V  PE +++  +L         +T+ + D+
Sbjct  8    VTGAGGFLGQRIVQLLVQEKDLKEVRVLDKVFRPETREEFFNL----GTSIKVTVLEGDI  63

Query  76   TVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVF  135
                    A QG   V H A  +D    +P   ++   ++G  +++E+C +A +V   ++
Sbjct  64   LDTQCLRRACQGISVVIHTAALIDVTGVNPRQTILDVNLKGTQNLLEACVQA-SVPAFIY  122

Query  136  TSSAGTLDVQEQQKLFYD-------QTSWSDLDFIYAKKM  168
             S+         +K+  +       +++WS+  + Y+KKM
Sbjct  123  CSTVDVAGPNSYKKIILNGHEEEHHESTWSN-PYPYSKKM  161
```

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RecName: Full=ADP-L-glycero-D-manno-heptose-6-epimerase; AltName: Full=ADP-L-glycero-beta-D-manno-heptose-6-epimerase; Short=ADP-glyceromanno-heptose 6-epimerase; Short=ADP-hep 6-epimerase; Short=AGME

Sequence ID: Q46Y59.1 **Length:** 331 **Number of Matches:** 1

Related Information

Range 1: 2 to 255 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
48.5 bits(114)	4e-05	Compositional matrix adjust.	70/279(25%)	110/279(39%)	43/279(15%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            T+ VTGAAGFIGS LV  L  RG N    V +     K  +L++    D    L K D
Sbjct  2    TIIVTGAAGFIGSNLVKGLNARGENHIVAVDNLHRADKFHNLVDCEIRD---YLDKDDFL  58

Query  77   VEGSFDEAIQG-CQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVF  135
                F+    G  + VFH+    D   +D    +++   R   +++E C   +T  + ++
Sbjct  59   --SRFERGEFGRVRAVFHLGACTDTMEQDGRY-LMENNYRYSKTLMELCLAQDT--QFIY  113

Query  136  TSSAGT----------------LDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKIL  179
             SSA                  L V    K  +DQ   + LD   + ++ G  YF   +
Sbjct  114  ASSAAVYGESHSFREAREYERPLSVYGYSKFLFDQAVRNRLDGALS-QVVGLRYF--NVY  170

Query  180  AEKSAMEETKKKNIDFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYV  239
                A +          + +  +V   F    F       L    G     C  +   +V
Sbjct  171  GPGEAHK----------ARMASIVCQQF--EQFRAEGTVKLFGEHGGHGPGC--QSHDFV  216

Query  240  HLDDLCEAHIFLYEHPKADGRFICSSHHAIIY-DVAKMV  277
             +DD+ + ++F  +HP+  G F   S HA  + DVA +V
Sbjct  217  SIDDVVKVNLFFLDHPRRSGIFNVGSGHARSFNDVACVV  255
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase type 3; AltName: Full=3 beta-hydroxysteroid dehydrogenase type III; Short=3-beta-HSD III; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=NADP-dependent 3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=Progesterone reductase

Sequence ID: O35296.3 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 161 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
48.1 bits(113)	6e-05	Compositional matrix adjust.	43/161(27%)	72/161(44%)	13/161(8%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPK--ADTNLTLWKAD  74
            +  VTGA GF+G   ++R+L +   +   VR        KH  EL K    T +T+ + D
Sbjct  5    SCLVTGAGGFLGQ-RIIRMLAQEKELQE-VRTLFRSFTPKHREELSKLQTKTKVTVLEGD  62

Query  75   LTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLV  134
            +        A QG   V H A  +D     P   VI   ++G   ++++C  A  V   +
Sbjct  63   ILDAQCLRRACQGISVVIHTAAAIDVFGAIPRQTVIDINLKGTQHLLDACIGAR-VPVFI  121

Query  135  FTSSAGT-------LDVQEQQKLFYDQTSWSDLDFIYAKKM  168
            ++SS          + +Q   +    +++WSD  + Y+KKM
Sbjct  122  YSSSVAVAGPNSYKVIIQNGSEEENHESTWSD-PYAYSKKM  161
```

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RecName: Full=Putative sugar dehydratase/epimerase YfnG

Sequence ID: O06485.2 **Length:** 322 **Number of Matches:** 1

Related Information

Range 1: 8 to 143 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
47.8 bits(112)	7e-05	Compositional matrix adjust.	43/145(30%)	71/145(48%)	15/145(10%)

```
Query  17    TVCVTGAAGFIGSWLVMRLLERGYNVHATVRD---PENKKKVKHLLELPKADTNLTLWKA  73
              V VTG  G +GS+LV  L+E+G NV   VRD     N  + +H+ ++     +L
Sbjct  8     NVFVTGCTGLLGSYLVKELIEQGANVTGLVRDHVPQSNLYQGEHIKKMNIVRGSL----E  63

Query  74    DLTV-EGSFDEAIQGCQGVFHVATP--MDFESKDPENEVIKPTVRGMLSIIESCAKANTV  130
             DL V E +  E       VFH+A    +   +++P +   +  + G  +I+E+C K   +
Sbjct  64    DLAVIERALGE--YEIDTVFHLAAQAIVGVANRNPIS-TFEANILGTWNILEACRKHPLI  120

Query  131   KRLVFTSSAGTLDVQEQQKLFYDQT  155
             KR++  SS       +Q+ L YD+
Sbjct  121   KRVIVASSDKAYG--DQENLPYDEN  143
```

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RecName: Full=UDP-D-apiose/UDP-D-xylose synthase 2

Sequence ID: Q9SGE0.1 **Length:** 389 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 14 to 335 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
47.8 bits(112)	9e-05	Compositional matrix adjust.	73/342(21%)	135/342(39%)	61/342(17%)

```
Query  12    PVAVPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADT-----  66
             P+   T+C+ GA GFIGS L  +L+      H  +       K+KHLLE    DT
Sbjct  14    PIKPMTICMIGAGGFIGSHLCEKLMTE--TPHKVLALDVYNDKIKHLLE---PDTVQWAG  68

Query  67    NLTLWKADLTVEGSFDEAIQGCQGVFHVA---TPMDFESKDPENEVIKPTVRGMLSIIES  123
              +   + ++  +   +  I+      ++A   TP D+ ++    + I       L +++
Sbjct  69    RIQFHRINIKHDSRLEGLIKMADLTINLAAICTPADYNTR--PLDTIYSNFIDALPVVKY  126

Query  124   CAKANTVKRLVFTSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTG----------WM  172
             C++ N  KRL+  S+           L  D     D +F   K+              W
Sbjct  127   CSENN--KRLIHFSTCEVYGKTIGSFLPKDHPLRQDPEFYVLKEDISPCIFGSIEKQRWS  184

Query  173   YFVSKILAEKSAMEETKKKNIDFISIIP-----------PLVVG-----PFITPTFPPSL  216
             Y  +K L E+    E  +  ++F  + P           P + G     P +   F  +L
Sbjct  185   YACAKQLIERLVYAEGAENGLEFTIVRPFNWIGPRMDFIPGIDGPSEGVPRVLACFSNNL  244

Query  217   ITA--LSLITGNEAHYCIIKQGQYVHLDDLCEAHIFLYEHP-KADGRFI---CSSHHAII  270
             +    L L+ G E+      Q  ++++ D  EA + + E+P +A+G        ++   +
Sbjct  245   LRREPLKLVDGGES------QRTFIYIKDAIEAVLLMIENPERANGHIFNVGNPNNEVTV  298

Query  271   YDVAKMVREKWPEYYVPTEFKGIDKDLPVVSFSSKKLTDMGF  312
               +A+M+ E + +    T  +      P +  SSK+    G+
Sbjct  299   RQLAEMMTEVYAKVSGETAIES-----PTIDVSSKEFYGEGY  335
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 3; AltName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type III; Short=3-beta-HSD III; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: P26150.3 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 8 to 161 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
47.4 bits(111)	9e-05	Compositional matrix adjust.	38/160(24%)	72/160(45%)	17/160(10%)

```
Query  20    VTGAAGFIGSWLVMRLLERG----YNVHATVRDPENKKKVKHLLELPKADTNLTLWKADL  75
             VTGA GF+G  ++  L++        V   V  PE +++  +L         +T+ + D+
Sbjct  8     VTGAGGFLGQRIIQLLVQEKDLEEIRVLDKVFKPETREQFFNL----GTSIKVTVLEGDI  63

Query  76    TVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVF  135
                     A QG   V H A  +D     P   ++   ++G  +++E+C +A +V   +F
Sbjct  64    LDTQYLRRACQGISVVIHTAAIIDVTGVIPRQTILDVNLKGTQNLLEACIQA-SVPAFIF  122

Query  136   TSSAGTLDVQEQQKLFYD-------QTSWSDLDFIYAKKM  168
             +SS         + +          +++WSD  + Y+KKM
Sbjct  123   SSSVDVAGPNSYKDIVLNGHEDEHRESTWSD-PYPYSKKM  161
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase type 4; AltName: Full=3 beta-hydroxysteroid dehydrogenase type IV; Short=3-beta-HSD IV; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=NADPH-dependent 3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=Progesterone reductase

Sequence ID: Q61767.3 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 8 to 161 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
47.4 bits(111)	1e-04	Compositional matrix adjust.	43/161(27%)	78/161(48%)	19/161(11%)

```
Query  20    VTGAAGFIGSWLVMRLL--ERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTV  77
             VTGA GF+G  +V  L+   E    + A  R    +K+ + L +L +  T +T+ K D+
Sbjct  8     VTGAGGFLGQRIVRMLVQEEELQEIRALFRT-FGRKQEEELSKL-QTKTKVTVLKGDILD  65

Query  78    EGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTS  137
```

```
                   A QG   V H A  +D         ++   ++G   ++++C +AN V   +++S
Sbjct  66   AQCLKRACQGMSAVIHTAAAIDPLGAASRQTILDVNLKGTQLLLDACVEAN-VPTFIYSS  124

Query  138  S---AG-------TLDVQEQQKLFYDQTSWSDLDFIYAKKM  168
            S   AG        L+  E++   + +++WS+  + Y+KKM
Sbjct  125  SVLVAGPNSYKEIILNAHEEE---HHESTWSN-PYPYSKKM  161
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase; Short=3-beta-HSD; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: P21097.1 **Length:** 346 **Number of Matches:** 1

Related Information

Range 1: 6 to 118 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
47.0 bits(110)	1e-04	Compositional matrix adjust.	33/123(27%)	58/123(47%)	14/123(11%)

```
Query  20   VTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTN----LTLWKADL  75
            VTG AGF+G ++V  L+           D   + +V  ++E P+  T+    +   + D+
Sbjct  6    VTGGAGFLGRYIVKLLISA---------DDVQEIRVIDIVEDPQPITSKVKVINYIQCDI  56

Query  76   TVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVF  135
                   EA+ G   + H A  +D   K  +NE++K    G  +I+ +C     +K L++
Sbjct  57   NDFDKVREALDGVNLIIHTAALVDVFGKYTDNEIMKVNYYGTQTILAACVDLG-IKYLIY  115

Query  136  TSS  138
            TSS
Sbjct  116  TSS  118
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase; Short=3-beta-HSD; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: P26670.1 **Length:** 346 **Number of Matches:** 1

Related Information

Range 1: 6 to 118 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
47.0 bits(110)	1e-04	Compositional matrix adjust.	33/123(27%)	58/123(47%)	14/123(11%)

```
Query  20   VTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTN----LTLWKADL  75
            VTG AGF+G ++V  L+           D   + +V  ++E P+  T+    +   + D+
Sbjct  6    VTGGAGFLGRYIVKLLISA---------DDVQEIRVIDIVEDPQPITSKVKVINYIQCDI  56

Query  76   TVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVF  135
                   EA+ G   + H A  +D   K  +NE++K    G  +I+ +C     +K L++
Sbjct  57   NDFDKVREALDGVNLIIHTAALVDVFGKYTDNEIMKVNYYGTQTILAACVDLG-IKYLIY  115

Query  136  TSS  138
            TSS
Sbjct  116  TSS  118
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase; Short=3-beta-HSD; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: O57245.1 **Length:** 346 **Number of Matches:** 1

Related Information

Range 1: 6 to 118 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
47.0 bits(110)	2e-04	Compositional matrix adjust.	33/123(27%)	58/123(47%)	14/123(11%)

```
Query  20   VTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTN----LTLWKADL  75
            VTG AGF+G ++V  L+           D   + +V  ++E P+  T+    +   + D+
Sbjct  6    VTGGAGFLGRYIVKLLISA---------DDVQEIRVIDIVEDPQPITSKVKVINYIQCDI  56

Query  76   TVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVF  135
                   EA+ G   + H A  +D   K  +NE++K    G  +I+ +C     +K L++
Sbjct  57   NDFDKVREALDGVNLIIHTAALVDVFGKYTDNEIMKVNYYGTQTILAACVDLG-IKYLIY  115

Query  136  TSS  138
            TSS
Sbjct  116  TSS  118
```

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RecName: Full=ADP-L-glycero-D-manno-heptose-6-epimerase; AltName: Full=ADP-L-glycero-beta-D-manno-heptose-6-epimerase; Short=ADP-glyceromanno-heptose 6-epimerase; Short=ADP-hep 6-epimerase; Short=AGME

Sequence ID: B3R3C0.1 **Length:** 331 **Number of Matches:** 1

Related Information

Range 1: 2 to 255 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
46.6 bits(109)	2e-04	Compositional matrix adjust.	67/279(24%)	109/279(39%)	43/279(15%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            T+ VTGAAGFIGS LV  L ERG      V +     K  +L++   +D    L K D
Sbjct  2    TIIVTGAAGFIGSNLVKGLNERGETNVIAVDNLTRADKFHNLVDCEISD---YLDKQDFL  58

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
               +  E     + VFH     D    D    +++   R  LS++ESC +  T  + ++
Sbjct  59   ARFARGE-FGKVRAVFHEGACSDTMETDGR-YMMENNYRYTLSLMESCLEQGT--QFLYA  114

Query  137  SSAGT----------------LDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILA  180
            SSA T                L+V    K  +DQ     L    + ++ G+ YF
Sbjct  115  SSAATYGASQVFREDREFERPLNVYGYSKFLFDQIVRRRLPSALS-QIVGFRYF------  167

Query  181  EKSAMEETKKKNIDFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQ-YV  239
                  ET K  +  ++              F          + G    Y    Q + ++
Sbjct  168  NVYGPRETHKGRMASVAF-----------HNFNQFRADGTVKLFGEYGGYGPGMQSRDFI  216

Query  240  HLDDLCEAHIFLYEHPKADGRFICSSHHAIIY-DVAKMV  277
             ++D+ + ++F ++HP+  G F   +  A  + D+A  V
Sbjct  217  SVEDVVKVNLFFFDHPEKSGIFNLGTGRAQPFNDIAATV  255
```

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RecName: Full=UDP-glucose 4-epimerase uge1; AltName: Full=Galactowaldenase

Sequence ID: Q9Y7X5.1 **Length:** 355 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 8 to 131 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
46.6 bits(109)	2e-04	Compositional matrix adjust.	42/127(33%)	61/127(48%)	7/127(5%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPK-ADTNLTLWKADL  75
            TV VTG AG+IGS   + LLE+GY+V   + D     +V+ +  + K     +   + DL
Sbjct  8    TVLVTGGAGYIGSHTCVVLLEKGYDV--VIVDNLCNSRVEAVHRIEKLTGKKVIFHQVDL  65

Query  76   TVEGSFDE--AIQGCQGVFHVATPMDF-ESKDPENEVIKPTVRGMLSIIESCAKANTVKR  132
              E + D+  A Q    V H A      ES        K  + G +++IE C K   V+
Sbjct  66   LDEPALDKVFANQNISAVIHFAGLKAVGESVQVPLSYYKNNISGTINLIE-CMKKYNVRD  124

Query  133  LVFTSSA  139
             VF+SSA
Sbjct  125  FVFSSSA  131
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase; AltName: Full=Cholesterol dehydrogenase; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; Short=3-beta-HSD; Short=3BHSD; AltName: Full=3-beta hydroxysterol dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: P9WQP6.1 **Length:** 370 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details

PubChem BioAssay - bioactivity screening

Identical Proteins - Identical proteins to P9WQP6.1

Range 1: 17 to 280 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
46.6 bits(109)	2e-04	Compositional matrix adjust.	65/288(23%)	113/288(39%)	43/288(14%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTV  77
            V VTG AGF+G+ LV  LL+RG+ V +  R P           L  A   L + + D+T
Sbjct  17   VLVTGGAGFVGANLVTTLLDRGHWVRSFDRAP----------SLLPAHPQLEVLQGDITD  66

Query  78   EGSFDEAIQGCQGVFHVATPMDFE-----SKDPENEVIKPTVRGMLSIIESCAKANTVKR  132
                  A+ G   +FH A  ++       + +         V G  +++ +  +A  V+R
Sbjct  67   ADVCAAAVDGIDTIFHTAAIIELMGGASVTDEYRQRSFAVNVGGTENLLHAGQRAG-VQR  125

Query  133  LVFTSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKN  192
             V+TSS     V   Q +     +  D    Y  +    +Y  +K++AE+  + +
Sbjct  126  FVYTSSNSV--VMGGQNI-----AGGDETLPYTDRFND-LYTETKVVAERFVLAQNGVDG  177

Query  193  IDFISIIPPLVVG----PFITPTFPPSLITALSLITGNEAHYCIIKQGQYVHLDDLCEAH  248
            +   +I P  + G          F   L   + ++ G ++         YVH  +L
Sbjct  178  MLTCAIRPSGIWGNGDQTMFRKLFESVLKGHVKVLVGRKSARL---DNSYVH--NLIHGF  232

Query  249  IFLYEHPKADGR------FICSSHHAIIYDVAKMVRE----KWPEYYV  286
            I    H   DG       FI  +    +++ A+ V E    +WP+  +
Sbjct  233  ILAAAHLVPDGTAPGQAYFINDAEPINMFEFARPVLEACGQRWPKMRI  280
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase; Short=3-beta-HSD; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: Q5IFP1.3 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 125 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
46.2 bits(108)	3e-04	Compositional matrix adjust.	31/122(25%)	57/122(46%)	1/122(0%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            +  VTGA GF+G  +V  L E          D   + ++       ++ T LT+ + D+
Sbjct  5    SCLVTGAGGFLGQRIVHLLAEEKELQEIRALDKAFRPELLEEFSKLQSKTKLTMVEGDIL  64

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
             E     A QG   V H A+ +D  +      ++   ++G   ++E+CA+A +V   ++T
Sbjct  65   DEQCLKRACQGTSVVIHTASVIDVMNVIHRETIMNVNLKGTQLLLEACAQA-SVPIFIYT  123

Query  137  SS  138
            S+
Sbjct  124  ST  125
```

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RecName: Full=Bifunctional polymyxin resistance protein ArnA; Includes: RecName: Full=UDP-4-amino-4-deoxy-L-arabinose formyltransferase; AltName: Full=ArnAFT; AltName: Full=UDP-L-Ara4N formyltransferase; Includes: RecName: Full=UDP-glucuronic acid oxidase, UDP-4-keto-hexauronic acid decarboxylating; AltName: Full=ArnADH; AltName: Full=UDP-GlcUA decarboxylase; AltName: Full=UDP-glucuronic acid dehydrogenase

Sequence ID: A8FRR2.1 **Length:** 660 **Number of Matches:** 1

Related Information

Range 1: 320 to 498 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
46.2 bits(108)	3e-04	Compositional matrix adjust.	52/194(27%)	93/194(47%)	20/194(10%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERG-YNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            V + GA GFIG+ L  RLL+ G Y ++A   D  + +  +HL     +  +    + D+T
Sbjct  320  VLIMGANGFIGNHLTKRLLDDGKYEIYAM--DMSSSQIEQHL-----SHPDFHFVEGDIT  372

Query  77   VEGSFDE-AIQGCQGVF---HVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKR  132
            +   + E  I+ C  V     +ATP+++ +++P   V +      L I+ +C K +  KR
Sbjct  373  IHNEWIEYHIKKCDIVLPLVAIATPIEY-TRNPL-RVFELDFEENLKIVRACVKYD--KR  428

Query  133  LVFTSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKKKN  192
            ++F S++    ++ F + TS      I  ++   W+Y  SK L ++      KK N
Sbjct  429  IIFPSTSEVYGMCTDEE-FDEDTSPLITGPINRQR---WIYSTSKQLLDRVIWAYGKKDN  484

Query  193  IDFISIIPPLVVGP  206
            + F    P   +GP
Sbjct  485  LKFTLFRPFNWMGP  498
```

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RecName: Full=ADP-L-glycero-D-manno-heptose-6-epimerase; AltName: Full=ADP-L-glycero-beta-D-manno-heptose-6-epimerase; Short=ADP-glyceromanno-heptose 6-epimerase; Short=ADP-hep 6-epimerase; Short=AGME

Sequence ID: Q2L2R8.1 **Length:** 332 **Number of Matches:** 1

Related Information

Range 1: 2 to 254 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
45.4 bits(106)	4e-04	Compositional matrix adjust.	68/278(24%)	115/278(41%)	43/278(15%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERG-YNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            + VTGAAGFIGS LV  L  RG Y++ A + D     K ++L++   AD         L
Sbjct  2    IVVTGAAGFIGSNLVRGLNRRGIYDIIA-IDDLTEGDKFRNLVDCRIADYMHHEDARALL  60

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
              G F       + V H     D   ++ +  ++    R  L   E C +AN V  L++
Sbjct  61   KAGQFPR----VRAVLHQGACSDTTERNGQ-YMMDNNYRVTLEWFEYC-QANRVP-LIYA  113

Query  137  SSA----------------GTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILA  180
            SSA                G L+V    KL +DQ   + +D + A ++ G  YF
Sbjct  114  SSAAVYGASTVYVEDPANEGPLNVYGYSKLLFDQVLRTRMDKLTA-QVVGLRYFNVYGPH  172

Query  181  EKSAMEETKKKNIDFISIIPPLVVGPFITPTFPPSLITALSLITGNEAHYCIIKQGQYVH  240
            E+    + +  ++ F ++   L  G              + L +G + +    +   ++
Sbjct  173  EQ---HKGRMASVAFHNMNQFLAEGH-------------VRLFSGWDGYADGGQSRDFIS  216

Query  241  LDDLCEAHIFLYEHPKADGRFICSSHHAIIY-DVAKMV  277
            ++D+ + ++   +HP   G F C +  A  + DVA  V
Sbjct  217  VEDVVDVNLHFLDHPGTSGIFNCGTGRAQPFNDVAAAV  254
```

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RecName: Full=GDP-mannose 4,6 dehydratase; AltName: Full=GDP-D-mannose dehydratase; Short=GMD

Sequence ID: Q8K3X3.1 **Length:** 372 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 28 to 164 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
45.4 bits(106)	5e-04	Compositional matrix adjust.	43/141(30%)	64/141(45%)	18/141(12%)

```
Query  20   VTGAAGFIGSWLVMRLLERGYNVHATVRDPE--NKKKVKHLLELPKA--DTNLTLWKADL  75
            +TG  G  GS+L   LLE+GY VH  VR     N  +++HL + P+A  + N+ L   DL
Sbjct  28   ITGITGQDGSYLAEFLLEKGYEVHGIVRRSSSFNTGRIEHLYKNPQAHIEGNMKLHYGDL  87

Query  76   TVEGSFDEAIQ----------GCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCA  125
            T      + I           G Q   HV    D      + + +  T+R +L  I++C
Sbjct  88   TDSTCLVKIINEVKPTEIYNLGAQS--HVKISFDLAEYTADVDGVG-TLR-LLDAIKTCG  143

Query  126  KANTVKRLVFTSSAGTLDVQE  146
              N+VK    ++S      VQE
Sbjct  144  LINSVKFYQASTSELYGKVQE  164
```

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RecName: Full=GDP-mannose 4,6 dehydratase; AltName: Full=GDP-D-mannose dehydratase; Short=GMD

Sequence ID: Q8K0C9.1 **Length:** 372 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 28 to 164 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
45.4 bits(106)	5e-04	Compositional matrix adjust.	43/141(30%)	64/141(45%)	18/141(12%)

```
Query  20   VTGAAGFIGSWLVMRLLERGYNVHATVRDPE--NKKKVKHLLELPKA--DTNLTLWKADL  75
            +TG  G  GS+L   LLE+GY VH  VR     N  +++HL + P+A  + N+ L   DL
Sbjct  28   ITGITGQDGSYLAEFLLEKGYEVHGIVRRSSSFNTGRIEHLYKNPQAHIEGNMKLHYGDL  87

Query  76   TVEGSFDEAIQ----------GCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCA  125
            T      + I           G Q   HV    D      + + +  T+R +L  I++C
Sbjct  88   TDSTCLVKIINEVKPTEIYNLGAQS--HVKISFDLAEYTADVDGVG-TLR-LLDAIKTCG  143

Query  126  KANTVKRLVFTSSAGTLDVQE  146
              N+VK    ++S      VQE
Sbjct  144  LINSVKFYQASTSELYGKVQE  164
```

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RecName: Full=dTDP-4-oxo-6-deoxy-D-allose reductase; AltName: Full=dTDP-4-dehydro-6-deoxy-D-allose reductase; AltName: Full=dTDP-4-keto-6-deoxyallose reductase

Sequence ID: Q5SFA6.1 **Length:** 326 **Number of Matches:** 1

Related Information

Range 1: 10 to 269 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
45.1 bits(105)	5e-04	Compositional matrix adjust.	69/274(25%)	109/274(39%)	27/274(9%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            TV VTGA GFIGS  V +L  RG  V A  R  E  +    L  L +     T  + +
Sbjct  10   TVLVTGALGFIGSHFVRQLEARGAEVLALYR-TERPQLQAELAALDRVRLIRTELRDESD  68

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESK---DPENEVIKPTVRGMLSIIESCAKANTVKRL  133
            V G+F         V H A  MD  ++   +   E++    R  +S + +C +   V
Sbjct  69   VRGAFKYLAPSIDTVVHCAA-MDGNAQFKLERSAEILDSNQR-TISHLLNCVRDFGVGEA  126

Query  134  VFTSSAGTLDVQEQQKLFY---DQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAMEETKK  190
            V  SS+         +L+       +  D DF  + + T   Y +SK   E  A    ++
Sbjct  127  VVMSSS---------ELYCAPPTAAAHEDDDFRRSMRYTDNGYVLSKTYGEILARLHREQ  177

Query  191  KNIDFISIIPPLVVGPFITPTFPPSLITAL-SLITGNEAHYCIIKQG------QYVHLDD  243
               +   + P  V GP     + PS    + S++   +A   I   G       ++H+ D
Sbjct  178  FGTNVFLVRPGNVYGP--GDGYDPSRGRVIPSMLAKADAGEEIEIWGDGSQTRSFIHVTD  235

Query  244  LCEAHIFLYEHPKADGRFICSSHHAIIYDVAKMV  277
            L  A + L E  K     +  +    I ++A+MV
Sbjct  236  LVRASLRLLETGKYPEMNVAGAEQVSILELARMV  269
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 2; AltName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type II; Short=3-beta-HSD II; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: P22072.3 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 161 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
45.4 bits(106)	5e-04	Compositional matrix adjust.	37/163(23%)	71/163(43%)	17/163(10%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRD----PENKKKVKHLLELPKADTNLTLWK  72
            +  VTGA GF+G  ++  L++          D    PE K++   L    +    +T+ +
Sbjct  5    SCLVTGAGGFVGQRIIRMLVQEKELQEVRALDKVFRPETKEEFSKL----QTKAKVTMLE  60
```

```
Query  73   ADLTVEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKR  132
             D+        A QG   V H A+ MDF    P   ++   ++G  +++E+   A +V
Sbjct  61   GDILDAQYLRRACQGISVVIHTASVMDFSRVLPRQTILDVNLKGTQNLLEAGIHA-SVPA  119

Query  133  LVFTSSAGTLDVQEQQKLFYD-------QTSWSDLDFIYAKKM  168
             ++ S+         +K   +       +++WS+  + Y+KKM
Sbjct  120  FIYCSTVDVAGPNSYKKTILNGREEEHHESTWSN-PYPYSKKM  161
```

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RecName: Full=UDP-D-apiose/UDP-D-xylose synthase

Sequence ID: Q8S9Z2.1 **Length:** 398 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 22 to 343 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
45.4 bits(106)	5e-04	Compositional matrix adjust.	70/333(21%)	133/333(39%)	43/333(12%)

```
Query  12   PVAVPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLE--LPKADTNLT  69
            P+A  T+C+ GA GFIGS L  +L+      H          K++HL++   P     ++
Sbjct  22   PIAPLTICMIGAGGFIGSHLCEKLMAE--TAHVVYAVDVYCDKIRHLVDPAPPHLHGRIS  79

Query  70   LWKADLTVEGSFDEAIQGCQGVFHVA---TPMDFESKDPENEVIKPTVRGMLSIIESCAK  126
              + ++  +   +  I+      ++A   TP D+ ++    + I       L +++ C++
Sbjct  80   FHRLNIKNDSRLEGLIKMADLTINLAAICTPADYNTR--PLDTIYSNFIDALPVVKYCSE  137

Query  127  ANTVKRLVFTSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKK-----------MTGWMYFV  175
             N  KRL+  S+           L  D     + +F   K+              W Y
Sbjct  138  NN--KRLIHFSTCEVYGKTIGSFLPTDHPLRKEPEFYVLKEDESPCIFGPIVKQRWSYAC  195

Query  176  SKILAEKSAMEETKKKNIDFISIIPPLVVGP---FITPTFPPS--LITALSLITGNEAHY  230
            +K L E+    E  +  ++F  + P   +GP   FI     PS  +   L+  + N
Sbjct  196  AKQLIERLIFAEGAENGLEFTIVRPFNWIGPRMDFIPGVDGPSEGVPRVLACFSNNLLRR  255

Query  231  CIIK-------QGQYVHLDDLCEAHIFLYEHP-KADGRFI---CSSHHAIIYDVAKMVRE  279
              +K       Q  +V++ D  EA   + E+P +A+G+       ++   +  +A+M+ E
Sbjct  256  EPLKLVDGGQSQRTFVYIKDAIEAVHLMIENPARANGQIFNVGNPNNEVTVRQLAEMMTE  315

Query  280  KWPEYYVPTEFKGIDKDLPVVSFSSKKLTDMGF  312
             +              D P++  SSK+    G+
Sbjct  316  VYANVSGEPPL-----DEPMIDVSSKQFYGEGY  343
```

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RecName: Full=GDP-mannose 4,6 dehydratase; AltName: Full=GDP-D-mannose dehydratase; Short=GMD

Sequence ID: O60547.1 **Length:** 372 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 28 to 164 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
44.7 bits(104)	8e-04	Compositional matrix adjust.	42/141(30%)	64/141(45%)	18/141(12%)

```
Query  20   VTGAAGFIGSWLVMRLLERGYNVHATVRDPE--NKKKVKHLLELPKA--DTNLTLWKADL  75
            +TG  G  GS+L   LLE+GY VH  VR     N  +++HL + P+A  + N+ L   DL
Sbjct  28   ITGITGQDGSYLAEFLLEKGYEVHGIVRRSSSFNTGRIEHLYKNPQAHIEGNMKLHYGDL  87

Query  76   TVEGSFDEAIQ----------GCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCA  125
            T      + I           G Q   HV    D      + + +  T+R +L  +++C
Sbjct  88   TDSTCLVKIINEVKPTEIYNLGAQS--HVKISFDLAEYTADVDGVG-TLR-LLDAVKTCG  143

Query  126  KANTVKRLVFTSSAGTLDVQE  146
              N+VK    ++S     VQE
Sbjct  144  LINSVKFYQASTSELYGKVQE  164
```

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RecName: Full=UDP-glucose 4-epimerase; AltName: Full=Galactowaldenase; AltName: Full=UDP-N-acetylglucosamine 4-epimerase; Short=UDP-GlcNAc 4-epimerase; AltName: Full=UDP-galactosamine 4-epimerase; Short=UDP-GalNAc 4-epimerase; AltName: Full=UDP-galactose 4-epimerase

Sequence ID: Q8R059.1 **Length:** 347 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 4 to 132 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
44.3 bits(103)	8e-04	Compositional matrix adjust.	44/139(32%)	65/139(46%)	27/139(19%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGY------NVHATVRD----PENKKKVKHL----LELPK  63
            V VTG AG+IGS  V+ LLE GY      N H  +R     PE+ ++V+ L    +E  +
Sbjct  4    VLVTGGAGYIGSHTVLELLEAGYSPVVIDNFHNAIRGEDSMPESLRRVQELTGRSVEFEE  63

Query  64   ADTNLTLWKADLTVEGSFDEAIQ--GCQGVFH-VATPMDFESKDPENEVIKPTVRGMLSI  120
             D         L  + SF   I   G + V   V  P+D+          +  + G + +
Sbjct  64   MDILDQAALQHLFKKHSFKAVIHFAGLKAVGESVQKPLDY---------YRVNLTGTIQL  114

Query  121  IESCAKANTVKRLVFTSSA  139
            +E   +A+ VK LVF+SSA
Sbjct  115  LE-IMRAHGVKNLVFSSSA  132
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 1; AltName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type I; Short=3-beta-HSD I; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: P27365.2 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 125 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
44.7 bits(104)	9e-04	Compositional matrix adjust.	31/122(25%)	55/122(45%)	1/122(0%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            +  VTGA GF+G  +V  L+E        V D   + +++      +  T LT+ + D+
Sbjct  5    SCLVTGAGGFLGQRIVRLLVEEKELKEIRVLDKAFRPELREEFSKLQNKTKLTVLEGDIL  64

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
             E     A Q    V H A  +D         ++   V+G   ++E+C +A +V   ++T
Sbjct  65   DEPFLKRACQDVSVVIHTACIIDVFGVTHRESIMNVNVKGTQLLLEACVQA-SVPVFIYT  123

Query  137  SS  138
            S+
Sbjct  124  ST  125
```

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RecName: Full=UDP-glucose 4-epimerase 2; Short=OsUGE-2; AltName: Full=UDP-galactose 4-epimerase 2

Sequence ID: Q6ZDJ7.1 **Length:** 408 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 8 to 139 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
44.3 bits(103)	0.001	Compositional matrix adjust.	46/140(33%)	65/140(46%)	20/140(14%)

```
Query  12   PVAVPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKK---VKHLLELPKADT-N  67
            P  V TV VTG AG+IGS  V++LL  G+   A V D  N      V+ +  L    + N
Sbjct  8    PGGVRTVLVTGGAGYIGSHAVLQLLLAGF--RAVVVDNLNNSSELAVRRVAALAGDHSRN  65

Query  68   LTLWKADLTVEGSFDEAIQGCQ--GVFHVATPMDFESKDPENEVIKP------TVRGMLS  119
            L   K DL  +G+ ++     +   V H A       K     V KP       V G ++
Sbjct  66   LAFHKVDLRDKGALEKVFASTRFDAVVHFAG-----LKAVGESVQKPLLYYDNNVNGTVN  120

Query  120  IIESCAKANTVKRLVFTSSA  139
            ++E    A+  K+LVF+SSA
Sbjct  121  LLE-VMSAHGCKKLVFSSSA  139
```

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RecName: Full=ADP-L-glycero-D-manno-heptose-6-epimerase; AltName: Full=ADP-L-glycero-beta-D-manno-heptose-6-epimerase; Short=ADP-glyceromanno-heptose 6-epimerase; Short=ADP-hep 6-epimerase; Short=AGME

Sequence ID: Q0KDH0.1 **Length:** 331 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 2 to 119 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
43.9 bits(102)	0.001	Compositional matrix adjust.	40/125(32%)	58/125(46%)	7/125(5%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            T+ VTGAAGFIGS LV  L +RG      V +     K  +L++   +D    L K D
Sbjct  2    TIIVTGAAGFIGSNLVKGLNDRGETNVIAVDNLTRADKFHNLVDCEISD---YLDKQDFL  58

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
               +  E     + VFH     D    D    +++   R  LS++ESC +  T  + ++
Sbjct  59   ARFARGE-FGKVRAVFHEGACSDTMETDGR-YMMENNYRYTLSLMESCLEQGT--QFLYA  114

Query  137  SSAGT  141
            SSA T
Sbjct  115  SSAAT  119
```

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RecName: Full=ADP-L-glycero-D-manno-heptose-6-epimerase; AltName: Full=ADP-L-glycero-beta-D-manno-heptose-6-epimerase; Short=ADP-glyceromanno-heptose 6-epimerase; Short=ADP-hep 6-epimerase; Short=AGME

Sequence ID: Q1LQG2.1 **Length:** 331 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 2 to 167 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
43.9 bits(102)	0.001	Compositional matrix adjust.	48/177(27%)	74/177(41%)	30/177(16%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            T+ VTGAAGFIGS +V  L ERG      V +    +K  +L++   AD    L K D
Sbjct  2    TIIVTGAAGFIGSNIVKGLNERGETNIIAVDNLTRAEKFNNLVDCEIAD---YLDKTDFV  58

Query  77   ---VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRL  133
                 G F       + VFH     D    D    +++   R  L+++E+C +     +
```

```
Sbjct  59   ARFARGDFGNV----RAVFHEGACSDTMETDGR-YMMENNYRYTLALLEACLEQGA--QF  111

Query  134  VFTSSAGT----------------LDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYF  174
            ++ SSA T                L+V    K  +DQ     L   ++ ++ G+ YF
Sbjct  112  LYASSAATYGASTMFREDRDYEKPLNVYGYSKFLFDQVVRRRLPSAHS-QIVGFRYF  167
```

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RecName: Full=ADP-L-glycero-D-manno-heptose-6-epimerase; AltName: Full=ADP-L-glycero-beta-D-manno-heptose-6-epimerase; Short=ADP-glyceromanno-heptose 6-epimerase; Short=ADP-hep 6-epimerase; Short=AGME

Sequence ID: Q21Y60.1 **Length:** 340 **Number of Matches:** 1

Related Information

Range 1: 4 to 149 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
43.5 bits(101)	0.002	Compositional matrix adjust.	40/153(26%)	64/153(41%)	23/153(15%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTV  77
            + VTGAAGFIGS ++  L  RG N    + D     K ++L  L  +D        DL  
Sbjct  4    IVVTGAAGFIGSNIIQGLNARGLNDIIAIDDLTQGDKFRNLAHLKISDYVDASVFYDLFA  63

Query  78   EGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFTS  137
             G++ +     + VFH     D    + +  ++       +++ ++C K     RL++ S
Sbjct  64   NGAYGQ----IEAVFHEGACSDTMESNGK-YMMDNNYATSVNLFQACQKRGA--RLLYAS  116

Query  138  SAGT----------------LDVQEQQKLFYDQ  154
            SA T                L+V    KL +DQ
Sbjct  117  SAATYGGSDTFREDPAFERPLNVYGYSKLLFDQ  149
```

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RecName: Full=UDP-glucose 4-epimerase; AltName: Full=Galactowaldenase; AltName: Full=UDP-N-acetylglucosamine 4-epimerase; Short=UDP-GlcNAc 4-epimerase; AltName: Full=UDP-galactosamine 4-epimerase; Short=UDP-GalNAc 4-epimerase; AltName: Full=UDP-galactose 4-epimerase

Sequence ID: Q3T105.2 **Length:** 348 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 133 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
42.7 bits(99)	0.003	Compositional matrix adjust.	44/139(32%)	65/139(46%)	27/139(19%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGY------NVHATVRD----PENKKKVKHL----LELPK  63
            V VTG AG+IGS  V+ LLE GY      N H  +R     PE+ ++V+ L    +E  +
Sbjct  5    VLVTGGAGYIGSHTVLELLEAGYSPMVIDNFHNAIRGGGSMPESLRRVQDLTGRSVEFEE  64

Query  64   ADTNLTLWKADLTVEGSFDEAIQ--GCQGVFH-VATPMDFESKDPENEVIKPTVRGMLSI  120
             D         L  + SF   I   G + V   V  P+D+          +  + G + +
Sbjct  65   MDILDQAALQRLFKKHSFMAVIHFAGLKAVGESVQKPLDY---------YRVNLTGTIQL  115

Query  121  IESCAKANTVKRLVFTSSA  139
            +E   +A+ VK LVF+SSA
Sbjct  116  LE-IMRAHGVKNLVFSSSA  133
```

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RecName: Full=UDP-glucose 4-epimerase; AltName: Full=Galactowaldenase; AltName: Full=UDP-N-acetylgalactosamine 4-epimerase; Short=UDP-GalNAc 4-epimerase; AltName: Full=UDP-N-acetylglucosamine 4-epimerase; Short=UDP-GlcNAc 4-epimerase; AltName: Full=UDP-galactose 4-epimerase

Sequence ID: Q14376.2 **Length:** 348 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 133 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
42.7 bits(99)	0.003	Compositional matrix adjust.	41/135(30%)	62/135(45%)	19/135(14%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGY------NVHATVRD----PENKKKVKHLLELPKADTN  67
            V VTG AG+IGS  V+ LLE GY      N H   R     PE+ ++V+ L        +
Sbjct  5    VLVTGGAGYIGSHTVLELLEAGYLPVVIDNFHNAFRGGGSLPESLRRVQEL-----TGRS  59

Query  68   LTLWKADLTVEGSFDEAIQ--GCQGVFHVATPMDF-ESKDPENEVIKPTVRGMLSIIESC  124
            +   + D+  +G+     +      V H A      ES     +  +  + G + ++E
Sbjct  60   VEFEEMDILDQGALQRLFKKYSFMAVIHFAGLKAVGESVQKPLDYYRVNLTGTIQLLE-I  118

Query  125  AKANTVKRLVFTSSA  139
             KA+ VK LVF+SSA
Sbjct  119  MKAHGVKNLVFSSSA  133
```

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RecName: Full=UDP-glucose 4-epimerase; AltName: Full=Galactowaldenase; AltName: Full=UDP-N-acetylglucosamine 4-epimerase; Short=UDP-GlcNAc 4-epimerase; AltName: Full=UDP-galactosamine 4-epimerase; Short=UDP-GalNAc 4-epimerase; AltName: Full=UDP-galactose 4-epimerase

Sequence ID: Q5R8D0.1 **Length:** 348 **Number of Matches:** 1

Related Information

Range 1: 5 to 133 GenPept Graphics Next Match Previous Match

Gene - associated gene details

Score	Expect	Method	Identities	Positives	Gaps
42.7 bits(99)	0.003	Compositional matrix adjust.	41/135(30%)	62/135(45%)	19/135(14%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGY------NVHATVRD----PENKKKVKHLLELPKADTN  67
            V VTG AG+IGS  V+ LLE GY      N H   R     PE+ ++V+ L        +
Sbjct  5    VLVTGGAGYIGSHTVLELLEAGYLPVVIDNFHNAFRGGGSLPESLRRVQEL-----TGRS  59

Query  68   LTLWKADLTVEGSFDEAIQ--GCQGVFHVATPMDF-ESKDPENEVIKPTVRGMLSIIESC  124
            +   + D+  +G+     +      V H A      ES     +  +  + G + ++E
Sbjct  60   VEFEEMDILDQGALQRLFKKHSFMAVIHFAGLKAVGESVQKPLDYYRVNLTGTIQLLE-I  118

Query  125  AKANTVKRLVFTSSA  139
             KA+ VK LVF+SSA
Sbjct  119  MKAHGVKNLVFSSSA  133
```

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RecName: Full=UDP-glucose 4-epimerase; AltName: Full=Galactowaldenase; AltName: Full=UDP-N-acetylglucosamine 4-epimerase; Short=UDP-GlcNAc 4-epimerase; AltName: Full=UDP-galactosamine 4-epimerase; Short=UDP-GalNAc 4-epimerase; AltName: Full=UDP-galactose 4-epimerase

Sequence ID: P18645.1 **Length:** 347 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 133 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
42.4 bits(98)	0.004	Compositional matrix adjust.	43/139(31%)	65/139(46%)	27/139(19%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGY------NVHATVRD----PENKKKVKHL----LELPK  63
            V VTG AG+IGS  V+ LLE GY      N H ++R     PE+ ++V+ L    +E  +
Sbjct  5    VLVTGGAGYIGSHTVLELLEAGYSPVVIDNFHNSIRGEDSMPESLRRVQELTGRSVEFEE  64

Query  64   ADTNLTLWKADLTVEGSFDEAIQ--GCQGVFH-VATPMDFESKDPENEVIKPTVRGMLSI  120
             D         L  + +F   I   G + V   V  P+D+          +  + G + +
Sbjct  65   MDILDQAALQHLFKKHNFKAVIHFAGLKAVGESVQKPLDY---------YRVNLTGTIQL  115

Query  121  IESCAKANTVKRLVFTSSA  139
            +E   +A  VK LVF+SSA
Sbjct  116  LE-IMRAMGVKSLVFSSSA  133
```

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RecName: Full=UDP-glucose 4-epimerase; AltName: Full=Galactowaldenase; AltName: Full=UDP-galactose 4-epimerase

Sequence ID: Q45291.2 **Length:** 329 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 3 to 118 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
42.4 bits(98)	0.004	Compositional matrix adjust.	40/128(31%)	64/128(50%)	16/128(12%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGYNVHATVRD---PENKKKVKHLLELPKADTNLTLWKAD  74
            + VTG AG++GS     LLE G++V  T+ D     N++ V     L + D N  +   +
Sbjct  3    LLVTGGAGYVGSVAAAVLLEHGHDV--TIIDNFSTGNREAVPADARLIEGDVNDVV--EE  58

Query  75   LTVEGSFDEAIQGCQGVFH-VATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRL  133
            +  EG F       +GV H  A  +  ES +  NE     V   L+++++  +A+ V  L
Sbjct  59   VLSEGGF-------EGVVHFAARSLVGESVEKPNEYWHDNVVTALTLLDAM-RAHGVNNL  110

Query  134  VFTSSAGT  141
            VF+S+A T
Sbjct  111  VFSSTAAT  118
```

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RecName: Full=Bifunctional polymyxin resistance protein ArnA; Includes: RecName: Full=UDP-4-amino-4-deoxy-L-arabinose formyltransferase; AltName: Full=ArnAFT; AltName: Full=UDP-L-Ara4N formyltransferase; Includes: RecName: Full=UDP-glucuronic acid oxidase, UDP-4-keto-hexauronic acid decarboxylating; AltName: Full=ArnADH; AltName: Full=UDP-GlcUA decarboxylase; AltName: Full=UDP-glucuronic acid dehydrogenase

Sequence ID: B5XTK9.1 **Length:** 661 **Number of Matches:** 1

Related Information

Range 1: 298 to 496 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
42.7 bits(99)	0.004	Compositional matrix adjust.	56/214(26%)	95/214(44%)	23/214(10%)

```
Query  1    MASEAVHAPSPPVAVPT---VCVTGAAGFIGSWLVMRLLE-RGYNVHATVRDPENKKKVK  56
            + S AV +  P VA+     V + G  GFIG+ L  RLL+   Y ++            +
Sbjct  298  LVSGAVISSKPVVAIKRRTRVLILGVNGFIGNHLTERLLQDDNYEIYGL---DIGSDAIS  354

Query  57   HLLELPKADTNLTLWKADLTVEGSFDE-AIQGCQGVF---HVATPMDFESKDPENEVIKP  112
              LE P+        + D+++   + E  I+ C  V     +ATP+++ +++P   V +
Sbjct  355  RFLESPR----FHFVEGDISIHSEWIEYHIKKCDVVLPLVAIATPIEY-TRNPL-RVFEL  408

Query  113  TVRGMLSIIESCAKANTVKRLVFTSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWM  172
                 L II  C K N  KR++F S++    +    K F + TS   +  I  ++   W+
Sbjct  409  DFEENLKIIRDCVKYN--KRIIFPSTSEVYGMC-TDKNFDEDTSNLVVGPINKQR---WI  462
```

```
Query  173  YFVSKILAEKSAMEETKKKNIDFISIIPPLVVGP  206
            Y VSK L ++       K ++ F    P   +GP
Sbjct  463  YSVSKQLLDRVIWAYGDKYDLKFTLFRPFNWMGP  496
```

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RecName: Full=GDP-mannose 4,6-dehydratase; AltName: Full=GDP-D-mannose dehydratase

Sequence ID: Q06952.1 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 7 to 67 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
41.6 bits(96)	0.007	Compositional matrix adjust.	25/61(41%)	32/61(52%)	3/61(4%)

```
Query  19  CVTGAAGFIGSWLVMRLLERGYNVHATVRDPE--NKKKVKHLLELP-KADTNLTLWKADL  75
            +TG  G  GS+L   LLE+GY VH   R     N ++V HL + P + D N  L   DL
Sbjct  7   LITGITGQDGSYLAEFLLEKGYEVHGIKRRSSLFNTQRVDHLYKDPHEEDVNFKLHYGDL  66

Query  76  T  76
           T
Sbjct  67  T  67
```

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RecName: Full=Bifunctional polymyxin resistance protein ArnA; Includes: RecName: Full=UDP-4-amino-4-deoxy-L-arabinose formyltransferase; AltName: Full=ArnAFT; AltName: Full=UDP-L-Ara4N formyltransferase; Includes: RecName: Full=UDP-glucuronic acid oxidase, UDP-4-keto-hexauronic acid decarboxylating; AltName: Full=ArnADH; AltName: Full=UDP-GlcUA decarboxylase; AltName: Full=UDP-glucuronic acid dehydrogenase

Sequence ID: A6TF98.1 **Length:** 661 **Number of Matches:** 1

Related Information

Range 1: 298 to 496 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
42.0 bits(97)	0.007	Compositional matrix adjust.	55/214(26%)	94/214(43%)	23/214(10%)

```
Query  1    MASEAVHAPSPPVAVPT---VCVTGAAGFIGSWLVMRLLE-RGYNVHATVRDPENKKKVK  56
            + S AV +  P VA+     V + G  GFIG+ L  RLL+   Y ++           +
Sbjct  298  LVSGAVISSKPVVAIKRRTRVLILGVNGFIGNHLTERLLQDDNYEIYGL---DIGSDAIS  354

Query  57   HLLELPKADTNLTLWKADLTVEGSFDE-AIQGCQGVF---HVATPMDFESKDPENEVIKP  112
              L+ P+        + D+++   + E  I+ C  V     +ATP+++ +++P   V +
Sbjct  355  RFLDCPR----FHFVEGDISIHSEWIEYHIKKCDVVLPLVAIATPIEY-TRNPL-RVFEL  408

Query  113  TVRGMLSIIESCAKANTVKRLVFTSSAGTLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWM  172
                 L II  C K N  KR++F S++    +   +   +D+ S S+L      K   W+
Sbjct  409  DFEENLKIIRDCVKYN--KRIIFPSTSEVYGMCTDKN--FDEDS-SNLVVGPINKQR-WI  462

Query  173  YFVSKILAEKSAMEETKKKNIDFISIIPPLVVGP  206
            Y VSK L ++       K  + F    P   +GP
Sbjct  463  YSVSKQLLDRVIWAYGDKNGLKFTLFRPFNWMGP  496
```

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RecName: Full=dTDP-4-oxo-6-deoxy-D-allose reductase; AltName: Full=dTDP-4-dehydro-6-deoxy-D-allose reductase; AltName: Full=dTDP-4-keto-6-deoxy-D-hexose reductase GerKI; AltName: Full=dTDP-4-keto-6-deoxyallose reductase

Sequence ID: Q331Q7.1 **Length:** 326 **Number of Matches:** 1

Related Information

Range 1: 10 to 269 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
41.6 bits(96)	0.007	Compositional matrix adjust.	70/279(25%)	112/279(40%)	37/279(13%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVR--DPENKKKVKHLLELPKADTNLTLWKAD  74
            TV VTGA GFIGS  V +L  RG  V A  R   PE + ++  L  +    T L   + +
Sbjct  10   TVLVTGALGFIGSHFVRQLDARGAEVLALYRTERPEIQAELAALNRVRLVRTEL---RDE  66

Query  75   LTVEGSFDEAIQGCQGVFHVATPMDFESK---DPENEVIKPTVRGMLSIIESCAKANTVK  131
              V G+F         V H A  MD  ++   +   E++    R + +++ +C +   V
Sbjct  67   SDVRGAFKYLAPSIDTVVHCAA-MDGNAQFKLERSAEILDSNQRTISNLL-NCVRDFGVG  124

Query  132  RLVFTSSAG------TLDVQEQQKLFYDQTSWSDLDFIYAKKMTGWMYFVSKILAEKSAM  185
             +V  SS+       T+  +E+             DF  + + T   Y +SK   E  A
Sbjct  125  EVVVMSSSELYSASPTVAAREED------------DFRRSMRYTDNGYVLSKTYGEILAR  172

Query  186  EETKKKNIDFISIIPPLVVGPFITPTFPPSLITAL-SLITGNEAHYCIIKQG------QY  238
               ++   +   + P  V GP     F  S    + S++   +A   I   G       +
Sbjct  173  LHREQFGTNVFLVRPGNVYGP--GDGFDCSRGRVIPSMLAKADAGEEIEIWGDGSQTRSF  230

Query  239  VHLDDLCEAHIFLYEHPKADGRFICSSHHAIIYDVAKMV  277
            VH+ DL  A + L E  K     +  +    I ++A MV
Sbjct  231  VHVADLVRASLRLLETGKYPEMNVAGAEQVSILELAGMV  269
```

