

Appendix 13

**Bioinformatics analysis of
deduced amino acid sequences of
Arabidopsis thaliana ahasl and SEC61 γ from
herbicide-tolerant soybean BPS-CV127-9 for
allergenicity and toxicity potential**

**BIOINFORMATICS ANALYSIS OF DEDUCED AMINO ACID SEQUENCES OF
ARABIDOPSIS THALIANA ahasI AND SEC61 γ FROM HERBICIDE-TOLERANT
SOYBEAN BPS-CV127-9 FOR ALLERGENICITY AND TOXICITY
POTENTIAL**

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STATEMENT OF NO DATA CONFIDENTIALITY CLAIMS

No claim of confidentiality is made for any information contained in this study on the basis of its falling within the scope of FIFRA §10(d) (1) (A), (B), or (C).

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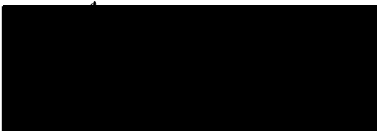
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STATEMENT OF COMPLIANCE

This study was not conducted in compliance with the requirements of 40 CFR Part 160.

The data generated by BASF Plant Science in support of product safety comply with generally accepted scientific procedures. Record keeping is consistent with procedures used throughout the research community. This report accurately presents the raw data developed during the study.

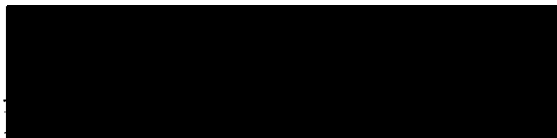
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ABBREVIATIONS AND DEFINITIONS

AHAS	acetohydroxyacid synthase enzyme
<i>ahasl</i>	imidazolinone-tolerant alleles of <i>Arabidopsis thaliana</i> acetohydroxyacid synthase large subunit gene; includes the <i>ahasl</i> (S653N) allele found in plasmid pAC321 and the <i>ahasl</i> (R272K, S653N) allele found in BPS-CV127-9
<i>AHASL</i>	wild-type <i>Arabidopsis thaliana</i> acetohydroxyacid synthase large subunit gene; also referred to in the literature as <i>CSR1</i>
<i>ahasl</i>	imidazolinone-tolerant <i>Arabidopsis thaliana</i> acetohydroxyacid synthase large subunit protein bearing two mutations (R272K, S653N)
BLASTP	protein-protein Basic Local Alignment Search Tool
BLOSUM	<u>blocks substitution matrix</u>
FARRP	Food Allergy Research and Resource Program
E value	expect value
GI number	GenInfo identifier, or GI number, is a sequence identification number assigned by the NCBI
IgE	immunoglobulin E
NCBI	National Center for Biotechnology Information (United States of America)
R272K	arginine residue at position 272 of <i>Arabidopsis thaliana</i> acetohydroxyacid synthase large subunit replaced with lysine
RT-PCR	reverse-transcription polymerase chain reaction
S653N	serine residue at position 653 of <i>Arabidopsis thaliana</i> acetohydroxyacid synthase large subunit replaced with asparagine
<i>SEC61γ</i>	wild-type <i>Arabidopsis thaliana</i> <i>SEC61γ</i> -subunit gene
SEC61γ	wild-type <i>Arabidopsis thaliana</i> SEC61γ-subunit protein

BIOINFORMATICS ANALYSIS OF DEDUCED AMINO ACID SEQUENCES OF *ARABIDOPSIS THALIANA* *ahasl* AND SEC61 γ FROM HERBICIDE-TOLERANT SOYBEAN BPS-CV127-9 FOR ALLERGENICITY AND TOXICITY POTENTIAL

SUMMARY

Soybean [*Glycine max* (L.) Merr.] plants have been developed that are tolerant to the imidazolinone class of agricultural herbicides. The herbicide-tolerant soybean plants, referred to as BPS-CV127-9, are derived from a single transformation event and were produced by the introduction of an imidazolinone-tolerant acetohydroxyacid synthase large subunit (*ahasl*) gene from *Arabidopsis thaliana* (L.) Heynh. into the soybean plant genome via biolistics using the PvuII fragment of transformation plasmid pAC321. The PvuII fragment of pAC321 includes what, at the time of transformation, was defined as the wild-type *Arabidopsis AHASL* promoter, the mutant *Arabidopsis ahasl* (S653N) coding sequence, and the wild-type *Arabidopsis AHASL* terminator. The mutant *Arabidopsis ahasl* (S653N) allele, which confers tolerance to imidazolinone herbicides, has also been referred to in the literature as *csr1-2* (Sathasivan *et al.*, 1990; Jander *et al.*, 2003). In addition to the S653N mutation, a second mutation was discovered in the *Arabidopsis ahasl* coding sequence integrated in the CV127 soybean genome. This second mutation, in which arginine at position 272 of the *ahasl* protein is replaced by lysine, does not impact the enzymatic function of the acetohydroxyacid synthase (AHAS) enzyme or its herbicide-tolerance properties. Also included in the region originally annotated as the *AHASL* promoter was the majority of an *Arabidopsis* putative SEC61 γ -subunit gene (*Arabidopsis* Genome Initiative locus code At3g48570), including the entire *Arabidopsis SEC61 γ* coding sequence. In this study, the deduced amino acid sequences of *ahasl* (R272K, S653N) and SEC61 γ from *A. thaliana* were subjected to bioinformatics analyses to assess their allergenicity and toxicity potential. These analyses confirmed that the two proteins do not share immunologically relevant amino acid sequence segments or structure with known allergens or have sequence homology to known protein toxins. Thus, the bioinformatics analyses of the *Arabidopsis ahasl* (R272K, S653N) and SEC61 γ -subunit proteins encoded within the BPS-CV127-9 transgene insert sequence do not provide any indication of a potential allergenicity or toxicity concern.

INTRODUCTION

Soybean [*Glycine max* (L.) Merr.] plants have been developed that are tolerant to the imidazolinone class of agricultural herbicides. The herbicide-tolerant soybean plants, referred to as BPS-CV127-9, are derived from a single transformation event. BPS-CV127-9 was produced by the introduction of an imidazolinone-tolerant acetohydroxyacid synthase large subunit (*ahasl*) gene from *A. thaliana* (L.) Heynh. into the soybean plant genome via biolistics using the PvuII fragment of transformation vector pAC321. The PvuII fragment includes what, at the time of transformation, was defined as the wild-type *Arabidopsis AHASL* promoter, the herbicide-tolerant *Arabidopsis ahasl*

coding sequence, and the wild-type Arabidopsis *AHASL* terminator. In addition to the S653N mutation, a second mutation was discovered in the *ahasl* coding sequence integrated in the BPS-CV127-9 soybean genome. This mutation, in which arginine at position 272 of the *ahasl* protein is replaced by lysine, does not impact the enzymatic function of the AHAS enzyme or its herbicide-tolerance properties (Stevenson Paulik, 2007). Also included in the region originally annotated as the *AHASL* promoter was the majority of the Arabidopsis putative *SEC61γ*-subunit gene (Arabidopsis Genome Initiative locus code At3g48570), including the entire Arabidopsis *SEC61γ* coding sequence.

Acetohydroxyacid synthase (AHAS) is found ubiquitously in the plant kingdom. The AHAS enzyme catalyzes the first step in the biosynthesis of branched-chain amino acids in plants. In conventional plants, inhibition of the AHAS enzyme by imidazolinone herbicides leads to a deficiency in branched-chain amino acids and other compounds derived from this pathway that are needed for plant survival. The *ahasl* gene from Arabidopsis confers tolerance to imidazolinone herbicides by encoding an AHAS catalytic subunit with altered herbicide-binding properties, while retaining its normal biosynthetic function in the soybean plant.

SEC61 is a heterotrimeric complex which forms a protein-conducting channel involved in transport across the endoplasmic reticulum membrane in eukaryotes. Two of the three subunits of SEC61, the α and γ subunits, are found in all organisms (Osborne *et al.*, 2005). Although the *SEC61γ*-subunit transcript is detectable in BPS-CV127-9 by reverse-transcription polymerase chain reaction (RT-PCR) analysis (Shen, 2007), the SEC61γ-subunit protein product is not detectable in BPS-CV127-9 soybean leaves or grain (Jiang, 2007).

The transgene insert of BPS-CV127-9 contains the coding sequences of two proteins from *A. thaliana*: *ahasl* (R272K, S653N) and SEC61γ. The purpose of this study was to conduct a bioinformatics analysis of these two protein sequences as part of a weight-of-evidence assessment of the potential allergenicity and toxicity of the proteins encoded within the BPS-CV127-9 transgene insert sequence.

MATERIALS AND METHODS

Databases. The Food Allergy Research and Resource Program (FARRP) Allergen Protein Database (version 8.00; allergenonline.com) containing 1313 entries was utilized for all bioinformatics assessments of potential allergenicity. These 1313 entries are comprised of known or putative food, respiratory, venom/salivary, or contact allergenic proteins. Glutenins and gliadins from *Triticum aestivum* L. (bread wheat) were included in the database if there was published evidence of immunoglobulin E (IgE) from sera of allergic individuals binding to the glutenin or gliadin in question. Some of these same glutenins and gliadins are involved in Celiac disease, although that disease is a non-IgE-mediated disorder. All allergen database entries have been vetted by a panel of seven academic allergy experts based on published evidence of allergenicity.

The GenBank non-redundant peptide sequence database was utilized for all bioinformatics assessments of potential toxicity. The GenBank non-redundant peptide sequence data (a total of 7,155,275 sequences) was downloaded October 26, 2008 from the National Center for Biotechnology Information (NCBI) website. This database is comprised of all non-redundant GenBank coding sequence translations, protein sequences from NCBI's Reference Sequence Project, sequences derived from the Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, the Protein Information Resource (PIR) Protein Sequence Database, and the Protein Research Foundation (PRF) Protein Sequence Database.

Database search for eight-amino acid regions of identity. Each protein sequence was submitted to an analysis using a custom comparison (word-match) program which provides an exhaustive search of all possible eight-amino acid subsegments of the query protein against all possible eight-amino acid segments in proteins in the FARRP Allergen Protein Database. Regions of at least eight consecutive amino acids which are identical between a submitted protein and a known allergen will be identified by this search.

This eight-amino acid search was originally suggested based on the concept that eight or more amino acids is a representative minimal size for an IgE-binding epitope (Metcalf *et al.*, 1996). Bannon and Ogawa (2006) compiled a list of characterized linear IgE-binding epitopes from major allergens and, although one epitope from a wheat ω -5 gliadin was only four amino acids long, the majority of characterized epitopes were indeed eight amino acids or longer. However, this search does not detect conformational epitopes which are formed when non-linear amino acids are brought together by the higher-order folding of the protein. Moreover, the utility of such an eight-amino acid analysis has been questioned due to the high rate of false positives identified by this search (Silvanovich *et al.*, 2006; Hileman *et al.*, 2002).

Database search with eighty-amino acid segments of query sequence. The deduced amino acid sequence of ahasl (R272K, S653N) was subdivided into all possible overlapping 80-amino acid segments while the deduced amino acid sequence of SEC61 γ was analyzed as a single intact sequence since it was shorter than 80 amino acids. Each of these 80-amino acid segments or, in the case of SEC61 γ , the entire protein sequence was compared *in silico* to all proteins in the FARRP Allergen Protein Database via a protein-protein FASTA (version 34.26.5; April 26, 2007) analysis. The default parameters of the FASTA program were used, including the default substitution scoring matrix of BLOSUM 50, with one exception: the threshold score for optimization was set to 20.

Since the total protein sequence was analyzed incrementally in 80 amino acid segments, the query length for each of the ahasl (R272K, S653N) analyses was 80 amino acids. Thus, the percent identity for a given alignment was determined by dividing the number of identical amino acids within the alignment by 80. In the case of SEC61 γ , which has a sequence length of less than 80 amino acids, the number of identical amino acids was still divided by 80 to determine the percent identity over 80 amino acids. In instances where

gaps were inserted into the query sequence to achieve the optimal alignment, percent identity was calculated by dividing the number of identical amino acid residues in the alignment by the alignment length of overlap if the overlap length was greater than 80. A query protein which showed >35% identity to a known or putative allergen would be identified as potentially requiring additional studies, on a case-by-case basis, to determine the likelihood of the protein being allergenic (Codex, 2003).

Database search for homology to known protein toxin sequences. Each protein sequence was submitted to a protein-protein Basic Local Alignment Search Tool (BLASTP), (NCBI version 2.2.18) analysis. All parameters were left at the default setting for this BLASTP analysis with the exception of the expect (E) value cut-off which was set to one. Thus, either the top 250 unique protein alignments (the default value) or all alignments with an E value less than one, whichever is fewer, were analyzed. This BLASTP analysis will identify regions of local similarity (i.e. similarity over a portion of the protein sequence rather than the entire protein sequence) between the query protein sequence [either ahasl (R272K, S653N) or SEC61 γ] and proteins in the downloaded October 26, 2008 GenBank non-redundant peptide sequence database.

Descriptions of the 250 proteins from the GenBank non-redundant database which show the most significant local homology to ahasl (R272K, S653N) were manually compared to known toxins which act on humans as listed in the United States Code of Federal Regulations ([40 CFR Part 725.421](#)). Only 123 proteins in the GenBank non-redundant database had an E value less than one when SEC61 γ was used as a query sequence. Descriptions of these 123 proteins were manually compared to known toxins which act on humans as listed in the United States Code of Federal Regulations ([40 CFR Part 725.421](#)).

RESULTS AND DISCUSSION

Database search for eight-amino acid regions of identity. The submitted protein sequences did not share a sequence of eight or more consecutive identical amino acids with any potential allergens found in the FARRP Allergen Protein Database. Because the eight-amino acid word-match search did not identify any common identical sequences of eight or more amino acids, there are no search results to report.

Database search with eighty-amino acid segments of query sequence. The analyzed proteins did not show 35% or greater identity over 80 amino acids to any potential allergens found in the FARRP Allergen Protein Database. The allergen homology search results for the ahasl (R272K, S653N) 80-amino acid segment which showed the highest homology to a known or potential allergen are shown in Appendix 1. The allergen homology search results for SEC61 γ are also shown in Appendix 1.

Database search for homology to known protein toxin sequences. The submitted protein sequences did not show significant homology to proteins that are toxic to humans as

listed in the United States Code of Federal Regulations ([40 CFR Part 725.421](#)). The toxin homology search results are shown in Appendix 2.

CONCLUSIONS

The transgene insert of BPS-CV127-9 contains the coding sequences for two proteins from *A. thaliana*: ahas1 (R272K, S653N) and SEC61 γ . In this study, the two protein sequences were subjected to a bioinformatics analysis as part of a weight-of-evidence assessment of the potential allergenicity and toxicity of the proteins encoded within the BPS-CV127-9 transgene insert sequence. Neither sequence showed significant homology to a known protein toxin as defined in the United States Code of Federal Regulations ([40 CFR Part 725.421](#)). Neither sequence showed 35% or greater identity over 80 amino acids to a potential allergen. And finally, neither sequence shared a sequence of eight or more consecutive identical amino acids with a potential allergen. Thus, the bioinformatics analyses of the ahas1 (R272K, S653N) and SEC61 γ -subunit proteins encoded within the BPS-CV127-9 transgene insert sequence do not provide any indication of a potential allergenicity or toxicity concern.

RECORDS RETENTION

Search records, the original copy of this report, and other relevant records are archived at BASF, 26 Davis Drive, Research Triangle Park, North Carolina 27709 U. S. A.

STUDY PERSONNEL

Bioinformatics scripts utilized for the work reported herein were written by [REDACTED], Ph.D., and [REDACTED], M.S., BASF Plant Science L. L. C., 26 Davis Drive, Research Triangle Park, North Carolina 27709.

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Figure 1. Deduced Amino Acid Sequence of Arabidopsis ahasl (R272K, S653N)

The deduced amino acid sequence of ahasl (R272K, S653N) from BPS-CV127-9 is shown below.

```

1  MAAATTTTTT SSSISFSTKP SPSSSKSPLP ISRFSLPFSL NPNKSSSSSR
51  RRGIKSSSPS SISAVLNNTT NVTTPSPPTK PTKPETFISR FAPDQPRKGA
101 DILVEALERQ GVETVFAYPG GASMEIHQAL TRSSSIRNVL PRHEQGGVFA
151 AEGYARSSGK PGICIATSGP GATNLVSGLA DALDSVPLV AITGQVPRRM
201 IGTDAFQETP IVEVTRSITK HNYLVMDVED IPRIIEEAFF LATSGRPGPV
251 LVDVPKDIQQ QLAIPNWEQA MKLPGYMSRM PKPPEDSHLE QIVRLISESK
301 KPVLYVGGGC LNSSDELGRF VELTGIPVAS TLMGLGSYPC DDELSLHMLG
351 MHGTVYANYA VEHSLLLLAF GVRFDDRVTG KLEAFASRAK IVHIDIDSAE
401 IGKNKTPHVS VCGDVKLALQ GMNKVLENRA EELKLDFGVW RNELNVQKQK
451 FPLSFKTFGE AIPPQYAIKV LDELTDGKAI ISTGVGQHQM WAAQFYNKYK
501 PRQWLSSGGL GAMGFGLPAA IGASVANPDA IVVDIDGDGS FIMNVQELAT
551 IRVENLPVKV LLLNNQHLGM VMQWEDRFYK ANRAHTFLGD PAQEDEIFPN
601 MLLFAAACGI PAARVTKKAD LREAIQTMLD TPGPYLLDVI CPHQEHVLP
651 IPNGGTFNDV ITEGDGRIKY

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Figure 2. Deduced Amino Acid Sequence of Arabidopsis SEC61 γ

The deduced amino acid sequence of SEC61 γ from BPS-CV127-9 is shown below.

```
1 MEAIDSAIDP LRDFAKSSVR LVQRCHKPDR KEFTKVAVRT AIGFVVMGFV
51 GFFVKLVFIP INNIIVGSS
```

APPENDIX 1. 80-AMINO ACID ALLERGEN HOMOLOGY SEARCH RESULTS

Typical output from the FASTA search of an allergen database using either an 80-amino acid segment from ahasl (R272K, S653N) or the entire 69-amino acid sequence of SEC61 γ as the query sequence is shown below in Appendix 1.

The highest observed percent identity to a known or putative allergen for any 80-amino acid segment of ahasl (R272K, S653N) was 33.75%. Four different 80-amino acid segments from ahasl (R272K, S653N) shared 33.75% identity with the putative allergen Tyr p 13 [GenInfo identifier (GI): 51860756], a putative fatty acid-binding protein from the mite *Tyrophagus putrescentiae* (Jeong *et al.*, 2005). Only the FASTA search result from the first of these four 80-amino acid segments of ahasl (R272K, S653N), corresponding to amino acids 352 through 431, is shown here in Appendix 1. The ahasl (R272K, S653N) alignment which shows 33.75% identity is highlighted in yellow on page 16; this alignment contained 27 identical amino acids over the length of the 80-amino acid ahasl segment.

When the entire 69-amino acid SEC61 γ sequence was used as the query sequence in a FASTA analysis, the highest observed percent identity to a known or putative allergen was 18.75%. In this alignment, highlighted in yellow on page 25, SEC61 γ shared 15 identical amino acids with allergen Ole e 1 from *Olea europaea* (common olive), (GI number: 1362130), (Villalba *et al.*, 1994). Because the query length was normalized to 80 amino acids to determine the percent identity, the calculated percent identity for this alignment is 15/80 or 18.75%.

FASTA searches a protein or DNA sequence data bank version 34.26.5 April 26, 2007

Please cite:

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

ahasl.R272K.S653N 352-431, 80 aa

vs /n/na4/bioinfo/refsets/PUB_AllergenOnline12Dec2007_V8.fasta library

292011 residues in 1313 sequences

Expectation_n fit: rho(ln(x))= 2.5793+/-0.00366; mu= 16.8140+/- 0.191

mean_var=42.0176+/-11.266, 0's: 8 Z-trim: 8 B-trim: 101 in 2/42

Lambda= 0.197860

FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2

join: 36, opt: 20, open/ext: -10/-2, width: 16

The best scores are:

					opt bits	E(1313)	%_id	%_sim	alen
gi 60280803	gi 60280803	gb AAX18294 (160)			59	22.8	2.3	0.228	0.667 57
gi 51860756	gi 51860756	gb AAU11502 (131)			56	21.8	3.8	0.346	0.551 78
gi 60280823	gi 60280823	gb AAX18304 (159)			56	21.9	4.2	0.228	0.632 57
gi 60280825	gi 60280825	gb AAX18305 (159)			56	21.9	4.2	0.228	0.632 57
gi 14285797	gi 14285797	sp O61379.1 (274)			57	22.6	4.6	0.269	0.615 52
gi 125995167	gi 125995167	dbj BAF47 (284)			57	22.6	4.6	0.269	0.615 52
gi 125995169	gi 125995169	dbj BAF47 (284)			57	22.6	4.6	0.269	0.615 52
gi 2660868	gi 2660868	gb AAC48288.1 (284)			57	22.6	4.6	0.269	0.615 52

gi 125995171	gi 125995171 dbj BAF47	(284)	57	22.6	4.6	0.269	0.615	52
gi 14285796	gi 14285796 sp O44119.1	(284)	57	22.6	4.6	0.269	0.615	52
gi 19338630	gi 19338630 gb AAL86739	(448)	58	23.2	4.8	0.230	0.557	61
gi 60280827	gi 60280827 gb AAX18306	(159)	54	21.4	6.2	0.214	0.643	70
gi 2739154	gi 2739154 gb AAC67308.1	(191)	54	21.5	6.9	0.298	0.526	57
gi 1531589	gi 1531589 gb AAB09632.1	(631)	57	23.2	7	0.588	0.765	17
gi 729764	gi 729764 sp P40918.1 HSP	(643)	57	23.2	7	0.237	0.593	59
gi 26190140	gi 26190140 emb CAD2055	(179)	53	21.1	8.1	0.292	0.492	65
gi 729979	gi 729979 sp P39673.1 MAG	(341)	54	21.9	9.2	0.260	0.560	50
gi 7024506	gi 7024506 gb AAF35431.1	(264)	53	21.4	9.9	0.269	0.596	52
gi 59800145	gi 59800145 sp P69198.1	(83)	50	19.7	9.9	0.230	0.554	74
gi 59800146	gi 59800146 sp P69199.1	(83)	50	19.7	9.9	0.230	0.554	74

>>>ahasl.R272K.S653N_352-431, 80 aa vs

/n/na4/bioinfo/refsets/PUB_AllergenOnline12Dec2007_V8.fasta library

>>gi|60280803 gi|60280803|gb|AAX18294.1| major allergen (160 aa)
initn: 26 initl: 26 opt: 59 Z-score: 94.9 bits: 22.8 E(): 2.3
Smith-Waterman score: 59; 22.807% identity (66.667% similar) in 57 aa overlap
(10-66:75-129)

```

gi|602 MGVTYETETFTSVIPAPRLFKAFILDGDNLPKIAPQAIKSTEIIIEGDGGVGTIKKVTFG
      10      20      30      40      50      60
      10      20      30      40      50
ahasl. HGTVYANYAVEHSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKT
      ..... : .. ::: .. ..... : ... : .. :
gi|602 EGSQYGYVKQVRVNGIDKDNFTYSYSMIEGDTLSDKLEKITYETKLI-ASPDGGSIIKT-T
      70      80      90      100     110
      60      70      80
ahasl. PHVSVC GDVKLALQGMNKVLENRAE
      : . : : : .
gi|602 SHYHAKGDVEIKEEHVKAGKEKASGLFKLLEAYLVANPDAYN
      120     130     140     150     160

```

>>gi|51860756 gi|51860756|gb|AAU11502.1| fatty acid-bidi (131 aa)
initn: 34 initl: 34 opt: 56 Z-score: 91.1 bits: 21.8 E(): 3.8
Smith-Waterman score: 56; 34.615% identity (55.128% similar) in 78 aa overlap
(7-80:7-76)

```

      10      20      30      40      50
ahasl. HGTVYANYAVEHSDLLLA----GVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKTP
      .: :.: : . : : : : : : : : : : : : : : : : : : :
gi|518 MVQLNGSYKLEKSDNFDAFLKELGVNF---VTRNLAKSASPTVEVIVDGDSTYTI---KTS
      10      20      30      40      50
      60      70      80
ahasl. HVSVC GDVKLALQGMNKVLENRAE
      . : : : : : : : : : : : : : : :
gi|518 STLKNSEIKFKL-G-EEFEEDRADGKKVQTSVTKEGDNKLVQVQKGDKPVTIVREFSEEG
      60      70      80      90      100     110
gi|518 LTVTATVNGVTSVRFYKRQ
      120     130

```

>>gi|60280823 gi|60280823|gb|AAX18304.1| major allergen (159 aa)
initn: 24 initl: 24 opt: 56 Z-score: 90.3 bits: 21.9 E(): 4.2
Smith-Waterman score: 56; 22.807% identity (63.158% similar) in 57 aa overlap
(10-66:75-128)

gi | 602 MGVLTYET EYASVIPPARLYNALVLDADNLIPKIAPQAVKTVEILEGDDGGVGTIKKVSFG
10 20 30 40 50 60

ahas1. HGTVYANYAVEHSDLLLAFGVRFD¹⁰DRVTGKLEAFASRAKIVHIDIDS²⁰AEIGKNKT³⁰
:::
:::
:::
:::
:::
:::
:::
:::
:::
:::

gi|602 EGSEYSYVKHKVEGIDKDNFVYSYNLIEGDAISDKIEKISYEIKLVASG--SGSIIKNIS
70 80 90 100 110

```

          60          70          80
ahas1. PHVSVCGDVKLALQGMNKVLENRAE
      :  .  : : : .

```

gi|602 -HYHTKGDVEIKEEHVKAGKERAHGLFKLIENHLVANPDAYN
120 130 140 150

```
>>gi|60280825 gi|60280825|gb|AAX18305.1| major allergen (159 aa)
  initn: 24 initl: 24 opt: 56 Z-score: 90.3 bits: 21.9 E(): 4.2
Smith-Waterman score: 56; 22.807% identity (63.158% similar) in 57 aa overlap
(10-66:75-128)
```

gi | 602 MGVLTYET EYASVIPPARLYNALVLDADNLIPKIAPQAVKTVEILEGDDGGVGTIKKVSFG
10 20 30 40 50 60

ahas1. HGTVYANYAVEHSDLLLAFGVRFD RVTGKLEAFASRAKIVHIDIDS AEIGKNKT

gi|602 EGSEYSYVKHKVEGIDKDNFVYSYSLIEGDAISDKIEKISYEIKLVASG--SGSIKKNIS
70 80 90 100 110

```

          60          70          80
ahas1. PHVSVCGDVKLALQGMNKVLENRAE
      :  .  : : : .

```

gi|602 -HYHTKGDVEIKEEHVKAGKERAHGLFKLIENHLVANPDAYN
120 130 140 150

```
>>gi|14285797 gi|14285797|sp|O61379.1|TPM_PANST Tropomyo (274 aa)
  initn: 37 initl: 37 opt: 57 Z-score: 89.7 bits: 22.6 E(): 4.6
Smith-Waterman score: 57; 26.923% identity (61.538% similar) in 52 aa overlap
(29-79:73-124)
```

```

                                     10
ahasl.                                HGTVYANYAVEHSDLL

```

gi | 142 MKLEKDNAMDRADTLEQQNKEANIRAEKAEFEVHNLQKRMQQLENDLDQVQESLLKANTQ
10 20 30 40 50 60

 20 30 40 50 60 70

aHasI.LAFGVRFDDRVTGKLEAFA~~SRAKIVHIDIDSAEIGKNK-TPHVSVCGDVKLALQGMNKVL~~

: : : : : : : : : : : : : :

gi|142 LEEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAADESERMRKVL
70 80 90 100 110 120

```

      80
ahas1. ENRAE
      :::

```

gi | 142 ENRSLSDEERMDALENQLKEARFLAAEADRKYDEVARKLAMVEADLERAEERAETGESKF
130 140 150 160 170 180

gi|142 VELEEEELRVVGNLKSLEVSEEEKANQREEAYKEQIKTLTNKLKAAEARAFAERSVQKLQ
190 200 210 220 230 240

gi|142 KEVDRLEDELVNEKEKYKSITDELDQTFSELSGY
250 260 270

Smith-Waterman score: 57; 26.923% identity (61.538% similar) in 52 aa overlap
(29-79:83-134)

```
ahasl.                                     HGTVYA

gi|266 MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANIRAEKSEEEVHNLQKRMQQLENDLDQV
      10      20      30      40      50      60
      10      20      30      40      50      60
ahasl. NYAVEHSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNK-TPHVSVCQDVK
      :.. :. : .... :.. :. : : ... ...
gi|266 QESLLKANTQLEEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
      70      80      90      100     110     120
      70      80
ahasl. LALQGMNKVLENRAE
      . : : : : .
gi|266 DESERMRKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
      130     140     150     160     170     180
gi|266 ERAETGESKIVELEEEELRVVGNNLKSLEVSSEKANQREEAYKEQIKTLANKLKAAEARAE
      190     200     210     220     230     240
gi|266 FAERSVQKLQKEVDRLDELVNEKEKYKSITDELDTQTFSELSGY
      250     260     270     280
```

>>gi|125995171 gi|125995171|dbj|BAF47269.1| tropomyosin (284 aa)
initn: 37 initl: 37 opt: 57 Z-score: 89.5 bits: 22.6 E(): 4.6
Smith-Waterman score: 57; 26.923% identity (61.538% similar) in 52 aa overlap
(29-79:83-134)

```
ahasl.                                     HGTVYA

gi|125 MDAIKKKMQAMKLEKDNAMDRAHTLEQQNKEANLRAEKTEEEIRATQKKMQQIENELDHA
      10      20      30      40      50      60
      10      20      30      40      50      60
ahasl. NYAVEHSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNK-TPHVSVCQDVK
      :.. :. : .... :.. :. : : ... ...
gi|125 QEQLSAANTKLDKEKALQNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
      70      80      90      100     110     120
      70      80
ahasl. LALQGMNKVLENRAE
      . : : : : .
gi|125 DESERMRKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
      130     140     150     160     170     180
gi|125 ERAESGESKIVELEEEELRVVGNNLKSLEVSSEKANQREETYKEQIKTLANKLKAAEARAE
      190     200     210     220     230     240
gi|125 FAERSVQKLQKEVDRLDELVNEKEKYKNIADEMDQAFSELSGF
      250     260     270     280
```

>>gi|14285796 gi|14285796|sp|O44119.1|TPM_HOMAM Tropomyo (284 aa)
initn: 37 initl: 37 opt: 57 Z-score: 89.5 bits: 22.6 E(): 4.6
Smith-Waterman score: 57; 26.923% identity (61.538% similar) in 52 aa overlap
(29-79:83-134)

ahasl. HGTVYA

gi|142 MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANIRAEKTEEEIRITHKKMQQVENELDQV
10 20 30 40 50 60

10 20 30 40 50 60
ahasl. NYAVEHSDLLLAFGVRFDDRVTKGLEAFASRAKIVHIDIDSAEIGKNK-TPHVSVCQDVK
... .. : : : : : : : : : : : : : : : :
gi|142 QEQLSLANTKLEEKEKALQNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
70 80 90 100 110 120

70 80
ahasl. LALQGMNKLLENRAE
. : : : : :
gi|142 DESERMKRVLENRSLDEERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
130 140 150 160 170 180

gi|142 ERAETGESKIVELEELRVVGNNLKSLEVSSEKANQREEAYKEQIKTLANKLKAAEARAE
190 200 210 220 230 240

gi|142 FAERSVQKLQKEVDRLEDELVNEKEKYKSITDELDTFSELSGY
250 260 270 280

>>gi|19338630 gi|19338630|gb|AAL86739.1|AF441864_1 48-kD (448 aa)
initn: 63 initl: 40 opt: 58 Z-score: 89.2 bits: 23.2 E(): 4.8
Smith-Waterman score: 58; 22.951% identity (55.738% similar) in 61 aa overlap
(2-59:277-337)

gi|193 MLPKEDPELKCKKHKCRDERQFDEQQRRDGKQICEEKARERQQEEGNSSEESYGKEQEEN
10 20 30 40 50 60

gi|193 PYVFQDEHFESRVKTEEGRVQVLENFTKRSRLLSGIENFRLAILEANPHTFISPAPHFAE
70 80 90 100 110 120

gi|193 LVLFAVGRATITMVREEKRESFNVEHGDIIIRIPAGTPVYMINRDENEKLFIVKILQPVVS
130 140 150 160 170 180

gi|193 APGHFEAFYGAGGEDPESFYRAFSWEVLEAALKVRREQLEKVFGEQSKGSIVKASREKIR
190 200 210 220 230 240

10 20
ahasl. HGTVYANYAVEHSDLL-LAFGVRFDD
: : : : : : : : : : : : : : : :
gi|193 ALSQHEEGPPRIWPFGESESGPINLLHKHPSQSNQFGRLYEAHPDDHKQLQDLMLVSFA
250 260 270 280 290 300

30 40 50 60 70 80
ahasl. DRVTGKLEA--FASRAKIVHIDIDSAEIGKNKTPHVSVCQDVKLALQGMNKLLENRAE
. : : : : : : : : : : : : : : : :
gi|193 NITKGSMAOPYNSRATKISVVVEGEGFFEMACPHLSSSSGSYQKISARLRGVVVFVAPA
310 320 330 340 350 360

gi|193 GHPVAVIASQNNNLQVLCFEVNAHGNSRFPLAGKGNIVNEFERDAKELAFNLPSREVERI
370 380 390 400 410 420

gi|193 FKNQDQAFFFPNPKQEEGGRGGRAFE
430 440

>>gi|60280827 gi|60280827|gb|AAX18306.1| major allergen (159 aa)
initn: 24 initl: 24 opt: 54 Z-score: 87.2 bits: 21.4 E(): 6.2
Smith-Waterman score: 54; 21.429% identity (64.286% similar) in 70 aa overlap
(10-79:75-140)

gi | 602 MGVLTYET EYASVIPPARLYNALVLDADNLIPKIAPQAVKTVEILEGDDGGVGTIKKVSFG
10 20 30 40 50 60

ahas1. HGT VYANYAVEHS D LLLAF GVR FDDRVTG KLEAFA SRAKIVH IDIDS A EIGKNKT

gi|602 EGSEYSYVKHKVEGIDKDNFVYSYSLIEGDAISDKIQKISYEIKLVASG--SGSIKKNIS
70 80 90 100 110

```

          60          70          80
ahas1. PHVSVCGDVKLALQGMNKVLENRAE
          :  .  :::.  ...  :  .  ::
gi|602 -HYHTKGDVEIKEENV-KAGKERAHGLFKLIENHLVANPDAYN
          120        130        140        150

```

```
>>gi|2739154 gi|2739154|gb|AAC67308.1| 22.6 kDa tegument (191 aa)
  initn: 31 init1: 31 opt: 54 Z-score: 86.5 bits: 21.5 E(): 6.9
Smith-Waterman score: 54; 29.825% identity (52.632% similar) in 57 aa overlap
(22-73:54-110)
```

```

                                     10      20
ahas1.                             HGTVYANYAVEHSDLLAFGVRFDDRVT
                                     :::
gi|273 MATTEYRLSLMEQFIRAFIEIDKDNNELIDKQELTKYCQQNQMDMKQIDPWIARFDTDKD
               10      20      30      40      50      60
```

```

          30          40          50          60          70          80
ahas1.  GK--LEAFASR--AKIVHIDIDSAEIGKNKTPHVSVCG-DVKLALQGMNKVLENRAE
        ::  ::  :      :.  .  .  .  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi|273  GKVSLEEFRCRGLKQVWEVRREKEELKKDKEGKVSTLPDIIQIIAATMSKAKQYNICCKF
          70          80          90          100         110         120

```

gi | 273 KELLDKTSRTGDEVRAVANDLKAFLDSEYGRVWQVIILTGSYWMNFSHEPFLSMQFKYSN
130 140 150 160 170 180gi|273 YVCLLW RTPSS
190

```
>>gi|1531589 gi|1531589|gb|AAB09632.1| allergen [Peripla (631 aa)
initn: 45 initl: 45 opt: 57 Z-score: 86.3 bits: 23.2 E(): 7
Smith-Waterman score: 57; 58.824% identity (76.471% similar) in 17 aa overlap
(42-58:5-20)
```

```

          10          20          30          40          50          60
ahas1. HGTVYANYAVEHSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSV
          :  ::  ::::  :  ::
gi|153          DIGDHYDIE-ANIGHYKYPHVVK
          10          20

```

```
              70          80
ahasl. CGDVKLALOGMNVLENRAE
```

gi|153 NFISYYKKGLLP³⁰RGEPFSVYYEKHRE⁴⁰QAIKLFELFFA⁵⁰ANDYDTFYKTACWARD⁶⁰RVNEG⁷⁰MF⁸⁰gi|153 MYALTVAAFHREDTKDLVLPPPYEVNPLYFVEDDVIQQAYKYWTKESGTDKHVEHVIPVN
90 100 110 120 130 140gi|153 FTARSQEDLVAYFREDVDLNAFNMYFRIYPSWFNTTLYGKSFDRRGEQFYTYHQIYAR
150 160 170 180 190 200

gi|153 YFLERLSNSLPDVKPFQYSKPLKTGYNPHLRYHNGEEMPARPSNMYPTNFDLIFYVSDIKN
210 220 230 240 250 260gi|153 YERRVEKAIDFGYAFDEHRTPYSLYHDQHGMMDYLGQMIEGTRNSPHQYFYGVSFHFYRLL
270 280 290 300 310 320gi | 153 VGHVVDPPYHKNGLAPSALEHPQTALRDPAFYQLWKRIDHIVQKYKNRLPRYTYDELSFPG
330 340 350 360 370 380gi|153 VKIENVDVGKLYTYFEHFEHSLGNAMYLGKLEDYMKASIRARHYRLNHKPFITYNIEVSSD
390 400 410 420 430 440gi|153 KAQDVYVRIFLGPKYDSLGECELDERRHYFVEMDRFVHKVEAGKTVIERKSHDSSIISD
450 460 470 480 490 500gi|153 SHDSYRNLFFKKVSDALQEKDQYYIDKSHKYCGYPENLLLPGKKGQTFTFYVIVTPYVK
510 520 530 540 550 560gi | 153 QDEHDFEPYHYKAFSYCGVGHGRKYPDDKPLGFPFDRKIHDFYFYPNMYFKDQVVI FHKK
570 580 590 600 610 620gi|153 YDEVHDTVH
630

```
>>gi|729764 gi|729764|sp|P40918.1|HSP70_CLAHE Heat shock (643 aa)
  initn: 31 init1: 31 opt: 57 Z-score: 86.3 bits: 23.2 E(): 7
Smith-Waterman score: 57; 23.729% identity (59.322% similar) in 59 aa overlap
(2-60:10-65)
```

```

          10          20          30          40          50
ahas1.      HGTVYANYAVEHSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSDAEIGK
             :::: ..:: . . . .::: . .::: . . . .:::
gi|729  MAPAIGIDLGTTYSCVGIYRDDRIEIIANDQGNRTTSPFVAFDTDERLIG---DSAKNQV
             10          20          30          40          50

```