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RecName: Full=UDP-glucose 4-epimerase; AltName: Full=Galactowaldenase; AltName: Full=UDP-galactose 4-epimerase

Sequence ID: P45602.1 **Length:** 139 **Number of Matches:** 1

Related Information

Range 1: 3 to 125 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
39.7 bits(91)	0.008	Compositional matrix adjust.	36/125(29%)	57/125(45%)	5/125(4%)

```
Query  18   VCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLTV  77
            V VTG +G+IGS   ++LL+RG+ V        +K+++  ++E        T  + D+
Sbjct  3    VLVTGGSGYIGSHTCVQLLQRGHEVVILDNLCNSKRRILPVIE-RLGGKEATFIEGDIRN  61

Query  78   EGSFDEAI--QGCQGVFHVATPMDF-ESKDPENEVIKPTVRGMLSIIESCAKANTVKRLV  134
            E    E +     + V H A      ES     E     V G L ++ S  +A  VK  +
Sbjct  62   EARMTEILHDHAIEAVIHFAGLKAVGESVAKPLEYYDNNVTGTLKLV-SAMRAAGVKNFI  120

Query  135  FTSSA  139
            F+SSA
Sbjct  121  FSSSA  125
```

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RecName: Full=UDP-glucose 4-epimerase 4; Short=OsUGE-4; AltName: Full=UDP-galactose 4-epimerase 4

Sequence ID: Q6K2E1.1 **Length:** 369 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 19 to 145 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
41.6 bits(96)	0.008	Compositional matrix adjust.	43/133(32%)	63/133(47%)	16/133(12%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYN-VHATVRDPENKKKVKHLLELPKADT-NLTLWKAD  74
            TV VTG AG+IGS  V++LL  G+  V A      ++  V+ +  L      NL+L K D
Sbjct  19   TVLVTGGAGYIGSHTVLQLLAAGFRVVVADSLGNSSELAVRRVAALAGDKARNLSLHKVD  78

Query  75   LTVEGSFDEAIQGCQ--GVFHVATPMDFESKDPENEVIKP------TVRGMLSIIESCAK  126
            +  +G  ++     +   V H A       K     V KP       V G + ++E  A
Sbjct  79   IRDKGGLEKVFSSTRFDAVVHFAG-----LKAVGESVQKPLLYYDHNVAGTIILLEVMA-  132

Query  127  ANTVKRLVFTSSA  139
            A+  K+LVF+SSA
Sbjct  133  AHGCKKLVFSSSA  145
```

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RecName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 1; AltName: Full=3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type I; Short=3-beta-HSD I; AltName: Full=Trophoblast antigen FDO161G; Includes: RecName: Full=3-beta-hydroxy-Delta(5)-steroid dehydrogenase; AltName: Full=3-beta-hydroxy-5-ene steroid dehydrogenase; AltName: Full=Progesterone reductase; Includes: RecName: Full=Steroid Delta-isomerase; AltName: Full=Delta-5-3-ketosteroid isomerase

Sequence ID: P14060.2 **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 125 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
41.6 bits(96)	0.009	Compositional matrix adjust.	29/122(24%)	54/122(44%)	1/122(0%)

```
Query  17   TVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPENKKKVKHLLELPKADTNLTLWKADLT  76
            +  VTGA GF+G  ++  L++        V D     +++      +  T LT+ + D+
Sbjct  5    SCLVTGAGGFLGQRIIRLLVKEKELKEIRVLDKAFGPELREEFSKLQNKTKLTVLEGDIL  64

Query  77   VEGSFDEAIQGCQGVFHVATPMDFESKDPENEVIKPTVRGMLSIIESCAKANTVKRLVFT  136
             E     A Q    + H A  +D         ++   V+G   ++E+C +A +V   ++T
Sbjct  65   DEPFLKRACQDVSVIIHTACIIDVFGVTHRESIMNVNVKGTQLLLEACVQA-SVPVFIYT  123

Query  137  SS  138
            SS
Sbjct  124  SS  125
```

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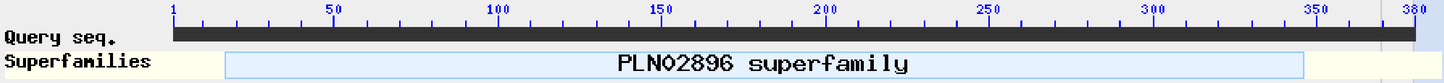

Distribution of the top 7 Blast Hits on 7 subject sequences

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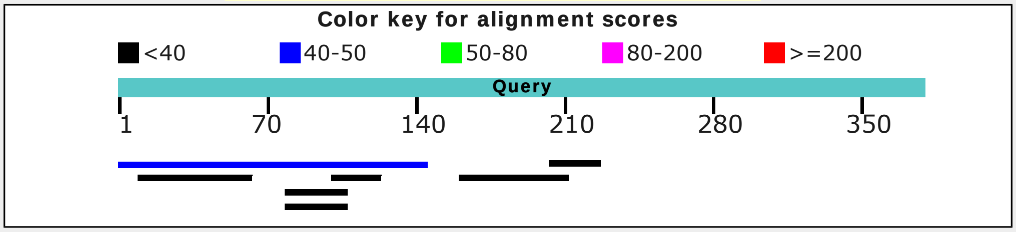

Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	RecName: Full=GDP-mannose 4,6 dehydratase 1; AltName: Full=Bacillus thuringiensis toxin-resista	40.0	40.0	38%	2e-04	25%	Q18801.3
☐	RecName: Full=Antitoxin PemI	27.3	27.3	6%	0.66	54%	P13975.1
☐	RecName: Full=Polycystic kidney disease 1 like 1; AltName: Full=Protein abecobe	27.7	27.7	13%	2.2	31%	E7FKV8.2
☐	RecName: Full=Lethal factor; Short=LF; AltName: Full=Anthrax lethal toxin endopeptidase compone	26.2	26.2	14%	5.9	34%	P15917.2
☐	RecName: Full=U12-ctenitoxin-Pn1a; Short=U12-CNTX-Pn1a; AltName: Full=Neurotoxin Pn3-6B; Fl	24.3	24.3	6%	7.5	44%	P0C2S8.1
☐	RecName: Full=Ecto-ADP-ribosyltransferase 4; AltName: Full=ADP-ribosyltransferase C2 and C3 to	25.4	25.4	7%	8.0	42%	Q95NE0.1
☐	RecName: Full=Ecto-ADP-ribosyltransferase 4; AltName: Full=ADP-ribosyltransferase C2 and C3 to	25.4	25.4	7%	8.0	42%	Q93070.2

Alignments

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RecName: Full=GDP-mannose 4,6 dehydratase 1; AltName: Full=Bacillus thuringiensis toxin-resistant protein 1; Short=Bt toxin-resistant protein 1; AltName: Full=GDP-D-mannose dehydratase; Short=GMD

Sequence ID: Q18801.3 **Length:** 399 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 32 to 192 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
40.0 bits(92)	2e-04	Compositional matrix adjust.	40/161(25%)	67/161(41%)	15/161(9%)

```
Query  1    MASEAVHAPSPPVAV----PTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPE--NKKK  54
            M+ E    P+  +A         +TG +G  GS+L   LL +GY VH  +R     N  +
Sbjct  32   MSHEVSTTPAAELAAFRARKVALITGISGQDGSYLAELLLSKGYKVHGIIRRSSSFNTAR  91

Query  55   VKHLLELP---KADTNLTLWKADLTVEGSFDEAIQGCQ--GVFHVA----TPMDFESKDP  105
            ++HL   P     D++ +L   D+T      + I   +   V+H+A      + F+  +
Sbjct  92   IEHLYSNPITHHGDSSFSLHYGDMTDSSCLIKLISTIEPTEVYHLAAQSHVKVSFDLPEY  151

Query  106  ENEVIKPTVRGMLSIIESCAKANTVKRLVFTSSAGTLDVQE  146
              EV       +L  I +C     V+    ++S     VQE
Sbjct  152  TAEVDAVGTLRLLDAIHACRLTEKVRFYQASTSELYGKVQE  192
```

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RecName: Full=Antitoxin PemI

Sequence ID: P13975.1 **Length:** 85 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 9 to 32 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
27.3 bits(59)	0.66	Composition-based stats.	13/24(54%)	16/24(66%)	0/24(0%)

```
Query  204  VGPFITPTFPPSLITALSLITGNE  227
            VG  +  T PP+L+ ALSL T NE
Sbjct  9    VGGSVMLTVPPALLNALSLGTDNE  32
```

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RecName: Full=Polycystic kidney disease 1 like 1; AltName: Full=Protein abecobe

Sequence ID: E7FKV8.2 **Length:** 2742 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 2193 to 2244 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
27.7 bits(60)	2.2	Compositional matrix adjust.	16/52(31%)	22/52(42%)	0/52(0%)

```
Query  161   DFIYAKKMTGWMYFVSKILAEKSAMEETKKKNIDFISIIPPLVVGPFITPTF  212
             DF+  KK   W  +    L       E++   + FISI  PLV    +  TF
Sbjct  2193  DFMSIKKYEDWWKWAQTSLLSSLYYNESENPQMSFISIGAPLVQKTEVCGTF  2244
```

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RecName: Full=Lethal factor; Short=LF; AltName: Full=Anthrax lethal toxin endopeptidase component; Flags: Precursor

Sequence ID: P15917.2 **Length:** 809 **Number of Matches:** 1

Related Information

Range 1: 23 to 74 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
26.2 bits(56)	5.9	Compositional matrix adjust.	19/56(34%)	26/56(46%)	6/56(10%)

```
Query  10  SPPVAVPTVCVTGAAGFIGSWLVMRLLERGYNVHATVRDPE--NKKKVKHLLELPK  63
           S PV +P V   G  G +G    M + E+  N     R  E  NK + +HL E+ K
Sbjct  23  SGPVFIPLVQGAGGHGDVG----MHVKEKEKNKDENKRKDEERNKTQEEHLKEIMK  74
```

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RecName: Full=U12-ctenitoxin-Pn1a; Short=U12-CNTX-Pn1a; AltName: Full=Neurotoxin Pn3-6B; Flags: Precursor

Sequence ID: P0C2S8.1 **Length:** 100 **Number of Matches:** 1

Related Information

Range 1: 27 to 51 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
24.3 bits(51)	7.5	Composition-based stats.	11/25(44%)	17/25(68%)	1/25(4%)

```
Query  101  ESKD-PENEVIKPTVRGMLSIIESC  124
            E+KD PE++ + P  RG L I ++C
Sbjct  27   EAKDEPESDALVPQERGCLDIGKTC  51
```

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RecName: Full=Ecto-ADP-ribosyltransferase 4; AltName: Full=ADP-ribosyltransferase C2 and C3 toxin-like 4; Short=ARTC4; AltName: Full=Dombrock molecule 1; AltName: Full=Mono(ADP-ribosyl)transferase 4; AltName: Full=NAD(P)(+)--arginine ADP-ribosyltransferase 4; AltName: CD_antigen=CD297; Flags: Precursor

Sequence ID: Q95NE0.1 **Length:** 314 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 60 to 90 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
25.4 bits(54)	8.0	Compositional matrix adjust.	13/31(42%)	18/31(58%)	1/31(3%)

```
Query  79   GSFDEAIQGC-QGVFHVATPMDFESKDPENE  108
            GSFD+  QGC + V     T  D+ +KD E +
Sbjct  60   GSFDDQYQGCSKQVMEKLTQGDYFTKDIEAQ  90
```

Download GenPept Graphics Next Previous Descriptions

RecName: Full=Ecto-ADP-ribosyltransferase 4; AltName: Full=ADP-ribosyltransferase C2 and C3 toxin-like 4; Short=ARTC4; AltName: Full=Dombrock blood group carrier molecule; AltName: Full=Mono(ADP-ribosyl)transferase 4; AltName: Full=NAD(P)(+)--arginine ADP-ribosyltransferase 4; AltName: CD_antigen=CD297; Flags: Precursor

Sequence ID: Q93070.2 **Length:** 314 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 60 to 90 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
25.4 bits(54)	8.0	Compositional matrix adjust.	13/31(42%)	18/31(58%)	1/31(3%)

```
Query  79   GSFDEAIQGC-QGVFHVATPMDFESKDPENE  108
            GSFD+  QGC + V     T  D+ +KD E +
Sbjct  60   GSFDDQYQGCSKQVMEKLTQGDYFTKDIEAQ  90
```

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BLAST Results

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Job title: Protein Sequence (506 letters)

RID	E945S3A7016 (Expires on 04-06 14:37 pm)		
Query ID	lcl|Query_358325	**Database Name**	swissprot
Description	None	**Description**	Non-redundant UniProtKB/SwissProt sequences
Molecule type	amino acid	**Program**	BLASTP 2.6.0+ Citation
Query Length	506		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment] [MSA viewer]

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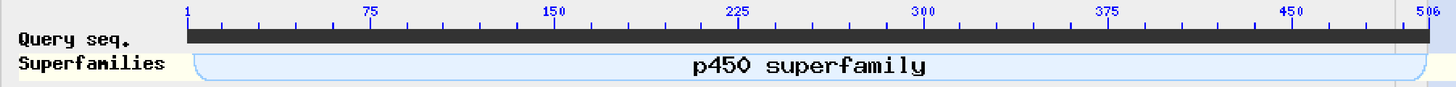
Graphic Summary

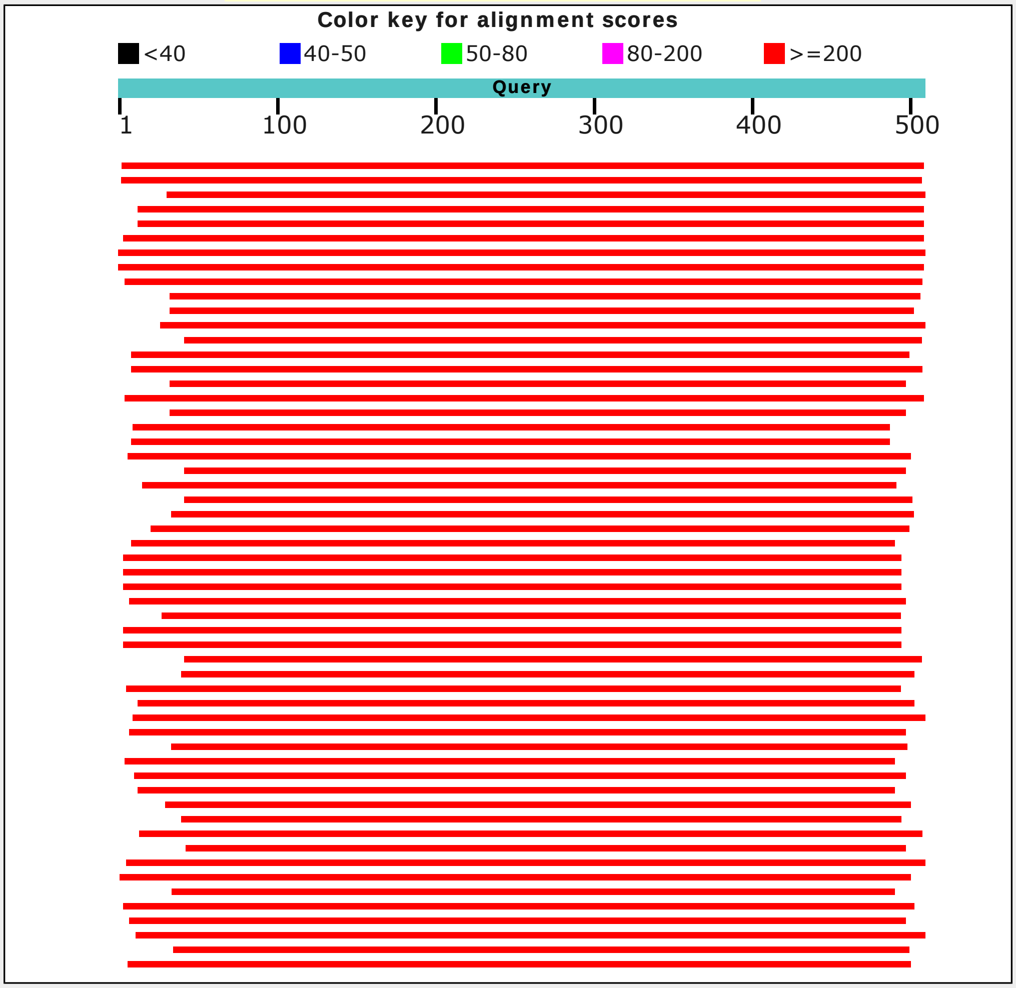
Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of the top 100 Blast Hits on 100 subject sequences

Mouse over to see the title, click to show alignments



Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	RecName: Full=Flavonoid 3',5'-hydroxylase 2; Short=F3'5'H; AltName: Full=CYPLXXVA3; AltNam	806	806	99%	0.0	76%	P48419.1
☐	RecName: Full=Flavonoid 3',5'-hydroxylase 1; Short=F3'5'H; AltName: Full=CYPLXXVA1; AltNam	800	800	99%	0.0	76%	P48418.1
☐	RecName: Full=Flavonoid 3',5'-hydroxylase; Short=F3'5'H; AltName: Full=CYPLXXVA2; AltName:	792	792	94%	0.0	77%	P37120.1
☐	RecName: Full=Flavonoid 3',5'-hydroxylase; Short=F3'5'H; AltName: Full=Cytochrome P450 75A5	763	763	97%	0.0	72%	Q96418.1
☐	RecName: Full=Flavonoid 3',5'-hydroxylase; Short=F3'5'H; AltName: Full=Cytochrome P450 75A7	761	761	97%	0.0	72%	O04790.1
☐	RecName: Full=Flavonoid 3',5'-hydroxylase; Short=F3'5'H; AltName: Full=Cytochrome P450 75A4	735	735	99%	0.0	71%	Q96581.1
☐	RecName: Full=Flavonoid 3',5'-hydroxylase; Short=F3'5'H; AltName: Full=Cytochrome P450 75A6	676	676	100%	0.0	64%	O04773.1
☐	RecName: Full=Flavonoid 3'-monooxygenase; AltName: Full=Cytochrome P450 75B1; AltName: F	506	506	99%	2e-175	48%	Q9SD85.1
☐	RecName: Full=Flavonoid 3'-monooxygenase; AltName: Full=Cytochrome P450 75B2; AltName: F	478	478	98%	1e-164	50%	Q9SBQ9.1
☐	RecName: Full=Cytochrome P450 750A1; AltName: Full=Cytochrome P450 CYPC	371	371	93%	2e-122	40%	Q50EK4.1
☐	RecName: Full=Cytochrome P450 CYP736A12	369	369	92%	4e-122	41%	H2DH18.1
☐	RecName: Full=3,9-dihydroxypterocarpan 6A-monooxygenase; AltName: Full=Cytochrome P450	367	367	94%	5e-121	40%	Q42798.1
☐	RecName: Full=Cytochrome P450 93A3; AltName: Full=Cytochrome P450 CP5	361	361	91%	9e-119	41%	O81973.1
☐	RecName: Full=Geraniol 8-hydroxylase; AltName: Full=Cytochrome P450 76B6; AltName: Full=G	357	357	96%	2e-117	40%	Q8VWZ7.1
☐	RecName: Full=Cytochrome P450 93A2	356	356	98%	5e-117	39%	Q42799.1
☐	RecName: Full=Cytochrome P450 76C4	350	350	91%	2e-114	40%	O64635.1
☐	RecName: Full=Beta-amyrin 24-hydroxylase; AltName: Full=Cytochrome P450 93E1; AltName: Fu	348	348	99%	1e-113	37%	Q9XHC6.1
☐	RecName: Full=Cytochrome P450 76C1	345	345	91%	2e-112	40%	O64636.1
☐	RecName: Full=Costunolide synthase; Short=LsCOS; AltName: Full=Cytochrome P450 71BL2	340	340	93%	5e-111	39%	F8S1I0.1
☐	RecName: Full=Costunolide synthase; Short=CiCOS; AltName: Full=Cytochrome P450 71BL3	340	340	94%	1e-110	38%	G3GBK0.1
☐	RecName: Full=Geraniol 8-hydroxylase; AltName: Full=Cytochrome P450 76B10; AltName: Full=	339	339	97%	3e-110	40%	D1MI46.1
☐	RecName: Full=Cytochrome P450 76C2; AltName: Full=Protein YELLOW-LEAF-SPECIFIC GENE	339	339	89%	3e-110	39%	O64637.1
☐	RecName: Full=Licodione synthase; AltName: Full=(2S)-flavanone 2-hydroxylase; AltName: Full=	336	336	93%	9e-109	36%	P93149.2
☐	RecName: Full=Cytochrome P450 71A1; AltName: Full=ARP-2; AltName: Full=CYPLXXIA1	328	328	90%	5e-106	37%	P24465.2
☐	RecName: Full=Cytochrome P450 98A1	327	327	92%	1e-105	37%	O48956.1
☐	RecName: Full=Cytochrome P450 71D11	325	325	94%	5e-105	37%	O22307.1
☐	RecName: Full=Cytochrome P450 71D8; AltName: Full=Cytochrome P450 CP7	325	325	94%	1e-104	35%	O81974.1
☐	RecName: Full=Germacrene A oxidase; Short=BsGAO; AltName: Full=Germacrene A alcohol deh	321	321	96%	2e-103	37%	D5JBX1.1
☐	RecName: Full=Germacrene A oxidase; Short=CiGAO; AltName: Full=Germacrene A alcohol deh	320	320	96%	4e-103	36%	D5JBW8.1
☐	RecName: Full=Germacrene A oxidase; Short=HaGAO; AltName: Full=Germacrene A alcohol deh	320	320	96%	6e-103	36%	D5JBX0.1
☐	RecName: Full=Cytochrome P450 71B11	319	319	96%	1e-102	35%	P58049.1
☐	RecName: Full=Cytochrome P450 71BL1; AltName: Full=Germacrene A acid 8-beta-hydroxylase;	319	319	91%	1e-102	38%	F8S1H3.1
☐	RecName: Full=Germacrene A oxidase; Short=LsGAO; AltName: Full=Germacrene A alcohol deh	319	319	96%	1e-102	36%	D5J9U8.1
☐	RecName: Full=Germacrene A oxidase; Short=SlGAO; AltName: Full=Germacrene A alcohol deh	318	318	96%	2e-102	36%	D5JBW9.1
☐	RecName: Full=Cytochrome P450 703A2; AltName: Full=Protein DEFECTIVE IN EXINE FORMA	319	319	91%	2e-102	35%	Q9LNJ4.1
☐	RecName: Full=Cytochrome P450 84A1; AltName: Full=Ferulate-5-hydroxylase; Short=F5H	319	319	90%	3e-102	36%	Q42600.1
☐	RecName: Full=Cytochrome P450 71AV8; AltName: Full=(+)-Valencene oxidase	318	318	96%	4e-102	36%	E1B2Z9.1
☐	RecName: Full=Cytochrome P450 71D10	318	318	96%	6e-102	36%	O48923.1
☐	RecName: Full=Cytochrome P450 82A3; AltName: Full=Cytochrome P450 CP6	317	317	98%	2e-101	36%	O49858.1
☐	RecName: Full=Cytochrome P450 71B12	315	315	96%	4e-101	35%	Q9ZU07.1
☐	RecName: Full=Cytochrome P450 71B10	315	315	91%	7e-101	37%	Q9LVD2.1

☐ RecName: Full=Cytochrome P450 71B34	314	314	95%	1e-100	36%	Q9LIP6.1
☐ RecName: Full=Cytochrome P450 76A2; AltName: Full=CYPLXXVIA2; AltName: Full=Cytochrome	311	311	95%	2e-99	36%	P37122.1
☐ RecName: Full=Cytochrome P450 71B35	311	311	93%	2e-99	36%	Q9LIP5.1
☐ RecName: Full=Premnaspirodiene oxygenase; Short=HPO; AltName: Full=Cytochrome P450 71D	310	310	92%	4e-99	36%	A6YIH8.1
☐ RecName: Full=(S)-N-methylcoclaurine 3'-hydroxylase isozyme 1; AltName: Full=Cytochrome P45	309	309	89%	8e-99	39%	Q9SP06.1
☐ RecName: Full=Cytochrome P450 98A2	309	309	97%	1e-98	36%	O48922.1
☐ RecName: Full=Cytochrome P450 76C3	310	310	89%	1e-98	39%	O64638.2
☐ RecName: Full=Cytochrome P450 82A4; AltName: Full=Cytochrome P450 CP9	310	310	99%	1e-98	36%	O49859.1
☐ RecName: Full=Cytochrome P450 71A2; AltName: Full=CYPLXXIA2; AltName: Full=Cytochrome	308	308	98%	3e-98	35%	P37118.1
☐ RecName: Full=Cytochrome P450 71B37	308	308	89%	4e-98	37%	Q9LIP3.2
☐ RecName: Full=Cytochrome P450 82C4	308	308	98%	8e-98	35%	Q9SZ46.1
☐ RecName: Full=Cytochrome P450 71B13	306	306	96%	2e-97	35%	P58050.1
☐ RecName: Full=Cytochrome P450 82A1; AltName: Full=CYPLXXXII	305	305	97%	1e-96	34%	Q43068.2
☐ RecName: Full=Cytochrome P450 71A23	303	303	91%	1e-96	37%	Q9STL0.1
☐ RecName: Full=7-ethoxycoumarin O-deethylase; Short=ECOD; AltName: Full=Cytochrome P450	303	303	97%	2e-96	36%	O23976.1
☐ RecName: Full=Cytochrome P450 71B4	303	303	93%	2e-96	34%	O65786.2
☐ RecName: Full=Cytochrome P450 71D7	302	302	92%	5e-96	34%	P93531.1
☐ RecName: Full=Cytochrome P450 98A3; AltName: Full=Protein REDUCED EPIDERMAL FLUOR	302	302	97%	8e-96	35%	O22203.1
☐ RecName: Full=2-methylbutanal oxime monooxygenase; AltName: Full=Cytochrome P450 71E7	301	301	86%	2e-95	35%	Q6XQ14.1
☐ RecName: Full=Cytochrome P450 71B2	301	301	97%	2e-95	33%	O65788.2
☐ RecName: Full=Cytochrome P450 71A9; AltName: Full=Cytochrome P450 CP1	301	301	93%	2e-95	36%	O81970.1
☐ RecName: Full=Tabersonine 16-hydroxylase; AltName: Full=Cytochrome P450 71D12	299	299	89%	1e-94	37%	P98183.1
☐ RecName: Full=Cytochrome P450 71B14	298	298	96%	1e-94	34%	P58051.1
☐ RecName: Full=Cytochrome P450 71B19	298	298	96%	2e-94	33%	Q9LTM4.1
☐ RecName: Full=Cytochrome P450 71A22	298	298	91%	2e-94	35%	Q9STL1.1
☐ RecName: Full=Cytochrome P450 82C2	298	298	99%	3e-94	34%	O49394.2
☐ RecName: Full=(S)-N-methylcoclaurine 3'-hydroxylase isozyme 1; AltName: Full=Cytochrome P45	297	297	96%	4e-94	38%	O64899.1
☐ RecName: Full=Cytochrome P450 71B36	297	297	91%	5e-94	35%	Q9LIP4.1
☐ RecName: Full=Cytochrome P450 71B20	296	296	96%	8e-94	33%	Q9LTM3.1
☐ RecName: Full=Amorpha-4,11-diene 12-monooxygenase; AltName: Full=Amorpha-4,11-diene C-1	296	296	96%	1e-93	36%	Q1PS23.1
☐ RecName: Full=(S)-N-methylcoclaurine 3'-hydroxylase isozyme 2; AltName: Full=Cytochrome P45	296	296	96%	1e-93	38%	O64900.1
☐ RecName: Full=Cytochrome P450 84A4	296	296	92%	1e-93	34%	F4JW83.1
☐ RecName: Full=Cytochrome P450 71A4; AltName: Full=CYPLXXIA4; AltName: Full=Cytochrome	296	296	91%	2e-93	35%	P37117.1
☐ RecName: Full=Cytochrome P450 71D6	295	295	92%	3e-93	34%	P93530.1
☐ RecName: Full=Psoralen synthase; AltName: Full=Cytochrome P450 CYP71AJ2	294	294	93%	3e-93	34%	C0SJS4.1
☐ RecName: Full=Cytochrome P450 71A6	295	295	91%	4e-93	35%	O04164.1
☐ RecName: Full=Psoralen synthase; AltName: Full=Cytochrome P450 CYP71AJ1	293	293	96%	1e-92	34%	Q6QNI4.1
☐ RecName: Full=5-epiaristolochene 1,3-dihydroxylase; Short=NtEAH; AltName: Full=Cytochrome	293	293	88%	2e-92	34%	Q94FM7.2
☐ RecName: Full=Cytochrome P450 71A25	292	292	96%	3e-92	34%	Q9STK8.1
☐ RecName: Full=Ferruginol synthase; AltName: Full=Cytochrome P450 76AH1	291	291	95%	1e-91	34%	S4UX02.1
☐ RecName: Full=Cytochrome P450 71B1; AltName: Full=CYPLXXIB1	290	290	96%	2e-91	32%	P49264.1
☐ RecName: Full=(S)-N-methylcoclaurine 3'-hydroxylase-like protein; AltName: Full=Cytochrome P4	288	288	86%	3e-91	39%	I3V6B1.1
☐ RecName: Full=Cytochrome P450 76AD1	290	290	90%	3e-91	36%	I3PFJ5.1
☐ RecName: Full=Protopine 6-monooxygenase; AltName: Full=Protopine 6-hydroxylase; Short=P6H	290	290	97%	6e-91	34%	F2Z9C1.1
☐ RecName: Full=Cytochrome P450 71B7	289	289	97%	6e-91	31%	Q96514.1
☐ RecName: Full=4-hydroxyphenylacetaldehyde oxime monooxygenase; AltName: Full=Cytochrome	290	290	90%	7e-91	33%	O48958.1

☐ RecName: Full=Cytochrome P450 71B26	288	288	90%	1e-90	36%	Q9LTL0.1
☐ RecName: Full=Psoralen synthase; AltName: Full=Cytochrome P450 CYP71AJ3	287	287	93%	2e-90	34%	C0SJS2.1
☐ RecName: Full=Cytochrome P450 83B1; AltName: Full=Protein ALTERED TRYPTOPHAN REGU	288	288	94%	2e-90	34%	O65782.1
☐ RecName: Full=Cytochrome P450 71A26	287	287	92%	3e-90	35%	Q9STK7.1
☐ RecName: Full=Probable (S)-N-methylcoclaurine 3'-hydroxylase isozyme 2; AltName: Full=Cytoch	287	287	93%	3e-90	40%	Q9FXW4.1
☐ RecName: Full=Cytochrome P450 71B23	287	287	90%	3e-90	32%	Q9LTM0.1
☐ RecName: Full=Cytochrome P450 82A2; AltName: Full=Cytochrome P450 CP4	287	287	93%	8e-90	35%	O81972.1
☐ RecName: Full=Berbamunine synthase; AltName: Full=(S)-N-methylcoclaurine oxidase [C-O phen	285	285	97%	2e-89	35%	P47195.1
☐ RecName: Full=Cytochrome P450 71D9; AltName: Full=Cytochrome P450 CP3	285	285	94%	2e-89	36%	O81971.1
☐ RecName: Full=Cytochrome P450 71B17	285	285	94%	3e-89	33%	Q9LTM6.1
☐ RecName: Full=Methyltetrahydroprotoberberine 14-monooxygenase; AltName: Full=(S)-cis-N-metl	285	285	93%	4e-89	33%	L7X3S1.1
☐ RecName: Full=Cytochrome P450 71A8	282	282	96%	3e-88	34%	Q42716.1
☐ RecName: Full=Cytochrome P450 82C3	282	282	98%	3e-88	35%	O49396.3

Alignments

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RecName: Full=Flavonoid 3',5'-hydroxylase 2; Short=F3'5'H; AltName: Full=CYPLXXVA3; AltName: Full=Cytochrome P450 75A3

Sequence ID: P48419.1 **Length:** 508 **Number of Matches:** 1

Related Information

Range 1: 2 to 505 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
806 bits(2082)	0.0	Compositional matrix adjust.	384/504(76%)	439/504(87%)	1/504(0%)

```
Query  3    ILVTDFVVAAIIFLITRFLVRSLFKKPT-RPLPPGPLGWPLVGALPLLGAMPHVALAKLA  61
            +L+++   A +IFL T   + +L      R LPPGP GWP++GALPLLGAMPHV+LAK+A
Sbjct  2    VLLSELAAATLIFLTTHIFISTLLSITNGRRLPPGPRGWPVIGALPLLGAMPHVSLAKMA  61

Query  62   KKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKY  121
            KKYG IM+LK+GTC MVVASTP++A+AFLKTLDLNFSNRPPNAGA+HLAYGAQD+VFA Y
Sbjct  62   KKYGAIMYLKVGTCGMVVASTPDAAKAFLKTLDLNFSNRPPNAGATHLAYGAQDMVFAHY  121

Query  122  GPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMA  181
            GPRWK LRKLSNLHMLGGKAL++WANVR  ELGHMLK+M + SR GE VV+AEMLT+AMA
Sbjct  122  GPRWKLLRKLSNLHMLGGKALENWANVRANELGHMLKSMFDMSREGERVVVAEMLTFAMA  181

Query  182  NMIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKK  241
            NMIGQVILS+RVFV KG E NEFKDMVVELMT+AGYFNIGDFIP +AWMDLQGIE+GMK+
Sbjct  182  NMIGQVILSKRVFVNKGVEVNEFKDMVVELMTTAGYFNIGDFIPCLAWMDLQGIEKGMKR  241

Query  242  LHTKFDVLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTA  301
            LH KFD LLTKM  EH+ATS+ERKGK DFLD ++E  DN+ GE+LS TNIKA+LLNLFTA
Sbjct  242  LHKKFDALLTKMFDEHKATSYERKGKPDFLDCVMENRDNSEGERLSTTNIKALLLNLFTA  301

Query  302  GTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYR  361
            GTDTSSS IEWAL EM+KNP ILKKAQ EMD+VIG +RRLLESDI +LPYL+AI KET+R
Sbjct  302  GTDTSSSAIEWALAEMMKNPAILKKAQGEMDQVIGNNRRLLESDIPNLPYLRAICKETFR  361

Query  362  KHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEEN  421
            KHPSTPLNLPRI+ + C VDGYYIPK+ RLSVNIWAIGRDP VWENPLEF PERFLS  N
Sbjct  362  KHPSTPLNLPRISNEPCIVDGYYIPKNTRLSVNIWAIGRDPEVWENPLEFYPERFLSGRN  421

Query  422  GKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMDESF  481
             KI+P GNDF+LIPFGAGRRICAGTRMG+V+V YILGTLVHSFDWKLP+ V ELNM+E+F
Sbjct  422  SKIDPRGNDFELIPFGAGRRICAGTRMGIVMVEYILGTLVHSFDWKLPSEVIELNMEEAF  481

Query  482  GLALQKAVPLSALVSPRLASNPYA  505
            GLALQKAVPL A+V+PRL  + YA
Sbjct  482  GLALQKAVPLEAMVTPRLPIDVYA  505
```

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RecName: Full=Flavonoid 3',5'-hydroxylase 1; Short=F3'5'H; AltName: Full=CYPLXXVA1; AltName: Full=Cytochrome P450 75A1

Sequence ID: P48418.1 **Length:** 506 **Number of Matches:** 1

Related Information

Range 1: 2 to 504 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
800 bits(2066)	0.0	Compositional matrix adjust.	381/503(76%)	438/503(87%)	1/503(0%)

```
Query  3    ILVTDFVVAAIIFLITRFLVRSLFKKPT-RPLPPGPLGWPLVGALPLLGAMPHVALAKLA  61
            +L+T+   A  IFLI   ++ +L  K T R LPPGP GWP++GALPLLGAMPHV+LAK+A
Sbjct  2    MLLTELGAATSIFLIAHIIISTLISKTTGRHLPPGPRGWPVIGALPLLGAMPHVSLAKMA  61

Query  62   KKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKY  121
            KKYG IM+LK+GTC M VASTP++A+AFLKTLD+NFSNRPPNAGA+HLAY AQD+VFA Y
Sbjct  62   KKYGAIMYLKVGTCGMAVASTPDAAKAFLKTLDINFSNRPPNAGATHLAYNAQDMVFAHY  121

Query  122  GPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMA  181
            GPRWK LRKLSNLHMLGGKAL++WANVR  ELGHMLK+M + SR G+ VV+AEMLT+AMA
Sbjct  122  GPRWKLLRKLSNLHMLGGKALENWANVRANELGHMLKSMSDMSREGQRVVVAEMLTFAMA  181

Query  182  NMIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKK  241
            NMIGQV+LS+RVFV KG E NEFKDMVVELMT AGYFNIGDFIP +AWMDLQGIE+ MK+
Sbjct  182  NMIGQVMLSKRVFVDKGVEVNEFKDMVVELMTIAGYFNIGDFIPCLAWMDLQGIEKRMKR  241

Query  242  LHTKFDVLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTA  301
            LH KFD LLTKM  EH+AT++ERKGK DFLDV++E  DN+ GE+LS TNIKA+LLNLFTA
Sbjct  242  LHKKFDALLTKMFDEHKATTYERKGKPDFLDVVMENGDNSEGERLSTTNIKALLLNLFTA  301

Query  302  GTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYR  361
            GTDTSSS IEWAL EM+KNP ILKKAQ EMD+VIGR+RRLLESDI +LPYL+AI KET+R
Sbjct  302  GTDTSSSAIEWALAEMMKNPAILKKAQAEMDQVIGRNRRLLESDIPNLPYLRAICKETFR  361

Query  362  KHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEEN  421
            KHPSTPLNLPRI+ + C VDGYYIPK+ RLSVNIWAIGRDP VWENPLEF PERFLS  N
Sbjct  362  KHPSTPLNLPRISNEPCIVDGYYIPKNTRLSVNIWAIGRDPQVWENPLEFNPERFLSGRN  421

Query  422  GKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMDESF  481
             KI+P GNDF+LIPFGAGRRICAGTRMG+V+V YILGTLVHSFDWKLP+ V ELNM+E+F
Sbjct  422  SKIDPRGNDFELIPFGAGRRICAGTRMGIVMVEYILGTLVHSFDWKLPSEVIELNMEEAF  481

Query  482  GLALQKAVPLSALVSPRLASNPY  504
            GLALQKAVPL A+V+PRL  + Y
Sbjct  482  GLALQKAVPLEAMVTPRLQLDVY  504
```

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RecName: Full=Flavonoid 3',5'-hydroxylase; Short=F3'5'H; AltName: Full=CYPLXXVA2; AltName: Full=Cytochrome P450 75A2; AltName: Full=P-450EG1

Sequence ID: P37120.1 **Length:** 513 **Number of Matches:** 1

Related Information

Range 1: 34 to 509 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
792 bits(2045)	0.0	Compositional matrix adjust.	366/476(77%)	427/476(89%)	0/476(0%)

```
Query  31   RPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFL  90
            R LPPGP GWP++GALPLLG MPHVALAK+AKKYGPIM+LK+GTC MVVASTP +A+AFL
Sbjct  34   RRLPPGPEGWPVIGALPLLGGMPHVALAKMAKKYGPIMYLKVGTCGMVVASTPNAAKAFL  93

Query  91   KTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRV  150
            KTLD+NFSNRPPNAGA+H+AY AQD+VFA YGPRWK LRKLSNLHMLGGKAL++WANVR
Sbjct  94   KTLDINFSNRPPNAGATHMAYNAQDMVFAPYGPRWKLLRKLSNLHMLGGKALENWANVRA  153

Query  151  TELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVE  210
             ELGHMLK+M +AS  GE +V+A+MLT+AMANMIGQV+LS+RVFV KG E NEFK+MVVE
Sbjct  154  NELGHMLKSMFDASHVGERIVVADMLTFAMANMIGQVMLSKRVFVEKGKEVNEFKNMVVE  213

Query  211  LMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKGKADF  270
            LMT AGYFNIGDFIP IAWMDLQGIE+GMKKLH KFD LLTKM +EH ATS+ERKGK DF
Sbjct  214  LMTVAGYFNIGDFIPQIAWMDLQGIEKGMKKLHKKFDDLLTKMFEEHEATSNERKGKPDF  273

Query  271  LDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEE  330
            LD ++   DN+ GE+LSITNIKA+LLNLFTAGTDTSSS+IEWALTEM+KNPTI KKAQ+E
Sbjct  274  LDFIMANRDNSEGERLSITNIKALLLNLFTAGTDTSSSVIEWALTEMMKNPTIFKKAQQE  333

Query  331  MDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDAR  390
            MD++IG++RR +ESDI +LPYL+AI KE +RKHPSTPLNLPR++  AC +DGYYIPK+ R
Sbjct  334  MDQIIGKNRRFIESDIPNLPYLRAICKEAFRKHPSTPLNLPRVSSDACTIDGYYIPKNTR  393

Query  391  LSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGM  450
            LSVNIWAIGRDP+VWENPLEF+PERFLSE+N KI   GNDF+LIPFGAGRRICAGTRMG+
Sbjct  394  LSVNIWAIGRDPDVWENPLEFIPERFLSEKNAKIEHRGNDFELIPFGAGRRICAGTRMGI  453

Query  451  VLVSYILGTLVHSFDWKLPNGVAELNMDESFGLALQKAVPLSALVSPRLASNPYAT  506
            V+V YILGTL+HSFDWKLPN V ++NM+E+FGLALQKAVPL A+V+PRL+ + Y +
Sbjct  454  VMVEYILGTLIHSFDWKLPNDVVDINMEETFGLALQKAVPLEAIVTPRLSFDIYQS  509
```

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RecName: Full=Flavonoid 3',5'-hydroxylase; Short=F3'5'H; AltName: Full=Cytochrome P450 75A5

Sequence ID: Q96418.1 **Length:** 510 **Number of Matches:** 1

Related Information

Range 1: 16 to 509 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
763 bits(1971)	0.0	Compositional matrix adjust.	357/494(72%)	426/494(86%)	1/494(0%)

```
Query  13   IIFLITRFLVRSLFKKPTRP-LPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLK  71
            ++F   + LV+ L+    R  LPPGP+GWP++GALPLLG MPHVALA +AKKYGP+M+LK
Sbjct  16   MLFFHVQKLVQYLWMNSRRHRLPPGPIGWPVLGALPLLGTMPHVALANMAKKYGPVMYLK  75
```

```
Query  72   MGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKL  131
            +G+C + VASTPE+A+AFLKTLD+NFSNRPPNAGA+HLAY AQD+VFA YGPRWK LRKL
Sbjct  76   VGSCGLAVASTPEAAKAFLKTLDMNFSNRPPNAGATHLAYNAQDMVFADYGPRWKLLRKL  135

Query  132  SNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSR  191
            SN+H+LGGKAL  W  VR  ELG+ML AM E+ R G+PVV++EMLTYAMANM+GQV+LS+
Sbjct  136  SNIHILGGKALQGWEEVRKKELGYMLYAMAESGRHGQPVVVSEMLTYAMANMLGQVMLSK  195

Query  192  RVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKFDVLLT  251
            RVF ++G+ESNEFKDMVVELMT AGYFNIGDFIPSIAWMDLQGI+ GMK+LH KFD LLT
Sbjct  196  RVFGSQGSESNEFKDMVVELMTVAGYFNIGDFIPSIAWMDLQGIQGGMKRLHKKFDALLT  255

Query  252  KMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIE  311
            ++++EH A++HERKG  DFLD ++   DN+ GE+L   NIKA+LLN+FTAGTDTSSS+IE
Sbjct  256  RLLEEHTASAHERKGSPDFLDFVVANRDNSEGERLHTVNIKALLLNMFTAGTDTSSSVIE  315

Query  312  WALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLP  371
            WAL E++KNP ILK+AQEEMD VIGRDRR LE+DIS LPYLQAI KE +RKHPSTPLNLP
Sbjct  316  WALAELLKNPIILKRAQEEMDGVIGRDRRFLEADISKLPYLQAICKEAFRKHPSTPLNLP  375

Query  372  RIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDF  431
            RIA QACEV+G+YIPK  RLSVNIWAIGRDP++WENP EF P+RFL  +N KI+P GNDF
Sbjct  376  RIASQACEVNGHYIPKGTRLSVNIWAIGRDPSLWENPNEFNPDRFLERKNAKIDPRGNDF  435

Query  432  KLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMDESFGLALQKAVPL  491
            +LIPFGAGRRICAGTR+G++LV YILGTLVHSFDW+LP+ V ELNMDE FGLALQKAVPL
Sbjct  436  ELIPFGAGRRICAGTRLGILLVEYILGTLVHSFDWELPSSVIELNMDEPFGLALQKAVPL  495

Query  492  SALVSPRLASNPYA  505
            +A+V+PRL  + Y
Sbjct  496  AAMVTPRLPLHIYC  509
```

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RecName: Full=Flavonoid 3',5'-hydroxylase; Short=F3'5'H; AltName: Full=Cytochrome P450 75A7

Sequence ID: O04790.1 **Length:** 510 **Number of Matches:** 1

Related Information

Range 1: 16 to 509 GenPept Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
761 bits(1964)	0.0	Compositional matrix adjust.	356/494(72%)	426/494(86%)	1/494(0%)

```
Query  13   IIFLITRFLVRSLFKKPTRP-LPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLK  71
            ++F   + LV+ L+    R  LPPGP+GWP++GAL LLG MPHVALA +AKKYGP+M+LK
Sbjct  16   MLFFHVQKLVQYLWMNSRRHRLPPGPIGWPVLGALRLLGTMPHVALANMAKKYGPVMYLK  75

Query  72   MGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKL  131
            +G+C + VASTPE+A+AFLKTLD+NFSNRPPNAGA+HLAY AQD+VFA YGPRWK LRKL
Sbjct  76   VGSCGLAVASTPEAAKAFLKTLDMNFSNRPPNAGATHLAYNAQDMVFADYGPRWKLLRKL  135

Query  132  SNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSR  191
            SN+H+LGGKAL  W  VR  ELG+ML AM E+ R G+PVV++EMLTYAMANM+GQV+LS+
Sbjct  136  SNIHILGGKALQGWEEVRKKELGYMLYAMAESGRHGQPVVVSEMLTYAMANMLGQVMLSK  195

Query  192  RVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKFDVLLT  251
            RVF ++G+ESNEFKDMVVELMT AGYFNIGDFIPSIAWMDLQGI+ GMK+LH KFD LLT
Sbjct  196  RVFGSQGSESNEFKDMVVELMTVAGYFNIGDFIPSIAWMDLQGIQGGMKRLHKKFDALLT  255

Query  252  KMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIE  311
            ++++EH A++HERKG  DFLD ++   DN+ GE+L   NIKA+LLN+FTAGTDTSSS+IE
Sbjct  256  RLLEEHTASAHERKGSPDFLDFVVANGDNSEGERLQTVNIKALLLNMFTAGTDTSSSVIE  315

Query  312  WALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLP  371
            WAL E++KNP IL++AQEEMD VIGRDRR LE+DIS LPYLQAI KE +RKHPSTPLNLP
Sbjct  316  WALAELLKNPIILRRAQEEMDGVIGRDRRFLEADISKLPYLQAICKEAFRKHPSTPLNLP  375

Query  372  RIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDF  431
            RIA QACEV+G+YIPK  RLSVNIWAIGRDP+VWENP EF P+RFL  +N KI+P GNDF
Sbjct  376  RIASQACEVNGHYIPKGTRLSVNIWAIGRDPSVWENPNEFNPDRFLERKNAKIDPRGNDF  435

Query  432  KLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMDESFGLALQKAVPL  491
            +LIPFGAGRRICAGTR+G++LV YILGTLVHSF W+LP+ V ELNMDESFGLALQKAVPL
Sbjct  436  ELIPFGAGRRICAGTRLGILLVEYILGTLVHSFVWELPSSVIELNMDESFGLALQKAVPL  495

Query  492  SALVSPRLASNPYA  505
            +A+V+PRL  + Y+
Sbjct  496  AAMVTPRLPLHIYS  509
```

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RecName: Full=Flavonoid 3',5'-hydroxylase; Short=F3'5'H; AltName: Full=Cytochrome P450 75A4

Sequence ID: Q96581.1 **Length:** 516 **Number of Matches:** 1

Related Information

Range 1: 8 to 515 GenPept Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
735 bits(1897)	0.0	Compositional matrix adjust.	359/508(71%)	421/508(82%)	6/508(1%)

```
Query  4    LVTDFVVAAIIFLITRFLVRSLFKKPT----RPLPPGPLGWPLVGALPLLGAMPHVALAK  59
            L      A  +F   + LV  L  K T    R LPPGP GWP++GALPLLG MPHV  A
Sbjct  8    LTLHLATALFLFFHVQKLVHYLHGKATGHRCRRLPPGPTGWPILGALPLLGNMPHVTFAN  67

Query  60   LAKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFA  119
            +AKKYG +M+LK+G+  + +ASTP++A+AFLKTLDLNFSNRPPNAGA+HLAY AQD+VFA
```

```
Sbjct  68   MAKKYGSVMYLKVGSHGLAIASTPDAAKAFLKTLDLNFSNRPPNAGATHLAYNAQDMVFA  127

Query  120  KYGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYA  179
             YGP+WK LRKLSNLHMLGGKAL++WA+VR TELG+MLKAM E+S+  EPV+++EMLTYA
Sbjct  128  HYGPKWKLLRKLSNLHMLGGKALENWADVRKTELGYMLKAMFESSQNNEPVMISEMLTYA  187

Query  180  MANMIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGM  239
            MANM+ QVILSRRVF  KG +SNEFKDMVVELMTSAGYFNIGDFIPSI WMDLQGIE GM
Sbjct  188  MANMLSQVILSRRVFNKKGAKSNEFKDMVVELMTSAGYFNIGDFIPSIGWMDLQGIEGGM  247

Query  240  KKLHTKFDVLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLF  299
            K+LH KFDVLLT+++ +H+ TS ERK K DFLD ++   DN++GE+L+  NIKA+LLNLF
Sbjct  248  KRLHKKFDVLLTRLLDDHKRTSQERKQKPDFLDFVIANGDNSDGERLNTDNIKALLLNLF  307

Query  300  TAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKET  359
            TAGTDTSSSIIEWAL E++KN T+L +AQ+EMDRVIGRDRRLLESDI +LPYLQAI KET
Sbjct  308  TAGTDTSSSIIEWALAELLKNRTLLTRAQDEMDRVIGRDRRLLESDIPNLPYLQAICKET  367

Query  360  YRKHPSTPLNLPRIAIQA-CEVDGYYIPKDARLSVNIWAIGRDPNVW-ENPLEFLPERFL  417
            +RKHPSTPLNLPR  I+   +V+GYYIPK  RL+VNIWAIGRDP+VW +NP EF PERFL
Sbjct  368  FRKHPSTPLNLPRNCIRGHVDVNGYYIPKGTRLNVNIWAIGRDPSVWGDNPNEFDPERFL  427

Query  418  SEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNM  477
               N KI+P GN F+LIPFGAGRRICAGTRMG++LV YILGTLVHSFDWKL     ELNM
Sbjct  428  YGRNAKIDPRGNHFELIPFGAGRRICAGTRMGILLVEYILGTLVHSFDWKLGFSEDELNM  487

Query  478  DESFGLALQKAVPLSALVSPRLASNPYA  505
            DE+FGLALQKAVPL+A+V PRL  + YA
Sbjct  488  DETFGLALQKAVPLAAMVIPRLPLHVYA  515
```

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RecName: Full=Flavonoid 3',5'-hydroxylase; Short=F3'5'H; AltName: Full=Cytochrome P450 75A6

Sequence ID: O04773.1   **Length:** 523   **Number of Matches:** 1

Related Information

Range 1: 5 to 523 GenPept   Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
676 bits(1743)	0.0	Compositional matrix adjust.	331/519(64%)	405/519(78%)	13/519(2%)

```
Query  1    MAILVTDFVVAAIIFLITRFLVRSLFK-KPTRPLPPGPLGWPLVGALPLLGAMPHVALAK  59
            ++ L  + V A  ++L T   +R LFK      LPPGP GWP++GALPLLG MPHV+LA
Sbjct  5    ISTLFYELVAAISLYLATYSFIRFLFKPSHHHHLPPGPTGWPIIGALPLLGTMPHVSLAD  64

Query  60   LAKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFA  119
            +A KYGPIM+LK+G+   VVAS P++ARAFLKT D NFSNRP + G ++LAY AQD+VFA
Sbjct  65   MAVKYGPIMYLKLGSKGTVVASNPKAARAFLKTHDANFSNRPIDGGPTYLAYNAQDMVFA  124

Query  120  KYGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLA--EMLT  177
            +YGP+WK LRKL +LHMLG KAL+DWA+V+V+E+GHMLK M E S    PV +   EMLT
Sbjct  125  EYGPKWKLLRKLCSLHMLGPKALEDWAHVKVSEVGHMLKEMYEQSSKSVPVPVVVPEMLT  184

Query  178  YAMANMIGQVILSRRVFVTKG---------TESNEFKDMVVELMTSAGYFNIGDFIPSIA  228
            YAMANMIG++ILSRR FV               +EF+ MV+ELM  AG FNIGDFIP IA
Sbjct  185  YAMANMIGRIILSRRPFVITSKLDSSASASASVSEFQYMVMELMRMAGLFNIGDFIPYIA  244

Query  229  WMDLQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKGKADFLDVLLEEC-DNTNGEKLS  287
            WMDLQGI+R MK +  KFDVLL KM+KEH  ++H+RK   DFLD+L+    +NT G +L+
Sbjct  245  WMDLQGIQRDMKVIQKKFDVLLNKMIKEHTESAHDRKDNPDFLDILMAATQENTEGIQLN  304

Query  288  ITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDIS  347
            + N+KA+LL+LFTAGTDTSSS+IEWAL EM+ +  IL +A EEMD+VIGR+RRL +SDI
Sbjct  305  LVNVKALLLDLFTAGTDTSSSVIEWALAEMLNHRQILNRAHEEMDQVIGRNRRLEQSDIP  364

Query  348  SLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWEN  407
            +LPY QAI KET+RKHPSTPLNLPRI+ +ACEVDG++IPK+ RL VNIWAIGRDP VWEN
Sbjct  365  NLPYFQAICKETFRKHPSTPLNLPRISTEACEVDGFHIPKNTRLIVNIWAIGRDPKVWEN  424

Query  408  PLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWK  467
            PL+F PERFLSE++ KI+P GN F+LIPFGAGRRICAG RMG   V YILGTLVHSFDWK
Sbjct  425  PLDFTPERFLSEKHAKIDPRGNHFELIPFGAGRRICAGARMGAASVEYILGTLVHSFDWK  484

Query  468  LPNGVAELNMDESFGLALQKAVPLSALVSPRLASNPYAT  506
            LP+GV E+NM+ESFG+ALQK VPLSA+V+PRL  + Y
Sbjct  485  LPDGVVEVNMEESFGIALQKKVPLSAIVTPRLPPSSYTV  523
```

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RecName: Full=Flavonoid 3'-monooxygenase; AltName: Full=Cytochrome P450 75B1; AltName: Full=Flavonoid 3'-hydroxylase; Short=AtF3'H; AltName: Full=Protein TRANSPARENT TESTA 7

Sequence ID: Q9SD85.1   **Length:** 513   **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 1 to 509 GenPept   Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
506 bits(1302)	2e-175	Compositional matrix adjust.	248/513(48%)	348/513(67%)	12/513(2%)

```
Query  1    MAILVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKL  60
            MA L    ++A ++FLI R       +     LPPGP  WP++G LP +G  PH  L+ +
Sbjct  1    MATLFLTILLATVLFLILRIFSHRRNRSHNNRLPPGPNPWPIIGNLPHMGTKPHRTLSAM  60

Query  61   AKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAK  120
               YGPI+HL++G  D+VVA++   A  FLK  D NF++RPPN+GA H+AY  QDLVFA
```

```
Sbjct  61   VTTYGPILHLRLGFVDVVVAASKSVAEQFLKIHDANFASRPPNSGAKHMAYNYQDLVFAP  120

Query  121  YGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCG-EPVVLAEMLTYA  179
            YG RW+ LRK+S++H+   KAL+D+ +VR  E+G + +   E  R G +PV L +++
Sbjct  121  YGHRWRLLRKISSVHLFSAKALEDFKHVRQEEVGTLTR---ELVRVGTKPVNLGQLVNMC  177

Query  180  MANMIGQVILSRRVF-VTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERG  238
            + N +G+ ++ RR+F      +++EF+ MV E+M  AG FNIGDF+PS+ W+DLQG+
Sbjct  178  VVNALGREMIGRRLFGADADHKADEFRSMVTEMMALAGVFNIGDFVPSLDWLDLQGVAGK  237

Query  239  MKKLHTKFDVLLTKMVKEHRATSHERKGKADFLDVL--LEECD-NTNGEKLSITNIKAVL  295
            MK+LH +FD  L+ ++KEH     ++K   D L  L  L+  D + +G  L+ T IKA+L
Sbjct  238  MKRLHKRFDAFLSSILKEHEMNGQDQK-HTDMLSTLISLKGTDLDGDGGSLTDTEIKALL  296

Query  296  LNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAI  355
            LN+FTAGTDTS+S ++WA+ E+I++P I+ KAQEE+D V+GRDR + ESDI+ LPYLQA+
Sbjct  297  LNMFTAGTDTSASTVDWAIAELIRHPDIMVKAQEELDIVVGRDRPVNESDIAQLPYLQAV  356

Query  356  AKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPER  415
             KE +R HP TPL+LP IA ++CE++GY+IPK + L  NIWAI RDP+ W +PL F PER
Sbjct  357  IKENFRLHPPTPLSLPHIASESCEINGYHIPKGSTLLTNIWAIARDPDQWSDPLAFKPER  416

Query  416  FL-SEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVA-  473
            FL   E   ++  G+DF+LIPFGAGRRICAG  +G+  + ++  TLV  FDW+L  GV
Sbjct  417  FLPGGEKSGVDVKGSDFELIPFGAGRRICAGLSLGLRTIQFLTATLVQGFDWELAGGVTP  476

Query  474  -ELNMDESFGLALQKAVPLSALVSPRLASNPYA  505
             +LNM+ES+GL LQ+AVPL     PRLA N Y
Sbjct  477  EKLNMEESYGLTLQRAVPLVVHPKPRLAPNVYG  509
```

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RecName: Full=Flavonoid 3'-monooxygenase; AltName: Full=Cytochrome P450 75B2; AltName: Full=Flavonoid 3'-hydroxylase

Sequence ID: Q9SBQ9.1 **Length:** 512 **Number of Matches:** 1

Related Information

Range 1: 3 to 510 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
478 bits(1231)	1e-164	Compositional matrix adjust.	257/518(50%)	357/518(68%)	28/518(5%)

```
Query  5    VTDFVVAAIIF-LITRFLVRSLFKKP-TRPLPPGPLGWPLVGALPLLGAMPHVALAKLAK  62
            +   ++  +IF  + +F++RS F+K    PLPPGP  WP++G L  LG  PH + A +A+
Sbjct  3    ILSLILYTVIFSFLLQFILRSFFRKRYPLPLPPGPKPWPIIGNLVHLGPKPHQSTAAMAQ  62

Query  63   KYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYG  122
             YGP+M+LKMG  D+VVA++   A  FLKT D NFS+RPPN+GA H+AY  QDLVFA YG
Sbjct  63   TYGPLMYLKMGFVDVVVAASASVAAQFLKTHDANFSSRPPNSGAEHMAYNYQDLVFAPYG  122

Query  123  PRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMAN  182
            PRW+ LRK+ ++H+   KALDD+ +VR  E+  + +A+  A +  +PV L ++L     N
Sbjct  123  PRWRMLRKICSVHLFSTKALDDFRHVRQDEVKTLTRALASAGQ--KPVKLGQLLNVCTTN  180

Query  183  MIGQVILSRRVFVTKGTESN----EFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERG  238
             + +V+L +RVF     + +    EFK MVVE+M  AG FNIGDFIP + W+D+QG+
Sbjct  181  ALARVMLGKRVFADGSGDVDPQAAEFKSMVVEMMVVAGVFNIGDFIPQLNWLDIQGVAAK  240

Query  239  MKKLHTKFDVLLTKMVKEHRATSHERKGK-----ADFLDVLL----EECDNTNGEKLSIT  289
            MKKLH +FD  LT +++EH       KGK      D L  L+    ++ DN +G KL+ T
Sbjct  241  MKKLHARFDAFLTDILEEH-------KGKIFGEMKDLLSTLISLKNDDADN-DGGKLTDT  292

Query  290  NIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSL  349
             IKA+LLNLF AGTDTSSS +EWA+ E+I+NP IL +AQ+E+D+V+GRDR + E D++ L
Sbjct  293  EIKALLLNLFVAGTDTSSSTVEWAIAELIRNPKILAQAQQEIDKVVGRDRLVGELDLAQL  352

Query  350  PYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPL  409
             YL+AI KET+R HPSTPL+LPRIA ++CE++GY+IPK + L +N+WAI RDPN W +PL
Sbjct  353  TYLEAIVKETFRLHPSTPLSLPRIASESCEINGYFIPKGSTLLLNVWAIARDPNAWADPL  412

Query  410  EFLPERFL-SEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKL  468
            EF PERFL   E  K++  GNDF++IPFGAGRRICAG  +G+ +V  ++ TL+H+F+W L
Sbjct  413  EFRPERFLPGGEKPKVDVRGNDFEVIPFGAGRRICAGMNLGIRMVQLMIATLIHAFNWDL  472

Query  469  PNGV--AELNMDESFGLALQKAVPLSALVSPRLASNPY  504
             +G     LNM+E++GL LQ+A PL     PRL +  Y
Sbjct  473  VSGQLPEMLNMEEAYGLTLQRADPLVVHPRPRLEAQAY  510
```

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RecName: Full=Cytochrome P450 750A1; AltName: Full=Cytochrome P450 CYPC

Sequence ID: Q50EK4.1 **Length:** 525 **Number of Matches:** 1

Related Information

Range 1: 42 to 525 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
371 bits(953)	2e-122	Compositional matrix adjust.	196/485(40%)	303/485(62%)	15/485(3%)

```
Query  33   LPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKT  92
            LPPGP  WP++G    +    H  L  LA+KYGPI+ L+ G+    VV S+ E A+ FLKT
Sbjct  42   LPPGPYPWPIIGNFHQVRLPLHRTLKNLAEKYGPILFLRFGSVPTVVVSSSEKAKHFLKT  101

Query  93   LDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTE  152
             DL F++RPP +   +  Y  +D+ F+ YG  W+ +RK+  L +L  K ++ + +VR  E
```

```
Sbjct  102  HDLIFASRPPTSVGKYFFYNFKDIAFSPYGDHWRKMRKICVLELLTSKRIESFKHVRQEE  161

Query  153  LGHMLKAMCEASRCGEPVV-LAEMLTYAMANMIGQVILSRRVFVTK--GTESNEFKDMVV  209
            L  M+ ++ E S  G   V +++ ++ ++AN++ + IL+R+ F     G +   F D+VV
Sbjct  162  LSAMIHSIWEESESGRIAVNVSKAISTSLANILWR-ILARKKFSDNDLGADGKGFADLVV  220

Query  210  ELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKGKAD  269
            E+  + G  NIGDFIP +  +DLQGI+R +KK + +FD    KM+ EH   S  R G+AD
Sbjct  221  EVSIAVGSLNIGDFIPYLDCLDLQGIKRALKKANARFDAFAEKMIDEHINASTIRNGEAD  280

Query  270  -------FLDVLLEECDNTN-GEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNP  321
                    +DVLLE   N N G K++   IKA+   LF+AG +TS++++EWA++E++++P
Sbjct  281  AGCHVKDIIDVLLEMAKNDNTGAKVTREIIKAITYELFSAGMETSANVLEWAMSELLRHP  340

Query  322  TILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVD  381
              +KK Q+E++ V+G+   + ESD++S+ YL  + KET R +PS PL LP  +++A  V
Sbjct  341  HAMKKLQQEIESVVGQQGTVKESDLASIVYLHCVVKETLRLYPSLPLALPHESLEAVTVG  400

Query  382  GYYIPKDARLSVNIWAIGRDPNVW-ENPLEFLPERFLS-EENG-KINPGGNDFKLIPFGA  438
            GYYIPK   + +N+WAIGRDP+VW  +  EF PERF+  EENG  ++ G +DF+++PFGA
Sbjct  401  GYYIPKKTMVIMNLWAIGRDPSVWGADASEFKPERFMQMEENGIDLSGGQSDFRMLPFGA  460

Query  439  GRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMDESFGLALQKAVPLSALVSPR  498
            GRR C G+ M ++ V + L  L+H+FDW++    +EL+M E+    + +  PL A    R
Sbjct  461  GRRTCPGSAMAILTVEFTLAQLLHTFDWRVEGDPSELDMKEACATKMPRQTPLLAYPRLR  520

Query  499  LASNP  503
            L   P
Sbjct  521  LPRCP  525
```

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RecName: Full=Cytochrome P450 CYP736A12

Sequence ID: H2DH18.1 **Length:** 500 **Number of Matches:** 1

Related Information

Range 1: 33 to 500 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
369 bits(948)	4e-122	Compositional matrix adjust.	193/476(41%)	289/476(60%)	17/476(3%)

```
Query  33   LPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKT  92
            LPPGP G P++G+L  LGA+PH  L  LAKKYGPIM +++G+   +V S+P++A  FLKT
Sbjct  33   LPPGPRGLPIIGSLHTLGALPHRTLQTLAKKYGPIMSMRLGSVPTIVVSSPQAAELFLKT  92

Query  93   LDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTE  152
             D  F++RP    A +++YG   + F  YGP W+ +RK   L +L    ++ +  +R  E
Sbjct  93   HDNIFASRPKLQAAEYMSYGTMGMSFTAYGPHWRNIRKFVVLELLTPAKINSFVGMRREE  152

Query  153  LGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVELM  212
            LG ++K++ EAS   E V L+  +   + NM  +++L R    TK  +  + K ++ E +
Sbjct  153  LGTVVKSIKEASAANEVVDLSAKVANIIENMTYRLLLGR----TK-DDRYDLKGIMNEAL  207

Query  213  TSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKGKADFLD  272
            T AG FNI DF+P +  +D+QG+ R  K    + D +L  ++ EH   S       DF+D
Sbjct  208  TLAGRFNIADFVPFLGPLDIQGLTRQFKDTGKRLDKILEFIIDEHEQNSSNGNASGDFID  267

Query  273  VLLE---ECDNTNGEKLSITN---IKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKK  326
             +L    +  NT+ E   + +   IKA+++++ +A  DTS + IEW LTE+IK+P  +KK
Sbjct  268  DMLSLKNKPSNTHDELSKVIDRSVIKAIMIDIISAAIDTSDTSIEWILTELIKHPRAMKK  327

Query  327  AQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIP  386
             QEE+D V+G DR + E+D+ +L Y+  + KE  R HP  PL  P  +++   ++GY+IP
Sbjct  328  CQEEIDAVVGVDRMVEETDLPNLEYVYMVVKEGLRLHPVAPLLGPHESMEDITINGYFIP  387

Query  387  KDARLSVNIWAIGRDPNVW-ENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAG  445
            K +R+ VN WA+GRDPNVW EN  EFLPERF   E   ++  G DF+L+PFG+GRR C G
Sbjct  388  KQSRVIVNSWALGRDPNVWSENAEEFLPERF---EGSNVDVRGRDFQLLPFGSGRRGCPG  444

Query  446  TRMGMVLVSYILGTLVHSFDWKLPNGVA--ELNMDESFGLALQKAVPLSALVSPRL  499
             ++G++ V  ++  LVH FDW LPNG     L+M E FGL   +   L A+   RL
Sbjct  445  MQLGLITVQLVVARLVHCFDWNLPNGTTPDNLDMTEKFGLTTPRVKHLLAVPKYRL  500
```

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RecName: Full=3,9-dihydroxypterocarpan 6A-monooxygenase; AltName: Full=Cytochrome P450 93A1; AltName: Full=Dihydroxypterocarpan 6a-hydroxylase; Short=D6aH

Sequence ID: Q42798.1 **Length:** 509 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 23 to 508 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
367 bits(942)	5e-121	Compositional matrix adjust.	195/490(40%)	291/490(59%)	14/490(2%)

```
Query  27   KKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESA  86
            K+  + LPP P   P++G L L+  +PH    KL+ ++GPIM L +G+   VVAST E+A
Sbjct  23   KQSKKNLPPSPKALPIIGHLHLVSPIPHQDFYKLSTRHGPIMQLFLGSVPCVVASTAEAA  82

Query  87   RAFLKTLDLNFSNRP-PNAGASHLAYGAQDLVFA--KYGPRWKTLRKLSNLHMLGGKALD  143
            + FLKT ++NFSNRP  N     LAY +QD +FA   +GP WK ++KL    +L G+ +D
Sbjct  83   KEFLKTHEINFSNRPGQNVAVKGLAYDSQDFLFAFAPFGPYWKFMKKLCMSELLSGRMMD  142

Query  144  DWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNE  203
             +  VR  E    +  +      GE V   + L     N++ ++ LS++       ++ E
```

```
Sbjct  143  QFLPVRQQETKRFISRVFRKGVAGEAVDFGDELMTLSNNIVSRMTLSQKT-SENDNQAEE  201

Query  204  FKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKFDVLLTKMVKEHRATSHE  263
             K +V  +    G FN+ DFI  +   DLQG  R +K+   +FDV++  ++K+ +    +
Sbjct  202  MKKLVSNIAELMGKFNVSDFIWYLKPFDLQGFNRKIKETRDRFDVVVDGIIKQRQEERRK  261

Query  264  RK--GKA----DFLDVLLEECDNTNGE-KLSITNIKAVLLNLFTAGTDTSSSIIEWALTE  316
             K  G A    D LDVLL+  ++ N E KL   NIKA ++++F AGTDTS+  IEWA+ E
Sbjct  262  NKETGTAKQFKDMLDVLLDMHEDENAEIKLDKKNIKAFIMDIFVAGTDTSAVSIEWAMAE  321

Query  317  MIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQ  376
            +I NP +L+KA++E+D V+G+ R + ESDI++LPYLQAI +ET R HP  PL + R + +
Sbjct  322  LINNPDVLEKARQEIDAVVGKSRMVEESDIANLPYLQAIVRETLRLHPGGPL-VVRESSK  380

Query  377  ACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPF  436
            +  V GY IP   RL VN+WAIGRDPN WE P EF PERF+ +   +++  G  +  IPF
Sbjct  381  SAVVCGYDIPAKTRLFVNVWAIGRDPNHWEKPFEFRPERFIRDGQNQLDVRGQHYHFIPF  440

Query  437  GAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMDESFGLALQKAVPLSALVS  496
            G+GRR C G  +   +V   L  ++  F WKL  G  +++M+E  G+ L +A P+  +
Sbjct  441  GSGRRTCPGASLAWQVVPVNLAIIIQCFQWKLVGGNGKVDMEEKSGITLPRANPIICVPV  500

Query  497  PRLASNPYAT  506
            PR+  NP+ T
Sbjct  501  PRI--NPFPT  508
```

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RecName: Full=Cytochrome P450 93A3; AltName: Full=Cytochrome P450 CP5

Sequence ID: O81973.1 **Length:** 510 **Number of Matches:** 1

Related Information

Range 1: 40 to 507 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
361 bits(927)	9e-119	Compositional matrix adjust.	195/471(41%)	281/471(59%)	11/471(2%)

```
Query  42   LVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRP  101
            ++G L LL   PH    KL+ +YGPI+HL +G+   VVAST E+A+ FLKT +  FSNRP
Sbjct  40   IIGHLHLLSPTPHQDFHKLSLRYGPIIHLFLGSVPCVVASTAEAAKEFLKTHEPAFSNRP  99

Query  102  PNAGASH-LAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAM  160
             N  A   L YG QD +FA YGP WK ++KL    +LGG  LD +  VR  E    +K +
Sbjct  100  ANTVAVETLTYGFQDFLFAPYGPYWKFMKKLCMSELLGGHMLDQFLPVRQXETKKFIKRV  159

Query  161  CEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNI  220
             +    GE V           N++ ++I+S+        E  E + +V +    +G FNI
Sbjct  160  LQKGISGEAVDFGGEFITLSNNIVSRMIVSQTSTTEDENEVEEMRKLVKDAAELSGKFNI  219

Query  221  GDFIPSIAWMDLQGIERGMKKLHTKFDVLLTKMVK---EHRATSHERKGKADF---LDVL  274
             DF+  +   DLQG  + ++K+   FD +L +++K   E R   +E  GK +F   LDVL
Sbjct  220  SDFVSFLKRFDLQGFNKRLEKIRDCFDTVLDRIIKQREEERRNKNETVGKREFKDMLDVL  279

Query  275  LEECDNTNGE-KLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDR  333
             +  ++ + E KL+  NIKA +L++  AGTDTS+  +EWA+ E+I NP +L+KA++EMD
Sbjct  280  FDISEDESSEIKLNKENIKAFILDILIAGTDTSAVTMEWAMAELINNPGVLEKARQEMDA  339

Query  334  VIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSV  393
            V+G+ R + ESDI++LPYLQ I +ET R HP+ PL L R + +   V GY IP   RL V
Sbjct  340  VVGKSRIVEESDIANLPYLQGIVRETLRLHPAGPL-LFRESSRRAVVCGYDIPAKTRLFV  398

Query  394  NIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLV  453
            N+WAIGRDPN WENPLEF PERF+     +++  G  + L+PFG+GRR C GT + + +V
Sbjct  399  NVWAIGRDPNHWENPLEFRPERFVENGKSQLDVRGQHYHLLPFGSGRRACPGTSLALQVV  458

Query  454  SYILGTLVHSFDWKLPNGVAELNMDESFGLALQKAVPLSALVSPRLASNPY  504
               L  L+  F WK+     ++NM+E  G+ L +A P+  +   RL  NP+
Sbjct  459  HVNLAVLIQCFQWKVDCDNGKVNMEEKAGITLPRAHPIICVPIRRL--NPF  507
```

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RecName: Full=Geraniol 8-hydroxylase; AltName: Full=Cytochrome P450 76B6; AltName: Full=Geraniol 10-hydroxylase; Short=CrG10H

Sequence ID: Q8VWZ7.1 **Length:** 493 **Number of Matches:** 1

Related Information

Range 1: 6 to 491 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
357 bits(916)	2e-117	Compositional matrix adjust.	197/491(40%)	294/491(59%)	8/491(1%)

```
Query  9    VVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIM  68
            ++  ++F +T +   S   + T+ LPPGP   P +G+L LLG  PH +LAKL+KK+GPIM
Sbjct  6    IILTLLFALTLYEAFSYLSRRTKNLPPGPSPLPFIGSLHLLGDQPHKSLAKLSKKHGPIM  65

Query  69   HLKMGTCDMVVASTPESARAFLKTLDLNFSNRP-PNAGASHLAYGAQDLVFAKYGPRWKT  127
             LK+G    +V S+   A+  L+  DL FS+R  PNA  +H   +    +V+      RW++
Sbjct  66   SLKLGQITTIVISSSTMAKEVLQKQDLAFSSRSVPNALHAHNQFKFS-VVWLPVASRWRS  124

Query  128  LRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQV  187
            LRK+ N ++  G  LD   ++R  ++  ++    + S+ GE V +         N++  +
Sbjct  125  LRKVLNSNIFSGNRLDANQHLRTRKVQELIAYCRKNSQSGEAVDVGRAAFRTSLNLLSNL  184

Query  188  ILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKFD  247
            I S+ +       + EFKD+V  +M  AG  N+ DF P +  +D QGI   M     +
```

```
Sbjct  185  IFSKDLTDPYSDSAKEFKDLVWNIMVEAGKPNLVDFFPLLEKVDPQGIRHRMTIHFGEVL  244

Query  248  VLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTDTSS  307
             L   +V E       +  K D LDVLL     +  E++  T+I+ + L+LF AGTDT+S
Sbjct  245  KLFGGLVNERLEQRRSKGEKNDVLDVLLTTSQES-PEEIDRTHIERMCLDLFVAGTDTTS  303

Query  308  SIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTP  367
            S +EWA++EM+KNP  +KK Q+E+ +VIGR + + ESDI+ LPYL+ + KET R HP  P
Sbjct  304  STLEWAMSEMLKNPDKMKKTQDELAQVIGRGKTIEESDINRLPYLRCVMKETLRIHPPVP  363

Query  368  LNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPG  427
              +PR   Q+ EV GY +PK +++ VN WAIGRD  VW++ L F PERF+  E   ++
Sbjct  364  FLIPRKVEQSVEVCGYNVPKGSQVLVNAWAIGRDETVWDDALAFKPERFMESE---LDIR  420

Query  428  GNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVA--ELNMDESFGLAL  485
            G DF+LIPFGAGRRIC G  + +  V  +LG+L++SF+WKL  G+A  +L+M+E FG+ L
Sbjct  421  GRDFELIPFGAGRRICPGLPLALRTVPLMLGSLLNSFNWKLEGGMAPKDLDMEEKFGITL  480

Query  486  QKAVPLSALVS  496
            QKA PL A+ S
Sbjct  481  QKAHPLRAVPS  491
```

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RecName: Full=Cytochrome P450 93A2

Sequence ID: Q42799.1 **Length:** 502 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 10 to 499 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
356 bits(914)	5e-117	Compositional matrix adjust.	198/506(39%)	296/506(58%)	26/506(5%)

```
Query  9    VVAAIIF--LITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGP  66
            VV++I+F  ++ R       K+  + LPP P G P++G L L+  +PH    KL+ ++GP
Sbjct  10   VVSSIVFAYIVWR-------KERKKKLPPSPKGLPIIGHLHLVSPIPHQDFYKLSLRHGP  62

Query  67   IMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRP-PNAGASHLAYGAQDLVFAKYGPRW  125
            IM L +G+   VVAST E+A+ FLKT ++NFSNRP  N     L Y     VF  YGP
Sbjct  63   IMQLFLGSVPCVVASTAEAAKEFLKTHEINFSNRPGQNVAVQFLTY-----VFGPYGPSV  117

Query  126  KTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIG  185
            K ++KL    +LGG+ LD +  VR  E    +K + +    GE V           N+I
Sbjct  118  KFIKKLCMSELLGGRMLDQFLPVRQQETKKFIKRVLQKGIAGEAVDFGGEFMRLSNNIIS  177

Query  186  QVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTK  245
            ++ +++        ++ E + +V ++    G FN+ DFI  +   DLQG  + ++K   +
Sbjct  178  RMTMNQ-TSSEDEKQAEEMRMLVADVAELMGTFNVSDFIWFLKPFDLQGFNKRIRKTRIR  236

Query  246  FDVLLTKMVK---EHRATSHERKGK---ADFLDVLLEECDNTNGE-KLSITNIKAVLLNL  298
            FD +L +++K   E R  + E  G     D LDVLL+  ++ + E KL+  NIKA ++++
Sbjct  237  FDAVLDRIIKQREEERRNNKEIGGTRQFKDILDVLLDIGEDDSSEIKLTKENIKAFIMDI  296

Query  299  FTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKE  358
            F AGTDTS++ +EWA+ E+I NP +L+KA++E+D V+G  R + ESDI +LPYLQAI +E
Sbjct  297  FVAGTDTSAATMEWAMAELINNPCVLEKARQEIDAVVGNSRIIEESDIVNLPYLQAIVRE  356

Query  359  TYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLS  418
            T R HP  PL + R + ++  V GY IP   RL VN+WAIGRDPN WENP EF PERF
Sbjct  357  TLRIHPGGPL-IVRESSKSVVVCGYEIPAKTRLFVNVWAIGRDPNHWENPFEFRPERFFE  415

Query  419  EENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMD  478
                +++  G  +  IPFG+GRR C GT + + +V   L  ++  F WK  NG  +++M+
Sbjct  416  NGQSQLDVRGQHYHFIPFGSGRRSCPGTSLALQIVHVNLAIMIQCFQWKFDNGNNKVDME  475

Query  479  ESFGLALQKAVPLSALVSPRLASNPY  504
            E  G+ L +A P+  +  PRL  NP+
Sbjct  476  EKSGITLPRAHPIICVPVPRL--NPF  499
```

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RecName: Full=Cytochrome P450 76C4

Sequence ID: O64635.1 **Length:** 511 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 38 to 503 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
350 bits(897)	2e-114	Compositional matrix adjust.	191/472(40%)	285/472(60%)	16/472(3%)

```
Query  33   LPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKT  92
            LPPGP   P++G +  +G  PH + A LAK YGPIM LK G  + VV ++PE+AR  L+T
Sbjct  38   LPPGPPRLPIIGNIHQVGKNPHSSFADLAKIYGPIMSLKFGCLNSVVITSPEAAREVLRT  97

Query  93   LDLNFSNRPPNAGASHLAYGAQDLVFAKYGP---RWKTLRKLSNLHMLGGKALDDWANVR  149
             D   S R  N   S   +G +++      P   RW+ LRKLS   M   +  +    +R
Sbjct  98   HDQILSGRKSND--SIRCFGHEEVSVIWLPPSSARWRMLRKLSVTLMFSPQRTEATKALR  155

Query  150  VTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVV  209
            + ++  ++  M E+S   E V ++      + N+I  ++ S  +      +SNEF+D V+
Sbjct  156  MKKVQELVSFMNESSERKEAVDISRASYTTVLNIISNILFSVDLGSYDSKKSNEFQDTVI  215

Query  210  ELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTK----FDVLLTKMVKEHRATSHERK  265
              M +AG  +  ++ P + ++DLQG  + M+ L  +    F   +   + E    ++ +
Sbjct  216  GAMEAAGKPDAANYFPFMGFLDLQGNRKAMRGLTERLFRVFRGFMDAKIAEKSLGNYSKD  275
```

```
Query  266  -GKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTIL  324
                DFLD LL   +    E L   +I+ +LL++FTAGTDTSSS +EWA+ E+++NP  +
Sbjct  276  VSNRDFLDSLLILNEGDEAE-LDNNDIEHLLLDMFTAGTDTSSSTLEWAMAELLRNPKTM  334

Query  325  KKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYY  384
             KAQ EMDRV+G++  + ESDIS LPYLQA+ KET+R HP+ PL +PR A    EV G+
Sbjct  335  VKAQAEMDRVLGQNSVVQESDISGLPYLQAVVKETFRLHPAAPLLVPRKAESDVEVLGFM  394

Query  385  IPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICA  444
            +PKD ++ VN+WAIGRDP+VWENP +F PERF+ ++   I+  G D++L PFG GRRIC
Sbjct  395  VPKDTQVLVNVWAIGRDPSVWENPSQFEPERFMGKD---IDVKGRDYELTPFGGGRRICP  451

Query  445  GTRMGMVLVSYILGTLVHSFDWKLPNGVA--ELNMDESFGLALQKAVPLSAL  494
            G  + +  VS +L +L++SFDWKLPNGV   +L+MDE+FG+ L +   L A+
Sbjct  452  GLPLAVKTVSLMLASLLYSFDWKLPNGVVSEDLDMDETFGITLHRTNTLYAI  503
```

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RecName: Full=Beta-amyrin 24-hydroxylase; AltName: Full=Cytochrome P450 93E1; AltName: Full=Sophoradiol 24-hydroxylase

Sequence ID: Q9XHC6.1 **Length:** 513 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 4 to 512 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
348 bits(893)	1e-113	Compositional matrix adjust.	193/515(37%)	310/515(60%)	20/515(3%)

```
Query  5    VTDFVVAAIIFLITRFLVRSLFKKPTR-PLPPGP-LGWPLVGALPLLGAMPHVALAKLAK  62
            +  ++V   ++ I+  L+RS+FKKP R  LPPGP +  PL+G  P L ++ H AL KL+
Sbjct  4    IKGYLVLFFLWFISTILIRSIFKKPQRLRLPPGPPISIPLLGHAPYLRSLLHQALYKLSL  63

Query  63   KYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYG  122
            +YGP++H+ +G+  +VVAS+ E+A+  LKT +  F NRP    +  L YGA D  F  YG
Sbjct  64   RYGPLIHVMIGSKHVVVASSAETAKQILKTSEEAFCNRPLMIASESLTYGAADYFFIPYG  123

Query  123  PRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCG--EPVVLAEMLTYAM  180
              W+ L+KL    +L GK L+ +  +R +E+   LK M E S  G  E V+  E++T+
Sbjct  124  TYWRFLKKLCMTELLSGKTLEHFVRIRESEVEAFLKRMMEISGNGNYEVVMRKELITHT-  182

Query  181  ANMIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMK  240
             N+I ++I+ ++    +  E    + +V E+    G FN+GD I  +  +DLQG  +
Sbjct  183  NNIITRMIMGKKS-NAENDEVARLRKVVREVGELLGAFNLGDVIGFMRPLDLQGFGKKNM  241

Query  241  KLHTKFDVLLTKMVKEHRATSHERKG----KADFLDVLLE--ECDNTNGEKLSITNIKAV  294
            + H K D ++ K+++EH     +       K D  D+LL   E D  +  KL+  + KA
Sbjct  242  ETHHKVDAMMEKVLREHEEARAKEDADSDRKKDLFDILLNLIEADGADN-KLTRESAKAF  300

Query  295  LLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQA  354
             L++F AGT+  +S++EW+L E+++NP + KKA+EE++ V+G++R + ESDI +LPYLQA
Sbjct  301  ALDMFIAGTNGPASVLEWSLAELVRNPHVFKKAREEIESVVGKERLVKESDIPNLPYLQA  360

Query  355  IAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPE  414
            + KET R HP TP+   R A++ C+V+GY IP+++ + ++ WAIGRDPN W++ LE+ PE
Sbjct  361  VLKETLRLHPPTPI-FAREAMRTCQVEGYDIPENSTILISTWAIGRDPNYWDDALEYKPE  419

Query  415  RFLSEEN---GKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG  471
            RFL  ++    KI+  G  ++L+PFG+GRR C G  + ++++   L +L+  FDW + +G
Sbjct  420  RFLFSDDPGKSKIDVRGQYYQLLPFGSGRRSCPGASLALLVMQATLASLIQCFDWIVNDG  479

Query  472  V-AELNMDESFGLALQKAVPLSALVSPRLASNPYA  505
                ++M E   + +  A PL     PR    P+A
Sbjct  480  KNHHVDMSEEGRVTVFLAKPLKCKPVPRF--TPFA  512
```

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RecName: Full=Cytochrome P450 76C1

Sequence ID: O64636.1 **Length:** 512 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 38 to 503 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
345 bits(884)	2e-112	Compositional matrix adjust.	187/471(40%)	290/471(61%)	14/471(2%)

```
Query  33   LPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKT  92
            LPPGP   P++G + L+G  PH + A+L+K YGP+M LK+G+ + VV ++PE+AR  L+T
Sbjct  38   LPPGPPRLPIIGNIHLVGKHPHRSFAELSKTYGPVMSLKLGSLNTVVIASPEAAREVLRT  97

Query  93   LDLNFSNRPPNAGASHLAYGAQDLVF-AKYGPRWKTLRKLSNLHMLGGKALDDWANVRVT  151
             D   S R P      + +    LV+      RW+ LR+LS   +L  + ++    +R+
Sbjct  98   HDQILSARSPTNAVRSINHQDASLVWLPSSSARWRLLRRLSVTQLLSPQRIEATKALRMN  157

Query  152  ELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTES-NEFKDMVVE  210
            ++  ++  + E+S   E V ++ +      N+I  ++ S  +       S N  +D V+
Sbjct  158  KVKELVSFISESSDREESVDISRVAFITTLNIISNILFSVDLGSYNAKASINGVQDTVIS  217

Query  211  LMTSAGYFNIGDFIPSIAWMDLQGIERGMK----KLHTKFDVLLTKMVKEHRATSHERK-  265
            +M +AG  +  ++ P + ++DLQG  +  K    +L   F   +   + E  + ++ +
Sbjct  218  VMDAAGTPDAANYFPFLRFLDLQGNVKTFKVCTERLVRVFRGFIDAKIAEKSSQNNPKDV  277

Query  266  GKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILK  325
             K DF+D LL+     +  +LSI++I+ +LL++FTAGTDTSSS +EWA+TE++KNP  +
Sbjct  278  SKNDFVDNLLDY--KGDESELSISDIEHLLLDMFTAGTDTSSSTLEWAMTELLKNPKTMA  335
```

```
Query  326  KAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYI  385
            KAQ E+D VIG++  + ESDIS LPYLQA+ KET+R H   PL +PR A    E+ G+ +
Sbjct  336  KAQAEIDCVIGQNGIVEESDISKLPYLQAVVKETFRLHTPVPLLIPRKAESDAEILGFMV  395

Query  386  PKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAG  445
             KD ++ VN+WAIGRDP+VW+NP +F PERFL ++   ++  G D++L PFGAGRRIC G
Sbjct  396  LKDTQVLVNVWAIGRDPSVWDNPSQFEPERFLGKD---MDVRGRDYELTPFGAGRRICPG  452

Query  446  TRMGMVLVSYILGTLVHSFDWKLPNGV--AELNMDESFGLALQKAVPLSAL  494
              + M  VS +L +L++SFDWKLP GV   +L+MDE+FGL L K  PL A+
Sbjct  453  MPLAMKTVSLMLASLLYSFDWKLPKGVLSEDLDMDETFGLTLHKTNPLHAV  503
```

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RecName: Full=Costunolide synthase; Short=LsCOS; AltName: Full=Cytochrome P450 71BL2

Sequence ID: F8S1I0.1 **Length:** 490 **Number of Matches:** 1

Related Information

Range 1: 9 to 475 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
340 bits(873)	5e-111	Compositional matrix adjust.	186/481(39%)	285/481(59%)	20/481(4%)

```
Query  10   VAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGA-MPHVALAKLAKKYGPIM  68
            +A   FL+  F   +L  K ++ LPPGP   P++G +  L +  PH  L  LAKKYGPIM
Sbjct  9    LAVASFLL--FAFWALSPKTSKNLPPGPPKLPIIGNIHQLKSPTPHRVLRNLAKKYGPIM  66

Query  69   HLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTL  128
            HL++G    VV STP  AR  +KT D++F++RP    +    Y AQD+ +A YG  W+ +
Sbjct  67   HLQLGQVSTVVVSTPRLAREIMKTNDISFADRPTTTTSQIFFYKAQDIGWAPYGEYWRQM  126

Query  129  RKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVI  188
            +K+  L +L  K +  ++++R  EL  + K +   S+ G PV   EM    + N+I +
Sbjct  127  KKICTLELLSAKKVRSFSSIREEELRRISKVL--ESKAGTPVNFTEMTVEMVNNVICKAT  184

Query  189  LSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKKLHTKFD  247
            L          +     +++ +++ +   FN+  + P + +++ + G +    K+  + D
Sbjct  185  LGDSC-----KDQATLIEVLYDVLKTLSAFNLASYYPGLQFLNVILGKKAKWLKMQKQLD  239

Query  248  VLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITN--IKAVLLNLFTAGTDT  305
             +L  ++KEHR+    +  + D +DVLL   D T G   ++T+  +KAV+L++ TAGTDT
Sbjct  240  DILEDVLKEHRSKGRNKSDQEDLVDVLLRVKD-TGGLDFTVTDEHVKAVVLDMLTAGTDT  298

Query  306  SSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPS  365
            SS+ +EWA+TE+++NP ++K+AQEE+  V+  D  + E+D+ SL YL+ I KET R H
Sbjct  299  SSATLEWAMTELMRNPHMMKRAQEEVRSVVKGD-TITETDLQSLHYLKLIVKETLRLHAP  357

Query  366  TPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKIN  425
            TPL +PR   QAC VDGY IP   ++ VN WA G DP+ W++   F+PERF   EN  IN
Sbjct  358  TPLLVPRECRQACNVDGYDIPAKTKILVNAWACGTDPDSWKDAESFIPERF---ENCPIN  414

Query  426  PGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVA--ELNMDESFGL  483
              G DF+ IPFGAGRRIC G   G+ +V Y L   ++ FDWKLPNG+   EL++ E  G+
Sbjct  415  YMGADFEFIPFGAGRRICPGLTFGLSMVEYPLANFLYHFDWKLPNGLKPHELDITEITGI  474

Query  484  A  484
            +
Sbjct  475  S  475
```

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RecName: Full=Costunolide synthase; Short=CiCOS; AltName: Full=Cytochrome P450 71BL3

Sequence ID: G3GBK0.1 **Length:** 494 **Number of Matches:** 1

Related Information

Range 1: 9 to 475 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
340 bits(871)	1e-110	Compositional matrix adjust.	183/482(38%)	286/482(59%)	21/482(4%)

```
Query  9    VVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGA-MPHVALAKLAKKYGPI  67
            +V A +FL   F   +L  K ++ LPPGP   P++G +  L +  PH  L  LA+KYGPI
Sbjct  9    LVVASLFL---FAFWALSPKTSKNLPPGPPKLPIIGNIHQLKSPTPHRVLRNLARKYGPI  65

Query  68   MHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKT  127
            MHL++G    VV STP  AR  +KT D++F++RP    +    Y AQD+ +A YG  W+
Sbjct  66   MHLQLGQVSTVVVSTPRLAREIMKTNDISFADRPTTTTSQIFFYKAQDIGWAPYGEYWRQ  125

Query  128  LRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQV  187
            ++K+  L +L  K +  ++++R  EL  + K +   S+ G P+   EM    + N+I +
Sbjct  126  MKKICTLELLSAKKVRSFSSIREEELSRISKVL--ESQAGTPINFTEMTVEMVNNVICKA  183

Query  188  ILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKKLHTKF  246
             L          +     +++ +++ +   FN+  + P + +++ + G +    K+  +
Sbjct  184  TLGDSC-----KDQATLIEVLYDVLKTLSAFNLASYYPGLQFLNVILGKKAKWLKMQKQL  238

Query  247  DVLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITN--IKAVLLNLFTAGTD  304
            D +L  ++KEHR+    +  + D +DVLL   D T G   ++T+  +KAV+L++ TAGTD
Sbjct  239  DDILEDVLKEHRSKGSNKSDQEDLVDVLLRVKD-TGGLDFTVTDEHVKAVVLDMLTAGTD  297

Query  305  TSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHP  364
            TSS+ +EWA+TE+++NP ++K+AQ+E+ R + +   + E+D+ SL YL+ I KET R H
Sbjct  298  TSSATLEWAMTELMRNPHMMKRAQDEV-RSVVKGNTITETDLQSLHYLKLIVKETLRLHA  356

Query  365  STPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKI  424
             TPL +PR   Q C VDGY IP   ++ VN WA G DP+ W++P  F+PERF   EN  I
```

```
Sbjct  357  PTPLLVPRECRQDCNVDGYDIPAKTKILVNAWACGTDPDSWKDPESFIPERF---ENCPI  413

Query  425  NPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVA--ELNMDESFG  482
            N  G DF+ IPFGAGRRIC G   G+ +V Y L   ++ FDWKLPNG+   EL++ E  G
Sbjct  414  NYMGADFEFIPFGAGRRICPGLTFGLSMVEYPLANFLYHFDWKLPNGLKPHELDITEITG  473

Query  483  LA  484
            ++
Sbjct  474  IS  475
```

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RecName: Full=Geraniol 8-hydroxylase; AltName: Full=Cytochrome P450 76B10; AltName: Full=Geraniol 10-hydroxylase; Short=SmG10H

Sequence ID: D1MI46.1 **Length:** 495 **Number of Matches:** 1

Related Information

Range 1: 4 to 494 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
339 bits(869)	3e-110	Compositional matrix adjust.	198/496(40%)	298/496(60%)	10/496(2%)

```
Query  7    DFVVAAIIFLITRFLVRSL--FKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKY  64
            DF+  AI FL T  L ++L  F + ++ LPPGP   PL+G L LLG  PH +LAKLAKK+
Sbjct  4    DFLTIAIGFLFTITLYQALNFFSRKSKNLPPGPSPLPLIGNLHLLGDQPHKSLAKLAKKH  63

Query  65   GPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRP-PNAGASHLAYGAQDLVFAKYGP  123
            GPIM L++G    +V ++   A+  L+  DL FS+R  PNA  +H  Y    +++
Sbjct  64   GPIMGLQLGQVTTIVVTSSGMAKEVLQKQDLAFSSRSIPNAIHAHDQY-KYSVIWLPVAS  122

Query  124  RWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANM  183
            RW+ LRK  N +M  G  LD   ++R  ++  ++    ++S+ G+ + +         N+
Sbjct  123  RWRGLRKALNSNMFSGNRLDANQHLRSRKVQELIAYCRKSSQTGDAIDVGRAAFRTSLNL  182

Query  184  IGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLH  243
            +   + S+ +       + EFKD+V  +M  AG  N+ D+ P +  +D QGI + M
Sbjct  183  LSNTMFSKDLTDPYSDSAKEFKDLVWNVMVEAGKPNLVDYFPLLDKVDPQGIRKRMTIHF  242

Query  244  TKFDVLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGT  303
             K   L   ++ E       +    D LDVLL   + +  E++  T+I+ + L+LF AGT
Sbjct  243  GKILELFGGLIDERLQQKKAKGVNDDVLDVLLTTSEES-PEEIDRTHIQRMCLDLFVAGT  301

Query  304  DTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKH  363
            DT+SS +EWA++EM+KNP  +K AQ E+ +VIG+ + + E+D++ LPYL+   KET R H
Sbjct  302  DTTSSTLEWAMSEMLKNPEKMKAAQAELAQVIGKGKAVEEADLARLPYLRCAIKETLRIH  361

Query  364  PSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGK  423
            P  PL +PR   Q  EV GY +PK++++ VN+WAI RD  +W++PL F PERFL  E
Sbjct  362  PPVPLLIPRRTEQEVEVCGYTVPKNSQVLVNVWAISRDDAIWKDPLSFKPERFLESE---  418

Query  424  INPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVA--ELNMDESF  481
            +   G DF+LIPFGAGRRIC G  + + +V  +LG+L++SFDWKL  G+A  +L+M+E F
Sbjct  419  LEMRGKDFELIPFGAGRRICPGLPLAVRMVPVMLGSLLNSFDWKLEGGIAPKDLDMEEKF  478

Query  482  GLALQKAVPLSALVSP  497
            G+ LQKA PL A+ +P
Sbjct  479  GITLQKAHPLRAVATP  494
```

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RecName: Full=Cytochrome P450 76C2; AltName: Full=Protein YELLOW-LEAF-SPECIFIC GENE 6

Sequence ID: O64637.1 **Length:** 512 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 47 to 504 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
339 bits(870)	3e-110	Compositional matrix adjust.	182/462(39%)	276/462(59%)	13/462(2%)

```
Query  42   LVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRP  101
            ++G + L+G  PH + A L+K YGPIM LK G+ + VV ++PE+AR  L+T D   S+R
Sbjct  47   IIGNIHLVGRNPHHSFADLSKTYGPIMSLKFGSLNTVVVTSPEAAREVLRTYDQILSSRT  106

Query  102  PNAGASHLAYGAQDLVF-AKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAM  160
            P      + +    +V+      RW+ LRKLS   +   + ++    +R  ++  ++  M
Sbjct  107  PTNSIRSINHDKVSVVWLPPSSSRWRLLRKLSATQLFSPQRIEATKTLRENKVKELVSFM  166

Query  161  CEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNI  220
             E+S   E V ++        N+I  ++ S  +      +S  F+D V+ +M + G  +
Sbjct  167  SESSEREEAVDISRATFITALNIISNILFSVDLGNYDSNKSGVFQDTVIGVMEAVGNPDA  226

Query  221  GDFIPSIAWMDLQGIERGMKKLHTKFDVLLTKMV------KEHRATSHERKGKADFLDVL  274
             +F P + ++DLQG  + +K    +   +    +      K  R T+ +   + DF+DVL
Sbjct  227  ANFFPFLGFLDLQGNRKTLKACSERLFKVFRGFIDAKLAEKSLRDTNSKDVRERDFVDVL  286

Query  275  LEECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRV  334
            L+  +    E L+  +I  +LL+LF AGTDT+SS +EWA+ E+++NP  + KAQ E+D V
Sbjct  287  LDLTEGDEAE-LNTNDIVHLLLDLFGAGTDTNSSTVEWAMAELLRNPETMVKAQAEIDCV  345

Query  335  IGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVN  394
            IG+   + ESDIS+LPYLQA+ KET+R HP+ PL +PR A    EV G+ +PKD ++ VN
Sbjct  346  IGQKGVVEESDISALPYLQAVVKETFRLHPAAPLLVPRKAESDVEVLGFMVPKDTQVFVN  405

Query  395  IWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVS  454
            +WAIGRDPNVWEN   F PERFL ++   I+  G D++L PFGAGRRIC G  + +  V
```

```
Sbjct  406  VWAIGRDPNVWENSSRFKPERFLGKD---IDLRGRDYELTPFGAGRRICPGLPLAVKTVP  462

Query  455  YILGTLVHSFDWKLPNGVA--ELNMDESFGLALQKAVPLSAL  494
             +L +L++SFDWKLPNGV   +L+MDE+FGL L K  PL A+
Sbjct  463  LMLASLLYSFDWKLPNGVGSEDLDMDETFGLTLHKTNPLHAV  504
```

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RecName: Full=Licodione synthase; AltName: Full=(2S)-flavanone 2-hydroxylase; AltName: Full=CYP GE-5; AltName: Full=Cytochrome P450 93B1; AltName: Full=Flavone synthase II

Sequence ID: P93149.2 **Length:** 523 **Number of Matches:** 1

Related Information

Range 1: 15 to 501 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
336 bits(861)	9e-109	Compositional matrix adjust.	181/498(36%)	288/498(57%)	36/498(7%)

```
Query  16   LITRFLVRSLFKKPTRPLPPGPL-GWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGT  74
            LI  F  R  F +  + LPP P    P++G + +LG + H +   L+ +YGP+  L  G+
Sbjct  15   LICYFFFRPYFHRYGKNLPPSPFFRLPIIGHMHMLGPLLHQSFHNLSHRYGPLFSLNFGS  74

Query  75   CDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNL  134
               VVASTP  A+  L+T +L F+ R  +     L Y +  L FA YG  W+ ++KLS
Sbjct  75   VLCVVASTPHFAKQLLQTNELAFNCRIESTAVKKLTYESS-LAFAPYGDYWRFIKKLSMN  133

Query  135  HMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVF  194
             +LG ++++++ ++R  E   +L+ +   +R  E V + E L     N+I  +++
Sbjct  134  ELLGSRSINNFQHLRAQETHQLLRLLSNRARAFEAVNITEELLKLTNNVISIMMVG----  189

Query  195  VTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKFDVLLTKMV  254
                 E+ E +D+V ++    G FN+ DFI     MDLQG  + ++ L  +FD L+ +++
Sbjct  190  -----EAEEARDVVRDVTEIFGEFNVSDFIWLFKKMDLQGFGKRIEDLFQRFDTLVERII  244

Query  255  KEHRATSHERK------------GKADFLDVLLEECDNTNGE-KLSITNIKAVLLNLFTA  301
             +   T  +R+            G  DFLD+LL+  ++ N E K+   +IKA++++ FTA
Sbjct  245  SKREQTRKDRRRNGKKGEQGSGDGIRDFLDILLDCTEDENSEIKIQRVHIKALIMDFFTA  304

Query  302  GTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYR  361
            GTDT++   EWAL E++K P++L+K +EE+D V+G+DR + ESD  +LPYLQAI KET+R
Sbjct  305  GTDTTAISTEWALVELVKKPSVLQKVREEIDNVVGKDRLVEESDCPNLPYLQAILKETFR  364

Query  362  KHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEE-  420
             HP  P+ + R  +  C V+ Y IP+D+ L VN+W+IGR+P  W+NPLEF PERFL  E
Sbjct  365  LHPPVPM-VTRRCVAECTVENYVIPEDSLLFVNVWSIGRNPKFWDNPLEFRPERFLKLEG  423