```

          60          70          80
ahas1. NKTPHVSVC GDVKLALQGMNKVLENRAE
      .::.:
gi|729 AINPHNTVFD AAKRLIGRK FQDAEVQADM KHFFPKVIEKAGK PVTQVEFKGETKD FTFPEEI
          60          70          80          90          100          110

```

gi | 729 SSMILTKMRETAESYLGGTVNNNAVITVPAYFNDSQRQATKDAGLIAGLNLVRIINEPTAA
120 130 140 150 160 170

gi|729 AIAYGLDKKQEGEKNVLIFDLGGGTFDVSFLTIEEGIFEVKSTAGDTHLGGEDFDNRLVN
180 190 200 210 220 230gi | 729 HFSNEFKRKHKDLSDNARALRRLRTACERAKRTLSSSAQTSIEIDSLFEGIDFFTSNTR
240 250 260 270 280 290gi | 729 ARFEEVGQDLFRGNMEPGERTLRDDKIDKSSVHEIVLGGGSTRIPKVQKLVSDFNGKEP
300 310 320 330 340 350gi | 729 CKSINPDEAVAYGA AVQA ILSGDTSSKSTKE ILLLDVAPLSLGIETAGGVMTALIKRNT
360 370 380 390 400 410gi | 729 TIPTKKSETFSTFSDNQPGVLIQVFEGEARTKDINLMGKFELSGIRPAPRGVPEIETF
420 430 440 450 460 470gi|729 DLDANGIMNVSALEKGTGKTNKIVITNDKGRLSKEEIERMLADA EKYKEEDEAEAGRIQA
480 490 500 510 520 530

gi | 729 KNGLESYAYS LKNTVSDPKVEEKLSAEDKETLTGAIDKTVAWIDENQTATKEEYEAQKQ
540 550 560 570 580 590

gi|729 LESVANPVMMKIYGAEGGAPGGMPGQAGAPPPGAGDDGPTVEEVD
600 610 620 630 640

```
>>gi|26190140 gi|26190140|emb|CAD20556.1| putative inver (179 aa)
  initn: 29 initl: 29 opt: 53 Z-score: 85.2 bits: 21.1 E(): 8.1
Smith-Waterman score: 53; 29.231% identity (49.231% similar) in 65 aa overlap
(15-79:15-72)
```

```

          10          20          30          40          50          60
ahas1. HGTVYANYAVEHSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDS AEIGKNKTPHVSV
          ::  . : : : . : : . : . : : . : . : : . : . : : . : .
gi|261 MKLSFSLCIIFFNLLLLQAVISADIVQGTCKKVAQRSPNPNYDFCVKSLGADPKSHTA-
          10          20          30          40          50

```

```

              70              80
ahas1. CGDVKLALQGMNKVLENRAE
              : : : : . . : :
gi|261 --D----LQGLGVISANLAIQHGSKIQTFIGRILKSKVDPALKKYLNDCVGLYADAKSSV
              60              70              80              90             100             110

```

gi | 261 QEAIADFKSKDYASANVKMSAALDDSVTCEDGFKEKKGIVSPVTKENKDYVQLTAISLAI
120 130 140 150 160 170

gi | 261 TKLLGA

```
>>gi|729979 gi|729979|sp|P39673.1|MAG_DERFA Allergen Mag (341 aa)
  initn: 34 initl: 34 opt: 54 Z-score: 84.2 bits: 21.9 E(): 9.2
Smith-Waterman score: 54; 26.000% identity (56.000% similar) in 50 aa overlap
(4-53:169-214)
```

gi | 729 FVMKREPLRFRDITVEGNENAYIKNGKLHLSLMDPSTLSLVTKADGKIDMTVDLISPVTK
10 20 30 40 50 60gi | 729 RASLKIDSKYNYLFHEGELSASIVNPRLSWHQYTKRDSREYKSDVELSLRSSDIALKITM
70 80 90 100 110 120

```

                                     10
ahasl.                                HGTVYANYAVEHSDL
                                   . : : : :
gi|729 PDYNSKIHYSRQGDQINMDIDGTLIEGHAQGTTIREGKIHIKGRQTDFEIESNRYEDGKL
      130          140          150          160          170          180

```

```

          20          30          40          50          60          70
ahas1.  LLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVCGDVKLALQGMNKVL
          ..  :.  ..  :::.  :.  :.  ..  ..  :
gi|729   IIE-PVKSEN--GKLEGLVSRKVPSHLTLETPRVKMNMKYDRYAPVKVFKLDYDGIHFE
          190          200          210          220          230

```

80
ahasl. ENRAE

gi | 729 KHTDIEYEGVRYKIIINGKCLKDDGRHYSIDVQGIPKAFNLADLMDFKLVSKPEDSN
240 250 260 270 280 290

gi|729 KAQFSYTFNEYTETEEYEFDPHRAYYVNWLSSIRKYIQNFIVEDN
300 310 320 330 340

80 residues in 1 query sequences
292011 residues in 1313 library sequences
Scomplib [34.26]
start: Fri Dec 5 18:19:28 2008 done: Fri Dec 5 18:19:29 2008
Total Scan time: 0.110 Total Display time: 0.050

Function used was FASTA [version 34.26.5 April 26, 2007]

FASTA searches a protein or DNA sequence data bank version 34.26.5 April 26, 2007

Please cite:

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

SEC61gamma, 69 aa

vs /n/na4/bioinfo/refsets/PUB_AllergenOnline12Dec2007_V8.fasta library

292011 residues in 1313 sequences
Expectation_n fit: $\rho(\ln(x)) = 4.1578 \pm 0.00347$; $\mu = 4.8928 \pm 0.182$
mean_var=40.0471 \pm 12.490, 0's: 11 Z-trim: 11 B-trim: 76 in 1/43
Lambda= 0.202670

FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 36, opt: 20, open/ext: -10/-2, width: 16

The best scores are:

					opt	bits	E(1313)	%_id	%_sim	alen
gi 1362130	gi 1362130	pir F53806	m (136)		54	22.4	2.2	0.366	0.537	41
gi 633938	gi 633938	gb AAB30434.1	(265)		54	22.6	3.9	0.500	0.615	26
gi 548449	gi 548449	sp Q06478.1	PA1 (317)		53	22.3	5.5	0.200	0.629	35
gi 897647	gi 897647	gb AAB48072.1	(336)		52	22.0	7.1	0.237	0.579	38
gi 3319897	gi 3319897	emb CAA76841.	(585)		54	22.7	7.5	0.500	0.615	26
gi 6687188	gi 6687188	emb CAB64867.	(608)		54	22.8	7.8	0.500	0.615	26
gi 14423833	gi 14423833	sp Q9U6W0.1	(301)		51	21.7	7.9	0.206	0.618	34
gi 13195753	gi 13195753	gb AAB32652	(130)		47	20.4	8.8	0.341	0.512	41
gi 1336811	gi 1336811	gb AAB36119.1	(25)		40	17.9	9	0.667	0.750	12
gi 1362133	gi 1362133	pir G53806	m (136)		47	20.4	9.1	0.341	0.512	41
gi 1709545	gi 1709545	sp P51528.1	P (300)		50	21.4	9.7	0.237	0.579	38

>>>SEC61gamma, 69 aa vs

/n/na4/bioinfo/refsets/PUB_AllergenOnline12Dec2007_V8.fasta library

>>gi|1362130 gi|1362130|pir|F53806 major allergen OLE19 (136 aa)
initn: 47 init1: 47 opt: 54 Z-score: 95.3 bits: 22.4 E(): 2.2
Smith-Waterman score: 54; 36.585% identity (53.659% similar) in 41 aa overlap
(8-47:18-58)

	10	20	30	40
SEC61g	MEAIDSAIDPLRDFAK-SSVRLVQRCHKPDRKEFTKVAVRTAIGFVVMGF			
	:	:	:	:
gi 136	QFHIQGVYCDTCRAGFINELSEFIPGASVRLQCREKKNGDITFTEVGVTAEGLYSMLV			
	10	20	30	40
	50	60		
SEC61g	VGFFVKLVFIPINNIIVGSS			
gi 136	ERDHKNEFCEITLISSGRKDCNEIPIEGWAKPSLKFILNTVNGTTRTINPLGFYKKEALP			
	70	80	90	100
	110	120		
gi 136	KCAQVYNKLGMYPPNM			
	130			

>>gi|633938 gi|633938|gb|AAB30434.1| albumin [Canis fami (265 aa)
initn: 53 initl: 53 opt: 54 Z-score: 90.9 bits: 22.6 E(): 3.9
Smith-Waterman score: 54; 50.000% identity (61.538% similar) in 26 aa overlap
(12-36:19-44)

```

                10         20         30         40         50
SEC61g      MEAIDSAIDPLRDF-AKSSVRLVQRCHKPDRKEFTKVAVRTAIGFVVMGFVGF
                : : : : : : : : : : : : : : : :
gi|633 LSSAKERFKCASLQKFGDRAFKAWSVARLSQRFPAKADFAEISKVVTDLTQVHKECCCHGDL
                10         20         30         40         50         60

                60
SEC61g FVKLVFIPINNIIVGSS

gi|633 LECADDRADLAKYMCENQDSISTKLKECCDKPVLEKSQCLAEVERDELPGDLPSLAADFV
                70         80         90        100        110        120

gi|633 EDKEVCKNYQEAKDVFLGTFLYEYSRRHPEYSVSLLLRLAKEYEATLEKCCATDDPPTCY
                130        140        150        160        170        180

gi|633 AKVLDEFKPLVDEPQNLVKTNCELFEKLGEGYGFQNALLVRYTKKAPQVSTPTLVVEVSRK
                190        200        210        220        230        240

gi|633 LGKVGTKCCKKPESERMSCADDFLS
                250        260

```

>>gi|548449 gi|548449|sp|Q06478.1|PA11_DOLMA Phospholipa (317 aa)
initn: 48 initl: 48 opt: 53 Z-score: 88.2 bits: 22.3 E(): 5.5
Smith-Waterman score: 53; 20.000% identity (62.857% similar) in 35 aa overlap
(32-66:53-87)

```

                10         20         30
SEC61g      MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVR
                : : : : :
gi|548 RLIMFVGDPSSSNELDRFSVCPFSNDTVKMIFLTRENKHDFTYTLDTMNRHNEFKKSIK
                10         20         30         40         50         60

                40         50         60
SEC61g TAIGFVVMGFVGFVFKLVFIPINNIIVGSS
                . . . : . . . : . . . . .
gi|548 RPVVFITHGFTSSATEKNFVAMSEALMHTGDFLIIMVDWRMAACTDEYPGLKYMFYKAAV
                70         80         90        100        110        120

gi|548 GNTRLVGNFIAMIAKKLVEQYKVPMTNIRLVGHSLGAHISGFAGKRVQELKLGKFSEIIG
                130        140        150        160        170        180

gi|548 LDPAGPSFKKNDCSERICETDAHYVQILHTSSNLGTERTLTGTVDIFYINNGSNQPGCRYII
                190        200        210        220        230        240

gi|548 GETCSHTRAVKYFTECIRRECCLIGVPQSKNPQPVSKCTRNECVCVGLNAKKYPKRGSFY
                250        260        270        280        290        300

gi|548 VPVEAEAPYCNNGKII
                310

```

>>gi|897647 gi|897647|gb|AAB48072.1| allergen and phosph (336 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.2 bits: 22.0 E(): 7.1
Smith-Waterman score: 52; 23.684% identity (57.895% similar) in 38 aa overlap
(29-66:69-106)

10 20

SEC61g MEAIDSAIDPLRDFAKSSVR

gi|897 MEENMNLKYLLLLFVYFVQVLNCCYGHGDPLSYELDRGPKPCPFNSDVTVSI I I I ETRENRRND
10 20 30 40 50 60

SEC61α IVORCHKPDRKEFTKVAVRTAIGFVVMGFVGFVVKLVFIPINNIIVGSS

gi|897 LYTLQTLQNHPEFKKKTITRPVVFITHGFTSSASETNFINLAKALVDDKNYMVISIDWQT

gi|897 AACTNEAAGLKYLYPTAARNTRLVGQYIATITQKLVKHYKISMANIRLIGHSLGAHASG
130 140 150 160 170 180gi|897 FAGKKVQELKLGKYSEIIIGLDPARPSFDSNHC SERLCETDAEYVQIIH TSNYLGTEKTLG
190 200 210 220 230 240gi|897 TVDFYMNNGKNQPGCGRFFSEVCSHSRAVIYMAECIKHECCLIGIPKSKSSQPISSCTKQ
250 260 270 280 290 300

gi|897 ECVCVGLNAKKYPSRGSFYVPVESTAPFCNNKGKII
310 320 330

```
>>gi|3319897 gi|3319897|emb|CAA76841.1| albumin [Canis f (585 aa)
  initn: 53 init1: 53 opt: 54 Z-score: 85.7 bits: 22.7 E(): 7.5
Smith-Waterman score: 54; 50.000% identity (61.538% similar) in 26 aa overlap
(12-36:210-235)
```

gi | 331 MDTYKSEIAHRYNDLGEEHFRGLVLVAFSQYLQQCPFEDHVKLAKEVTEFAKACAAEESG
10 20 30 40 50 60gi | 331 ANCDKSLHTLFGDKLCTVASLRDKYGDMA DCCCKQEPDRNECFLAHKDDNPGFPPLVAPE
70 80 90 100 110 120gi | 331 PDRLCAAFQDNEQLFLGKYLYEIAARRHPYFYAPELLYYAQQYKGVFAECCQAADKAACLG
130 140 150 160 170 180

SEC61g MEAIDSAIDPLRDF-AKSSVRLVQRCHKPDRKEFTKVAVRTA

gi | 331 PKTEALREKVL LSSAKERFKCASLQKFGDRAFKAWSVARLSQRFPKADFAEISKVVTDLT
190 200 210 220 230 240

50 60
SEC61α IGFVVMGFVGFFVKLVFIPINNIIVGSS

gi | 331 KVVHKECCHGDLLECADDRADLAKYMCENQDSISTKLKECCDKPVLEKSQCLAEVERDELDP
250 260 270 280 290 300gi | 331 GDLPSLAADFVEDKEVCKNYQEAQDAFLGTFLYEYSRRRHPEYSVSLLLLRLAKEYEATLEK
310 320 330 340 350 360

gi | 331 CCATDDPPTCYAKVLDEFKPLVDEPQNLVKTNCELFEKLGEYGFQNALLVRYTKKAPQVS
370 380 390 400 410 420

gi | 331 TPTLVEVSRKLGKVGTKCKKPESEMSCADDFLSVVLNRLCVLHEKTPVSESVTKCCSE
430 440 450 460 470 480

gi | 331 SLVNRPPCFSGLEVDETYVPKEFNAETFTTFHADLCTLPEAEKQVKKQTALVELLKHKPKA
490 500 510 520 530 540

gi|331 TDEQLKTVMGDFGAFVEKCCAAENKEGCFSEEGPKLVAAAQAALV
550 560 570 580

>>gi|6687188 gi|6687188|emb|CAB64867.1| albumin [Canis f (608 aa)
initn: 53 init1: 53 opt: 54 Z-score: 85.5 bits: 22.8 E(): 7.8
Smith-Waterman score: 54; 50.000% identity (61.538% similar) in 26 aa overlap
(12-36:233-258)

gi|668 MKWVTFISLFFLFSSAYSRLVRREAYKSEIAHRYNDLGEEHFRGLVLVAFSQYLQQCPF
10 20 30 40 50 60

gi|668 EDHVKLAKKEVTEFAKACAAEESGANCDKSLHTLFGDKLCTVASLRDKYGMADCCCKQEP
70 80 90 100 110 120

gi|668 DRNECFLAHKDDNPGFPPLVAPEPDALCAAFQDNEQLFLGKYLIEIARRHPYFYAPELLY
130 140 150 160 170 180

SEC61g 10
MEAIDSAIDPLRDF-AKSS
: : :
gi|668 YAQQYKGVFAECCQAADKAACLGPKIEALREKVLLSSAKERFKCASLQKFGDRAFKAWSV
190 200 210 220 230 240

20 30 40 50 60
SEC61g VRLVQRCHKPDRKEFTKVAVRTAIGFVVMGFVGVFFVKLVFIPINNIIVGSS
.: : : : :
gi|668 ARLSQRFPKADFAEISKVVTDLTKVHKECCHGDLLECADDRADLAKYMCENQDSISTKLK
250 260 270 280 290 300

gi|668 ECCDKPVLEKSQCLAEVERDELPGDLPSLAADFVEDKEVCKNYQEAQDVFLGTFLEYEAR
310 320 330 340 350 360

gi|668 RHPEYSVSLLLRLAKEYEATLEKCCATDDPPTCYAKVLDEFKPLVDEPQNLVKTNCLEFE
370 380 390 400 410 420

gi|668 KLGEYGFQNALLVRYTKKAPQVSTPTLVEVSRKLGKVGTKCKKPESERMSCAEDFLSVV
430 440 450 460 470 480

gi|668 LNRLCVLHEKTPVSESVTKCCSESLVNRRCFSGLEVDETYVPKEFNAETFTFHADLCTL
490 500 510 520 530 540

gi|668 PEAQKQVKKQTALVELLKHKPKATDEQLKTVMGDFGAFVEKCCAAENKEGCFSEEGPKLV
550 560 570 580 590 600

gi|668 AAAQAALV

>>gi|14423833 gi|14423833|sp|Q9U6W0.1|PA1_POLAN Phosphol (301 aa)
initn: 47 init1: 47 opt: 51 Z-score: 85.4 bits: 21.7 E(): 7.9
Smith-Waterman score: 51; 20.588% identity (61.765% similar) in 34 aa overlap
(33-66:38-71)

SEC61g 10 20 30 40 50
MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIGFVVMGFVGVFFVK
: : : : :
gi|144 MSPDCTFNEKDIFVYVSRDKRDGIILKKETLTNYDLFTKSTISKQVFLIHGFLSTGN
10 20 30 40 50 60

60
SEC61g LVFIPINNIIVGSS
.: : : : :
gi|144 ENFVAMSKALIEKDDFLVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGVKQVADFTKL
70 80 90 100 110 120

gi|144 LVEKYKVLISNIRLIGHSLGAHTSGFAGKEVQKLKLGKYKEIIGLDPAGPYFHRSDCPDR
130 140 150 160 170 180

gi|144 LCVTDAEYVQVIHTSIILGVYYNVGSVDFYVNYGKNQPGCNEPSCSHTKAVKYLTECIKH
190 200 210 220 230 240

gi|144 ECCLIGTPWKKYFSTPKPISQCRGDTCCVGLNAKSYPARGAIFYAPVEANAPYCHNEGIK
250 260 270 280 290 300

gi|144 L

>>gi|13195753 gi|13195753|gb|AAB32652.2| main olive alle (130 aa)
initn: 43 initl: 43 opt: 47 Z-score: 84.6 bits: 20.4 E(): 8.8
Smith-Waterman score: 47; 34.146% identity (51.220% similar) in 41 aa overlap
(8-47:12-52)

10 20 30 40 50
SEC61g MEAIDSAIDPLRDFAK-SSVRLVQRCHKPDRKEFTKVAVRTAIGFVVMGFVGVFFVK
: : .: .::: . .: :::. : :.
gi|131 QVYCDTCRAGFITELSEFIPGASVRLQCKEKKNGDITFTEVGYTRAEGLYSMLVERDHKN
10 20 30 40 50 60

60
SEC61g LVFIPINNIIVGSS

gi|131 EFCEITLISSGSKDCNEIPTEGWAKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQVY
70 80 90 100 110 120

gi|131 NKLGMYPPNM
130

>>gi|1336811 gi|1336811|gb|AAB36119.1| Sol i l=antigen { (25 aa)
initn: 36 initl: 36 opt: 40 Z-score: 84.3 bits: 17.9 E(): 9
Smith-Waterman score: 40; 66.667% identity (75.000% similar) in 12 aa overlap
(59-69:3-14)

10 20 30 40 50 60
SEC61g MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIGFVVMGFVGVFFVKLVFIP
:
gi|133 WKIP

SEC61g INNI-IVGSS
.: : :
gi|133 LNNIQYVGHSLGSHVSGFAAK
10 20

>>gi|1362133 gi|1362133|pir||G53806 major allergen OLE26 (136 aa)
initn: 43 initl: 43 opt: 47 Z-score: 84.3 bits: 20.4 E(): 9.1
Smith-Waterman score: 47; 34.146% identity (51.220% similar) in 41 aa overlap
(8-47:18-58)

10 20 30 40
SEC61g MEAIDSAIDPLRDFAK-SSVRLVQRCHKPDRKEFTKVAVRTAIGFVVMGF
: : .: .::: . .: :::. : :.
gi|136 QFHIQGVYCDTCRAGFITELSEFIPGASVRLQCKEKKNGDITFTEVGYTRAEGLYSMLV
10 20 30 40 50 60

```

      50      60
SEC61g VGFFVKLVFIPINNIIVGSS

gi|136 ERDHKNEFCEITLISSGSKDCNEIPTEGWGKPSLKFILNTVNGTTTRTVNPLGFYKKEALP
      70      80      90     100     110     120

gi|136 KCAQVYNKLGMYPPNM
      130

>>gi|1709545 gi|1709545|sp|P51528.1|PA1_VESMC Phospholip (300 aa)
  initn: 45 initl: 45 opt: 50 Z-score: 83.8 bits: 21.4 E(): 9.7
Smith-Waterman score: 50; 23.684% identity (57.895% similar) in 38 aa overlap
(29-66:33-70)

      10      20      30      40      50
SEC61g MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIGFVVMGFVVGFFVKL
      .. :: : .. . :.. :... .
gi|170 GPKCFNSDTVSIIIE TRENRNRDL YTLQTLQNHPEFKKKTITRPVVFITHGFTSSASEK
      10      20      30      40      50      60

      60
SEC61g VFIPINNIIVGSS
      :: . . . :
gi|170 NFINLAKALVDKDN YVISIDWQTA ACTNEYPGLKYAYYPTAASNTRLVGQYIATITQKL
      70      80      90     100     110     120

gi|170 VKDYKISMANIRLIGHSLGAHVSGFAGKRVQELKLGKYSEIIGLDPARPSFDSNHCSERL
      130     140     150     160     170     180

gi|170 CETDAEYVQIIHTSN YLGTEKILGTVD FYMNGKNNPGCGRFFSEVCSHTRAVIYMAECI
      190     200     210     220     230     240

gi|170 KHECCLIGIPRSKSSQ PISRCTKQECVCVGLN AKKYP SRGSFYVPVESTAPFCNNKGKII
      250     260     270     280     290     300

69 residues in 1 query sequences
292011 residues in 1313 library sequences
Scomplib [34.26]
start: Fri Dec 5 18:28:25 2008 done: Fri Dec 5 18:28:25 2008
Total Scan time: 0.090 Total Display time: 0.020

Function used was FASTA [version 34.26.5 April 26, 2007]

```

APPENDIX 2. TOXIN HOMOLOGY SEARCH RESULTS

The BLASTP results for the search of the GenBank non-redundant database with ahasl (R272K, S653N) and SEC61 γ are shown below. All descriptions of proteins from the GenBank non-redundant database which show the most significant local homology to ahasl (R272K, S653N) or SEC61 γ were manually compared to known toxins which act on humans as listed in the United States Code of Federal Regulations ([40 CFR Part 725.421](#)) to ensure that neither ahasl (R272K, S653N) nor SEC61 γ shared significant homology to a known toxin.

BLASTP 2.2.18 [Mar-02-2008]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Query= ahasl.R272K.S653N
(670 letters)

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
from WGS projects
7,155,275 sequences; 2,468,333,968 total letters

Searching.....done

Sequences producing significant alignments:		Score (bits)	E Value
emb CAA35887.1	unnamed protein product [Arabidopsis thaliana]	1215	0.0
ref NP_190425.1	CSR1 (CHLORSULFURON/IMIDAZOLINONE RESISTANT 1) ...	1213	0.0
gb AAK68759.1	acetolactate synthase [Arabidopsis thaliana]	1212	0.0
gb AAM92569.1	acetolactate synthase [Arabidopsis thaliana]	1210	0.0
gb ABJ80681.1	acetolactate synthase catalytic subunit [Arabidop...	1203	0.0
pdb 1YBH A	Chain A, Crystal Structure Of Arabidopsis Thaliana Ac...	1194	0.0
gb AAR06607.1	acetolactate synthase 2 [Camelina microcarpa]	1170	0.0
gb AAR07633.1	acetolactate synthase 1 [Camelina microcarpa]	1165	0.0
gb AAR07632.1	acetolactate synthase 1 [Camelina microcarpa]	1165	0.0
sp P27818 ILV1_BRANA	Acetolactate synthase 1, chloroplast precur...	1142	0.0
sp P27819 ILV3_BRANA	Acetolactate synthase 3, chloroplast precur...	1142	0.0
emb CAC86700.1	putative acetolactate synthase [Raphanus raphani...	1135	0.0
emb CAC86694.1	putative acetolactate synthase [Raphanus raphani...	1134	0.0
emb CAC86692.1	putative acetolactate synthase [Raphanus raphani...	1134	0.0
emb CAC86701.1	putative acetolactate synthase [Raphanus raphani...	1134	0.0
gb ACB12188.1	acetolactate synthase [Descurainia sophia]	1133	0.0
emb CAC86698.1	putative acetolactate synthase [Raphanus raphani...	1132	0.0
emb CAC86696.1	putative acetolactate synthase [Raphanus raphani...	1131	0.0
gb ACB12189.1	acetolactate synthase [Descurainia sophia]	1131	0.0
emb CAC86699.1	putative acetolactate synthase [Raphanus raphani...	1130	0.0
gb ACB12190.1	acetolactate synthase [Descurainia sophia]	1129	0.0
emb CAC86695.1	putative acetolactate synthase [Raphanus raphani...	1129	0.0

gb AAA62705.1	acetolactate synthase	1128	0.0
emb CAC86702.1	putative acetolactate synthase [Raphanus raphani...	1124	0.0
gb AAY46011.1	putative acetolactate synthase [Sinapis arvensis]	1123	0.0
emb CAC86703.1	putative acetolactate synthase [Raphanus raphani...	1122	0.0
gb AAY46010.1	putative acetolactate synthase [Sinapis arvensis]	1121	0.0
gb AAY46004.1	putative acetolactate synthase [Sinapis arvensis]	1120	0.0
gb AAY46012.1	putative acetolactate synthase [Sinapis arvensis]	1120	0.0
gb AAY46008.1	putative acetolactate synthase [Sinapis arvensis]	1119	0.0
gb AAY45998.1	putative acetolactate synthase [Sinapis arvensis]...	1118	0.0
gb AAY45995.1	putative acetolactate synthase [Sinapis arvensis]...	1117	0.0
gb AAY46007.1	putative acetolactate synthase [Sinapis arvensis]	1117	0.0
gb AAY46013.1	putative acetolactate synthase [Sinapis arvensis]	1115	0.0
gb AAY46005.1	putative acetolactate synthase [Sinapis arvensis]	1115	0.0
emb CAC86693.1	putative acetolactate synthase [Raphanus raphani...	1112	0.0
gb AAY46006.1	putative acetolactate synthase [Sinapis arvensis]...	1104	0.0
emb CAA87083.1	acetohydroxyacid synthase [Gossypium hirsutum]	1055	0.0
emb CAA87084.1	acetohydroxyacid synthase [Gossypium hirsutum]	1055	0.0
gb AAT07322.1	acetohydroxyacid synthase 1 [Helianthus annuus]	1050	0.0
gb AAT07323.1	acetohydroxyacid synthase 1 [Helianthus annuus]	1048	0.0
gb AAT07325.1	acetohydroxyacid synthase 1 [Helianthus annuus]	1047	0.0
gb AAT07324.1	acetohydroxyacid synthase 1 [Helianthus annuus]	1045	0.0
gb AAT07326.1	acetohydroxyacid synthase 1 [Helianthus annuus]	1043	0.0
gb AAT07327.1	acetohydroxyacid synthase 2 [Helianthus annuus]	1042	0.0
gb AAT07328.1	acetohydroxyacid synthase 2 [Helianthus annuus]	1042	0.0
gb AAA74913.1	acetolactate synthase precursor	1042	0.0
gb ABN08612.1	Thiamine pyrophosphate enzyme, central region [Me...	1041	0.0
sp P09114 ILV2_TOBAC	Acetolactate synthase 2, chloroplast precu...	1035	0.0
gb AAB60297.1	acetolactate synthase precursor	1034	0.0
prf 1407140B	acetolactate synthase SuRB	1034	0.0
gb AAK50820.1 AF363369_1	acetolactate synthase [Amaranthus retro...	1033	0.0
gb AAK50821.1 AF363370_1	acetolactate synthase [Amaranthus powel...	1033	0.0
gb ABY57316.1	acetolactate synthase [Medicago littoralis]	1031	0.0
gb ABS72164.1	acetolactate synthase [Amaranthus hypochondriacus]	1030	0.0
sp P09342 ILV1_TOBAC	Acetolactate synthase 1, chloroplast precu...	1030	0.0
gb ABM53021.1	acetolactate synthase [Amaranthus tuberculatus]	1030	0.0
gb ABY57317.1	acetolactate synthase [Medicago truncatula]	1029	0.0
gb ABY57318.1	acetolactate synthase [Medicago truncatula]	1029	0.0
prf 1407140A	acetolactate synthase SuRA	1029	0.0
gb ABY57315.1	acetolactate synthase [Medicago littoralis]	1028	0.0
gb ACF47583.1	acetolactate synthase 1 [Sonchus asper]	1026	0.0
sp P14874 ILV2_BRANA	Acetolactate synthase 2, chloroplast precu...	1025	0.0
gb ABM53020.1	acetolactate synthase [Amaranthus tuberculatus]	1023	0.0
gb ACF47582.1	acetolactate synthase 1 [Sonchus asper]	1022	0.0
gb ACF17639.1	putative acetolactate synthase [Capsicum annuum]	1022	0.0
gb ABM53018.1	acetolactate synthase [Amaranthus tuberculatus]	1021	0.0
gb ABM53019.1	acetolactate synthase [Amaranthus tuberculatus]	1021	0.0
emb CAE18088.1	acetolactate synthase [Papaver rhoeas]	1017	0.0
gb AAC69629.1	herbicide resistant acetolactate synthase precurs...	1016	0.0
emb CAO49020.1	unnamed protein product [Vitis vinifera]	1016	0.0
gb AAB67839.1	acetolactate synthase precursor [Amaranthus sp.]	1015	0.0
gb AAG40279.1 AF308648_1	acetolactate synthase [Solanum tychant...	1004	0.0
gb AAG40280.1 AF308649_1	acetolactate synthase [Solanum tychant...	1003	0.0
gb ABR68865.1	acetohydroxyacid synthase [Solanum tychanthum]	1000	0.0
gb ABR68866.1	acetohydroxyacid synthase [Solanum tychanthum]	999	0.0
gb AAT07329.1	acetohydroxyacid synthase 3 [Helianthus annuus]	990	0.0
gb ABR68867.1	acetohydroxyacid synthase [Solanum tychanthum]	980	0.0
dbj BAF57909.1	acetolactate synthase [Sagittaria trifolia]	968	0.0
dbj BAE97677.1	acetolactate synthase [Schoenoplectus juncooides]...	950	0.0
dbj BAE97675.1	acetolactate synthase [Schoenoplectus juncooides]...	948	0.0
gb AAM03119.1 AF488771_1	acetolactate synthase [Bromus tectorum]	941	0.0
gb AAX14281.1	acetolactate synthase [Oryza sativa] >gi 99079641...	939	0.0
gb AAL93207.1 AF487459_1	acetolactate synthase [Bromus tectorum]	939	0.0
gb AAX14282.1	acetolactate synthase [Oryza sativa (japonica cul...	937	0.0
gb ABM92357.2	acetolactate synthase [Cyperus difformis]	937	0.0
gb EAY86003.1	hypothetical protein OsI_007236 [Oryza sativa (in...	937	0.0
ref NP_001046931.1	Os02g0510200 [Oryza sativa (japonica cultiva...	935	0.0
gb ACD74789.1	acetolactate synthase [Oryza sativa Indica Group]...	935	0.0
gb AAX14283.1	acetolactate synthase [Oryza sativa]	935	0.0
gb ABF66052.1	acetolactate synthase [Oryza sativa (indica culti...	932	0.0
gb ABF66048.1	acetolactate synthase [Oryza sativa (indica culti...	931	0.0

gb ABF66051.1	acetolactate synthase [Oryza sativa (indica culti...	931	0.0
dbj BAE53597.1	acetolactate synthase [Monochoria vaginalis] >gi...	931	0.0
dbj BAE53591.1	acetolactate synthase [Monochoria vaginalis] >gi...	929	0.0
dbj BAE53587.1	acetolactate synthase [Monochoria vaginalis] >gi...	928	0.0
dbj BAB20813.1	acetolactate synthase [Oryza sativa (japonica cu...	928	0.0
dbj BAE53596.1	acetolactate synthase [Monochoria vaginalis]	927	0.0
dbj BAE53598.1	acetolactate synthase [Monochoria vaginalis] >gi...	927	0.0
dbj BAE53602.1	acetolactate synthase [Monochoria vaginalis]	927	0.0
emb CAD24801.2	acetolactate synthase [Alopecurus myosuroides]	927	0.0
dbj BAE53593.1	acetolactate synthase [Monochoria vaginalis]	926	0.0
gb AAO53551.1	acetohydroxyacid synthase [Triticum aestivum]	926	0.0
dbj BAE53588.1	acetolactate synthase [Monochoria vaginalis]	926	0.0
sp Q41768 ILV1_MAIZE	Acetolactate synthase 1, chloroplast precur...	925	0.0
gb AAO53549.1	acetohydroxyacid synthase [Triticum aestivum]	924	0.0
gb AAO53550.1	acetohydroxyacid synthase [Triticum aestivum]	924	0.0
dbj BAE53610.1	acetolactate synthase [Monochoria vaginalis]	923	0.0
dbj BAE53605.1	acetolactate synthase [Monochoria vaginalis] >gi...	923	0.0
gb AAO53548.1	acetohydroxyacid synthase [Triticum aestivum]	922	0.0
dbj BAE53612.1	acetolactate synthase [Monochoria vaginalis]	922	0.0
gb ABF66049.1	acetolactate synthase [Oryza sativa (indica culti...	922	0.0
dbj BAE53611.1	acetolactate synthase [Monochoria vaginalis]	920	0.0
gb AAG30931.1 AF310684_1	acetolactate synthase precursor [Lolium...	920	0.0
dbj BAE53608.1	acetolactate synthase [Monochoria vaginalis]	917	0.0
dbj BAE53604.1	acetolactate synthase [Monochoria vaginalis]	915	0.0
gb ACF87819.1	unknown [Zea mays]	911	0.0
sp Q41769 ILV2_MAIZE	Acetolactate synthase 2, chloroplast precur...	910	0.0
ref XP_001759950.1	predicted protein [Physcomitrella patens sub...	894	0.0
gb EAZ23185.1	hypothetical protein OsJ_006668 [Oryza sativa (ja...	891	0.0
ref XP_001758473.1	predicted protein [Physcomitrella patens sub...	890	0.0
emb CAH66432.1	OSIGBa0096P03.6 [Oryza sativa (indica cultivar-g...	877	0.0
gb EAY93888.1	hypothetical protein OsI_015121 [Oryza sativa (in...	874	0.0
gb AAC14572.1	acetohydroxyacid synthase [Hordeum vulgare]	872	0.0
sp Q7XKQ8 ILV2_ORYSJ	Probable acetolactate synthase 2, chloropla...	872	0.0
emb CAN73760.1	hypothetical protein [Vitis vinifera]	858	0.0
emb CAO17032.1	unnamed protein product [Vitis vinifera]	834	0.0
gb AAB88296.1	acetolactate synthase [Volvox carterii]	832	0.0
emb CAO42659.1	unnamed protein product [Vitis vinifera]	829	0.0
emb CAL58226.1	acetolactate synthase 1 (ISS) [Ostreococcus tauri]	829	0.0
gb ABQ85870.1	acetolactate synthase [Lolium rigidum]	823	0.0
gb AAB88292.1	acetolactate synthase [Chlamydomonas reinhardtii]	819	0.0
gb AAC03784.1	acetolactate synthase [Chlamydomonas reinhardtii]	818	0.0
gb ABQ85869.1	acetolactate synthase [Lolium rigidum]	818	0.0
gb AAC04854.1	acetolactate synthase [Volvox carterii]	812	0.0
ref XP_001421626.1	predicted protein [Ostreococcus lucimarinus ...	801	0.0
dbj BAE53595.1	acetolactate synthase [Monochoria vaginalis]	792	0.0
emb CAC86697.1	putative acetolactate synthase [Raphanus raphani...	788	0.0
gb EAZ30535.1	hypothetical protein OsJ_014018 [Oryza sativa (ja...	758	0.0
gb EAZ30530.1	hypothetical protein OsJ_014013 [Oryza sativa (ja...	726	0.0
gb AAT72502.1	AT3G48560 [Arabidopsis lyrata subsp. lyrata]	706	0.0
emb CAP09635.1	acetolactate-synthase-N-DnaE intein-N fusion pro...	701	0.0
ref XP_001695168.1	acetolactate synthase, large subunit [Chlamy...	701	0.0
ref ZP_03129981.1	acetolactate synthase, large subunit, biosynt...	675	0.0
emb CAO45071.1	unnamed protein product [Vitis vinifera]	673	0.0
ref ZP_01089063.1	acetolactate synthase III (Precursor) [Blasto...	669	0.0
ref YP_001941018.1	Acetolactate synthase large subunit or other...	667	0.0
ref ZP_02966895.1	acetolactate synthase, large subunit, biosynt...	653	0.0
ref ZP_01857674.1	acetolactate synthase III (Precursor) [Planct...	653	0.0
ref ZP_02737021.1	acetolactate synthase III [Gemmata obscuriglo...	650	0.0
ref NP_870771.1	acetolactate synthase III [precursor] [Rhodopir...	642	0.0
gb EDY84597.1	acetolactate synthase, large subunit, biosyntheti...	629	e-178
ref ZP_02013682.1	acetolactate synthase, large subunit, biosynt...	611	e-173
ref YP_001818911.1	acetolactate synthase, large subunit, biosyn...	606	e-171
ref YP_001878250.1	acetolactate synthase, large subunit, biosyn...	598	e-169
dbj BAF37288.1	acetolactate synthase [Monochoria vaginalis]	597	e-169
ref ZP_01922597.1	acetolactate synthase, large subunit, biosynt...	574	e-162
ref YP_001930430.1	acetolactate synthase, large subunit, biosyn...	556	e-156
ref ZP_01923625.1	acetolactate synthase, large subunit, biosynt...	549	e-154
ref ZP_01188450.1	Acetolactate synthase, large subunit, biosynt...	548	e-154
ref ZP_02177150.1	acetolactate synthase large subunit [Hydrogen...	548	e-154
ref NP_213319.1	acetolactate synthase large subunit [Aquifex ae...	542	e-152

ref ZP_03135286.1	acetolactate synthase, large subunit, biosynt...	538	e-151
ref YP_001111655.1	acetolactate synthase, large subunit, biosyn...	538	e-151
ref YP_001568611.1	acetolactate synthase, large subunit, biosyn...	538	e-151
ref NP_952960.1	acetolactate synthase, large subunit, biosynthe...	536	e-150
ref YP_001046985.1	acetolactate synthase, large subunit, biosyn...	536	e-150
ref YP_002249089.1	acetolactate synthase, large subunit, biosyn...	536	e-150
gb ABV24338.1	indole-3-pyruvate decarboxylase [Paenibacillus po...	533	e-149
ref YP_004823.1	acetolactate synthase large subunit [Thermus th...	533	e-149
ref NP_831551.1	acetolactate synthase 3 catalytic subunit [Baci...	532	e-149
ref ZP_02179310.1	acetolactate synthase large subunit [Hydrogen...	531	e-149
ref YP_144479.1	acetolactate synthase, large subunit [Thermus t...	531	e-148
ref YP_502706.1	acetolactate synthase, large subunit, biosynthe...	530	e-148
ref ZP_01389342.1	acetolactate synthase, large subunit, biosynt...	529	e-148
ref ZP_03038955.1	acetolactate synthase, large subunit, biosynt...	528	e-148
ref ZP_03024969.1	acetolactate synthase, large subunit, biosynt...	528	e-148
ref YP_002121866.1	acetolactate synthase, large subunit, biosyn...	528	e-148
ref NP_693544.1	acetolactate synthase large subunit [Oceanobaci...	527	e-147
ref YP_388660.1	acetolactate synthase, large subunit [Desulfovi...	527	e-147
ref YP_894460.1	acetolactate synthase 3 catalytic subunit [Baci...	526	e-147
ref YP_384221.1	acetolactate synthase, large subunit [Geobacter...	526	e-147
ref ZP_02585109.1	acetolactate synthase 3 catalytic subunit [Ba...	526	e-147
gb EDZ37939.1	acetolactate synthase, large subunit [Leptospiril...	525	e-147
ref YP_001232446.1	acetolactate synthase, large subunit, biosyn...	525	e-147
ref ZP_00740942.1	Acetolactate synthase large subunit [Bacillus...	525	e-147
ref YP_036023.1	acetolactate synthase 3 catalytic subunit [Baci...	525	e-147
ref YP_002139546.1	acetolactate synthase, large subunit, biosyn...	525	e-147
ref ZP_03231724.1	acetolactate synthase, large subunit, biosynt...	525	e-147
ref NP_844268.1	acetolactate synthase 3 catalytic subunit [Baci...	524	e-147
ref ZP_03100840.1	acetolactate synthase, large subunit, biosynt...	524	e-147
ref ZP_03108556.1	acetolactate synthase, large subunit, biosynt...	524	e-147
ref NP_978250.1	acetolactate synthase 3 catalytic subunit [Baci...	524	e-147
ref YP_359378.1	acetolactate synthase, large subunit, biosynthe...	522	e-146
dbj BAF37287.1	acetolactate synthase [Monochoria vaginalis]	521	e-146
ref ZP_02850743.1	acetolactate synthase, large subunit, biosynt...	521	e-146
ref YP_001833518.1	acetolactate synthase, large subunit, biosyn...	521	e-146
ref ZP_02577817.1	acetolactate synthase 3 catalytic subunit [Ba...	520	e-145
ref YP_357321.1	acetolactate synthase, large subunit, biosynthe...	520	e-145
ref YP_001126680.1	acetolactate synthase catalytic subunit [Geo...	520	e-145
ref YP_001413730.1	acetolactate synthase, large subunit, biosyn...	520	e-145
ref YP_010595.1	acetolactate synthase, large subunit, biosynthe...	519	e-145
ref YP_967136.1	acetolactate synthase, large subunit, biosynthe...	519	e-145
ref YP_864823.1	acetolactate synthase, large subunit [Magnetoco...	519	e-145
ref ZP_02956061.1	acetolactate synthase, large subunit, biosynt...	519	e-145
ref YP_002250909.1	acetolactate synthase, large subunit, biosyn...	518	e-145
ref YP_001030046.1	acetolactate synthase, large subunit [Methan...	518	e-145
ref ZP_00236615.1	acetolactate synthase, large subunit, biosynt...	517	e-144
ref ZP_02326419.1	acetolactate synthase catalytic subunit [Paen...	517	e-144
ref ZP_02912696.1	acetolactate synthase, large subunit, biosynt...	517	e-144
ref YP_148514.1	acetolactate synthase catalytic subunit [Geobac...	517	e-144
ref YP_083261.1	acetolactate synthase 3 catalytic subunit [Baci...	516	e-144
ref ZP_01695377.1	acetolactate synthase, large subunit, biosynt...	516	e-144
ref YP_565425.1	acetolactate synthase 3 catalytic subunit [Meth...	516	e-144
ref YP_754808.1	acetolactate synthase large subunit [Syntrophom...	516	e-144
ref YP_821479.1	acetolactate synthase, large subunit [Solibacte...	515	e-144
ref ZP_03286153.1	acetolactate synthase, large subunit, biosynt...	515	e-144
ref YP_001644574.1	acetolactate synthase 3 catalytic subunit [B...	515	e-144
ref ZP_01104189.1	Acetolactate synthase [gamma proteobacterium ...	515	e-144
ref ZP_02118763.1	acetolactate synthase, large subunit, biosynt...	514	e-144
ref YP_001952737.1	acetolactate synthase, large subunit, biosyn...	514	e-144
ref NP_632694.1	acetolactate synthase 3 catalytic subunit [Meth...	514	e-144
ref ZP_02257502.1	acetolactate synthase 3 catalytic subunit [Ba...	513	e-143
gb EDZ60585.1	acetolactate synthase, large subunit, biosyntheti...	513	e-143
ref NP_618663.1	acetolactate synthase 3 catalytic subunit [Meth...	512	e-143
ref ZP_03039219.1	acetolactate synthase, large subunit, biosynt...	511	e-143
ref YP_001642303.1	acetolactate synthase, large subunit, biosyn...	511	e-143
ref YP_001404604.1	acetolactate synthase, large subunit, biosyn...	511	e-143
ref ZP_01311443.1	acetolactate synthase, large subunit, biosynt...	511	e-143
ref ZP_02059000.1	acetolactate synthase, large subunit, biosynt...	510	e-142
ref YP_706419.1	acetolactate synthase 1 catalytic subunit [Rhod...	510	e-142
gb AAL99356.1	acetohydroxy acid synthase large subunit; acetola...	510	e-142

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ref|YP_001211077.1| thiamine pyrophosphate-requiring enzymes [Pe... 510 e-142
ref|YP_431088.1| acetolactate synthase, large subunit [Moorella ... 510 e-142
ref|YP_001487695.1| acetolactate synthase catalytic subunit [Bac... 510 e-142
ref|YP_001416393.1| acetolactate synthase, large subunit, biosyn... 509 e-142
ref|YP_902220.1| acetolactate synthase, large subunit, biosynthe... 509 e-142
ref|YP_080105.1| acetolactate synthase catalytic subunit [Bacill... 509 e-142
ref|YP_066505.1| acetolactate synthase isozyme III, large subuni... 509 e-142
ref|ZP_00051726.2| COG0028: Thiamine pyrophosphate-requiring enz... 508 e-142
ref|ZP_03056016.1| acetolactate synthase, large subunit, biosynt... 508 e-142
ref|ZP_02169902.1| acetolactate synthase [Bacillus selenitireduc... 508 e-142
ref|YP_001529918.1| acetolactate synthase, large subunit, biosyn... 507 e-141
ref|YP_359375.1| acetolactate synthase, large subunit, biosynthe... 507 e-141
ref|ZP_01288118.1| Acetolactate synthase, large subunit, biosynt... 506 e-141
ref|YP_001261115.1| acetolactate synthase, large subunit [Sphing... 506 e-141
ref|YP_001757953.1| acetolactate synthase, large subunit, biosyn... 506 e-141
ref|YP_001928031.1| acetolactate synthase, large subunit, biosyn... 506 e-141
emb|CAJ72436.1| strongly similar to acetohydroxy acid synthase I... 506 e-141
ref|YP_176141.1| acetolactate synthase large subunit [Bacillus c... 506 e-141