Query  421  --NGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAE----  474
              +G ++  G+ F+L+PFG+GRR+C G  + M  V  +LG ++  FD+ +     E
Sbjct  424  DSSGVVDVRGSHFQLLPFGSGRRMCPGVSLAMQEVPALLGAIIQCFDFHVVGPKGEILKG  483

Query  475  ----LNMDESFGLALQKA  488
                +N+DE  GL   +A
Sbjct  484  DDIVINVDERPGLTAPRA  501
```

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RecName: Full=Cytochrome P450 71A1; AltName: Full=ARP-2; AltName: Full=CYPLXXIA1

Sequence ID: P24465.2 **Length:** 502 **Number of Matches:** 1

Related Information

Range 1: 40 to 499 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
328 bits(841)	5e-106	Compositional matrix adjust.	174/465(37%)	279/465(60%)	13/465(2%)

```
Query  42   LVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRP  101
            ++G L  LG +PH +L  LA + GP++ L +G    ++ ST E A   LKT DL F++RP
Sbjct  40   IIGNLHQLGNLPHRSLRSLANELGPLILLHLGHIPTLIVSTAEIAEEILKTHDLIFASRP  99

Query  102  PNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMC  161
                A  + Y   D+ F+ YG  W+ +RK+  L +L  K ++ + ++R  E+G M++ +
Sbjct  100  STTAARRIFYDCTDVAFSPYGEYWRQVRKICVLELLSIKRVNSYRSIREEEVGLMMERIS  159

Query  162  EASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIG  221
            ++   GE V L+E+L    +  I +V   ++ +  +    N+F D+  EL T  G F +G
Sbjct  160  QSCSTGEAVNLSELLLLLSSGTITRVAFGKK-YEGEEERKNKFADLATELTTLMGAFFVG  218

Query  222  DFIPSIAWMD-LQGIERGMKKLHTKFDVLLTKMVKEH----RATSHERKGKADFLDVLLE  276
            D+ PS AW+D L G++  +K+ H + D  +  ++ +H    +A   +   + D +DVLL
Sbjct  219  DYFPSFAWVDVLTGMDARLKRNHGELDAFVDHVIDDHLLSRKANGSDGVEQKDLVDVLLH  278

Query  277  -ECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVI  335
             + D++ G  L+  N+KAV+L++F+ GTDT++  +EWA+ E+IK+P +++KAQ+E+ RV+
Sbjct  279  LQKDSSLGVHLNRNNLKAVILDMFSGGTDTTAVTLEWAMAELIKHPDVMEKAQQEVRRVV  338

Query  336  GRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNI  395
            G+  ++ E D+  L YL+ I KET R HP  PL +PR + +   + GY+IP   R+ +N
Sbjct  339  GKKAKVEEEDLHQLHYLKLIIKETLRLHPVAPLLVPRESTRDVVIRGYHIPAKTRVFINA  398

Query  396  WAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSY  455
            WAIGRDP  WEN  EFLPERF+   N  ++  G DF+LIPFGAGRR C G   G+  V
Sbjct  399  WAIGRDPKSWENAEEFLPERFV---NNSVDFKGQDFQLIPFGAGRRGCPGIAFGISSVEI  455

Query  456  ILGTLVHSFDWKLPNGVA--ELNMDESFGLALQKAVPLSALVSPR  498
             L  L++ F+W+LP  +   +L+M E+ G+ +    PL  LV+ R
```

```
Sbjct  456  SLANLLYWFNWELPGDLTKEDLDMSEAVGITVHMKFPLQ-LVAKR  499
```

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RecName: Full=Cytochrome P450 98A1

Sequence ID: O48956.1 **Length:** 512 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 32 to 499 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
327 bits(839)	1e-105	Compositional matrix adjust.	178/476(37%)	270/476(56%)	18/476(3%)

```
Query  34   PPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTL  93
            PPGP  WP++G L  +  +      + A++YGP++ +  G+   VV ST E A+  LK
Sbjct  32   PPGPRPWPVLGNLRQIKPIRCRCFQEWAERYGPVISVWFGSGLTVVVSTSELAKEVLKEN  91

Query  94   DLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTEL  153
            D   ++RP N      +   QDL++A YGP +  +RKL NL +   K L+    +R  E+
Sbjct  92   DQQLADRPRNRSTQRFSRNGQDLIWADYGPHYIKVRKLCNLELFTPKRLEALRPIREDEV  151

Query  154  GHMLKAMCEASRC----GEPVVLAEMLTYAMANMIGQVILSRRVFVTKG---TESNEFKD  206
              M++++  A+      G+P+V+   L+    N I ++   +R     G    +  EFK
Sbjct  152  TAMVESVYRAATAPGNEGKPMVVRNHLSMVAFNNITRLAFGKRFMNANGDIDEQGREFKT  211

Query  207  MVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHT-KFDVLLTKMVKEHRATSHERK  265
            +V   +      ++ +FI  + W  L  +    + K H  + D L  K+++EH  +  E
Sbjct  212  IVNNGIKIGASLSVAEFIWYLRW--LCPLNEELYKTHNERRDRLTMKIIEEHAKSLKESG  269

Query  266  GKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILK  325
             K  F+D L       +   LS   +  +L ++ TAG DT+   +EWA+ E+++NP + K
Sbjct  270  AKQHFVDALFTLKQQYD---LSEDTVIGLLWDMITAGMDTTVISVEWAMAELVRNPRVQK  326

Query  326  KAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYI  385
            K QEE+DRV+GRDR +LE+D  +LPYLQA+ KE+ R HP TPL LP  A    ++ GY I
Sbjct  327  KLQEELDRVVGRDRVMLETDFQNLPYLQAVVKESLRLHPPTPLMLPHKASTNVKIGGYDI  386

Query  386  PKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAG  445
            PK A + VN+WA+ RDP VW NPLE+ PERFL E    I+  G+DF+++PFGAGRR+C G
Sbjct  387  PKGANVMVNVWAVARDPKVWSNPLEYRPERFLEE---NIDIKGSDFRVLPFGAGRRVCPG  443

Query  446  TRMGMVLVSYILGTLVHSFDWKLPNGV--AELNMDESFGLALQKAVPLSALVSPRL  499
             ++G+ LV+ ++G L+H F+W LP G    ++NM ES GL      PL A+  PRL
Sbjct  444  AQLGINLVASMIGHLLHHFEWSLPEGTRPEDVNMMESPGLVTFMGTPLQAVAKPRL  499
```

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RecName: Full=Cytochrome P450 71D11

Sequence ID: O22307.1 **Length:** 490 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 482 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
325 bits(834)	5e-105	Compositional matrix adjust.	181/489(37%)	285/489(58%)	24/489(4%)

```
Query  21   LVRSLFKKPTR--PLPPGPLGWPLVGALP-LLGAMPHVALAKLAKKYGPIMHLKMGTCDM  77
            ++R   KKP     +PPGP   P++G++P L+G+ PH  L  LAKKYGP+MHL++G
Sbjct  5    ILRKNLKKPDSIPNIPPGPWKLPIIGSIPHLVGSPPHRKLRDLAKKYGPLMHLQLGEVIF  64

Query  78   VVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHML  137
            ++ S+ E A+  +KT D+ F++RP +     + YG+ D+ F+ YG  W+ +RK+ N+ +L
Sbjct  65   IIVSSAEYAKEVMKTHDVTFASRPRSLFTDIVFYGSTDIGFSPYGDYWRQVRKICNVELL  124

Query  138  GGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTK  197
              K +     +R  E+ ++++ +  AS  G  V L++    A+ ++I   I SR  F  +
Sbjct  125  SMKRVQSLWPIREEEVKNLIQRI--ASEEGSVVNLSQ----AIDSLIF-TITSRSAFGKR  177

Query  198  GTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKKLHTKFDVLLTKMVKE  256
              E  EF   V E+M  AG FNI D  PS  W++ L  +    + LH K D +L  ++ +
Sbjct  178  YMEQEEFISCVREVMKLAGGFNIADLFPSAKWLENLTRMRSKFEYLHQKMDRILETIIDD  237

Query  257  HRATSHERKGKA-----DFLDVLLEECDNTNGE--KLSITNIKAVLLNLFTAGTDTSSSI  309
            H+A S  ++G+      D +DVLL+  +++  +   L+I NIKA+L ++F AG++TS++
Sbjct  238  HKANSRTKEGQVEGGEEDLIDVLLKYENSSTDQDFHLTIRNIKAILFDIFIAGSETSATT  297

Query  310  IEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLN  369
            I W + EM+K+P +LKKAQ+E+  +  R  ++ E+ I  L YL+A   E  R HP  PL
Sbjct  298  INWTMAEMMKDPILLKKAQDEVREIFQRRGKVDETCIYELKYLKAFINEVLRLHPPGPLV  357

Query  370  LPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGN  429
              R   QACE++GY+IP  + + VN +AIG D   W  P  F PERF+   +  I+  G
Sbjct  358  F-RECRQACEINGYHIPAKSTVLVNTFAIGTDSKYWAEPERFCPERFI---DSSIDYKGT  413

Query  430  DFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGV--AELNMDESFGLALQK  487
            +F+ +PFGAGRRIC G   GM  V  +L  L++ FDW LP G+   +L++ E FG+ + K
Sbjct  414  NFEHLPFGAGRRICPGINYGMANVELVLALLLYHFDWTLPKGIKNEDLDLTEEFGVTVSK  473

Query  488  AVPLSALVS  496
               L  + S
Sbjct  474  KEDLCLIPS  482
```

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RecName: Full=Cytochrome P450 71D8; AltName: Full=Cytochrome P450 CP7

Sequence ID: O81974.1 **Length:** 504 **Number of Matches:** 1

Related Information

Range 1: 9 to 490 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
325 bits(832)	1e-104	Compositional matrix adjust.	174/493(35%)	290/493(58%)	25/493(5%)

```
Query  9    VVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVG---ALPLLGAMPHVALAKLAKKYG  65
            V+   +FL+  +LV++  +K +  LPPGP   P++G    L L  ++P  AL KL +KYG
Sbjct  9    VITFFVFLLLHWLVKTYKQKSSHKLPPGPWRLPIIGNLHQLALAASLPDQALQKLVRKYG  68

Query  66   PIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRW  125
            P+MHL++G    +V S+P+ A   +KT D++F  RP        + YGA D+ FA YG  W
Sbjct  69   PLMHLQLGEISTLVVSSPKMAMEMMKTHDVHFVQRPQLLAPQFMVYGATDIAFAPYGDYW  128

Query  126  KTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIG  185
            + +RK+  L +L  K +  ++++R  E   +++++   S  G P+ L+  L     +++G
Sbjct  129  RQIRKICTLELLSAKRVQSFSHIRQDENKKLIQSI--HSSAGSPIDLSGKL----FSLLG  182

Query  186  QVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERG-MKKLHT  244
              + SR  F  +  + +EF  +V + +T  G F + D  PS+  + L   ++  ++ +H
Sbjct  183  TTV-SRAAFGKENDDQDEFMSLVRKAITMTGGFEVDDMFPSLKPLHLLTRQKAKVEHVHQ  241

Query  245  KFDVLLTKMVKEH---RATSHERKG----KADFLDVLLEECDNTNGE-KLSITNIKAVLL  296
            + D +L  ++++H   R    E  G    + D +DVLL   ++ + E  +++ NIKAV+
Sbjct  242  RADKILEDILRKHMEKRTRVKEGNGSEAEQEDLVDVLLRLKESGSLEVPMTMENIKAVIW  301

Query  297  NLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIA  356
            N+F AGTDTS+S +EWA++EM+KNP + +KAQ E+ ++      + E+D+  L YL+++
Sbjct  302  NIFAAGTDTSASTLEWAMSEMMKNPKVKEKAQAELRQIFKGKEIIRETDLEELSYLKSVI  361

Query  357  KETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERF  416
            KET R HP + L +PR  I +  +DGY IP   ++ +N WAIGRDP  W +   F+PERF
Sbjct  362  KETLRLHPPSQL-IPRECIISTNIDGYEIPIKTKVMINTWAIGRDPQYWSDADRFIPERF  420

Query  417  LSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGV--AE  474
                +  I+  GN F+ IPFGAGRR+C G   G+  ++  L  L++ F+W+LPN +   +
Sbjct  421  ---NDSSIDFKGNSFEYIPFGAGRRMCPGMTFGLASITLPLALLLYHFNWELPNKMKPED  477

Query  475  LNMDESFGLALQK  487
            L+MDE FG+ + +
Sbjct  478  LDMDEHFGMTVAR  490
```

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RecName: Full=Germacrene A oxidase; Short=BsGAO; AltName: Full=Germacrene A alcohol dehydrogenase; AltName: Full=Germacrene A hydroxylase

Sequence ID: D5JBX1.1 **Length:** 496 **Number of Matches:** 1

Related Information

Range 1: 5 to 482 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
321 bits(823)	2e-103	Compositional matrix adjust.	180/492(37%)	276/492(56%)	18/492(3%)

```
Query  4    LVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALP-LLGAMPHVALAKLAK  62
            L T   +A  +F++ + L  S   K T+   P     P++G +  L+G +PH  +  +A+
Sbjct  5    LTTSLGLAVFVFILFKLLTGS---KSTKNSLPEAWRLPIIGHMHHLVGTLPHRGVTDMAR  61

Query  63   KYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYG  122
            KYG +MHL++G    +V S+P  A+  L T D+ F+NRP       +AY   D+V + YG
Sbjct  62   KYGSLMHLQLGEVSTIVVSSPRWAKEVLTTYDITFANRPETLTGEIVAYHNTDIVLSPYG  121

Query  123  PRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMAN  182
              W+ LRKL  L +L  K +  + ++R  E  +++K +  +S  G PV L+E +   +A
Sbjct  122  EYWRQLRKLCTLELLSAKKVKSFQSLREEECWNLVKEV-RSSGSGSPVDLSESIFKLIA-  179

Query  183  MIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKK  241
                 ILSR  F     +  EF ++V E++   G F++ D  PS   +  L G    +
Sbjct  180  ----TILSRAAFGKGIKDQREFTEIVKEILRLTGGFDVADIFPSKKILHHLSGKRAKLTN  235

Query  242  LHTKFDVLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTA  301
            +H K D L+  +V EH   S     +   LDVLL   D+     L+  N+KAV+L++F A
Sbjct  236  IHNKLDSLINNIVSEHPG-SRTSSSQESLLDVLLRLKDSAE-LPLTSDNVKAVILDMFGA  293

Query  302  GTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYR  361
            GTDTSS+ IEWA++E+I+ P  ++K Q E+ + +    R+ E DI  L YL+ + KET R
Sbjct  294  GTDTSSATIEWAISELIRCPRAMEKVQTELRQALNGKERIQEEDIQELSYLKLVIKETLR  353

Query  362  KHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEEN  421
             HP  PL +PR   + C + GY IP   +L VN++AI RDP  W++   F+PERF   EN
Sbjct  354  LHPPLPLVMPRECREPCVLAGYEIPTKTKLIVNVFAINRDPEYWKDAETFMPERF---EN  410

Query  422  GKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG--VAELNMDE  479
              IN  G++++ +PFGAGRR+C G  +G+  V   L  +++ F+WKLPNG  + EL+M E
Sbjct  411  SPINIMGSEYEYLPFGAGRRMCPGAALGLANVELPLAHILYYFNWKLPNGARLDELDMSE  470

Query  480  SFGLALQKAVPL  491
             FG  +Q+   L
Sbjct  471  CFGATVQRKSEL  482
```

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RecName: Full=Germacrene A oxidase; Short=CiGAO; AltName: Full=Germacrene A alcohol dehydrogenase; AltName: Full=Germacrene A hydroxylase

Sequence ID: D5JBW8.1 **Length:** 488 **Number of Matches:** 1

Related Information

Range 1: 5 to 482 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
320 bits(821)	4e-103	Compositional matrix adjust.	175/492(36%)	276/492(56%)	18/492(3%)

```
Query  4    LVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALP-LLGAMPHVALAKLAK  62
            L T   +A I+ ++ +   R    K  +   P     P++G +  L+G MPH  + +LA+
Sbjct  5    LTTSIALATIVLILYKLATRP---KSNKKRLPEASRLPIIGHMHHLIGTMPHRGVMELAR  61

Query  63   KYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYG  122
            K+G +MHL++G    +V S+P+ A+  L T D+ F+NRP       +AY   D+V A YG
Sbjct  62   KHGSLMHLQLGEVSTIVVSSPKWAKEILTTYDITFANRPETLTGEIIAYHNTDIVLAPYG  121

Query  123  PRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMAN  182
              W+ LRKL  L +L  K +  + ++R  E  +++K + E S  G+P+ L+E +   +A
Sbjct  122  EYWRQLRKLCTLELLSVKKVKSFQSIREEECWNLVKEVKE-SGSGKPISLSESIFKMIA-  179

Query  183  MIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKK  241
                 ILSR  F     +  EF ++V E++   G F++ D  PS  ++  L G    +
Sbjct  180  ----TILSRAAFGKGIKDQREFTEIVKEILRQTGGFDVADIFPSKKFLHHLSGKRARLTS  235

Query  242  LHTKFDVLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTA  301
            +H K D L+  +V EH  ++   K     LDVLL   D+     L+  N+KA++L++F A
Sbjct  236  IHKKLDTLINNIVAEHHVST-SSKANETLLDVLLRLKDSAEF-PLTADNVKAIILDMFGA  293

Query  302  GTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYR  361
            GTDTSS+ +EWA++E+I+ P  ++K Q E+ + +    ++ E DI  LPYL  + +ET R
Sbjct  294  GTDTSSATVEWAISELIRCPRAMEKVQAELRQALNGKEQIHEEDIQDLPYLNLVIRETLR  353

Query  362  KHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEEN  421
             HP  PL +PR   +   + GY I    +L VN++AI RDP  W++   F+PERF   EN
Sbjct  354  LHPPLPLVMPRECREPVNLAGYEIANKTKLIVNVFAINRDPEYWKDAEAFIPERF---EN  410

Query  422  GKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVA--ELNMDE  479
               N  G D++ +PFGAGRR+C G  +G+  V   L  +++ F+WKLPNG +  +L+M E
Sbjct  411  NPNNIMGADYEYLPFGAGRRMCPGAALGLANVQLPLANILYHFNWKLPNGASHDQLDMTE  470

Query  480  SFGLALQKAVPL  491
            SFG  +Q+   L
Sbjct  471  SFGATVQRKTEL  482
```

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RecName: Full=Germacrene A oxidase; Short=HaGAO; AltName: Full=Germacrene A alcohol dehydrogenase; AltName: Full=Germacrene A hydroxylase

Sequence ID: D5JBX0.1 **Length:** 488 **Number of Matches:** 1

Related Information

Range 1: 5 to 482 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
320 bits(819)	6e-103	Compositional matrix adjust.	178/494(36%)	275/494(55%)	22/494(4%)

```
Query  4    LVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGW--PLVGALP-LLGAMPHVALAKL  60
            L T   +A I+F + + L R    K   P P     W  P++G +  L+G MPH  +  L
Sbjct  5    LTTSIALATIVFFLYKLLTRPTSSKNRLPEP-----WRLPIIGHMHHLIGTMPHRGVMDL  59

Query  61   AKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAK  120
            A+KYG +MHL++G    +V S+P+ A+  L T D+ F+NRP       +AY   D+V A
Sbjct  60   ARKYGSLMHLQLGEVSAIVVSSPKWAKEILTTYDIPFANRPETLTGEIIAYHNTDIVLAP  119

Query  121  YGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAM  180
            YG  W+ LRKL  L +L  K +  + ++R  E  ++++ + +AS  G P  L+E +   +
Sbjct  120  YGEYWRQLRKLCTLELLSVKKVKSFQSLREEECWNLVQEI-KASGSGTPFNLSEGIFKVI  178

Query  181  ANMIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERG-M  239
            A      +LSR  F     +  +F ++V E++   G F++ D  PS  ++     +RG +
Sbjct  179  A-----TVLSRAAFGKGIKDQKQFTEIVKEILRETGGFDVADIFPSKKFLHHLSGKRGRL  233

Query  240  KKLHTKFDVLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLF  299
              +H K D L+  +V EH   S   K     LDVLL    N+    L+  N+KA++L++F
Sbjct  234  TSIHNKLDSLINNLVAEH-TVSKSSKVNETLLDVLLR-LKNSEEFPLTADNVKAIILDMF  291

Query  300  TAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKET  359
             AGTDTSS+ +EWA++E+I+ P  ++K Q E+ + +    R+ E +I  LPYL  + +ET
Sbjct  292  GAGTDTSSATVEWAISELIRCPRAMEKVQAELRQALNGKERIKEEEIQDLPYLNLVIRET  351

Query  360  YRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSE  419
             R HP  PL +PR   QA  + GY +    +L VN++AI RDP  W++   F PERF
Sbjct  352  LRLHPPLPLVMPRECRQAMNLAGYDVANKTKLIVNVFAINRDPEYWKDAESFNPERF---  408

Query  420  ENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVA--ELNM  477
            EN      G D++ +PFGAGRR+C G+ +G+  V   L  +++ F WKLPNG +  +L+M
Sbjct  409  ENSNTTIMGADYEYLPFGAGRRMCPGSALGLANVQLPLANILYYFKWKLPNGASHDQLDM  468

Query  478  DESFGLALQKAVPL  491
             ESFG  +Q+   L
Sbjct  469  TESFGATVQRKTEL  482
```

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RecName: Full=Cytochrome P450 71B11

Sequence ID: P58049.1 **Length:** 496 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 489 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
319 bits(818)	1e-102	Compositional matrix adjust.	174/495(35%)	282/495(56%)	18/495(3%)

```
Query  8    FVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPI  67
            +++ A +F  T  +VR+  +K  + LPPGP   P++G L  LG+ PH ++ KL++KYGP+
Sbjct  5    YIIVAFVFFSTIIIVRNT-RKTKKNLPPGPPRLPIIGNLHQLGSKPHSSMFKLSEKYGPL  63

Query  68   MHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKT  127
            M L+ G+   VVASTPE+ +  LKT D    +RP     + L Y  +D+ F  Y   W+
Sbjct  64   MALRFGSVSTVVASTPETVKEVLKTFDAECCSRPYMTYPARLTYNLKDIGFCPYTKYWRE  123

Query  128  LRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQV  187
            +RK++ + +   K +  + + R  E+  ++  + +A+   +PV L   L     ++I +V
Sbjct  124  VRKMTVVELYTAKRVQSFQHTRKEEVASLVDFITQAASLEKPVNLNTKLMKLSGSVICRV  183

Query  188  ILSRRVFVTKGTE-SNEFKDMVVELMTSAGYFNIGDFIPSIAWM--DLQGIERGMKKLHT  244
            +    +   KG++  N +++++   M   G F   D+ P I  +   + G+    +K+
Sbjct  184  VFGINL---KGSKLENLYEEVIQGTMEVVGSFAAADYFPIIGRIIDRITGLHSKCEKIFK  240

Query  245  KFDVLLTKMVKEHRATSHERKGKADFLDVLL--EECDNTNGE-KLSITNIKAVLLNLFTA  301
              D    + +K H     +   K D +D+LL  E  +   GE +L+  N K +L N+  A
Sbjct  241  AMDAFFDQSIKHHL---EDESIKDDIIDLLLKMERGEIELGEFQLTRDNTKGILFNILNA  297

Query  302  GTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYR  361
            G DTS+ ++ W +T +I NP ++KKAQ E+  VI     ++E DI  L YL+ + KET+R
Sbjct  298  GIDTSAQVMTWVMTYLISNPRVMKKAQAEVREVIKNKDDIIEEDIERLEYLKMVVKETFR  357

Query  362  KHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEEN  421
              P  PL +PR A +  ++ GY IPK    + VNIWAI R+PNVW++P  F+PERF+   +
Sbjct  358  VLPLVPLLIPREASKDVKIGGYDIPKKTWIHVNIWAIHRNPNVWKDPEAFIPERFM---D  414

Query  422  GKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG--VAELNMDE  479
             +I+  G +F+ +PFG+GRR+C G  MGM LV   L  L++ FDWKLP G  V +++++E
Sbjct  415  NQIDYKGLNFEFLPFGSGRRMCPGIGMGMALVHLTLINLLYRFDWKLPEGMEVEDVDLEE  474

Query  480  SFGLALQKAVPLSAL  494
            S+GL   K VPL  +
Sbjct  475  SYGLVCPKKVPLQLI  489
```

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RecName: Full=Cytochrome P450 71BL1; AltName: Full=Germacrene A acid 8-beta-hydroxylase; Short=HaG8H

Sequence ID: F8S1H3.1 **Length:** 488 **Number of Matches:** 1

Related Information

Range 1: 23 to 479 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
319 bits(817)	1e-102	Compositional matrix adjust.	178/471(38%)	271/471(57%)	21/471(4%)

```
Query  28   KPTRPLPPGPLGWPLVGALPLLGAM-PHVALAKLAKKYGPIMHLKMGTCDMVVASTPESA  86
            K  + LPPGP   P++G + LL  + PH  L  LA+KYGPIMHL++G    VV S+P  A
Sbjct  23   KVPKNLPPGPPKLPIIGNIHLLDKIAPHRNLRNLARKYGPIMHLRLGQVSTVVISSPRLA  82

Query  87   RAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWA  146
               +KT DL+F++RP    +    Y A ++ +A+YG  W+ ++K+  L +L  K    +
Sbjct  83   HEIMKTQDLSFADRPTTTTSQIFFYKASNIAWARYGNYWRQMKKICTLELLSAKKSRSFF  142

Query  147  NVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEF-K  205
             +R  EL    K +  +S  G P+ L + +   + N++ +  L         +E  +F
Sbjct  143  YIREEELTRTYKFLDFSS--GTPITLRDTIQEMVNNVVSRATLG------DVSEDRQFII  194

Query  206  DMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKKLHTKFDVLLTKMVKEHRATSHER  264
            D    ++ S   FN+ ++ PS+++++ + G +    K+H + DV+L K+++EHR+    +
Sbjct  195  DSTYTMLKSFNSFNLFNYYPSLSFINVISGKQAQWLKMHKEVDVILEKILREHRSRPRGK  254

Query  265  KGKADFLDVLLEECDNTNGEKLSIT--NIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPT  322
                D +DVL+     T    ++IT  NIKA++L + TAGT +SS  IEWA TEM++NP
Sbjct  255  NDHEDLVDVLI-RIKETGDLDMAITDDNIKAIILEMLTAGTSSSSMTIEWAFTEMMRNPK  313

Query  323  ILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDG  382
            I+KKAQ E+  V+  D R+ E+DI +L Y + + KET R H   P+ +PR   + C V+G
Sbjct  314  IMKKAQTEVRSVVKGD-RVTEADIQNLDYTKLVIKETLRLH-GVPILVPRENQEDCVVNG  371

Query  383  YYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRI  442
            Y IP   RL VN WA   DP+ WE+P  F+PERF   EN  I   G DF+ IPFGAGRRI
Sbjct  372  YDIPAKTRLLVNAWACATDPDSWEDPDSFIPERF---ENNSIGYSGADFEFIPFGAGRRI  428

Query  443  CAGTRMGMVLVSYILGTLVHSFDWKLPNGVA--ELNMDESFGLALQKAVPL  491
            C G   GM  V Y++  L+  +DWKLP+G+   +++M E  G++     PL
Sbjct  429  CPGMNFGMGTVEYVVANLLLHYDWKLPDGMKPHDIDMREITGISTLPIHPL  479
```

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RecName: Full=Germacrene A oxidase; Short=LsGAO; AltName: Full=Germacrene A alcohol dehydrogenase; AltName: Full=Germacrene A hydroxylase

Sequence ID: D5J9U8.1 **Length:** 488 **Number of Matches:** 1

Related Information

Range 1: 5 to 482 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
319 bits(817)	1e-102	Compositional matrix adjust.	175/492(36%)	275/492(55%)	18/492(3%)

```
Query  4    LVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALP-LLGAMPHVALAKLAK  62
            + T   +A I+F + +   R    K T+   P     P++G +  L+G MPH  +  LA+
Sbjct  5    ITTSIALATIVFFLYKLATRP---KSTKKQLPEASRLPIIGHMHHLIGTMPHRGVMDLAR  61

Query  63   KYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYG  122
            K+G +MHL++G    +V S+P+ A+  L T D+ F+NRP       +AY   D+V A YG
Sbjct  62   KHGSLMHLQLGEVSTIVVSSPKWAKEILTTYDITFANRPETLTGEIIAYHNTDIVLAPYG  121

Query  123  PRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMAN  182
              W+ LRKL  L +L  K +  + ++R  E  +++K + E S  G+P+ L+E +   +A
Sbjct  122  EYWRQLRKLCTLELLSVKKVKSFQSIREEECWNLVKEVKE-SGSGKPINLSESIFTMIA-  179

Query  183  MIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKK  241
                 ILSR  F     +  EF ++V E++   G F++ D  PS  ++  L G    +
Sbjct  180  ----TILSRAAFGKGIKDQREFTEIVKEILRQTGGFDVADIFPSKKFLHHLSGKRARLTS  235

Query  242  LHTKFDVLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTA  301
            +H K D L+  +V EH  ++   K     LDVLL   D+     L+  N+KA++L++F A
Sbjct  236  IHKKLDNLINNIVAEHHVST-SSKANETLLDVLLRLKDSAEF-PLTADNVKAIILDMFGA  293

Query  302  GTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYR  361
            GTDTSS+ +EWA++E+I+ P  ++K Q E+ + +    ++ E DI  L YL  + +ET R
Sbjct  294  GTDTSSATVEWAISELIRCPRAMEKVQAELRQALNGKEKIQEEDIQDLAYLNLVIRETLR  353

Query  362  KHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEEN  421
             HP  PL +PR   +   + GY I    +L VN++AI RDP  W++   F+PERF   EN
Sbjct  354  LHPPLPLVMPRECREPVNLAGYEIANKTKLIVNVFAINRDPEYWKDAEAFIPERF---EN  410

Query  422  GKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVA--ELNMDE  479
               N  G D++ +PFGAGRR+C G  +G+  V   L  +++ F+WKLPNG +  +L+M E
Sbjct  411  NPNNIMGADYEYLPFGAGRRMCPGAALGLANVQLPLANILYHFNWKLPNGASHDQLDMTE  470

Query  480  SFGLALQKAVPL  491
            SFG  +Q+   L
Sbjct  471  SFGATVQRKTEL  482
```

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RecName: Full=Germacrene A oxidase; Short=SlGAO; AltName: Full=Germacrene A alcohol dehydrogenase; AltName: Full=Germacrene A hydroxylase

Sequence ID: D5JBW9.1 **Length:** 488 **Number of Matches:** 1

Related Information

Range 1: 5 to 482 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
318 bits(816)	2e-102	Compositional matrix adjust.	178/492(36%)	275/492(55%)	18/492(3%)

```
Query  4    LVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALP-LLGAMPHVALAKLAK  62
              T   VA I+F++ +   R    K  + L P P   P++G +  L+G MPH  +  LA+
Sbjct  5    FTTSIAVATIVFVLFKLATRP---KSNKKLLPEPWRLPIIGHMHHLIGTMPHRGVMDLAR  61

Query  63   KYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYG  122
            KYG +MHL++G    +V S+P+ A+  L T D+ F+NRP       +AY   D+V A YG
Sbjct  62   KYGSLMHLQLGEVSTIVVSSPKWAKEILTTHDITFANRPETLTGEIIAYHNTDIVLAPYG  121

Query  123  PRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMAN  182
              W+ LRKL  L +L  K +  + ++R  E  ++++ + E S  G PV L+E +   +A
Sbjct  122  EYWRQLRKLCTLELLSVKKVKSFQSLREEECWNLVQEVKE-SGSGRPVDLSENIFKMIA-  179

Query  183  MIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKK  241
                 ILSR  F     +  EF ++V E++   G F++ D  PS  ++  L G    +
Sbjct  180  ----TILSRAAFGKGIKDQKEFTEIVKEILRQTGGFDVADIFPSKKFLHHLSGKRARLTS  235

Query  242  LHTKFDVLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTA  301
            +H K D L+  +V EH   ++  K     LDV+L   D+     L+  N+KA++L++F A
Sbjct  236  IHKKLDNLINNIVAEHPG-NNSSKSNETLLDVMLRLKDSVEF-PLTADNVKAIILDMFGA  293

Query  302  GTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYR  361
            GTDTSS+ +EWA++E+I+ P  ++K Q E+ + +    ++ E DI  L YL  + KET R
Sbjct  294  GTDTSSATVEWAISELIRCPRAMEKVQAELRQALKGKDKVKEEDIQDLSYLDLVIKETLR  353

Query  362  KHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEEN  421
             HP  PL +PR   Q   + GY I    +L VN++AI RDP  W++   F+PERF   EN
Sbjct  354  LHPPLPLVMPRECRQPVNLAGYDIANKTKLIVNVFAINRDPEYWKDAESFIPERF---EN  410

Query  422  GKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVA--ELNMDE  479
              I   G +++ +PFGAGRR+C G  +G+  V   L  +++ F+WKLPNG +  +L+M E
Sbjct  411  SPITVMGAEYEYLPFGAGRRMCPGAALGLANVQLPLANILYHFNWKLPNGASHDQLDMTE  470

Query  480  SFGLALQKAVPL  491
            SFG  +Q+   L
Sbjct  471  SFGATVQRKTHL  482
```

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RecName: Full=Cytochrome P450 703A2; AltName: Full=Protein DEFECTIVE IN EXINE FORMATION 2

Sequence ID: Q9LNJ4.1 **Length:** 510 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 41 to 509 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
319 bits(817)	2e-102	Compositional matrix adjust.	163/472(35%)	266/472(56%)	12/472(2%)

```
Query  42   LVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRP  101
            ++G L  LG +PH  LA L  KYGP+++L++G  D +  + P++ R  L   D  FS+RP
Sbjct  41   ILGNLLQLGPLPHRDLASLCDKYGPLVYLRLGNVDAITTNDPDTIREILLRQDDVFSSRP  100

Query  102  PNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMC  161
                A HLAYG  D+  A  GP WK +R++   H+L  K L+ +   R  E  ++++ +
Sbjct  101  KTLAAVHLAYGCGDVALAPMGPHWKRMRRICMEHLLTTKRLESFTTQRAEEARYLIRDVF  160

Query  162  EASRCGEPVVLAEMLTYAMANMIGQVILSRRVF----VTKGTESNEFKDMVVELMTSAGY  217
            + S  G+P+ L E+L     N + +++L ++ F    +    E+ EF  +  +L    G
Sbjct  161  KRSETGKPINLKEVLGAFSMNNVTRMLLGKQFFGPGSLVSPKEAQEFLHITHKLFWLLGV  220

Query  218  FNIGDFIPSIAWMDLQGIERGMKKLHTKFDVLLTKMVKEHRATSHE---RKGKADFLDVL  274
              +GD++P   W+D  G E+ M+ +  + D   TK++ EHR    E   + G  DF+DVL
Sbjct  221  IYLGDYLPFWRWVDPSGCEKEMRDVEKRVDEFHTKIIDEHRRAKLEDEDKNGDMDFVDVL  280

Query  275  LEECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRV  334
            L          +    IKA++ ++  A TDTS+   EWA+ E IK P +++K QEE+D V
Sbjct  281  LSLPGENGKAHMEDVEIKALIQDMIAAATDTSAVTNEWAMAEAIKQPRVMRKIQEELDNV  340

Query  335  IGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVN  394
            +G +R + ESD+  L YL+ + +ET+R HP+ P  +P  +++A  ++GYYIP   R+ +N
Sbjct  341  VGSNRMVDESDLVHLNYLRCVVRETFRMHPAGPFLIPHESVRATTINGYYIPAKTRVFIN  400

Query  395  IWAIGRDPNVWENPLEFLPERFLS-EENGKIN-PGGNDFKLIPFGAGRRICAGTRMGMVL  452
               +GR+  +W++  +F PER    E +G++    G DFK++PF AG+R C G  +G+ +
Sbjct  401  THGLGRNTKIWDDVEDFRPERHWPVEGSGRVEISHGPDFKILPFSAGKRKCPGAPLGVTM  460

Query  453  VSYILGTLVHSFDWKLPNGVAELNMDESFGLALQKAVPLSALVSPRLASNPY  504
            V   L  L H F+W  P  +  +   E +G+ + KA PL A+  PRLA++ Y
Sbjct  461  VLMALARLFHCFEWSSPGNIDTV---EVYGMTMPKAKPLRAIAKPRLAAHLY  509
```

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RecName: Full=Cytochrome P450 84A1; AltName: Full=Ferulate-5-hydroxylase; Short=F5H

Sequence ID: Q42600.1 **Length:** 520 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 47 to 516 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
319 bits(818)	3e-102	Compositional matrix adjust.	174/481(36%)	267/481(55%)	32/481(6%)

```
Query  40   WPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSN  99
            WP++G + ++  + H  LA LAKKYG + HL+MG   M   S+PE AR  L+  D  FSN
Sbjct  47   WPIIGNMLMMDQLTHRGLANLAKKYGGLCHLRMGFLHMYAVSSPEVARQVLQVQDSVFSN  106

Query  100  RPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKA  159
            RP     S+L Y   D+ FA YGP W+ +RK+  + +   K  + WA+VR  E+  M+++
Sbjct  107  RPATIAISYLTYDRADMAFAHYGPFWRQMRKVCVMKVFSRKRAESWASVR-DEVDKMVRS  165

Query  160  MCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTE-SNEFKDMVVELMTSAGYF  218
            +  +   G+P+ + E +     N     I  R  F +   +  +EF  ++ E     G F
Sbjct  166  V--SCNVGKPINVGEQIFALTRN-----ITYRAAFGSACEKGQDEFIRILQEFSKLFGAF  218

Query  219  NIGDFIPSIAWMDLQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKGK-----------  267
            N+ DFIP   W+D QGI + + K     D  +  ++ EH      +
Sbjct  219  NVADFIPYFGWIDPQGINKRLVKARNDLDGFIDDIIDEHMKKKENQNAVDDGDVVDTDMV  278

Query  268  -------ADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKN  320
                   ++   ++ E  D  N  KL+  NIKA+++++   GT+T +S IEWALTE++++
Sbjct  279  DDLLAFYSEEAKLVSETADLQNSIKLTRDNIKAIIMDVMFGGTETVASAIEWALTELLRS  338

Query  321  PTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEV  380
            P  LK+ Q+E+  V+G DRR+ ESDI  L YL+   KET R HP  PL L   A +   +
Sbjct  339  PEDLKRVQQELAEVVGLDRRVEESDIEKLTYLKCTLKETLRMHPPIPLLLHETA-EDTSI  397

Query  381  DGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGR  440
            DG++IPK +R+ +N +AIGRDP  W +P  F P RFL  E G  +  G++F+ IPFG+GR
Sbjct  398  DGFFIPKKSRVMINAFAIGRDPTSWTDPDTFRPSRFL--EPGVPDFKGSNFEFIPFGSGR  455

Query  441  RICAGTRMGMVLVSYILGTLVHSFDWKLPNGV--AELNMDESFGLALQKAVPLSALVSPR  498
            R C G ++G+  +   +  ++H F WKLP+G+  +EL+M++ FGL   KA  L A+ + R
Sbjct  456  RSCPGMQLGLYALDLAVAHILHCFTWKLPDGMKPSELDMNDVFGLTAPKATRLFAVPTTR  515

Query  499  L  499
            L
Sbjct  516  L  516
```

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RecName: Full=Cytochrome P450 71AV8; AltName: Full=(+)-Valencene oxidase

Sequence ID: E1B2Z9.1 **Length:** 496 **Number of Matches:** 1

Related Information

Range 1: 7 to 482 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps

318 bits(814)	4e-102	Compositional matrix adjust.	178/490(36%)	278/490(56%)	18/490(3%)

```
Query  6    TDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALP-LLGAMPHVALAKLAKKY  64
            T   +A IIF+I + L R+  KK    L P P   P++G +  L+G MPH  + +LA+K+
Sbjct  7    TTLGLAVIIFIIFKLLTRTTSKKN---LLPEPWRLPIIGHMHHLIGTMPHRGVMELARKH  63

Query  65   GPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPR  124
            G +MHL++G    +V S+P  A+  L T D+ F+NRP       +AY   D+V A YG
Sbjct  64   GSLMHLQLGEVSTIVVSSPRWAKEVLTTYDITFANRPETLTGEIVAYHNTDIVLAPYGEY  123

Query  125  WKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMI  184
            W+ LRKL  L +L  K +  + ++R  E  +++K +  ++  G P+ L+E +   +A
Sbjct  124  WRQLRKLCTLELLSNKKVKSFQSLREEECWNLVKDI-RSTGQGSPINLSENIFKMIA---  179

Query  185  GQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKKLH  243
               ILSR  F     +  +F ++V E++   G F++ D  PS   +  L G    +  +H
Sbjct  180  --TILSRAAFGKGIKDQMKFTELVKEILRLTGGFDVADIFPSKKLLHHLSGKRAKLTNIH  237

Query  244  TKFDVLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGT  303
             K D L+  ++ EH   +     +   LDVLL   ++     L+  N+KAV+L++F AGT
Sbjct  238  NKLDNLINNIIAEHPG-NRTSSSQETLLDVLLRLKESAEF-PLTADNVKAVILDMFGAGT  295

Query  304  DTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKH  363
            DTSS+ IEWA++E+I+ P  ++K Q E+ + +    R+ E D+  L YL+ + KET R H
Sbjct  296  DTSSATIEWAISELIRCPRAMEKVQTELRQALNGKERIQEEDLQELNYLKLVIKETLRLH  355

Query  364  PSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGK  423
            P  PL +PR   + C + GY IP   +L VN++AI RDP  W++   F+PERF   EN
Sbjct  356  PPLPLVMPRECREPCVLGGYDIPSKTKLIVNVFAINRDPEYWKDAETFMPERF---ENSP  412

Query  424  INPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG--VAELNMDESF  481
            I   G++++ +PFGAGRR+C G  +G+  V   L  +++ F+WKLPNG    +L+M ESF
Sbjct  413  ITVMGSEYEYLPFGAGRRMCPGAALGLANVELPLAHILYYFNWKLPNGKTFEDLDMTESF  472

Query  482  GLALQKAVPL  491
            G  +Q+   L
Sbjct  473  GATVQRKTEL  482
```

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RecName: Full=Cytochrome P450 71D10

Sequence ID: O48923.1 **Length:** 510 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 22 to 509 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
318 bits(814)	6e-102	Compositional matrix adjust.	180/497(36%)	282/497(56%)	19/497(3%)

```
Query  13   IIFLITRFLVRSLFK-KPTRPLPPGPLGWPLVGAL-PLLGAMP-HVALAKLAKKYGPIMH  69
            I F+  + + RS  K   T  LPPGP   PL+G +  ++G++P H  L  LA KYGP+MH
Sbjct  22   IFFVFFKLVQRSDSKTSSTCKLPPGPRTLPLIGNIHQIVGSLPVHYYLKNLADKYGPLMH  81

Query  70   LKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLR  129
            LK+G    ++ ++PE A+  +KT DLNFS+RP    +  ++Y    +VF+++G  W+ LR
Sbjct  82   LKLGEVSNIIVTSPEMAQEIMKTHDLNFSDRPDFVLSRIVSYNGSGIVFSQHGDYWRQLR  141

Query  130  KLSNLHMLGGKALDDWANVRVTELGHMLKAMC-EASRCGEPVVLAEMLTYAMANMIGQVI  188
            K+  + +L  K +  + ++R  E+  ++K +   AS  G  +       Y+M   I
Sbjct  142  KICTVELLTAKRVQSFRSIREEEVAELVKKIAATASEEGGSIFNLTQSIYSMTFGIA---  198

Query  189  LSRRVFVTKGTESNEF-KDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKFD  247
             +R  F  K      F  +M  +LM   G F++ D  PS     + G    ++K+H   D
Sbjct  199  -ARAAFGKKSRYQQVFISNMHKQLMLLGG-FSVADLYPSSRVFQMMGATGKLEKVHRVTD  256

Query  248  VLLTKMVKEHR---ATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTD  304
             +L  ++ EH+    +S ER+   D +DVLL+     +  +L+  NIKAV+ ++F  G +
Sbjct  257  RVLQDIIDEHKNRNRSSEEREAVEDLVDVLLK-FQKESEFRLTDDNIKAVIQDIFIGGGE  315

Query  305  TSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHP  364
            TSSS++EW ++E+I+NP ++++AQ E+ RV      + E+++  L YL++I KET R HP
Sbjct  316  TSSSVVEWGMSELIRNPRVMEEAQAEVRRVYDSKGYVDETELHQLIYLKSIIKETMRLHP  375

Query  365  STPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKI  424
              PL +PR++ + C+++GY IP   R+ +N WAIGR+P  W     F PERFL   N  I
Sbjct  376  PVPLLVPRVSRERCQINGYEIPSKTRIIINAWAIGRNPKYWGETESFKPERFL---NSSI  432

Query  425  NPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGV--AELNMDESFG  482
            +  G DF+ IPFGAGRRIC G    +  +   L  L++ FDWKLPN +   EL+M ES G
Sbjct  433  DFRGTDFEFIPFGAGRRICPGITFAIPNIELPLAQLLYHFDWKLPNKMKNEELDMTESNG  492

Query  483  LALQKAVPLSALVSPRL  499
            + L++   L  +   RL
Sbjct  493  ITLRRQNDLCLIPITRL  509
```

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RecName: Full=Cytochrome P450 82A3; AltName: Full=Cytochrome P450 CP6

Sequence ID: O49858.1 **Length:** 527 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 15 to 526 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
317 bits(812)	2e-101	Compositional matrix adjust.	188/519(36%)	284/519(54%)	29/519(5%)

```
Query  10   VAAIIFLITRFLVRSLFKKPTR----PLPPGPLGWPLVGALPLLGA--MPHVALAKLAKK  63
            +A+I+ LI  FL    L++K +R    P+  G   WP++G L LL     PH  L  LA K
Sbjct  15   IASILSLI--FLCLFLYRKNSRGKDAPVVSG--AWPILGHLSLLNGSQTPHKVLGALADK  70

Query  64   YGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGP  123
            YGP+  +K+G    +V S  E ++    T DL  S+RP       ++Y    +  A YGP
Sbjct  71   YGPLFTIKLGMKPALVLSNWEMSKELFTTNDLAVSSRPKLVAVEVMSYNQAFVGLAPYGP  130

Query  124  RWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEP-------VVLAEML  176
             W+ LRK+     L  + ++   ++RV+E+   +K + +    G         V + + L
Sbjct  131  YWRELRKIVTFEFLSNRRIEQRNHIRVSEVRTSIKELFDIWSNGNKNESRYTLVDIKQWL  190

Query  177  TYAMANMIGQVILSRRVF----VTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDL  232
             Y   NM+ ++++ +R F    V    ++  F   + E M   G F + D +P + W+DL
Sbjct  191  AYLTFNMVVRMVVGKRYFGVMHVEGKDKAQRFMKNIREFMNLMGTFTVADGVPCLRWLDL  250

Query  233  QGIERGMKKLHTKFDVLLTKMVKEHRATS---HERKGKADFLDVLLEECDNTN-GEKLSI  288
             G E+ MK    + D LL++ ++EHR         +   DF+DV++   +    G   +
Sbjct  251  GGHEKAMKANAKEVDKLLSEWLEEHRQKKLLGENVESDRDFMDVMISALNGAQIGAFDAD  310

Query  289  TNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISS  348
            T  KA  L L   GTD+++  + WAL+ +++NP  L KA+EE+D  IG+D  + ESDIS
Sbjct  311  TICKATSLELILGGTDSTAVTLTWALSLLLRNPLALGKAKEEIDMQIGKDEYIRESDISK  370

Query  349  LPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENP  408
            L YLQAI KET R +P  P + PR   + C + GY+I K  RL  N+W I RDP+VW +P
Sbjct  371  LVYLQAIVKETLRLYPPAPFSSPREFTENCILGGYHIKKGTRLIHNLWKIHRDPSVWSDP  430

Query  409  LEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKL  468
            LEF PERFL+     ++  G++F+L+PFG+GRR+CAG  +G+ +V + L  L+HSFD  +
Sbjct  431  LEFKPERFLTTHK-DVDLRGHNFELLPFGSGRRVCAGMSLGLNMVHFTLANLLHSFD--I  487

Query  469  PNGVAE-LNMDESFGLALQKAVPLSALVSPRLASNPYAT  506
             N  AE ++M E FG    KA PL  LV PR + N Y T
Sbjct  488  LNPSAEPVDMTEFFGFTNTKATPLEILVKPRQSPNYYET  526
```

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RecName: Full=Cytochrome P450 71B12

Sequence ID: Q9ZU07.1 **Length:** 496 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 489 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
315 bits(808)	4e-101	Compositional matrix adjust.	170/492(35%)	281/492(57%)	12/492(2%)

```
Query  8    FVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPI  67
            +++ A +F  +  +VR + +K  + LPPGP   P++G L  LG+ PH ++ KL++ YGP+
Sbjct  5    YIIVAFVFFSSMIIVR-IIRKTKKNLPPGPPRLPIIGNLHQLGSKPHRSMFKLSETYGPL  63

Query  68   MHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKT  127
            M LK G+   VVASTPE+ +  LKT D+   +RP     + + Y  +DL F+ Y   W+
Sbjct  64   MSLKFGSVSTVVASTPETVKEVLKTFDVECCSRPNMTYPARVTYNLKDLCFSPYSKYWRE  123

Query  128  LRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQV  187
            +RK++ + +   K +  + + R  E+  ++  + +A+   +PV L + L     ++I +V
Sbjct  124  VRKMTVVELYTAKRVQSFQHTRKEEVAALVDFIKQAASLEKPVNLNKKLMKLSGSVICRV  183

Query  188  ILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWM--DLQGIERGMKKLHTK  245
                 + +      N +++++   +   G F   D+ P +  +   + G+    +KL
Sbjct  184  AFG--INLQGSKLENTYEEVIQGTVELVGSFAAADYFPVVGRIIDRITGLHSKCEKLFKA  241

Query  246  FDVLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGE-KLSITNIKAVLLNLFTAGTD  304
             D    + +K H      +    D L + +E  + T GE +L+  + K +L N+  AG D
Sbjct  242  MDAFFDQSIKHHLEDEIIKDDIID-LLLKMERGETTLGEFQLTRDHTKGILANILNAGID  300

Query  305  TSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHP  364
            TS+ ++ W +T +I NP +LKKAQ E+  VI     ++E DI  L YL+ + KET+R +P
Sbjct  301  TSAQVMTWVMTYLISNPRVLKKAQAEVREVIKHKDDIIEEDIERLQYLKMVIKETFRINP  360

Query  365  STPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKI  424
              PL +PR A +  ++ GY IPK   + VNIWAI R+PNVW++P  F+PERF+   + +I
Sbjct  361  LVPLLIPREASKDVKIGGYNIPKKTWIHVNIWAIHRNPNVWKDPEAFIPERFM---DSQI  417

Query  425  NPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG--VAELNMDESFG  482
            +  G +F+L+PFG+GRRIC G  MGM LV   L  L++ FDWKLP G  VA+++++ES+G
Sbjct  418  DYKGLNFELLPFGSGRRICPGIGMGMALVHLTLINLLYRFDWKLPEGMKVADVDLEESYG  477

Query  483  LALQKAVPLSAL  494
            L   K +PL  +
Sbjct  478  LVCPKKIPLQLI  489
```

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RecName: Full=Cytochrome P450 71B10

Sequence ID: Q9LVD2.1 **Length:** 502 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 31 to 502 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
315 bits(807)	7e-101	Compositional matrix adjust.	175/478(37%)	272/478(56%)	22/478(4%)

```
Query  34   PPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTL  93
            PP P G P++G L  LG +PH +L KL+KKYGP+M LK+G    V+ STPE+A+  LK
```

```
Sbjct  31   PPSPPGLPIIGNLHQLGELPHQSLCKLSKKYGPVMLLKLGRVPTVIVSTPETAKQVLKDY  90

Query  94   DLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTEL  153
            DL+  +RP   G   L+Y   D+ F+++   WK LRKL    +   K ++    ++  E+
Sbjct  91   DLHCCSRPSLEGTRKLSYNYLDIAFSRFDDYWKELRKLCVEELFCNKRINSIQPIKEAEM  150

Query  154  GHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVELMT  213
              ++ ++ E++     V L++       N+I + +     F      +++F+D+V E +
Sbjct  151  EKLIDSIAESASQKTLVNLSDTFLSLNVNVICKAVFGVN-FQGTVLNNDKFQDLVHEALE  209