```

```

>emb|CAA35887.1| unnamed protein product [Arabidopsis thaliana]
Length = 670

```

```

Score = 1215 bits (3144), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 587/607 (96%), Positives = 588/607 (96%)

```

```

Query: 64 AVLNXXXXXXXXXXXXXXXXXXXXFISRFAPDQPRKGADILVEALERQGVETVFAYPGGAS 123
AVLN FISRFAPDQPRKGADILVEALERQGVETVFAYPGGAS
Sbjct: 64 AVLNTTNTVTTPSPSTKPTKPTTFISRFAPDQPRKGADILVEALERQGVETVFAYPGGAS 123

```

```

Query: 124 MEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSSGKPGICIATSGPGATNLVSGLADAL 183
MEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSSGKPGICIATSGPGATNLVSGLADAL
Sbjct: 124 MEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSSGKPGICIATSGPGATNLVSGLADAL 183

```

```

Query: 184 LDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLAT 243
LDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLAT
Sbjct: 184 LDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLAT 243

```

```

Query: 244 SGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPV 303
SGRPGPVLVDVPKDIQQQLAIPNWEQAM+LPGYMSRMPKPPEDSHLEQIVRLISESKKPV
Sbjct: 244 SGRPGPVLVDVPKDIQQQLAIPNWEQAMRLPGYMSRMPKPPEDSHLEQIVRLISESKKPV 303

```

```

Query: 304 LYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEH 363
LYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEH
Sbjct: 304 LYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEH 363

```

```

Query: 364 SDLLAFGVRFD DRTVGKLEAFASRAKIVHIDIDS AEIGKNKTPHVSVC G DVKLALQGMN 423
SDLLAFGVRFD DRTVGKLEAFASRAKIVHIDIDS AEIGKNKTPHVSVC G DVKLALQGMN
Sbjct: 364 SDLLAFGVRFD DRTVGKLEAFASRAKIVHIDIDS AEIGKNKTPHVSVC G DVKLALQGMN 423

```

```

Query: 424 KVLENRAEELKLDFGVWRNELNVQKQKFP LSFKTFGEAIPPQYAIKVLDELTDGKAIIST 483
KVLENRAEELKLDFGVWRNELNVQKQKFP LSFKTFGEAIPPQYAIKVLDELTDGKAIIST
Sbjct: 424 KVLENRAEELKLDFGVWRNELNVQKQKFP LSFKTFGEAIPPQYAIKVLDELTDGKAIIST 483

```

```

Query: 484 GVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGFLPAAIGASVANPD AIVVDIDGDSFIM 543
GVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGFLPAAIGASVANPD AIVVDIDGDSFIM
Sbjct: 484 GVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGFLPAAIGASVANPD AIVVDIDGDSFIM 543

```

```

Query: 544 NVQELATIRVENLPVKVLLNNQHLMVMQWEDRFYKANRAHTFLGDP AQEDEIFPNMLL 603
NVQELATIRVENLPVKVLLNNQHLMVMQWEDRFYKANRAHTFLGDP AQEDEIFPNMLL
Sbjct: 544 NVQELATIRVENLPVKVLLNNQHLMVMQWEDRFYKANRAHTFLGDP AQEDEIFPNMLL 603

```

```

Query: 604 FAAACGIPAARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLP MIPNGGTFNDVITE 663
FAAACGIPAARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLP MIPNGGTFNDVITE
Sbjct: 604 FAAACGIPAARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLP MIPNGGTFNDVITE 663

```

```

Query: 664 GDGRIKY 670
GDGRIKY
Sbjct: 664 GDGRIKY 670

```

```
>ref|NP_190425.1| CSR1 (CHLORSULFURON/IMIDAZOLINONE RESISTANT 1) [Arabidopsis
    thaliana]
sp|P17597|ILVB_ARATH Acetolactate synthase, chloroplast precursor (Acetohydroxy-acid
    synthase) (ALS)
emb|CAB62345.1| acetolactate synthase [Arabidopsis thaliana]
gb|AAW70386.1| At3g48560 [Arabidopsis thaliana]
prf||1501386B acetolactate synthase
    Length = 670
```

Score = 1213 bits (3138), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 586/607 (96%), Positives = 588/607 (96%)

```
Query: 64  AVLNXXXXXXXXXXXXXXXXXXXXFISRFAPDQPRKGADILVEALERQGVETVFAYPGGAS 123
    AVLN FISRFAPDQPRKGADILVEALERQGVETVFAYPGGAS
Sbjct: 64  AVLNTTTNTTTTTPSPTKPTKPTFISRFAPDQPRKGADILVEALERQGVETVFAYPGGAS 123
```

```
Query: 124 MEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSSGKPGICIATSGPGATNLVSLADAL 183
    MEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSSGKPGICIATSGPGATNLVSLADAL
Sbjct: 124 MEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSSGKPGICIATSGPGATNLVSLADAL 183
```

```
Query: 184 LDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLAT 243
    LDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLAT
Sbjct: 184 LDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLAT 243
```

```
Query: 244 SGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPV 303
    SGRPGPVLVDVPKDIQQQLAIPNWEQAM+LPGYMSRMPKPPEDSHLEQIVRLISESKKPV
Sbjct: 244 SGRPGPVLVDVPKDIQQQLAIPNWEQAMRLPGYMSRMPKPPEDSHLEQIVRLISESKKPV 303
```

```
Query: 304 LYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSYPCDDEL$HMLGMHGT$VYANYAVEH 363
    LYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSYPCDDEL$HMLGMHGT$VYANYAVEH
Sbjct: 304 LYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSYPCDDEL$HMLGMHGT$VYANYAVEH 363
```

```
Query: 364 SDLLAFGVRFD$RVTGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVC$GDKLALQGMN 423
    SDLLAFGVRFD$RVTGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVC$GDKLALQGMN
Sbjct: 364 SDLLAFGVRFD$RVTGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVC$GDKLALQGMN 423
```

```
Query: 424 KVLENRAEELKLD$FGVWRNELNVQKQK$FPLSF$KTFGEAIPPQYAIKVLDELTDGKAIIST 483
    KVLENRAEELKLD$FGVWRNELNVQKQK$FPLSF$KTFGEAIPPQYAIKVLDELTDGKAIIST
Sbjct: 424 KVLENRAEELKLD$FGVWRNELNVQKQK$FPLSF$KTFGEAIPPQYAIKVLDELTDGKAIIST 483
```

```
Query: 484 GVGQHQMWAAQF$YNYKKPRQWLSS$GGLGAMG$FLPAAIGASVANPDAIVVDIDG$G$FIM 543
    GVGQHQMWAAQF$YNYKKPRQWLSS$GGLGAMG$FLPAAIGASVANPDAIVVDIDG$G$FIM
Sbjct: 484 GVGQHQMWAAQF$YNYKKPRQWLSS$GGLGAMG$FLPAAIGASVANPDAIVVDIDG$G$FIM 543
```

```
Query: 544 NVQELATIRVENLPVKVLLLNQHLGMVMQWEDRFYKANRAHTFLGDPAQE$E$IFPNMLL 603
    NVQELATIRVENLPVKVLLLNQHLGMVMQWEDRFYKANRAHTFLGDPAQE$E$IFPNMLL
Sbjct: 544 NVQELATIRVENLPVKVLLLNQHLGMVMQWEDRFYKANRAHTFLGDPAQE$E$IFPNMLL 603
```

```
Query: 604 F$AAACGIPAA$RVT$K$KADLREAIQTMLDTPGPYLLDVICPHQE$H$VLPMP$NGGTFNDVITE 663
    F$AAACGIPAA$RVT$K$KADLREAIQTMLDTPGPYLLDVICPHQE$H$VLPMP$NGGTFNDVITE
Sbjct: 604 F$AAACGIPAA$RVT$K$KADLREAIQTMLDTPGPYLLDVICPHQE$H$VLPMP$SGGTFNDVITE 663
```

```
Query: 664 GDGRIKY 670
    GDGRIKY
Sbjct: 664 GDGRIKY 670
```

```
>gb|AAK68759.1| acetolactate synthase [Arabidopsis thaliana]
    Length = 670
```

Score = 1212 bits (3135), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 585/607 (96%), Positives = 588/607 (96%)

```
Query: 64  AVLNXXXXXXXXXXXXXXXXXXXXFISRFAPDQPRKGADILVEALERQGVETVFAYPGGAS 123
    AVLN FISRFAPDQPRKGADILVEALERQGVETVFAYPGGAS
Sbjct: 64  AVLNTTTNTTTTTPSPTKPTKPTFISRFAPDQPRKGADILVEALERQGVETVFAYPGGAS 123
```

```
Query: 124 MEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSSGKPGICIATSGPGATNLVSLADAL 183
    MEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSSGKPGICIATSGPGATNLVSLADAL
Sbjct: 124 MEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSSGKPGICIATSGPGATNLVSLADAL 183
```

Query: 184 LDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLAT 243
LDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLAT
Sbjct: 184 LDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLAT 243

Query: 244 SGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPV 303
SGRPGPVLVDVPKDIQQQLAIPNWEQAM+LPGYMSRMPKPPEDSHLEQIVRLISESKKPV
Sbjct: 244 SGRPGPVLVDVPKDIQQQLAIPNWEQAMRLPGYMSRMPKPPEDSHLEQIVRLISESKKPV 303

Query: 304 LYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSPCDDEL SLHMLGMHGT VYANYAVEH 363
LYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSPCDDEL SLHMLGMHGT VYANYAVEH
Sbjct: 304 LYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSPCDDEL SLHMLGMHGT VYANYAVEH 363

Query: 364 SDLLAFGVRFDRTVTGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMN 423
SDLLAFGVRFDRTVTGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMN
Sbjct: 364 SDLLAFGVRFDRTVTGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMN 423

Query: 424 KVLNRAEELKLDGFWRNELNVQKQKPLSFKTFGEAIPPQYAIKVLDELTDGKAIIST 483
KVLNRAEELKLDGFWRNELNVQKQKPLSFKTFGEAIPPQYAIKVLDELTDGKAIIST
Sbjct: 424 KVLNRAEELKLDGFWRNELNVQKQKPLSFKTFGEAIPPQYAIKVLDELTDGKAIIST 483

Query: 484 GVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGFLPAAIGASVANPD AIVVDIDGDGSFIM 543
GVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGFLPAAIGASVANPD AIVVDIDGDGSFIM
Sbjct: 484 GVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGFLPAAIGASVANPD AIVVDIDGDGSFIM 543

Query: 544 NVQELATIRVENLPVKVLLLNQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLL 603
NVQELATIRVENLPVKVLLLNQHLGMVMQW+DRFYKANRAHTFLGDPAQEDEIFPNMLL
Sbjct: 544 NVQELATIRVENLPVKVLLLNQHLGMVMQWQDRFYKANRAHTFLGDPAQEDEIFPNMLL 603

Query: 604 FAAACGIPAARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITE 663
FAAACGIPAARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMP+GGTFNDVITE
Sbjct: 604 FAAACGIPAARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMPSGGTFNDVITE 663

Query: 664 GDGRIKY 670
GDGRIKY
Sbjct: 664 GDGRIKY 670

>gb|AAM92569.1| acetolactate synthase [Arabidopsis thaliana]
Length = 670

Score = 1210 bits (3131), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 584/607 (96%), Positives = 587/607 (96%)

Query: 64 AVLNXXXXXXXXXXXXXXXXXXXXFISRFAPDQPRKGADILVEALERQGVETVFAYPPGGAS 123
AVLN FISRFAPDQPRKGADILVEALERQGVETVFAYPPGGAS
Sbjct: 64 AVLNTTNTVTTPSPKPTKPTETFISRFAPDQPRKGADILVEALERQGVETVFAYPPGGAS 123

Query: 124 MEIHQALTRSSSIRNVLP RHEQGGVF AAEGYARSSGKPGICIATSGPGATNLV SGLADAL 183
MEIHQALTRSSSIRNVLP RHEQGGVF AAEGYARSSGKPGICIATSGPGATNLV SGLADAL
Sbjct: 124 MEIHQALTRSSSIRNVLP RHEQGGVF AAEGYARSSGKPGICIATSGPGATNLV SGLADAL 183

Query: 184 LDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLAT 243
LDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLAT
Sbjct: 184 LDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLAT 243

Query: 244 SGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPV 303
SGRPGPVLVDVPKDIQQQLAIPNWEQAM+LPGYMSRMPKPPEDSHLEQIVRLISESKKPV
Sbjct: 244 SGRPGPVLVDVPKDIQQQLAIPNWEQAMRLPGYMSRMPKPPEDSHLEQIVRLISESKKPV 303

Query: 304 LYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSPCDDEL SLHMLGMHGT VYANYAVEH 363
LYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSPCDDEL SLHMLGMHGT VYANYAVEH
Sbjct: 304 LYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSPCDDEL SLHMLGMHGT VYANYAVEH 363

Query: 364 SDLLAFGVRFDRTVTGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMN 423
SDLLAFGVRFDRTVTGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMN
Sbjct: 364 SDLLAFGVRFDRTVTGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMN 423

Query: 424 KVLNRAEELKLDGFWRNELNVQKQKPLSFKTFGEAIPPQYAIKVLDELTDGKAIIST 483
KVLNRAEELKLDGFWRNELNVQKQKPLSFKTFGEAIPPQYAIKVLDELTDGKAIIST
Sbjct: 424 KVLNRAEELKLDGFWRNELNVQKQKPLSFKTFGEAIPPQYAIKVLDELTDGKAIIST 483

Query: 484 GVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGFLPAAIGASVANPDAIVVDIDGDSFIM 543
GVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGFLPAAIGASVANPDAIVVDIDGDSFIM
Sbjct: 484 GVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGFLPAAIGASVANPDAIVVDIDGDSFIM 543

Query: 544 NVQELATIRVENLPVKVLLNNQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLL 603
NVQELATIRVE LPVK+LLLNNQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLL
Sbjct: 544 NVQELATIRVEQLPVKILLNNQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLL 603

Query: 604 FAAACGIPAARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITE 663
FAAACGIPAARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMP+GGTFNDVITE
Sbjct: 604 FAAACGIPAARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMPGGGTFNDVITE 663

Query: 664 GDGRIKY 670
GDGRIKY
Sbjct: 664 GDGRIKY 670

>gb|ABJ80681.1| acetolactate synthase catalytic subunit [Arabidopsis thaliana]
Length = 670

Score = 1203 bits (3113), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 582/607 (95%), Positives = 585/607 (96%)

Query: 64 AVLNXXXXXXXXXXXXXXXXXXXXFISRFAPDQPRKGADILVEALERQGVETVFAYPGGAS 123
AVLN FISRFAPDQPRKGADIL EALERQGVETVFAYPGGAS
Sbjct: 64 AVLNTTNTVTTPSPKPTKPTFISRFAPDQPRKGADILAEALERQGVETVFAYPGGAS 123

Query: 124 MEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSSGKPGICIATSGPGATNLVSGLADAL 183
MEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSSGK GICIATSGPGATNLVSGLADAL
Sbjct: 124 MEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSSGKSGICIATSGPGATNLVSGLADAL 183

Query: 184 LDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLAT 243
LDSVPLVAITGQVPRRMIGTDAFQ TPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLAT
Sbjct: 184 LDSVPLVAITGQVPRRMIGTDAFQGTPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLAT 243

Query: 244 SGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPV 303
SGRPGPVLVDVPKDIQQQLAIPNWEQAM+LPGYMSRMPKPPEDSHLEQIVRLISESKKPV
Sbjct: 244 SGRPGPVLVDVPKDIQQQLAIPNWEQAMRLPGYMSRMPKPPEDSHLEQIVRLISESKKPV 303

Query: 304 LYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSLYPCDDELSLHMLGMHGTVYANYAVEH 363
LYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSLYPCDDELSLHMLGMHGTVYANYAVEH
Sbjct: 304 LYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSLYPCDDELSLHMLGMHGTVYANYAVEH 363

Query: 364 SDLLAFGVRFDRTVGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVCQDVKLALQGMN 423
SDLLAFGVRFDRTVGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVCQDVKLALQGMN
Sbjct: 364 SDLLAFGVRFDRTVGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVCQDVKLALQGMN 423

Query: 424 KVLNRAEELKLDGFWRNELNVQKQKPLSFKTFGEAIPPQYAIKVLDELTDGKAIIST 483
KVLNRAEELKLDGFWRNELNVQKQKPLSFKTFGEAIPPQYAIKVLDELTDGKAIIST
Sbjct: 424 KVLNRAEELKLDGFWRNELNVQKQKPLSFKTFGEAIPPQYAIKVLDELTDGKAIIST 483

Query: 484 GVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGFLPAAIGASVANPDAIVVDIDGDSFIM 543
GVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGFLPAAIGASVANPDAIVVDIDGDSFIM
Sbjct: 484 GVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGFLPAAIGASVANPDAIVVDIDGDSFIM 543

Query: 544 NVQELATIRVENLPVKVLLNNQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLL 603
NVQELATIRVENLPVKVLLNNQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLL
Sbjct: 544 NVQELATIRVENLPVKVLLNNQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLL 603

Query: 604 FAAACGIPAARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITE 663
FAAACGIPAARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMP+GGTFNDVITE
Sbjct: 604 FAAACGIPAARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMPGGGTFNDVITE 663

Query: 664 GDGRIKY 670
GDGRIKY
Sbjct: 664 GDGRIKY 670

```
>pdb|1YBH|A Chain A, Crystal Structure Of Arabidopsis Thaliana Acetohydroxyacid
Synthase In Complex With A Sulfonylurea Herbicide
Chlorimuron Ethyl
pdb|1YHY|A Chain A, Crystal Structure Of Arabidopsis Thaliana Acetohydroxyacid
Synthase In Complex With A Sulfonylurea Herbicide,
Metsulfuron Methyl
pdb|1YHZ|A Chain A, Crystal Structure Of Arabidopsis Thaliana Acetohydroxyacid
Synthase In Complex With A Sulfonylurea Herbicide,
Chlorsulfuron
pdb|1YI0|A Chain A, Crystal Structure Of Arabidopsis Thaliana Acetohydroxyacid
Synthase In Complex With A Sulfonylurea Herbicide,
Sulfometuron Methyl
pdb|1YI1|A Chain A, Crystal Structure Of Arabidopsis Thaliana Acetohydroxyacid
Synthase In Complex With A Sulfonylurea Herbicide,
Tribenuron Methyl
pdb|1Z8N|A Chain A, Crystal Structure Of Arabidopsis Thaliana Acetohydroxyacid
Synthase In Complex With An Imidazolinone Herbicide,
Imazaquin
Length = 590
```

Score = 1194 bits (3088), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 578/584 (98%), Positives = 583/584 (99%)

```
Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG
Sbjct: 2 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 61

Query: 147 GVFAAEGYARSSGKPGICIAATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARSSGKPGICIAATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF
Sbjct: 62 GVFAAEGYARSSGKPGICIAATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 121

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN
Sbjct: 122 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 181

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYVGGGCLNSSDELGRFVELTGI 326
WEQAM+LPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYVGGGCLNSSDELGRFVELTGI
Sbjct: 182 WEQAMRLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYVGGGCLNSSDELGRFVELTGI 241

Query: 327 PVASTLMGLGSYPDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DVRTGKLEAFA 386
PVASTLMGLGSYP DDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DVRTGKLEAFA
Sbjct: 242 PVASTLMGLGSYPXDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DVRTGKLEAFA 301

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV
Sbjct: 302 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 361

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QKQKFPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS
Sbjct: 362 QKQKFPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 421

Query: 507 SGGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ
Sbjct: 422 SGGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 481

Query: 567 HLGVMVQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGVMVQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQ
Sbjct: 482 HLGVMVQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQ 541

Query: 627 TMLDTPGPYLLDVICPHQEHVLP MIPNGGT FNDVITEGDGRIKY 670
TMLDTPGPYLLDVICPHQEHVLP MIP+GGTFNDVITEGDGR+++
Sbjct: 542 TMLDTPGPYLLDVICPHQEHVLP MIPSGGT FNDVITEGDGRLEH 585
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>gb|AAR06607.1| acetolactate synthase 2 [Camelina microcarpa]
Length = 665
```

Score = 1170 bits (3026), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 557/584 (95%), Positives = 576/584 (98%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F+SRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG
Sbjct: 82 FVS RFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 141

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARS+GKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF
Sbjct: 142 GVFAAEGYARSTGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 201

Query: 207 QETPIVEVTRSI TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSI TKHNYLVMDVEDIPRI+EEAFFLATSGRPGPVLVDVPKDIQQQLAIPN
Sbjct: 202 QETPIVEVTRSI TKHNYLVMDVEDIPRIVEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 261

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCLNSSDELGRFVELTGI 326
WEQ+M+LPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCLNSS+ELGRFVELTGI
Sbjct: 262 WEQSMRLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCLNSSSEELGRFVELTGI 321

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DVRTGKLEAFA 386
PVASTLMGLG+YPCDDELSLHMLGMHGT VYANY+VEHSDLLAFGVRFD DVRTGKLEAFA
Sbjct: 322 PVASTLMGLGAYPCDDELSLHMLGMHGT VYANYSVEHSDLLAFGVRFD DVRTGKLEAFA 381

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENR EELKLD FGVWR+ELN
Sbjct: 382 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRGEELKLD FGVWRSELNE 441

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLS 506
QKQKFPLSFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWA AQFY YKKPRQWLS
Sbjct: 442 QKQKFPLSFKTFGEAIPPQYAIQVLDELTDGKAIISTGVGQHQMWA AQFYKYKKPRQWLS 501

Query: 507 SGGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
S GLGAMGFGLPAAIGASVANPD A+VVDIDGDSFIMNVQELATIRVENLPVK+L+LNNQ
Sbjct: 502 SAGLGAMGFGLPAAIGASVANPD A VVDIDGDSFIMNVQELATIRVENLPVKILILNNQ 561

Query: 567 HLGVMVMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPARVTKKADLREAIQ 626
HLGVMVMQWEDRFYKANRAHT+LG+PA EDEIFPNML FA+ACGIP+ARVTKKA+LREAIQ
Sbjct: 562 HLGVMVMQWEDRFYKANRAHTYLGNPATEDEIFPNMLQFASACGIPSARVTKKAELREAIQ 621

Query: 627 TMLDTPGPYLLDVICPHQEHLVPMIPNGGTFNDVITEGDGR IKY 670
MLDTPGPYLLDVICPHQEHLVPMIP+GGTFNDVITEGDGR KY
Sbjct: 622 KMLDTPGPYLLDVICPHQEHLVPMIPSGGTFNDVITEGDGR TKY 665

>gb|AAR07633.1| acetolactate synthase 1 [Camelina microcarpa]
Length = 668

Score = 1165 bits (3013), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 555/584 (95%), Positives = 575/584 (98%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F+SRFAP QPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG
Sbjct: 85 FVS RFAPGQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 144

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARS+GKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF
Sbjct: 145 GVFAAEGYARSTGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 204

Query: 207 QETPIVEVTRSI TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSI TKHNYLVMDVEDIPRI+EEAFFLATSGRPGPVLVDVPKDIQQQLAIPN
Sbjct: 205 QETPIVEVTRSI TKHNYLVMDVEDIPRIVEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 264

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCLNSSDELGRFVELTGI 326
WEQ+M+LPGYMSRMPKPPEDSHLEQ VRLISESKKPVLVYGGGCLNSS+ELGRFVELTGI
Sbjct: 265 WEQSMRLPGYMSRMPKPPEDSHLEQTVRLISESKKPVLVYGGGCLNSSSEELGRFVELTGI 324

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DVRTGKLEAFA 386
PVASTLMGLG+YPCDDELSLHMLGMHGT VYANY+VEHSDLLAFGVRFD DVRTGKLEAFA
Sbjct: 325 PVASTLMGLGAYPCDDELSLHMLGMHGT VYANYSVEHSDLLAFGVRFD DVRTGKLEAFA 384

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWR+ELN
Sbjct: 385 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRSELNE 444

Query: 447 QKQKFPLSFKTFGEAIPPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QKQKFPLSFKTFGEAIPPPQYAI+VLDELTDG+AIISTGVGQHQMWAQFY YKKPRQWLS
Sbjct: 445 QKQKFPLSFKTFGEAIPPPQYAIQVLDELTDGRAIISTGVGQHQMWAQFYKYKKPRQWLS 504

Query: 507 SGGLGAMGFGLPAAIGASVANPDIAIVVDIDGDGSFIMNVQELATIRVENLPVKVLLLNQ 566
S GLGAMGFGLPAAIGASVANPD+IVVDIDGDGSFIMNVQELATIRVENLPVK+L+LNNQ
Sbjct: 505 SAGLGAMGFGLPAAIGASVANPDSIVVDIDGDGSFIMNVQELATIRVENLPVKILILNNQ 564

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGMMVQWEDRFYKANRAHT+LG+PA+EDEFIPNML FA+ACGIPAARVTK A+LREAIQ
Sbjct: 565 HLGMMVQWEDRFYKANRAHTYLGNAPEEDEFIPNMLQFASACGIPAARVTKIAELREAIQ 624

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
MLDTPGPYLLDVICPHQEHVLPMP+GGTFNDVITEGDGR KY
Sbjct: 625 KMLDTPGPYLLDVICPHQEHVLPMPISGGTFNDVITEGDGRTKY 668

>gb|AAR07632.1| acetolactate synthase 1 [Camelina microcarpa]
Length = 668

Score = 1165 bits (3013), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 555/584 (95%), Positives = 575/584 (98%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
F+SRFAPDQPRKGADILVEALERQGVET FAYPGGASMEIHQALTRSSSIRNVLPHEQG
Sbjct: 85 FVS RFAPDQPRKGADILVEALERQGVETAFAYPGGASMEIHQALTRSSSIRNVLPHEQG 144

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARS+GKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF
Sbjct: 145 GVFAAEGYARSTGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 204

Query: 207 QETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSIKHNLYLMDVEDIPRI+EEAFFLATSGRPGPVLVDVPKDIQQQLAIPN
Sbjct: 205 QETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 264

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
WEQ+M+LPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSS+ELGRFVELTGI
Sbjct: 265 WEQSMRLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSSEELGRFVELTGI 324

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFA 386
PVASTLMGLG+YPCDDELSLHMLGMHGTVYANY+VEHSDLLAFGVRFDRTGKLEAFA
Sbjct: 325 PVASTLMGLGAYPCDDELSLHMLGMHGTVYANYVEHSDLLAFGVRFDRTGKLEAFA 384

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWRNELNV 446
SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWWR+ELN
Sbjct: 385 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWWRSELNE 444

Query: 447 QKQKFPLSFKTFGEAIPPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QKQKFPLSFKTFGEAIPPPQYAI+VLDELTDG+AIISTGVGQHQMWAQFY YKKPRQWLS
Sbjct: 445 QKQKFPLSFKTFGEAIPPPQYAIQVLDELTDGRAIISTGVGQHQMWAQFYKYKKPRQWLS 504

Query: 507 SGGLGAMGFGLPAAIGASVANPDIAIVVDIDGDGSFIMNVQELATIRVENLPVKVLLLNQ 566
S GLGAMGFGLPAAIGASVANPD+IVVDIDGDGSFIMNVQELATIRVENLPVK+L+LNNQ
Sbjct: 505 SAGLGAMGFGLPAAIGASVANPDSIVVDIDGDGSFIMNVQELATIRVENLPVKILILNNQ 564

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGMMVQWEDRFYKANRAHT+LG+PA+EDEFIPNML FA+ACGIPAARVTK A+LREAIQ
Sbjct: 565 HLGMMVQWEDRFYKANRAHTYLGNAPEEDEFIPNMLQFASACGIPAARVTKIAELREAIQ 624

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
MLDTPGPYLLDVICPHQEHVLPMP+GGTFNDVITEGDGR KY
Sbjct: 625 KMLDTPGPYLLDVICPHQEHVLPMPISGGTFNDVITEGDGRTKY 668

>sp|P27818|ILV1_BRANA Acetolactate synthase 1, chloroplast precursor (Acetolactate
synthase I) (Acetohydroxy-acid synthase I) (ALS I)
emb|CAA77613.1| actohydroxyacid synthase I [Brassica napus]
Length = 655

Score = 1142 bits (2953), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 543/584 (92%), Positives = 570/584 (97%)

```
Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQG 146
      F+SR+APD+PRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLP RHEQG
Sbjct: 72 FVSRYAPDEPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQG 131

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
      GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADA+LDSVPLVAITGQVPRRMIGTDAF
Sbjct: 132 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADAMLDSVPLVAITGQVPRRMIGTDAF 191

Query: 207 QETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
      QETPIVEVTRSIKHNLYLMDV+DIPRI++EAFFLATSGRPGPVLVDVPKDIQQQLAIPN
Sbjct: 192 QETPIVEVTRSIKHNLYLMDVDDIPRIVQEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 251

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
      W+Q M+LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSS+ELGRFVELTGI
Sbjct: 252 WDQPMRLPGYMSRLPQPPEVSQLGQIVRLISESKRPVLYVGGGSLNSSEELGRFVELTGI 311

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTVGKLEAFA 386
      PVASTLMGLGSYPC+DELSL MLGMHGT VYANYAVEHSDLLAFGVRFD DRTVGKLEAFA
Sbjct: 312 PVASTLMGLGSYPCNDELSLQMLGMHGT VYANYAVEHSDLLAFGVRFD DRTVGKLEAFA 371

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLDFGVWRNELNV 446
      SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLDFGVWR+EL+
Sbjct: 372 SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLDFGVWRSE LSE 431

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
      QKQKFPLSFKTFGEAIPPQYAI++LDELTDGKAIISTGVGQHQMWAQFY Y+KPRQWLS
Sbjct: 432 QKQKFPLSFKTFGEAIPPQYAIQILDELTDGKAIISTGVGQHQMWAQFYK YRKP RQWLS 491

Query: 507 SSSLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
      S GLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVK+LLNNQ
Sbjct: 492 SSSLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQ 551

Query: 567 HLGVMVMQWEDRFYKANRAHTFLGDPAQEDEIFPNMMLFAAACGIPAARVTKKADLREAIQ 626
      HLGVMVMQWEDRFYKANRAHT+LGDP A+E+EIFPNML FA ACGIPAARVTKK +LREAIQ
Sbjct: 552 HLGVMVMQWEDRFYKANRAHTYLGDPARENEIFPNMLQFAGACGIPAARVTKKEELREAIQ 611

Query: 627 TMLDTPGPYLLDVICPHQEHVLP MIPNGGTFNDVITEGDGRIKY 670
      TMLDTPGPYLLDVICPHQEHVLP MIP+GGTF DVITEGDGR KY
Sbjct: 612 TMLDTPGPYLLDVICPHQEHVLP MIPSGGTFKDVITEGDGR TKY 655
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>sp|P27819|ILV3_BRANA Acetolactate synthase 3, chloroplast precursor (Acetolactate synthase III) (Acetohydroxy-acid synthase III) (ALS III)
emb|CAA77615.1| acetohydroxyacid synthase III [Brassica napus]
Length = 652

Score = 1142 bits (2953), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 545/584 (93%), Positives = 569/584 (97%)

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Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQG 146
      FISR+APD+PRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLP RHEQG
Sbjct: 69 FISRYAPDEPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQG 128

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
      GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADA+LDSVPLVAITGQVPRRMIGTDAF
Sbjct: 129 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADAMLDSVPLVAITGQVPRRMIGTDAF 188

Query: 207 QETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
      QETPIVEVTRSIKHNLYLMDV+DIPRI++EAFFLATSGRPGPVLVDVPKDIQQQLAIPN
Sbjct: 189 QETPIVEVTRSIKHNLYLMDVDDIPRIVQEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 248

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
      W+Q M+LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSS+ELGRFVELTGI
Sbjct: 249 WDQPMRLPGYMSRLPQPPEVSQLGQIVRLISESKRPVLYVGGGSLNSSEELGRFVELTGI 308

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTVGKLEAFA 386
      PVASTLMGLGSYPC+DELSL MLGMHGT VYANYAVEHSDLLAFGVRFD DRTVGKLEAFA
Sbjct: 309 PVASTLMGLGSYPCNDELSLQMLGMHGT VYANYAVEHSDLLAFGVRFD DRTVGKLEAFA 368
```

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWR+EL+
Sbjct: 369 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRSELS 428

Query: 447 QKQKFPLSF KTFGEAIP PQYAIKVLDEL TDGKAIISTGVGQHQM WAAQFYNYKKPRQWLS 506
QKQKFPLSF KTFGEAIP PQYAI+VLDEL TDGKAIISTGVGQHQM WAAQFY Y+KPRQWLS
Sbjct: 429 QKQKFPLSF KTFGEAIP PQYAIQVLDEL TDGKAIISTGVGQHQM WAAQFYKYRKPRQWLS 488

Query: 507 S SGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
S GLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVK+LLLNNQ
Sbjct: 489 S SGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQ 548

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEIFPNM LFAAACGIPAARVTKKADLREAIQ 626
HLGMMVQWEDRFYKANRAHT+LGDPA+E+EIFPNM L FA ACGIPAARVTKK +LREAIQ
Sbjct: 549 HLGMMVQWEDRFYKANRAHTYLGDPARENEIFPNM LQFAGACGIPAARVTKKEELREAIQ 608

Query: 627 TMLDTPGPYLLDVICPHQEHVLP MIPNGGTFNDVITEGDGR IKY 670
TMLDTPGPYLLDVICPHQEHVLP MIP+GGTF DVITEGDGR KY
Sbjct: 609 TMLDTPGPYLLDVICPHQEHVLP MIPSGGTFKDVITEGDGR TKY 652

>emb|CAC86700.1| putative acetolactate synthase [Raphanus raphanistrum]
Length = 585

Score = 1135 bits (2936), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 541/584 (92%), Positives = 568/584 (97%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F+SR+APD+PRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS+IRNVLP RHEQG
Sbjct: 2 FVSRYAPDEPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 61

Query: 147 GVFAAEGYARSSGKPGIC IATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARSSGKPGIC IATSGPGATNLVSGLADA+LDSVPLVAITGQVPRRMIGTDAF
Sbjct: 62 GVFAAEGYARSSGKPGIC IATSGPGATNLVSGLADAM LDSVPLVAITGQVPRRMIGTDAF 121

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLVMDV+DIPRI++EAFFLATSGRPGPVLVDVPKDIQQQLAIPN
Sbjct: 122 QETPIVEVTRSITKHNYLVMDVDDIPRIVQEAF FLATSGRPGPVLVDVPKDIQQQLAIPN 181

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKPVLVYVGGGCLNSSDELGRFVELTGI 326
W+Q M+LPGYMSR+P+PPE S L QIVRLISESK+PVLVYVGGG LNSS+ELGRFVELTGI
Sbjct: 182 WQPMRLPGYMSRLPQPPEVSQLRQIVRLISESKR PVLVYVGGGSLNSS EELGRFVELTGI 241

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTGKLEAFA 386
PVASTLMGLGSYPC+DELSL MLGMHGT VYANY+VEHSDLLAFGVRFDDRVTGKLEAFA
Sbjct: 242 PVASTLMGLGSYPCNDELSLQMLGMHGT VYANYSVEHSDLLAFGVRFDDRVTGKLEAFA 301

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMN++LENRAEELKLD FGVWR+EL+
Sbjct: 302 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNEILENRAEELKLD FGVWRSELS 361

Query: 447 QKQKFPLSF KTFGEAIP PQYAIKVLDEL TDGKAIISTGVGQHQM WAAQFYNYKKPRQWLS 506
QKQKFPLSF KTFGEAIP PQYAI+VLDEL TDGKAIISTGVGQHQM WAAQFY Y+KPRQWLS
Sbjct: 362 QKQKFPLSF KTFGEAIP PQYAIQVLDEL TDGKAIISTGVGQHQM WAAQFYKYRKPRQWLS 421

Query: 507 S SGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
S GLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVK+LLLNNQ
Sbjct: 422 S SGLGAMGFGLPAAIGASVANPD AIXVDIDGDSFIMNVQELATIRVENLPVKILLNNQ 481

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEIFPNM LFAAACGIPAARVTKKADLREAIQ 626
HLGMMVQWEDRFYKANRAHT+LGDPA+E EIFPNM L FA ACGIPAARVTKK +LREAIQ
Sbjct: 482 HLGMMVQWEDRFYKANRAHTYLGDPARESEIFPNM LQFAGACGIPAARVTKKEELREAIQ 541

Query: 627 TMLDTPGPYLLDVICPHQEHVLP MIPNGGTFNDVITEGDGR IKY 670
TMLDTPGPYLLDVICPHQEHVLP MIP+GGTF DVITEGDGR KY
Sbjct: 542 TMLDTPGPYLLDVICPHQEHVLP MIPSGGTFKDVITEGDGR TKY 585

>emb|CAC86694.1| putative acetolactate synthase [Raphanus raphanistrum]
Length = 585

Score = 1134 bits (2934), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 541/584 (92%), Positives = 567/584 (97%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F+SR+APD+PRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLP RHEQG
Sbjct: 2 FVSRYAPDEPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLP RHEQG 61

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARSSGKPGICIATSGPGATNLVSLADA+LDSVPLVAITGQVPRRMIGTDAF
Sbjct: 62 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADAMLDVPLVAITGQVPRRMIGTDAF 121

Query: 207 QETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSIKHNLYLMDV+DIPRI++EAFFLATSGRPGPVLVDVPKDIQ QL AIPN
Sbjct: 122 QETPIVEVTRSIKHNLYLMDVDDIPRIVQEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 181

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W+Q M+LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSS+ELGRFVELTGI
Sbjct: 182 WDQPMRLPGYMSRLPQPPEVSQLRQIVRLISESKRPVLYVGGGSLNSSEELGRFVELTGI 241

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTVGKLEAFA 386
PVASTLMGLGSYPC+DELSL MLGMHGT VYANY+VEHSDLLAFGVRFD DRTVGKLEAFA
Sbjct: 242 PVASTLMGLGSYPCNDELSLQMLGMHGT VYANY+VEHSDLLAFGVRFD DRTVGKLEAFA 301

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNK+LENR EELKLD FGVWR+EL+
Sbjct: 302 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKILENRGEELKLD FGVWRSELS 361

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMMAAQFYNYKKPRQWLS 506
QKQKFPLSFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMMAAQFY Y+KPRQWLS
Sbjct: 362 QKQKFPLSFKTFGEAIPPQYAIQVLDELTDGKAIISTGVGQHQMMAAQFYKYRKPQWLS 421

Query: 507 SSGGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
S GLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVK+LLNNQ
Sbjct: 422 SSGGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQ 481

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFIPNMLFAAACGIPAA RVTKKADLREAIQ 626
HLGMMVQWEDRFYKANRAHT+LGDPA+E EIFPNML FA ACGIPAA RVTKK +LREAIQ
Sbjct: 482 HLGMMVQWEDRFYKANRAHTYLGDPA RESEIFPNMLQFAGACGIPAA RVTKKEELREAIQ 541

Query: 627 TMLDTPGPYLLDVICPHQEHVLP MIPNGGTFNDVITEGDGR IKY 670
TMLDTPGPYLLDVICPHQEHVLP MIP+GGTF DVITEGDGR KY
Sbjct: 542 TMLDTPGPYLLDVICPHQEHVLP MIPSGGTFKDVITEGDGR TKY 585

>emb|CAC86692.1| putative acetolactate synthase [Raphanus raphanistrum]
Length = 585

Score = 1134 bits (2933), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 542/584 (92%), Positives = 567/584 (97%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F+SR+APD+PRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLP RHEQG
Sbjct: 2 FVSRYAPDEPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLP RHEQG 61

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARSSGKPGICIATSGPGATNLVSLADA+LDSVPLVAITGQVPRRMIGTDAF
Sbjct: 62 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADAMLDVPLVAITGQVPRRMIGTDAF 121

Query: 207 QETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSIKHNLYL M V+DIPRI++EAFFLATSGRPGPVLVDVPKDIQQQLAIPN
Sbjct: 122 QETPIVEVTRSIKHNLYLVMXVDDIPRIVQEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 181

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W+Q M+LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSS+ELGRFVELTGI
Sbjct: 182 WDQPMRLPGYMSRLPQPPEVSQLRQIVRLISESKRPVLYVGGGSLNSSEELGRFVELTGI 241

Query: 327 PVASTLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRVTGKLEAFA 386
PVASTLMGLGSYPC+DELSL MLGMHGT VYANYAVEHSDLLLAFGVRFDDRVTGKLEAFA
Sbjct: 242 PVASTLMGLGSYPCNDELSLQMLGMHGT VYANYAVEHSDLLLAFGVRFDDRVTGKLEAFA 301

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNK+LENRAEELKLD FGVWR+EL+
Sbjct: 302 SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKILENRAEELKLD FGVWRSELSE 361

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QKQKFPLSFKTFGEAIPPQYAI+VLDELTDGKAIISTGVG HQMWAQFY Y+KPRQWLS
Sbjct: 362 QKQKFPLSFKTFGEAIPPQYAIQVDELTDGKAIISTGVGXHQMWAQFYKYRKPRQWLS 421

Query: 507 SGGLGAMGFGLPAAIGASVANPDAIVVDIDGGSFIMNVQELATIRVENLPVKVLLNNQ 566
S GLGAMGFGLPAAIGASVANPDAIVVDIDGGSFIMNVQELATIRVENLPVK+LLNNQ
Sbjct: 422 SSGLGAMGFGLPAAIGASVANPDAIVVDIDGGSFIMNVQELATIRVENLPVKILLNNQ 481

Query: 567 HLGVMVQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGVMVQWEDRFYKANRAHT+LGDP A+E EIFPNML FA ACGIPAARVTKK +LREAIQ
Sbjct: 482 HLGVMVQWEDRFYKANRAHTYLGDPARESEIFPNMLQFAGACGIPAARVTKKEELREAIQ 541

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
TMLDTPGPYLLDVICPHQEHVLPMP+GGTF DVITEGDGR KY
Sbjct: 542 TMLDTPGPYLLDVICPHQEHVLPMPISGGTFKDVITEGDGRKY 585

>emb|CAC86701.1| putative acetolactate synthase [Raphanus raphanistrum]
Length = 585

Score = 1134 bits (2933), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 541/584 (92%), Positives = 568/584 (97%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F+SR+APD+PRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS+IRNVLP RHEQG
Sbjct: 2 FVSRYAPDEPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS TIRNVLP RHEQG 61

Query: 147 GVFAAEGYARSSGKPGICIA TSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARSSGKPGICIA TSGPGATNLVSLADA+LDSVPLVAITGQV RRMIGTDAF
Sbjct: 62 GVFAAEGYARSSGKPGICIA TSGPGATNLVSLADAMLDSVPLVAITGQVXR RMIGTDAF 121

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNLYLMDV+DIPRI++EAFFLATSGRPGPVLVDVPKDIQQQLAIPN
Sbjct: 122 QETPIVEVTRSITKHNLYLMDVDDIPRIVQEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 181

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKPVLYVGGGCLNSSDELGRFVELTGI 326
W+Q M+LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSS+ELGRFVELTGI
Sbjct: 182 WDQPMRLPGYMSRLPQPPEVSQLRQIVRLISESKRPVLYVGGGSLNSS EELGRFVELTGI 241

Query: 327 PVASTLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRVTGKLEAFA 386
PVASTLMGLGSYPC+DELSL MLGMHGT VYANY+VEHSDLLLAFGVRFDDRVTGKLEAFA
Sbjct: 242 PVASTLMGLGSYPCNDELSLQMLGMHGT VYANY SVEHSDLLLAFGVRFDDRVTGKLEAFA 301

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMN++LENRAEELKLD FGVWR+EL+
Sbjct: 302 SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNEILENRAEELKLD FGVWRSELSE 361

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QKQKFPLSFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQFY Y+KPRQWLS
Sbjct: 362 QKQKFPLSFKTFGEAIPPQYAIQVDELTDGKAIISTGVGQHQMWAQFYKYRKPRQWLS 421

Query: 507 SGGLGAMGFGLPAAIGASVANPDAIVVDIDGGSFIMNVQELATIRVENLPVKVLLNNQ 566
S GLGAMGFGLPAAIGASVANPDAIVVDIDGGSFIMNVQELATIRVENLPVK+LLNNQ
Sbjct: 422 SSGLGAMGFGLPAAIGASVANPDAIVVDIDGGSFIMNVQELATIRVENLPVKILLNNQ 481

Query: 567 HLGVMVQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGVMVQWEDRFYKANRAHT+LGDP A+E EIFPNML FA ACGIPAARVTKK +LREAIQ
Sbjct: 482 HLGVMVQWEDRFYKANRAHTYLGDPARESEIFPNMLQFAGACGIPAARVTKKEELREAIQ 541

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
TMLDTPGPYLLDVICPHQEHVLPMP+GGTF DVITEGDGR KY
Sbjct: 542 TMLDTPGPYLLDVICPHQEHVLPMPISGGTFKDVITEGDGRKY 585

>gb|ACB12188.1| acetolactate synthase [Descurainia sophia]
Length = 566

Score = 1133 bits (2931), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 546/566 (96%), Positives = 557/566 (98%)

Query: 94 DQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEG 153
DQPRKGADILVEALERQGV FAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEG
Sbjct: 1 DQPRKGADILVEALERQGVENVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEG 60

Query: 154 YARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVE 213
YARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVE
Sbjct: 61 YARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVE 120

Query: 214 VTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKL 273
VTRSITKHNYLVMDVEDIPRI+EEAFFLATSGRPGPVLVDVPKDIQQQLAIPNW+Q M+L
Sbjct: 121 VTRSITKHNYLVMDVEDIPRIVEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWDQPMRL 180

Query: 274 PGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVASTLM 333
PGY+SRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDEL RFVELTGIPVASTLM
Sbjct: 181 PGYLSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELRRFVELTGIPVASTLM 240

Query: 334 GLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVH 393
GLGSYPCDDELSLHMLGMHGT VYANY+VEHSDLLAFGVRFDRTGKLEAFASRAKIVH
Sbjct: 241 GLGSYPCDDELSLHMLGMHGT VYANY+VEHSDLLAFGVRFDRTGKLEAFASRAKIVH 300

Query: 394 IDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWRNELNVQKQKFPL 453
IDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLE RAEELKLDGFWRNELN QKQKFPL
Sbjct: 301 IDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLEKRAEELKLDGFWRNELNEQKQKFPL 360

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAM 513
SFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQFY YKKPRQWLSSGGLGAM
Sbjct: 361 SFKTFGEAIPPQYAIQVLDELTDGKAIISTGVGQHQMWAQFYKYKKPRQWLSSGGLGAM 420

Query: 514 GFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQ 573
GFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVK+LLLNNQHLGMVMQ
Sbjct: 421 GFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQHLGMVMQ 480

Query: 574 WEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPG 633
WEDRFYKANRAHTFLGDPAQE+EIFPNMLLFAAACGIPAARVTKK LR+AIQ MLDTPG
Sbjct: 481 WEDRFYKANRAHTFLGDPAQENEIFPNMLLFAAACGIPAARVTKKEHLRDAIQKMLDTPG 540

Query: 634 PYLLDVICPHQEHVLPMPINGGTFND 659
PYLLDVICPHQEHVLPMP+GGTF+D
Sbjct: 541 PYLLDVICPHQEHVLPMPISGGTFSD 566

>emb|CAC86698.1| putative acetolactate synthase [Raphanus raphanistrum]
Length = 585

Score = 1132 bits (2927), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 540/584 (92%), Positives = 567/584 (97%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
F+SR+APD+PRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS+IRNVLPHEQG
Sbjct: 2 FVSRYAPDEPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS+IRNVLPHEQG 61

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARSSGKPGICIATSGPGATNLVSLADA+LDSVPLVAITGQVPRRMIGTDAF
Sbjct: 62 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADAMLDVPLVAITGQVPRRMIGTDAF 121

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLV V+DIPRI++EAFFLATSGRPGPVLVDVPKDIQQQLAIPN
Sbjct: 122 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 181

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W+Q M+LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSS+ELGRFVELTGI
Sbjct: 182 WDQPMRLPGYMSRLPQPPEVSQLRQIVRLISESKRPVLYVGGGSLNSSEELGRFVELTGI 241

Query: 327 PVASTLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLLA FGVRFD DVRTGKLEAFA 386
PVASTLMGLGSYPC+DELSL MLGMHGT VYANY+VEHSDLLLA FGVRFD DVRTGKLEAFA
Sbjct: 242 PVASTLMGLGSYPCNDELSLQMLGMHGT VYANYAVEHSDLLLA FGVRFD DVRTGKLEAFA 301

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMN++LENRAEELKLD FGVWR+EL+
Sbjct: 302 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNEILENRAEELKLD FGVWRSELSE 361

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLS 506
QKQKFPLSFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWA AQFY Y+KPRQWLS
Sbjct: 362 QKQKFPLSFKTFGEAIPPQYAIQVLDELTDGKAIISTGVGQHQMWA AQFYK YRKPQWLS 421

Query: 507 SSGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
S GLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVK+LLNNQ
Sbjct: 422 SSGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQ 481

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAA RVTKKADLREAIQ 626
HLGMMVQWEDRFYKANRAHT+LGDPA+E EIFPNML FA ACGIPAA RVTKK +LREAIQ
Sbjct: 482 HLGMMVQWEDRFYKANRAHTYLGDPA RESEIFPNMLQFAGACGIPAA RVTKKEELREAIQ 541

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
TMLDTPGPYLLDVICPHQEHVLPMP+GGTF DVITEG GR KY
Sbjct: 542 TMLDTPGPYLLDVICPHQEHVLPMPISGGTFKDVITEGXGR TKY 585

>emb|CAC86696.1| putative acetolactate synthase [Raphanus raphanistrum]
Length = 585

Score = 1131 bits (2926), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 541/584 (92%), Positives = 565/584 (96%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F+SR+APD+PRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS+IRNVLP RHEQG
Sbjct: 2 FVSRYAPDEPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS TIRNVLP RHEQG 61

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARSSGKPGICIATSGPGATNLVSLADA+LDSVPLVAITGQV RRMIGTDAF
Sbjct: 62 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADAMLDSVPLVAITGQVXR RMIGTDAF 121

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDV PKDIQQQLAIPN 266
QETPIVEVTRSITKHNLYLMDV+DIPRI++EAFFLATSGRPGPVLVDV PKDIQQQLAIPN
Sbjct: 122 QETPIVEVTRSITKHNLYLMDVDDIPRIVQEAFFLATSGRPGPVLVDV PKDIQQQLAIPN 181

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W+Q M+LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSS+ELGRFVELTGI
Sbjct: 182 WDQPMRLPGYMSRLPQPPEVSQLRQIVRLISESKRPVLYVGGGSLNSS EELGRFVELTGI 241

Query: 327 PVASTLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLLA FGVRFD DVRTGKLEAFA 386
PVASTLMGLGSYPC+DELSL MLGMHGT VYANYAVEHSDLLLA FGVRFD DVRTGKLEAFA
Sbjct: 242 PVASTLMGLGSYPCNDELSLQMLGMHGT VYANYAVEHSDLLLA FGVRFD DVRTGKLEAFA 301

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNK+LENRAEELKLD FGVWR+EL
Sbjct: 302 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKILENRAEELKLD FGVWRSELKE 361

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLS 506
QKQKFPLSFKTFGEAIPPQYAI+VLDELTDGKAIISTGVG QHMWA AQFY Y+KPRQWLS
Sbjct: 362 QKQKFPLSFKTFGEAIPPQYAIQVLDELTDGKAIISTGVGXHQMWA AQFYK YRKPQWLS 421

Query: 507 SSGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
S GLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVK+LLNNQ
Sbjct: 422 SSGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQ 481

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAA RVTKKADLREAIQ 626
HLGMMVQWEDRFYKANRAHT+LGDPA+E EIFPNML FA ACGIPAA RVTKK +LREAIQ
Sbjct: 482 HLGMMVQWEDRFYKANRAHTYLGDPA RESEIFPNMLQFAGACGIPAA RVTKKEELREAIQ 541

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
TMLDTPGPYLLDVICPHQEHVLPMP+GGTF DVITEG DGR KY
Sbjct: 542 TMLDTPGPYLLDVICPHQEHVLPMPISGGTFKDVITEGXGR TKY 585

>gb|ACB12189.1| acetolactate synthase [Descurainia sophia]
Length = 566

Score = 1131 bits (2925), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 545/566 (96%), Positives = 556/566 (98%)

Query: 94 DQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEG 153
DQPRKGADILVEALERQGV E VFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEG
Sbjct: 1 DQPRKGADILVEALERQGVENVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEG 60

Query: 154 YARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVE 213
YARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQV RRMIGTDAFQETPIVE
Sbjct: 61 YARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVTRRMIGTDAFQETPIVE 120

Query: 214 VTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKL 273
VTRSITKHNYLVMDVEDIPRI+EEAFFLATSGRPGPVLVDVPKDIQQQLAIPNW+Q M+L
Sbjct: 121 VTRSITKHNYLVMDVEDIPRIVEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWDQPMRL 180

Query: 274 PGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVASTLM 333
PGY+SRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDEL RFVELTGIPVASTLM
Sbjct: 181 PGYLSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELRRFVELTGIPVASTLM 240

Query: 334 GLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVH 393
GLGSYPCCDELSLHMLGMHGT VYANY+VEHSDLLAFGVRFDRTGKLEAFASRAKIVH
Sbjct: 241 GLGSYPCCDELSLHMLGMHGT VYANY+VEHSDLLAFGVRFDRTGKLEAFASRAKIVH 300

Query: 394 IDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWRNELNVQKQKFPL 453
IDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLE RAEELKLDGFWRNELN QKQKFPL
Sbjct: 301 IDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLEKRAEELKLDGFWRNELNEQKQKFPL 360

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAM 513
SFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQFY YKKPRQWLSSGGLGAM
Sbjct: 361 SFKTFGEAIPPQYAIQVLDELTDGKAIISTGVGQHQMWAQFYKYKKPRQWLSSGGLGAM 420

Query: 514 GFGLPAAIGASVANPD AIVVDIDGGSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQ 573
GFGLPAAIGASVANPD AIVVDIDGGSFIMNVQELATIRVENLPVK+LLLNNQHLGMVMQ
Sbjct: 421 GFGLPAAIGASVANPD AIVVDIDGGSFIMNVQELATIRVENLPVKILLNNQHLGMVMQ 480

Query: 574 WEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPG 633
WEDRFYKANRAHTFLGDPAQE+EIFPNMLLFAAACGIPAARVTKK LR+AIQ MLDTPG
Sbjct: 481 WEDRFYKANRAHTFLGDPAQENEIFPNMLLFAAACGIPAARVTKKEHLRDAIQKMLDTPG 540

Query: 634 PYLLDVICPHQEHVLPMPINGGTFND 659
PYLLDVICPHQEHVLPMP+GGTF+D
Sbjct: 541 PYLLDVICPHQEHVLPMPISGGTFSD 566

>emb|CAC86699.1| putative acetolactate synthase [Raphanus raphanistrum]
Length = 585

Score = 1130 bits (2923), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 540/584 (92%), Positives = 566/584 (96%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
F+SR+APD+PRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS+IRNVLPHEQG
Sbjct: 2 FVSRYAPDEPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS+IRNVLPHEQG 61

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARSSGKPGICIATSGPGATNLVSLADA+LDSVPLVAITGQVPRRMIGTDAF
Sbjct: 62 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADAMLDVPLVAITGQVPRRMIGTDAF 121

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLVMDV+DIPRI++EAFFLATSGRPGPVLVDVPKDIQQQLAIPN
Sbjct: 122 QETPIVEVTRSITKHNYLVMDVDDIPRIVQEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 181

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W+Q M+LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSS+ELG FVELTGI
Sbjct: 182 WDQPMRLPGYMSRLPQPPEVSQLRQIVRLISESKRPVLYVGGGSLNSSEELGXFVELTGI 241

Query: 327 PVASTLMGLGSPCDDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRVTGKLEAFA 386
PVASTLMGLGSPC+DELSL MLGMHGT VYANY+VEHSDLLLAFGVRFDDRVTGKLEA A
Sbjct: 242 PVASTLMGLGSPCNDELSLQMLGMHGT VYANYAVEHSDLLLAFGVRFDDRVTGKLEAXA 301

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNK+LENRAEELKLD FGVWR+EL+
Sbjct: 302 SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKILENRAEELKLD FGVWRSELS 361

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QKQKFPLSFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQFY Y+KPRQWLS
Sbjct: 362 QKQKFPLSFKTFGEAIPPQYAXQVDELTDGKAIISTGVGQHQMWAQFYKYRKRPRQWLS 421

Query: 507 SSGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
S GLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVK+LLNNQ
Sbjct: 422 SSGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQ 481

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDP AQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGMMVQWEDRFYKANRAHT+LGDPA+E EIFPNML FA ACGIPAARVTKK +LREAIQ
Sbjct: 482 HLGMMVQWEDRFYKANRAHTYLGDPARESEIFPNMLQFAGACGIPAARVTKKEELREAIQ 541

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRKY 670
TMLDTPGPYLLDVICPHQEHVLPMP+GGTF DVITEGDGR KY
Sbjct: 542 TMLDTPGPYLLDVICPHQEHVLPMPISGGTFKDVITEGDGRKY 585

>gb|ACB12190.1| acetolactate synthase [Descurainia sophia]
Length = 566

Score = 1129 bits (2920), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 545/566 (96%), Positives = 556/566 (98%)

Query: 94 DQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEG 153
DQPRKGADILVEALERQGV E VFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEG
Sbjct: 1 DQPRKGADILVEALERQGVENVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEG 60

Query: 154 YARSSGKPGICIATSGPGATNLVSG LADALLDSVPLVAITGQVPRRMIGTDAFQETPIVE 213
YARSSGKPGICIATSGPGATNLVSG LADALLDSVPLVAITGQV RRMIGTDAFQETPIVE
Sbjct: 61 YARSSGKPGICIATSGPGATNLVSG LADALLDSVPLVAITGQVLR RMIGTDAFQETPIVE 120

Query: 214 VTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKL 273
VTRSITKHNYLVMDVEDIPRI+EEAFFLATSGRPGPVLVDVPKDIQQQLAIPN+Q M+L
Sbjct: 121 VTRSITKHNYLVMDVEDIPRIVEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWDQPMRL 180

Query: 274 PGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVASTLM 333
PGY+SRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDEL RFVELTGIPVASTLM
Sbjct: 181 PGYLSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELR RFVELTGIPVASTLM 240

Query: 334 GLGSPYPCDDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRVTGKLEAFASRAKIVH 393
GLGSPYPCDDELSLHMLGMHGT VYANY+VEHSDLLLAFGVRFDDRVTGKLEAFASRAKIVH
Sbjct: 241 GLGSPYPCDDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRVTGKLEAFASRAKIVH 300

Query: 394 IDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKFPL 453
IDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLE RAEELKLD FGVWRNELN QKQKFPL
Sbjct: 301 IDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLEKRAEELKLD FGVWRNELNEQKQKFPL 360

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAM 513
SFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQFY YKKPRQWLSSGGLGAM
Sbjct: 361 SFKTFGEAIPPQYAIQVDELTDGKAIISTGVGQHQMWAQFYKYKKPRQWLSSGGLGAM 420

Query: 514 GFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQ 573
GFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVK+LLNNQHLGMVMQ
Sbjct: 421 GFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQHLGMVMQ 480

Query: 574 WEDRFYKANRAHTFLGDP AQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQ TMLDTPG 633
WEDRFYKANRAHTFLGDP AQE+EIFPNMLLFAAACGIPAARVTKK LR+AIQ MLDTPG
Sbjct: 481 WEDRFYKANRAHTFLGDP AQENEIFPNMLLFAAACGIPAARVTKKEHLRDAIQKMLDTPG 540

Query: 634 PYLLDVICPHQEHVLPMPINGGTFND 659
PYLLDVICPHQEHVLPMP+GGTF+D
Sbjct: 541 PYLLDVICPHQEHVLPMPISGGTFSD 566

>emb|CAC86695.1| putative acetolactate synthase [Raphanus raphanistrum]
Length = 585

Score = 1129 bits (2919), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 539/584 (92%), Positives = 565/584 (96%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F+SR+APD+PRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS+IRNVLP RHEQG
Sbjct: 2 FVSRYAPDEPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS+IRNVLP RHEQG 61

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADA+LDSVPLVAITGQVPRRMIGTDAF
Sbjct: 62 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 121

Query: 207 QETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSIKHNLYLMDV+DIPRI++EAFFLATSGRPGPVLVDVPKDIQQQLAIPN
Sbjct: 122 QETPIVEVTRSIKHNLYLMDVDDIPRIVQEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 181

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKPVLVYGGGCLNSSDELGRFVELTGI 326
W+Q M+LPGYMSR+P+PP S L QIVRLISESK+PVLVYGGG LNSS+ELGRFVELTGI
Sbjct: 182 WDQPMRLPGYMSRLPQPXVSQLRQIVRLISESKRPVLVYGGGSLNSSEELGRFVELTGI 241

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTGKLEAFA 386
PVASTLMGLGSYPC+DELSL MLGMHGT VYANY+VEHSDLLAFGVRFD DRTGKLEAFA
Sbjct: 242 PVASTLMGLGSYPCNDELSLQMLGMHGT VYANY+VEHSDLLAFGVRFD DRTGKLEAFA 301

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNK+LENR EELKLD FGVWR+EL+
Sbjct: 302 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKILENRGEELKLD FGVWRSELS 361

Query: 447 QKQKFPLSFKTFGEAIP PQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLS 506
QKQKFPLSFKTFGEAIP PQYAI+VLDELTDGKAIISTGVGQHQMWA AQFY Y+KPRQWLS
Sbjct: 362 QKQKFPLSFKTFGEAIP PQYAIQVLDELTDGKAIISTGVGQHQMWA AQFYKPRQWLS 421

Query: 507 SSGGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
S GLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVK+LLNNQ
Sbjct: 422 SSGGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQ 481

Query: 567 HLGVMVQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVT K KADLREAIQ 626
HLGVMVQWEDRFYKANRAHT+LGDPA+E EIFPNML FA ACGIPAARVT K K+LREAIQ
Sbjct: 482 HLGVMVQWEDRFYKANRAHTYLGDPARESEIFPNMLQFAGACGIPAARVT K KEELREAIQ 541

Query: 627 TMLDTPGPYLLDVICPHQEHVLP MIPNGGTFNDVITEGDRIKY 670
TMLDTPGPYLLDVICPHQEHVLP MIP+GGTF DVITE GR KY
Sbjct: 542 TMLDTPGPYLLDVICPHQEHVLP MIPSGGTFKDVITEEXGRKY 585

>gb|AAA62705.1| acetolactate synthase
Length = 599

Score = 1128 bits (2917), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 539/578 (93%), Positives = 564/578 (97%)

Query: 93 PDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAE 152
PD+PRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS+IRNVLP RHEQGGVFAAE
Sbjct: 22 PDEPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS+IRNVLP RHEQGGVFAAE 81

Query: 153 GYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIV 212
GYARSSGKPGICIATSGPGATNLVSGLADA+LDSVPLVAITGQVPRRMIGTDAFQETPIV
Sbjct: 82 GYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIV 141

Query: 213 EVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMK 272
EVTRSIKHNLYLMDV+DIPRI++EAFFLATSGRPGPVLVDVPKDIQQQLAIPN+Q M+
Sbjct: 142 EVTRSIKHNLYLMDVDDIPRIVQEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWDQPMR 201

Query: 273 LPGYMSRMPKPPEDSHLEQIVRLISESKPVLVYGGGCLNSSDELGRFVELTGIPVASTL 332
LPGYMSR+P+PPE S L QIVRLISESK+PVLVYGGG LNSS+ELGRFVELTGIPVASTL
Sbjct: 202 LPGYMSRLPQPPEVSQLQIVRLISESKRPVLVYGGGSLNSSEELGRFVELTGIPVASTL 261

Query: 333 MGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLLA FGVRFDDRVTGKLEAFASRAKIV 392
MGLGSYPC+DELSL MLGMHGT VYANYAVEHSDLLLA FGVRFDDRVTGKLEAFASRAKIV
Sbjct: 262 MGLGSYPCNDELSLQMLGMHGT VYANYAVEHSDLLLA FGVRFDDRVTGKLEAFASRAKIV 321

Query: 393 HIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKFP 452
HIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWR+EL+ QKQKFP
Sbjct: 322 HIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRSELSEQKQKFP 381

Query: 453 LSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGLGA 512
LSFKTFGEAIPPQYAI++LDELTDGKAIISTGVGQHQMWA AQFY Y+KPRQWLSS GLGA
Sbjct: 382 LSFKTFGEAIPPQYAIQILDELTDGKAIISTGVGQHQMWA AQFYKRYKPRQWLSSGGLGA 441

Query: 513 MGFGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLMVM 572
MGFGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVK+LLNNQHLMVM
Sbjct: 442 MGFGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQHLMVM 501

Query: 573 QWEDRFYKANRAHTFLGDP AQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLDTP 632
QWEDRFYKANRAHT+LGDP A+E+EIFPNML FA ACGIPAARVTKK +LREAIQTMLDTP
Sbjct: 502 QWEDRFYKANRAHTYLGDPARENEIFPNMLQFAGACGIPAARVTKKEELREAIQTMLDTP 561

Query: 633 GPYLLDVICPHQEHVLP MIPNGGTFNDVITEGDGRIKY 670
GPYLLDVICPHQEHVLP MIP+GGTF DVITEGDGR KY
Sbjct: 562 GPYLLDVICPHQEHVLP MIPSGGTFKDVITEGDGR TKY 599

>emb|CAC86702.1| putative acetolactate synthase [Raphanus raphanistrum]
Length = 585

Score = 1124 bits (2907), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 538/584 (92%), Positives = 563/584 (96%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F+SR+APD+PRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS+IRNVLP RHEQG
Sbjct: 2 FVSRYAPDEPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS TIRNVLP RHEQG 61

Query: 147 GVFAAEYARSSGKPGICIA TSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEYARSSGKPGICIA TSGPGATNLVSLADA+LDSVPLVAITGQV RRMIGTDAF
Sbjct: 62 GVFAAEYARSSGKPGICIA TSGPGATNLVSLADAMLDVPLVAITGQVXR RMIGTDAF 121

Query: 207 QETPIVEVTRSITKHN YLVM DVEDIPRIIEEAFFLATSGRPGPVLVDV PKDIQQQLAIPN 266
QETPIVEVTRSITKHN YLVM DV+DIPRI++EAFFLATSGRPGPVLVDV PKDIQQQLAIPN
Sbjct: 122 QETPIVEVTRSITKHN YLVM DDDIPRIVQEAFFLATSGRPGPVLVDV PKDIQQQLAIPN 181

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W+Q M+ PGYMSR+P+PPE S L Q VRLISESK PVLYVGGG LNSS+ELGRFVELTGI
Sbjct: 182 WDQPMRXPGYMSRLPQPPEVSLXQXVRLISESKKPVLYVGGGSLNSS EELGRFVELTGI 241

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLLA FGVRFDDRVTGKLEAFA 386
PVASTLMGLGSYPC+DE SL MLGMHGT VYANY+VEHSDLLLA FGVRFDDRVTGKLEA A
Sbjct: 242 PVASTLMGLGSYPCNDEXSLQMLGMHGT VYANY+VEHSDLLLA FGVRFDDRVTGKLEAXA 301

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNK+LENRAEELKLD FGVWR+EL+
Sbjct: 302 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKILENRAEELKLD FGVWRSELSE 361

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLS 506
QKQKFPLSFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWA AQFY Y+KPRQWLS
Sbjct: 362 QKQKFPLSFKTFGEAIPPQYAIQVLDELTDGKAIISTGVGQHQMWA AQFYKRYKPRQWLS 421

Query: 507 SSGGLGAMGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
S GLGAMGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVK+LLNNQ
Sbjct: 422 SSGGLGAMGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQ 481

Query: 567 HLGVMVQWEDRFYKANRAHTFLGDP AQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGVMVQWEDRFYKANRAHT+LGDP A+E EIFPNML FA ACGIPAARVTKK +LREAIQ
Sbjct: 482 HLGVMVQWEDRFYKANRAHTYLGDPARESEIFPNMLQFAGACGIPAARVTKKEELREAIQ 541

Query: 627 TMLDTPGPYLLDVICPHQEHVLP MIPNGGTFNDVITEGDGRIKY 670
TMLDTPGPYLLDVICPHQEHVLP MIP+GGTF DVITEGDGR KY
Sbjct: 542 TMLDTPGPYLLDVICPHQEHVLP MIPSGGTFKDVITEGDGR TKY 585

>gb|AAY46011.1| putative acetolactate synthase [Sinapis arvensis]
Length = 577

Score = 1123 bits (2904), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 538/577 (93%), Positives = 563/577 (97%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVFA 150
+APD+PRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLPHEQGG+FA
Sbjct: 1 YAPDEPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLPHEQGGIFA 60

Query: 151 AEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
AEGYARSSGKPGICIATSGPGATNLVSGGLADA+LDVPLVAITGQVPRRMIGTDAFQETP
Sbjct: 61 AEGYARSSGKPGICIATSGPGATNLVSGGLADAMLDVPLVAITGQVPRRMIGTDAFQETP 120

Query: 211 IVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNLYLMDV+DIPRI++EAFFLATSGRPGPVLVDVDPKDIQQQLAIPNW+Q
Sbjct: 121 IVEVTRSITKHNLYLMDVDDIPRIVQEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWDQP 180

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M+LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSSDELGRFVELTGIPVAS
Sbjct: 181 MRLPGYMSRLPQPPEVSQLGQIVRLISESKRPVLYVGGGSLNSSDELGRFVELTGIPVAS 240

Query: 331 TLMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAK 390
TLMGLGSYPC+DELSL MLGMHGTVYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAK
Sbjct: 241 TLMGLGSYPCNDELSLQMLGMHGTVYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAK 300

Query: 391 IVHIDIDSAEIGKNKTPHVSVCDDVKLALQGMNKVLENRAEELKLDGFWVRNENLVQKQK 450
IVHIDIDSAEIGKNKTPHVSVCDDVKLALQGMNKVLENRAEELKLDGFWVR+EL+ QKQK
Sbjct: 301 IVHIDIDSAEIGKNKTPHVSVCDDVKLALQGMNKVLENRAEELKLDGFWVRSELSEKQKQK 360

Query: 451 FPLSFKTFGEAIPPQYAIKVLELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
FPLSFKTFGEAIPPQYAI+VLELTDGKAIISTGVGQHQMWAQFY Y+KPRQWLSS GL
Sbjct: 361 FPLSFKTFGEAIPPQYAIQVLELTDGKAIISTGVGQHQMWAQFYKYRKPQWLSSSGL 420

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVK+LLNNQHLGM
Sbjct: 421 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQHLGM 480

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNPMMLFAAACGIPAARVTKKADLREAIQTMLD 630
VMQWEDRFYKANRAHT+LGDPA+E+EIFNPMML FA ACGIPAARVTKK +LR+AIQTMLD
Sbjct: 481 VMQWEDRFYKANRAHTYLGDPAKENEIFNPMMLQFAGACGIPAARVTKKEELRDAIQTMLD 540

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGR 667
TPGPYLLDVICPHQEHVLPMP+GGTF DVITEGDGR
Sbjct: 541 TPGPYLLDVICPHQEHVLPMPSGGTFKDVITEGDGR 577

>emb|CAC86703.1| putative acetolactate synthase [Raphanus raphanistrum]
Length = 585

Score = 1122 bits (2902), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 537/584 (91%), Positives = 562/584 (96%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQG 146
F+SR+APD+PRKGADILVEALERQGVETVFAYPPGGASM IHQALTRSS+IRNVLPHEQG
Sbjct: 2 FVSRYAPDEPRKGADILVEALERQGVETVFAYPPGGASMXIHQALTRSS+IRNVLPHEQG 61

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADA+LDVPLVAITGQVPRRMIGTDAF
Sbjct: 62 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADAMLDVPLVAITGQVPRRMIGTDAF 121

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPN 266
QETPIVEVTRSITKHNLYLMDV+DIPRI++EAFFLATSGRPGPVLVDVDPKDIQQQLAIP
Sbjct: 122 QETPIVEVTRSITKHNLYLMDVDDIPRIVQEAFFLATSGRPGPVLVDVDPKDIQQQLAIPX 181

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W+Q M+LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSS+ELGRFVELTGI
Sbjct: 182 WDQPMRLPGYMSRLPQPPEVSQLRQIVRLISESKRPVLYVGGGSLNSSDELGRFVELTGI 241