Query  214  SAGYFNIGDFIPSIAWMD--LQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKGKADFL  271
              G F+  DF P + W+     G+    ++     D    +M+  H   + E + + DF+
Sbjct  210  MLGSFSASDFFPYVGWIVDWFTGLHARRERSVRDLDAFYEQMIDLHLQKNRE-ESEDDFV  268

Query  272  DVLL----EECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKA  327
            D+LL    EE     G KL+  +IKA+L+N+   G +TS+  + WA+ E+I+NP ++KK
Sbjct  269  DLLLRLEKEEAVLGYG-KLTRNHIKAILMNILLGGINTSAITMTWAMAELIRNPRVMKKV  327

Query  328  QEEMDRVIGRDR--RLLESD-ISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYY  384
            Q E+   IG++   R++  D I+ L YL  + KET R HP  PL +PR  I   +++GY
Sbjct  328  QSEIRAQIGKNNKTRIISLDEINHLSYLNMVIKETCRLHPVAPLLVPREVISEFKINGYT  387

Query  385  IPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICA  444
            I    RL VN+WAIGRDP +W++P EFLPERF+   +  I+  G D++L+PFG+GRRIC
Sbjct  388  IQPKTRLHVNVWAIGRDPEIWKDPEEFLPERFM---DCDIDVKGQDYELLPFGSGRRICP  444

Query  445  GTRMGMVLVSYILGTLVHSFDWKLPNGVA--ELNMDESFGLALQKA-----VPLSALV  495
               MG+  V + L  L++ FDWKLP GVA  ++ MDE+ GL   K      VP+ +LV
Sbjct  445  AVYMGITTVEFGLANLLYHFDWKLPEGVAVEDIYMDEASGLTSHKKHDLLLVPVKSLV  502
```

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RecName: Full=Cytochrome P450 71B34

Sequence ID: Q9LIP6.1 **Length:** 500 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 1 to 486 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
314 bits(805)	1e-100	Compositional matrix adjust.	180/498(36%)	279/498(56%)	27/498(5%)

```
Query  5    VTDFVVAAIIFLITRFLVRSLFKKPTRP----LPPGPLGWPLVGALPLLGAMPHVALAKL  60
            +T+  + ++IF+I   ++ ++F    R      PP P G P++G L  LG +PH +L KL
Sbjct  1    MTNIWLLSLIFVIC--ILVAVFNHKNRRNYQRTPPSPPGCPIIGNLHQLGELPHQSLWKL  58

Query  61   AKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAK  120
            +KKYGP+M LK+G    V+ S+ E+A+  LK  DL+  +RP  AGA  L+Y   D+ F+
Sbjct  59   SKKYGPVMLLKLGRVPTVIVSSSETAKQALKIHDLHCCSRPGFAGARELSYNYLDIAFSP  118

Query  121  YGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAM  180
            Y   WK +RKL+   +   K +     ++  E+  ++ ++ E++    P+ L + L
Sbjct  119  YDDYWKEVRKLAVQELFSSKQVHSIQPIKDEEVKKLIDSISESAAQKTPINLNKTLLALT  178

Query  181  ANMIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWM-----DLQGI  235
             +++ +   S   F      S  F ++V E +   G F+  DFIP +  +      LQG
Sbjct  179  VSVVCRTAFSVN-FEGTVLNSERFNNIVREALEMLGSFSASDFIPYVGRIIDLLTGLQGR  237

Query  236  -ERGMKKLHTKFDVLLTKMVKEHRATSHERKGKADFLDVLL---EECDNTNGEKLSITNI  291
             ER M+ L    D    +M   H+    E  G  DF+D+LL   +E      +KL+  +I
Sbjct  238  RERSMRDL----DAFYEQMFDLHKQKKEE--GSEDFVDLLLRLEKEEAVLGNDKLTRNHI  291

Query  292  KAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPY  351
            KA+L+++  AG DTS+  + WA+ E+ KNP ++KK Q E+   I    R+   D   L Y
Sbjct  292  KAILMDVLLAGMDTSAITMTWAMAELAKNPRVMKKVQSEIRSQIKNKERISFDDTDKLEY  351

Query  352  LQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEF  411
            L+ + KET+R HP+TPL +PR A+   E++GY IP   RL VN+WAIGRDP+ W++P  F
Sbjct  352  LKMVIKETWRLHPTTPLLIPREAMSEFEINGYTIPVKTRLHVNVWAIGRDPDTWKDPEVF  411

Query  412  LPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG  471
            LPERF    +  I+  G  F+L+PFG GRR+C    MG  +V + L  L++ FDWKLP G
Sbjct  412  LPERF---TDNNIDAKGQHFELLPFGGGRRMCPAVYMGTTMVEFGLANLLYHFDWKLPEG  468

Query  472  --VAELNMDESFGLALQK  487
              V +++M+E+ GL + K
Sbjct  469  MKVDDIDMEEAPGLTVNK  486
```

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RecName: Full=Cytochrome P450 76A2; AltName: Full=CYPLXXVIA2; AltName: Full=Cytochrome P-450EG7

Sequence ID: P37122.1 **Length:** 505 **Number of Matches:** 1

Related Information

Range 1: 18 to 501 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
311 bits(798)	2e-99	Compositional matrix adjust.	177/494(36%)	279/494(56%)	20/494(4%)

```
Query  11   AAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHL  70
            A I+F   +   +S +K      PPGP G P+ G +  LG  P+  +A L +KYGP++ L
Sbjct  18   AFILFFSQKNTTKSSYK-----FPPGPPGLPIFGNMFELGTEPYKKMAVLRQKYGPVLWL  72

Query  71   KMGTCDMVVASTPESARAFLKTLDLNFSNRP-PNAGASHLAYGAQDLVFAKYGPRWKTLR  129
            K+G+   +V  T +++    K  D++F+NR  P+   +H +Y    L  A YGP W+  R
Sbjct  73   KLGSTYTMVVQTAQASEELFKNHDISFANRVIPDVNQAH-SYYQGSLAIAPYGPFWRFQR  131
```

```
Query  130  KLSNLHMLGGKALDDWANVRVTELGHMLKAM---CEASRCGEPVVLAEMLTYAMANMIGQ  186
            ++  + M   K + +   VR   + +MLK +     ++  G  + +   +  A  NM+G
Sbjct  132  RICTIEMFVHKKISETEPVRRKCVDNMLKWIEKEANSAEKGSGIEVTRFVFLASFNMLGN  191

Query  187  VILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKF  246
            +ILS+ +   +  E++EF   +  +   +G  N+ D  P +   DLQ + + M +   K
Sbjct  192  LILSKDLADLESEEASEFFIAMKRINEWSGIANVSDIFPFLKKFDLQSLRKKMARDMGKA  251

Query  247  DVLLTKMVKEHRATSHE--RKGKADFLDVLLEECDNTNGE--KLSITNIKAVLLNLFTAG  302
              +++  +KE      +   KGK DFLDVLLE       E  KLS   IK  +L +F AG
Sbjct  252  VEIMSMFLKEREEERKKGTEKGK-DFLDVLLEFQGTGKDEPAKLSEHEIKIFVLEMFLAG  310

Query  303  TDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRK  362
            T+T+SS +EWALTE++++P  + K + E+ + I  +R+  +SDI +LPY+QA+ KE+ R
Sbjct  311  TETTSSSVEWALTELLRHPEAMAKVKTEISQAIEPNRKFEDSDIENLPYMQAVLKESLRL  370

Query  363  HPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENG  422
            HP  P  +PR  IQ  +  GY +PKD ++ VN WAIGRDP  W++P+ F PERFL
Sbjct  371  HPPLPFLIPRETIQDTKFMGYDVPKDTQVLVNAWAIGRDPECWDDPMSFKPERFL---GS  427

Query  423  KINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVA--ELNMDES  480
            KI+  G  + LIPFGAGRR+C G  +G  ++ + LG+L+  F+W+LP+GV+   +NMD S
Sbjct  428  KIDVKGQHYGLIPFGAGRRMCVGLPLGHRMMHFALGSLLREFEWELPDGVSPKSINMDGS  487

Query  481  FGLALQKAVPLSAL  494
             G+  +K   L  +
Sbjct  488  MGVTARKRDSLKVI  501
```

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RecName: Full=Cytochrome P450 71B35

Sequence ID: Q9LIP5.1 **Length:** 500 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 9 to 485 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
311 bits(796)	2e-99	Compositional matrix adjust.	172/483(36%)	268/483(55%)	14/483(2%)

```
Query  13   IIFLITRFL-VRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLK  71
            +IFL+   L V +  K P     P P G+P++G L  +G +PH  L KL+KKYGP+MHL
Sbjct  9    LIFLVCILLAVFNHKKHPKYRQFPCPPGFPIIGNLHQIGELPHQTLWKLSKKYGPVMHLM  68

Query  72   MGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKL  131
            +G    VV S+ ++AR  L+  DL+   RP  +G   L+Y   D+ F+ Y   WK +RKL
Sbjct  69   LGRVPTVVVSSSDTARQVLRVHDLHCCTRPSLSGPRELSYNYLDIAFSPYDDYWKEVRKL  128

Query  132  SNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSR  191
                +   K +     ++  E+  M+ ++ E++    PV L         +++ +
Sbjct  129  CVQELFSTKQVHSIQPIKDEEVKKMIDSIAESASQKNPVNLNNKCLELTVSVVCRTAFGV  188

Query  192  RVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMD--LQGIERGMKKLHTKFDVL  249
              F      S+ F  +V E +   G F+  DFIP + W+   L G++   ++     +
Sbjct  189  S-FEGTVLNSDRFNKIVREALEMLGSFSAADFIPYVGWIIDVLTGLQGRRERSKRDLNAF  247

Query  250  LTKMVKEHRATSHERKGKADFLDVLL---EECDNTNGEKLSITNIKAVLLNLFTAGTDTS  306
              +M   H+    E  G  DF+D+LL   +E      +KL+  +IKA+LL++  AG DTS
Sbjct  248  FEQMFDLHKEGKKE--GNEDFVDLLLRLEKEEAVLGNDKLTRNHIKAILLDVLLAGIDTS  305

Query  307  SSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPST  366
            +  + WA+TE+ +NP ++KK Q E+   +G    +   D+  L YL+ + KET+R HP+T
Sbjct  306  AITMTWAMTELARNPRVMKKVQSEIRTQMGNRSMISFEDMDQLEYLKMVIKETWRLHPTT  365

Query  367  PLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINP  426
            PL LPR A+   +++GY IP   RL VN+WAIGRDP+ W++P  FLPERF+   +  I+
Sbjct  366  PLLLPREAMSEFDINGYTIPVKTRLHVNVWAIGRDPDTWKDPEVFLPERFM---DNNIDA  422

Query  427  GGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVA--ELNMDESFGLA  484
             G  F+L+PFG GRRIC    MG  +V + L  L++ FDWKLP GV   +++++E+ GL
Sbjct  423  KGQHFELLPFGGGRRICPAIYMGTTMVEFGLANLLYHFDWKLPEGVEVKDIDVEEAPGLT  482

Query  485  LQK  487
            + K
Sbjct  483  VNK  485
```

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RecName: Full=Premnaspirodiene oxygenase; Short=HPO; AltName: Full=Cytochrome P450 71D55

Sequence ID: A6YIH8.1 **Length:** 502 **Number of Matches:** 1

Related Information

Range 1: 29 to 496 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
310 bits(795)	4e-99	Compositional matrix adjust.	172/479(36%)	267/479(55%)	22/479(4%)

```
Query  30   TRPLPPGPLGWPLVGA-LPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARA  88
            ++ LPPGP   PL+G+ L ++G +PH  L  LAKKYGP+MHL++G    VV ++P+ A+
Sbjct  29   SKKLPPGPWKLPLLGSMLHMVGGLPHHVLRDLAKKYGPLMHLQLGEVSAVVVTSPDMAKE  88

Query  89   FLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANV  148
             LKT D+ F++RP       + Y   D+ F  YG  W+ +RK+  L +L  K +  ++++
Sbjct  89   VLKTHDIAFASRPKLLAPEIVCYNRSDIAFCPYGDYWRQMRKICVLEVLSAKNVRSFSSI  148

Query  149  RVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMV  208
            R  E+  ++  +   S   EPV   E L    ++M       R  F     E   F  ++
```

```
Sbjct  149  RRDEVLRLVNFV--RSSTSEPVNFTERLFLFTSSMT-----CRSAFGKVFKEQETFIQLI  201

Query  209  VELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKKLHTKFDVLLTKMVKEHR-----ATSH  262
             E++  AG F++ D  PS+ ++  L G+E  + K H K D ++  ++ EH+       ++
Sbjct  202  KEVIGLAGGFDVADIFPSLKFLHVLTGMEGKIMKAHHKVDAIVEDVINEHKKNLAMGKTN  261

Query  263  ERKGKADFLDVLLEECDNTNGEKLSITN--IKAVLLNLFTAGTDTSSSIIEWALTEMIKN  320
               G  D +DVLL    N  G +  ITN  IKA++ ++F AGT+TSSS + WA+ +M++N
Sbjct  262  GALGGEDLIDVLLR-LMNDGGLQFPITNDNIKAIIFDMFAAGTETSSSTLVWAMVQMMRN  320

Query  321  PTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEV  380
            PTIL KAQ E+           E+D+  L YL+ + KET R HP  PL +PR   +  E+
Sbjct  321  PTILAKAQAEVREAFKGKETFDENDVEELKYLKLVIKETLRLHPPVPLLVPRECREETEI  380

Query  381  DGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGR  440
            +GY IP   ++ VN+WA+GRDP  W++   F PERF   E   ++  GN+F+ +PFG GR
Sbjct  381  NGYTIPVKTKVMVNVWALGRDPKYWDDADNFKPERF---EQCSVDFIGNNFEYLPFGGGR  437

Query  441  RICAGTRMGMVLVSYILGTLVHSFDWKLPNGV--AELNMDESFGLALQKAVPLSALVSP  497
            RIC G   G+  V   L  L++ FDWKLP G+   +L++ E  G+   +   L  + +P
Sbjct  438  RICPGISFGLANVYLPLAQLLYHFDWKLPTGMEPKDLDLTELVGVTAARKSDLMLVATP  496
```

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RecName: Full=(S)-N-methylcoclaurine 3'-hydroxylase isozyme 1; AltName: Full=Cytochrome P450 80B1; AltName: Full=Cytochrome P450 80B3

Sequence ID: Q9SP06.1 **Length:** 481 **Number of Matches:** 1

Related Information

Range 1: 30 to 473 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
309 bits(791)	8e-99	Compositional matrix adjust.	178/458(39%)	259/458(56%)	20/458(4%)

```
Query  40   WPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSN  99
            WP+VG L  LG  PH   A+LA+ YG +  LK+G+  +VVASTP +A   LKT D   S
Sbjct  30   WPIVGNLLQLGEKPHSQFAQLAETYGDLFSLKLGSETVVVASTPLAASEILKTHDRVLSG  89

Query  100  RPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKA  159
            R          +    +V+++    WK LRK+    +   K ++  A VR ++   M++
Sbjct  90   RYVFQSFRVKEHVENSIVWSECNETWKKLRKVCRTELFTQKMIESQAEVRESKAMEMVEY  149

Query  160  MCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESN---EFKDMVVELMTSAG  216
            +      G  V +AE++   + N+ G +I S+ +F   G ES+   E K+ +  ++
Sbjct  150  L--KKNVGNEVKIAEVVFGTLVNIFGNLIFSQNIF-KLGDESSGSVEMKEHLWRMLELGN  206

Query  217  YFNIGDFIPSIAWMDLQGIERGMKKLHTKFDVLLTKMVKEHR-ATSHERKGKADFLDVLL  275
              N  D+ P +   DL G  + +         +   M+KE + A  H    K DF+++LL
Sbjct  207  STNPADYFPFLGKFDLFGQSKDVADCLQGIYSVWGAMLKERKIAKQHNNSKKNDFVEILL  266

Query  276  EECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVI  335
            +         L    I A+L+ +F AGT+TS+S IEWAL+E+ KNP +    + E+  V+
Sbjct  267  DS-------GLDDQQINALLMEIFGAGTETSASTIEWALSELTKNPQVTANMRLELLSVV  319

Query  336  GRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNI  395
            G+ R + ESDI ++PYLQA  KET R HP+TPL LPR A++ C+V  Y IPK+ ++ VN
Sbjct  320  GK-RPVKESDIPNMPYLQAFVKETLRLHPATPLLLPRRALETCKVLNYTIPKECQIMVNA  378

Query  396  WAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSY  455
            W IGRDP  W +PL+F PERFL   N  I+  GNDF+LIPFGAGRRIC G  +    +S
Sbjct  379  WGIGRDPKRWTDPLKFSPERFL---NSSIDFKGNDFELIPFGAGRRICPGVPLATQFISL  435

Query  456  ILGTLVHSFDWKLPNGV--AELNMDESFGLALQKAVPL  491
            I+ +LV +FDW  P G+  ++L M+E FGL LQK  PL
Sbjct  436  IVSSLVQNFDWGFPKGMDPSQLIMEEKFGLTLQKEPPL  473
```

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RecName: Full=Cytochrome P450 98A2

Sequence ID: O48922.1 **Length:** 509 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 9 to 502 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
309 bits(792)	1e-98	Compositional matrix adjust.	181/502(36%)	284/502(56%)	19/502(3%)

```
Query  14   IFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMG  73
            I L+T +L  +L+++    LPPGP  WP+VG L  +  +     A+ A+ YGPI+ +  G
Sbjct  9    ISLVTLWLGYTLYQRLRFKLPPGPRPWPVVGNLYDIKPVRFRCFAEWAQSYGPIISVWFG  68

Query  74   TCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSN  133
            +   V+ S  E A+  LK  D   ++R  +  A+  +   +DL++A YGP +  +RK+
Sbjct  69   STLNVIVSNSELAKEVLKEHDQLLADRHRSRSAAKFSRDGKDLIWADYGPHYVKVRKVCT  128

Query  134  LHMLGGKALDDWANVRVTELGHMLKAM---CEASR-CGEPVVLAEMLTYAMANMIGQVIL  189
            L +   K L+    +R  E+  M+ ++   C ++   G+ ++L + L     N I ++
Sbjct  129  LELFSPKRLEALRPIREDEVTSMVDSVYNHCTSTENLGKGILLRKHLGVVAFNNITRLAF  188

Query  190  SRRVFVTKGT---ESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLH-TK  245
             +R   ++G    +  EFK +V   +       + + IP + WM    +E G    H  +
Sbjct  189  GKRFVNSEGVMDEQGVEFKAIVENGLKLGASLAMAEHIPWLRWM--FPLEEGAFAKHGAR  246

Query  246  FDVLLTKMVKEHRATSHERKG-KADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTD  304
             D L   ++ EH     +  G K  F+D LL   D  +   LS   I  +L ++ TAG D
```

```
Sbjct  247  RDRLTRAIMAEHTEARKKSGGAKQHFVDALLTLQDKYD---LSEDTIIGLLWDMITAGMD  303

Query  305  TSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHP  364
            T++  +EWA+ E+I+NP + +K QEE+DRVIG +R + E+D S+LPYLQ + KE  R HP
Sbjct  304  TTAISVEWAMAELIRNPRVQQKVQEELDRVIGLERVMTEADFSNLPYLQCVTKEAMRLHP  363

Query  365  STPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKI  424
             TPL LP  A    +V GY IPK + + VN+WA+ RDP VW++PLEF PERFL E+   +
Sbjct  364  PTPLMLPHRANANVKVGGYDIPKGSNVHVNVWAVARDPAVWKDPLEFRPERFLEED---V  420

Query  425  NPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGV--AELNMDESFG  482
            +  G+DF+L+PFG+GRR+C G ++G+ L + +LG L+H F W  P G+   E++M E+ G
Sbjct  421  DMKGHDFRLLPFGSGRRVCPGAQLGINLAASMLGHLLHHFCWTPPEGMKPEEIDMGENPG  480

Query  483  LALQKAVPLSALVSPRLASNPY  504
            L      P+ A+VSPRL S+ Y
Sbjct  481  LVTYMRTPIQAVVSPRLPSHLY  502
```

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RecName: Full=Cytochrome P450 76C3

Sequence ID: O64638.2 **Length:** 515 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 48 to 504 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
310 bits(793)	1e-98	Compositional matrix adjust.	178/462(39%)	268/462(58%)	15/462(3%)

```
Query  43   VGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPP  102
            VG +  LG  PH +LA  +K YGPIM LK+G    VV S+PE+A+  L+T D   S R
Sbjct  48   VGNIFQLGFNPHRSLAAFSKTYGPIMSLKLGRLTAVVISSPEAAKEALRTHDHVMSARTF  107

Query  103  NAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCE  162
            N       +    +V+     RW+ L+K    ++L  + LD   ++R+ ++  ++  + E
Sbjct  108  NDALRAFDHHKHSIVWIPPSARWRFLKKTITKYLLSPQNLDAIQSLRMRKVEELVSLVNE  167

Query  163  ASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESN-EFKDMVVELMTSAGYFNIG  221
                GE + LA        N+I   + S  +       S+ EF + VV L   AG  N+G
Sbjct  168  FRERGEAIDLARASFVTSFNIISNALFSVDLATYDSNSSSYEFHNTVVHLTDIAGIPNVG  227

Query  222  DFIPSIAWMDLQGIERG----MKKLHTKFDVLL-TKMVKEHRATSHERKGKA--DFLDVL  274
            D+   + ++DLQG  +     ++KL   F   +  ++ K    T  E K  +  D LD L
Sbjct  228  DYFQYMRFLDLQGTRKKAVLCIEKLFRVFQEFIDARLAKRFSRTEKEPKEASSIDMLDSL  287

Query  275  LEECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRV  334
            L+       E L++ ++K +LL++F AGTDT+SS +EWA+TE+ ++    + KAQ E+ +V
Sbjct  288  LDLTQQNEAE-LTMNDLKHLLLDVFVAGTDTNSSTMEWAMTELFRSTEKMVKAQSEIRQV  346

Query  335  IGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVN  394
            IG++  + ESDI SLPYLQAI KET R HP+ PL +PR +    ++ G+ +PK+ ++ VN
Sbjct  347  IGQNGFVQESDIPSLPYLQAIVKETLRLHPAAPL-IPRKSESDVQIMGFLVPKNTQVVVN  405

Query  395  IWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVS  454
            +WAIGRD +VWENP++F PERFL  E    +  G DF+LIPFG+GRR+C G  M +  +
Sbjct  406  VWAIGRDASVWENPMKFEPERFLLRET---DVKGRDFELIPFGSGRRMCPGISMALKTMH  462

Query  455  YILGTLVHSFDWKLPNGV--AELNMDESFGLALQKAVPLSAL  494
             +L +L++SFDWKL NGV    ++M E+FGL L KA  L A+
Sbjct  463  MVLASLLYSFDWKLQNGVVPGNIDMSETFGLTLHKAKSLCAV  504
```

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RecName: Full=Cytochrome P450 82A4; AltName: Full=Cytochrome P450 CP9

Sequence ID: O49859.1 **Length:** 525 **Number of Matches:** 1

Related Information

Range 1: 11 to 524 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
310 bits(793)	1e-98	Compositional matrix adjust.	185/517(36%)	281/517(54%)	19/517(3%)

```
Query  6    TDFVVAAIIFLITRFLVRSLFK--KPTRPLPPGPLGWPLVGALPLL--GAMPHVALAKLA  61
            T   V ++IFL+  FL   L K    ++  P     WP+ G LPLL     PH AL  LA
Sbjct  11   TTIGVVSLIFLLCLFLYGPLKKVHGSSKEAPTVGGAWPIFGHLPLLIGSKSPHKALGALA  70

Query  62   KKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKY  121
            +K+GP+  +K+G    +V S  E AR    T D+  S RP    A  + Y    L+ A Y
Sbjct  71   EKHGPLFTIKLGAKKALVVSDWEMARECFTTNDVAVSARPKLLVAELMCYNNAMLLVAPY  130

Query  122  GPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGE------PVVLAEM  175
            GP W+ LRK+    +L     ++  +VRV+E+ + +  + +  R  +       V L +
Sbjct  131  GPYWRELRKIIVTEILSSSRVEQLQDVRVSEVQNSIVELYDVWRSQKNESDYASVELKQW  190

Query  176  LTYAMANMIGQVILSRRVFVTKGTESNEFKDM--VVELMTSAGYFNIGDFIPSIAWMDLQ  233
                + NM+ ++++ +R      T+    K +  V E M  AG F +GD IP + W+D
Sbjct  191  FAQPIFNMVLRMVVGKRFLSATATDEKAEKCVKAVDEFMRLAGVFTVGDAIPYLRWLDFG  250

Query  234  GIERGMKKLHTKFDVLLTKMVKEHR---ATSHERKGKADFLDVLLEECDNTNGEKLSI-T  289
            G E+ MK+   + DV++++ ++EHR   A      G  DF++V+L   D    + +   T
Sbjct  251  GYEKAMKETAKELDVMISEWLEEHRQKRALGEGVDGAQDFMNVMLSSLDGKTIDGIDADT  310

Query  290  NIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSL  349
             IK+ +L +  AGT+ S S I WA+  ++KNP IL+  + E+D  +G+DR + ESDIS+L
Sbjct  311  LIKSTVLTIIQAGTEASISTIIWAMCLILKNPLILEN-KAELDIQVGKDRCICESDISNL  369
```

```
Query  350  PYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPL  409
             YLQA+ KET R +   PL+ PR   + C + GY++ K  RL  NIW I  DPNVW +P
Sbjct  370  VYLQAVVKETLRLYAPGPLSSPREFAEDCTLGGYHVKKGTRLITNIWKIHTDPNVWSDPF  429

Query  410  EFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLP  469
            EF P+RFL+     I+  G+ F+L+PFG+GRR+C G   G+  V   L + +HSF+   P
Sbjct  430  EFKPDRFLTTHK-DIDVKGHHFQLLPFGSGRRVCPGISFGLQTVHLALASFLHSFEILNP  488

Query  470  NGVAELNMDESFGLALQKAVPLSALVSPRLASNPYAT  506
            +    L+M E+FG+   KA PL  LV P L+ + Y +
Sbjct  489  S-TEPLDMTEAFGVTNTKATPLEVLVKPCLSPSCYKS  524
```

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RecName: Full=Cytochrome P450 71A2; AltName: Full=CYPLXXIA2; AltName: Full=Cytochrome P-450EG4

Sequence ID: P37118.1 **Length:** 505 **Number of Matches:** 1

Related Information

Range 1: 9 to 504 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
308 bits(789)	3e-98	Compositional matrix adjust.	176/508(35%)	294/508(57%)	24/508(4%)

```
Query  2    AILVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLA  61
            ++L+  FV    IFL+      +  KK    L P P   P++G L  LG++PH +L KL+
Sbjct  9    SLLIPLFV---FIFLLIHHCFFTTSKKQNMLLLPSPRKLPIIGNLHQLGSLPHRSLHKLS  65

Query  62   KKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKY  121
            +KYGP+M L  G+  ++VAS+ ++AR  +KT D+ +++RP ++    L+YG++D+ F+ +
Sbjct  66   QKYGPVMLLHFGSKPVIVASSVDAARDIMKTHDVVWASRPKSSIVDRLSYGSKDVGFSPF  125

Query  122  GPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVV-LAEMLTYAM  180
            G  W+  + ++ LH+L    +  + NVR  E  +M+  + +   C   V+ L E L
Sbjct  126  GEYWRRAKSITVLHLLSNTRVQSYRNVRAEETANMIGKIRQG--CDSSVINLGEHLCSLT  183

Query  181  ANMIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGM  239
             N+I +V L  R +  K +      +  VEL+   G FN+GD+IP + W++   G++  +
Sbjct  184  NNIISRVALG-RTYDEKESGIEHIIEQFVELL---GIFNVGDYIPRLEWVNKFTGLDAKV  239

Query  240  KKLHTKFDVLLTKMVKEH----RATSHERKGKA-DFLDVLLE-ECDNTNGEKLSITNIKA  293
            KK+  + D+ L  +++EH    +   +   G+A DF+DVLLE +  N     L   ++KA
Sbjct  240  KKVAKELDMFLEIVIEEHIIRKKKEEYTSTGEAKDFVDVLLEIQNGNETDFPLQRDSLKA  299

Query  294  VLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQ  353
            +LL+ F AGTDT+ + ++W + E+++ P  LK  Q+E+  +      + E D+ ++ YL+
Sbjct  300  ILLDSFAAGTDTTFATLDWTMAELLRQPRALKTLQDEVRGLAQGKSEITEDDLKNMQYLR  359

Query  354  AIAKETYRKHPST-PLNLPRIAIQACEVDGYY-IPKDARLSVNIWAIGRDPNVWENPLEF  411
            A+ KE+ R HP+   L +PR +++   + GYY IP   +  +N WAIGRDP  WENP E+
Sbjct  360  AVIKESLRLHPTQESLLVPRESMEDVNLLGYYHIPARTQAIINAWAIGRDPLSWENPEEY  419

Query  412  LPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG  471
             PERFL   N   +  G +FKL+PFGAGRR C G+   + ++   L  LVH FD+ LP G
Sbjct  420  QPERFL---NSDADVKGLNFKLLPFGAGRRGCPGSSFAIAVIELALARLVHKFDFALPEG  476

Query  472  V--AELNMDESFGLALQKAVPLSALVSP  497
            +   +L+M E+ G+  ++ +PL  + +P
Sbjct  477  IKPEDLDMTETIGITTRRKLPLLVVATP  504
```

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RecName: Full=Cytochrome P450 71B37

Sequence ID: Q9LIP3.2 **Length:** 500 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 32 to 486 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
308 bits(788)	4e-98	Compositional matrix adjust.	169/461(37%)	259/461(56%)	13/461(2%)

```
Query  34   PPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTL  93
            PP P G+P++G L  LG +PH +L  L+KKYGP+M LK G+   VV S+ E+A+  LK
Sbjct  32   PPSPPGFPIIGNLHQLGELPHQSLWSLSKKYGPVMLLKFGSIPTVVVSSSETAKQALKIH  91

Query  94   DLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTEL  153
            DLN  +RP  AG   L+Y   D+VF+ +   WK LR++    +   K +      +R  E+
Sbjct  92   DLNCCSRPSLAGPRALSYNYLDIVFSPFNDYWKELRRMCVQELFSPKQVHLIQPIREEEV  151

Query  154  GHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVELMT  213
              ++ +  E++    PV L+E L      +I +       F      S+ F  ++ +
Sbjct  152  KKLMNSFSESAAQKTPVNLSEKLASLTVGVICKAAFGVS-FQGTVLNSDNFDKLIHDAFL  210

Query  214  SAGYFNIGDFIPSIAWMD--LQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKGKADFL  271
              G F+  D+ P++ W+   L G++   ++     D    +M   H+  + E  G  DF+
Sbjct  211  FLGSFSASDYFPNVGWIIDWLTGLQGQRERSVRGLDAFYEQMFDLHKQGNKE--GVEDFV  268

Query  272  DVLL--EECDNTNGE-KLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQ  328
            D+LL  E+ +   G  KL+  +IKAVL+N+   G  TS+  + WA+TE+++NP ++KK Q
Sbjct  269  DLLLKLEKEETVLGYGKLTRNHIKAVLMNVLLGGIGTSAITMTWAMTELMRNPRVMKKVQ  328

Query  329  EEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKD  388
             E+   IG    +   DI  L YL+ +  ET+R HP  PL +PR  +   E++GY IP
Sbjct  329  SEIRNQIGGKSMICLDDIDQLHYLKMVINETWRLHPPAPLLVPREVMSEFEINGYTIPAK  388

Query  389  ARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRM  448
             RL VN+W IGRDP+ W++P EFLPERF+   N  I+  G +F+L+PFG+GRR+C    M
```

```
Sbjct  389  TRLYVNVWGIGRDPDTWKDPEEFLPERFV---NSNIDAKGQNFELLPFGSGRRMCPAMYM  445

Query  449  GMVLVSYILGTLVHSFDWKLPNG--VAELNMDESFGLALQK  487
            G  +V + L  L++ FDWKLP G  V +++M+ES GL   K
Sbjct  446  GTTMVEFGLANLLYHFDWKLPEGMVVEDIDMEESPGLNASK  486
```

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RecName: Full=Cytochrome P450 82C4

Sequence ID: Q9SZ46.1 **Length:** 524 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 518 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
308 bits(788)	8e-98	Compositional matrix adjust.	181/517(35%)	282/517(54%)	24/517(4%)

```
Query  4     LVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHV---ALAKL  60
             L + FV   +   I  F      K    P P G   WP++G L LLG    +    L K+
Sbjct  5     LFSLFVPILVFVFIALFKKSKKPKYVKAPAPSG--AWPIIGHLHLLGGKEQLLYRTLGKM  62

Query  61    AKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAK  120
             A  YGP M L++G+ +  V S+ E A+      D   ++RP  A A H+ Y      FA
Sbjct  63    ADHYGPAMSLQLGSNEAFVVSSFEVAKDCFTVNDKALASRPMTAAAKHMGYNFAVFGFAP  122

Query  121   YGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCE---ASRCGEPVV--LAEM  175
             Y   W+ +RK++ + +L  + L    +VRV+E+   +K +      +   +PV+  L
Sbjct  123   YSAFWREMRKIATIELLSNRRLQMLKHVRVSEITMGVKDLYSLWFKNGGTKPVMVDLKSW  182

Query  176   LTYAMANMIGQVILSRRVFVTKGTESNE-------FKDMVVELMTSAGYFNIGDFIPSIA  228
             L     NMI +++  +R F   G+ S+E        K  + +     G F + D  P+++
Sbjct  183   LEDMTLNMIVRMVAGKRYFGGGGSVSSEDTEEAMQCKKAIAKFFHLIGIFTVSDAFPTLS  242

Query  229   WMDLQGIERGMKKLHTKFDVLLTKMVKEHRAT---SHERKGKADFLDVLLEECDNTNGEK  285
             + DLQG E+ MK+  ++ DV+L + ++ HR     S  ++  +DF+DV++   +
Sbjct  243   FFDLQGHEKEMKQTGSELDVILERWIENHRQQRKFSGTKENDSDFIDVMMSLAEQGKLSH  302

Query  286   LSI---TNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLL  342
             L     T+IK+  L L   G+DTS+S + WA++ ++ N  +LKKAQ+E+D  +GRDR +
Sbjct  303   LQYDANTSIKSTCLALILGGSDTSASTLTWAISLLLNNKEMLKKAQDEIDIHVGRDRNVE  362

Query  343   ESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDP  402
             +SDI +L YLQAI KET R +P+ PL  PR A++ C V GYY+P   RL VN+W I RDP
Sbjct  363   DSDIENLVYLQAIIKETLRLYPAGPLLGPREAMEDCTVAGYYVPCGTRLIVNVWKIQRDP  422

Query  403   NVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVH  462
              V+  P EF PERF++ E  + +  G +F+L+PFG+GRR C G+ + M ++   L   +H
Sbjct  423   KVYMEPNEFRPERFITGEAKEFDVRGQNFELMPFGSGRRSCPGSSLAMQVLHLGLARFLH  482

Query  463   SFDWKLPNGVAELNMDESFGLALQKAVPLSALVSPRL  499
             SFD K    +  ++M E+ GL + KA PL  L+SPR+
Sbjct  483   SFDVKTVMDMP-VDMSENPGLTIPKATPLEVLISPRI  518
```

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RecName: Full=Cytochrome P450 71B13

Sequence ID: P58050.1 **Length:** 496 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 489 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
306 bits(783)	2e-97	Compositional matrix adjust.	171/494(35%)	277/494(56%)	16/494(3%)

```
Query  8     FVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPI  67
             +++   +F  + F+ ++  +K  + LPPGP   P++G L  LG+ PH ++ KL++KYGP+
Sbjct  5     YIIVVFVFFASIFIAKNT-RKTKKNLPPGPPRLPIIGNLHQLGSKPHRSMFKLSEKYGPL  63

Query  68    MHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKT  127
             ++LK+G    VVASTPE+ +  LKT D +  +R      + ++Y  +DL FA Y   WK
Sbjct  64    VYLKLGKVPSVVASTPETVKDVLKTFDKDCCSRAFLTYPARISYNLKDLAFAPYSKYWKA  123

Query  128   LRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQV  187
             +RK++ + +   K +  + N+R  E+   ++ +  ++   E V L + L     ++I +V
Sbjct  124   VRKMTVVELYTAKRVKSFRNIREEEVASFVEFIKHSASLEEIVNLNQTLVKLSGSVICRV  183

Query  188   ILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWM--DLQGIERGMKKLHTK  245
                  + +      N +++++   M   G F   D+ P I  +   + G+    +K+
Sbjct  184   GFG--INLEGSKLENTYEEVIHGTMEVLGSFAASDYFPVIGGIIDRITGLHNKCEKVFKG  241

Query  246   FDVLLTKMVKEHRATSHERKGKADFLDVLL--EECDNTNGE-KLSITNIKAVLLNLFTAG  302
              D      +K H     +   K D +D+LL  E  +   GE + +  + K +LL++  AG
Sbjct  242   TDSFFDHCIKHHL---EDGGSKDDIVDLLLKVERGEIGLGEFQFTRNHTKGILLDILLAG  298

Query  303   TDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRK  362
              DTS   I W +T +IKNP ++KKAQ E+  VI     + E DI  L YL+ + KET R
Sbjct  299   VDTSGHTITWVMTHLIKNPRVMKKAQAEVREVIKNKDNITEEDIEGLEYLKMVVKETLRI  358

Query  363   HPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENG  422
             +P  PL  PR A +  ++ GY IPK   + VNIWAI R+PNVW++P  F+PERF+   +
Sbjct  359   NPLVPLLTPREASKDVKIGGYNIPKKTWIHVNIWAIHRNPNVWKDPEAFIPERFM---DN  415

Query  423   KINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG--VAELNMDES  480
             +I+  G +F+L+PFG+GRRIC G  MGM L+   L  L++ FDWKLP G  V +++++ES
Sbjct  416   QIDYKGLNFELLPFGSGRRICPGIGMGMALIHLTLINLLYRFDWKLPEGMEVEDVDLEES  475
```

```
Query  481  FGLALQKAVPLSAL  494
            +GL   K VPL  +
Sbjct  476  YGLVCPKKVPLELI  489
```

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RecName: Full=Cytochrome P450 82A1; AltName: Full=CYPLXXXII

Sequence ID: Q43068.2 **Length:** 544 **Number of Matches:** 1

Related Information

Range 1: 18 to 543 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
305 bits(782)	1e-96	Compositional matrix adjust.	181/532(34%)	285/532(53%)	43/532(8%)

```
Query  12   AIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLL--GAMPHVALAKLAKKYGPIMH  69
            +++F + RF   S  K+P  P+  G   WPL+G LPL+     PH  L  L  KYGPI
Sbjct  18   SLLFFLFRFSKVSHTKEP--PIISG--SWPLLGHLPLMRNTQTPHKTLGALVDKYGPIFT  73

Query  70   LKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLR  129
            +K+G  + +V S  E A+      D+  S+RP       ++Y    + +A YG  W+ LR
Sbjct  74   IKLGATNALVLSNWELAKECFTKNDIVVSSRPKPVAVELMSYNQAFIGWAPYGAYWRQLR  133

Query  130  KLSNLHMLGGKALDDWANVRVTELGHMLKAMC------------------EASRCGEP--  169
            K+  L +L  + ++  +++RV+E+   +K +                    +S   EP
Sbjct  134  KIVTLEILSNRRIELLSHIRVSEVQTSIKELVNVWSNQISSQYGLLDDTKSSSTNDEPST  193

Query  170  -----VVLAEMLTYAMANMIGQVILSRRVF----VTKGTESNEFKDMVVELMTSAGYFNI  220
                 V L +       NM+ ++++ +R F    V    E+  F + + + M   G F +
Sbjct  194  TDYVSVELKKWFAQLTLNMVLRMVVGKRCFGDVDVENKEEAKRFLENIRDFMRLIGTFTV  253

Query  221  GDFIPSIAWMDLQGIERGMKKLHTKFDVLLTKMVKEHR-----ATSHERKGKADFLDVLL  275
            GD +P + W+DL G E+ MKK   KFDV+L + ++EHR      +  +  G+ DF+D +L
Sbjct  254  GDGVPFLKWLDLGGHEKEMKKCAKKFDVMLNEWLEEHREKKGLGSEDKVVGERDFMDAML  313

Query  276  EECDNTNGEKLSI-TNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRV  334
                +   E   + T IKA  L L   G+DT++  + WA+  ++K+P +L+K +EE++
Sbjct  314  LVLKDKPIEGFDVDTIIKATTLELILGGSDTTAGTLTWAMCLLLKHPHVLEKLKEELNTY  373

Query  335  IGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVN  394
            IG++R + ESDI+ L YL AI KET R +P  P + PR   + C + GY+I K  RL  N
Sbjct  374  IGKERCVNESDINKLVYLHAIIKETLRLYPPAPFSSPREFTEDCTIGGYHIKKGTRLMPN  433

Query  395  IWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVS  454
            +W I RDP+VW +PLEF PERFLS  +  ++  G +F+L+PFG+GRR+CAG  +G+ +V
Sbjct  434  LWKIHRDPSVWPDPLEFKPERFLS-THKDVDVRGQNFELLPFGSGRRMCAGMSLGLHMVH  492

Query  455  YILGTLVHSFDWKLPNGVAELNMDESFGLALQKAVPLSALVSPRLASNPYAT  506
            YIL   +HSF+   P+    +++ E       KA PL  LV P L+   Y +
Sbjct  493  YILANFLHSFEILNPSP-ESIDVTEVLEFVTTKATPLEVLVKPCLSFKCYES  543
```

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RecName: Full=Cytochrome P450 71A23

Sequence ID: Q9STL0.1 **Length:** 483 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 31 to 480 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
303 bits(777)	1e-96	Compositional matrix adjust.	171/465(37%)	272/465(58%)	18/465(3%)

```
Query  35   PGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTLD  94
            P P   PL+G L  L   PH +L  L+ +YGP+M L  G+  ++VAST E+AR  LKT D
Sbjct  31   PSPPRLPLIGNLHQLSQHPHRSLCYLSHRYGPLMLLHFGSVPVIVASTAEAARDVLKTHD  90

Query  95   LNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTELG  154
              F++RP +     L Y ++++  A YG  W+ ++ +S LH+L  K +  + +VR  E+
Sbjct  91   RVFASRPRSKIFEKLLYKSRNMASAPYGEYWRQMKSVSVLHLLSNKMVRSFQDVRQEEIT  150

Query  155  HMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVELMTS  214
             M++ + ++S   +PV L+++L+    ++I +V L R+  V  GT+   FK+++  LM
Sbjct  151  LMMETIRKSS--SKPVNLSKILSSLTNDVICRVALGRKYGV--GTD---FKELIDRLMRQ  203

Query  215  AGYFNIGDFIPSIAWMD-LQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKGKADFLDV  273
             G F IG ++P +AW D + G+E  ++K    FD LL ++V++H     +   K DF+DV
Sbjct  204  LGTFTIGSYVPWLAWTDWVSGLEARLEKTANDFDKLLERIVQDHEDGDGD---KTDFVDV  260

Query  274  LLE-ECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMD  332
            LL  + D + G  +   +IKA++L+ F  GTDTSS+++EW +TE++++PT LKK QEE+
Sbjct  261  LLAAQRDKSFGFDIDRLSIKAIVLDAFVGGTDTSSTLVEWEMTELLRHPTCLKKLQEEVR  320

Query  333  RVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLS  392
             +      + E DI  + YL+A+ KE  R HP  PL +P  + Q   +   +IP   ++
Sbjct  321  TICKGKSSVSEDDIQGMEYLKAVVKEALRLHPPVPLMVPHQSTQDVRLRDNHIPAGTQVI  380

Query  393  VNIWAIGRDPNVW-ENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMV  451
            VN+WA+GR+   W  +  EF PER L   +   +  G DF+LIPFGAGRR+C G    +V
Sbjct  381  VNLWAVGREAATWGPDANEFRPERHLESPS---DFRGQDFELIPFGAGRRMCPGISFAVV  437

Query  452  LVSYILGTLVHSFDWKLPNGVAELNMDESFGLALQKAVPLSALVS  496
            L   +L  LVH FDW+  +   E ++ ES G  +++  PL  + S
Sbjct  438  LNEVVLANLVHGFDWQSIDD--ETDVAESIGSVIRRMHPLYVIPS  480
```

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RecName: Full=7-ethoxycoumarin O-deethylase; Short=ECOD; AltName: Full=Cytochrome P450 76B1; AltName: Full=Phenylurea dealkylase

Sequence ID: O23976.1 **Length:** 490 **Number of Matches:** 1

Related Information

Range 1: 2 to 488 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
303 bits(776)	2e-96	Compositional matrix adjust.	179/493(36%)	277/493(56%)	8/493(1%)

```
Query  7    DFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGP  66
            DF++     L++  L+  L     + LPPGP   P++G L LLGA+PH +LAKLAK +GP
Sbjct  2    DFLIIVSTLLLSYILIWVLGVGKPKNLPPGPTRLPIIGNLHLLGALPHQSLAKLAKIHGP  61

Query  67   IMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWK  126
            IM L++G    +V S+  +A   LK  DL FS R          +    + F      W+
Sbjct  62   IMSLQLGQITTLVISSATAAEEVLKKQDLAFSTRNVPDAVRAYNHERHSISFLHVCTEWR  121

Query  127  TLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQ  186
            TLR++ + ++    +L+   ++R  ++  ++    +A+   E V +         N++
Sbjct  122  TLRRIVSSNIFSNSSLEAKQHLRSKKVEELIAYCRKAALSNENVHIGRAAFRTSLNLLSN  181

Query  187  VILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKF  246
             I S+ +         EF++++  +M  +   N+ D  P +  +D QGI+RGM +  +K
Sbjct  182  TIFSKDLTDPYEDSGKEFREVITNIMVDSAKTNLVDVFPVLKKIDPQGIKRGMARHFSKV  241

Query  247  DVLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTDTS  306
              +  ++++E   T    +G  D LDV L+   + N  + + TNIKA+ L+LF AGTDT+
Sbjct  242  LGIFDQLIEERMRTGRFEQG--DVLDVCLKMMQD-NPNEFNHTNIKALFLDLFVAGTDTT  298

Query  307  SSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPST  366
            S  IEWA+TE+++ P I+ KA+EE+++VIG+   + E D+  LPYL  I KE  R HP +
Sbjct  299  SITIEWAMTELLRKPHIMSKAKEELEKVIGKGSIVKEDDVLRLPYLSCIVKEVLRLHPPS  358

Query  367  PLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINP  426
            PL LPR  +   E+ GY IP    + VN WAIGRDP VW++ LEF P+RFL     +++
Sbjct  359  PLLLPRKVVTQVELSGYTIPAGTLVFVNAWAIGRDPTVWDDSLEFKPQRFLE---SRLDV  415

Query  427  GGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAE--LNMDESFGLA  484
             G+DF LIPFGAGRRIC G  +   +V  +LG+L+++FDWK+   V    L+M E  G
Sbjct  416  RGHDFDLIPFGAGRRICPGIPLATRMVPIMLGSLLNNFDWKIDTKVPYDVLDMTEKNGTT  475

Query  485  LQKAVPLSALVSP  497
            + KA PL  +  P
Sbjct  476  ISKAKPLCVVPIP  488
```

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RecName: Full=Cytochrome P450 71B4

Sequence ID: O65786.2 **Length:** 504 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 26 to 503 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
303 bits(777)	2e-96	Compositional matrix adjust.	164/483(34%)	268/483(55%)	14/483(2%)

```
Query  27   KKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESA  86
            K+  + LPPGP   P++G L  L  + H  L  L+KK+GP+MHL++G   MVV S+ E+A
Sbjct  26   KESKQNLPPGPAKLPIIGNLHQLQGLLHKCLHDLSKKHGPVMHLRLGFAPMVVISSSEAA  85

Query  87   RAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWA  146
               LKT DL   +RP    +   +   +D+ F  YG  W+ LRKLS       K +  +
Sbjct  86   EEALKTHDLECCSRPITMASRVFSRNGKDIGFGVYGDEWRELRKLSVREFFSVKKVQSFK  145

Query  147  NVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKD  206
             +R  E   M+K + E +    PV L+++L    A++I +    +  F  K  +    K+
Sbjct  146  YIREEENDLMIKKLKELASKQSPVDLSKILFGLTASIIFRTAFGQSFFDNKHVDQESIKE  205

Query  207  MVVELMTSAGYFNIGDFIPS--IAWMD--LQGIERGMKKLHTKFDVLLTKMVKEHRATSH  262
            ++ E +++   F   DF P+  + W    + G  + +  +  + D     +V +H +
Sbjct  206  LMFESLSNMT-FRFSDFFPTAGLKWFIGFVSGQHKRLYNVFNRVDTFFNHIVDDHHSKK-  263

Query  263  ERKGKADFLDVLLEECDNTNGE---KLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIK  319
              + + D +D +L+  DN       KL++ ++K VL N++ AG DTS+  + WA+ E+++
Sbjct  264  ATQDRPDMVDAILDMIDNEQQYASFKLTVDHLKGVLSNIYHAGIDTSAITLIWAMAELVR  323

Query  320  NPTILKKAQEEMDRVIG--RDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQA  377
            NP ++KKAQ+E+   IG  ++ R++E D+  L YL+ + KET R HP+ PL LPR  +
Sbjct  324  NPRVMKKAQDEIRTCIGIKQEGRIMEEDLDKLQYLKLVVKETLRLHPAAPLLLPRETMAD  383

Query  378  CEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFG  437
             ++ GY IP+   L VN W+IGRDP  W+NP EF PERF+   +  ++  G+ F+L+PFG
Sbjct  384  IKIQGYDIPQKRALLVNAWSIGRDPESWKNPEEFNPERFI---DCPVDYKGHSFELLPFG  440

Query  438  AGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMDESFGLALQKAVPLSALVSP  497
            +GRRIC G  M +  +   L  L++ FDW +P    +++M+E+  L + K VPL  L
Sbjct  441  SGRRICPGIAMAIATIELGLLNLLYFFDWNMPEKKKDMDMEEAGDLTVDKKVPLELLPVI  500

Query  498  RLA  500
            R++
Sbjct  501  RIS  503
```

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RecName: Full=Cytochrome P450 71D7

Sequence ID: P93531.1 **Length:** 500 **Number of Matches:** 1

Related Information

Range 1: 28 to 497 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
302 bits(774)	5e-96	Compositional matrix adjust.	163/483(34%)	269/483(55%)	28/483(5%)

```
Query  30   TRPLPPGPLGWPLVGALP-LLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARA  88
            T+ LPPGP   P +G +  L G +PH  L  LA+KYGP+MHL++G    VV ++PE A+
Sbjct  28   TKKLPPGPWKLPFIGGMHHLAGGLPHRVLRDLAEKYGPLMHLQLGEVSAVVVTSPEMAKQ  87

Query  89   FLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANV  148
             LKT D+ F++RP       + Y  +D+ F+ YG  W+ +RK+  + +L  K++  ++++
Sbjct  88   VLKTHDIAFASRPKLLAMDIICYNRRDIAFSPYGDYWRQMRKICIMEVLSAKSVRSFSSI  147

Query  149  RVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANM-----IGQVILSRRVFVTKGTESNE  203
            R  E+  ++ ++      GE V   E + +  ++M      GQV+  + VF+
Sbjct  148  RHDEVVRLIDSIQPCFTSGELVNFTERIIWFTSSMTCRSAFGQVLKEQEVFIK-------  200

Query  204  FKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKKLHTKFDVLLTKMVKEHRATSH  262
               ++ E+++ A  F++ D  PS  ++    G ++ +   H K D ++  ++KEH+
Sbjct  201  ---LIREVISLAEGFDVADIFPSYKFLHGFGGAKQKLLNAHRKVDSIVEDVIKEHKKNLA  257

Query  263  ERK-----GKADFLDVLLEECDNTNGE-KLSITNIKAVLLNLFTAGTDTSSSIIEWALTE  316
             RK     G  D +D L+   ++ + +  ++  NIKAV+++LF AGT+TSS+   WA+ E
Sbjct  258  TRKSDDAIGGEDLVDALVRLMNDKSLQFPINNDNIKAVIIDLFAAGTETSSTTTVWAMAE  317