Query: 327 PVASTLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTVGKLEAFA 386
PVASTLMGLGSYPC+DE SL MLGMHGT VYANY+VEHSD LLAFGVRFD DRTVGKLEAFA
Sbjct: 242 PVASTLMGLGSYPCNDESLQMLGMHGT VYANYAVEHSDXLLAFGVRFD DRTVGKLEAFA 301

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNK+LENRAEELKLD FGVWR+ELN
Sbjct: 302 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKILENRAEELKLD FGVWRSELNE 361

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDEL TDGKAIISTGVGQHQMWA AQFYNYKKPRQWLS 506
QKQKFPLSFKTFGEAIPPQYAI+VLDEL TDGKAIISTGVGQHQMWA AQFY Y+KPRQWLS
Sbjct: 362 QKQKFPLSFKTFGEAIPPQYAIQVLDEL TDGKAIISTGVGQHQMWA AQFYK YRKPQWLS 421

Query: 507 SSGGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLL LNNQ 566
S GLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVK+LL LNNQ
Sbjct: 422 SSGGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKILL LNNQ 481

Query: 567 HLGMMVMQWEDRFYKANRAHTFLGDPAQE DEIFPNMLFAAACGIPAARVTKKADLREAIQ 626
HLGMMVMQ EDRFYKANRAHT+LGDPA+E EIFPNML FA ACGIPAARVTKK +LREAIQ
Sbjct: 482 HLGMMVMQXEDRFYKANRAHTYLGDPARESEIFPNMLQFAGACGIPAARVTKKEELREAIQ 541

Query: 627 TMLDTPGPYLLDVICPHQEHVLP MIPNGGTFNDVITEGDGR IKY 670
TMLDTP PYLLDVICPHQEHVLP MIP+GGTF DVITEGDGR KY
Sbjct: 542 TMLDTPXPYLLDVICPHQEHVLP MIPSGGTFKDVITEGDGR TKY 585

>gb|AA46010.1| putative acetolactate synthase [Sinapis arvensis]
Length = 576

Score = 1121 bits (2900), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 538/576 (93%), Positives = 562/576 (97%)

Query: 92 APDQPRKGADILVEALERQGVETVFAYPG GASMEIHQALTRSSIRNVLP RHEQGGVF AA 151
APD+PRKGADILVEALERQGVETVFAYPG GASMEIHQALTRSS+IRNVLP RHEQGG+FAA
Sbjct: 1 APDEPRKGADILVEALERQGVETVFAYPG GASMEIHQALTRSSIRNVLP RHEQGGIF AA 60

Query: 152 EGYARSSGKPGICIA TSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPI 211
EGYARSSGKPGICIA TSGPGATNLVSLADA+LDSVPLVAITGQVPRRMIGTDAFQETPI
Sbjct: 61 EGYARSSGKPGICIA TSGPGATNLVSLADAMLDSVPLVAITGQVPRRMIGTDAFQETPI 120

Query: 212 VEVTRSI TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAM 271
VEVTRSI TKHNYLVMDV+DIPRI++EAFFLATSGRPGPVLVDVPKDIQQQLAIPNW+Q M
Sbjct: 121 VEVTRSI TKHNYLVMDVDDIPRIVQEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWDQPM 180

Query: 272 KLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAST 331
+LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSSDELGRFVELTGIPVAST
Sbjct: 181 RLPGYMSRLPQPPEVSLGQIVRLISESKRPVLYVGGGSLNSSDELGRFVELTGIPVAST 240

Query: 332 LMGLGSYPCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTVGKLEAFASRAKI 391
LMGLGSYPC+DELSL MLGMHGT VYANYAVEHSDLLAFGVRFD DRTVGKLEAFASRAKI
Sbjct: 241 LMGLGSYPCNDESLQMLGMHGT VYANYAVEHSDLLAFGVRFD DRTVGKLEAFASRAKI 300

Query: 392 VHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKF 451
VHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWR+EL+ QKQKF
Sbjct: 301 VHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRSELSEQKQKF 360

Query: 452 PLSFKTFGEAIPPQYAIKVLDEL TDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGLG 511
PLSFKTFGEAIPPQYAI+VLDEL T GKAIISTGVGQHQMWA AQFY Y+KPRQWLSS GLG
Sbjct: 361 PLSFKTFGEAIPPQYAIQVLDEL THGKAIISTGVGQHQMWA AQFYK YRKPQWLSSSGLG 420

Query: 512 AMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLL LNNQHLMGV 571
AMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVK+LL LNNQHLMGV
Sbjct: 421 AMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKILL LNNQHLMGV 480

Query: 572 MQWEDRFYKANRAHTFLGDPAQE DEIFPNMLFAAACGIPAARVTKKADLREAIQTMLDT 631
MQWEDRFYKANRAHT+LGDPA+E+EIFPNML FA ACGIPAARVTKK +LR+AIQTMLDT
Sbjct: 481 MQWEDRFYKANRAHTYLGDPAKENEIFPNMLQFAGACGIPAARVTKKEELRDAIQTMLDT 540

Query: 632 PGPYLLDVICPHQEHVLP MIPNGGTFNDVITEGDGR 667
PGPYLLDVICPHQEHVLP MIP+GGTF DVITEGDGR
Sbjct: 541 PGPYLLDVICPHQEHVLP MIPSGGTFKDVITEGDGR 576

>gb|AAY46004.1| putative acetolactate synthase [Sinapis arvensis]
Length = 576

Score = 1120 bits (2897), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 536/576 (93%), Positives = 561/576 (97%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVFA 150
+APD+PRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLPHEQGG+FA
Sbjct: 1 YAPDEPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLPHEQGGIFA 60

Query: 151 AEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
AEGYARSSGKPGICIATSGPGATNLVSGLADA+LDSVPLVAITGQV RRMIGTDAFQETP
Sbjct: 61 AEGYARSSGKPGICIATSGPGATNLVSGLADAMLDVPLVAITGQVSRRMIGTDAFQETP 120

Query: 211 IVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNLYLMDV+DIPRI++EAFFLATSGRPGPVLVDVPKDIQQQLAIPNW+Q
Sbjct: 121 IVEVTRSITKHNLYLMDVDDIPRIVQEAFLLATSGRPGPVLVDVPKDIQQQLAIPNWDQP 180

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M+LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSSDELGRFVELTGIPVAS
Sbjct: 181 MRLPGYMSRLQPPEVSQLSQIVRLISESKRPVLYVGGGSLNSSDELGRFVELTGIPVAS 240

Query: 331 TLMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASRAK 390
TLMGLGSYPC+DELSL MLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASRAK
Sbjct: 241 TLMGLGSYPCNDELSLQMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASRAK 300

Query: 391 IVHIDIDSAEIGKKNKTPHVSVCDDVKLALQGMNKVLENRAEELKLDGFWVRNENLVQKQK 450
IVHIDIDSAEIGKKNKTPHVSVCDDVKLALQGMNKVLENRAEELKLDGFWVR+EL+ QKQK
Sbjct: 301 IVHIDIDSAEIGKKNKTPHVSVCDDVKLALQGMNKVLENRAEELKLDGFWVRSELSEKQKQK 360

Query: 451 FPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
FPLSFKTFGEAIPPQYAI+VDELTDGKAIISTGVGQHQMWAQFY Y+KPRQWLSS GL
Sbjct: 361 FPLSFKTFGEAIPPQYAIQVDELTDGKAIISTGVGQHQMWAQFYKYRKPQWLSSSGL 420

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVK+LLNNQHLGM
Sbjct: 421 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQHLGM 480

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNPMMLFAAACGIPAARVTKKADLREAIQTMLD 630
VMQWEDRFYKANRAHT+LGDPA+E+EIFNPMML FA ACGIPAARVTKK +LR+AIQTMLD
Sbjct: 481 VMQWEDRFYKANRAHTYLGDPAKENEIFNPMMLQFAGACGIPAARVTKKEELRDIAQTMLD 540

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDG 666
TPGPYLLDVICPHQEHVLPMP+GGTF DVITEGDG
Sbjct: 541 TPGPYLLDVICPHQEHVLPMPSGGTFKDVITEGDG 576

>gb|AAY46012.1| putative acetolactate synthase [Sinapis arvensis]
Length = 577

Score = 1120 bits (2896), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 537/577 (93%), Positives = 562/577 (97%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVFA 150
+APD+PRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLPHEQGG+FA
Sbjct: 1 YAPDEPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLPHEQGGIFA 60

Query: 151 AEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
AEGYARSSGKPGICIATSGPGATNLVSGLADA+LDSVPLVAITGQVPRRMIGTDAFQETP
Sbjct: 61 AEGYARSSGKPGICIATSGPGATNLVSGLADAMLDVPLVAITGQVPRRMIGTDAFQETP 120

Query: 211 IVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNLYLMDV+DIPRI++EAFFLATSGRPGPVLVDVPKDIQQQLAIPNW+Q
Sbjct: 121 IVEVTRSITKHNLYLMDVDDIPRIVQEAFLLATSGRPGPVLVDVPKDIQQQLAIPNWDQP 180

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M+LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSSDELGRFVELTGIPVAS
Sbjct: 181 MRLPGYMSRLQPPEVSQLGQIVRLISESKRPVLYVGGGSLNSSDELGRFVELTGIPVAS 240

Query: 331 TLMGLGSYPCCDELSLHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTKLEAFASRAK 390
TLMGLGSYPC+DELSL MLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTKLEAFASRAK
Sbjct: 241 TLMGLGSYPCCNDELSLQMLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTKLEAFASRAK 300

Query: 391 IVHIDIDSAEIGKNKTPHVSVCADVCLALQGMNKVLENRAEELKLDGFGVWRNENLVQKQK 450
IVHIDIDSAEIGKNKTPHVSVCADVCLALQGMNKVLENRAEELKLDGFGVWR+EL+ QKQK
Sbjct: 301 IVHIDIDSAEIGKNKTPHVSVCADVCLALQGMNKVLENRAEELKLDGFGVWRSELSEQKQK 360

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
FPLSFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQFY Y+KPRQWLSS GL
Sbjct: 361 FPLSFKTFGEAIPPQYAIQVLDELTDGKAIISTGVGQHQMWAQFYKYRKPRQWLSSGGL 420

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVK+LLLNNQHLGM
Sbjct: 421 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQHLGM 480

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
VMQ EDRFYKANRAHT+LGDP+E+EIFPNML FA ACGIPAARVTKK +LR+AIQTMLD
Sbjct: 481 VMQLEDRFYKANRAHTYLGDPAKENEIFPNMLQFAGACGIPAARVTKKEELRDAIQTMLD 540

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGR 667
TPGPYLLDVICPHQEHVLPMP+GGTF DVITEGDGR
Sbjct: 541 TPGPYLLDVICPHQEHVLPMPSSGGTFKDVITEGDGR 577

>gb|AA46008.1| putative acetolactate synthase [Sinapis arvensis]
Length = 575

Score = 1119 bits (2895), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 537/575 (93%), Positives = 561/575 (97%)

Query: 93 PDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHEQGGVFAAE 152
PD+PRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS+IRNVLPRHEQGG+FAAE
Sbjct: 1 PDEPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHEQGGIFAAE 60

Query: 153 GYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITQVPRRMIGTDAFQETPIV 212
GYARSSGKPGICIATSGPGATNLVSGLADA+LDSVPLVAITQVPRRMIGTDAFQETPIV
Sbjct: 61 GYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITQVPRRMIGTDAFQETPIV 120

Query: 213 EVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMK 272
EVTRSITKHNYLVMDV+DIPRI++EAFFLATSGRPGPVLVDVPKDIQQQLAIPNW+Q M+
Sbjct: 121 EVTRSITKHNYLVMDVDIPRIVQEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWDQPMR 180

Query: 273 LPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGCLNSSDELGRFVELTGIPVASTL 332
LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSSDELGRFVELTGIPVASTL
Sbjct: 181 LPGYMSRPLQPPEVSQLQIVRLISESKRPVLYVGGGSLNSSDELGRFVELTGIPVASTL 240

Query: 333 MGLGSYPCCDELSLHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTKLEAFASRAKIV 392
MGLGSYPC+DELSL MLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTKLEAFASRAKIV
Sbjct: 241 MGLGSYPCCNDELSLQMLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTKLEAFASRAKIV 300

Query: 393 HIDIDSAEIGKNKTPHVSVCADVCLALQGMNKVLENRAEELKLDGFGVWRNENLVQKQKFP 452
HIDIDSAEIGKNKTPHVSVCADVCLALQGMNKVLENRAEELKLDGFGVWR+EL+ QKQKFP
Sbjct: 301 HIDIDSAEIGKNKTPHVSVCADVCLALQGMNKVLENRAEELKLDGFGVWRSELSEQKQKFP 360

Query: 453 LSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGA 512
LSFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQFY Y+KPRQWLSS GLGA
Sbjct: 361 LSFKTFGEAIPPQYAIQVLDELTDGKAIISTGVGQHQMWAQFYKYRKPRQWLSSGGLGA 420

Query: 513 MGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVM 572
MGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVK+LLLNNQHLGMVM
Sbjct: 421 MGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQHLGMVM 480

Query: 573 QWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDTP 632
QWEDRFYKANRAHT+LGDP+E+EIFPNML FA ACGIPAARVTKK +LR+AIQTMLDTP
Sbjct: 481 QWEDRFYKANRAHTYLGDPAKENEIFPNMLQFAGACGIPAARVTKKEELRDAIQTMLDTP 540

Query: 633 GPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGR 667
GPYLLDVICPHQEHVLPMP+GGTF DVITEGDGR
Sbjct: 541 GPYLLDVICPHQEHVLPMPSSGGTFKDVITEGDGR 575

>gb|AA45998.1| putative acetolactate synthase [Sinapis arvensis]
gb|AA45999.1| putative acetolactate synthase [Sinapis arvensis]
Length = 574

Score = 1118 bits (2891), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 535/574 (93%), Positives = 560/574 (97%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVFA 150
+APD+PRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLPHEQGG+FA
Sbjct: 1 YAPDEPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLPHEQGGIFA 60

Query: 151 AEGYARSSGKPGICIAATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
AEGYARSSGKPGICIAATSGPGATNLVSGGLADA+LDSVPLVAITGQVPRRMIGTDAFQETP
Sbjct: 61 AEGYARSSGKPGICIAATSGPGATNLVSGGLADAMLDVPLVAITGQVPRRMIGTDAFQETP 120

Query: 211 IVEVTRSTITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQA 270
IVEVTRSTITKHNYLVMDV+DIPRI++EAFFLATSGRPGPVLVDVPKDIQQQLAIPNW+Q
Sbjct: 121 IVEVTRSTITKHNYLVMDVDDIPRIVQEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWDQP 180

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M+LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSSDELGRFVELTGIPVAS
Sbjct: 181 MRLPGYMSRLQPPEVSQLXQIVRLISESKRPVLYVGGGSLNSSDELGRFVELTGIPVAS 240

Query: 331 TLMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRTVGKLEAFASRAK 390
TLMGLGSYPC+DELSL MLGMHGTVYANYAVEHSDLLAFGVRFDDRTVGKLEAFASRAK
Sbjct: 241 TLMGLGSYPCNDELSLQMLGMHGTVYANYAVEHSDLLAFGVRFDDRTVGKLEAFASRAK 300

Query: 391 IVHIDIDSAEIGKNKTPHVSVCADVKLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQK 450
IVHIDIDSAEIGKNKTPHVSVCADVKLALQGMNKVLENRAEELKLDGFGVWR+EL+ QKQK
Sbjct: 301 IVHIDIDSAEIGKNKTPHVSVCADVKLALQGMNKVLENRAEELKLDGFGVWRSELSEKQKQK 360

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMMAAQFYNYKKPRQWLSSGGL 510
FPLSFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMMAAQFY Y+KPRQWLSS GL
Sbjct: 361 FPLSFKTFGEAIPPQYAIQVLDELTHGKAIISTGVGQHQMMAAQFYKPRQWLSSGGL 420

Query: 511 GAMGFGLPAAIGASVANPDIAVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAAIGASVANPDIAVVDIDGDSFIMNVQELATIRVENLPVK+LLNNQHLGM
Sbjct: 421 GAMGFGLPAAIGASVANPDIAVVDIDGDSFIMNVQELATIRVENLPVKILLNNQHLGM 480

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
VMQWEDRFYKANRAHT+LGDP+A+E+EIFPNML FA ACGIPAARVTKK +LR+AIQTMLD
Sbjct: 481 VMQWEDRFYKANRAHTYLGDPAKENEIFPNMLQFAGACGIPAARVTKKEELRDAIQTMLD 540

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEG 664
TPGPYLLDVICPHQEHVLPMP+GGTF DVITEG
Sbjct: 541 TPGPYLLDVICPHQEHVLPMPSGGTFKDVITEG 574

>gb|AA45995.1| putative acetolactate synthase [Sinapis arvensis]
gb|AA45996.1| putative acetolactate synthase [Sinapis arvensis]
gb|AA45997.1| putative acetolactate synthase [Sinapis arvensis]
gb|AA46000.1| putative acetolactate synthase [Sinapis arvensis]
gb|AA46001.1| putative acetolactate synthase [Sinapis arvensis]
gb|AA46002.1| putative acetolactate synthase [Sinapis arvensis]
gb|AA46003.1| putative acetolactate synthase [Sinapis arvensis]
Length = 574

Score = 1117 bits (2890), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 535/574 (93%), Positives = 560/574 (97%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVFA 150
+APD+PRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLPHEQGG+FA
Sbjct: 1 YAPDEPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLPHEQGGIFA 60

Query: 151 AEGYARSSGKPGICIAATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
AEGYARSSGKPGICIAATSGPGATNLVSGGLADA+LDSVPLVAITGQVPRRMIGTDAFQETP
Sbjct: 61 AEGYARSSGKPGICIAATSGPGATNLVSGGLADAMLDVPLVAITGQVPRRMIGTDAFQETP 120

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLVMDV+DIPRI++EAAFFLATSGRPGPVLVDVPKDIQQQLAIPNW+Q
Sbjct: 121 IVEVTRSITKHNYLVMDVDDIPRIVQEAAFFLATSGRPGPVLVDVPKDIQQQLAIPNWDQP 180

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M+LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSSDELGRFVELTGIPVAS
Sbjct: 181 MRLPGYMSRLQPPEVSQLGQIVRLISESKRPVLYVGGGSLNSSDELGRFVELTGIPVAS 240

Query: 331 TLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAK 390
TLMGLGSYPC+DELSL MLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAK
Sbjct: 241 TLMGLGSYPCNDELSLQMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAK 300

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQK 450
IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWR+EL+ QKQK
Sbjct: 301 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRSELSEQKQK 360

Query: 451 FPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQQFYNYKKPRQWLSSGGL 510
FPLSFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQQFY Y+KPRQWLSS GL
Sbjct: 361 FPLSFKTFGEAIPPQYAIQVDELTDGKAIISTGVGQHQMWAQQFYKPRQWLSSGGL 420

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLLNNQHLGM 570
GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVK+LLLNNQHLGM
Sbjct: 421 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQHLGM 480

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
VMQWEDRFYKANRAHT+LGDP+A+E+EIFNML FA ACGIPAARVTKK +LR+AIQTMLD
Sbjct: 481 VMQWEDRFYKANRAHTYLGDPAKENEIFNMLQFAGACGIPAARVTKKEELRDAIQTMLD 540

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEG 664
TPGPYLLDVICPHQEHVLPMP+GGTF DVITEG
Sbjct: 541 TPGPYLLDVICPHQEHVLPMPSGGTFKDVITEG 574

>gb|AAY46007.1| putative acetolactate synthase [Sinapis arvensis]
Length = 574

Score = 1117 bits (2890), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 536/574 (93%), Positives = 560/574 (97%)

Query: 93 PDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHEQGGVFAAE 152
PD+PRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS+IRNVLPRHEQGG+FAAE
Sbjct: 1 PDEPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSIRNVLPRHEQGGIFAAE 60

Query: 153 GYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIV 212
GYARSSGKPGICIATSGPGATNLVSGLADA+LDSVPLVAITGQVPRRMIGTDAFQETPIV
Sbjct: 61 GYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIV 120

Query: 213 EVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMK 272
EVTRSITKHNYLVMDV+DIPRI++EAAFFLATSGRPGPVLVDVPKDIQQQLAIPNW+Q M+
Sbjct: 121 EVTRSITKHNYLVMDVDDIPRIVQEAAFFLATSGRPGPVLVDVPKDIQQQLAIPNWDQPMR 180

Query: 273 LPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVASTL 332
LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSSDELGRFVELTGIPVASTL
Sbjct: 181 LPGYMSRLQPPEVSQLGQIVRLISESKRPVLYVGGGSLNSSDELGRFVELTGIPVASTL 240

Query: 333 MGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIV 392
MGLGSYPC+DELSL MLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIV
Sbjct: 241 MGLGSYPCNDELSLQMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIV 300

Query: 393 HIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKFP 452
HIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWR+EL+ QKQKFP
Sbjct: 301 HIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRSELSEQKQKFP 360

Query: 453 LSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQQFYNYKKPRQWLSSGGLGA 512
LSFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQQFY Y+KPRQWLSS GLGA
Sbjct: 361 LSFKTFGEAIPPQYAIQVDELTDGKAIISTGVGQHQMWAQQFYKPRQWLSSGGLGA 420

Query: 513 MGFGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLLNNQHLGMVM 572
MGFGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVK+LLLNNQHLGMVM
Sbjct: 421 MGFGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQHLGMVM 480

Query: 573 QWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLDTP 632
QWEDRFYKANRAHT+LGDP+E+EIFPNML FA ACGIPAARVTKK +LR+AIQTMLDTP
Sbjct: 481 QWEDRFYKANRAHTYLGDPAKENEIFPNMLQFAGACGIPAARVTKKEELRDAIQTMLDTP 540

Query: 633 GPYLLDVICPHQEHVLPMPNGGTFNDVITEGDG 666
GPYLLDVICPHQEHVLPMP+GGTF DVITEGDG
Sbjct: 541 GPYLLDVICPHQEHVLPMPISGGTFKDVITEGDG 574

>gb|AA46013.1| putative acetolactate synthase [Sinapis arvensis]
Length = 575

Score = 1115 bits (2884), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 535/575 (93%), Positives = 560/575 (97%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVFA 150
+APD+PRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLPHEQGG+FA
Sbjct: 1 YAPDEPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSIRNVLPHEQGGIFA 60

Query: 151 AEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
AEGYARSSGKPGICIATSGPGATNLVSGLADA+LDSVPLVAITGQVPRRMIGTDAFQETP
Sbjct: 61 AEGYARSSGKPGICIATSGPGATNLVSGLADAMLDVPLVAITGQVPRRMIGTDAFQETP 120

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLVMDV+DIPRI++EAFFLATSGRPGPVLVDVPKDIQQQLAIPNW+Q
Sbjct: 121 IVEVTRSITKHNYLVMDVDDIPRIVQEAFLLATSGRPGPVLVDVPKDIQQQLAIPNWDQP 180

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGCLNSSDELGRFVELTGIPVAS 330
M+LPGYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSSDELGRFVELTGIPVAS
Sbjct: 181 MRLPGYMSRLQPPEVSQLGQIVRLISESKRPVLYVGGSLNSSDELGRFVELTGIPVAS 240

Query: 331 TLMGLGSYPCDELDSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRTVGKLEAFASRAK 390
TLMGLGSYPC+DELSL MLGMHGTVYANYAVEHSDLLAFGVRFDDRTVGKLEAFASRAK
Sbjct: 241 TLMGLGSYPCDELDSLQMLGMHGTVYANYAVEHSDLLAFGVRFDDRTVGKLEAFASRAK 300

Query: 391 IVHIDIDSAEIGKNKTPHVSVCADVCLALQGMNKVLENRAEELKLDGFWVRNENLVQKQK 450
IVHIDIDSAEIGKNKTPHVSVCADVCLALQGMNKVLENRAEELKLDGFWVR+EL+ QKQK
Sbjct: 301 IVHIDIDSAEIGKNKTPHVSVCADVCLALQGMNKVLENRAEELKLDGFWVRSELSEKQKQK 360

Query: 451 FPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
FPLSFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQFY Y+KPRQWLSS GL
Sbjct: 361 FPLSFKTFGEAIPPQYAIQVDELTDGKAIISTGVGQHQMWAQFYKYRKPRQWLSSGGL 420

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVK+LLNNQHLGM
Sbjct: 421 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQHLGM 480

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
VMQ EDRFYKANRAHT+LGDP+E+EIFPNML FA ACGIPAARVTKK +LR+AIQTMLD
Sbjct: 481 VMQXEDRFYKANRAHTYLGDPAKENEIFPNMLQFAGACGIPAARVTKKEELRDAIQTMLD 540

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGD 665
TPGPYLLDVICPHQEHVLPMP+GGTF DVITEGD
Sbjct: 541 TPGPYLLDVICPHQEHVLPMPISGGTFKDVITEGD 575

>gb|AA46005.1| putative acetolactate synthase [Sinapis arvensis]
Length = 573

Score = 1115 bits (2883), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 534/573 (93%), Positives = 558/573 (97%)

Query: 95 QPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGY 154
+PRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSS+IRNVLPHEQGG+FAAEGY
Sbjct: 1 EPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSIRNVLPHEQGGIFAEGY 60

Query: 155 ARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEV 214
ARSSGKPGICIATSGPGATNLVSGLADA+LDSVPLVAITGQV RRMIGTDAFQETPIVEV
Sbjct: 61 ARSSGKPGICIATSGPGATNLVSGLADAMLDVPLVAITGQVSRRMIGTDAFQETPIVEV 120

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Query: 215 TRSITKHNYLVMDEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQAMKLP 274
          TRSITKHNYLMDV+DIPRI++EAAFFLATSGRPGPVLVDVDPKDIQQQLAIPNW+Q M+LP
Sbjct: 121 TRSITKHNYLMDVDDIPRIVQEAAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWDQPMRLP 180

Query: 275 GYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVASTLMG 334
          GYMSR+P+PPE S L QIVRLISESK+PVLYVGGG LNSSDELGRFVELTGIPVASTLMG
Sbjct: 181 GYMSRLPQPPEVSQLSQIVRLISESKRPVLYVGGGSLNSSDELGRFVELTGIPVASTLMG 240

Query: 335 LGSYPCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVHI 394
          LGSYPC+DELSL MLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVHI
Sbjct: 241 LGSYPCNDELSLQMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVHI 300

Query: 395 DIDS AEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKFP LS 454
          DIDS AEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWR+EL+ QKQKFP LS
Sbjct: 301 DIDS AEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRSELSEQKQKFP LS 360

Query: 455 FKT FGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMG 514
          FKT FGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQFY Y+KPRQWLSS GLGAMG
Sbjct: 361 FKT FGEAIPPQYAIQVLDELTDGKAIISTGVGQHQMWAQFYKYRKPRQWLSSGGLGAMG 420

Query: 515 FGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQW 574
          FGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVK+LLNNQHLGMVMQW
Sbjct: 421 FGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQHLGMVMQW 480

Query: 575 EDRFYKANRAHTFLGDP AQEDEFIPNMLLFAACGIPAARVTKKADLREAIQTMLDTPGP 634
          EDRFYKANRAHT+LGDPA+E+EIPNML FA ACGIPAARVTKK +LR+AIQTMLDTPGP
Sbjct: 481 EDRFYKANRAHTYLGDPAKENEIIPNMLQFAGACGIPAARVTKKEELRDAIQTMLDTPGP 540

Query: 635 YLLDVICPHQEHVLP MIPNGGTFNDVITEGDGR 667
          YLLDVICPHQEHVLP MIP+GGTF DVITEGDGR
Sbjct: 541 YLLDVICPHQEHVLP MIPSGGTFKDVITEGDGR 573

>emb|CAC86693.1| putative acetolactate synthase [Raphanus raphanistrum]
      Length = 585

      Score = 1112 bits (2877), Expect = 0.0, Method: Compositional matrix adjust.
      Identities = 533/584 (91%), Positives = 559/584 (95%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQG 146
          F+SR+APD+PRKGADILVEALERQGVETVFAYPPGGASM IHQALTRSS+IRNVLP RHEQG
Sbjct: 2 FVSRYAPDEPRKGADILVEALERQGVETVFAYPPGGASMXIHQALTRSSSIRNVLP RHEQG 61

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
          GVFAAEGYARSSGKPGICIATSGPGATNLVSLADA+LD VPLVAITGQVPRRMIGTDAF
Sbjct: 62 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADAML DXVPLVAITGQVPRRMIGTDAF 121

Query: 207 QETPIVEVTR S I T K H N Y L V M D E D I P R I I E E A F F L A T S G R P G P V L V D V P K D I Q Q Q L A I P N 266
          QETPIVEVTR S I T K H N Y L V M V + D I P R I I E E A F F L A T S G R P G P V L V D V P K D I Q Q Q L A I P N
Sbjct: 122 QETPIVEVTR S I T K H N Y L V M X V D D I P R I V Q E A F F L A T S G R P G P V L V D V P K D I Q Q Q L A I P N 181

Query: 267 WEQAMKLP G Y M S R M P K P P E D S H L E Q I V R L I S E S K K P V L Y V G G G C L N S S D E L G R F V E L T G I 326
          W+Q M+LPGYMSR+P+PPE S L QIVRLISESK PVLYVGGG LNSS+ELGRFVELTG
Sbjct: 182 WDQPMRLPGYMSRLPQPPEVSQLRQIVRLISESKXPVLYVGGGSLNSSEELGRFVELTGX 241

Query: 327 PVASTLMGLGSYPCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFA 386
          PVASTLMGLGS PC+DE SL MLGMHGT VYANY+VEHSDLLAFGVRFDRTGKLEAFA
Sbjct: 242 PVASTLMGLGSXPCNDEXSLQMLGMHGT VYANY+VEHSDLLAFGVRFDRTGKLEAFA 301

Query: 387 SRAKIVHIDIDS AEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
          SRAKIVH DIDS AEIGKNKTPHVSVC G DVKLALQGMN++LENRAEELKLD FGVWR+EL+
Sbjct: 302 SRAKIVHXDIDS AEIGKNKTPHVSVC G DVKLALQGMNEILENRAEELKLD FGVWRSELSE 361

Query: 447 QKQKFP L S F K T F G E A I P P Q Y A I K V L D E L T D G K A I I S T G V G Q H Q M W A A Q F Y N Y K K P R Q W L S 506
          QKQKFP L S F K T F G E A I P P Q Y A I + V L D E L T D G K A I I S T G V G Q H Q M W A A Q F Y Y + K P R Q W L S
Sbjct: 362 QKQKFP L S F K T F G E A I P P Q Y A I Q V L D E L T D G K A I I S T G V G Q H Q M W A A Q F Y K Y R K P R Q W L S 421

Query: 507 S S G L G A M G F G L P A A I G A S V A N P D A I V V D I D G D S F I M N V Q E L A T I R V E N L P V K V L L L N N Q 566
          S GLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVK+LLNNQ
Sbjct: 422 S S G L G A M G F G L P A A I G A S V A N P D A I V V D I D G D S F I M N V Q E L A T I R V E N L P V K I L L L N N Q 481

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Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGMMVQ EDRFYKANRAHT+LGDPA+E EIFPNM FA ACGIPAARVTKK +LREAIQ
Sbjct: 482 HLGMMVQLEDRFYKANRAHTYLGDPAESEIFPNMXQFAGACGIPAARVTKKXELREAIQ 541

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
TMLDTPGPYLLDVICPHQEHVLPMP+GGTF DVITEGDGR KY
Sbjct: 542 TMLDTPGPYLLDVICPHQEHVLPMPSSGGTFKDVITEGDGRKY 585

>gb|AA46006.1| putative acetolactate synthase [Sinapis arvensis]
gb|AA46009.1| putative acetolactate synthase [Sinapis arvensis]
Length = 567

Score = 1104 bits (2855), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 530/567 (93%), Positives = 553/567 (97%)

Query: 101 DILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSSGK 160
DILVEALERQGVETVFAYPGGASMEIHQALTRSS+IRNVLPHEQGG+FAAEGYARSSGK
Sbjct: 1 DILVEALERQGVETVFAYPGGASMEIHQALTRSS+IRNVLPHEQGGIFAAEGYARSSGK 60

Query: 161 PGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITK 220
PGICIATSGPGATNLVSLADALA+LDVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITK
Sbjct: 61 PGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITK 120

Query: 221 HNYLVMVDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMSRM 280
HNYLVMVDV+DIPRI++EAFFLATSGRPGPVLVDVPKDIQQQLAIPNW+Q M+LPGYMSR+
Sbjct: 121 HNYLVMVDVDDIPRIVQEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWDQPMRLPGYMSRL 180

Query: 281 PKPPEDSHLEQIVRLISESKPVLVVGGLNSSDELGRFVELTGIPVASTLMGLGSYPC 340
P+PPE S L QIVRLISESK+PVLVVGGLNSSDELGRFVELTGIPVASTLMGLGSYPC
Sbjct: 181 PQPPEVSQLGQIVRLISESKPVLVVGGLNSSDELGRFVELTGIPVASTLMGLGSYPC 240

Query: 341 DDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVHIDIDSAE 400
+DELSL MLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVHIDIDSAE
Sbjct: 241 NDELSLQMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVHIDIDSAE 300

Query: 401 IGKNKTPHVSVCQDVKLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQKFLSFKTFGE 460
IGKNKTPHVSVCQDVKLALQGMNKVLENRAEELKLDGFGVWR+EL+ QKQKFLSFKTFGE
Sbjct: 301 IGKNKTPHVSVCQDVKLALQGMNKVLENRAEELKLDGFGVWRSELSEQKQKFLSFKTFGE 360

Query: 461 AIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGFLPAA 520
AIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQFY Y+KPRQWLSS GLGAMGFLPAA
Sbjct: 361 AIPPQYAIQVLDELTDGKAIISTGVGQHQMWAQFYKRYKPRQWLSSGGLGAMGFLPAA 420

Query: 521 IGASVANPDAIVVDIDGGSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWEDRFYK 580
IGASVANPDAIVVDIDGGSFIMNVQELATIRVENLPVK+LLNNQHLGMVMQWEDRFYK
Sbjct: 421 IGASVANPDAIVVDIDGGSFIMNVQELATIRVENLPVKILLNNQHLGMVMQWEDRFYK 480

Query: 581 ANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPYLLDVI 640
ANRAHT+LGDPA+E+EIFPNM FA ACGIPAARVTKK +LR+AIQTMLDTPGPYLLDVI
Sbjct: 481 ANRAHTYLGDPAKENEIFPNMLQFAGACGIPAARVTKKEELRDAIQTMLDTPGPYLLDVI 540

Query: 641 CPHQEHVLPMPNGGTFNDVITEGDGR 667
CPHQEHVLPMP+GGTF DVITEGDGR
Sbjct: 541 CPHQEHVLPMPSSGGTFKDVITEGDGR 567

>emb|CAA87083.1| acetohydroxyacid synthase [Gossypium hirsutum]
Length = 659

Score = 1055 bits (2729), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 497/584 (85%), Positives = 541/584 (92%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
FISR+A D+PRKGADILVEALER+GV+ VFAYPGGASMEIHQALTRS IRNVLPHEQG
Sbjct: 76 FISRYADDEPRKGADILVEALEREKVDFAYPGGASMEIHQALTRSKIIRNVLPHEQG 135

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARSSG G+CIATSGPGATNLVSLADALA+LD+PLVAITGQVPRRMIGTDAF
Sbjct: 136 GVFAAEGYARSSGISGVCATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 195

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLV+DV+DIPRI+ EAFFLA+SGRPGPVL+DVPKDIQQQLA+P
Sbjct: 196 QETPIVEVTRSITKHNYLVLDVDDIPRIVSEAFFLASSGRPGPVLIDVPKDIQQQLAVPK 255

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCLNSSDELGRFVELTGI 326
W +++LPGY+SR+PK P ++HLEQIVRL+SESKKPVLVYGGGCLNSS+EL RFVELTGI
Sbjct: 256 WNHSRLRLPGYLSRLPKAPAEAHLEQIVRLVSESKKPVLVYGGGCLNSSSEELKRFVELTGI 315

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRTVGKLEAFA 386
PVASTLMGLG++P DELSL MLGMHGT VYANYAV+ SDLLLAFGVRFDDRTVGKLEAFA
Sbjct: 316 PVASTLMGLGAFPI SDELSLQMLGMHGT VYANYAVDKSDLLLAFGVRFDDRTVGKLEAFA 375

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC DVKLALQGMNKVLENRAEELKLDGFWVRNELNV 446
SRAKIVHIDIDSAEIGKNK PH+SVC DVKLALQG+NK+LE +L LD+ WR ELN
Sbjct: 376 SRAKIVHIDIDSAEIGKNKQPHMSVCS DVKLALQGINKILETTGAKLNLDYSEWRQELNE 435

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK KFPLS+KTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQFY YKKPRQWL+
Sbjct: 436 QKLFPLSYKTFGEAIPPQYAIQVLDELTDGNAIISTGVGQHQMWAQFYKYKKPRQWLT 495

Query: 507 SGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+VANP+A+VVDIDGDSFIMNVQELAT+RVENLPVK+LLNNQ
Sbjct: 496 SGGLGAMGFGLPAAIGAAVANPEAVVVDIDGDSFIMNVQELATMRVENLPVKILLNNQ 555

Query: 567 HLGVMVQWEDRFYKANRAHTFLGDPAQEDEFIPNMLFAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LGDP+ E EIFPNML FA ACGIPAARVTKK DL+ AIQ
Sbjct: 556 HLGVMVQWEDRFYKANRAHTYLGDPSENEEIFPNMLKFAEACGIPAARVTKKEDLKAAIQ 615

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGT FNDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP+GG F DVITEGDGR +Y
Sbjct: 616 KMLDTPGPYLLDVIVPHQEHVLPMPISGGAFKDVITEGDGRTQY 659

>emb|CAA87084.1| acetohydroxyacid synthase [Gossypium hirsutum]
Length = 659

Score = 1055 bits (2728), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 497/584 (85%), Positives = 542/584 (92%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
FISR+A D+PRKGADILVEAL R+GV+ VFAYPGGASMEIHQALTRS IRNVLP RHEQG
Sbjct: 76 FISRYADDEPRKGADILVEALVREGVDVFAYPGGASMEIHQALTRSKIIRNVLP RHEQG 135

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARSSG PG+CIATSGPGATNLVSGLADA+LDS+PLVAITGQVPRRMIGTDAF
Sbjct: 136 GVFAAEGYARSSGIPGVCIATSGPGATNLVSGLADAMLDSIPLVAITGQVPRRMIGTDAF 195

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLV+DV+DIPRI+ EAFFLA+SGRPGPVL+DVPKDIQQQLA+P
Sbjct: 196 QETPIVEVTRSITKHNYLVLDVDDIPRIVSEAFFLASSGRPGPVLIDVPKDIQQQLAVPK 255

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCLNSSDELGRFVELTGI 326
W +++LPGY+SR+PK P ++HLEQIVRL+SESKKPVLVYGGGCLNSS+EL RFVELTGI
Sbjct: 256 WNHSRLRLPGYLSRLPKAPGEAHLEQIVRLVSESKKPVLVYGGGCLNSSSEELKRFVELTGI 315

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRTVGKLEAFA 386
PVASTLMGLG++P D+LSL MLGMHGT VYANYAV+ SDLLLAFGVRFDDRTVGKLEAFA
Sbjct: 316 PVASTLMGLGAFPI SDDLSLQMLGMHGT VYANYAVDKSDLLLAFGVRFDDRTVGKLEAFA 375

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC DVKLALQGMNKVLENRAEELKLDGFWVRNELNV 446
SRAKIVHIDIDSAEIGKNK PHVSVC DVKLALQG+NK+LE + +L LD+ WR ELN
Sbjct: 376 SRAKIVHIDIDSAEIGKNKQPHVSVCSDVKLALQGINKILETKVAKLNLDYSEWRQELNE 435