Query  317  MIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQ  376
            M+KNP++  KAQ ++           E+D+  L YL+ + KET R H   PL +PR   +
Sbjct  318  MLKNPSVFAKAQAKVREAFRDKVTFDENDVEELKYLKLVIKETMRLHAPVPLLVPRECRE  377

Query  377  ACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPF  436
              E++GY IP   ++ VN+WA+GRDP  W++   F PERF   E   I+  GN+F+ +PF
Sbjct  378  ETEINGYTIPVKTKVMVNVWALGRDPKYWDDAESFKPERF---EQCSIDFIGNNFEYLPF  434

Query  437  GAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGV--AELNMDESFGLALQKAVPLSAL  494
            G GRRIC G   G+  V   L  L++ FDWKLP G+   +L++ ES G+   +   L  +
Sbjct  435  GGGRRICPGISFGLANVYLPLAQLLYHFDWKLPTGMEPKDLDLTESAGITAARKGDLYLI  494

Query  495  VSP  497
             +P
Sbjct  495  ATP  497
```

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RecName: Full=Cytochrome P450 98A3; AltName: Full=Protein REDUCED EPIDERMAL FLUORESCENCE 8; AltName: Full=p-coumaroylshikimate/quinate 3'-hydrolxylase; Short=C3'H

Sequence ID: O22203.1 **Length:** 508 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 8 to 501 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
302 bits(773)	8e-96	Compositional matrix adjust.	179/507(35%)	274/507(54%)	25/507(4%)

```
Query  10   VAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMH  69
            VA I  +++  L++ L  K     PPGP   P+VG L  +  +      + A+ YGPI+
Sbjct  8    VATIAAVVSYKLIQRLRYK----FPPGPSPKPIVGNLYDIKPVRFRCYYEWAQSYGPIIS  63

Query  70   LKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLR  129
            + +G+   VV S+ E A+  LK  D   ++R  N      +   QDL++A YGP +  +R
Sbjct  64   VWIGSILNVVVSSAELAKEVLKEHDQKLADRHRNRSTEAFSRNGQDLIWADYGPHYVKVR  123

Query  130  KLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEP------VVLAEMLTYAMANM  183
            K+  L +   K L+    +R  E+  M++++     C  P      + L + L     N
Sbjct  124  KVCTLELFTPKRLESLRPIREDEVTAMVESVFRD--CNLPENRAKGLQLRKYLGAVAFNN  181

Query  184  IGQVILSRRVFVTKGT---ESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMK  240
            I ++   +R    +G    +  EFK +V   +      +I + IP + WM     E+
Sbjct  182  ITRLAFGKRFMNAEGVVDEQGLEFKAIVSNGLKLGASLSIAEHIPWLRWM-FPADEKAFA  240

Query  241  KLHTKFDVLLTKMVKEHRATSHERKG-KADFLDVLLEECDNTNGEKLSITNIKAVLLNLF  299
            +   + D L   +++EH     +  G K  F+D LL   D  +   LS   I  +L ++
Sbjct  241  EHGARRDRLTRAIMEEHTLARQKSSGAKQHFVDALLTLKDQYD---LSEDTIIGLLWDMI  297

Query  300  TAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKET  359
            TAG DT++   EWA+ EMIKNP + +K QEE DRV+G DR L E+D S LPYLQ + KE+
Sbjct  298  TAGMDTTAITAEWAMAEMIKNPRVQQKVQEEFDRVVGLDRILTEADFSRLPYLQCVVKES  357

Query  360  YRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSE  419
            +R HP TPL LP  +    ++ GY IPK + + VN+WA+ RDP VW+NP EF PERFL E
Sbjct  358  FRLHPPTPLMLPHRSNADVKIGGYDIPKGSNVHVNVWAVARDPAVWKNPFEFRPERFLEE  417

Query  420  ENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGV--AELNM  477
            +   ++  G+DF+L+PFGAGRR+C G ++G+ LV+ ++  L+H F W  P G    E++M
Sbjct  418  D---VDMKGHDFRLLPFGAGRRVCPGAQLGINLVTSMMSHLLHHFVWTPPQGTKPEEIDM  474

Query  478  DESFGLALQKAVPLSALVSPRLASNPY  504
             E+ GL      P+ A+ +PRL S+ Y
Sbjct  475  SENPGLVTYMRTPVQAVATPRLPSDLY  501
```

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RecName: Full=2-methylbutanal oxime monooxygenase; AltName: Full=Cytochrome P450 71E7

Sequence ID: Q6XQ14.1 **Length:** 511 **Number of Matches:** 1

Related Information

Range 1: 43 to 479 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
301 bits(771)	2e-95	Compositional matrix adjust.	156/447(35%)	259/447(57%)	18/447(4%)

```
Query  33   LPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKT  92
            LPPGP   PL+G L  LG  P+V   K+AKKYGP+M+L++G C  VV S+ E+++  +K
Sbjct  43   LPPGPRQLPLIGNLHQLGGQPYVDFWKMAKKYGPVMYLQLGRCPTVVLSSTETSKELMKD  102

Query  93   LDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTE  152
             D+   +RP + G   L+Y   D+ F+ Y   W+ +RKL    +L  + +  +   R  +
Sbjct  103  RDVECCSRPLSVGPGQLSYNFLDVAFSPYSDYWREMRKLFIFELLSMRRVQTFWYAREEQ  162

Query  153  LGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVELM  212
            +  M++ +  A     PV L E +   M  +IG +   R  +  +     EF+D  V+++
Sbjct  163  MDKMIEILDGAY--PNPVNLTEKVFNMMDGIIGTIAFGRTTYAQQ-----EFRDGFVKVL  215

Query  213  TSA----GYFNIGDFIPSIA-WMD-LQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKG  266
             +       F+  +F P +  ++D L G     ++  T  D    K++++H   +  +
Sbjct  216  AATMDMLDNFHAENFFPVVGRFIDSLTGALAKRQRTFTDVDRYFEKVIEQHLDPNRPKPE  275

Query  267  KADFLDVLLEEC-DNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILK  325
              D +DVL+    D +   K++  ++KA+L+N+F  G DTS+  I WA +E++KNP ++K
Sbjct  276  TEDIVDVLIGLMKDESTSFKITKDHVKAILMNVFVGGIDTSAVTITWAFSELLKNPKLMK  335

Query  326  KAQEEMDRVIGRDRRLLE-SDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYY  384
            KAQEE+ R +G ++R +E  ++  + Y+  I KET+RKHP  PL +P  +++ C++ GY
Sbjct  336  KAQEEVRRAVGPNKRRVEGKEVEKIKYIDCIVKETFRKHPPVPLLVPHFSMKHCKIGGYD  395

Query  385  IPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICA  444
            I     + VN WA+G+DP +WENP E+ P+RF+   N +++  G+DF+L+PFGAGRRIC
Sbjct  396  ILPGTTIYVNAWAMGKDPTIWENPEEYNPDRFM---NSEVDFRGSDFELVPFGAGRRICP  452

Query  445  GTRMGMVLVSYILGTLVHSFDWKLPNG  471
            G  MG   V YIL  L++ +D+++P G
Sbjct  453  GLAMGTTAVKYILSNLLYGWDYEMPRG  479
```

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RecName: Full=Cytochrome P450 71B2

Sequence ID: O65788.2 **Length:** 502 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 1 to 495 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
301 bits(770)	2e-95	Compositional matrix adjust.	166/505(33%)	285/505(56%)	23/505(4%)

```
Query  1    MAILVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKL  60
            M IL+  F+V+ +  + + FL ++  K     LPP P   P++G L  L  +PH    KL
Sbjct  1    MTILLCFFLVSLLTIVSSIFLKQN--KTSKFNLPPSPSSLPIIGNLHHLAGLPHRCFHKL  58

Query  61   AKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAK  120
            + KYGP++ L++G+  +VV S+ E+A A LKT DL   +RP   G+  L+YG +D+ FA
Sbjct  59   SIKYGPLVFLRLGSVPVVVISSSEAAEAVLKTNDLECCSRPKTVGSGKLSYGFKDITFAP  118

Query  121  YGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAM  180
            YG  W+ +RKL+ + +   K +  +  +R  E+  ++K + E++    PV L++
Sbjct  119  YGEYWREVRKLAVIELFSSKKVQSFRYIREEEVDFVVKKVSESALKQSPVDLSKTFFSLT  178

Query  181  ANMIGQVILSRRVFVTKG--TESNEFKDMVVELMTSAGYFNIGDFIPS-----IAWMDLQ  233
            A++I +V L +  F   G   + +  +++V E   + G F   DF P      + W+  +
Sbjct  179  ASIICRVALGQN-FNESGFVIDQDRIEELVTESAEALGTFTFSDFFPGGLGRFVDWLFQR  237

Query  234  GIERGMKKLHTKFDVLLTKMVKEHRATSHERKGKADFLDVLLEECD---NTNGEKLSITN  290
               + + K+  + D     ++ +H     E +   D + ++L+  D   +++  KL++ N
Sbjct  238  --HKKINKVFKELDAFYQHVIDDH--LKPEGRKNQDIVTLILDMIDKQEDSDSFKLNMDN  293

Query  291  IKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIG-RDRRLLESDISSL  349
            +KA+++++F AG DTS+  + WA+TE+I+NP ++KKAQE +   +G +  R+ E D+  +
Sbjct  294  LKAIVMDVFLAGIDTSAVTMIWAMTELIRNPRVMKKAQESIRTTLGLKKERITEEDLGKV  353

Query  350  PYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPL  409
             YL  I KET+R HP+ P  +PR  +   ++ GY IP   ++ +N+W IGRDP  W +P
Sbjct  354  EYLNHILKETFRLHPALPFVVPRETMSHIKIQGYDIPPKTQIQLNVWTIGRDPKRWNDPE  413

Query  410  EFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLP  469
            EF PERF    N  ++  G  F L+PFG+GRRIC G  M +  V   L  L++ FDW +P
Sbjct  414  EFNPERF---ANSSVDFRGQHFDLLPFGSGRRICPGMPMAIASVELALMNLLYYFDWSMP  470

Query  470  NGV--AELNMDESFGLALQKAVPLS  492
            +G    +++M+E+  +++ K +PL
Sbjct  471  DGTKGEDIDMEEAGNISIVKKIPLQ  495
```

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RecName: Full=Cytochrome P450 71A9; AltName: Full=Cytochrome P450 CP1

Sequence ID: O81970.1 **Length:** 499 **Number of Matches:** 1

Related Information

Range 1: 22 to 496 GenPept Graphics Next Match Previous Match

Gene - associated gene details

Score	Expect	Method	Identities	Positives	Gaps
301 bits(770)	2e-95	Compositional matrix adjust.	175/484(36%)	272/484(56%)	21/484(4%)

```
Query  26   FKKPT----RPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVAS  81
             +KPT    R LPPGP   P +G L  LG +PH +L  L+ K+GP+M L++G+   +V S
Sbjct  22   LRKPTAEKRRLLPPGPRKLPFIGNLHQLGTLPHQSLQYLSNKHGPLMFLQLGSIPTLVVS  81

Query  82   TPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKA  141
            + E AR   K  D  FS RP    A+ L YG+  + FA YG  W+ +RK+  L +L  K
Sbjct  82   SAEMAREIFKNHDSVFSGRPSLYAANRLGYGST-VSFAPYGEYWREMRKIMILELLSPKR  140

Query  142  LDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTES  201
            +  +  VR  E+  +L+ +  +     PV L+E+      N++ ++ L +R   +   ++
Sbjct  141  VQSFEAVRFEEVKLLLQTIALSH---GPVNLSELTLSLTNNIVCRIALGKRN-RSGADDA  196

Query  202  NEFKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKKLHTKFDVLLTKMVKEHRA-  259
            N+  +M+ E     G F   DF P + W++   G+E  ++K+  + D    +++KEH A
Sbjct  197  NKVSEMLKETQAMLGGFFPVDFFPRLGWLNKFSGLENRLEKIFREMDNFYDQVIKEHIAD  256

Query  260  TSHERKG--KADFLDVLLEECDNTNGEKLSITN--IKAVLLNLFTAGTDTSSSIIEWALT  315
             S ER G    D +DVLL    + N + ++IT+  IK VL+++F AGTDT+S+ I W ++
Sbjct  257  NSSERSGAEHEDVVDVLLRVQKDPN-QAIAITDDQIKGVLVDIFVAGTDTASATIIWIMS  315

Query  316  EMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAI  375
            E+I+NP  +K+AQEE+  ++     + E D+S L Y++++ KE  R HP  PL +PR
Sbjct  316  ELIRNPKAMKRAQEEVRDLVTGKEMVEEIDLSKLLYIKSVVKEVLRLHPPAPLLVPREIT  375

Query  376  QACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIP  435
            + C + G+ IP   R+ VN  +I  DP  WENP EFLPERFL      I+  G  F+++P
Sbjct  376  ENCTIKGFEIPAKTRVLVNAKSIAMDPCCWENPNEFLPERFLV---SPIDFKGQHFEMLP  432

Query  436  FGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLP--NGVAELNMDESFGLALQKAVPLSA  493
            FG GRR C G    M +V   L  L+  FDW+LP   G+ +L+M+E+ G+ + K   L
Sbjct  433  FGVGRRGCPGVNFAMPVVELALANLLFRFDWELPLGLGIQDLDMEEAIGITIHKKAHLWL  492

Query  494  LVSP  497
              +P
Sbjct  493  KATP  496
```

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RecName: Full=Tabersonine 16-hydroxylase; AltName: Full=Cytochrome P450 71D12

Sequence ID: P98183.1 **Length:** 495 **Number of Matches:** 1

Related Information

Range 1: 26 to 478 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
299 bits(765)	1e-94	Compositional matrix adjust.	173/465(37%)	272/465(58%)	22/465(4%)

```
Query  33   LPPGPLGWPLVG-ALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLK  91
            LPPGP   P++G A  L G   H  L  LAKKYGP+MHLK+G    +VAS+P+ A    +
Sbjct  26   LPPGPPQIPILGNAHQLSGGHTHHILRDLAKKYGPLMHLKIGEVSTIVASSPQIAEEIFR  85

Query  92   TLDLNFSNRPPNAGASHL-AYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRV  150
            T D+ F++RP N  +  + +Y   D+V + YG  W+ LRK+S + +L  K++  + ++R
Sbjct  86   THDILFADRPSNLESFKIVSYDFSDMVVSPYGNYWRQLRKISMMELLSQKSVQSFRSIRE  145

Query  151  TELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVE  210
             E+ + +K++   S+ G  + L++ ++  +       I +R  F  K   + EF  ++ +
Sbjct  146  EEVLNFIKSI--GSKEGTRINLSKEISLLIYG-----ITTRAAFGEKNKNTEEFIRLLDQ  198

Query  211  LMTSAGYFNIGDFIPSIAWMDLQGIER-GMKKLHTKFDVLLTKMVKEHRA------TSHE  263
            L  +    NI D  PS+ ++ L    +  ++K+H +FDV++  ++K H+       +
Sbjct  199  LTKAVAEPNIADMFPSLKFLQLISTSKYKIEKIHKQFDVIVETILKGHKEKINKPLSQEN  258

Query  264  RKGKADFLDVLLEECDNTNGEK-LSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPT  322
             + K D +DVLL      + E  L   NIKA++ N+F+AGT+TSS+ ++WA+ EMIKNPT
Sbjct  259  GEKKEDLVDVLLNIQRRNDFEAPLGDKNIKAIIFNIFSAGTETSSTTVDWAMCEMIKNPT  318

Query  323  ILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDG  382
            ++KKAQEE+ +V   +  + E+ +  L YLQA+ KET R HP  PL LPR   + C++ G
Sbjct  319  VMKKAQEEVRKVFNEEGNVDETKLHQLKYLQAVIKETLRLHPPVPLLLPRECREQCKIKG  378

Query  383  YYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRI  442
            Y IP  +R+ VN WAIGRDPN W  P +F P+RFL     K++  GN F+ +PFG GRRI
Sbjct  379  YTIPSKSRVIVNAWAIGRDPNYWIEPEKFNPDRFLE---SKVDFKGNSFEYLPFGGGRRI  435

Query  443  CAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMDESFGLALQK  487
            C G    +  +   L  L+  FDW+  +   +LNM ES G+ +++
Sbjct  436  CPGITFALANIELPLAQLLFHFDWQ--SNTEKLNMKESRGVTVRR  478
```

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RecName: Full=Cytochrome P450 71B14

Sequence ID: P58051.1 **Length:** 496 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 489 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
298 bits(764)	1e-94	Compositional matrix adjust.	170/494(34%)	272/494(55%)	16/494(3%)

```
Query  8    FVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPI  67
```

```
            F+V A F     + +   +   + LPPGP   P++G L  LG+ P  +L KL++KYG +
Sbjct  5    FIVGASFFFAFILIAKDT-RTTKKNLPPGPPRLPIIGNLHQLGSKPQRSLFKLSEKYGSL  63

Query  68   MHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKT  127
            M LK G    VVASTPE+ +  LKT D    +RP     + + Y   DL F+ Y   W+
Sbjct  64   MSLKFGNVSAVVASTPETVKDVLKTFDAECCSRPYMTYPARVTYNFNDLAFSPYSKYWRE  123

Query  128  LRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQV  187
            +RK++ + +   K +  + NVR  E+   +  + + +   + V + + L     ++I +V
Sbjct  124  VRKMTVIELYTAKRVKSFQNVRQEEVASFVDFIKQHASLEKTVNMKQKLVKLSGSVICKV  183

Query  188  ILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWM--DLQGIERGMKKLHTK  245
                 +  +K   +N +++++   M   G F   D+ P I  +   + G+    +K+  +
Sbjct  184  GFGISLEWSK--LANTYEEVIQGTMEVVGRFAAADYFPIIGRIIDRITGLHSKCEKVFKE  241

Query  246  FDVLLTKMVKEHRATSHERKGKADFLDVLL--EECDNTNGE-KLSITNIKAVLLNLFTAG  302
             D    + +K H   ++    K D + +LL  E+ +   GE +L+  + K +LLN+  AG
Sbjct  242  MDSFFDQSIKHHLEDTN---IKDDIIGLLLKMEKGETGLGEFQLTRNHTKGILLNVLIAG  298

Query  303  TDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRK  362
             DTS   + W +T +IKNP ++KKAQ E+  VI     + E DI  L YL+ + KET R
Sbjct  299  VDTSGHTVTWVMTHLIKNPRVMKKAQAEVREVIKNKDDITEEDIERLEYLKMVIKETLRI  358

Query  363  HPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENG  422
            +P  PL +PR A +  ++ GY IPK   + VNIWA+ R+PNVW++P  F+PERF+  E
Sbjct  359  NPLVPLLIPREASKYIKIGGYDIPKKTWIYVNIWAVQRNPNVWKDPEVFIPERFMHSE--  416

Query  423  KINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG--VAELNMDES  480
             I+  G DF+L+PFG+GRR+C G  +GM LV   L  L++ FDWKLP G  + +++++ES
Sbjct  417  -IDYKGVDFELLPFGSGRRMCPGMGLGMALVHLTLINLLYRFDWKLPEGMNIEDVDLEES  475

Query  481  FGLALQKAVPLSAL  494
            +GL   K VPL  +
Sbjct  476  YGLVCPKKVPLQLI  489
```

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RecName: Full=Cytochrome P450 71B19

Sequence ID: Q9LTM4.1 **Length:** 502 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 1 to 494 GenPept Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
298 bits(763)	2e-94	Compositional matrix adjust.	167/499(33%)	277/499(55%)	16/499(3%)

```
Query  4    LVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKK  63
            +   F+   +I  ++        K+    LPP P  +P++G L  +G +PH +L  LA++
Sbjct  1    MAISFLCVFLITFVSLIFFAKKIKRSKWNLPPSPPKFPVIGNLHQIGELPHRSLQHLAER  60

Query  64   YGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGP  123
            YGP+M L  G   + V S+ E+A   L+T DL+  +RP   G   L+   +D+ F  YG
Sbjct  61   YGPVMLLHFGFVPITVVSSREAAEEVLRTHDLDCCSRPKLVGTRLLSRDFKDIGFTPYGN  120

Query  124  RWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANM  183
             WK  RK +   +   K +  + ++R  E   ++K + E++    PV L++ L +  A++
Sbjct  121  EWKARRKFALRELFCLKKVQSFRHIREEECNFLVKQLSESAVDRSPVDLSKSLFWLTASI  180

Query  184  IGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIP--SIAWMD--LQGIERGM  239
            + +V L +    +   +  + +++V E  T+   F   DF P   + W+     G  + +
Sbjct  181  LFRVALGQNFHESDFIDKEKIEELVFEAETALASFTCSDFFPVAGLGWLVDWFSGQHKRL  240

Query  240  KKLHTKFDVLLTKMVKEH----RATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVL  295
              +  K D L   ++ +H    R+  HE    +  LDV+ ++ ++++ E L+I +IK  L
Sbjct  241  NDVFYKLDALFQHVIDDHLNPGRSKEHEDIIDS-MLDVIHKQGEDSSLE-LTIDHIKGFL  298

Query  296  LNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDR-RLLESDISSLPYLQA  354
             N+F AG DT +  + WA+TE++KNP ++KK Q ++   +G ++ R+ E DI  +PYL+
Sbjct  299  ANIFLAGIDTGAITMIWAVTELVKNPKLIKKVQGDIREQLGSNKERITEEDIEKVPYLKM  358

Query  355  IAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPE  414
            + KET+R HP+ PL LPR  +   +V GY IP   R+ VN+ AIGRDP +W NP EF PE
Sbjct  359  VIKETFRLHPAAPLILPRETMAHIKVQGYDIPPKRRILVNVSAIGRDPKLWTNPKEFDPE  418

Query  415  RFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAE  474
            RF+   +  ++  G  ++L+PFG+GRRIC G  MG+  V   L  L++ FDWKLP+G+
Sbjct  419  RFM---DSFVDYRGQHYELLPFGSGRRICPGMPMGIAAVELGLLNLLYFFDWKLPDGMTH  475

Query  475  LNMD--ESFGLALQKAVPL  491
             ++D  E+  L + K VPL
Sbjct  476  KDIDTEEAGTLTIVKKVPL  494
```

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RecName: Full=Cytochrome P450 71A22

Sequence ID: Q9STL1.1 **Length:** 490 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 33 to 487 GenPept Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
298 bits(762)	2e-94	Compositional matrix adjust.	165/468(35%)	266/468(56%)	18/468(3%)

```
Query  34   PPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTL  93
            P  P   PL+G L  LG  PH +L  L+ +YGP+M L+ G   ++V S+ + AR  LKT
Sbjct  33   PASPPRLPLIGNLHQLGRHPHRSLCSLSNRYGPLMLLRFGLVPVLVVSSADVARDILKTY  92
```

```
Query  94   DLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTEL  153
            D  F++RP +     + Y A+D+  A YG  W+ ++ +  LH+L  K +  + NVR  E+
Sbjct  93   DRVFASRPRSKIFEKIFYEARDVALAPYGEYWRQMKSVCVLHLLTNKMVRSFRNVRQEEI  152

Query  154  GHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVELMT  213
              M++ + ++S     V L+E+L     ++I +V L R     K ++  +FK+++  L
Sbjct  153  SLMMEKIQKSSSL--QVNLSELLGSLTNDVISRVALGR-----KYSDETDFKELMKRLTK  205

Query  214  SAGYFNIGDFIPSIAWMD-LQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKGKADFLD  272
              G F +G ++P +AW+D + G++  +KK     D  L K+V++H     +R    DF+D
Sbjct  206  LLGEFCVGTYVPWLAWIDWISGLDGQLKKTGNDLDEFLEKVVQDHEDGDAQR---TDFVD  262

Query  273  VLLE-ECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEM  331
            VLL  + + + G ++   +IKA++L++   GTDTS +++EWA+TE++  P  L + QEE+
Sbjct  263  VLLRIQREKSVGFEIDRLSIKAIILDVVVGGTDTSYALMEWAMTELLHRPECLNRLQEEV  322

Query  332  DRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARL  391
              +   +  + E DI  + YL+A+ KET R HP  PL +P  + Q   +  Y+IP   ++
Sbjct  323  RTICKGNSSVSEDDIKDMNYLKAVIKETMRLHPPLPLMVPHESTQDVRLGDYHIPAGTQV  382

Query  392  SVNIWAIGRDPNVWENPLE-FLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGM  450
             +N WAIGR+   W    E F PER L   N  ++  G++F+LIPFGAGRRIC      +
Sbjct  383  MINAWAIGREAATWGPDAEKFRPERHL---NSSVDFRGHNFELIPFGAGRRICPAISFAV  439

Query  451  VLVSYILGTLVHSFDWKLPNGVAE--LNMDESFGLALQKAVPLSALVS  496
            +L+   L  LVH +DW+LP    E   N+ ES G+ + +  PL A+VS
Sbjct  440  ILIEVTLANLVHRYDWRLPEEYIEDQTNVAESTGMVIHRLFPLYAIVS  487
```

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RecName: Full=Cytochrome P450 82C2

Sequence ID: O49394.2 **Length:** 523 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 522 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
298 bits(764)	3e-94	Compositional matrix adjust.	178/521(34%)	278/521(53%)	23/521(4%)

```
Query  4    LVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHV---ALAKL  60
            L + FV   +   I  F      K    P P G   WP++G L LL     +    L K+
Sbjct  5    LFSLFVPILVFVFIALFKKSKKPKHVKAPAPSG--AWPIIGHLHLLSGKEQLLYRTLGKM  62

Query  61   AKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAK  120
            A +YGP M L++G+ +  V S+ E A+      D   ++RP  A A H+ Y      FA
Sbjct  63   ADQYGPAMSLRLGSSETFVVSSFEVAKDCFTVNDKALASRPITAAAKHMGYDCAVFGFAP  122

Query  121  YGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCE--ASRCG-EPVV--LAEM  175
            Y   W+ +RK++ L +L  + L    +VRV+E+  +++ +      + G EPV+  L
Sbjct  123  YSAFWREMRKIATLELLSNRRLQMLKHVRVSEISMVMQDLYSLWVKKGGSEPVMVDLKSW  182

Query  176  LTYAMANMIGQVILSRRVF------VTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAW  229
            L     NM+ +++  +R F           E+ + +  V       G F + D  P + W
Sbjct  183  LEDMSLNMMVRMVAGKRYFGGGSLSPEDAEEARQCRKGVANFFHLVGIFTVSDAFPKLGW  242

Query  230  MDLQGIERGMKKLHTKFDVLLTKMVKEHRA---TSHERKGKADFLDVLL---EECDNTNG  283
             D QG E+ MK+   + DV+L + ++ HR     S  +   +DF+DV+L   E+   ++
Sbjct  243  FDFQGHEKEMKQTGRELDVILERWIENHRQQRKVSGTKHNDSDFVDVMLSLAEQGKFSHL  302

Query  284  EKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLE  343
            +  +IT+IK+  L L   G++TS S + WA++ ++ N  +LKKAQ+E+D  +GRDR + +
Sbjct  303  QHDAITSIKSTCLALILGGSETSPSTLTWAISLLLNNKDMLKKAQDEIDIHVGRDRNVED  362

Query  344  SDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPN  403
            SDI +L Y+QAI KET R +P+ PL   R AI+ C V GY + +  R+ VN+W I RDP
Sbjct  363  SDIENLVYIQAIIKETLRLYPAGPLLGHREAIEDCTVAGYNVRRGTRMLVNVWKIQRDPR  422

Query  404  VWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHS  463
            V+  P EF PERF++ E  + +  G +F+L+PFG+GRR C G+ + M ++   L   + S
Sbjct  423  VYMEPNEFRPERFITGEAKEFDVRGQNFELMPFGSGRRSCPGSSLAMQVLHLGLARFLQS  482

Query  464  FDWKLPNGVAELNMDESFGLALQKAVPLSALVSPRLASNPY  504
            FD K    +  ++M ES GL + KA PL  L+SPRL    Y
Sbjct  483  FDVKTVMDMP-VDMTESPGLTIPKATPLEILISPRLKEGLY  522
```

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RecName: Full=(S)-N-methylcoclaurine 3'-hydroxylase isozyme 1; AltName: Full=Cytochrome P450 80B1

Sequence ID: O64899.1 **Length:** 487 **Number of Matches:** 1

Related Information

Range 1: 5 to 487 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
297 bits(760)	4e-94	Compositional matrix adjust.	189/496(38%)	269/496(54%)	19/496(3%)

```
Query  10   VAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMH  69
            VA I  +I+  L         + LPPGP  WP+VG L  LG  PH   A+LA+ YG I
Sbjct  5    VALIAVIISSILYLLFGGSGHKNLPPGPKPWPIVGNLLQLGEKPHAQFAELAQTYGDIFT  64

Query  70   LKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLR  129
            LKMGT  +VVAST  +A   LKT D   S R          +    +V++      WK LR
Sbjct  65   LKMGTETVVVASTSSAASEILKTHDRILSARYVFQSFRVKGHVENSIVWSDCTETWKNLR  124

Query  130  KLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVIL  189
```

```
            K+    +   K ++  A+VR  +   M++ + +  + GE V + E++   + N+ G +I
Sbjct  125  KVCRTELFTQKMIESQAHVREKKCEEMVEYLMK--KQGEEVKIVEVIFGTLVNIFGNLIF  182

Query  190  SRRVFV--TKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKFD  247
            S+ +F      + S+EFK+ +  ++      N  D+ P +   DL G  + + +
Sbjct  183  SQNIFELGDPNSGSSEFKEYLWRMLELGNSTNPADYFPMLGKFDLFGQRKEVAECLKGIY  242

Query  248  VLLTKMVKEHRATSH--ERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTDT  305
             +   M++E +        K K DF+DV L+         L+   I A+L+ LF AGT+T
Sbjct  243  AIWGAMLQERKLAKKVDGYKSKNDFVDVCLDS-------GLNDYQINALLMELFGAGTET  295

Query  306  SSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPS  365
            S+S IEWA+TE+ KNP I  K + E+  V+G +R + ESD  +LPYL+A  KET R HP
Sbjct  296  SASTIEWAMTELTKNPKITAKIRSEIQTVVG-ERSVKESDFPNLPYLEATVKETLRLHPP  354

Query  366  TPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKIN  425
            TPL LPR A++ C +  Y IPKD ++ VN W IGRDP  W +PL F PERFL   N  ++
Sbjct  355  TPLLLPRRALETCTILNYTIPKDCQIMVNAWGIGRDPKTWTDPLTFSPERFL---NSSVD  411

Query  426  PGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG--VAELNMDESFGL  483
              GNDF LIPFGAGRRIC G  +    ++ ++ T V + DW LPNG  V  L ++E FGL
Sbjct  412  FRGNDFSLIPFGAGRRICPGLPIANQFIALLVATFVQNLDWCLPNGMSVDHLIVEEKFGL  471

Query  484  ALQKAVPLSALVSPRL  499
             LQK  PL  +   R+
Sbjct  472  TLQKEPPLFIVPKSRV  487
```

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RecName: Full=Cytochrome P450 71B36

Sequence ID: Q9LIP4.1 **Length:** 500 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 32 to 498 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
297 bits(761)	5e-94	Compositional matrix adjust.	166/473(35%)	264/473(55%)	18/473(3%)

```
Query  34   PPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTL  93
            PP P G+P++G L  LG +PH +L +L+KKYG +M LK G+   VV S+ E+A+  LK
Sbjct  32   PPSPPGFPIIGNLHQLGELPHQSLWRLSKKYGHVMLLKFGSIPTVVVSSSETAKQVLKIH  91

Query  94   DLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTEL  153
            DL+  +RP  AG   L+Y   D+ F+ +   WK LR++    +   K +  +  ++  E+
Sbjct  92   DLHCCSRPSLAGPRALSYNYLDIAFSPFDDYWKELRRICVQELFSVKRVQSFQPIKEDEV  151

Query  154  GHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVELMT  213
              ++ ++ E++  G PV L+E  T     +  +       F      S+ F+ ++ +
Sbjct  152  KKLIDSVSESASQGTPVNLSEKFTSLTVRVTCKATFGVN-FQGTVLNSDRFEKLIHDTYL  210

Query  214  SAGYFNIGDFIPSIAWMD--LQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKGKADFL  271
              G F+  D+ P+  W+   L G+    ++     D    +M   H+  + E  G  DF+
Sbjct  211  FLGSFSASDYFPNGGWIIDWLTGLHGQRERSVRALDAFYEQMFDLHKQGNKE--GVEDFV  268

Query  272  DVLL--EECDNTNGE-KLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQ  328
            D+LL  E+ +   G  KL+  +IKA+L+N+   G  TS+  + WA+TE+++NP ++KK Q
Sbjct  269  DLLLRLEKEETVIGYGKLTRNHIKAILMNVLIGGIGTSAITMTWAMTELMRNPRVMKKVQ  328

Query  329  EEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKD  388
             E+   IG+   +   DI  L YL+ +  ET+R HP +P  +PR  +   E++ Y IP
Sbjct  329  SEIRNQIGKKSMITLDDIDQLHYLKMVINETWRLHPPSPFLIPRQVMSEFELNDYVIPVK  388

Query  389  ARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRM  448
             RL VN+WAIGRDP+ W++P EFLPERF+   N  I+  G  F+L+PFG+GRR+C    M
Sbjct  389  TRLYVNVWAIGRDPDTWKDPEEFLPERFV---NSSIDAKGQHFELLPFGSGRRMCPAMYM  445

Query  449  GMVLVSYILGTLVHSFDWKLPNG-VAE-LNMDESFGLALQKA-----VPLSAL  494
            G  +V + L  +++ FDWK+P G VAE ++++ES GL   K      VPL  L
Sbjct  446  GTTMVEFGLANMLYHFDWKIPVGMVAEDIDLEESPGLNASKKNELVLVPLKYL  498
```

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RecName: Full=Cytochrome P450 71B20

Sequence ID: Q9LTM3.1 **Length:** 502 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 1 to 495 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
296 bits(759)	8e-94	Compositional matrix adjust.	168/503(33%)	270/503(53%)	22/503(4%)

```
Query  4    LVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKK  63
            +   F+   +I L +        K     LPP P  +P++G L  +G +PH +L  LA++
Sbjct  1    MAISFLCFCLITLASLIFFAKKIKHLKWNLPPSPPKFPVIGNLHQIGELPHRSLQHLAER  60

Query  64   YGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGP  123
            YGP+M L  G   + V S+ E+A   L+T DL+  +RP   G   L+   +D+ F  YG
Sbjct  61   YGPVMLLHFGFVPVTVVSSREAAEEVLRTHDLDCCSRPKLVGTRLLSRNFKDVCFTPYGN  120

Query  124  RWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANM  183
             WK  RK +   +   K +  + ++R  E   ++K + E++    PV L++ L +  A++
Sbjct  121  EWKARRKFALRELFCLKKVQSFRHIREEECNFLVKQLSESAVNRSPVDLSKSLFWLTASI  180

Query  184  IGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIP--SIAWMD--LQGIERGM  239
              +V L +    +   +  + +++V E  T+   F   DF P   + W+     G  + +
Sbjct  181  FFRVALGQNFHESNFIDKEKIEELVFEAETALASFTCSDFFPVAGLGWLVDWFSGQHKRL  240
```

```
Query  240  KKLHTKFDVLLTKMVKEH----RATSHERKGKADFLDVLLEECDNTNGE---KLSITNIK  292
              +  K D L   ++ +H    R+  HE     D +D +L+       +   +L I +IK
Sbjct  241  NDVFYKLDALFQHVIDDHLNPGRSKEHE-----DIIDSMLDAIHKEGKDSSLELIIDHIK  295

Query  293  AVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDR-RLLESDISSLPY  351
              L N+F AG DT +  + WA+TE++KNP ++KK Q E+   +G ++ R+ E DI  +PY
Sbjct  296  GFLANIFLAGIDTGALTMIWAMTELVKNPKLIKKVQGEIREQLGSNKARITEEDIDKVPY  355

Query  352  LQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEF  411
            L+ + KET+R HP+ PL LPR  +   +V GY IP   R+ VN+ AIGRDP +W NP EF
Sbjct  356  LKMVIKETFRLHPAAPLILPRETMAHIKVQGYDIPPKRRILVNVSAIGRDPKLWTNPEEF  415

Query  412  LPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG  471
             PERF+   +  ++  G  ++L+PFG+GRRIC G  MG+  V   L  L++ FDWKLP+G
Sbjct  416  DPERFM---DSSVDYRGQHYELLPFGSGRRICPGMPMGIAAVELGLLNLLYFFDWKLPDG  472

Query  472  VAELNMD--ESFGLALQKAVPLS  492
            +   ++D  E+  L + K VPL
Sbjct  473  MTHKDIDTEEAGTLTIVKKVPLQ  495
```

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RecName: Full=Amorpha-4,11-diene 12-monooxygenase; AltName: Full=Amorpha-4,11-diene C-12 oxidase; AltName: Full=Cytochrome P450 71AV1

Sequence ID: Q1PS23.1 **Length:** 495 **Number of Matches:** 1

Related Information

Range 1: 12 to 489 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
296 bits(758)	1e-93	Compositional matrix adjust.	179/492(36%)	273/492(55%)	18/492(3%)

```
Query  4    LVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALP-LLGAMPHVALAKLAK  62
            L T   +A I+  + +F  RS   K T+   P P   P++G +  L+G  PH  +  LA+
Sbjct  12   LTTSIALATILLFVYKFATRS---KSTKKSLPEPWRLPIIGHMHHLIGTTPHRGVRDLAR  68

Query  63   KYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYG  122
            KYG +MHL++G    +V S+P+ A+  L T D+ F+NRP       + Y   D+V A YG
Sbjct  69   KYGSLMHLQLGEVPTIVVSSPKWAKEILTTYDITFANRPETLTGEIVLYHNTDVVLAPYG  128

Query  123  PRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMAN  182
              W+ LRK+  L +L  K +  + ++R  E  ++++ + +AS  G PV L+E +   +A
Sbjct  129  EYWRQLRKICTLELLSVKKVKSFQSLREEECWNLVQEI-KASGSGRPVNLSENVFKLIA-  186

Query  183  MIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKK  241
                 ILSR  F     +  E  ++V E++   G F++ D  PS  ++  L G    +
Sbjct  187  ----TILSRAAFGKGIKDQKELTEIVKEILRQTGGFDVADIFPSKKFLHHLSGKRARLTS  242

Query  242  LHTKFDVLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTA  301
            L  K D L+  +V EH   +  +  +   LDVLL   D+     L+  NIKA++L++F A
Sbjct  243  LRKKIDNLIDNLVAEHTVNTSSKTNET-LLDVLLRLKDSAEF-PLTSDNIKAIILDMFGA  300

Query  302  GTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYR  361
            GTDTSSS IEWA++E+IK P  ++K Q E+ + +    ++ E DI  L YL  + KET R
Sbjct  301  GTDTSSSTIEWAISELIKCPKAMEKVQAELRKALNGKEKIHEEDIQELSYLNMVIKETLR  360

Query  362  KHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEEN  421
             HP  PL LPR   Q   + GY IP   +L VN++AI RDP  W++   F+PERF   EN
Sbjct  361  LHPPLPLVLPRECRQPVNLAGYNIPNKTKLIVNVFAINRDPEYWKDAEAFIPERF---EN  417

Query  422  GKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVA--ELNMDE  479
                  G +++ +PFGAGRR+C G  +G+  V   L  +++ F+WKLPNGV+  +++M E
Sbjct  418  SSATVMGAEYEYLPFGAGRRMCPGAALGLANVQLPLANILYHFNWKLPNGVSYDQIDMTE  477

Query  480  SFGLALQKAVPL  491
            S G  +Q+   L
Sbjct  478  SSGATMQRKTEL  489
```

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RecName: Full=(S)-N-methylcoclaurine 3'-hydroxylase isozyme 2; AltName: Full=Cytochrome P450 80B2

Sequence ID: O64900.1 **Length:** 488 **Number of Matches:** 1

Related Information

Range 1: 6 to 488 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
296 bits(757)	1e-93	Compositional matrix adjust.	188/496(38%)	269/496(54%)	19/496(3%)

```
Query  10   VAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMH  69
            VA I  +I+  L         + LPPGP  WP+VG L  LG  PH   A+LA+ YG I
Sbjct  6    VALIAVIISSILYLLFGSSGHKNLPPGPKPWPIVGNLLQLGEKPHAQFAELAQTYGDIFT  65

Query  70   LKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLR  129
            LKMGT  +VVAST  +A   LKT D   S R          +    +V++     WK LR
Sbjct  66   LKMGTETVVVASTSSAASEILKTHDRILSARYVFQSFRVKGHVENSIVWSDCTETWKNLR  125

Query  130  KLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVIL  189
            K+    +   K ++  A+VR  +   M++ + +  + GE V + E++   + N+ G +I
Sbjct  126  KVCRTELFTQKMIESQAHVREKKCEEMVEYLMK--KQGEEVKIVEVIFGTLVNIFGNLIF  183

Query  190  SRRVFV--TKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKFD  247
            S+ +F      + S+EFK+ +  ++      N  D+ P +   DL G  + + +
Sbjct  184  SQNIFELGXPNSGSSEFKEYLWRMLELGNSTNPADYFPMLGKFDLFGQRKEVAECLKGIY  243
```

```
Query  248  VLLTKMVKEHRATSH--ERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTDT  305
             +   M++E +        + K DF+DV L+         L+   I A+L+ LF AGT+T
Sbjct  244  AIWGAMLQERKLAKKVDGYQSKNDFVDVCLDS-------GLNDYQINALLMELFGAGTET  296

Query  306  SSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPS  365
            S+S IEWA+TE+ KNP I  K + E+  V+G +R + ESD  +LPYL+A  KET R HP
Sbjct  297  SASTIEWAMTELTKNPKITAKLRSELQTVVG-ERSVKESDFPNLPYLEATVKETLRLHPP  355

Query  366  TPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKIN  425
            TPL LPR A++ C +  Y IPKD ++ VN W IGRDP  W +PL F PERFL   N  ++
Sbjct  356  TPLLLPRRALETCTILNYTIPKDCQIMVNAWGIGRDPKTWIDPLTFSPERFL---NSSVD  412

Query  426  PGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG--VAELNMDESFGL  483
              GNDF LIPFGAGRRIC G  +    ++ ++ T V + DW LPNG  V  L ++E FGL
Sbjct  413  FRGNDFSLIPFGAGRRICPGLPIANQFIALLVATFVQNLDWCLPNGMSVDHLIVEEKFGL  472

Query  484  ALQKAVPLSALVSPRL  499
             LQK  PL  +   R+
Sbjct  473  TLQKEPPLFIVPKSRV  488
```

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RecName: Full=Cytochrome P450 84A4

Sequence ID: F4JW83.1 **Length:** 512 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 30 to 505 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
296 bits(759)	1e-93	Compositional matrix adjust.	166/484(34%)	272/484(56%)	23/484(4%)

```
Query  31   RPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFL  90
            +P PPGP G P++G + ++    H  LAKL++ YG ++HL++G   + V S+P+ AR  L
Sbjct  30   KPYPPGPKGLPVIGNILMMNQFNHRGLAKLSRIYGGLLHLRLGFSHIFVVSSPDIARQVL  89

Query  91   KTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRV  150
            +  D  FSNRP      +L YG  DL F  YGP W+ +RKL  + +   K  + W  V V
Sbjct  90   QVQDHVFSNRPTTIAIRYLTYGGSDLAFCNYGPFWRRMRKLYVMMLFSRKRAESW--VSV  147

Query  151  TELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVE  210
             E  H    +  AS  G+P+ + ++      ++  +         +  +  +EF +++ E
Sbjct  148  DEEVHKSVRLV-ASNVGKPLNICKLAFSLSRDITFRAAFGSSSSTSDESRLDEFLEIIQE  206

Query  211  LMTSAGYFNIGDFIPS-IAWMDLQGIERGMKKLHTKFDVLLTKMVKEH---RATSHER-K  265
                 G FN+ D++PS ++W+D QGI   ++K     D  +  ++ +H   +   H+
Sbjct  207  FSKLFGEFNVADYVPSWLSWIDPQGINGRVEKARKSLDGFIESVIDDHLHKKKREHDNVD  266

Query  266  GKADFLDVLL----EECD-NTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKN  320
             + D +D LL    EE   N +  K+++ NIK +++++   GT+T +  IEW LTE++++
Sbjct  267  EETDMVDQLLAFYEEEVKVNNSVTKINLDNIKGIIMDVMFGGTETVALAIEWVLTEILRS  326

Query  321  PTILKKAQEEMDRVIGRDR-RLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACE  379
            P  +K+ Q+E+  V+G DR R+ ++ +  L +L+ I KET R HP  PL L    ++  E
Sbjct  327  PENMKRVQDELTSVVGLDRWRVEDTHLEKLTFLKCILKETLRLHPPFPLLLHE-TVKDTE  385

Query  380  VDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPG--GNDFKLIPFG  437
            + GY+IPK +R+ VN +A+GRDPN W +P  F P RFL+     I P   GN+F+ +PFG
Sbjct  386  ISGYFIPKGSRVMVNTYALGRDPNSWSDPESFNPGRFLN----PIAPDLKGNNFEFVPFG  441

Query  438  AGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMD--ESFGLALQKAVPLSALV  495
            +GRR C G ++G+      +  L+H F W LP+G+   ++D  E  GL + KA+PL A+
Sbjct  442  SGRRSCPGMQLGLYAFELAVAHLLHCFTWSLPDGMNPGDVDTVEGPGLTVPKAIPLVAVP  501

Query  496  SPRL  499
            + RL
Sbjct  502  TTRL  505
```

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RecName: Full=Cytochrome P450 71A4; AltName: Full=CYPLXXIA4; AltName: Full=Cytochrome P-450EG2

Sequence ID: P37117.1 **Length:** 507 **Number of Matches:** 1

Related Information

Range 1: 36 to 504 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
296 bits(757)	2e-93	Compositional matrix adjust.	170/483(35%)	278/483(57%)	32/483(6%)

```
Query  33   LPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKT  92
            LPP P   P++G L  LG+ PH +L KL++KYGP+M L +G+  ++VAS+ ++AR  LKT
Sbjct  36   LPPSPRKLPIIGNLHQLGSHPHRSLRKLSQKYGPVMLLHLGSKPVIVASSVDAARDILKT  95

Query  93   LDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTE  152
             D  ++ RP  + A  L YG++D+ F+ +G  W  +R +  LH+L  K +  + +VR  E
Sbjct  96   HDHVWATRPKYSIADSLLYGSKDVGFSPFGEYWWQVRSIVVLHLLSNKRVQSYRDVREEE  155

Query  153  LGHMLKAMCEASRCGEPVV-LAEMLTYAMANMIGQVILSRRVFVTKGTESN-EFKDMVVE  210
              +M++ + +   C   V+ L E L +   N+  +V L R        ES  + KD++ +
Sbjct  156  TANMIEKIRQG--CDASVINLGEHLCFLTNNITSRVALGR---TYDERESGIDAKDILEQ  210

Query  211  LMTSAGYFNIGDFIPSIAWMD-LQGIERGMKKLHTKFDVLLTKMVKEH--------RATS  261
             +     FN+GD+IP + W++ + G++  ++K+  K D  L  +++EH         A +
Sbjct  211  FLQLLDTFNVGDYIPWLKWVNKITGLDTKVEKIAKKLDTFLDSVIEEHIIRNKKEEYAIT  270

Query  262  HERKGKADFLDVLLEECDNTNGEK----LSITNIKAVLLNLFTAGTDTSSSIIEWALTEM  317
             E K   DF+DVLLE     NG++    L   ++KA+LL+ F AGTDT  + ++W + ++
```

```
Sbjct  271  DEAK---DFVDVLLE---IQNGKETDFPLQRDSLKAILLDAFAAGTDTIYTNLDWTMADV  324

Query  318  IKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQA  377
            ++ P  +K  Q E+  +      + E D+ ++ YL+A+ KE+ R HP   L +PR +++
Sbjct  325  LRQPRAMKTLQNEVRGLAQGKSEITEDDLKNMQYLRAVIKESLRLHPPNSLLVPRESMED  384

Query  378  CEVDGYY-IPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPF  436
             ++ GYY IP   +  +N+WAIGRDP  WENP EF PERFL   N  I+  G  F+L+PF
Sbjct  385  VKLLGYYHIPARTQALINVWAIGRDPLSWENPEEFCPERFL---NNDIDMKGLKFELLPF  441

Query  437  GAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGV--AELNMDESFGLALQKAVPLSAL  494
            G+GRR C G+   + ++   L  LVH F++ LP G    +L+M E  G+A ++  PL  +
Sbjct  442  GSGRRGCPGSSFAIAVIELALARLVHKFNFALPKGTKPEDLDMTECTGIATRRKSPLPVV  501

Query  495  VSP  497
             +P
Sbjct  502  ATP  504
```

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RecName: Full=Cytochrome P450 71D6

Sequence ID: P93530.1 **Length:** 501 **Number of Matches:** 1

Related Information

Range 1: 28 to 498 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
295 bits(755)	3e-93	Compositional matrix adjust.	164/479(34%)	266/479(55%)	19/479(3%)

```
Query  30    TRPLPPGPLGWPLVGALP-LLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARA  88
             T+ LPPGP   P +G++  L G  PH  L  LAKKYGP+MHL++G    VV ++P+ A+
Sbjct  28    TKKLPPGPWKLPFIGSMHHLAGGRPHRVLRDLAKKYGPLMHLQLGEVSAVVVTSPDMAKE  87

Query  89    FLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANV  148
              LKT D+ F++RP       + Y   D+ F+ YG  WK +RK+    +L  K++  ++++
Sbjct  88    VLKTHDIAFASRPKLLAMDIICYDRCDIAFSPYGEYWKQMRKICVTEVLSAKSVRSFSSI  147

Query  149   RVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMV  208
             R  E+  ++ ++  +S  GE V   E + +  ++M       R  F     E + F  ++
Sbjct  148   RCDEVVRLIDSIQSSSSSGELVNFKERVIWFTSSMT-----CRSAFGQLPKEQDMFIKLI  202

Query  209   VELMTSAGYFNIGDFIPSIAWMDLQG-IERGMKKLHTKFDVLLTKMVKEHRATSHERK--  265
              E++  A  F++ D  PS  ++ + G  +R +  +H K D ++  ++ EH+      RK
Sbjct  203   REVIRLAEGFDVADIFPSYKFLHVFGRAKRKLLNVHRKVDAIVEDVINEHKKNFATRKND  262

Query  266   ----GKADFLDVLLEECDNTNGE-KLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKN  320
                 G  + +DVLL+  ++ + +  ++  NIKA+++++F AGT+TSS+   WA+ EM+KN
Sbjct  263   DHALGGENLIDVLLKLMNDKSLQFPINNDNIKAIIIDMFAAGTETSSTTTVWAMVEMLKN  322

Query  321   PTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEV  380
             P +L KAQ E+           E+D+  L YL+ + KET R H   PL +PR   +  E+
Sbjct  323   PRVLAKAQAEVREAFRNKVTFDENDVEDLKYLKLVIKETMRLHAPIPLLVPRECRKETEI  382

Query  381   DGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGR  440
             +GY IP   ++ VN+WA+GRDP  W++   F PERF   E   I+  GN+F+ +PFG GR
Sbjct  383   NGYTIPVKTKVMVNVWALGRDPKYWDDVECFKPERF---EQCSIDFIGNNFEYLPFGGGR  439

Query  441   RICAGTRMGMVLVSYILGTLVHSFDWKLPNGV--AELNMDESFGLALQKAVPLSALVSP  497
             RIC GT  G+      L  L+  FDWKLP G+   +L++ E  G++      L  + +P
Sbjct  440   RICPGTSFGLANDYLPLAQLLCHFDWKLPTGMEPKDLDLTELAGMSAASKDDLYLIATP  498
```

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RecName: Full=Psoralen synthase; AltName: Full=Cytochrome P450 CYP71AJ2

Sequence ID: C0SJS4.1 **Length:** 476 **Number of Matches:** 1

Related Information

Range 1: 5 to 475 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
294 bits(753)	3e-93	Compositional matrix adjust.	165/483(34%)	281/483(58%)	21/483(4%)

```
Query  14    IFLITRFLVR--SLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLK  71
             +FL+T F+ +  +L K P++ LPP P  +P++G L  +G  P  +L  LA KYGP+M LK
Sbjct  5     LFLVTVFVYKLLTLKKTPSKNLPPSPPRYPIIGNLHQIGPDPQHSLRDLALKYGPLMSLK  64