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK KFPLS+KTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQFY YKKPRQWL+
Sbjct: 436 QKLFPLSYKTFGEAIPPQYAIQVLDELTDGNAIISTGVGQHQMWAQFYKYKKPRQWLT 495

Query: 507 SGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+VANP+A+VVDIDGDSFIMNVQELATIRVENLPVK+LLNNQ
Sbjct: 496 SGGLGAMGFGLPAAIGAAVANPEAVVVDIDGDSFIMNVQELATIRVENLPVKILLNNQ 555

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LGDP+ E EIFPNML FA ACGIPAARVTKK DL+ A+Q
Sbjct: 556 HLGMMVQWEDRFYKANRAHTYLGDPNSSEIFNMLKFAEACGIPAARVTKKEDLKAAMQ 615

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP+GG F DVITEGDGR +Y
Sbjct: 616 KMLDTPGPYLLDVIVPHQEHVLPMPISGGAFKDVITEGDGRTQY 659

>gb|AAT07322.1| acetohydroxyacid synthase 1 [Helianthus annuus]
Length = 655

Score = 1050 bits (2715), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 494/584 (84%), Positives = 539/584 (92%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHEQG 146
F+SR+APDQPRKGAD+LVEALER+GV VFAYPGGASMEIHQALTRSS+IRNVLPRHEQG
Sbjct: 72 FVSRYAPDQPRKGADVLVEALEREVDVFAYPGGASMEIHQALTRSS+IRNVLPRHEQG 131

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR+SG PG+CIATSGPGATNLVSGGLADALLDSVP+VAITGQVPRRMIGTDAF
Sbjct: 132 GVFAAEGYARASGLPGVCIATSGPGATNLVSGGLADALLDSVPMVAITGQVPRRMIGTDAF 191

Query: 207 QETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSIKHNLYL+DVEDIPRI+ EAF+LA+SGRPGPVL+DVPKDIQQQL +P
Sbjct: 192 QETPIVEVTRSIKHNLYLMDVEDIPRIVREAFYLASSGRPGPVLVDVPKDIQQQLVVPK 251

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W++ M+LPGY+SRMPKP D HLEQIVRL+ E+K+PVLYVGGGCLNS DEL RFVELTGI
Sbjct: 252 WDEPMRLPGYLSRMPKPYDGHLEQIVRLVGEAKRPVLYVGGGCLNSDELRRFVELTGI 311

Query: 327 PVASTLMGLGSGYPCDDDESLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFA 386
PVASTLMGLG+YP +LSLHMLGMHGTVYANYAV+ SDLLAFGVRFDRTGKLEAFA
Sbjct: 312 PVASTLMGLGAYPASSDLSLHMLGMHGTVYANYAVDKSDLLAFGVRFDRTGKLEAFA 371

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVCGDVKLALQGMNKVLENRAEELKLDGFWRNELNV 446
SRAKIVHIDID AEIGKNK PHVS+CGD+K+ALQG+NK+LE + LDF WR EL+
Sbjct: 372 SRAKIVHIDIDPAEIGKNKQPHVSIKQIKVALQGLNKILEKNSVTNLDFTWRKELDE 431

Query: 447 QKQKFPLSFKTFGEAIPQYAIKVLDELTDGKAIISTGVGQHQMMAAQFYNYKKPRQWLS 506
QK KFPPLSFKTFGEAIPQYAI+VLDELTD G AIISTGVGQHQMMAAQFY Y KPRQWL+
Sbjct: 432 QKMKFPLSFKTFGEAIPQYAIQVLDDELTDGNAIISTGVGQHQMMAAQFYKYNKPRQWLT 491

Query: 507 SGGLGAMGFGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGFLPAAIGA+VA PDA+VVDIDGDSF+MNVQELATIRVENLPVK+LLLNNQ
Sbjct: 492 SGGLGAMGFGFLPAAIGA+AVRPDAVVVDIDGDSFMMNVQELATIRVENLPVKILLNNQ 551

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LG+P++E EIFPNM+ FA AC IPAARVT+KADLR AIQ
Sbjct: 552 HLGMMVQWEDRFYKANRAHTYLGPNPSKESEIFPNMVKFAEACDIPAARVTQKADLRAAIQ 611

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP GG F+DVITEGDGR KY
Sbjct: 612 KMLDTPGPYLLDVIVPHQEHVLPMPAGGGFSDVITEGDGRTKY 655

>gb|AAT07323.1| acetohydroxyacid synthase 1 [Helianthus annuus]
Length = 654

Score = 1048 bits (2710), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 494/584 (84%), Positives = 539/584 (92%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHEQG 146
F+SR+APDQPRKGAD+LVEALER+GV VFAYPGGASMEIHQALTRSS+IRNVLPRHEQG
Sbjct: 71 FVSRYAPDQPRKGADVLVEALEREVDVFAYPGGASMEIHQALTRSS+IRNVLPRHEQG 130

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR+SG PG+CIATSGPGATNLVSGGLADALLDSVP+VAITGQVPRRMIGTDAF
Sbjct: 131 GVFAAEGYARASGLPGVCIATSGPGATNLVSGGLADALLDSVPMVAITGQVPRRMIGTDAF 190

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLV+DVEDIPRI+ EAF+LA+SGRPGPVL+DVPKDIQQQL +P
Sbjct: 191 QETPIVEVTRSITKHNYLVLDVEDIPRIVREAFYLASSGRPGPVLIDVPKDIQQQLVVPK 250

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W++ M+LPGY+SRMPKP D HLEQIVRL+ E+K+PVLYVGGGCLNS DEL RFVELTGI
Sbjct: 251 WDEPMRLPGYLSRMPKPQYDGHLEQIVRLVGEAKRPVLYVGGGCLNSDELRRFVELTGI 310

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTGKLEAFA 386
PVASTLMGLG+YP +LSLHMLGMHGT VYANYAV+ SDLLAFGVRFD DRTGKLEAFA
Sbjct: 311 PVASTLMGLGAYPASSDLSLHMLGMHGT VYANYAVDKSDLLAFGVRFD DRTGKLEAFA 370

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDID AEIGKNK PHVS+CGD+K+ALQG+NK+LE + LDF WR EL+
Sbjct: 371 SRAKIVHIDIDPAEIGKNKQPHVSICGDIKVALQGLNKILEEKNSVTNLDFSNWRKELDE 430

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK KFPLSFKTFGEAIPPQYAI+VLDEL T G AIIISTGVGQHQMWAQFY Y KPRQWL+
Sbjct: 431 QKVKFPLSFKTFGEAIPPQYAIQVLDELTDGNAIISTGVGQHQMWAQFYKYNKPRQWLT 490

Query: 507 SGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+VA PDA+VVDIDGDSF+MNVQELATIRVENLPVK+LLNNQ
Sbjct: 491 SGGLGAMGFGLPAAIGAAVARPD VVDIDGDSFMMNVQELATIRVENLPVKILLNNQ 550

Query: 567 HLGVMVQWEDRFYKANRAHTFLGDPAQEDEIFPNMLFAAACGIPAARVT KADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LG+P++E EIFPNML FA AC IPAARVT+KADLR AIQ
Sbjct: 551 HLGVMVQWEDRFYKANRAHTYLGNSKESEIFPNMLKFAEACDIPAARVTQKADLRAAIQ 610

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP GG F+DVITEGDGR KY
Sbjct: 611 KMLDTPGPYLLDVIVPHQEHVLPMPAGGGFSDVITEGDGRTKY 654

>gb|AAT07325.1| acetohydroxyacid synthase 1 [Helianthus annuus]
Length = 652

Score = 1047 bits (2707), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 493/584 (84%), Positives = 539/584 (92%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F+SR+APDQPRKGAD+LVEALER+GV VFAYPGGASMEIHQALTRS++IRNVLP RHEQG
Sbjct: 69 FVSRYAPDQPRKGADVLVEALEREGVTDVFAYPGGASMEIHQALTRSN TIRNVLP RHEQG 128

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR+SG PG+CIATSGPGATNLVSGLADALLDSVP+VAITGQVPRRMIGTDAF
Sbjct: 129 GVFAAEGYARASGLPGVC IATSGPGATNLVSGLADALLDSVPMVAITGQVPRRMIGTDAF 188

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLV+DVEDIPRI+ EAF+LA+SGRPGPVL+DVPKDIQQQL +P
Sbjct: 189 QETPIVEVTRSITKHNYLVLDVEDIPRIVREAFYLASSGRPGPVLIDVPKDIQQQLVVPK 248

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W++ M+LPGY+SRMPKP D HLEQIVRL+ E+K+PVLYVGGGCLNS DEL RFVELTGI
Sbjct: 249 WDEPMRLPGYLSRMPKPQYDGHLEQIVRLVGEAKRPVLYVGGGCLNSDELRRFVELTGI 308

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTGKLEAFA 386
PVASTLMGLG+YP +LSLHMLGMHGT VYANYAV+ SDLLAFGVRFD DRTGKLEAFA
Sbjct: 309 PVASTLMGLGAYPASSDLSLHMLGMHGT VYANYAVDKSDLLAFGVRFD DRTGKLEAFA 368

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDID AEIGKNK PHVS+CGD+K+ALQG+NK+LE + LDF WR EL+
Sbjct: 369 SRAKIVHIDIDPAEIGKNKQPHVSICGDIKVALQGLNKILEEKNSVTNLDFSNWRKELDE 428

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK KFPLSFKTFGEAIPPQYAI+VLDEL T G AIIISTGVGQHQMWAQFY Y KPRQWL+
Sbjct: 429 QKVKFPLSFKTFGEAIPPQYAIQVLDELTDGNAIISTGVGQHQMWAQFYKYNKPRQWLT 488

Query: 507 SGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+VA PDA+VVDIDGDSF+MNVQELATIRVENLPVK+LLNNQ
Sbjct: 489 SGGLGAMGFGLPAAIGAAVARPD VVDIDGDSFMMNVQELATIRVENLPVKILLNNQ 548

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LG+P++E EIFPNM+ FA AC IPAARVT+KADLR AIQ
Sbjct: 549 HLGMMVQWEDRFYKANRAHTYLGNPSEKEIFPNMVKFAEACDIPAARVTQKADLRAAIQ 608

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP GG F+DVITEGDGR KY
Sbjct: 609 KMLDTPGPYLLDVIVPHQEHVLPMPAGGGFSDVITEGDGRTKY 652

>gb|AAT07324.1| acetohydroxyacid synthase 1 [Helianthus annuus]
Length = 658

Score = 1045 bits (2701), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 493/584 (84%), Positives = 538/584 (92%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
F+SR+APDQPRKGAD+LVEALER+GV VFAYPGGASMEIHQALTRSS+IRNVLPHEQG
Sbjct: 75 FVSRYAPDQPRKGADVLVEALEREVDVFAYPGGASMEIHQALTRSS+IRNVLPHEQG 134

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR+SG PG+CIATSGPGATNLVSGGLADALLDSVP+VAITGQV RRMIGTDAF
Sbjct: 135 GVFAAEGYARASGLPGVCIATSGPGATNLVSGGLADALLDSVPMVAITGQVLRMIGTDAF 194

Query: 207 QETPIVEVTRISITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRISITKHNYLV+DVEDIPRI+ EAF+LA+SGRPGPVL+DVPKDIQQQL +P
Sbjct: 195 QETPIVEVTRISITKHNYLVLDVEDIPRIVREAFYLASSGRPGPVLIDVPKDIQQQLVVPK 254

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W++ M+LPGY+SRMPKP D HLEQIVRL+ E+K+PVLYVGGGCLNS DEL RFVELTGI
Sbjct: 255 WDEPMRLPGYLSRMPKPYDGHLEQIVRLVGEAKRPVLYVGGGCLNSDELRRFVELTGI 314

Query: 327 PVASTLMGLGSGYPCDDSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFA 386
PVASTLMGLG+YP +LSLHMLGMHGTVYANYAV+ SDLLAFGVRFDRTGKLEAFA
Sbjct: 315 PVASTLMGLGAYPASSDLSLHMLGMHGTVYANYAVDKSDLLAFGVRFDRTGKLEAFA 374

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVCGDVKLALQGMNKVLENRAEELKLDGFWRNELNV 446
SRAKIVHIDID AEIGKNK PHVS+CGD+K+ALQG+NK+LE + LDF WR EL+
Sbjct: 375 SRAKIVHIDIDPAEIGKNKQPHVSIKQIKVALQGLNKILEKNSVTNLDGFWRNELNDE 434

Query: 447 QKQKFPLSFKTFGEAIPQYAIKVLDELTDGKAIISTGVGQHQMMAAQFYNYKKPRQWLS 506
QK KPLSFKTFGEAIPQYAI+VLDELTDGKAIISTGVGQHQMMAAQFY Y KPRQWL+
Sbjct: 435 QKVKFPLSFKTFGEAIPQYAIQVLDDELTDGNAIISTGVGQHQMMAAQFYKYNKPRQWLT 494

Query: 507 SGGLGAMGFGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGFLPAAIGA+VA PDA+VVDIDGDSF+MNVQELATIRVENLPVK+LLLNNQ
Sbjct: 495 SGGLGAMGFGFLPAAIGA+AVRPAVVDIDGDSFMMNVQELATIRVENLPVKILLNNQ 554

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LG+P++E EIFPNM+ FA AC IPAARVT+KADLR AIQ
Sbjct: 555 HLGMMVQWEDRFYKANRAHTYLGNPSEKEIFPNMVKFAEACDIPAARVTQKADLRAAIQ 614

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP GG F+DVITEGDGR KY
Sbjct: 615 KMLDTPGPYLLDVIVPHQEHVLPMPAGGGFSDVITEGDGRTKY 658

>gb|AAT07326.1| acetohydroxyacid synthase 1 [Helianthus annuus]
Length = 652

Score = 1043 bits (2696), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 491/584 (84%), Positives = 538/584 (92%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
F+SR+APDQPRKGAD+LVEALER+GV VFAYPGGASMEIHQALTRSS+IRNVLPHEQG
Sbjct: 69 FVSRYAPDQPRKGADVLVEALEREVDVFAYPGGASMEIHQALTRSS+IRNVLPHEQG 128

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR+SG PG+CIATSGPGATNLVSGGLADALLDSVP+VAITGQVPRRMIGTDAF
Sbjct: 129 GVFAAEGYARASGLPGVCIATSGPGATNLVSGGLADALLDSVPMVAITGQVPRRMIGTDAF 188

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLV+DVEDIPRI+ EAF+LA+SGRPGPVL+DVPKDIQQQL +P
Sbjct: 189 QETPIVEVTRSITKHNYLVLDVEDIPRIVREAFYLASSGRPGPVLIDVPKDIQQQLVVPK 248

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W++ M+LPGY+SRMPKP D HLEQIVRL+ E+K+PVLYVGGGCLNS DEL RFVELTGI
Sbjct: 249 WDEPMRLPGYLSRMPKPQYDGHLEQIVRLVGEAKRPVLYVGGGCLNSDELRRFVELTGI 308

Query: 327 PVASTLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRTVGKLEAFA 386
PVASTLMGLG+YP +LSLHMLGMHGT VYANYAV+ SDLLLAFGVRFDDRTVGKLEAFA
Sbjct: 309 PVASTLMGLGAYPASSDLSLHMLGMHGT VYANYAVDKSDLLLAFGVRFDDRTVGKLEAFA 368

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDID AEIGKNK PHVS+CGD+K+ALQG+NK+LE + LDF WR EL+
Sbjct: 369 SRAKIVHIDIDPAEIGKNKQPHVSICGDIKVALQGLNKILEEKNSTVNLDFSNWRKELDE 428

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK KFPLSFKTFGEAIPPQ+AI+VLDELTD G AIISTGVGQHQMWAQFY Y KPRQWL+
Sbjct: 429 QKVKFPLSFKTFGEAIPPQYAIQVLDELTDGNAIISTGVGQHQMWAQFYKYNKPRQWLT 488

Query: 507 SGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+VA PDA+VVDIDGDSF+MNVQELATIRVENLPVK+LLNNQ
Sbjct: 489 SGGLGAMGFGLPAAIGAAVARPDAVVVDIDGDSFMMNVQELATIRVENLPVKILLNNQ 548

Query: 567 HLGVMVQWEDRFYKANRAHTFLGDPAQEDEIFPNMMLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LG+P++E EIFPNM+ FA AC IPAARVT+KADLR AIQ
Sbjct: 549 HLGVMVQWEDRFYKANRAHTYLGNSKESEIFPNMVKFAEACDIPAARVTQKADLRAAIQ 608

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP GG F+DVITEGDGR KY
Sbjct: 609 KMLDTPGPYLLDVIVPHQEHVLPMPAGGGFSDVITEGDGRTKY 652

>gb|AAT07327.1| acetohydroxyacid synthase 2 [Helianthus annuus]
Length = 646

Score = 1042 bits (2695), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 494/584 (84%), Positives = 539/584 (92%), Gaps = 3/584 (0%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F+SR+APDQPRKGAD+LVEALER+GV VFAYPGGASMEIHQALTRS++IRNVLP RHEQG
Sbjct: 66 FVSRYAPDQPRKGADVLVEALEREGVTDVFAYPGGASMEIHQALTRSNITIRNVLP RHEQG 125

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR+SG PG+CIATSGPGATNLVSGGLADALLDSVP+VAITGQVPRRMIGTDAF
Sbjct: 126 GVFAAEGYARASGVPGVCIATSGPGATNLVSGGLADALLDSVPMVAITGQVPRRMIGTDAF 185

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLV+DVEDIPRI+ EAF+LA+SGRPGPVL+DVPKDIQQQL +P
Sbjct: 186 QETPIVEVTRSITKHNYLVLDVEDIPRIVREAFYLASSGRPGPVLIDVPKDIQQQLVVPK 245

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W++ M+LPGY+SRMPKP D HLEQIVRL+ E+K+PVLYVGGGCLNS DEL RFVELTGI
Sbjct: 246 WDEPMRLPGYLSRMPKPQYDGHLEQIVRLVGEAKRPVLYVGGGCLNSDELRRFVELTGI 305

Query: 327 PVASTLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRTVGKLEAFA 386
PVASTLMGLG+YP +LSLHMLGMHGT VYANYAV+ SDLLLAFGVRFDDRTVGKLEAFA
Sbjct: 306 PVASTLMGLGAYPASSDLSLHMLGMHGT VYANYAVDKSDLLLAFGVRFDDRTVGKLEAFA 365

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDID AEIGKNK PHVS+CGD+K+ALQG+NK+LE E+ LDF WR EL+
Sbjct: 366 SRAKIVHIDIDPAEIGKNKQPHVSICGDIKVALQGLNKILE--EKNLDFSNWRKELDE 422

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK KFPLSFKTFGEAIPPQYAI VLDELTD G AIISTGVGQHQMWAQFY Y KPRQWL+
Sbjct: 423 QKVKFPLSFKTFGEAIPPQYAIHVDELTDGNAIISTGVGQHQMWAQFYKYNKPRQWLT 482

Query: 507 SGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+VA PDA+VVDIDGDSF+MNVQELATIRVENLPVK+LLNNQ
Sbjct: 483 SGGLGAMGFGLPAAIGAAVARPDAVVVDIDGDSFMMNVQELATIRVENLPVKILLNNQ 542

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LG+P++E EIFPNML FA AC IPAARVT+K DLR AIQ
Sbjct: 543 HLGMMVQWEDRFYKANRAHTYLGNPSEKEIFNMLKFAEACDIPAARVTRKGDRLAAIQ 602

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP GG F+DVITEGDGR+KY
Sbjct: 603 KMLDTPGPYLLDVIVPHQEHVLPMPAGGGFSDVITEGDGRMKY 646

>gb|AAT07328.1| acetohydroxyacid synthase 2 [Helianthus annuus]
Length = 648

Score = 1042 bits (2695), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 494/584 (84%), Positives = 539/584 (92%), Gaps = 3/584 (0%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
F+SR+APDQPRKGAD+LVEALER+GV VFAYPGGASMEIHQALTR++IRNVLPHEQG
Sbjct: 68 FVSRYAPDQPRKGADVLVEALEREVTDVFAYPGGASMEIHQALTRSTIRNVLPHEQG 127

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR+SG PG+CIATSGPGATNLVSGLADALLDSVP+VAITGQVPRRMIGTDAF
Sbjct: 128 GVFAAEGYARASGVPGVCIATSGPGATNLVSGLADALLDSVPMVAITGQVPRRMIGTDAF 187

Query: 207 QETPIVEVTRISITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRISITKHNYLV+DVEDIPRI+ EAF+LA+SGRPGPVL+DVPKDIQQQL +P
Sbjct: 188 QETPIVEVTRISITKHNYLVLDVEDIPRIVREAFYLASSGRPGPVLIDVPKDIQQQLVVPK 247

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W++ M+LPGY+SRMPKP D HLEQIVRL+ E+K+PVLYVGGGCLNS DEL RFVELTGI
Sbjct: 248 WDEPMRLPGYLSRMPKPYDGHLEQIVRLVGEAKRPVLYVGGGCLNSDELRRFVELTGI 307

Query: 327 PVASTLMGLGSGYPCDDLSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFA 386
PVASTLMGLG+YP +LSLHMLGMHGTVYANYAV+ SDLLAFGVRFDRTGKLEAFA
Sbjct: 308 PVASTLMGLGAYPASSDLSLHMLGMHGTVYANYAVDKSDLLAFGVRFDRTGKLEAFA 367

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVCGDVKLALQGMNKVLENRAEELKLDGFWRNELNV 446
SRAKIVHIDID AEIGKNK PHVS+CGD+K+ALQG+NK+LE E+ LDF WR EL+
Sbjct: 368 SRAKIVHIDIDPAEIGKNKQPHVSIKDIKVALQGLNKILE---EKNLDFSNWRKELDE 424

Query: 447 QKQKFPLSFKTFGEAIPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK KPLSFKTFGEAIPQYAI VLDELTD G AIISTGVGQHQMWAQFY Y KPRQWL+
Sbjct: 425 QKVKFPLSFKTFGEAIPQYAIHVLDELTDGNAIISTGVGQHQMWAQFYKYNKPRQWLT 484

Query: 507 SGGLGAMGFGLPAAIGASVANPDIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+VA PDA+VVDIDGDSF+MNVQELATIRVENLPVK+LLLNNQ
Sbjct: 485 SGGLGAMGFGLPAAIGA+AVRPDAVVVDIDGDSFMMNVQELATIRVENLPVKILLNNQ 544

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LG+P++E EIFPNML FA AC IPAARVT+K DLR AIQ
Sbjct: 545 HLGMMVQWEDRFYKANRAHTYLGNPSEKEIFNMLKFAEACDIPAARVTRKGDRLAAIQ 604

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP GG F+DVITEGDGR+KY
Sbjct: 605 KMLDTPGPYLLDVIVPHQEHVLPMPAGGGFSDVITEGDGRMKY 648

>gb|AAA74913.1| acetolactate synthase precursor
Length = 648

Score = 1042 bits (2695), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 492/584 (84%), Positives = 538/584 (92%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
FISRFAPDQPRKGAD+LVEALER+GV VFAYPGGASMEIHQALTR++IRNVLPHEQG
Sbjct: 65 FISRYAPDQPRKGADVLVEALEREVTDVFAYPGGASMEIHQALTRSTIRNVLPHEQG 124

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR+SG PG+CIATSGPGATNLVSGLADALLDSVP+VAITGQVPRRMIGTDAF
Sbjct: 125 GVFAAEGYARASGLPGVCIATSGPGATNLVSGLADALLDSVPMVAITGQVPRRMIGTDAF 184

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNLYLVDVEDIPRI+ EAF+LA+SGRPGPVL+DVPKDIQQQL +P
Sbjct: 185 QETPIVEVTRSITKHNLYLVDVEDIPRIVREAFYLASSGRPGPVLIDVDPKDIQQQLVVPK 244

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W++ ++LPGY+SR PK + LEQIVRL+SE+K+PVLYVGGGCLNS DEL RFVELTGI
Sbjct: 245 WDEPIRLPGYLSRFPKTENNGLEQIVRLVSEAKRPVLYVGGGCLNSGDELRRFVELTGI 304

Query: 327 PVASTLMGLGSGPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTGKLEAFA 386
PVASTLMGLG+YP +LSLHMLGMHGT VYANYAV+ SDLLAFGVRFD DRTGKLEAFA
Sbjct: 305 PVASTLMGLGAYPASSDLSLHMLGMHGT VYANYAVDKSDLLAFGVRFD DRTGKLEAFA 364

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNK PHVS+CGD+K+ALQG+NK+LE + LDF WR EL+
Sbjct: 365 SRAKIVHIDIDSAEIGKNKQPHVSICGDIKVALQGLNKILEVKNSTVNLDFSNWRKELDE 424

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK K+PLSFKTFGEAIPPQYAI+VLDELTD G AIISTGVGQHQMWAQFY Y KPRQWL+
Sbjct: 425 QKVYKPLSFKTFGEAIPPQYAIQVLDELTDGNAIISTGVGQHQMWAQFYKYNKPRQWLT 484

Query: 507 SGGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+VA PDA+VVDIDGDSFIMNVQELATIRVENLPVK+LLNNQ
Sbjct: 485 SGGLGAMGFGLPAAIGAAVARPD AIVVDIDGDSFIMNVQELATIRVENLPVKILLNNQ 544

Query: 567 HLGVMVQWEDRFYKANRAHTFLGDPAQEDEIFPNMLFAAACGIPAARVT KADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LG+P++E EIFPNML FA AC IPAARVT+KADLR AIQ
Sbjct: 545 HLGVMVQWEDRFYKANRAHTYLGNSKESEIFPNMLKFAEACDIPAARVTRKADLRAAIQ 604

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGT FNDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP GG F DVITEGDGR+KY
Sbjct: 605 KMLDTPGPYLLDVIVPHQEHVLPMPAGGGFMDVITEGDGRMKY 648

>gb|ABN08612.1| Thiamine pyrophosphate enzyme, central region [Medicago truncatula]
Length = 655

Score = 1041 bits (2693), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 490/584 (83%), Positives = 545/584 (93%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
FISRFAP++PRKGADILVE+LERQGV VFAYPGGASMEIHQALTRS++IRNVLP RHEQG
Sbjct: 72 FISRFAPNEPRKGADILVESLERQGVTVNFAYPGGASMEIHQALTRSTAIRNVLP RHEQG 131

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSG LADALLDSVPLVAITGQVPRRMIGTDAF 206
G+FAAEGYARSSG PG+CIATSGPGATNLVSG LADA+LDSVPL+AITGQVPRRMIGTDAF
Sbjct: 132 GIFAAEGYARSSGLPGVCIATSGPGATNLVSG LADAMLDSVPLIAITGQVPRRMIGTDAF 191

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNLYLVD+DIPRI++EAF LA+SGRPGPVL+D+PKDIQQQ+++PN
Sbjct: 192 QETPIVEVTRSITKHNLYLVDVDDIPRIVKEAFLASSGRPGPVLIDIPKDIQQQVSLPN 251

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W+Q ++L GYM+R+PK P+++HLEQIVRL+ ESKKPVLYVGGG LN S+EL RFVELTG+
Sbjct: 252 WDQPIRLTGYMNLKAPDEAHLEQIVRLLESKPVLYVGGGSLNCSEELRRFVELTGV 311

Query: 327 PVASTLMGLGSGPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTGKLEAFA 386
PVASTLMGLGSGP DE SL MLGMHGT VYANYAV+ SDLLAFGVRFD DRTGKLEAFA
Sbjct: 312 PVASTLMGLGSGPSLDENSLQMLGMHGT VYANYAVDKSDLLAFGVRFD DRTGKLEAFA 371

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDID+AEIGKNK PHVSVC G+KLAL+G+N++LE+ E KLDFG WR ELN
Sbjct: 372 SRAKIVHIDIDAAEIGKNKQPHVSVC GDLKLALKGINQILESNGIERKLDFGGWREELND 431

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK +FP+S+KTF EAIPPQYAI+VLDELTD+G+AIISTGVGQHQMWAQFY YK+PRQWL+
Sbjct: 432 QKVRFPMSYKTFDEAIPPQYAIQVLDELTDNGEAIISTGVGQHQMWAQFYRYKRPRQWLT 491

Query: 507 SGGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
S GLGAMGFGLPAA+GA+VANPD AIVVDIDGDSF+MNVQELATI+VENLPVK+LLNNQ
Sbjct: 492 SAGLGAMGFGLPAAMGA+VANPD AIVVDIDGDSFMMNVQELATIKVENLPVKILLNNQ 551

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LGDP A EIFPNML FA ACGIPAARVTK+ADLR AIQ
Sbjct: 552 HLGMMVQWEDRFYKANRAHTYLGDPANEKEIFPNMLKFAGACGIPAARVTKRADLRAAIQ 611

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP G+F DVITEGDGRI Y
Sbjct: 612 KMLDTPGPYLLDVIVPHQEHVLPMPANGSFEDVITEGDGRISY 655

>sp|P09114|ILV2_TOBAC Acetolactate synthase 2, chloroplast precursor (Acetolactate
synthase II) (Acetohydroxy-acid synthase II) (ALS II)
emb|CAA30485.1| unnamed protein product [Nicotiana tabacum]
Length = 664

Score = 1035 bits (2677), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 489/584 (83%), Positives = 537/584 (91%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSIRNVLPHEQG 146
F+SRFAPD+PRKG+D+LVEALER+GV VFAYPGGASMEIHQALTRSS IRNVLPHEQG
Sbjct: 81 FVSRFAPDEPRKGSVDLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLPHEQG 140

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR++G PG+CIATSGPGATNLVSGGLADALLDSVP+VAITGQVPRRMIGTDAF
Sbjct: 141 GVFAAEGYARATGFPVCIAATSGPGATNLVSGGLADALLDSVPIVAITGQVPRRMIGTDAF 200

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLVMDVEDIPR++ EAAFLA SGRPGPVL+DVPKDIQQQL IP+
Sbjct: 201 QETPIVEVTRSITKHNYLVMDVEDIPRVVREAAFLARSGRPGPVLIDVPKDIQQQLVIPD 260

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W+Q M+LPGYMSR+PK P + LEQIVRLISESKKPVLYVGGGC SS+EL RFVELTGI
Sbjct: 261 WDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFVELTGI 320

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFA 386
PVASTLMGLG++P DELSL MLGMHGT VYANYAV+ SDLLAFGVRFDRTGKLEAFA
Sbjct: 321 PVASTLMGLGAFPTGDELSLMLGMHGT VYANYAVDSSDLLAFGVRFDRTGKLEAFA 380

Query: 387 SRAKIVHIDIDS AEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDS AEIGKNK PHVS+C D+KLALQG+N +LE++ +LKLD F WR EL V
Sbjct: 381 SRAKIVHIDIDS AEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLD FSAWRQELTV 440

Query: 447 QKQKFPPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK K+PL+FKTFG+AIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQ+Y Y+KPRQWL+
Sbjct: 441 QKVKYPLNFKTFGDAIPPQYAIQVLDELTDGSAIISTGVGQHQMWAQYKYKPRQWLT 500

Query: 507 SGGGLGAMGFLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGGLGAMGFLPAAIGA+V PD +VVDIDGDSFIMNVQELATI+VENLPVK++LLNNQ
Sbjct: 501 SGGGLGAMGFLPAAIGAAVGRPDVVDIDGDSFIMNVQELATIKVENLPVKIMLLNNQ 560

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LG+P+ E EIFPNML FA ACG+PAARVT + DLR AIQ
Sbjct: 561 HLGMMVQWEDRFYKANRAHTYLGPNSEAEIFPNMLKFAEACGVPAARVTHRDDLRAAIQ 620

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP+GG F DVITEGDGR Y
Sbjct: 621 KMLDTPGPYLLDVIVPHQEHVLPMPSGGAFKDVITEGDGRSSY 664

>gb|AAB60297.1| acetolactate synthase precursor
Length = 648

Score = 1034 bits (2674), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 489/584 (83%), Positives = 537/584 (91%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSIRNVLPHEQG 146
FISR+APDQPRKGAD+LVEALER+GV VFAYPGGASMEIHQALTRSS+IRNVLPHEQG
Sbjct: 65 FISRYAPDQPRKGADVLVEALEREGVTDVFAYPGGASMEIHQALTRSTTIRNVLPHEQG 124

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR+SG PG+CIATSGPGATNLVSGGLADALLDSVP+VAITGQVPRRMIGTDAF
Sbjct: 125 GVFAAEGYARASGLPGVCIAATSGPGATNLVSGGLADALLDSVPMVAITGQVPRRMIGTDAF 184

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNLYLMDVEDIPRI+ EAF+LA+SGRPGPVL+DVPKDIQQQL +P
Sbjct: 185 QETPIVEVTRSITKHNLYLMDVEDIPRIVREAFYLASSGRPGPVLIDVPKDIQQQLVVPK 244

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYVGGGCLNSSDELGRFVELTGI 326
W++ ++LPGY+SR+PK + LE IVRL+SE+K+PVLVYVGGGCLNS DEL RFVELTGI
Sbjct: 245 WDEPIRLPGYLSRLPKTENNGQLEHIVRLVSEAKRPVLVYVGGGCLNSGDELRRFVELTGI 304

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRTGKLEAFA 386
PVASTLMGLG+YP +LSLHMLGMHGT VYANYAV+ SDLLLAFGVRFDDRTGKLEAFA
Sbjct: 305 PVASTLMGLGAYPASSDLSLHMLGMHGT VYANYAVDKSDLLLAFGVRFDDRTGKLEAFA 364

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNK PHVS+CGD+K+ALQG+NK+LE + LDF WR EL+
Sbjct: 365 SRAKIVHIDIDSAEIGKNKQPHVSICGDIKVALQGLNKILEVKNSVTNLDFSNWRKELDE 424

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK K+PLSFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQFY Y KPRQWL+
Sbjct: 425 QKVYKPLSFKTFGEAIPPQYAIQVLDELTDGKAIISTGVGQHQMWAQFYKYNKPRQWLT 484

Query: 507 SGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+VA PDA+VVDIDGDSFIM+VQELATIRVENLPVK+LLNNQ
Sbjct: 485 SGGLGAMGFGLPAAIGAAVARPDVVVDIDGDSFIMSVQELATIRVENLPVKILLNNQ 544

Query: 567 HLGVMVQWEDRFYKANRAHTFLGDPAQEDEIFPNMLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+Q EDRFYKANRAHT+LG+P++E EIFPNML FA AC IPAARVT+KADLR AIQ
Sbjct: 545 HLGVMVQLED RFYKANRAHTYLGNPSEKESEIFPNMLKFAEACDIPAARVTRKADLRAAIQ 604

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP GG F DVITEGDGR+KY
Sbjct: 605 KMLDTPGPYLLDVIVPHQEHVLPMPAGGGFMDVITEGDGRMKY 648

>prf||1407140B acetolactate synthase SuRB
Length = 664

Score = 1034 bits (2673), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 489/584 (83%), Positives = 536/584 (91%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F+SRFAPD+PRKG+D+LVEALER+GV VFAYPGGASMEIHQALTRSS IRNVLP RHEQG
Sbjct: 81 FVS RFAPDEPRKGS DVLVEALEREGVTDVFAYPGGASMEIHQALTRSSIIRNVLP RHEQG 140

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR++G PG+CIATSGPGATNLVSGLADALLDSVP+VAITGQVPRRMIGTDAF
Sbjct: 141 GVFAAEGYARATGFPGVCIATSGPGATNLVSGLADALLDSVP IVAITGQVPRRMIGTDAF 200

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNLYLMDVEDIPRI++ EAFFLA SGRPGPVL+DVPKDIQQQL IP+
Sbjct: 201 QETPIVEVTRSITKHNLYLMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPD 260

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYVGGGCLNSSDELGRFVELTGI 326
W+Q M+LPGYMSR+PK P + LEQIVRLISESKKPVLVYVGGC SS+EL RFVELTGI
Sbjct: 261 WDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLVYVGGGCSQSSEELRRFVELTGI 320

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRTGKLEAFA 386
PVASTLMGLG++P DELSL MLGMHGT VYANYAV+ SDLLLAFGVRFDDRTGKLEAFA
Sbjct: 321 PVASTLMGLGAFPTGDELSLMLGMHGT VYANYAVDSSDLLLAFGVRFDDRTGKLEAFA 380

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNK PHVS+C D+KLALQG+N +LE++ +LKLDF WR EL V
Sbjct: 381 SRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLD FSAWRQELTV 440

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK K+PL+FKTFG+AIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQ+Y Y+KPRQWL+
Sbjct: 441 QKVYKPLNFKTFGDAIPPQYAIQVLDELTDGSAIISTGVGQHQMWAQYYKPRQWLT 500

Query: 507 SGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+V PD +VVDIDGDSFIMNVQELATI+VENLPVK++LLNNQ
Sbjct: 501 SGGLGAMGFGLPAAIGAAVGRPDEVVDIDGDSFIMNVQELATIKVENLPVKIMLLNNQ 560

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LG+P+ E EIFPNML FA ACG PAARVT + DLR AIQ
Sbjct: 561 HLGMMVQWEDRFYKANRAHTYLGPNSEAEIFPNMLKFAEACGNPAARVTHRDDLRRAIQ 620

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP+GG F DVITEGDGR Y
Sbjct: 621 KMLDTPGPYLLDVIVPHQEHVLPMPISGGAFKDVITEGDGRSSY 664

>gb|AAK50820.1|AF363369_1 acetolactate synthase [Amaranthus retroflexus]
Length = 669

Score = 1033 bits (2671), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 484/588 (82%), Positives = 540/588 (91%), Gaps = 4/588 (0%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHEQG 146
F+SRF+P++PRKG D+LVEALER+GV VFAYPGGASMEIHQALTRS+ IRNVLPRHEQG
Sbjct: 82 FVSRFSPEEPRKGCDVLVEALEREVTDVFAYPGGASMEIHQALTRSNIRNVLPRHEQG 141

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR++G+ G+CIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF
Sbjct: 142 GVFAAEGYARATGRVGVCIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 201

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLV+DVEDIPRI++EAFFLA SGRPGPVL+D+PKDIQQQL +PN
Sbjct: 202 QETPIVEVTRSITKHNYLVLDVEDIPRIVKEAFFLANSGRPGPVLIDIPKDIQQQLVVPN 261

Query: 267 WEQAMKLPGYMSRMPKPP----EDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVE 322
WEQ +KL GY+SR+PKP E+ L+QIVRL+ ESK+PVLY GGGCLNSS+EL +FVE
Sbjct: 262 WEQPIKLGGYLSRLPKPTYSANEGLLDQIVRLVGESKRPVLYTGGGCLNSSSEELRKFVE 321

Query: 323 LTGIPVASTLMGLGSYPCCDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKL 382
LTGIPVASTLMGLG++PC D+LSLHMLGMHGTVYANYAV+ +DLLAFGVRFDDRVTGKL
Sbjct: 322 LTGIPVASTLMGLGAFPCDDLSLHMLGMHGTVYANYAVDKADLLAFGVRFDDRVTGKL 381

Query: 383 EAFASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWRN 442
EAFASRAKIVHIDIDSAEIGKNK PHVS+CGDVK+ALQG+NK+LE+R ++KLDF WR
Sbjct: 382 EAFASRAKIVHIDIDSAEIGKNKQPHVSICGDVKVALQGLNKILESRSRKGKVKLDFSNWRE 441

Query: 443 ELNVQKQKFPLSFKTFGEAIPPQYAIKVLDDELTDGKAIISTGVGQHQMWAAQFYNYKKPR 502
ELN QK+KFPLSFKTFG+AIPPQYAI+VLDELTD G A++STGVGQHQMWAAQFY Y+ PR
Sbjct: 442 ELNEQKKKFPLSFKTFGDAIPPQYAIQVLDDELTDGDAVVSTGVGQHQMWAAQFYKYRNPR 501