Query  72    MGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKL  131
              GT  ++V S+ ++AR  LKT DL F++RP ++ A+ + Y  +D+VFA+Y   W+ ++ +
Sbjct  65    FGTVPVLVVSSADAAREVLKTHDLIFADRPYSSVANKVFYNGKDMVFARYTEYWRQVKSI  124

Query  132   SNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSR  191
                 +L  K ++ + NVR  E+  +++ +   + C + + L E+L     N++
Sbjct  125   CVTQLLSNKRVNSFQNVREEEVDLLVQNI--ENSCSKVINLTELLIEVTGNVVC------  176

Query  192   RVFVTKGTESNEFKDMVVELMTSAGYF-NIGDFIPSIAWMD-LQGIERGMKKLHTKFDVL  249
             +V V  G + + +K +++E+M   GY  +I DF P   W+D L G+   + K     D
Sbjct  177   KVSVGSGDKVDSYKILILEIMEMLGYSRSIEDFFPMFGWVDWLTGLRGKVAKAAKGVDDF  236

Query  250   LTKMVKEHRAT--SHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTDTSS  307
             L  ++KEH     S+      DF+ +LLE  +   G  +    IK+++ ++  AGT+T S
Sbjct  237   LEGVLKEHLTARASNNASADNDFVSILLEIQEADAGSTMDNECIKSLIWDMLGAGTETIS  296

Query  308   SIIEWALTEMIKNPTILKKAQEEMDRVIGRDR-RLLESDISSLPYLQAIAKETYRKHPST  366
             + +EW L  +IKNP  + K Q E+ R IG+ + ++ E+D+  + YLQA+ KE+ R + +
Sbjct  297   TALEWTLAALIKNPDAMLKLQNEV-REIGKGKSKISEADLGKMTYLQAVMKESMRLYFTA  355
```

```
Query  367  PLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINP  426
            PL +PR + Q  +  GY I    ++ +N+WAI RDP++WE P EF PERFL   N  I+
Sbjct  356  PLLVPRESRQDVKFMGYDISAGTQVLINVWAIARDPSLWEKPEEFRPERFL---NSHIDY  412

Query  427  GGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG--VAELNMDESFGLA  484
             G +++ +PFGAGRR C G +  M +   ++  ++H F+++LP+G  + +L+M    G+
Sbjct  413  KGFNYEYLPFGAGRRGCPGIQFAMAVNELVVANVIHKFNFELPDGERLEDLDMTAVSGIT  472

Query  485  LQK  487
            L+K
Sbjct  473  LRK  475
```

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RecName: Full=Cytochrome P450 71A6

Sequence ID: O04164.1 **Length:** 511 **Number of Matches:** 1

Related Information

Range 1: 36 to 511 GenPept Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
295 bits(755)	4e-93	Compositional matrix adjust.	167/479(35%)	259/479(54%)	21/479(4%)

```
Query  42   LVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRP  101
            ++G L  LG  PH +L  L+++YGP+M L  G+  ++VAS+PE+AR  +K  DLNFSNRP
Sbjct  36   VLGNLHQLGTFPHRSLQSLSRRYGPVMQLHFGSVPVLVASSPEAAREIMKNQDLNFSNRP  95

Query  102  PNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMC  161
              +    L Y   D+ FA YG  W+ +R +  L +L  K +  +  VR  E   M++ +
Sbjct  96   NLSIPRRLLYDNHDVAFAPYGEYWRQIRSICVLQLLSNKRVQSFRRVREEETSIMVEKIM  155

Query  162  EASRCG--EPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESN----EFKDMVVELMTSA  215
            +  +      V L ++LT    ++  ++ L ++   T   +        K  + E
Sbjct  156  QLQKTTPTAAVNLTDLLTCLTNDVFCRIALGKKYGGTTTGDGEYHVRSLKKNLAEFYVLL  215

Query  216  GYFNIGDFIPSIAWMD-LQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKGKA------  268
            G   + ++IP + W     G++R ++++   FD  L K+++EHR
Sbjct  216  GISPLWEYIPWLEWTRRFDGVDRRIEEVSRTFDEFLGKVIQEHRVRDKREDTTVVGDTVG  275

Query  269  -DFLDVLLE--ECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILK  325
             DF+D+LL+    +  +   +    IKAV+L++F AGTDT+ + +EWAL+E+IKNP  +K
Sbjct  276  LDFVDLLLQFQRENERSSSPVDDLTIKAVILDMFLAGTDTTVTALEWALSELIKNPRAMK  335

Query  326  KAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYI  385
              Q+E+  V G    + ESD+  +PYL+A+ KE+ R H   PL +PR + +  +V GY +
Sbjct  336  ILQKEVRGVAGSKGEIEESDLEKMPYLKAVMKESLRLHAPVPLLVPRESTRDTKVLGYDV  395

Query  386  PKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAG  445
                R+ +N WAIGRD +VWE    FLPERFL      I+  G  F+LIPFG+GRR C G
Sbjct  396  ASGTRVLINCWAIGRDSSVWEESETFLPERFL---ETSIDYRGMHFELIPFGSGRRGCPG  452

Query  446  TRMGMVLVSYILGTLVHSFDWKLPNG--VAELNMDESFGLALQKAVPLSALVSPRLASN  502
                  +    L TLVH FD+KLPNG  V +L+M E  G  + K  PL  + +P    ++
Sbjct  453  ATFAAAIDELALATLVHKFDFKLPNGVRVEDLDMSEGSGFTIHKKFPLLVVPTPHACTS  511
```

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RecName: Full=Psoralen synthase; AltName: Full=Cytochrome P450 CYP71AJ1

Sequence ID: Q6QNI4.1 **Length:** 494 **Number of Matches:** 1

Related Information

Range 1: 16 to 494 GenPept Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
293 bits(750)	1e-92	Compositional matrix adjust.	169/493(34%)	284/493(57%)	21/493(4%)

```
Query  14   IFLITRFLVR--SLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLK  71
            +FL+T FL +  +L K P + LPP P  +P++G L  +G  P  +L  LA+KYGP+M LK
Sbjct  16   LFLVTIFLYKWLTLKKTPLKNLPPSPPQYPIIGNLHQIGPDPQASLRDLAQKYGPLMFLK  75

Query  72   MGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKL  131
             GT  ++V S+ ++AR  LKT DL F++RP ++ A+ + Y  +D+VFA+Y   W+ ++ +
Sbjct  76   FGTVPVLVVSSADAAREALKTHDLVFADRPYSSVANKIFYNGKDMVFARYTEYWRQVKSI  135

Query  132  SNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSR  191
                +L  K ++ +  VR  E+  +++ +  +    +   L E+L     N++
Sbjct  136  CVTQLLSNKRVNSFHYVREEEVDLLVQNLENSH--SKVANLTELLIEVTGNVVC------  187

Query  192  RVFVTKGTESNEFKDMVVELMTSAGYF-NIGDFIPSIAWMD-LQGIERGMKKLHTKFDVL  249
            RV V  G + + +K +++E+M   GY  +I DF P + W+D L G+   + +     D
Sbjct  188  RVSVGSGDKVDSYKILILEIMDMLGYSRSIEDFFPLLGWVDWLTGLRGKVAEAAKGVDTF  247

Query  250  LTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSI  309
            L  ++KEH +T+  +    DF+ +LLE  +   G  +    IK+++ ++  AGT+T S+
Sbjct  248  LEGVLKEHLSTTGSKYN--DFVSILLEIQEADAGSSMDNECIKSLIWDMLGAGTETISTA  305

Query  310  IEWALTEMIKNPTILKKAQEEMDRVIGRDR-RLLESDISSLPYLQAIAKETYRKHPSTPL  368
            +EW L  +IKNP  + K Q E+ R IG+ + ++ E+D+  + YLQA+ KE+ R + + PL
Sbjct  306  LEWTLAALIKNPDAMFKLQNEV-REIGKGKSKISEADLVKMNYLQAVMKESMRLYFTAPL  364

Query  369  NLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGG  428
             +PR A Q  +  GY I    ++ +N WAI RDP +W+ P EF PERFL   N  I+  G
Sbjct  365  LVPREARQDIKFMGYDISSGTQVLINAWAIARDPLLWDKPEEFRPERFL---NSPIDYKG  421

Query  429  NDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG--VAELNMDESFGLALQ  486
              ++ +PFGAGRR C G +  M +   ++  LVH F+++LP+G  + +L+M  + G+ L+
```

```
Sbjct  422  FHYEFLPFGAGRRGCPGIQFAMCINELVVANLVHKFNFELPDGKRLEDLDMTAASGITLR  481

Query  487  KAVPLSALVSPRL  499
            K  PL  +  P +
Sbjct  482  KKSPLLVVARPHV  494
```

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RecName: Full=5-epiaristolochene 1,3-dihydroxylase; Short=NtEAH; AltName: Full=Cytochrome P450 71D20

Sequence ID: Q94FM7.2 **Length:** 504 **Number of Matches:** 1

Related Information

Range 1: 29 to 477 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
293 bits(751)	2e-92	Compositional matrix adjust.	156/462(34%)	262/462(56%)	26/462(5%)

```
Query  30    TRPLPPGPLGWPLVGA-LPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARA  88
             ++ LPPGP   P++G+ L ++G  PH  L  LAKKYGP+MHL++G    VV ++ + A+
Sbjct  29    SKKLPPGPWKIPILGSMLHMIGGEPHHVLRDLAKKYGPLMHLQLGEISAVVVTSRDMAKE  88

Query  89    FLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANV  148
              LKT D+ F++RP       + Y   D+ F+ YG  W+ +RK+  + +L  K +  ++++
Sbjct  89    VLKTHDVVFASRPKIVAMDIICYNQSDIAFSPYGDHWRQMRKICVMELLNAKNVRSFSSI  148

Query  149   RVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANM-----IGQVILSRRVFVTKGTESNE  203
             R  E+  ++ ++   S  GE V   + + +  ++M      GQV+  + +F  K
Sbjct  149   RRDEVVRLIDSIRSDSSSGELVNFTQRIIWFASSMTCRSAFGQVLKGQDIFAKK------  202

Query  204   FKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKKLHTKFDVLLTKMVKEHR----  258
                 + E++  A  F++ D  P+  ++  L G++R +   H K D ++  ++ EH+
Sbjct  203   ----IREVIGLAEGFDVVDIFPTYKFLHVLSGMKRKLLNAHLKVDAIVEDVINEHKKNLA  258

Query  259   -ATSHERKGKADFLDVLLEECDNTNGE-KLSITNIKAVLLNLFTAGTDTSSSIIEWALTE  316
                S+   G  D +DVLL   ++T+ +  ++  NIKAV++++F AGT+TSS+   WA+ E
Sbjct  259   AGKSNGALGGEDLIDVLLRLMNDTSLQFPITNDNIKAVIVDMFAAGTETSSTTTVWAMAE  318

Query  317   MIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQ  376
             M+KNP++  KAQ E+           E+D+  L YL+ + KET R HP +PL +PR   +
Sbjct  319   MMKNPSVFTKAQAEVREAFRDKVSFDENDVEELKYLKLVIKETLRLHPPSPLLVPRECRE  378

Query  377   ACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPF  436
               +++GY IP   ++ VN+WA+GRDP  W++   F PERF   E   ++  GN+F+ +PF
Sbjct  379   DTDINGYTIPAKTKVMVNVWALGRDPKYWDDAESFKPERF---EQCSVDFFGNNFEFLPF  435

Query  437   GAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMD  478
             G GRRIC G   G+  +   L  L++ FDWKLP G+   ++D
Sbjct  436   GGGRRICPGMSFGLANLYLPLAQLLYHFDWKLPTGIMPRDLD  477
```

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RecName: Full=Cytochrome P450 71A25

Sequence ID: Q9STK8.1 **Length:** 490 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 10 to 490 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
292 bits(747)	3e-92	Compositional matrix adjust.	167/494(34%)	277/494(56%)	18/494(3%)

```
Query  12    AIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLK  71
             +IIF+   FL + L  K  +  PP P G PL+G L  LG   H +L  L+++YGP+M L
Sbjct  10    SIIFMTILFLKKQLSGKKGKT-PPSPPGLPLIGNLHQLGRHTHRSLCDLSRRYGPLMLLH  68

Query  72    MGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKL  131
             +G   +++ S+ + A+  LKT D  F+NRP +  +  L Y  +D+  A YG  W+ ++ +
Sbjct  69    LGRVPVLIVSSADMAQEILKTHDQAFANRPRSKLSQKLLYNNRDVASAPYGEYWRQMKSV  128

Query  132   SNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSR  191
               +H+L  K +  + +VR  E+  M+  + ++S    P  ++++L     ++I +V L R
Sbjct  129   CVIHLLSNKMVRSFRDVREEEITLMMAKIRKSSSL--PFNVSKVLECLTNDVICRVALGR  186

Query  192   RVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKKLHTKFDVLL  250
             +     G E++ FK +   L    G F+IG F+P +AW+D ++G +  + K+    D
Sbjct  187   KY----GGETD-FKKLTDRLSELLGTFSIGSFVPWLAWVDWIRGWDAQLDKMGKDLDDFF  241

Query  251   TKMVKEHRATSHERKGKADFLDVLLE-ECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSI  309
              K+V++H     +R+   D +D LL  + + + G ++   +IKA+ L++F  G+DTS ++
Sbjct  242   EKVVQDHE--DGDRRDGTDLIDALLRVKREKSPGFEIERVSIKAITLDVFVGGSDTSFTL  299

Query  310   IEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLN  369
             +EWA+TE++++P  L + QEE+  +     R+ E DI  + YL+A+ KE  R HP  P+
Sbjct  300   LEWAMTELLRHPKSLNRLQEEVRTICKGKSRVSEDDIQGMKYLKAVIKEALRLHPPFPMM  359

Query  370   LPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVW-ENPLEFLPERFLSEENGKINPGG  428
              P  + +  ++  Y+IP   ++ +N WAIGR+   W  +  EF PER L   +  ++  G
Sbjct  360   APHESTEDVKLRDYHIPAGTQVMMNAWAIGREVATWGPDAEEFKPERHL---DTSVDFRG  416

Query  429   NDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMD--ESFGLALQ  486
              +F+L+PFGAGRRIC      +VL   +L  LVH FDWKLP    E   D  ES G ++
Sbjct  417   QNFELLPFGAGRRICPAVSFAVVLNEVVLANLVHGFDWKLPEESKEDKTDVAESSGFSVH  476

Query  487   KAVPLSALVSPRLA  500
             +  PL A+ SP L
Sbjct  477   REFPLYAVASPYLT  490
```

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RecName: Full=Ferruginol synthase; AltName: Full=Cytochrome P450 76AH1

Sequence ID: S4UX02.1 **Length:** 495 **Number of Matches:** 1

Related Information

Range 1: 4 to 487 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
291 bits(744)	1e-91	Compositional matrix adjust.	165/490(34%)	266/490(54%)	12/490(2%)

```
Query  8    FVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPI  67
            F + A +F I   +    F++  R LPPGP  +P+VG +  LGA PH   AKL+K+YGP+
Sbjct  4    FPLLAALFFIAATITFLSFRR-RRNLPPGPFPYPIVGNMLQLGANPHQVFAKLSKRYGPL  62

Query  68   MHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKT  127
            M + +G+   V+ S+PE A+  L      FS R          +    + F      W+
Sbjct  63   MSIHLGSLYTVIVSSPEMAKEILHRHGQVFSGRTIAQAVHACDHDKISMGFLPVASEWRD  122

Query  128  LRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQV  187
            +RK+    M   ++++    +R  +L  +L  + + S  G  V + E       N++
Sbjct  123  MRKICKEQMFSNQSMEASQGLRRQKLQQLLDHVQKCSDSGRAVDIREAAFITTLNLMSAT  182

Query  188  ILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERG----MKKLH  243
            + S +        + EFK+++  + T  G  N  D+ P +   D QG++R       KL
Sbjct  183  LFSSQATEFDSKATMEFKEIIEGVATIVGVPNFADYFPILRPFDPQGVKRRADVFFGKLL  242

Query  244  TKFDVLLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGT  303
             K +  L + ++  RA  +  K K DFL+++++     N  KL   +   ++L+LF  G+
Sbjct  243  AKIEGYLNERLESKRANPNAPK-KDDFLEIVVDII-QANEFKLKTHHFTHLMLDLFVGGS  300

Query  304  DTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKH  363
            DT+++ IEWA++E++ NP  + + + E+  V G ++ + ES +  LPYLQA+ KE  R H
Sbjct  301  DTNTTSIEWAMSELVMNPDKMARLKAELKSVAGDEKIVDESAMPKLPYLQAVIKEVMRIH  360

Query  364  PSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGK  423
            P  PL LPR A    EV+GY IPK  ++ +N +AIGRDP++W +P  F PERFL   + K
Sbjct  361  PPGPLLLPRKAESDQEVNGYLIPKGTQILINAYAIGRDPSIWTDPETFDPERFL---DNK  417

Query  424  INPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG--VAELNMDESF  481
            I+  G D++L+PFG+GRR+C G  +   ++     TLVH+FDWKL +    A  +  E F
Sbjct  418  IDFKGQDYELLPFGSGRRVCPGMPLATRILHMATATLVHNFDWKLEDDSTAAADHAGELF  477

Query  482  GLALQKAVPL  491
            G+A+++AVPL
Sbjct  478  GVAVRRAVPL  487
```

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RecName: Full=Cytochrome P450 71B1; AltName: Full=CYPLXXIB1

Sequence ID: P49264.1 **Length:** 496 **Number of Matches:** 1

Related Information

Range 1: 5 to 489 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
290 bits(742)	2e-91	Compositional matrix adjust.	156/494(32%)	280/494(56%)	16/494(3%)

```
Query  8    FVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPI  67
            ++VAA++   +  + +S  +KP + LPPGP   P++G L  LG  PH A+ +L+K YGP+
Sbjct  5    YIVAALVIFASLLIAKSK-RKPKKNLPPGPPRLPIIGNLHQLGEKPHRAMVELSKTYGPL  63

Query  68   MHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKT  127
            M LK+G+   VVA++ E+ R  LKT DL   +RP     + + Y  +DLVF+ Y   W+
Sbjct  64   MSLKLGSVTTVVATSVETVRDVLKTYDLECCSRPYMTYPARITYNLKDLVFSPYDKYWRQ  123

Query  128  LRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQV  187
            +RKL+ + +   K +  + ++R  E+   ++   +A+   E V L++ +     ++I ++
Sbjct  124  VRKLTVVELYTAKRVQSFRHIREEEVASFVRFNKQAASSEETVNLSQKILKMSGSVICRI  183

Query  188  ILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWM--DLQGIERGMKKLHTK  245
                 + +      N +++++V+     G     D+ P I  +   + G+    +K+
Sbjct  184  GFG--INLEGSKLENTYQEIIVQAFEVLGSLAAVDYFPVIGTIIDRITGLHAKCEKVFHG  241

Query  246  FDVLLTKMVKEHRATSHERKGKADFLDVLL--EECDNTNGE-KLSITNIKAVLLNLFTAG  302
             D    + ++ H     +   K D +D+LL  E  + + GE +L+  + K +L+N+ TAG
Sbjct  242  IDSFFDQAIQRH---IDDPSIKDDIIDLLLKMERGEGSLGEYELTREHTKGILMNILTAG  298

Query  303  TDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRK  362
             DTS+  + WA+T ++ NP ++KK Q E+   I     + + D+  L Y + + KET+R
Sbjct  299  IDTSAQTMTWAMTHLLANPRVMKKLQAEIREKIKNIDEITDDDVEQLDYFKLVLKETFRI  358

Query  363  HPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENG  422
             P  P+ +PR+A +  ++ GY +P+   + VN+WA+   P++W++P  F PERF+   +
Sbjct  359  SPIVPVLVPRVAAKDLKIAGYDVPEKTWIHVNMWAVHMSPSIWKDPETFNPERFI---DN  415

Query  423  KINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGV--AELNMDES  480
            + +  G +F+L+PFG+GRR+C G  MG+ +V   L  L++ FDWKLPNG+   EL+++E+
Sbjct  416  QTDFKGLNFELLPFGSGRRMCPGMGMGLAVVHLTLINLLYRFDWKLPNGMKAEELSIEEN  475

Query  481  FGLALQKAVPLSAL  494
            +GL   K +PL A+
Sbjct  476  YGLICVKKLPLEAI  489
```

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RecName: Full=(S)-N-methylcoclaurine 3'-hydroxylase-like protein; AltName: Full=Cytochrome P450 80BX

Sequence ID: I3V6B1.1 **Length:** 440 **Number of Matches:** 1

Related Information

Range 1: 6 to 436 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
288 bits(737)	3e-91	Compositional matrix adjust.	172/445(39%)	245/445(55%)	19/445(4%)

```
Query  10   VAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMH  69
            VA I  + T FL   + +     LPPGP  WP+VG L  LG  PH   A+LA+ YG +
Sbjct  6    VALIAIVFTTFLYLIVRESSPNGLPPGPKPWPIVGNLLQLGEKPHSQFAQLAETYGDLFT  65

Query  70   LKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLR  129
            LK+GT  +VVASTP +A   LK  D     R          +    +V+ +    WK LR
Sbjct  66   LKLGTQTVVVASTPLAASEVLKAHDRTLCGRYVFQSFRVKNHVENSIVWNECNETWKKLR  125

Query  130  KLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVIL  189
            K+    +   K +++ A VR  +   M+K + +    G  V + E++   + NM G +I
Sbjct  126  KVCRTQLFTQKMIENQAEVREIKTMEMVKYLKKNE--GIEVKIVEVIFGTLVNMFGNLIF  183

Query  190  SRRVFVTKGTESN---EFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKF  246
            S+ +F   G ES+   E K  +  ++      N GD++P +  +DL G  + +
Sbjct  184  SQDIF-KLGDESSGSLEMKQHIWRMLELGNSANPGDYVPLLGSLDLFGQRKDVADCLQGV  242

Query  247  DVLLTKMVKEHRATSHERKG--KADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTD  304
              +   M+KE R    +  G  K DF+DVLL+         L    I ++LL++F+AGT+
Sbjct  243  YGVWGAMLKERRIAKRQINGDTKNDFVDVLLDS-------GLDDQQINSLLLDMFSAGTE  295

Query  305  TSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHP  364
            T++S IEWALTE+ KNP +    + E+  V+G+ R + ESDI +LPYLQA  KET R HP
Sbjct  296  TTASTIEWALTELTKNPQVTADIRSELLSVVGK-RAVKESDILNLPYLQAFVKETLRLHP  354

Query  365  STPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKI  424
             TPL +PR A++ C+V  Y IPK+ ++ VN W IGRDP  W +PL+F P+RFL   N  I
Sbjct  355  PTPLLIPRRALETCQVLNYTIPKECQIMVNAWGIGRDPKTWTDPLKFSPDRFL---NSSI  411

Query  425  NPGGNDFKLIPFGAGRRICAGTRMG  449
            +  GNDF+LIPFGAGRRIC G   G
Sbjct  412  DFKGNDFELIPFGAGRRICPGVPPG  436
```

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RecName: Full=Cytochrome P450 76AD1

Sequence ID: I3PFJ5.1 **Length:** 497 **Number of Matches:** 1

Related Information

Range 1: 41 to 496 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
290 bits(742)	3e-91	Compositional matrix adjust.	167/463(36%)	262/463(56%)	13/463(2%)

```
Query  42   LVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRP  101
            ++G +  +G  PH + A LAK +GP++ L++G+   +V S+ + A+      D   SNR
Sbjct  41   IIGNILEVGKKPHRSFANLAKIHGPLISLRLGSVTTIVVSSADVAKEMFLKKDHPLSNRT  100

Query  102  -PN---AGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHML  157
             PN   AG  H       + +    P+W+  RK++ +H+L  + LD     R  ++  +
Sbjct  101  IPNSVTAGDHH----KLTMSWLPVSPKWRNFRKITAVHLLSPQRLDACQTFRHAKVQQLY  156

Query  158  KAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGY  217
            + + E ++ G+ V + +       N++ ++  S  +   K   S EFK+++ +M    G
Sbjct  157  EYVQECAQKGQAVDIGKAAFTTSLNLLSKLFFSVELAHHKSHTSQEFKELIWNIMEDIGK  216

Query  218  FNIGDFIPSIAWMDLQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKGKADFLDVLLEE  277
             N  D+ P +  +D  GI R +     K   +   ++ E  A            DVL
Sbjct  217  PNYADYFPILGCVDPSGIRRRLACSFDKLIAVFQGIICERLAPDSSTTTTTTTDDVLDVL  276

Query  278  CDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGR  337
                   +L++  I  +L+++F AGTDT+SS  EW +TE+I+NP +++KAQEE+ +V+G+
Sbjct  277  LQLFKQNELTMGEINHLLVDIFDAGTDTTSSTFEWVMTELIRNPEMMEKAQEEIKQVLGK  336

Query  338  DRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWA  397
            D+++ ESDI +LPYLQAI KET R HP T   LPR A    E+ GY +PKDA++ VN+WA
Sbjct  337  DKQIQESDIINLPYLQAIIKETLRLHPPTVFLLPRKADTDVELYGYIVPKDAQILVNLWA  396

Query  398  IGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYIL  457
            IGRDPN W+N   F PERF+  E   I+  G DF L+PFGAGRRIC G  + + +++ +L
Sbjct  397  IGRDPNAWQNADIFSPERFIGCE---IDVKGRDFGLLPFGAGRRICPGMNLAIRMLTLML  453

Query  458  GTLVHSFDWKLPNGVA--ELNMDESFGLALQKAVPLSALVSPR  498
             TL+  F+WKL   ++  +L+MDE FG+ALQK  PL  +  PR
Sbjct  454  ATLLQFFNWKLEGDISPKDLDMDEKFGIALQKTKPLKLIPIPR  496
```

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RecName: Full=Protopine 6-monooxygenase; AltName: Full=Protopine 6-hydroxylase; Short=P6H

Sequence ID: F2Z9C1.1 **Length:** 524 **Number of Matches:** 1

Related Information

Range 1: 17 to 523 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
290 bits(742)	6e-91	Compositional matrix adjust.	176/514(34%)	274/514(53%)	26/514(5%)

```
Query  10   VAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGA--MPHVALAKLAKKYGPI  67
            + A +FL   F  R+L  K  R  P     WP++G L L G+  +PH  LA +A KYG
Sbjct  17   IIAFVFLYNLFSSRTLKNKKIRTAPMATGAWPVLGHLHLFGSGELPHKMLAAMADKYGSA  76

Query  68   MHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKT  127
              +K G    +V S     +    T D  FSNRP        + Y  + + F  YG  W+
Sbjct  77   FRMKFGKHTTLVVSDTRIVKECFTTNDTLFSNRPSTKAFQLMTYDNESVAFTPYGSYWRE  136

Query  128  LRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASR--CGEPVVLAEMLTY---AMAN  182
            +RK+S L +L    L    +VR +E+    K + +  +   G   +L +M  +      N
Sbjct  137  IRKISTLKLLSNHRLQAIKDVRASEVNVCFKTLYDQCKNPSGSAPILIDMKKWFEEVSNN  196

Query  183  MIGQVILSRRVFVTKGTESNE----FKDMVVELMTSAGYFNIGDFIPSIAWMDL-QGIER  237
            ++ +VI+ R+ F +K  +  E    +K ++ EL+  A      DF P + ++D+ QG
Sbjct  197  VVMRVIVGRQNFGSKIVQGEEEAIHYKKVMDELLRLASLSMFSDFAPLLGFVDIFQGNLS  256

Query  238  GMKKLHTKFDVLLTKMVKEHRATSHE-RKGKADFLDVLL---EECDNTNGEKLSITNIKA  293
             MK+   K D +L   ++EHR   +   + + DF+DV+L   EE   +  +  ++  IKA
Sbjct  257  AMKRNAKKVDAILENWLEEHRKKKNSVAESQQDFMDVMLSIVEESKLSGHDADAV--IKA  314

Query  294  VLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQ  353
              L +   GTDT++  + W ++ ++ N   LKKA+EE+D ++G+DR++ +SD+ +L Y+
Sbjct  315  TCLAMIMGGTDTTAVSLTWIISLLMNNRHALKKAREELDALVGKDRQVEDSDLKNLVYMN  374

Query  354  AIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLP  413
            AI KET R +P   L L R   + CE+DG+++    RL VN+W + RDPNVW +P EF P
Sbjct  375  AIVKETMRMYPLGTL-LERETKEDCEIDGFHVKGGTRLLVNVWKLQRDPNVWVDPTEFRP  433

Query  414  ERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVA  473
            ERFL+ EN  I+ GG  F+L+PFGAGRR+C G    +  +  +L  L+H +D    N +
Sbjct  434  ERFLT-ENADIDVGGQHFELLPFGAGRRVCPGVXFALQFMHLVLARLIHGYDL---NTLN  489

Query  474  ELNMD--ES-FGLALQKAVPLSALVSPRLASNPY  504
            E N+D  ES  G    KA PL  +++PRL    Y
Sbjct  490  EENVDLTESPEGHVNHKASPLDLILTPRLHYKLY  523
```

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RecName: Full=Cytochrome P450 71B7

Sequence ID: Q96514.1 **Length:** 504 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 1 to 497 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
289 bits(740)	6e-91	Compositional matrix adjust.	155/501(31%)	271/501(54%)	13/501(2%)

```
Query  1    MAILVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKL  60
            M+IL+  F+    +FL++  ++    K     LPPGP   P++G L  L  +PH     L
Sbjct  1    MSILLC-FLCLLPVFLVSLSILSKRLKPSKWKLPPGPKTLPIIGNLHNLTGLPHTCFRNL  59

Query  61   AKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAK  120
            ++K+GP+M L  G   +VV S+ E A   LKT DL   +RP       ++Y  +D+ FA
Sbjct  60   SQKFGPVMLLHFGFVPVVVISSKEGAEEALKTQDLECCSRPETVATRMISYNFKDIGFAP  119

Query  121  YGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAM  180
            YG  WK LRKL  + +L  K    +  +R  E   ++K + E++    PV L + L   +
Sbjct  120  YGEEWKALRKLVVMELLNTKKFQSFRYIREEENDLLIKKLTESALKKSPVNLKKTLFTLV  179

Query  181  ANMIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWM--DLQGIERG  238
            A+++ ++     +   +  + +   D+V +           DF P + W+   + G  +
Sbjct  180  ASIVCRLAFGVNIHKCEFVDEDNVADLVNKFEMLVAGVAFTDFFPGVGWLVDRISGQNKT  239

Query  239  MKKLHTKFDVLLTKMVKEHRATSHERKGKADFLDVLLE--ECDNTNGE--KLSITNIKAV  294
            +  + ++ D     ++ +H     +     D +DV+L+  +    +GE  KL+  ++K +
Sbjct  240  LNNVFSELDTFFQNVLDDHIKPGRQVSENPDVVDVMLDLMKKQEKDGESFKLTTDHLKGI  299

Query  295  LLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIG-RDRRLLESDISSLPYLQ  353
            + ++F AG +TS+  + WA+ E+I+NP ++KK Q+E+   +G + +R+ E D+S + Y +
Sbjct  300  ISDIFLAGVNTSAVTLNWAMAELIRNPRVMKKVQDEIRTTLGDKKQRITEQDLSQVHYFK  359

Query  354  AIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLP  413
             + KE +R HP+ PL LPR  +   ++ GY IP   ++ +NI++I RDP +W NP EF P
Sbjct  360  LVVKEIFRLHPAAPLLLPRETMSHVKIQGYDIPVKTQMMINIYSIARDPKLWTNPDEFNP  419

Query  414  ERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG--  471
            +RFL   +  I+  G +F+L+PFG+GRRIC G  +G+  V   L  L++ FDW +P G
Sbjct  420  DRFL---DSSIDYRGLNFELLPFGSGRRICPGMTLGITTVELGLLNLLYFFDWVVPVGKN  476

Query  472  VAELNMDESFGLALQKAVPLS  492
            V ++N++E+  + + K   L
Sbjct  477  VKDINLEETGSIIISKKTTLE  497
```

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RecName: Full=4-hydroxyphenylacetaldehyde oxime monooxygenase; AltName: Full=Cytochrome P450 71E1

Sequence ID: O48958.1 **Length:** 531 **Number of Matches:** 1

Related Information

Range 1: 55 to 518 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
290 bits(742)	7e-91	Compositional matrix adjust.	156/467(33%)	255/467(54%)	11/467(2%)

```
Query  33   LPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKT  92
```

```
            LPPGP   P++G L LLG +PH  L +LA++YGP+M L++GT   VV S+ E+AR  LK
Sbjct  55   LPPGPAQLPILGNLHLLGPLPHKNLRELARRYGPVMQLRLGTVPTVVVSSAEAAREVLKV  114

Query  93   LDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTE  152
             D++  +RP + G   L+Y  +++ FA YG  W+ +RKL  L +L  + +      R  E
Sbjct  115  HDVDCCSRPASPGPKRLSYDLKNVGFAPYGEYWREMRKLFALELLSMRRVKAACYAREQE  174

Query  153  LGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVELM  212
            +  ++  +  A+     +VL + +      +IG V         +      F+ ++ + M
Sbjct  175  MDRLVADLDRAAASKASIVLNDHVFALTDGIIGTVAFGNIYASKQFAHKERFQHVLDDAM  234

Query  213  TSAGYFNIGDFIPSIAWM---DLQGIERGMKKLHTKFDVLLTKMVKEHRATSHE-RKGKA  268
                 F+  DF P+ A      L G     +++  + DV   K++ +H   +
Sbjct  235  DMMASFSAEDFFPNAAGRLADRLSGFLARRERIFNELDVFFEKVIDQHMDPARPVPDNGG  294

Query  269  DFLDVLLEECDNTNGE-KLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKA  327
            D +DVL+  C   +G  + +  ++KA++L+ F    DTSS  I WA++E+++ P +L+KA
Sbjct  295  DLVDVLINLCKEHDGTLRFTRDHVKAIVLDTFIGAIDTSSVTILWAMSELMRKPQVLRKA  354

Query  328  QEEMDRVIGRDR-RLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIP  386
            Q E+   +G D+ R+   D + +PYL+ + KET R HP   L +PR  ++   + GY +P
Sbjct  355  QAEVRAAVGDDKPRVNSEDAAKIPYLKMVVKETLRLHPPATLLVPRETMRDTTICGYDVP  414

Query  387  KDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGT  446
             + R+ VN WAIGRDP  W  P EF P+RF+  +   ++  G+ F+LIPFGAGRRIC G
Sbjct  415  ANTRVFVNAWAIGRDPASWPAPDEFNPDRFVGSD---VDYYGSHFELIPFGAGRRICPGL  471

Query  447  RMGMVLVSYILGTLVHSFDWKLPNGVA--ELNMDESFGLALQKAVPL  491
             MG   V++ L  L++ +DW LP  +   +++M+E+  L   +  PL
Sbjct  472  TMGETNVTFTLANLLYCYDWALPGAMKPEDVSMEETGALTFHRKTPL  518
```

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RecName: Full=Cytochrome P450 71B26

Sequence ID: Q9LTL0.1   **Length:** 500   **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 33 to 490 GenPept   Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
288 bits(737)	1e-90	Compositional matrix adjust.	167/465(36%)	255/465(54%)	15/465(3%)

```
Query  35   PGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTLD  94
            P P G+P++G L  LG + H +L KL+KKYGP+M LK+G    ++ S+ E+A+  L+  D
Sbjct  33   PSPPGFPIIGNLHQLGELQHQSLWKLSKKYGPVMLLKLGKVPTLILSSSETAKQALRDYD  92

Query  95   LNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTELG  154
            L+  +RP  AG   L+Y   D+  + Y   WK LRKL +  +     +     ++  E+
Sbjct  93   LHCCSRPSLAGGRELSYNNLDMSSSPYNEYWKELRKLCSQELFSANKIQSIQPIKDEEVK  152

Query  155  HMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVELMTS  214
             ++ ++ E+S    PV L++       +++ +       F      S+ F  +V +
Sbjct  153  KVIDSIAESSSLKNPVNLSKTFLALTTSVVCKAAFGVS-FEGSVLNSDRFNKLVRDTFEM  211

Query  215  AGYFNIGDFIPSIAWM--DLQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKGKADFLD  272
             G F+  DFIP + W+     G++   KK     D    ++   H+    +  G  D +D
Sbjct  212  LGSFSASDFIPYVGWIIDKFNGLQGWRKKSFRDLDAFYEQIFDLHK--EEKEVGSEDLVD  269

Query  273  VLL----EECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQ  328
            VLL    EE    NG KL+  +IKA+L+N+   G DTS+  + WA+ E+ KNP ++KK Q
Sbjct  270  VLLRLEKEEIVVGNG-KLTRNHIKAILMNILLGGIDTSAITMTWAMAELAKNPRVMKKVQ  328

Query  329  EEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKD  388
             E+   I    R+   D   L YL+ + KET+R HP TPL LPR  I   E++GY IP
Sbjct  329  AEIRNQIKNKERISFDDTDKLEYLKMVIKETWRLHPPTPLLLPRDVITEFEINGYTIPAK  388

Query  389  ARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRM  448
             RL VN+WAIGRDP+ W++P  FLPERF    +  I+  G +F+L+ FG+GRRIC G  M
Sbjct  389  TRLHVNVWAIGRDPDTWKDPEMFLPERF---NDSNIDAKGQNFELLSFGSGRRICPGLYM  445

Query  449  GMVLVSYILGTLVHSFDWKLPNG--VAELNMDESFGLALQKAVPL  491
            G  +V + L  +++ FDWKLP G  V +++M+E+ GL + K   L
Sbjct  446  GTTMVEFGLANMLYHFDWKLPEGMVVEDIDMEEAPGLTVSKKSEL  490
```

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RecName: Full=Psoralen synthase; AltName: Full=Cytochrome P450 CYP71AJ3

Sequence ID: C0SJS2.1   **Length:** 473   **Number of Matches:** 1

Related Information

Range 1: 5 to 471 GenPept   Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
287 bits(735)	2e-90	Compositional matrix adjust.	164/480(34%)	279/480(58%)	19/480(3%)

```
Query  14   IFLITRFLVRSLFKK-PTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKM  72
            +FL+T FL + L KK P++ LPP P   P++G L  +G  P ++L  LA++YGP+MHLK
Sbjct  5    LFLVTIFLYKWLVKKTPSKNLPPSPPRLPIIGNLHQIGPDPQISLRDLAREYGPVMHLKF  64

Query  73   GTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLS  132
            G+  ++V S+ + AR   KT DL F++RP ++ A+ + Y  +D+VFA+Y   W+ ++
Sbjct  65   GSVPVLVVSSADGAREIFKTHDLVFADRPYSSVANRIFYNGRDMVFARYTEYWRQVKSTC  124

Query  133  NLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRR  192
               +L  K +  + NVR  E+  +L  + E S+  + + L+EML     N++ +  L
Sbjct  125  VTQLLSVKRVQSFHNVREEEVALLLDNI-ENSKS-KVINLSEMLIELTGNVVCRAALG--  180
```

```
Query  193  VFVTKGTESNEFKDMVVELMTSAGYF-NIGDFIPSIAWMD-LQGIERGMKKLHTKFDVLL  250
                 G   + +K +++++M   GY  +I DF PS+ W+D + G++  ++K     D  L
Sbjct  181  ----SGYNVDSYKSLLLQIMDMLGYSRSIEDFFPSLGWVDWITGLKGKVEKAANGVDAFL  236

Query  251  TKMVKEHRATSHERKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSII  310
              ++K H   S     K DF+ +LLE  +   G  +    IK+++ ++  AGT+T ++ +
Sbjct  237  EGVLKNHTNPSTSSANK-DFVSILLEIQEADAGSSMDKECIKSLIWDMLGAGTETIATAL  295

Query  311  EWALTEMIKNPTILKKAQEEMDRVIGRDR-RLLESDISSLPYLQAIAKETYRKHPSTPLN  369
            EW +  +IK+P  + K Q+E+ R IG+ + R+ E D+  + YL+A+ KE+ R + + PL
Sbjct  296  EWTIGALIKSPDAMSKLQKEV-REIGKGKSRIEEGDLVKMDYLKAVMKESMRLYFTAPLL  354

Query  370  LPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGN  429
            +PR A Q  +  GY I    ++ +N WAI RDP+ W+NP EF PERFL   N  I+  G
Sbjct  355  VPREARQDVKFMGYDIKSGTQVLINAWAIARDPSSWDNPEEFRPERFL---NSPIDYKGF  411

Query  430  DFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNG--VAELNMDESFGLALQK  487
            +++ IPFGAGRR C G +  + +   ++  +V+ F+++LP+G  + E++M  S G+   K
Sbjct  412  NYEYIPFGAGRRGCPGIQFAISVNELVVANVVNKFNFELPDGKRLEEMDMTASTGITFHK  471
```

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RecName: Full=Cytochrome P450 83B1; AltName: Full=Protein ALTERED TRYPTOPHAN REGULATION 4; AltName: Full=Protein RED ELONGATED 1; AltName: Full=Protein SUPERROOT 2

Sequence ID: O65782.1 **Length:** 499 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 6 to 487 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
288 bits(736)	2e-90	Compositional matrix adjust.	163/485(34%)	266/485(54%)	9/485(1%)

```
Query  9    VVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAM-PHVALAKLAKKYGPI  67
            ++A ++     F +RS  KK  R LPPGP G P++G L  +    P   L +L+K YGPI
Sbjct  6    IIAGLVAAAAFFFLRSTTKKSLR-LPPGPKGLPIIGNLHQMEKFNPQHFLFRLSKLYGPI  64

Query  68   MHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKT  127
              +K+G   + V S+ E A+  LKT DLNF+ RP   G   ++Y  ++L F +Y   ++
Sbjct  65   FTMKIGGRRLAVISSAELAKELLKTQDLNFTARPLLKGQQTMSYQGRELGFGQYTAYYRE  124

Query  128  LRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQV  187
            +RK+  +++     +  +  VR  E   M+  + +A+     V L+E+L      ++ +
Sbjct  125  MRKMCMVNLFSPNRVASFRPVREEECQRMMDKIYKAADQSGTVDLSELLLSFTNCVVCRQ  184

Query  188  ILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKKLHTKF  246
               +R +   GTE   F D++ E     G     D  P   ++D L G+   +KK   +
Sbjct  185  AFGKR-YNEYGTEMKRFIDILYETQALLGTLFFSDLFPYFGFLDNLTGLSARLKKAFKEL  243

Query  247  DVLLTKMVKEHRATSHERKGKADFLDVLLE-ECDNTNGEKLSITNIKAVLLNLFTAGTDT  305
            D  L +++ E    +  ++    F+D+L++   D     K +  N+KA++L++   GTDT
Sbjct  244  DTYLQELLDETLDPNRPKQETESFIDLLMQIYKDQPFSIKFTHENVKAMILDIVVPGTDT  303

Query  306  SSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPS  365
            +++++ WA+T +IK P  +KKAQ+E+  VIG    + E DI +LPYL+A+ KE+ R  P
Sbjct  304  AAAVVVWAMTYLIKYPEAMKKAQDEVRSVIGDKGYVSEEDIPNLPYLKAVIKESLRLEPV  363

Query  366  TPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVW-ENPLEFLPERFLSEENGKI  424
             P+ L R  I   ++ GY IP    + VN WA+ RD   W +NP EF+PERF++E  G +
Sbjct  364  IPILLHRETIADAKIGGYDIPAKTIIQVNAWAVSRDTAAWGDNPNEFIPERFMNEHKG-V  422

Query  425  NPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGV--AELNMDESFG  482
            +  G DF+L+PFG+GRR+C    +G+ +V      L++ FDW LP G+   ++ MD   G
Sbjct  423  DFKGQDFELLPFGSGRRMCPAMHLGIAMVEIPFANLLYKFDWSLPKGIKPEDIKMDVMTG  482

Query  483  LALQK  487
            LA+ K
Sbjct  483  LAMHK  487
```

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RecName: Full=Cytochrome P450 71A26

Sequence ID: Q9STK7.1 **Length:** 489 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 28 to 486 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
287 bits(735)	3e-90	Compositional matrix adjust.	167/476(35%)	274/476(57%)	23/476(4%)

```
Query  27   KKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESA  86
            K+ T P PPG    PL+G L  LG  PH +L  L+ +YGP+M L  G   ++V S+ E A
Sbjct  28   KRNTLPSPPG---LPLIGNLHQLGRHPHRSLCSLSHRYGPLMLLHFGRVPVLVVSSAELA  84

Query  87   RAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWA  146
            R  LKT D  F++RP +     L Y   D+  A YG  W+ ++ +  LH+   K +  +
Sbjct  85   RDVLKTHDRVFASRPRSKIFEKLLYDKHDVASAPYGEYWRQMKSVCVLHLFSNKMVRSFR  144

Query  147  NVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKD  206
             VR  E+  M++ + ++     PV L+++L     ++I +V L R+     G E++ FK+
Sbjct  145  EVREEEISLMMEKIRKS--ISLPVNLSKILVSLTNDVICKVALGRKY----GGETD-FKE  197

Query  207  MVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKKLHTKFDVLLTKMVKEHRATSHERK  265
            ++  L    G F++G ++P +AW+D ++G++  ++K     D    ++V++H   +   +
Sbjct  198  LMERLNKLLGTFSVGSYVPWLAWIDWIRGLDCQLEKTANDVDKFFERVVQDHVDGN---R  254
```

```
Query  266  GKADFLDVLLE-ECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTIL  324
               DF+DVLL  + D T G +++  +IKA+++N+F  GTDTSS+++EWA+TE++++P  L
Sbjct  255  DMTDFVDVLLAIQRDKTVGFEINRVSIKAIVMNVFVGGTDTSSTLMEWAMTELLRHPKCL  314

Query  325  KKAQEEMDRVIGRDR-RLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGY  383
            K+ QEE+ R I +D+  + E +I ++ YL+A+ KE  R HP  PL +P  + Q   +  +
Sbjct  315  KRLQEEV-RTICKDKSSVSEEEIQNMSYLKAVIKEALRLHPPLPLMVPHESTQDVRLGDH  373

Query  384  YIPKDARLSVNIWAIGRDPNVW-ENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRI  442
            +IP   ++ +N WAIGR+   W  +  EF PER L   +  ++  G  F+LIPFG+GRRI
Sbjct  374  HIPAGTQVLINAWAIGREAATWGPDVEEFRPERHL---DSSVDYRGQAFELIPFGSGRRI  430

Query  443  CAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMD--ESFGLALQKAVPLSALVS  496
            C      +VL   +L  LVH FDW+L     E   +  ES G+A+ +  PL A+ S
Sbjct  431  CPAISFAVVLNEVVLANLVHRFDWRLSVESTEDQTEVAESTGIAIHRMFPLYAIAS  486
```

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RecName: Full=Probable (S)-N-methylcoclaurine 3'-hydroxylase isozyme 2; AltName: Full=Cytochrome P450 80B2

Sequence ID: Q9FXW4.1 **Length:** 488 **Number of Matches:** 1

Related Information

Range 1: 22 to 487 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
287 bits(734)	3e-90	Compositional matrix adjust.	193/481(40%)	275/481(57%)	21/481(4%)

```
Query  28   KPTRP--LPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPES  85
            + +RP  LPPGP   P+VG L  LG  PH   AKLA+KYG +  LK+G+  +VVAS+P +
Sbjct  22   RDSRPKNLPPGPRPSPIVGNLLQLGDKPHAEFAKLAQKYGELFSLKLGSQTVVVASSPAA  81

Query  86   ARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDW  145
            A   LKT D   S R          +    +V+++    WK LRK+    +   K ++
Sbjct  82   AAEILKTHDKILSGRYVFQSFRVKEHVENSIVWSECNDNWKLLRKVCRTELFTPKMIESQ  141

Query  146  ANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTE--SNE  203
            + +R  +   M+K +    + GE V + E++   + N+ G +I S+ VF  +     S E
Sbjct  142  SEIREAKAREMVKFL--RGKEGEVVKIVEVVFGTLVNIFGNLIFSKDVFDLEDPTGGSVE  199

Query  204  FKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKFDVLLTKMVKEHRATSHE  263
             K+ + +L+      N  D+ P +  +DL G  R + ++  +   +   M+KE R T
Sbjct  200  LKEHLWKLLDMGNSTNPADYFPIMGKLDLFGQRRAVAEVLQQIYDVWGVMLKERRGTKGS  259

Query  264  RKGKADFLDVLLEECDNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTI  323
             + K DF+DVLL          L    I A+L+ LF AGT+TS+S IEWA+TE+ K P +
Sbjct  260  -ESKNDFVDVLL-------NAGLDDQKINALLMELFGAGTETSASTIEWAITELTKKPLV  311

Query  324  LKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGY  383
            + K + E+  V+G D  + ESD+  LPYLQA  KET R HP TPL LPR A++ C V  Y
Sbjct  312  VSKIRLELVNVVG-DNTVKESDLPHLPYLQAFVKETLRLHPPTPLLLPRRALETCTVMNY  370

Query  384  YIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRIC  443
             IPK+ ++ VN WAIGRDP  W++PL F PERFLS +   ++  GNDF+LIPFG GRRIC
Sbjct  371  TIPKECQIMVNAWAIGRDPKTWDDPLNFKPERFLSSD---VDYKGNDFELIPFGGGRRIC  427

Query  444  AGTRMGMVLVSYILGTLVHSFDWKLPNGV--AELNMDESFGLALQKAVPLSALVSPRLAS  501
             G  +     + I+ TLV +F+W LP G+  +EL+MDE FGL LQK  PL  ++  R AS
Sbjct  428  PGLPLASQFSNLIVATLVQNFEWSLPQGMSTSELSMDEKFGLTLQKDPPLLIVLKAR-AS  486

Query  502  N  502
            N
Sbjct  487  N  487
```

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RecName: Full=Cytochrome P450 71B23

Sequence ID: Q9LTM0.1 **Length:** 501 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 40 to 500 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
287 bits(735)	3e-90	Compositional matrix adjust.	150/464(32%)	265/464(57%)	10/464(2%)

```
Query  42   LVGALPLLGAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRP  101
            ++G L  L  +PH  L  L K +GP+M L++G   +VV S+ ++A   LKT DL+  +RP
Sbjct  40   IIGNLHYLNGLPHKCLLNLWKIHGPVMQLQLGYVPLVVISSNQAAEEVLKTHDLDCCSRP  99

Query  102  PNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMC  161
                +  ++Y  +D+ FA YG  W+ LRKL+ + +   K  + +  +R  E   ++K +
Sbjct  100  ETIASKTISYNFKDIGFAPYGEEWRALRKLAVIELFSLKKFNSFRYIREEENDLLVKKLS  159

Query  162  EASRCGEPVVLAEMLTYAMANMIGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIG  221
            EAS    PV L + L    A+++ ++   + +  ++  + +  +D+          F
Sbjct  160  EASEKQSPVNLKKALFTLSASIVCRLAFGQNLHESEFIDEDSMEDLASRSEKIQAKFAFS  219

Query  222  DFIPSIAWMD-LQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKGKADFLDVLLEECDN  280
            +F P    +D + G  + + ++    D    +++ +H     +     D +DV+++  +
Sbjct  220  NFFPGGWILDKITGQSKSLNEIFADLDGFFNQVLDDHLKPGRKVLETPDVVDVMIDMMNK  279

Query  281  TNGE---KLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGR  337
             + +   KL+  +IK ++ ++F AG +TS++ I WA+TE+I+NP ++KK Q+E+  V+G
Sbjct  280  QSQDGSFKLTTDHIKGIISDIFLAGVNTSATTILWAMTELIRNPRVMKKVQDEVRTVLGE  339

Query  338  DR-RLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIW  396
             R R+ E D++ L Y + + KET+R HP+ PL LPR A+   ++ GY IP+  ++ VN++
```

```
Sbjct  340  KRDRITEQDLNQLNYFKLVIKETFRLHPAAPLLLPREAMAKIKIQGYDIPEKTQIMVNVY  399

Query  397  AIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYI  456
            AIGRDP++WENP EF PERF+   +  ++  G +F+L+PFG+GRRIC G  MG+  V
Sbjct  400  AIGRDPDLWENPEEFKPERFV---DSSVDYRGLNFELLPFGSGRRICPGMTMGIATVELG  456

Query  457  LGTLVHSFDWKLPNG--VAELNMDESFGLALQKAVPLSALVSPR  498
            L  L++ FDW LP G  V +++++E   + + K V L  + + R
Sbjct  457  LLNLLYFFDWGLPEGRTVKDIDLEEEGAIIIGKKVSLELVPTRR  500
```

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RecName: Full=Cytochrome P450 82A2; AltName: Full=Cytochrome P450 CP4

Sequence ID: O81972.1 **Length:** 522 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 37 to 521 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
287 bits(734)	8e-90	Compositional matrix adjust.	169/487(35%)	257/487(52%)	16/487(3%)

```
Query  34   PPGPLG-WPLVGALPLL--GAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTPESARAFL  90
            PP   G WP++G LPLL     PH  L  LA KYGPI  +K+G  + VV S  E A+
Sbjct  37   PPTVAGAWPIIGHLPLLLGSKTPHKTLGDLADKYGPIFSIKIGAKNAVVVSNWEMAKECY  96

Query  91   KTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALDDWANVRV  150
             T D+  S+ P    A+ L Y    +V A YGP W+ LRK+     L    ++   +VRV
Sbjct  97   TTNDIAVSSLPDLISANLLCYNRSMIVVAPYGPYWRQLRKILMSEFLSPSRVEQLHHVRV  156

Query  151  TELGHMLKAMCEASRCGE-------PVVLAEMLTYAMANMIGQVILSRRVF---VTKGTE  200
            +E+   +  +    R  +        V L +  +  + NMI +++  +R F    +   +
Sbjct  157  SEVQSSITELFRDWRSNKNVQSGFATVELKQWFSLLVFNMILRMVCGKRYFSASTSDDEK  216

Query  201  SNEFKDMVVELMTSAGYFNIGDFIPSIAWMDLQGIERGMKKLHTKFDVLLTKMVKEHRAT  260
            +N     V E +  A  F +GD IP + W D  G E  M++   + D ++ + + EHR
Sbjct  217  ANRCVKAVDEFVRLAATFTVGDAIPYLRWFDFGGYENDMRETGKELDEIIGEWLDEHRQK  276

Query  261  SHERKGKADFLDVLLEECDNTNGEKLSI-TNIKAVLLNLFTAGTDTSSSIIEWALTEMIK  319
                +   D + VLL   +    E +++   IK+ +L +  AGT+ S + + WA + ++
Sbjct  277  RKMGENVQDLMSVLLSLLEGKTIEGMNVDIVIKSFVLTVIQAGTEASITTLIWATSLILN  336

Query  320  NPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACE  379
            NP++L+K + E+D  +G++R + ESD+S L YLQA+ KET R +P  PL+ PR   + C
Sbjct  337  NPSVLEKLKAELDIQVGKERYICESDLSKLTYLQAVVKETLRLYPPAPLSRPREFEEDCT  396

Query  380  VDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAG  439
            + GY + K  RL  N+  I  D NVW NPLEF PERFL+ +   I+  G  F+L+PFG G
Sbjct  397  IGGYTVKKGTRLITNLSKIHTDHNVWSNPLEFKPERFLTTDK-DIDMKGQHFQLLPFGGG  455

Query  440  RRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMDESFGLALQKAVPLSALVSPRL  499
            RRIC G  +G+  V   L + +HSF+   P+    L+M E F     KA PL  L+ PRL
Sbjct  456  RRICPGINLGLQTVRLTLASFLHSFEILNPS-TEPLDMTEVFRATNTKATPLEILIKPRL  514

Query  500  ASNPYAT  506
            + + Y +
Sbjct  515  SPSCYES  521
```

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RecName: Full=Berbamunine synthase; AltName: Full=(S)-N-methylcoclaurine oxidase [C-O phenol-coupling]; AltName: Full=CYPLXXX; AltName: Full=Cytochrome P450 80

Sequence ID: P47195.1 **Length:** 487 **Number of Matches:** 1

Related Information

Range 1: 2 to 487 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
285 bits(729)	2e-89	Compositional matrix adjust.	175/501(35%)	267/501(53%)	23/501(4%)

```
Query  7    DFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLL---GAMPHV-ALAKLAK  62
            D++V  +   +   L   LFK     LPP P  WP+VG LP L    + P +  ++ +A+
Sbjct  2    DYIVGFVSISLVALLYFLLFKPKHTNLPPSPPAWPIVGHLPDLISKNSPPFLDYMSNIAQ  61

Query  63   KYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYG  122
            KYGP++HLK G    + AST E+A   L+T D   S R P        +    ++++
Sbjct  62   KYGPLIHLKFGLHSSIFASTKEAAMEVLQTNDKVLSGRQPLPCFRIKPHIDYSILWSDSN  121

Query  123  PRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMAN  182
              WK  RK+ +  +   K L      R    G+++  +   ++ G+ V L   L     N
Sbjct  122  SYWKKGRKILHTEIFSQKMLQAQEKNRERVAGNLVNFI--MTKVGDVVELRSWLFGCALN  179

Query  183  MIGQVILSRRVFVTKGTESNEFKDMVVE-LMTSAGYFNIGDFIPSIAWMDLQGIERGMKK  241
            ++G V+ S+ VF           D ++  ++ + G F++  + P +A  DL G++R   K
Sbjct  180  VLGHVVFSKDVFEYSDQSDEVGMDKLIHGMLMTGGDFDVASYFPVLARFDLHGLKR---K  236

Query  242  LHTKFDVLLTKMVKEHRATSHERKGK-ADFLDVLLEECDNTNGEKLSITNIKAVLLNLFT  300
            +  +F +L+     E  A    R  +  D LDVL+    N +        I A+ +  F
Sbjct  237  MDEQFKLLIKIWEGEVLARRANRNPEPKDMLDVLIANDFNEH-------QINAMFMETFG  289

Query  301  AGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETY  360
             G+DT+S+IIEWAL ++IKNP  L K +EE+DRV+GR   + ES  S LPYLQA  KET
Sbjct  290  PGSDTNSNIIEWALAQLIKNPDKLAKLREELDRVVGRSSTVKESHFSELPYLQACVKETM  349

Query  361  RKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEE  420
            R +P   + +P   ++ C+V GY IPK   + VN  AIGRDP  W++PL+F PERFL  +
```

```
Sbjct  350  RLYPPISIMIPHRCMETCQVMGYTIPKGMDVHVNAHAIGRDPKDWKDPLKFQPERFLDSD  409

Query  421  NGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGV--AELNMD  478
               I   G  F+ IPFG+GRRIC G  + + ++  +L +LVH+F W+LP+GV   +L+M+
Sbjct  410  ---IEYNGKQFQFIPFGSGRRICPGRPLAVRIIPLVLASLVHAFGWELPDGVPNEKLDME  466

Query  479  ESFGLALQKAVPLSALVSPRL  499
            E F L+L  A PL  +   R+
Sbjct  467  ELFTLSLCMAKPLRVIPKVRI  487
```

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RecName: Full=Cytochrome P450 71D9; AltName: Full=Cytochrome P450 CP3

Sequence ID: O81971.1 **Length:** 496 **Number of Matches:** 1

Related Information

Range 1: 12 to 483 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
285 bits(729)	2e-89	Compositional matrix adjust.	175/491(36%)	266/491(54%)	30/491(6%)

```
Query  8    FVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALP-LLGA-MPHVALAKLAKKYG  65
            F +   +F+  + + +     P+  LPPGP   P++G +  L+G+ +PH  L  L+ KYG
Sbjct  12   FSIFIFMFMTHKIVTKKSNSTPS--LPPGPWKLPIIGNMHNLVGSPLPHHRLRDLSAKYG  69

Query  66   PIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRW  125
             +MHLK+G    +V S+PE A+  +KT D  F++RP    A  + Y  + + F  YG  W
Sbjct  70   SLMHLKLGEVSTIVVSSPEYAKEVMKTHDHIFASRPYVLAAEIMDYDFKGVAFTPYGDYW  129

Query  126  KTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMC--EASRCGEPVVLAEMLTYAMANM  183
            + LRK+  L +L  K +  +  +R   L   +K M   E S+     V  E+++
Sbjct  130  RQLRKIFALELLSSKRVQSFQPIREEVLTSFIKRMATIEGSQVN---VTKEVISTVFT--  184

Query  184  IGQVILSRRVFVTKGTESNEFKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKKL  242
                I +R    +K     +   +V E    +G F++GD  PS+ ++  + G++  ++KL
Sbjct  185  ----ITARTALGSKSRHHQKLISVVTEAAKISGGFDLGDLYPSVKFLQHMSGLKPKLEKL  240

Query  243  HTKFDVLLTKMVKEHRATSHERKGKAD----FLDVLLEECDNTNGEKLSITNIKAVLLNL  298
            H + D ++  ++ EHR       G        LDVLL++        LS  +IKAV+ ++
Sbjct  241  HQQADQIMQNIINEHREAKSSATGDQGEEEVLLDVLLKKEFG-----LSDESIKAVIWDI  295

Query  299  FTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKE  358
            F  G+DTSS+ I WA+ EMIKNP  ++K Q E+ RV  ++ R   S   +L YL+++  E
Sbjct  296  FGGGSDTSSATITWAMAEMIKNPRTMEKVQTEVRRVFDKEGRPNGSGTENLKYLKSVVSE  355

Query  359  TYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLS  418
            T R HP  PL LPR   QACE++GY+IP  +R+ VN WAIGRDP +W     F PERF+
Sbjct  356  TLRLHPPAPLLLPRECGQACEINGYHIPAKSRVIVNAWAIGRDPRLWTEAERFYPERFIE  415

Query  419  EENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGV--AELN  476
                 I    N F+ IPFGAGRR+C G   G+  V Y+L  L++ FDWKLP G    +L
Sbjct  416  R---SIEYKSNSFEFIPFGAGRRMCPGLTFGLSNVEYVLAMLMYHFDWKLPKGTKNEDLG  472

Query  477  MDESFGLALQK  487
            M E FG+ + +
Sbjct  473  MTEIFGITVAR  483
```

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RecName: Full=Cytochrome P450 71B17

Sequence ID: Q9LTM6.1 **Length:** 502 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 10 to 494 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
285 bits(729)	3e-89	Compositional matrix adjust.	161/489(33%)	270/489(55%)	14/489(2%)

```
Query  13   IIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPIMHLKM  72
            +I  ++  +V    K+    LPP P   P++G L  +G +PH +  +LA++ G +M L +
Sbjct  10   LITFVSLTIVGCKIKRSIWNLPPSPPKLPVIGNLHQVGELPHRSFRRLAERTGHVMLLHL  69

Query  73   GTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLS  132
            G   + V S+ E+A   L+T DL+  +RP   G+  ++ G +DL F  YG  WK  R+
Sbjct  70   GFVPVTVISSREAAEEVLRTHDLDCCSRPNLVGSRLISRGFKDLNFTPYGEEWKERRRFL  129

Query  133  NLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMANMIGQVILSRR  192
               +   K L  +  ++  E   ++K + E++    PV L++ L +  A+++ +V   +
Sbjct  130  VGELFCSKKLQSFIYIKEVECNFLVKKLSESAVDQSPVDLSKTLFWLAASILFRVAFGQS  189

Query  193  VFVTKGTESNEFKDMVVELMTSAGYFNIGDFIP--SIAWMD--LQGIERGMKKLHTKFDV  248
               ++ T++++  ++V E  T+ G F   DF P   + W+   + G  + +  +  K D
Sbjct  190  FHESEFTDTDKIDELVFETETAQGSFTCSDFFPIAGLGWLVDWISGQHKRLNDVFLKLDA  249

Query  249  LLTKMVKEHRATSHERKGKADFLDVLLEECDNTNGE---KLSITNIKAVLLNLFTAGTDT  305
            LL  ++ +H      +  K D +DV+L+       +   +L+I +IK +L N+  AG DT
Sbjct  250  LLQHVIDDHSNPGRSKDHK-DIVDVMLDVMHKQGKDDSLRLTIDHIKGLLTNIIIAGIDT  308

Query  306  SSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDR-RLLESDISSLPYLQAIAKETYRKHP  364
             +  + W +TE+ +NP I+KK Q E+   +G +R R+ + D+  +P+L  + KET+R HP
Sbjct  309  GALTMIWTMTELARNPEIMKKVQGEIRDRLGNNRERITKEDLDKVPFLNLVIKETFRLHP  368

Query  365  STPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSEENGKI  424
              PL LPR  +   +V GY IP   R+ VN WAIGRDP +W +P EF PERF+   +  +
Sbjct  369  VAPLLLPRETMAHVKVQGYDIPPKRRILVNAWAIGRDPKLWTDPEEFKPERFI---DSPV  425
```

```
Query  425  NPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMD--ESFG  482
            +  G  F+L+PFG+GRRIC G  MGM  +   L  L++ FDWKLP+G++  ++D  E+
Sbjct  426  DYRGQHFELLPFGSGRRICPGMAMGMATLELGLLNLLYFFDWKLPDGMSHKDIDTEEAGT  485

Query  483  LALQKAVPL  491
            L + K V L
Sbjct  486  LTVVKKVHL  494
```

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RecName: Full=Methyltetrahydroprotoberberine 14-monooxygenase; AltName: Full=(S)-cis-N-methylstylopine 14-hydroxylase; AltName: Full=(S)-cis-N-methyltetrahydroprotoberberine-14-hydroxylase; AltName: Full=Methyltetrahydroprotoberberine 14-hydroxylase; AltName: Full=N-methylstylopine hydroxylase; Short=MSH

Sequence ID: L7X3S1.1 **Length:** 526 **Number of Matches:** 1

Related Information

Range 1: 38 to 524 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
285 bits(729)	4e-89	Compositional matrix adjust.	163/490(33%)	277/490(56%)	20/490(4%)

```
Query  27   KKPTRPL-PPGPLGWPLVGALPLL--GAMPHVALAKLAKKYGPIMHLKMGTCDMVVASTP  83
            + PT+ L P    G P++G L L   G + H  L  +A  YGP+ +++ G+   +V S
Sbjct  38   RNPTKKLAPEASGGRPIMGHLHLFNDGELTHRKLGAMADTYGPVFNIRFGSHKTLVVSDW  97

Query  84   ESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYGPRWKTLRKLSNLHMLGGKALD  143
            E  +    T D  FSNRP   G    + Y A  + +A YG  W+ LRK+S L +L    +D
Sbjct  98   EIVKECFTTNDKLFSNRPGTLGIKLMFYDADSVGYAPYGAYWRDLRKISTLKLLSNHRID  157

Query  144  DWANVRVTELGHMLKAMCEASRCGE------PVVLAEMLTYAMANMIGQVILSRRVFVTK  197
               ++R +E+    +++       GE      PV +    L     N++ +++  ++ F
Sbjct  158  TIKHLRSSEVESCFESLYSQWGNGEKSGEFAPVRMDSWLGDLTFNVVARIVAGKKNFSAN  217

Query  198  G-TESNEFKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMKKLHTKFDVLLTKMVK  255
            G   +  +K  + E M    +F   D IPS++W+D L+G+ R MKK  ++ D ++   V+
Sbjct  218  GDVGAQRYKAAMDEAMRLMRFFAFSDVIPSLSWLDNLRGLVREMKKCASEIDSIMATWVE  277

Query  256  EHRATSHE---RKGKADFLDVLLEECDNTN--GEKLSITNIKAVLLNLFTAGTDTSSSII  310
            EHR   +     + + DF+DV L+   ++++  G+   +  +K+  L++   G+DT++  +
Sbjct  278  EHRVKRNSGGNSQLEHDFIDVCLDIMEHSSLPGDDPDLV-VKSTCLDMILGGSDTTTVTL  336

Query  311  EWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNL  370
             WA++ ++ +P +L+KA+EE++  +G++R++ +SDI +LP++QAI KET R +P+ PL +
Sbjct  337  TWAMSLLLNHPQVLQKAKEELETQVGKNRQVDDSDIPNLPFIQAIIKETMRLYPAGPL-I  395

Query  371  PRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWE-NPLEFLPERFLSEENGKINPGGN  429
             R  ++ CEV GY +P   RL VN+W + RD NV++ +PLEF P+RFL+  N  ++  G
Sbjct  396  ERRTMEDCEVAGYQVPAGTRLLVNVWKMQRDGNVYKGDPLEFRPDRFLT-SNADVDLKGQ  454

Query  430  DFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMDESFGLALQKAV  489
             ++LIPFGAGRRIC G    + L+  +L  L+H F+        +++M ES GL   K +
Sbjct  455  HYELIPFGAGRRICPGVSFAVQLMHLVLARLLHEFEITTVEPETKVDMAESGGLLCYKIM  514

Query  490  PLSALVSPRL  499
            PL  L+ PRL
Sbjct  515  PLEVLIKPRL  524
```

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RecName: Full=Cytochrome P450 71A8

Sequence ID: Q42716.1 **Length:** 502 **Number of Matches:** 1

Related Information

Range 1: 26 to 498 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
282 bits(722)	3e-88	Compositional matrix adjust.	168/495(34%)	284/495(57%)	31/495(6%)

```
Query  9    VVAAIIFL-ITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHVALAKLAKKYGPI  67
            +V+ I+ + IT++L  S   K + P  P P   P++G L  LG++PH  L  +A+K+GPI
Sbjct  26   LVSLILLISITKWLSNSPKNKNSSP--PSPRKLPILGNLLQLGSLPHHNLRSMARKHGPI  83

Query  68   MHLKMGTCDMVVA-----STPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAKYG  122
            M L +G+   V +        E++R+ L+        RP  + ++ L    +      YG
Sbjct  84   MLLHLGSVRPVSSRRRPRGNHENSRSRLR--------RPRGSRSAALQLQGR---VGGYG  132

Query  123  PRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCEASRCGEPVVLAEMLTYAMAN  182
              W+ L+ +  + +L  K +  + +VR  E   ++K + ++S     V L+ M T    +
Sbjct  133  EYWRQLKTICVVQLLSNKRVQSFRSVREEETELLMKKIGDSS---GNVNLSHMFTQLTND  189

Query  183  MIGQVILSRRVFVTKGTESNE-FKDMVVELMTSAGYFNIGDFIPSIAWMD-LQGIERGMK  240
            ++ +  + R+     G E+ E F +++ E +    G  +IGDF+PS+ W++ + G +R +
Sbjct  190  VVCRSAIGRKY--GAGDENGEKFLEILREFLELLGAISIGDFVPSLWWINRINGFDRRVD  247

Query  241  KLHTKFDVLLTKMVKEHRATSHERKGKADFLDVLLE-ECDNTNGEKLSITNIKAVLLNLF  299
            ++  + D  L K++ E R  +   K + +F+D+LLE   +N+ G  +   +IKA++L++F
Sbjct  248  RIAKEMDEFLEKVIHE-RLENPAAKAEENFVDILLEIYRNNSAGVSIDRDSIKAIILDVF  306

Query  300  TAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLLESDISSLPYLQAIAKET  359
             AGTDT++ ++EWA+TE++++P I+KK Q E+ +V+     + + DI  + YL+A+ KET
Sbjct  307  AAGTDTTAVVLEWAMTELLRHPEIMKKLQSEVRQVVKDKHNITDDDIEKMHYLKAVMKET  366

Query  360  YRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPLEFLPERFLSE  419
             R H   PL +PR+A     EV GY +P    + +N WAIGRDP  W+ P +F PERFL
Sbjct  367  MRFHTPIPLLVPRVARNDVEVMGYDVPVGTMVMINAWAIGRDPTSWDEPEKFRPERFL--  424
```

```
Query  420  ENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMDE  479
             N  ++  G DF+LIPFGAGRR C GT   M  + + L  L+  FDW+LP+   EL+M E
Sbjct  425  -NSSVDFKGLDFELIPFGAGRRGCPGTTFPMATLEFTLANLMQKFDWELPHECRELDMSE  483

Query  480  SFGLALQKAVPLSAL  494
              G+A+++ +PL A+
Sbjct  484  RPGVAIRRVIPLLAI  498
```

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RecName: Full=Cytochrome P450 82C3

Sequence ID: O49396.3 **Length:** 512 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 5 to 506 GenPept Graphics   Next Match   Previous Match

Score	Expect	Method	Identities	Positives	Gaps
282 bits(722)	3e-88	Compositional matrix adjust.	180/517(35%)	270/517(52%)	36/517(6%)

```
Query  4    LVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLGWPLVGALPLLGAMPHV---ALAKL  60
            L + FV   +   I  F      K    P P G   WP++G L LLG    +    L K+
Sbjct  5    LFSLFVSILVFVFIALFKKSKKPKYVKAPAPSG--AWPIIGHLHLLGGKEQLLYRTLGKM  62

Query  61   AKKYGPIMHLKMGTCDMVVASTPESARAFLKTLDLNFSNRPPNAGASHLAYGAQDLVFAK  120
            A  YGP M L++G+ +  V S+ E A+      D   ++    A A H+ Y     VF
Sbjct  63   ADHYGPAMSLRLGSSETFVGSSFEVAKDCFTVNDKALASLM-TAAAKHMGY-----VF--  114

Query  121  YGPRWKTLRKLSNLHMLGGKALDDWANVRVTELGHMLKAMCE--ASRCG-EPVV--LAEM  175
                W  +RK++ + +L  + L    NVRV+E+   +K +      + G EPV+  L
Sbjct  115  ----WLEMRKIAMIELLSNRRLQMLNNVRVSEISMGVKDLYSLWVKKGGSEPVMVDLKSW  170

Query  176  LTYAMANMIGQVILSRRVFVTKGTESNE-------FKDMVVELMTSAGYFNIGDFIPSIA  228
            L   +ANMI +++  +R F   G ES+E       ++  + +     G F + D  P +
Sbjct  171  LEDMIANMIMRMVAGKRYFGGGGAESSEHTEEARQWRKGIAKFFHLVGIFTVSDAFPKLG  230

Query  229  WMDLQGIERGMKKLHTKFDVLLTKMVKEHRA---TSHERKGKADFLDVLLEECDNTNGEK  285
            W+DLQG E+ MK+   + DV+L + ++ HR     S  +   +DF+DV+L   +
Sbjct  231  WLDLQGHEKEMKQTRRELDVILERWIENHRQQRKVSGTKHNDSDFVDVMLSLAEQGKLSH  290

Query  286  LSI---TNIKAVLLNLFTAGTDTSSSIIEWALTEMIKNPTILKKAQEEMDRVIGRDRRLL  342
            L     T IK   L L   G++TS S + WA++ ++ N  +LKK Q+E+D  +GRDR +
Sbjct  291  LQYDANTCIKTTCLALILGGSETSPSTLTWAISLLLNNKDMLKKVQDEIDIHVGRDRNVE  350

Query  343  ESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDP  402
            +SDI +L YLQAI KET R +P+ PL   R A++ C V GY +P   RL VN+W I RDP
Sbjct  351  DSDIKNLVYLQAIIKETLRLYPAAPLLGHREAMEDCTVAGYNVPCGTRLIVNVWKIQRDP  410

Query  403  NVWENPLEFLPERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVH  462
             V+  P EF PERF++ E    +  G +F+L+PFG+GRR C G  + M ++   L   +H
Sbjct  411  KVYMEPNEFRPERFITGEAKDFDVRGQNFELMPFGSGRRSCPGPSLAMQMLHLGLARFLH  470

Query  463  SFDWKLPNGVAELNMDESFGLALQKAVPLSALVSPRL  499
            SF+ K       ++M ES GL + KA PL  L++PRL
Sbjct  471  SFEVKTVLD-RPVDMSESPGLTITKATPLEVLINPRL  506
```

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BLAST Results

Your search is limited to records matching entrez query: toxin.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

Job title: Protein Sequence (506 letters)

RID E94APRYP013 (Expires on 04-06 14:40 pm)

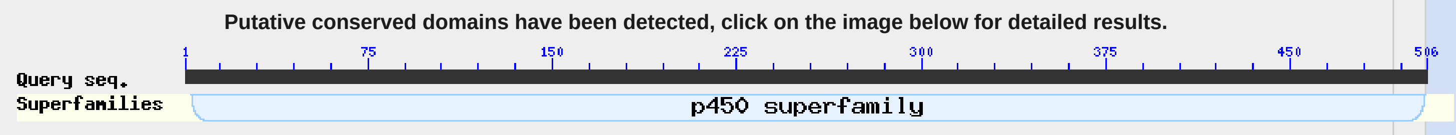
Query ID	lcl|Query_298952	**Database Name**	swissprot
Description	None	**Description**	Non-redundant UniProtKB/SwissProt sequences
Molecule type	amino acid	**Program**	BLASTP 2.6.0+ Citation
Query Length	506		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment] [MSA viewer]

New Analyze your query with SmartBLAST

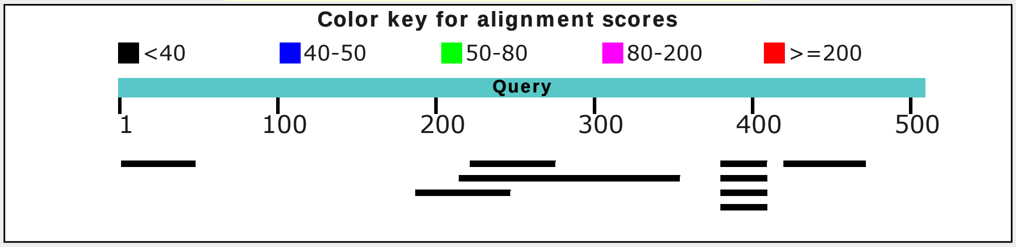
Graphic Summary

Show Conserved Domains



Distribution of the top 9 Blast Hits on 9 subject sequences

Mouse over to see the title, click to show alignments



Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	RecName: Full=Delta-actitoxin-Bgr2b; Short=Delta-AITX-Bgr2b; AltName: Full=Bg III; Short=BgIII; Al	25.4	25.4	5%	2.0	40%	P0C1F5.1
☐	RecName: Full=Uncharacterized 14.9 kDa protein in rep-hol intergenic region; AltName: Full=ORF14	26.6	26.6	10%	2.6	28%	P51716.1
☐	RecName: Full=Delta-actitoxin-Bgr2a; Short=Delta-AITX-Bgr2a; AltName: Full=Bg II; Short=BgII; Alt	24.6	24.6	5%	3.4	37%	P0C1F4.1
☐	RecName: Full=Hemolysin C	26.6	26.6	27%	4.6	25%	Q68W10.1
☐	RecName: Full=Acidic phospholipase A2; Short=svPLA2; AltName: Full=Phosphatidylcholine 2-acylh	25.8	25.8	10%	4.7	35%	Q7SID6.2
☐	RecName: Full=Orphan toxin OrtT	23.9	23.9	9%	6.6	43%	P64453.2
☐	RecName: Full=Delta-actitoxin-Bcg1b; Short=Delta-AITX-Bcg1b; AltName: Full=Cangitoxin II; AltNan	23.5	23.5	5%	7.9	37%	P0C7P9.1
☐	RecName: Full=Delta-actitoxin-Bcg1c; Short=Delta-AITX-Bcg1c; AltName: Full=Cangitoxin III; AltNar	23.5	23.5	5%	8.0	37%	P0C7Q0.1
☐	RecName: Full=Snake venom metalloproteinase neuwiedase; Short=SVMP	25.4	25.4	11%	8.4	28%	Q9I9R4.1

Alignments

Download GenPept Graphics Next Previous Descriptions

RecName: Full=Delta-actitoxin-Bgr2b; Short=Delta-AITX-Bgr2b; AltName: Full=Bg III; Short=BgIII; AltName: Full=Neurotoxin Bg-3

Sequence ID: P0C1F5.1 **Length:** 48 **Number of Matches:** 1

Related Information

Range 1: 6 to 34 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
25.4 bits(54)	2.0	Composition-based stats.	12/30(40%)	16/30(53%)	1/30(3%)

```
Query  378  CEVDGYYIPKDARLSVNIWAIGRDPNVWEN  407
            C+ DG     D  L+  +W IGR P+ W N
Sbjct  6    CDSDGPTSRGDT-LTGTLWLIGRCPSGWHN  34
```

Download GenPept Graphics Next Previous Descriptions

RecName: Full=Uncharacterized 14.9 kDa protein in rep-hol intergenic region; AltName: Full=ORF14

Sequence ID: P51716.1 **Length:** 133 **Number of Matches:** 1

Related Information

Range 1: 73 to 125 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
26.6 bits(57)	2.6	Compositional matrix adjust.	15/53(28%)	27/53(50%)	0/53(0%)

```
Query  222  DFIPSIAWMDLQGIERGMKKLHTKFDVLLTKMVKEHRATSHERKGKADFLDVL  274
            DFI ++  +DL  +    +K++     LL   + +  AT  E K +++FL  L
Sbjct  73   DFIVTVVDVDLTHLMGKAEKINITVPALLLHRIDQFIATHPEYKNRSNFLSQL  125
```

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RecName: Full=Delta-actitoxin-Bgr2a; Short=Delta-AITX-Bgr2a; AltName: Full=Bg II; Short=BgII; AltName: Full=Neurotoxin Bg-2

Sequence ID: P0C1F4.1 **Length:** 48 **Number of Matches:** 1

Related Information

Range 1: 6 to 34 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
24.6 bits(52)	3.4	Composition-based stats.	11/30(37%)	16/30(53%)	1/30(3%)

```
Query  378  CEVDGYYIPKDARLSVNIWAIGRDPNVWEN  407
            C+ DG    +   L+  +W IGR P+ W N
Sbjct  6    CDSDGP-TSRGNTLTGTLWLIGRCPSGWHN  34
```

Download GenPept Graphics Next Previous Descriptions

RecName: Full=Hemolysin C

Sequence ID: Q68W10.1 **Length:** 305 **Number of Matches:** 1

Related Information

Range 1: 123 to 264 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
26.6 bits(57)	4.6	Compositional matrix adjust.	39/153(25%)	67/153(43%)	26/153(16%)

```
Query  215  AGYFNIGDFIPSIAWMDLQGIERGMKKLHT------KFDVLLTKMVKE--HRATSHERKG  266
             G+ +I D   ++A      ++R ++K H       K   LL KM +E  H A   +  G
Sbjct  123  VGFIHIKDLFKALATKQNSTLKRLIRK-HIIAAPSMKLLDLLAKMRRERTHIAIVVDEYG  181

Query  267  KADFL---DVLLEEC----DNTNGEKLSITNIKAVLLNLFTAGTDTSSSIIEWALTEMIK  319
              D L   + L+EE     D+ + ++L  TN K +  +   A       ++E  + E IK
Sbjct  182  GTDGLVTIEDLIEEIVGRIDDEHDQQLDSTNFKVINNSTIIANARIEVELLEEIIKEKIK  241

Query  320  NPTILKKAQEEMDRVIGRDRRLLESDISSLPYL  352
            N        +E D + G    L+ + +SS+P +
Sbjct  242  ND------DDEFDTIGG----LVLTRVSSVPAI  264
```

Download GenPept Graphics Next Previous Descriptions

RecName: Full=Acidic phospholipase A2; Short=svPLA2; AltName: Full=Phosphatidylcholine 2-acylhydrolase

Sequence ID: Q7SID6.2 **Length:** 123 **Number of Matches:** 1

Related Information

Range 1: 67 to 112 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
25.8 bits(55)	4.7	Composition-based stats.	18/52(35%)	21/52(40%)	6/52(11%)

```
Query  418  SEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLP  469
            SEENG I  GG+D         R IC   R+  V     L T      W+ P
Sbjct  67   SEENGDIVCGGDD------PCKREICECDRVAAVCFRDNLDTYNSDTYWRYP  112
```

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RecName: Full=Orphan toxin OrtT

Sequence ID: P64453.2 **Length:** 57 **Number of Matches:** 1

See 1 more title(s)

Related Information

Identical Proteins - Identical proteins to P64453.2

Range 1: 7 to 53 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
23.9 bits(50)	6.6	Composition-based stats.	21/49(43%)	26/49(53%)	4/49(8%)

```
Query  3    ILVTDFVVAAIIFLITRFLVRSLFKKPTRPLPPGPLG--WPLVGALPLL  49
            +LV   V+AAI FLIT FL     KK  R L    +G  WP+   + LL
Sbjct  7    MLVFYAVMAAIAFLITWFLSHD--KKRIRFLSAFLVGATWPMSFPVALL  53
```

Download GenPept Graphics Next Previous Descriptions

RecName: Full=Delta-actitoxin-Bcg1b; Short=Delta-AITX-Bcg1b; AltName: Full=Cangitoxin II; AltName: Full=Cangitoxin-2; AltName: Full=Cangitoxin-II; Short=CGTX-II

Sequence ID: P0C7P9.1 **Length:** 48 **Number of Matches:** 1

Related Information

Range 1: 6 to 34 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
23.5 bits(49)	7.9	Composition-based stats.	11/30(37%)	16/30(53%)	1/30(3%)

```
Query  378  CEVDGYYIPKDARLSVNIWAIGRDPNVWEN  407
            C+ DG  +  D+ LS  +W  G  P+ W N
Sbjct  6    CDSDGPTVRGDS-LSGTLWLTGGCPSGWHN  34
```

Download GenPept Graphics Next Previous Descriptions

RecName: Full=Delta-actitoxin-Bcg1c; Short=Delta-AITX-Bcg1c; AltName: Full=Cangitoxin III; AltName: Full=Cangitoxin-3; AltName: Full=Cangitoxin-III; Short=CGTX-III

Sequence ID: P0C7Q0.1 **Length:** 48 **Number of Matches:** 1

Related Information

Range 1: 6 to 34 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
23.5 bits(49)	8.0	Composition-based stats.	11/30(37%)	16/30(53%)	1/30(3%)

```
Query  378  CEVDGYYIPKDARLSVNIWAIGRDPNVWEN  407
            C+ DG  +  D+ LS  +W  G  P+ W N
Sbjct  6    CDSDGPTVHGDS-LSGTLWLTGGCPSGWHN  34
```

Download GenPept Graphics Next Previous Descriptions

RecName: Full=Snake venom metalloproteinase neuwiedase; Short=SVMP

Sequence ID: Q9I9R4.1 **Length:** 198 **Number of Matches:** 1

Related Information

Range 1: 14 to 80 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
25.4 bits(54)	8.4	Compositional matrix adjust.	19/67(28%)	33/67(49%)	7/67(10%)

```
Query  187  VILSRRVFVTKGTESNEFKDMVVELM-TSAGYFNIGDFIPSIA----W--MDLQGIERGM  239
            ++  RR++    ++SN+ +  V EL+ T  G+F    +  S+A    W   DL  +E+
Sbjct  14   IVADRRMYTKYNSDSNKIRTRVHELVNTVNGFFRSMNVDASLANLEVWSKKDLIKVEKDS  73

Query  240  KKLHTKF  246
             K  T F
Sbjct  74   SKTLTSF  80
```

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Appendix 4. Results of search of FARRP allergen database

HYPERLINKS

*SuR*B (ALS)

DFR

F3’5’H

AllergenOnline Search Results

Note: As of August 2015 we have included gid: groupid in the fasta results that provides detailed information on the allergenicity references for the group, type of allergen, other sequences belonging to the same group and more.

%_id 1 = 100% identity, alen=alignment length

AllergenOnline Database v17 (January 18, 2017)

fasta35.exe -q -H -B -m 9i -w 80 -E 1 -d 20 C:\Windows\Temp\all2B6.tmp fasta/version17.fasta
User Query #1 >query

User Query #1

```
>query
MAAAAAAPSP SFSKTLSSSS SKSSTLLPRS TFPFPHHPHK TTPPPLHLTP THIHSQRRRF TISNVISTTQ KVSETQKAET FVSRFAPDEP RKGSDVLVEA LEREGVTDVF AYPGGASMEI
HQALTRSSII RNVLPRHEQG GVFAAEGYAR ATGFPGVCIA TSGPGATNLV SGLADALLDS VPIVAITGQV PRRMIGTDAF QETPIVEVTR SITKHNYLVM DVEDIPRVVR EAFFLARSGR
PGPVLIDVPK DIQQQLVIPD WDQPMRLPGY MSRLPKLPNE MLLEQIVRLI SESKKPVLYV GGGCSQSSEE LRRFVELTGI PVASTLMGLG AFPTGDELSL SMLGMHGTVY ANYAVDSSDL
LLAFGVRFDD RVTGKLEAFA SRAKIVHIDI DSAEIGKNKQ PHVSICADIK LALQGLNSIL ESKEGKLKLD FSAWRQELTV QKVKYPLNFK TFGDAIPPQY AIQVLDELTN GSAIISTGVG
QHQMWAAQYY KYRKPRQWLT SGGLGAMGFG LPAAIGAAVG RPDEVVVDID GDGSFIMNVQ ELATIKVENL PVKIMLLNNQ HLGMVVQWED RFYKANRAHT YLGNPSNEAE IFPNMLKFAE
ACGVPAARVT HRDDLRAAIQ KMLDTPGPYL LDVIVPHQEH VLPMIPSGGA FKDVITEGDG RSSY
```

```
# fasta35.exe -q -H -B -m 9i -w 80 -E 1 -d 20 C:\Windows\Temp\all2B6.tmp fasta/version17.fasta
FASTA searches a protein or DNA sequence data bank
 version 35.04 Jan. 15, 2009
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

Query: C:\Windows\Temp\all2B6.tmp
  1>>>query - 664 aa
Library: fasta/version17.fasta  481602 residues in  2035 sequences

 481602 residues in  2035 sequences
Statistics:  Expectation_n fit: rho(ln(x))= 4.2239+/- 0.004; mu= 20.3703+/- 0.212
 mean_var=82.8044+/-20.798, 0's: 1 Z-trim: 1  B-trim: 285 in 1/43
 Lambda= 0.140944
Algorithm: FASTA (3.5 Sept 2006) [optimized]
```

```
Parameters: BL50 matrix (15:-5) ktup: 2
 join: 38, opt: 26, open/ext: -10/-2, width:  16
 Scan time:  0.000

The best scores are:                                           opt z-sc E(2035) %_id  %_sim  alen
gi|34851180|gid|40|profilin-like protein [Ambrosia arte ( 131)   91 105.0    0.99 0.362 0.638   47

>>>query, 664 aa vs fasta/version17.fasta library

>>gi|34851180|gid|40|profilin-like protein [Ambrosia artemisiifolia]          (131 aa)
 initn:  49 init1:  49 opt:  91  Z-score: 105.0  bits: 27.4 E(): 0.99
Smith-Waterman score: 91; 36.2% identity (63.8% similar) in 47 aa overlap (239-285:85-129)

      200       210       220       230       240       250       260       270
query  AFQETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPDWDQPMRLPGYMSRLPKLP
                                               :. ::  . . :   ..:.:  .:.::  ::  . : . :
gi|348 EEITGIMNDFNEPGSLAPTGLYLGGTKYMVIQGEPGAVIRGKKGPGGVTI-KKTTMSLIIGIYDEPMT-PGQCNMLVERP
           50        60        70        80        90        100       110        120

      280       290       300       310       320       330       340       350
query  NEMLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSLSMLGMHGTVYANYAVDSS
       ...::::
gi|348 GDYLLEQGF
            130



664 residues in 1 query   sequences
481602 residues in 2035 library sequences
 Scomplib [35.04]
 start: Wed Apr 12 03:37:34 2017 done: Wed Apr 12 03:37:34 2017
 Total Scan time:  0.000 Total Display time:  0.000

Function used was FASTA [version 35.04 Jan. 15, 2009]
```

AllergenOnline Search Results

Note: As of August 2015 we have included gid: groupid in the fasta results that provides detailed information on the allergenicity references for the group, type of allergen, other sequences belonging to the same group and more.

%_id 1 = 100% identity, alen=alignment length

AllergenOnline Database v17 (January 18, 2017)

fasta35.exe -q -H -B -m 9i -w 80 -E 1 -d 20 C:\Windows\Temp\all3079.tmp fasta/version17.fasta
User Query #1 >query

User Query #1

```
>query
MASEAVHAPS PPVAVPTVCV TGAAGFIGSW LVMRLLERGY NVHATVRDPE NKKKVKHLLE LPKADTNLTL WKADLTVEGS FDEAIQGCQG VFHVATPMDF ESKDPENEVI KPTVRGMLSI
IESCAKANTV KRLVFTSSAG TLDVQEQQKL FYDQTSWSDL DFIYAKKMTG WMYFVSKILA EKSAMEETKK KNIDFISIIP PLVVGPFITP TFPPSLITAL SLITGNEAHY CIIKQGQYVH
LDDLCEAHIF LYEHPKADGR FICSSHHAII YDVAKMVREK WPEYYVPTEF KGIDKDLPVV SFSSKKLTDM GFQFKYTLED MYKGAIETCR QKQLLPFSTR SAADNGHNRE AIAISAQNYA
SGKENAPVAN HTEMLTNVEV
```

```
# fasta35.exe -q -H -B -m 9i -w 80 -E 1 -d 20 C:\Windows\Temp\all3079.tmp fasta/version17.fasta
FASTA searches a protein or DNA sequence data bank
 version 35.04 Jan. 15, 2009
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

Query: C:\Windows\Temp\all3079.tmp
  1>>>query - 380 aa
Library: fasta/version17.fasta  481602 residues in  2035 sequences

 481602 residues in  2035 sequences
Statistics:  Expectation_n fit: rho(ln(x))= 2.9729+/-0.00311; mu= 21.1892+/- 0.163
 mean_var=53.3979+/-14.394, 0's: 1 Z-trim: 1  B-trim: 79 in 1/43
 Lambda= 0.175514
Algorithm: FASTA (3.5 Sept 2006) [optimized]
Parameters: BL50 matrix (15:-5) ktup: 2
 join: 37, opt: 25, open/ext: -10/-2, width:  16
```

```
 Scan time:  0.000
!! No sequences with E() < 1.000000


380 residues in 1 query   sequences
481602 residues in 2035 library sequences
 Scomplib [35.04]
 start: Wed Apr 12 03:38:51 2017 done: Wed Apr 12 03:38:51 2017
 Total Scan time:  0.000 Total Display time:  0.000

Function used was FASTA [version 35.04 Jan. 15, 2009]
```

AllergenOnline Search Results

Note: As of August 2015 we have included gid: groupid in the fasta results that provides detailed information on the allergenicity references for the group, type of allergen, other sequences belonging to the same group and more.

%_id 1 = 100% identity, alen=alignment length

AllergenOnline Database v17 (January 18, 2017)

fasta35.exe -q -H -B -m 9i -w 80 -E 1 -d 20 C:\Windows\Temp\all28D4.tmp fasta/version17.fasta
User Query #1 >query

User Query #1

```
    >query
    MAILVTDFVV AAIIFLITRF LVRSLFKKPT RPLPPGPLGW PLVGALPLLG AMPHVALAKL AKKYGPIMHL KMGTCDMVVA STPESARAFL KTLDLNFSNR PPNAGASHLA YGAQDLVFAK
    YGPRWKTLRK LSNLHMLGGK ALDDWANVRV TELGHMLKAM CEASRCGEPV VLAEMLTYAM ANMIGQVILS RRVFVTKGTE SNEFKDMVVE LMTSAGYFNI GDFIPSIAWM DLQGIERGMK
    KLHTKFDVLL TKMVKEHRAT SHERKGKADF LDVLLEECDN TNGEKLSITN IKAVLLNLFT AGTDTSSSII EWALTEMIKN PTILKKAQEE MDRVIGRDRR LLESDISSLP YLQAIAKETY
    RKHPSTPLNL PRIAIQACEV DGYYIPKDAR LSVNIWAIGR DPNVWENPLE FLPERFLSEE NGKINPGGND FKLIPFGAGR RICAGTRMGM VLVSYILGTL VHSFDWKLPN GVAELNMDES
    FGLALQKAVP LSALVSPRLA SNPYAT
```

```
# fasta35.exe -q -H -B -m 9i -w 80 -E 1 -d 20 C:\Windows\Temp\all28D4.tmp fasta/version17.fasta
FASTA searches a protein or DNA sequence data bank
 version 35.04 Jan. 15, 2009
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

Query: C:\Windows\Temp\all28D4.tmp
  1>>>query - 506 aa
Library: fasta/version17.fasta  481602 residues in  2035 sequences

 481602 residues in  2035 sequences
Statistics:  Expectation_n fit: rho(ln(x))= 4.4678+/-0.00343; mu= 15.3463+/- 0.183
 mean_var=53.5914+/-13.695, 0's: 1 Z-trim: 1  B-trim: 285 in 1/43
 Lambda= 0.175197
Algorithm: FASTA (3.5 Sept 2006) [optimized]
Parameters: BL50 matrix (15:-5) ktup: 2
```

```
 join: 37, opt: 25, open/ext: -10/-2, width:  16
 Scan time:  0.000

The best scores are:                                           opt z-sc E(2035) %_id  %_sim  alen
gi|994779|gid|195|proteinase inhibitor [Solanum tuberos ( 221)   82 108.1    0.66 0.269 0.538   119
gi|75306610|gid|78|RecName: Full=Profilin; AltName: Ful ( 131)   78 105.8    0.89 0.333 0.540    63
gi|548948850|gid|159|profilin, partial [Triticum aestiv ( 131)   78 105.8    0.89 0.339 0.559    59
gi|190684061|gid|159|profilin [Triticum aestivum]       ( 131)   78 105.8    0.89 0.339 0.559    59
gi|548948848|gid|159|profilin, partial [Triticum aestiv ( 131)   78 105.8    0.89 0.339 0.559    59
gi|576017879|gid|390|RecName: Full=Profilin-5; AltName: ( 131)   78 105.8    0.89 0.250 0.476   124

>>>query, 506 aa vs fasta/version17.fasta library

>>gi|994779|gid|195|proteinase inhibitor [Solanum tuberosum]                  (221 aa)
 initn:  34 init1:  34 opt:  82  Z-score: 108.1  bits: 28.4 E(): 0.66
Smith-Waterman score: 82; 26.9% identity (53.8% similar) in 119 aa overlap (367-475:26-140)

        330       340       350       360       370       380       390            400
query  AQEEMDRVIGRDRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNI----W-AIGRD
                                               :.:::  :  . .: :  .  :.:::  :    : :.: :
gi|994                MKCLFLLCLCLVPIVVFSSTFTSKNPINLPSDATPVLDVAGKEL--DSRLSYRIISTFWGALGGD
                              10        20        30        40          50        60

             410        420       430       440       450          460        470
query  PNVWENPLEFLP-ERFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVL-VSYILGT--LVHSFD-WKLPNGVAELN
         . ..:    :    . . :. ..:.:.  ..:  :.. ..  :   . .: ... ..:  :  :.  ::. .  : :
gi|994 VYLGKSPNSDAPCANGIFRYNSDVGPSGTPVRFI--GSSSHFGQGIFENELLNIQFAISTSKLCVSYTIWKVGDYDASLG
            70        80        90          100       110       120       130       140

        480       490       500
query  MDESFGLALQKAVPLSALVSPRLASNPYAT

gi|994 TMLLETGGTIGQADSSWFKIVKSSQFGYNLLYCPVTSTMSCPFSSDDQFCLKVGVVHQNGKRRLALVKDNPLDVSFKQVQ
             150       160       170       180       190       200       210       220

>>gi|75306610|gid|78|RecName: Full=Profilin; AltName: Full=Minor food allerg  (131 aa)
 initn:  75 init1:  52 opt:  78  Z-score: 105.8  bits: 27.2 E(): 0.89
Smith-Waterman score: 78; 33.3% identity (54.0% similar) in 63 aa overlap (378-437:13-64)
```

```
       340       350       360       370       380       390       400          410
query  DRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVW-ENPL--EFLPE
                                               ::.:: .. . : :       :.: .:: ..:   .: ::
gi|753                             MSWQAYVDDHLMCEIDGQHLSSAAIL-------GHDSTVWAQSPNFPQFKPE
                                           10        20               30        40

          420       430       440       450       460       470       480       490
query  RFLSEENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMDESFGLALQKAVPLSAL
       .. .  :   :::.    : : :
gi|753 EISAILNDFENPGS----LAPTGLYLGGTKYMVIQGEPGVVIRGKKGTGGITVKKTNLALIIGVYDEPMTPGQCNMVVER
          50            60        70        80        90       100       110       120

>>gi|548948850|gid|159|profilin, partial [Triticum aestivum]                  (131 aa)
 initn:  49 init1:  49 opt:  78  Z-score: 105.8  bits: 27.2 E(): 0.89
Smith-Waterman score: 78; 33.9% identity (55.9% similar) in 59 aa overlap (378-428:13-64)

       340       350       360       370       380       390       400          410
query  DRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVW-ENPL--EFLPE
                                               ::.:: .. . : :       :.: .:: :.:   .: ::
gi|548                             MSWQAYVDDHLCCEIDGQHLTSAAIL-------GHDGSVWAESPNFPKFKPE
                                           10        20               30        40

               420       430       440       450       460       470       480
query  RFLS-----EENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMDESFGLALQKAV
       .. .     :: :.. : :
gi|548 EIAGIVKDFEEPGHLAPTGLFLGGTKYMVIQGEPGVVIRGKKGTGGITIKKTGMALILGIYDEPMTPGQCNLVVERLGDY
          50        60        70        80        90       100       110       120

>>gi|190684061|gid|159|profilin [Triticum aestivum]                           (131 aa)
 initn:  49 init1:  49 opt:  78  Z-score: 105.8  bits: 27.2 E(): 0.89
Smith-Waterman score: 78; 33.9% identity (55.9% similar) in 59 aa overlap (378-428:13-64)

       340       350       360       370       380       390       400          410
query  DRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVW-ENPL--EFLPE
                                               ::.:: .. . : :       :.: .:: :.:   .: ::
gi|190                             MSWQTYVDDHLCCEIDGQHLTSAAIL-------GHDGSVWAESPNFPKFKPE
                                           10        20               30        40

               420       430       440       450       460       470       480
```

```
query  RFLS-----EENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMDESFGLALQKAV
       .. .     :: :.. : :
gi|190 EIAGIVKDFEEPGHLAPTGLFLGGTKYMVIQGEPGVVIRGKKGTGGITIKKTGMALILGIYDEPMTPGQCNLVVERLGDY
          50        60        70        80        90       100       110       120

>>gi|548948848|gid|159|profilin, partial [Triticum aestivum]                  (131 aa)
 initn:  47 init1:  47 opt:  78  Z-score: 105.8  bits: 27.2 E(): 0.89
Smith-Waterman score: 78; 33.9% identity (55.9% similar) in 59 aa overlap (378-428:13-64)

       340       350       360       370       380       390       400          410
query  DRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVW-ENPL--EFLPE
                                               ::.:: .. . : :       :.: .:: :.:   .: ::
gi|548                             MSWQTYVDDHLCCEIDGQHLTSAAIL-------GHDGSVWTESPNFPKFKPE
                                           10        20               30        40

               420       430       440       450       460       470       480
query  RFLS-----EENGKINPGGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHSFDWKLPNGVAELNMDESFGLALQKAV
       .. .     :: :.. : :
gi|548 EIAGIVKDFEEPGHLAPTGLFLGGTKYMVIQGEPGVVIRGKKGTGGITIKKTGMALILGIYDEPMTPGQCNLVVERLGDY
          50        60        70        80        90       100       110       120

>>gi|576017879|gid|390|RecName: Full=Profilin-5; AltName: Full=Allergen Cor   (131 aa)
 initn:  72 init1:  46 opt:  78  Z-score: 105.8  bits: 27.2 E(): 0.89
Smith-Waterman score: 78; 25.0% identity (47.6% similar) in 124 aa overlap (378-487:13-128)

       340       350       360       370       380       390       400          410
query  DRRLLESDISSLPYLQAIAKETYRKHPSTPLNLPRIAIQACEVDGYYIPKDARLSVNIWAIGRDPNVWENPL---EFLPE
                                               ::.::...   :        ::.: .:: .     .: ::
gi|576                             MSWQAYVDEHLMCEIDGHHLSAAA-------IIGHDGSVWAQSSTFPQFKPE
                                           10        20               30        40

               420            430       440       450       460        470       480
query  RFLS-----EENGKINP-----GGNDFKLIPFGAGRRICAGTRMGMVLVSYILGTLVHS-FDWKLPNGVAELNMDESFGL
       .. .     .: :.. :     ::  . .:   .:  : .    : . :.    .:. . .:  :  :  .. . : .:
gi|576 EIAAIIKDFDEPGSLAPTGLHLGGIKYMVIQGESGAVIRGKKGAGGITVKKTSQALIFGIYDEPLTPGQCNM-IVERLGD
          50        60        70        80        90       100       110        120

           490       500
query  ALQKAVPLSALVSPRLASNPYAT
```

```
        : :
gi|576 YLLKQGL
          130



506 residues in 1 query   sequences
481602 residues in 2035 library sequences
 Scomplib [35.04]
 start: Wed Apr 12 03:39:55 2017 done: Wed Apr 12 03:39:55 2017
 Total Scan time:  0.000 Total Display time:  0.000

Function used was FASTA [version 35.04 Jan. 15, 2009]
```