Query: 503 QWLSSGGLGAMGFLPAAIGASVANPDAIVVDIDGDGFSFIMNVQELATIRVENLPVKVLL 562
QWL+SSGGLGAMGFLPAAIGA+VA PDA+VVDIDGDGFSFIMNVQELATIRVENLPV++L
Sbjct: 502 QWLTSSGGLGAMGFLPAAIGA+AVARPDAVVVDIDGDGFSFIMNVQELATIRVENLPVKIML 561

Query: 563 LNNQHLMGMVQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLR 622
LNNQHLMGMV+QWEDRFYKANRAHT+LG+P+ EIFP+ML FA AC IPAARVTK +DLR
Sbjct: 562 LNNQHLMGMVQWEDRFYKANRAHTYLGPNSEAEIFPDMLKFAEACDIPAARVTKVSDLR 621

Query: 623 EAIQTMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
AIQTMLDTPGPYLLDVI PHQEHVLPMP+G F D ITEGDGR Y
Sbjct: 622 AAIQTMLDTPGPYLLDVIVPHQEHVLPMPISGAFAFKDTITEGDGRRAY 669

>gb|AAK50821.1|AF363370_1 acetolactate synthase [Amaranthus powellii]
Length = 669

Score = 1033 bits (2670), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 484/588 (82%), Positives = 540/588 (91%), Gaps = 4/588 (0%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHEQG 146
F+SRF+P++PRKG D+LVEALER+GV VFAYPGGASMEIHQALTRS+ IRNVLPRHEQG
Sbjct: 82 FVSRFSPEEPRKGCDVLVEALEREVTDVFAYPGGASMEIHQALTRSNIRNVLPRHEQG 141

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR++G+ G+CIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF
Sbjct: 142 GVFAAEGYARATGRVGVCIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 201

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLV+DVEDIPRI++EAFFLA SGRPGPVL+D+PKDIQQQL +PN
Sbjct: 202 QETPIVEVTRSITKHNYLVLDVEDIPRIVKEAFFLANSGRPGPVLIDIPKDIQQQLVVPN 261

Query: 267 WEQAMKLPGYMSRMPKPP----EDSHLEQIVRLISESKKPVLVYGGGCLNSSDELGRFVE 322
WEQ +KL GY+SR+PKP E+ L+QIVRL+ ESK+PVLV GGGCLNSS+EL +FVE
Sbjct: 262 WEQPIKLGGLSRLPKPTYSANEEGLLDQIVRLVGESKRVPVLYTGGGCLNSSSEELRKFVE 321

Query: 323 LTGIPVASTLMGLGSYPDCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTGKGL 382
LTGIPVASTLMGLG++PC D+LSLHMLGMHGT VYANYAV+ +DLLAFGVRFD DRTGKGL
Sbjct: 322 LTGIPVASTLMGLGAFPCD DLSLHMLGMHGT VYANYAVDKADLLAFGVRFD DRTGKGL 381

Query: 383 EAFASRAKIVHIDIDSAEIGKNKTPHVSVC DVKLALQGMNKVLENRAEELKLD FGVWRN 442
EAFASRAKIVHIDIDSAEIGKNK PHVS+CGDVK+ALQG+NK+LE+R ++KLDF WR
Sbjct: 382 EAFASRAKIVHIDIDSAEIGKNKQPHVSIC DVKVALQGLNKILESRKGKVKLDFSNWRE 441

Query: 443 ELNVQKQKFP LSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPR 502
ELN QK+KFP LSFKTFG+AIPPQYAI+VLDELTD G A++STGVGQHQMWA AQFY Y+ PR
Sbjct: 442 ELNEQKKKFP LSFKTFGDAIPPQYAIQVLDELTDGDAVVSTGVGQHQMWA AQFYKYRNP 501

Query: 503 QWLSSGGLGAMGFLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLL 562
QWL+SGGLGAMGFLPAAIGA+VA PDA+VVDIDGDSFIMNVQELATIRVENLPVK++L
Sbjct: 502 QWLTSGGLGAMGFLPAAIGA AAVRPDAVVVDIDGDSFIMNVQELATIRVENLPVKIML 561

Query: 563 LNNQHLGMVQWEDRFYKANRAHTFLGDP AQEDEFIPNMLLFAAACGIPAARVTKKADLR 622
LNNQHLGMV+QWEDRFYKANRAHT+LG+P+ EIFP+ML FA AC IPAARVTK +DLR
Sbjct: 562 LNNQHLGMVVQWEDRFYKANRAHTYLG NPSNSSEIFPDMLKFAEACDIPAARVTKVSDLR 621

Query: 623 EAIQTMLDTPGPYLLDVICPHQEHVLP MIPNGGTFNDVITEGDGRIKY 670
AIQTMLDTPGPYLLDVI PHQEHVLP MIP+G F D ITEGDGR Y
Sbjct: 622 TAIQTMLDTPGPYLLDVIVPHQEHVLP MIPSGAAFKDTITEGDGRRAY 669

>gb|ABY57316.1| acetolactate synthase [Medicago littoralis]
Length = 651

Score = 1031 bits (2666), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 485/584 (83%), Positives = 541/584 (92%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F SRF+ QPRKG+DILVEALER+GV VFAYPGGASMEIHQALTRS +IRN+LPRHEQG
Sbjct: 68 FTSRFSSSQPRKGS DILVEALEREGVTNVFAYPGGASMEIHQALTRSKTIRNLP RHEQG 127

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLV SGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARSSG PG+CIATSGPGATNLV SGLADAL+DSVPL+AITGQVPRRMIGTDAF
Sbjct: 128 GVFAAEGYARSSGLPGVCIATSGPGATNLV SGLADALMDSVPLIAITGQVPRRMIGTDAF 187

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYL++DVEDIPR+++EAFFLATSGRPGPVL+DVPKDIQQQLA+PN
Sbjct: 188 QETPIVEVTRSITKHNYLILDVEDIPRVVKEAFFLATSGRPGPVLIDVPKDVQQQLAVPN 247

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCLNSSDELGRFVELTGI 326
W + +KL GY+SR+PK P ++ LEQ++RL+ ESKKPVLVYGGGCLNSSDEL RFVELTG+
Sbjct: 248 WSEPIKLTGYLSRLPKIPGEAQLEQVLRLLLESKKPVLVYGGGCLNSSDELKRFVELTGV 307

Query: 327 PVASTLMGLGSYPDCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTGKLEAFA 386
PVASTLMGLGSYP E SL MLGMHGT VYANYAV++SDLLAFGVRFD DRTGKLEAFA
Sbjct: 308 PVASTLMGLGSYPIGGEHSLMLGMHGT VYANYAVDNSDLLAFGVRFD DRTGKLEAFA 367

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC DVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNK PH+S+C D+K+AL+G+N+VLE++ + KLDF WR ELNV
Sbjct: 368 SRAKIVHIDIDSAEIGKNKIPHLSICADMKVALEGLNRVLESKGIKGLDFEAWRQELNV 427

Query: 447 QKQKFP LSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLS 506
QK KFP LFKTF +AI PQYAI+VLDELTDG AI+STGVGQHQMWA AQFY YK+PRQWL+
Sbjct: 428 QKLKFP LFGKTFEDAISPQYAIQVLDELTDNGDAIVSTGVGQHQMWA AQFYKYKRPRQWLT 487

Query: 507 SGGLGAMGFLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFLPAAIGA+VANPD AIVVDIDGDSF+MNVQELATIRVENLPVK+LLNNQ
Sbjct: 488 SGGLGAMGFLPAAIGA AAVANPD AIVVDIDGDSFMMNVQELATIRVENLPVKILLNNQ 547

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LGDP++EDEFNML FA ACGIPAARVTKK +LREAIQ
Sbjct: 548 HLGMMVQWEDRFYKANRAHTYLGDPskeDEFNMLGFADACGIPAARVTKKEELREAIQ 607

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
ML+TPGPYLLDVI PHQEHVLPMP+ G+F DVITEGDGR Y
Sbjct: 608 KMLETPGPYLLDVIVPHQEHVLPMPISNGSFKDVITEGDGRSY 651

>gb|ABS72164.1| acetolactate synthase [Amaranthus hypochondriacus]
Length = 669

Score = 1030 bits (2664), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 484/588 (82%), Positives = 540/588 (91%), Gaps = 4/588 (0%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
F+SRF+P++PRKG D+LVEALER+GV VFAYPGGASMEIHQALTRS+ IRNVLPHEQG
Sbjct: 82 FVSRFSPEEPRKGCDVLEALEREVDVFAYPGGASMEIHQALTRSNIRNVLPHEQG 141

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR++G+ G+CIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF
Sbjct: 142 GVFAAEGYARATGRVGVCIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 201

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNLYL+DVEDIPRI++EAFFLA SGRPGPVL+D+PKDIQQQL +PN
Sbjct: 202 QETPIVEVTRSITKHNLYLMDVEDIPRIVKEAFLANSRPGPVLIDIPKDIQQQLVVPN 261

Query: 267 WEQAMKLPGYMSRMPKPP----EDSHLEQIVRLISESKKPVLYVGGCLNSSDELGRFVE 322
WEQ +KL GY+SR+PKP E+ L+QIVRL+ ESK+PVLY GGGCLNSS+EL +FVE
Sbjct: 262 WEQPIKLGGLSRLPKPTYSANEEGLDQIVRLVGESKRPVLYTGGCLNSSSEELRKFE 321

Query: 323 LTGIPVASTLMGLGSPCDELHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKL 382
LTGIPVASTLMGLG++PC D+LSHMLGMHGTVYANYAV+ +DLLAFGVRFDDRVTGKL
Sbjct: 322 LTGIPVASTLMGLGAFPCDDELHMLGMHGTVYANYAVDKADLLAFGVRFDDRVTGKL 381

Query: 383 EAFASRAKIVHIDIDSAEIGKNKTPHVSVCVDKALQGMNVLENRAEELKLDGFWRN 442
EAFASRAKIVHIDIDSAEIGKNK PHVS+CGDVK+ALQG+NK+LE+R ++KLDF WR
Sbjct: 382 EAFASRAKIVHIDIDSAEIGKNKQPHVSICGVDKVALQGLNKILESRSRKGKVLDFSNWRE 441

Query: 443 ELNVQKQKFPKFTFGAIPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPR 502
ELN QK+KFPKFTFGAIPQYAI+VLDELTD G A++STGVGQHQMWAAQFY Y+ PR
Sbjct: 442 ELNVQKQKFPKFTFGAIPQYAIQVLDELTDGKDAVVDSTGVGQHQMWAAQFYKYRNP 501

Query: 503 QWLSSGGLGAMGFLPAAIGASVANPDAIVVDIDGDGFSIMNVQELATIRVENLPVKVLL 562
QWL+SSGGLGAMGFLPAAIGA+VA PDA+VVDIDGDGFSIMNVQELATIRVENLPVK++L
Sbjct: 502 QWLSSGGLGAMGFLPAAIGA+AVARPDAVVDIDGDGFSIMNVQELATIRVENLPVKIML 561

Query: 563 LNNQHLMGMVQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLR 622
LNNQHLMGMV+QWEDRFYKANRAHT+LG+P+ EIFP+ML FA AC IPAARVTK +DLR
Sbjct: 562 LNNQHLMGMVQWEDRFYKANRAHTYLGDPNSSEIFPDMLKFAEACDIPAARVTKVSDLR 621

Query: 623 EAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
AIQTMLDTPGPYLLDVI PHQEHVLPMP+G F D ITEGDGR Y
Sbjct: 622 AAIQTMLDTPGPYLLDVIVPHQEHVLPMPISGAFAFKTITEGDGRRAY 669

>sp|P09342|ILV1_TOBAC Acetolactate synthase 1, chloroplast precursor (Acetolactate
synthase I) (Acetohydroxy-acid synthase I) (ALS I)
emb|CAA30484.1| unnamed protein product [Nicotiana tabacum]
prf||1501386A acetolactate synthase
Length = 667

Score = 1030 bits (2664), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 486/584 (83%), Positives = 535/584 (91%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
F+SRFAPD+PRKG+D+LVEALER+GV VFAYPGGASMEIHQALTRSS IRNVLPHEQG
Sbjct: 84 FVSRFAPDEPRKGSVDLVEALEREVDVFAYPGGASMEIHQALTRSSIRNVLPHEQG 143

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR++G PG+CIATSGPGATNLVSLADALLDSVP+VAITGQVPRRMIGTDAF
Sbjct: 144 GVFAAEGYARATGFPGVCIATSGPGATNLVSLADALLDSVP+VAITGQVPRRMIGTDAF 203

Query: 207 QETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSIKHNLYLMDVEDIPR++ EAFFLA SGRPGP+L+DVPKDIQQQL IP+
Sbjct: 204 QETPIVEVTRSIKHNLYLMDVEDIPRVVREAFFLARSGRPGPILIDVPKDIQQQLVIPD 263

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCLNSSDELGRFVELTGI 326
W+Q M+LPGYMSR+PK P + LEQIVRLISESKKPVLVYGGGC SS++L RFVELTGI
Sbjct: 264 WDQPMRLPGYSRLPKLPNEMLLEQIVRLISESKKPVLVYGGGCSQSSDELRRFVELTGI 323

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTVTGKLEAFA 386
PVASTLMGLG++P DELSL MLGMHGTVYANYAV+ SDLLAFGVRFDRTVTGKLEAFA
Sbjct: 324 PVASTLMGLGAFPTGDELSLMLGMHGTVYANYAVDSSDLLAFGVRFDRTVTGKLEAFA 383

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNVLENRAEELKLDGFGVWRNELNV 446
SRAKIVHIDIDSAEIGKNK PHVS+C D+KLALQG+N +LE++ +LKLDG WR EL
Sbjct: 384 SRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLKLDGSAWRQELTE 443

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK K PL+FKTFG+AIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQ+Y Y+KPRQWL+
Sbjct: 444 QKVKHPLNFKTFGDAIPPQYAIQVLDELTDGKAIISTGVGQHQMWAQYKYKPRQWLT 503

Query: 507 SGGLGAMGFGLPAAIGASVANPDIAIVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+V PD +VVDIDGDSFIMNVQELATI+VENLPVK++LNNQ
Sbjct: 504 SGGLGAMGFGLPAAIGAAVGRPDEVVDIDGDSFIMNVQELATIKVENLPVKIMLNNQ 563

Query: 567 HLGVMVQWEDRFYKANRAHTFLGDPAQEDEFIPNMLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LG+P+ E EIFPNML FA ACG+PAARVT + DLR AIQ
Sbjct: 564 HLGVMVQWEDRFYKANRAHTYLGPNPSNEAEIFPNMLKFAEACGVPAARVTHRDDLRRAIQ 623

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTENDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP+GG F DVITEGDGR Y
Sbjct: 624 KMLDTPGPYLLDVIVPHQEHVLPMPISGGAFKDVITEGDGRSSY 667

>gb|ABM53021.1| acetolactate synthase [Amaranthus tuberculatus]
Length = 671

Score = 1030 bits (2664), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 484/588 (82%), Positives = 538/588 (91%), Gaps = 4/588 (0%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPREHQQ 146
F+SRF+PD+PRKG D+LVEALER+GV VFAYPGGASMEIHQALTRS+ IRNVLPREHQQ
Sbjct: 84 FVSRSFSPDEPRKGC DVLVEALEREGVTDVFAYPGGASMEIHQALTRSNIRNVLPREHQQ 143

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR++G+ G+CIATSGPGATNLVSG ADALLDSVPLVAITGQVPRRMIGTDAF
Sbjct: 144 GVFAAEGYARATGRVGVCIATSGPGATNLVSGFADALLDSVPLVAITGQVPRRMIGTDAF 203

Query: 207 QETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSIKHNLYLMDVEDIPRI++EAFFLA SGRPGPVL+D+PKDIQQQL +PN
Sbjct: 204 QETPIVEVTRSIKHNLYLMDVEDIPRIVKEAFFLANSRPGPVLIDIPKDIQQQLVVPN 263

Query: 267 WEQAMKLPGYMSRMPKPP-----EDSHLEQIVRLISESKKPVLVYGGGCLNSSDELGRFVE 322
WEQ +KL GY+SR+PKP E+ L+QIVRL+ ESK+PVLY GGGCLNSS+EL +FVE
Sbjct: 264 WEQPIKLGGLSRLPKPTFSANEGLLDQIVRLVGESKRPVLYTGGGCLNSSSEELRKFVE 323

Query: 323 LTGIPVASTLMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTVTGKL 382
LTGIPVASTLMGLG++PC D+LSL MLGMHGTVYANYAV+ +DLLAFGVRFDRTVTGKL
Sbjct: 324 LTGIPVASTLMGLGAFPTDDELSLQMLGMHGTVYANYAVDKADLLAFGVRFDRTVTGKL 383

Query: 383 EAFASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNVLENRAEELKLDGFGVWRN 442
EAFASRAKIVHIDIDSAEIGKNK PHVS+CGD+K+ALQG+NK+LE+R +LKLDG WR
Sbjct: 384 EAFASRAKIVHIDIDSAEIGKNKQPHVSICGDIKVALQGLNKILES RKGKLKLDGFSNWR 443

Query: 443 ELNVQKQKFLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPR 502
ELN QK+KFLSFKTFG+AIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQFY Y+ PR
Sbjct: 444 ELNEQKKKFLSFKTFGDAIPPQYAIQVLDELTDGDAIVSTGVGQHQMWAQFYKYRNPR 503

Query: 503 QWLSSGGLGAMGFGLPAAIGASVANPDAIVVDIDGDGSFIMNVQELATIRVENLPVKVLL 562
QWL+SGGLGAMGFGLPAAIGA+VA PDA+VVDIDGDGSFIMNVQELATIRVENLPVK++L
Sbjct: 504 QWLTSGGLGAMGFGLPAAIGA+AVARPDAVVVDIDGDGSFIMNVQELATIRVENLPVKIML 563

Query: 563 LNNQHLMVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLR 622
LNNQHLMGV+QWEDRFYKANRAHT+LG+P++ EIFP+ML FA AC IPAARVTK +DLR
Sbjct: 564 LNNQHLMVVQWEDRFYKANRAHTYLGNDPSKSEIFPDMLKFAEACDIPAARVTKVSDLR 623

Query: 623 EAIQTMLDTPGPYLLDVICPHQEHVLPMPINGGTNDVITEGDGRIKY 670
AIQTMLDTPGPYLLDVI PHQEHVLPMPIP G F D ITEGDGR Y
Sbjct: 624 AAIQTMLDTPGPYLLDVIVPHQEHVLPMPITGAAFKDTITEGDGRRAY 671

>gb|ABY57317.1| acetolactate synthase [Medicago truncatula]
Length = 651

Score = 1029 bits (2660), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 484/584 (82%), Positives = 541/584 (92%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
F SRF+ QPRKG+DILVEALER+GV VFAYPGGASMEIHQALTRS +IRN+LPRHEQG
Sbjct: 68 FTSRFSSTQPRKGS DILVEALEREQVTNVFAYPGGASMEIHQALTRSKTIRNLPHEQG 127

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARSSG PG+CIATSGPGATNLVSGGLADAL+DSVPL+AITGQVPRRMIGTDAF
Sbjct: 128 GVFAAEGYARSSGLPGVCIATSGPGATNLVSGGLADALMDSVPLIAITGQVPRRMIGTDAF 187

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYL++DVEDIPR+++EAFFLATSGRPGPVL+DVPKD+QQQLA+PN
Sbjct: 188 QETPIVEVTRSITKHNYLILDVEDIPRVVKEAFAFFLATSGRPGPVLIDVPKDVQQQLAVPN 247

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W + +KL GY+SR+PK P ++ LEQ++RL+ ES+KPVLYVGGGCLNSSDEL RFVELTG+
Sbjct: 248 WSEPIKLTGYLSRLPKIPGEAQLEQVLRLLLESEKPVLYVGGGCLNSSDELKRFVELTGV 307

Query: 327 PVASTLMGLGSYP CDDDESLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRVTGKLEAFA 386
PVASTLMGLGSYP E SL MLGMHGT VYANYAV++SDLLLAFGVRFDDRVTGKLEAFA
Sbjct: 308 PVASTLMGLGSYP IGGHSL SMLGMHGT VYANYAVDNDLLLAFGVRFDDRVTGKLEAFA 367

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNK PH+S+C D+K+AL+G+N+VLE++ + KLDF WR ELNV
Sbjct: 368 SRAKIVHIDIDSAEIGKNKIPHLSICADMKVALEGLNRVLESKGIGKLD FEAWRQELNV 427

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK KFPL FKTF +AI PQYAI+VLDELTDG AI+STGVGQHQMWAQFY YK+PRQWL+
Sbjct: 428 QKLFPLGFKTFEDAISPQYAIQVDELTDGDAIVSTGVGQHQMWSAQFYKYKRPRQWLT 487

Query: 507 SGGLGAMGFGLPAAIGASVANPDAIVVDIDGDGSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+VANPDAIVVDIDGDGSF+MNVQELATIRVENLPVK+LLLNNQ
Sbjct: 488 SGGLGAMGFGLPAAIGA+AVANPDAIVVDIDGDGSFMMNVQELATIRVENLPVKILLNNQ 547

Query: 567 HLGVMVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LGD++EDEFIPNML FA ACGIPAARVTKK +LREAIQ
Sbjct: 548 HLGMMVQWEDRFYKANRAHTYLGDPKKEDEFIPNMLGFADACGIPAARVTKKEELREAIQ 607

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTNDVITEGDGRIKY 670
ML+TPGPYLLDVI PHQEHVLPMPIP+ G+F DVITEGDGR Y
Sbjct: 608 KMLETPGPYLLDVIVPHQEHVLPMPISNGSFKDVITEGDGRRSY 651

>gb|ABY57318.1| acetolactate synthase [Medicago truncatula]
Length = 651

Score = 1029 bits (2660), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 484/584 (82%), Positives = 541/584 (92%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
F SRF+ QPRKG+DILVEALER+GV VFAYPGGASMEIHQALTRS +IRN+LPRHEQG
Sbjct: 68 FTSRFSSTQPRKGS DILVEALEREQVTNVFAYPGGASMEIHQALTRSKTIRNLPHEQG 127

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARSSG PG+CIATSGPGATNLVSLADALLDSVPL+AITGQVPRRMIGTDAF
Sbjct: 128 GVFAAEGYARSSGLPGVCIATSGPGATNLVSLADALLDSVPLIAITGQVPRRMIGTDAF 187

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYL++DVEDIPR+++EAFFLATSGRPGPVL+DVPKD+QQQLA+PN
Sbjct: 188 QETPIVEVTRSITKHNYLILDVEDIPRVVKEAFLATSGRPGPVLIDVPKDVQQQLAVPN 247

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYVGGGCLNSSDELGRFVELTGI 326
W + +KL GY+SR+PK P ++ LEQ++RL+ ES+KPVLYVGGGCLNSSDEL RFVELTG+
Sbjct: 248 WSEPIKLTGYLSRLPKIPGEAQLEQVLRLLLESEKPVLYVGGGCLNSSDELKRFVELTGV 307

Query: 327 PVASTLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRTVGKLEAFA 386
PVASTLMGLGSYP E SL MLGMHGT VYANYAV++SDLLLAFGVRFDDRTVGKLEAFA
Sbjct: 308 PVASTLMGLGSYPIGGEHSLMLGMHGT VYANYAVDNSDLLLAFGVRFDDRTVGKLEAFA 367

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNK PH+S+C D+K+AL+G+N+VLE++ + KLDF WR ELNV
Sbjct: 368 SRAKIVHIDIDSAEIGKNKIPHSICADMKVALEGLNRVLESGIKGKLDFAWRQELNV 427

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQAQFYNYKKPRQWLS 506
QK KFPL FKTF +AI PQYAI+VLDELTDG AI+STGVGQHQMWAQAQFY YK+PRQWL+
Sbjct: 428 QKLKFPPLGFKTFEDAI SPQYAIQVLDELTDGDAIVSTGVGQHQMWAQAQFYKYKPRQWLT 487

Query: 507 SGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+VANPDAIVVDIDGDSF+MNVQELATIRVENLPVK+LLNNQ
Sbjct: 488 SGGLGAMGFGLPAAIGAAVANPDAIVVDIDGDSFMMNVQELATIRVENLPVKILLNNQ 547

Query: 567 HLGVMVQWEDRFYKANRAHTFLGDPAQEDEIFPNMLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LGDP++EDEIFPNML FA ACGIPAARVTKK +LREAIQ
Sbjct: 548 HLGMMVQWEDRFYKANRAHTYLGDPKDEDEIFPNMLGFADACGIPAARVTKKKEELREAIQ 607

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPNPGGT FNDVITEGDGRIKY 670
ML+TPGPYLLDVI PHQEHVLPMP+ G+F DVITEGDGR Y
Sbjct: 608 KMLETPGPYLLDVIVPHQEHVLPMPNNGSFKDVITEGDGRSY 651

>prf||1407140A acetolactate synthase SuRA
Length = 667

Score = 1029 bits (2660), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 487/584 (83%), Positives = 534/584 (91%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F+SRFAPD+PRKG+D+LVEALER+GV VFAYPGGASMEIHQALTRSS IRNVLP RHEQG
Sbjct: 84 FVS RFAPDEPRKGS DVLVEALERE GVTDFVAYPGGASMEIHQALTRSSIIRNVLP RHEQG 143

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR++G PG+CIATSGPGATNLVSLADALLDSVP+VAITGQVPRRMIGTDAF
Sbjct: 144 GVFAAEGYARATGFPGVCIATSGPGATNLVSLADALLDSVP+VAITGQVPRRMIGTDAF 203

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLVMDVEDIPR++ EAFFLA SGRPGPVL+DVPKDIQQQL IP+
Sbjct: 204 QETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLARSGRPGPVLIDVPKDIQQQLVIPD 263

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYVGGGCLNSSDELGRFVELTGI 326
W+Q M+LPGYMSR+PK P + LEQIVRLISESKKPVLVYVGGGC SS++L RFVELTGI
Sbjct: 264 WDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLVYVGGGCSQSSDELRRFVELTGI 323

Query: 327 PVASTLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRTVGKLEAFA 386
PVASTLMGLG++P DELSL MLGMHGT VYANYAV+ SDLLLAFGVRFDDRTVGKLEAFA
Sbjct: 324 PVASTLMGLGAFPTGDELSLMLGMHGT VYANYAVDSSDLLLAFGVRFDDRTVGKLEAFA 383

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNK PHVS+C D+KLALQG+N +LE++ +LKLD F WR EL
Sbjct: 384 SRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILESKEGKLD FSAWRQELTE 443

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQAQFYNYKKPRQWLS 506
QK K PL+FKTFG+AIPPQYAI+VLDELTDG AIISTGVGQHQMWAQAQY Y+KPRQWL+
Sbjct: 444 QKVKHPLNFKTFGDAIPPQYAIQVLDELTDGNAIISTGVGQHQMWAQAQYKYKPRQWLT 503

Query: 507 SGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+V PD +VVDIDGDSFIMNVQELATI+VENLPVK++LLNNQ
Sbjct: 504 SGGLGAMGFGLPAAIGAAVGRPDEVVDIDGDSFIMNVQELATIKVENLPVKIMLLNNQ 563

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFIPNMLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LG+P+ E EIFPNML FA ACG PAARVT + DLR AIQ
Sbjct: 564 HLGMMVQWEDRFYKANRAHTYLGNPSEAEIFPNMLKFAEACGNPAARVTHRDDLRRAIQ 623

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTNDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP+GG F DVITEGDGR Y
Sbjct: 624 KMLDTPGPYLLDVIVPHQEHVLPMPISGGAFKDVITEGDGRSSY 667

>gb|ABY57315.1| acetolactate synthase [Medicago littoralis]
Length = 651

Score = 1028 bits (2657), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 484/584 (82%), Positives = 540/584 (92%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHEQG 146
F SRF+ QPRKG+DILVEALER+GV VFAYPGGASMEIHQALTRS +IRN+LPRHEQG
Sbjct: 68 FTSRFSSSQPRKGSIDLVEALEREQVTVNFAYPGGASMEIHQALTRSKTIRNLPHEQG 127

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYARSSG PG+CIATSGPGATNLVSGGLADAL+DSVPL+AITGQV RRMIGTDAF
Sbjct: 128 GVFAAEGYARSSGLPGVICIATSGPGATNLVSGGLADALMDSVPLIAITGQVLRMIGTDAF 187

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYL++DVEDIPR+++EAFFLATSGRPGPVL+DVPKD+QQQLA+PN
Sbjct: 188 QETPIVEVTRSITKHNYLILDVEDIPRVVKEAFAFFLATSGRPGPVLIDVPKDVQQQLAVPN 247

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W + +KL GY+SR+PK P ++ LEQ++RL+ ESKKPVLYVGGGCLNSSDEL RFVELTG+
Sbjct: 248 WSEPIKLTGYLSRLPKIPGEAQLEQVLRLLLESKKPVLYVGGGCLNSSDELKRFVELTGV 307

Query: 327 PVASTLMGLGSYPCCDESLHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTGKLEAFA 386
PVASTLMGLGSYP E SL MLGMHGTVYANYAV++SDLLLAFGVRFDDRVTGKLEAFA
Sbjct: 308 PVASTLMGLGSYPIGGEHSLMLGMHGTVYANYAVDNDLLLAFGVRFDDRVTGKLEAFA 367

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVCQDVKLALQGMNVLENRAEELKLDGFWRNELNV 446
SRAKIVHIDIDSAEIGKNK PH+S+C D+K+AL+G+N+VLE++ + KLDF WR ELNV
Sbjct: 368 SRAKIVHIDIDSAEIGKNKIPHLSICADMKVALEGLNRVLESKGKGLDFEAWRQELNV 427

Query: 447 QKQKFPLSFKTFGEAIPPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK KFPL FKTF +AI PQYAI+VLDELTDG AI+STGVGQHQMWAQFY YK+PRQWL+
Sbjct: 428 QKLFPLGFKTFEDAISPQYAIQVLDELTDGDAIVSTGVGQHQMWSAQFYKYRPRQWLT 487

Query: 507 SGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+VANPDAIVVDIDGDSF+MNVQELATIRVENLPVK+LLNNQ
Sbjct: 488 SGGLGAMGFGLPAAIGAAVANPDAIVVDIDGDSFMMNVQELATIRVENLPVKILLNNQ 547

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFIPNMLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LGD++EDEFIPNML FA ACGIPAARVTKK +LREAIQ
Sbjct: 548 HLGMMVQWEDRFYKANRAHTYLGDPKKEDEFIPNMLGFADACGIPAARVTKKEELREAIQ 607

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTNDVITEGDGRIKY 670
ML+TPGPYLLDVI PHQEHVLPMP+ G+F DVITEGDGR Y
Sbjct: 608 KMLETPGPYLLDVIVPHQEHVLPMPISNGSFKDVITEGDGRSY 651

>gb|ACF47583.1| acetolactate synthase 1 [Sonchus asper]
Length = 658

Score = 1026 bits (2654), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 484/584 (82%), Positives = 537/584 (91%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHEQG 146
F+SRFAPDQPRKG+D+LVEALER+GV+ VFAYPGGASMEIHQALTRS++IRNVLPRHEQG
Sbjct: 75 FVS RFAPDQPRKGSIDLVEALEREQVHVFAYPGGASMEIHQALTRSNITIRNVLPRHEQG 134

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR+ GKPG+CIATSGPGATNLVSLADALLDSVP+VAITGQVPRRMIGTDAF
Sbjct: 135 GVFAAEGYARALGKPGVCIATSGPGATNLVSLADALLDSVPIVAITGQVPRRMIGTDAF 194

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNLYLV+DVEDIPR++ EAF+LATSGRPGPVL+DVPKDIQQQL +P
Sbjct: 195 QETPIVEVTRSITKHNLYLMDVEDIPRVVHEAFYLATSGRPGPVLIDVPKDIQQQLVVPK 254

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCLNSSDELGRFVELTGI 326
W++ +L GY+SR+PKPP D+HLEQI+RLI+ESK+PVLV GGGCL+SS EL RFVELTGI
Sbjct: 255 WDEPKRLSGYLSRLPKPPNDAHLEQIIRLITESKRPLVYTGCGCLDSSVELCRFVELTGI 314

Query: 327 PVASTLMGLGSPYCDDELHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRTVGKLEAFA 386
PVASTLMGLG+YP +LSL MLGMHGT VYANYAV+ SDLLLAFGVRFDDRTVGKLEAFA
Sbjct: 315 PVASTLMGLGAYPASGDLSQLMLGMHGT VYANYAVDKSDLLLAFGVRFDDRTVGKLEAFA 374

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDIDSAEIGKNK PHVS+CGD+K+AL+G+N++LE R+E LDF WR EL+
Sbjct: 375 SRAKIVHIDIDSAEIGKNKQPHVSICGDIKIALKGLNEILEKRSEMRNLDFSSWRQELDE 434

Query: 447 QKQKPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK PLSFKTFG+AIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQFY Y +PRQWL+
Sbjct: 435 QKLTHPLSFKTFGDAIPPQYAIQVLDELTDGKAIISTGVGQHQMWAQFYKYNRPQWLT 494

Query: 507 SGGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+VA PD IVDIDGDSF+MNVQELATIRVENLPVK+LLNNQ
Sbjct: 495 SGGLGAMGFGLPAAIGAAVARPDCIVVDIDGDSFMMNVQELATIRVENLPVKILLNNQ 554

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFIPNMLFAAACGIPAAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LG+P+ E EIFPNML FA AC IPAAARVTK DLR AIQ
Sbjct: 555 HLGMMVQWEDRFYKANRAHTYLGNSPSENEIFPNMLKFAEACDIPAAARVTKIGDLRAAIQ 614

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
ML+TPGPYLLDVI PHQEHVLPMP GG F DVIT+GDGR+K+
Sbjct: 615 KMLETPGPYLLDVIVPHQEHVLPMPAGGGFMDVITDGDGRMKH 658

>sp|P14874|ILV2_BRANA Acetolactate synthase 2, chloroplast precursor (Acetolactate
synthase II) (Acetohydroxy-acid synthase II) (ALS II)
emb|CAA77614.1| acetohydroxyacid synthase II [Brassica napus]
emb|CAA34680.1| unnamed protein product [Brassica napus]
Length = 637

Score = 1025 bits (2649), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 484/576 (84%), Positives = 535/576 (92%), Gaps = 3/576 (0%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F S++AP+ PR GADILVEALERQGV+ VFAYPGGASMEIHQALTRS++IRNVLP RHEQG
Sbjct: 63 FSSKYAPNVPRSGADILVEALERQGVDDVVFAYPGGASMEIHQALTRNTIRNVLP RHEQG 122

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
G+FAAEGYARSSGKPGICIATSGPGA NLVSLADAL DSVPL+AITGQVPRRMIGT AF
Sbjct: 123 GIFA AEGYARSSGKPGICIATSGPGAMNLVSLADALFDSVPLIAITGQVPRRMIGTMAF 182

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETP+VEVTR+ITKHNLYLV+V+DIPRI+ EAFFLAT S RGPVL+DVPKD+QQQ AIPN
Sbjct: 183 QETPVVEVTRTITKHNLYLMEVDDIPRIVREAFFLATSVRPGPVLIDVPKDVQQQFAIPN 242

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCLNSSDELGRFVELTGI 326
WEQ M+LP YMS MPKPP+ SHLEQI+RL+SESK+PVLVYGGGCLNSS+EL RFVELTGI
Sbjct: 243 WEQPMRLPLYMSTMPKPPKVSHLEQILRLVSESKRPVLVYGGGCLNSSSEELRRFVELTGI 302

Query: 327 PVASTLMGLGSPYCDDELHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRTVGKLEAF 385
PVAST MGLGSPYCDDE E SL MLGMHGT VYANYAVE+SDLLLAFGVRFDDRTVGKLEAF
Sbjct: 303 PVASTMGLGSPYCDDEEFLQMLGMHGT VYANYAVEYSDLLLAFGVRFDDRTVGKLEAF 362

Query: 386 ASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELN 445
ASRAKIVHIDIDS EIGKNKTPHVSVC DV+LALQGMN+VLENR + LDFG WR ELN
Sbjct: 363 ASRAKIVHIDIDSTEIGKNKTPHVSVCDDVQLALQGMNEVLENRRD--VLDFGEWRCELN 420

Query: 446 VQKQKFPLSFKTFGEAIPPQYAIKVLDDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWL 505
Q+ KFPL +KTFGE IPPQYAI++LDELTDGKAIITGVGQHQMWAQFY +KKPRQWL
Sbjct: 421 EQRLKFLPLRYKTFGEEIPPQYAIQLDELTDGKAIITGVGQHQMWAQFYRFKKPRQWL 480

Query: 506 SSGGLGAMGFLPAAIGASVANPDAIVVDIDGDGSFIMNVQELATIRVENLPVKVLLNN 565
SSGGLGAMGFLPAA+GA++ANP A+VVDIDGDGSFIMN+QELATIRVENLPVKVLL+NN
Sbjct: 481 SSGGLGAMGFLPAAAGAAIANPGAVVVDIDGDGSFIMNIQELATIRVENLPVKVLLINN 540

Query: 566 QHLGMVMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAI 625
QHLGMV+QWED FY ANRA +FLGDPA + +FP+MLLFAA+CGIPAARVT++ DLREAI
Sbjct: 541 QHLGMVLQWEDHFYAAANRADSFLGDPAPEAVFPDMLLFAASCGIPAARVTRREDLREAI 600

Query: 626 QTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
QTMLDTPGP+LLDV+CPHQ+HVLPI+IP+GGTF D+I
Sbjct: 601 QTMLDTPGPFLLDVVCPHQDHVLPPIPSGGTFKDII 636

>gb|ABM53020.1| acetolactate synthase [Amaranthus tuberculatus]
Length = 669

Score = 1023 bits (2644), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 481/588 (81%), Positives = 535/588 (90%), Gaps = 4/588 (0%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
F+SRF+P +PRKG D+LVEALER+GV VFAYPGGASMEIHQALTRS+ IRNVLPHEQG
Sbjct: 82 FVSRFSPXEPKRGCDVLVEALEREVDVVFAYPGGASMEIHQALTRSNIRNVLPHEQG 141

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR++G+ G+CIATSGPGATNLVSG ADALLDSVPLVAITGQVPRRMIGTDAF
Sbjct: 142 GVFAAEGYARATGRVGVCIATSGPGATNLVSGFADALLDSVPLVAITGQVPRRMIGTDAF 201

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLV+DVEDIPRI++EAFFLA SGRPGPVL+D+PKDIQQQL +PN
Sbjct: 202 QETPIVEVTRSITKHNYLVLDVEDIPRIKAEFFLANSGRPGPVLIDIPKDIQQQLVVPN 261

Query: 267 WEQAMKLPGYMSRMPKPP----EDSHLEQIVRLISESKKPVLYVGGCLNSSDELGRFVE 322
WEQ +KL GY+SR+PKP E+ L+QIVRL+ ESK+PVLY GGGCLNSS+EL +FVE
Sbjct: 262 WEQPIKLGGYLSRLPKPTFSANEGLLDQIVRLVGESKRPVLYTGGCLNSSSEELRKFVE 321

Query: 323 LTGIPVASTLMGLGSYPDCDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTVGKL 382
LTGIPVASTLMGLG++PC D+LSL MLGMHGTVYANYAV+ +DLLAFGVRFDRTVGKL
Sbjct: 322 LTGIPVASTLMGLGAFPCDDLSLQMLGMHGTVYANYAVDKADLLAFGVRFDRTVGKL 381

Query: 383 EAFASRAKIVHIDIDSAEIGKNKTPHVSVCGDVKLALQGMNKVLENRAEELKLDGFWRN 442
EAFASRAKIVHIDIDSAEIGKNK PHVS+CGD K+AL+G+N +LE+R ++KLDF WR
Sbjct: 382 EAFASRAKIVHIDIDSAEIGKNKQPHVSICGDXXKVALRGLNNILESRKGVKLDGFSNWR 441

Query: 443 ELNVQKQKFPLSFKTFGEAIPPQYAIKVLDDELTDGKAIISTGVGQHQMWAQFYNYKKPR 502
ELN QK+KFPLSFKTFG+AIPPQYAI+VLDELTD G AI+STGVGQHQMWAQFY Y+ PR
Sbjct: 442 ELNEQKKKFPLSFKTFGDAIPPQYAIQVLDDELTDGDAIVSTGVGQHQMWAQFYKYRNPR 501

Query: 503 QWLSSGGLGAMGFLPAAIGASVANPDAIVVDIDGDGSFIMNVQELATIRVENLPVKVLL 562
QWL+SSGGLGAMGFLPAAIGA+VA PDA+VVDIDGDGSFIMNVQELATIRVENLPVK++L
Sbjct: 502 QWLTSGLGAMGFLPAAIGA+AVARPDVVDIDGDGSFIMNVQELATIRVENLPVKIML 561

Query: 563 LNNQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLR 622
LNNQHLGMV+QWEDRFYKANRAHT+LG+P+ EIFP+ML FA AC IPAARVTK +DLR
Sbjct: 562 LNNQHLGMVVQWEDRFYKANRAHTYLGNPXSSEIFPDMLKFAEACDIPAARVTKVSDLR 621

Query: 623 EAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
AIQTMLDTPGPYLLDVI PHQEHVLPMPNG F D ITEGDGR Y
Sbjct: 622 AAIQTMLDTPGPYLLDVIVPHQEHVLPMPNGAFAFKDTITEGDGRRAY 669

>gb|ACF47582.1| acetolactate synthase 1 [Sonchus asper]
Length = 658

Score = 1022 bits (2643), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 483/584 (82%), Positives = 536/584 (91%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPREHQQ 146
F+SRFAPDQPRKG+D+LVEALER+GV+ VFAYPGGASMEIHQALTRS++IRNVLPREHQQ
Sbjct: 75 FVSRFAPDQPRKGSVDLVEALEREKVHVFAYPGGASMEIHQALTRSNIRNVLPREHQQ 134

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR+ GKPG+CIATSGPGATNLVSGGLADALLDSVP+VAITGQV RRMIGTDAF
Sbjct: 135 GVFAAEGYARALGKPGVCIATSGPGATNLVSGGLADALLDSVPIVAITGQVLRMMIGTDAF 194

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLV+DVEDIPR++ EAF+LATSGRPGPVL+DVPKDIQQQL +P
Sbjct: 195 QETPIVEVTRSITKHNYLVLDVEDIPRVVHEAFYLATSGRPGPVLIDVPKDIQQQLVVPK 254

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYVGGCLNSSDELGRFVELTGI 326
W++ +L GY+SR+PKPP D+HLEQI+RLI+ESK+PVLV GGGCL+SS EL RFVELTGI
Sbjct: 255 WDEPKRLSGYLSRLPKPPNDAHLEQIIRLITESKRVPVLYTGGGCLDSSVELCRFVELTGI 314

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRTVGKLEAFA 386
PVASTLMGLG+YP +LSL MLGMHGTVYANYAV+ SDLLLAFGVRFDDRTVGKLEAFA
Sbjct: 315 PVASTLMGLGAYPASGDLSQLMLGMHGTVYANYAVDKSDLLLAFGVRFDDRTVGKLEAFA 374

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVCADVCLALQGMNKVLENRAEELKLDGFWVRNELNV 446
SRAKIVHIDIDSAEIGKNK PHVS+CGD+K+AL+G+N++LE R+E LDF WR EL+
Sbjct: 375 SRAKIVHIDIDSAEIGKNKQPHVSICGDIKIALKGLNEILEKRSEMRNLDFSSWRQELDE 434

Query: 447 QKQKPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMMAAQFYNYKKPRQWLS 506
QK PLSFKTFG+AIPPQYAI+VLDELTDGKAIISTGVGQHQMMAAQFY Y +PRQWL+
Sbjct: 435 QKLTHPLSFKTFGDAIPPQYAIQVLDELTDGKAIISTGVGQHQMMAAQFYKYNRPQWLT 494

Query: 507 SGGLGAMGFGLPAAIGASVANPDIAIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGLPAAIGA+VA PD IVDDIDGDSF+MNVQELATIRVENLPVK+LLNNQ
Sbjct: 495 SGGLGAMGFGLPAAIGAAVARPDCIVDDIDGDSFMMNVQELATIRVENLPVKILLNNQ 554

Query: 567 HLGVMVQWEDRFYKANRAHTFLGDPAQEDEFIPNMLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LG+P+ E EIFPNML FA AC IPAARVTK DLR AIQ
Sbjct: 555 HLGVMVQWEDRFYKANRAHTYLGNSPNESEIFPNMLKFAEACDIPAARVTKIGDLRAAIQ 614

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
ML+TPGPYLLDVI PHQEHVLPMP GG F DVIT+GDGR+K+
Sbjct: 615 KMLETPGPYLLDVIVPHQEHVLPMPAGGGFMDVITDGDGRMKH 658

>gb|ACF17639.1| putative acetolactate synthase [Capsicum annuum]
Length = 653

Score = 1022 bits (2642), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 483/585 (82%), Positives = 535/585 (91%), Gaps = 1/585 (0%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPREHQQ 146
FI+RFAPD+PRKG D+LVEALER+GV VFAYPGGAS+EIHQALTRS+ IRNVLPREHQQ
Sbjct: 69 FITRFAPDEPRKGCVDLVEALEREKVTDVFAYPGGASVEIHQALTRSNIRNVLPREHQQ 128

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR++G PG+CIATSGPGATNLVSGGLADALLDS+P+VAITGQVPRRMIGTDAF
Sbjct: 129 GVFAAEGYARATGFPVCIATSGPGATNLVSGGLADALLDSIPVAITGQVPRRMIGTDAF 188

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLVMDVEDIPR++ EAFFLA SGRPGPVL+DVPKDIQQQL IPN
Sbjct: 189 QETPIVEVTRSITKHNYLVMDVEDIPRVVREAFFLAKSGRPGPVLIDVPKDIQQQLVIPN 248

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYVGGCLNSSDELGRFVELTGI 326
W+Q M+LPGYMSR+PK P + LEQIVRLISESKKPVLVYVGGC SS+EL RFVELTGI
Sbjct: 249 WDQPMRLPGYMSRLPKLPNEMLLEQIVRLISESKKPVLVYVGGCSQSSEELRRFVELTGI 308

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRTVGKLEAFA 386
PVA+TLMGLG++P D+LSL MLGMHGTVYANYAV+ SDLLLAFGVRFDDRTVGKLEAFA
Sbjct: 309 PVATTLMGLGAFPTGDDLSLQMLGMHGTVYANYAVDSSDLLLAFGVRFDDRTVGKLEAFA 368

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVCADVCLALQGMNKVLENRAEEL-KLDGFWVRNELN 445
SRAKIVHIDIDSAEIGKNK PHVS+C D+KLALQG+N +LE + +L KLDF WR ELN
Sbjct: 369 SRAKIVHIDIDSAEIGKNKQPHVSICADIKLALQGLNSILEKEAKLKKLDFSAWRQELN 428

Query: 446 VQKQKFLPSFKTFGEAIPPPQYAIKVDELDTGKAIISTGVGQHQMWAQFYNYKKPRQWL 505
 QK K+PL++KTFG+AIPPPQYAI+VLDELDTG AI+STGVGQHQMWAQ+Y +KKPRQWL
 Sbjct: 429 EQKVKYPLNYKTFGDAIPPPQYAIQVDELDTGNAIVSTGVGQHQMWAQYYKFKKPRQWL 488

Query: 506 SSGGLGAMGFLPAAIGASVANPDAIVVDIDGDGSFIMNVQELATIRVENLPVKVLLNN 565
 +SSGGLGAMGFLPAAIGA+V P IVVDIDGDGSFIMNVQELATI+VENLPVK++LLNN
 Sbjct: 489 TSSGGLGAMGFLPAAIGA+VGRPEIVVDIDGDGSFIMNVQELATIKVENLPVKIMLLNN 548

Query: 566 QHLGMVMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAI 625
 QHLGMV+QWEDRFYKANRAHT+LG+PA E+EIFPNML FA ACG+PAARVT + D+R AI
 Sbjct: 549 QHLGMVVQWEDRFYKANRAHTYLGPNANEEEIFPNMLKFAEACGVPAARVTHRDDVRAAI 608

Query: 626 QTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
 Q MLDTPGPYLLDVI PHQEHVLPMP+GG F DVITEGDGR +
 Sbjct: 609 QKMLDTPGPYLLDVIVPHQEHVLPMPISGGAFKDVITEGDGRCSH 653

>gb|ABM53018.1| acetolactate synthase [Amaranthus tuberculatus]
 Length = 668

Score = 1021 bits (2641), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 480/588 (81%), Positives = 536/588 (91%), Gaps = 4/588 (0%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
 F+ RF+PD+PRKG D+LVEALER+GV VFAYPGGASMEIHQALTRS+ IRNVLPHEQG
 Sbjct: 81 FVFRFSPDEPRKGCDELVEALEREVTDVFAYPGGASMEIHQALTRSNIRNVLPHEQG 140

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGADALLDSVPLVAITGQVPRRMIGTDAF 206
 GVFAAEGYAR++G+ G+CIATSGPGATNLVSG ADALLDSVPLVAITGQVPRRMIGTDAF
 Sbjct: 141 GVFAAEGYARATGRVGVCIATSGPGATNLVSGFADALLDSVPLVAITGQVPRRMIGTDAF 200

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
 QETPIVEVTRSITKHNYLV+DVEDIPRI++EAFFLA SGRPGPVL+D+PKDIQQQL +PN
 Sbjct: 201 QETPIVEVTRSITKHNYLVLDVEDIPRIKAEFFLANSGRPGPVLIDIPKDIQQQLVVPN 260

Query: 267 WEQAMKLPGYMSRMPKPP----EDSHLEQIVRLISESKKPVLYVGGCLNSSDELGRFVE 322
 WEQ +KL GY+SR+PKP E+ L+QIVRL+ ESK+PVLY GGGCLNSS+EL +FV+
 Sbjct: 261 WEQPIKLGGLSRLPKPTFSANEGLLDQIVRLVGESEKRPVLYTGGCLNSSSEELRKFFVK 320

Query: 323 LTGIPVASTLMGLGSYPDCDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTVGKL 382
 LTGIPVASTLMGLG++PC D+LSL MLGMHGTVYANYAV+ +DLLAFGVRFDRTVGKL
 Sbjct: 321 LTGIPVASTLMGLGAFPCDDLSLQMLGMHGTVYANYAVDKADLLAFGVRFDRTVGKL 380

Query: 383 EAFASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWRN 442
 EAFASRAKIVHIDIDSAEIGKNK PHVS+CGDVK+AL+G+N +LE+R ++KLDF WR
 Sbjct: 381 EAFASRAKIVHIDIDSAEIGKNKQPHVSICGDVKVALRGLNNILESRKGVKLDGFSNWR 440

Query: 443 ELNVQKQKFLPSFKTFGEAIPPPQYAIKVDELDTGKAIISTGVGQHQMWAQFYNYKKPR 502
 ELN QK+KFLPSFKTFG+AIPPPQYAI+VLDELDT G AI+STGVGQHQMWAQFY Y+ PR
 Sbjct: 441 ELNEQKKKFLPSFKTFGDAIPPPQYAIQVDELDTGDAIVSTGVGQHQMWAQFYKYRNP 500

Query: 503 QWLSSGGLGAMGFLPAAIGASVANPDAIVVDIDGDGSFIMNVQELATIRVENLPVKVLL 562
 QWL+SSGGLGAMGFLPAAIGA+VA PDA+VVDIDGDGSFIMNVQELATIRVENLPVK++L
 Sbjct: 501 QWLTSSGGLGAMGFLPAAIGA+VARPDAVVVDIDGDGSFIMNVQELATIRVENLPVKIML 560

Query: 563 LNNQHLMVMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLR 622
 LNNQHLMV+QWEDRFYKANRAHT+LG+P+ EIFP+ML FA AC IPAARVTK +DLR
 Sbjct: 561 LNNQHLMVVQWEDRFYKANRAHTYLGPNNSSEIFPDMLKFAEACDIPAARVTKVSDLR 620

Query: 623 EAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
 AIQTMLDTPGPYLLDVI PHQEHVLPMP+G F D ITEGDGR Y
 Sbjct: 621 AAIQTMLDTPGPYLLDVIVPHQEHVLPMPISGAFAFKDTITEGDGRRAY 668

>gb|ABM53019.1| acetolactate synthase [Amaranthus tuberculatus]
 Length = 669

Score = 1021 bits (2640), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 481/588 (81%), Positives = 536/588 (91%), Gaps = 4/588 (0%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F+SRF+PD+PRKG D+LVEALER+GV VFAYPGGASMEIHQALTRS+ IRNVLP RHEQG
Sbjct: 82 FVSRFSDEPRKGC DVLVEALERE GVTDFVAYPGGASMEIHQALTRSNIRNVLP RHEQG 141

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSG LADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR++G+ G+CIATSGPGATNLVSG ADALLDSVPLVAITGQVPRRMIGTDAF
Sbjct: 142 GVFAAEGYARATGRVGVCIATSGPGATNLVSGFADALLDSVPLVAITGQVPRRMIGTDAF 201

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNLYL+DVEDIPRI++EAFFLA SGRPGPVL+D+PKDIQQQL +PN
Sbjct: 202 QETPIVEVTRSITKHNLYLVDVEDIPRIVKEAFFLANSGRPGPVLIDIPKDIQQQLVVPN 261

Query: 267 WEQAMKLPGYMSRMPKPP---EDSHLEQIVRLISESKKPVLVYGGGCLNSSDELGRFVE 322
WEQ +KL GY+SR+PKP E+ L+QIVRL+ ESK+PVLY GGGCLNSS+EL +FVE
Sbjct: 262 WEQPIKLG GYLSRLPKPTFSANE EGLDQIVRLVGE SKRPVLYTGGGCLNSS EELRK FVE 321

Query: 323 LTGIPVASTLMGLGSYP CDEL SLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTGKL 382
LTGIPVASTLMGLG++PC D+LSL MLGMHGT VYANYAV+ +DLLAFGVRFDDRVTGKL
Sbjct: 322 LTGIPVASTLMGLGAFPCTD DLSLQMLGMHGT VYANYAVDKADLLAFGVRFDDRVTGKL 381

Query: 383 EAFASRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRN 442
EAFASRAKIVHIDIDSAEIGKNK PHVS+CGDVK+AL+G+N +LE+R ++KLDF WR
Sbjct: 382 EAFASRAKIVHIDIDSAEIGKNKQPHVSIC G DVKVALRGLNNILESRKGKVLDFSNWRE 441

Query: 443 ELNVQKQKFP LSFKT FG EAI PPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPR 502
ELN QK+KFPLSFKT FG+AIPPQYAI+VLDELTD G AI+STGVGQHQMWA AQFY Y+ PR
Sbjct: 442 ELNEQKKKFP LSFKT FGDAIPPQYAIQVLDELTDGDAIVSTGVGQHQMWA AQFYKYRNPR 501

Query: 503 QWLSSGGLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLL 562
QWL+SGGLGAMGFGLPAAIGA+VA PDA+VVDIDGDSFIMNVQELATIRVENLPVK++L
Sbjct: 502 QWLTSGGLGAMGFGLPAAIGAAVARPD AVVDIDGDSFIMNVQELATIRVENLPVKIML 561

Query: 563 LNNQHLMGMVQWEDRFYKANRAHTFLGDPAQEDEIFPNM L LFAAACGIPAARVTKKADLR 622
LNNQHLMGMV+Q EDRFYKANRAHT+LG+P+ EIFP+ML FA AC IPAARVTK +DLR
Sbjct: 562 LNNQHLMGMVQLEDRFYKANRAHTYLG NPSNSSEIFPDMLKFAEACDIPAARVTKVSDLR 621

Query: 623 EAIQTMLDTPGPYLLDVICPHQEHLVPMIPNGGT FNDVITEGDGRIKY 670
AIQTMLDTPGPYLLDVI PHQEHLVPMIP+G F D ITEGDGR Y
Sbjct: 622 AAIQTMLDTPGPYLLDVIVPHQEHLVPMIPSGAAFKDTITEGDGRRAY 669

>emb|CAE18088.1| acetolactate synthase [Papaver rhoeas]
Length = 662

Score = 1017 bits (2629), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 474/584 (81%), Positives = 535/584 (91%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F+SR+ D+PRKGAD+LVEALER+GV VFAYPGGASMEIHQALTRSSSIRNVLP RHEQG
Sbjct: 79 FVSRYKDDEPRK GADVLVEALERE GVTNVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 138

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSG LADALLDSVPLVAITGQVPRRMIGTDAF 206
G+F+AEGYAR+SG PG+CIATSGPGATNLVSG LADALLDS+P+VA+TGQVPRRMIGTDAF
Sbjct: 139 GIFSAEGYARASGLPGVCIATSGPGATNLVSG LADALLDSIPIVAVTGQVPRRMIGTDAF 198

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNLYL+DVEDIPR+++EAFFLATSGRPGPVL+DVPKD+QQQL +P
Sbjct: 199 QETPIVEVTRSITKHNLYLVDVEDIPRVVKEAFFLATSGRPGPVLIDVPKDVQQQLVVPK 258

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCLNSSDELGRFVELTGI 326
W+ MKLPGYMSR PK PE + LEQ+VRLISESKKPVLVYGGGC+N S+EL RFV+LTGI
Sbjct: 259 WDTPMKLPGYMSRAPKSPEHNLLEQVRLISESKKPVLVYGGGCIN YSEELRRFVDLTGI 318

Query: 327 PVASTLMGLGSYP CDEL SLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTGKLEAFA 386
PVASTLMGLG++ C D LSL MLGMHGT VYANYAV+ +DLLAFGVRFDDRVTGK+EAFA
Sbjct: 319 PVASTLMGLGAHSCTDVL SLQMLGMHGT VYANYAVDKADLLAFGVRFDDRVTGKIEAFA 378

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SR+KIVHIDID AEIGKNK PHVS+C D+ +AL+G+NK+LE + +LKLDF WR EL
Sbjct: 379 SRSKIVHIDIDPAEIGKNKQPHVSICADMGVALKGLNKLLEKMSKLKLD FVSWREELME 438

Query: 447 QKQKPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK+ +PLS+KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQ+Y Y+ PRQWL+
Sbjct: 439 QKKNYPLSYKTFGEAIPPQYAIKVLDELTEGKAIISTGVGQHQMWAQWYKYRGPRQWLT 498

Query: 507 SGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
S GLGAMGFGLPAAIGA+VA P+AIVVDIDGDSF+MNVQELA +RVENLPVK+LLLNNQ
Sbjct: 499 SAGLGAMGFGLPAAIGAAVAKPEAIVVDIDGDSFMMNVQELAAVRVENLPVKILLNNQ 558

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LG+PA++ EIFP+ML FA AC IPAARVTK ++LR AIQ
Sbjct: 559 HLGMMVQWEDRFYKANRAHTYLGPNPAKDTEIFPDMLKFAEACDIPAARVTKVSELRAAIQ 618

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
MLDTPGPYLLDVI PHQEHVLPMP GG+FN+VI EGDGR KY
Sbjct: 619 KMLDTPGPYLLDVIVPHQEHVLPMPAGGSFNEVIIIEGDGRTKY 662

>gb|AAC69629.1| herbicide resistant acetolactate synthase precursor [Bassia
scoparia]
Length = 666

Score = 1016 bits (2628), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 480/588 (81%), Positives = 537/588 (91%), Gaps = 4/588 (0%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPREHQQ 146
F+SRFAPDQPRKG D+LVEALER+GV VFAYPGGASMEIHQALTRS SIRNVLPREHQQ
Sbjct: 79 FVSRFAPDQPRKGCDVLVEALEREGVTDVFAYPGGASMEIHQALTRSDSIRNVLPREHQQ 138

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGADALLDSVPLVAITGQVPRRMIGTDAF 206
G+FAAEGYAR++G+ G+CIATSGPGATNLVSG ADALLDSVPLVAITGQVPRRMIGTDAF
Sbjct: 139 GIFAAEGYARATGRVGVCIATSGPGATNLVSGFADALLDSVPLVAITGQVPRRMIGTDAF 198

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLV+DVEDIPRI++EAFFLA SGRPGPVL+D+PKDIQQQL +P+
Sbjct: 199 QETPIVEVTRSITKHNYLVLDVEDIPRIVKEAFFLANSGRPGPVLIDIPKDIQQQLVVPD 258

Query: 267 WEQAMKLPGYMSRMPKP---PEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVE 322
W+Q ++L GY+SR+PK ++ LEQIVRL+SE+KKPVLYVGGGCLNS +EL +FVE
Sbjct: 259 WDQGVRLGGYVSRPLKSVFSANDEGLLEQIVRLMSEAKKPVLYVGGGCLNSGEELRKFVE 318

Query: 323 LTGIPVASTLMGLGSPCDDLSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKL 382
LTGIPVASTLMGLG+YPC+D+LSLHMLGMHGTVYANYAV+ +DLLAFGVRFDDRVTGKL
Sbjct: 319 LTGIPVASTLMGLGAYPCNDDLHMLGMHGTVYANYAVDKADLLAFGVRFDDRVTGKL 378

Query: 383 EAFASRAKIVHIDIDSAEIGKNKTPHVSVCADVCLALQGMNVLENRAEELKLDGFWWRN 442
EAFASRAKIVHIDIDSAEIGKNK PHVS+C DVK AL+GMNK+LE+R +LKL++ WR
Sbjct: 379 EAFASRAKIVHIDIDSAEIGKNKQPHVSICADVCLALQGMNVLENRAEELKLDGFWWRN 438

Query: 443 ELNVQKQKPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPR 502
EL QK+KFPLSFKTFGEAIPPQYAI++LDELTDGKAIISTGVGQHQMWAQ Y Y+ PR
Sbjct: 439 ELGEQKKKPLSFKTFGEAIPPQYAIQMLDELTDGKAIISTGVGQHQMWAQHYKYRNPR 498

Query: 503 QWLSSGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLL 562
QWL+SGGLGAMGFGLPAAIGA+VA PDA+VVDIDGDSFIMNVQELATIRVENLPVK++L
Sbjct: 499 QWLTSGGLGAMGFGLPAAIGAAVARPDVVDIDGDSFIMNVQELATIRVENLPVKIML 558

Query: 563 LNNQHLMGMVQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLR 622
LNNQHLMGV+Q EDRFYKANRAHT+LG+P++E EIFP+ML FA AC IPAARVTK DLN
Sbjct: 559 LNNQHLMGMVQLEDRFYKANRAHTYLGPNPSKESEIFPDMLKFAEACDIPAARVTKVGDLR 618

Query: 623 EAIQTMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
A+QTMLDTPGPYLLDVI PHQEHVLPMP+G F D+I EGDGR Y
Sbjct: 619 AAMQTMLDTPGPYLLDVIVPHQEHVLPMPGAAFKDIINEGDGRTSY 666

>emb|CAO49020.1| unnamed protein product [Vitis vinifera]
Length = 657

Score = 1016 bits (2627), Expect = 0.0, Method: Compositional matrix adjust.

Identities = 478/584 (81%), Positives = 529/584 (90%), Gaps = 7/584 (1%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQG 146
FISRFAPD+PRKG D+LVEALER+GV+ VFAYPPGGASMEIHQALTRS+ IRNVLP RHEQG

Sbjct: 81 FISRFAPDEPRKGC DVLVEALEREKVHVFAYPPGGASMEIHQALTRSNIRNVLP RHEQG 140

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAAEGYAR+SG+PG+CIATSGPGATNLVSGLADALLDS+P+VAITGQVPRRMIGTDAF

Sbjct: 141 GVFAAEGYARASGRPGVCIATSGPGATNLVSGLADALLDSIPVAITGQVPRRMIGTDAF 200

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNLYL+DVEDIP I+ EAFFLATSGRPGPVL+DVPKDIQQQL +PN

Sbjct: 201 QETPIVEVTRSITKHNLYLVDVEDIPHIVREAFFLATSGRPGPVLIDVPKDIQQQLVVPN 260

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W + ++LPGY R+PK PE +HLEQIVRLISESK+PVLYVGGGC+NSS+EL RFV+LTGI

Sbjct: 261 WNKGLRLPGYTFRLPKSPEKAHLEQIVRLISESKRPVLYVGGGCMNSSEELKRFVDLTGI 320

Query: 327 PVASTLMGLGSGPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTVGKLEAFA 386
PVASTLMGLG++PC D+LSL MLGMHGT+YANYAV+ SDLLAFGVRFD DRTVGK+EAFA

Sbjct: 321 PVASTLMGLGAFPCTDKLSLQMLGMHGTMYANYAVDRSDLLAFGVRFD DRTVGKIEAFA 380

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC DVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDID AEIGKNK PHVS AL GMN +LE + K DF WR+ELN

Sbjct: 381 SRAKIVHIDIDPAEIGKNKQPHVS-----ALTGMNSLLEETGAKSKYDFSSWRDELNE 433

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
QK K+PLSFKTFGEAIPPQYAI+VLDELTDG AIIS+GVGQHQMWAQFY Y+ PRQWLS

Sbjct: 434 QKAKYPLSFKTFGEAIPPQYAIQVLDELTDGNAIISGVGQHQMWAQFYKYRGPRQWLS 493

Query: 507 SSGGLGAMGFGLPAAIGASVANPD AIVVDIDGDGSFIMNVQELATIRVENLPVKVLLNNQ 566
S GLGAMGFGLPAA+GA+VA PDA+VVDIDGDGSFIMNVQELATIRVENLPV++LNNQ

Sbjct: 494 SSGGLGAMGFGLPAAAMGA AVAKPD A VVDIDGDGSFIMNVQELATIRVENLPVKIMLNNQ 553

Query: 567 HLGVMVQWEDRFYKANRAHTFLGDPAQEDEIFPNMMLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LG+P+ E EIFPNML FA AC IPAARVTKK+++REAI+

Sbjct: 554 HLGVMVQWEDRFYKANRAHTYLG NPSNEAEIFPNMLKFAEACDIPAARVTKKSEVREAIK 613

Query: 627 TMLDTPGPYLLDVICPHQEHVLP MIPNGGT FNDVITEGDGRIKY 670
ML+TPGPYLLDVI PHQEHVLP MIP+GG F D I EGDGR Y

Sbjct: 614 KMLETPGPYLLDVIVPHQEHVLP MIPSGGAFKDAINEGDGREAY 657

>gb|AAB67839.1| acetolactate synthase precursor [Amaranthus sp.]
Length = 665

Score = 1015 bits (2625), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 477/588 (81%), Positives = 535/588 (90%), Gaps = 4/588 (0%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQG 146
F+SRF+P++PRKG D+LVEALER+GV VFAYPPGGASMEIHQALTRS+ IRNVLP RHEQG

Sbjct: 78 FVSRSFP EEPKGC DVLVEALEREKVTDVFAYPPGGASMEIHQALTRSNIRNVLP RHEQG 137

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
GVFAA+GYAR++G+ G+CIATSGPGATNLVSG ADALLDSVPLVAITGQVPRRMIGTDAF

Sbjct: 138 GVFAAQGYARATGRVGVC IATSGPGATNLVSGFADALLDSVPLVAITGQVPRRMIGTDAF 197

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNLYL+DVEDIPRI++EAFFLA SGRPGPVL+D+PKDIQQQL +PN

Sbjct: 198 QETPIVEVTRSITKHNLYLVDVEDIPRIVKEAFFLANSGRPGPVLIDIPKDIQQQLVVPN 257

Query: 267 WEQAMKLPGYMSRMPKPP----EDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVE 322
WEQ +KL GY+SR+PKP E+ L+QIVRL+ ESK+PVLY GGGCLNSS+EL +FVE

Sbjct: 258 WEQPIKLG GYLSRLPKPTFSANEGLLDQIVRLVGESKRVPVLYTGGGCLNSSSEELKRFVE 317

Query: 323 LTGIPVASTLMGLGSGPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTVGKL 382
LTGIPVASTLMGLG++PC D+LSL MLGMHGT VYANYAV+ +DLLAFGVRFD DRTVGKL

Sbjct: 318 LTGIPVASTLMGLGAFPCTDDLSLQMLGMHGT VYANYAVDKADLLAFGVRFD DRTVGKL 377

Query: 383 EAFASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFGVWRN 442
EAFASRAKIVHIDIDSAEIGKNK PHVS+CG++K+ALQG+NK+LE+R +LKLDG WR
Sbjct: 378 EAFASRAKIVHIDIDSAEIGKNKQPHVSICGEIKVALQGLNKILES SRKGLKLDGFSNWRE 437

Query: 443 ELNVQKQKFPPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPR 502
ELN QK+KFPPLSFK+FG+AIPPQYAI+VLDELTD G AI+STGVGQHQMWAQFY Y+ PR
Sbjct: 438 ELNEQKKKFPPLSFKSFGDAIPPQYAIQVDELTDGDAIVSTGVGQHQMWAQFYKYRNPR 497

Query: 503 QWLSSGGLGAMGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLL 562
QWL+SGGLGAMGFLPAA GA+VA PDA+VVDIDGDSFIMNVQELATIRVENLPVK++L
Sbjct: 498 QWLTSGGLGAMGFLPACYGAAVRPDAVVVDIDGDSFIMNVQELATIRVENLPVKIML 557

Query: 563 LNNQHLGMVMQWEDRFYKANRAHTFLGDPQAQDEIFPNMLLFAAACGIPAARVTKKADLR 622
LNNQHLGMV+Q EDRFYKANRAHT+LG+P+ EIFP+ML FA AC IPAARVTK +DLR
Sbjct: 558 LNNQHLGMVVQLED RFYKANRAHTYLGPNPSNSEIFPDMLKFAEACDIPAARVTKVSDLR 617

Query: 623 EAIQTMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
AIQTMLDTPGPYLLDVI PHQEHVLPMP+G F D ITEGDGR Y
Sbjct: 618 AAIQTMLDTPGPYLLDVIVPHQEHVLPMPISGA AFKDTITEGDGRRAY 665

>gb|AAG40279.1|AF308648_1 acetolactate synthase [Solanum ptychanthum]
Length = 567

Score = 1004 bits (2597), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 477/567 (84%), Positives = 519/567 (91%)

Query: 96 PRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVF AAEGYA 155
PRKG D+LVEALER+GV VFAYPPGGASMEIHQALTRS+ IRNVLP RHEQGGVF AAEGYA
Sbjct: 1 PRKGC DVLVEALERE GVTDFAYPPGGASMEIHQALTRSNIIRNVLP RHEQGGVF AAEGYA 60

Query: 156 RSSGKPGIC IATSGPGATNLVSG LADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVT 215
R++G PG+CIATSGPGATNLVSG LADALLDS+P+VAITGQVPRRMIGTDAFQETPIVEVT
Sbjct: 61 RATGFP GVIC IATSGPGATNLVSG LADALLDSIPIVAITGQVPRRMIGTDAFQETPIVEVT 120

Query: 216 RSITKHNLYLMDVEDIPRIIEEAF FLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLP 275
RSITKHNLYLMDVEDIPRI+ EAF FLA SGRPGPVL+DVPKDIQQQL IPNW+Q M+LPG
Sbjct: 121 RSITKHNLYLMDVEDIPRI REAF FLAKSGRPGPVLIDVPKDIQQQLVIPNWDQPMRLPG 180

Query: 276 YMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVASTLMGL 335
YMSR+PK P + LEQIVRLISESKKPVLYVGGG SS+EL RFVELTGIPVASTLMGL
Sbjct: 181 YMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGGCSQSS EELRRFVELTGIPVASTLMGL 240

Query: 336 GSYPCDEL SLHMLGMHGT VYANYAVEHSDLLLA FGVRFD DRVTGKLEAFASRAKIVHID 395
G++P DELSL MLGMHGT VYANYAV+ SDLLLA FGVRFD DRVTGKLEAFASRAKIVHID
Sbjct: 241 GAFFTGD ELSLQMLGMHGT VYANYAVDSSDLLLA FGVRFD DRVTGKLEAFASRAKIVHID 300

Query: 396 IDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQKFPPLSF 455
IDSAEIGKNK PH S+C D+KLALQG+N +LE + +LKLDG WR ELN QK K+PL+P
Sbjct: 301 IDSAEIGKNKLP HASICADIKLALQGLNSILEGKEGKLKLDGSAWRQELNEQKVKYPLNF 360

Query: 456 KTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGF 515
KTFGEAIPPQYAI+VLDELTD+G AIIISTGVGQHQMWAQFY YKKPRQWL+SGGLGAMGF
Sbjct: 361 KTFGEAIPPQYAIQVDELTDNGNAIISTGVGQHQMWAQFYKYKKPRQWLSSGGLGAMGF 420

Query: 516 GLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
GLPAA+GA+V P IVVDIDGDSF+MNVQELATI+VENLPVK++LLNNQHLGMV+QWE
Sbjct: 421 GLPAAMGA AVGRPGEIVVDIDGDSFMMNVQELATIKVENLPVKIMLLNNQHLGMVVQWE 480

Query: 576 DRFYKANRAHTFLGDPQAQDEIFPNMLLFAAACGIPAARVTKKADLR EAIQTMLDTPGPY 635
DRFYKANRAHT+LGDP A E+EIFPNML FA ACG+PAARVT + +LR AIQ MLDTPGPY
Sbjct: 481 DRFYKANRAHTYLGDPAN EEEIFPNMLKFAEACGVP AARVTHRDELRAAIQKMLDTPGPY 540

Query: 636 LLDVICPHQEHVLPMPINGGTFNDVIT 662
LLDVI PHQEHVLPMP+GG F DVIT
Sbjct: 541 LLDVIVPHQEHVLPMPISGGA F KD VIT 567

>gb|AAG40280.1|AF308649_1 acetolactate synthase [Solanum ptychanthum]
gb|AAG40281.1|AF308650_1 acetolactate synthase [Solanum ptychanthum]
Length = 567

Score = 1003 bits (2592), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 476/567 (83%), Positives = 518/567 (91%)

Query: 96 PRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYA 155
PRKG D+LVEALER+GV VFAYPPGGASMEIHQALTRS+ IRNVLPHEQGGVFAAEGYA
Sbjct: 1 PRKGCIDLVEALEREGVTDVFAYPPGGTSMIEHQALTRSNIIRNVLPHEQGGVFAAEGYA 60

Query: 156 RSSGKPGICIAATSGPGATNLVSGLDALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVT 215
R++G PG+CIATSGPGATNLVSGLDALLDS+P+VAITGQVPRRMIGTDAFQETPIVEVT
Sbjct: 61 RATGFPVGVCIATSGPGATNLVSGLDALLDSIPIVAITGQVPRRMIGTDAFQETPIVEVT 120

Query: 216 RSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLP 275
RSITKHNLYLMDVEDIPRI+ EAFFLA SGRPGPVL+DVPKDIQQQL IPNW+Q M+LPG
Sbjct: 121 RSITKHNLYLMDVEDIPRIVREAFFLAKSGRPGPVLIDVPKDIQQQLVIPNWDQPMRLPG 180

Query: 276 YMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGCLNSSDELGRFVELTGIPVASTLMGL 335
YMSR+PK P + LEQIVRLISESKKPVLYVGGC SS+EL RFVELTGIPVASTLMGL
Sbjct: 181 YMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGCSQSSEELRRFVELTGIPVASTLMGL 240

Query: 336 GSYPCDELSDLHMLGMHGT VYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAKIVHID 395
G++P DELSL MLGMHGT VYANYAV+ SDLLAFGVRFDRTVGKLEAFASRAKIVHID
Sbjct: 241 GAFPTGDELSLQMLGMHGT VYANYAVDSSDLLAFGVRFDRTVGKLEAFASRAKIVHID 300

Query: 396 IDSAEIGKNKTPHVSVC GDVKLALQGMNVLENRAELKLD FGVWRNELNVQKQKFLPSF 455
IDSAEIGKNK PH S+C D+KLALQG+N +LE + +LKLD F WR ELN QK K+PL+F
Sbjct: 301 IDSAEIGKNKLPHASICADIKLALQGLNSILEGKEGKLKLD FSAWRQELNEQKVKYPLNF 360

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGF 515
KTFGEAIPPQYAI+VLDELTDG AIISTGVGQHQMWAQFY YKKPRQWL+SGGLGAMGF
Sbjct: 361 KTFGEAIPPQYAIQVLDELTDGNAIISTGVGQHQMWAQFYKYKKPRQWLSSGGLGAMGF 420

Query: 516 GLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
GLPAA+GA+V P IVVDIDGDSF+MNVQELATI+VENLPVK++LLNNQHLGMV+QWE
Sbjct: 421 GLPAAMGAAGVGRPGIIVVDIDGDSFMMNVQELATIKVENLPVKIMLLNNQHLGMVQWE 480

Query: 576 DRFYKANRAHTFLGDP AQEDEFPNMLLFAAACGIPAARVTKADLREAIQTMLDTPGPY 635
DRFYKANRAHT+LGDP A E+EIFPNML FA ACG+PAARV + +LR AIQ MLDTPGPY
Sbjct: 481 DRFYKANRAHTYLGDPANEEEIFPNMLKFAEACGVPAARVTHRDELRAAIQMLDTPGPY 540

Query: 636 LLDVICPHQEHVLPMPNGGTFNDVIT 662
LLDVI PHQEHVLPMP+GG F DVIT
Sbjct: 541 LLDVIVPHQEHVLPMPISGGAFKDVIT 567

>gb|ABR68865.1| acetohydroxyacid synthase [Solanum ptychanthum]
Length = 565

Score = 1000 bits (2585), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 475/565 (84%), Positives = 517/565 (91%)

Query: 96 PRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYA 155
PRKG D+LVEALER+GV VFAYPPGGASMEIHQALTRS+ IRNVLPHEQGGVFAAEGYA
Sbjct: 1 PRKGCIDLVEALEREGVTDVFAYPPGGASMEIHQALTRSNIIRNVLPHEQGGVFAAEGYA 60

Query: 156 RSSGKPGICIAATSGPGATNLVSGLDALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVT 215
R++G PG+CIATSGPGATNLVSGLDALLDS+P+VAITGQVPRRMIGTDAFQETPIVEVT
Sbjct: 61 RATGFPVGVCIATSGPGATNLVSGLDALLDSIPIVAITGQVPRRMIGTDAFQETPIVEVT 120

Query: 216 RSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLP 275
RSITKHNLYLMDVEDIPRI+ EAFFLA SGRPGPVL+DVPKDIQQQL IPNW+Q M+LPG
Sbjct: 121 RSITKHNLYLMDVEDIPRIVREAFFLAKSGRPGPVLIDVPKDIQQQLVIPNWDQPMRLPG 180

Query: 276 YMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGCLNSSDELGRFVELTGIPVASTLMGL 335
YMSR+PK P + LEQIVRLISESKKPVLYVGGC SS+EL RFVELTGIPVASTLMGL
Sbjct: 181 YMSRLPKLPNEMLLEQIVRLISESKKPVLYVGGCSQSSEELRRFVELTGIPVASTLMGL 240

Query: 336 GSYPCDELSDLHMLGMHGT VYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAKIVHID 395
G++P DELSL MLGMHGT VYANYAV+ SDLLAFGVRFDRTVGKLEAFASRAKIVHID
Sbjct: 241 GAFPTGDELSLQMLGMHGT VYANYAVDSSDLLAFGVRFDRTVGKLEAFASRAKIVHID 300

Query: 396 IDSAEIGKNKTPHVSVCQDVKLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQKPLSF 455
IDSAEIGKNK PH S+C D+KLALQG+N +LE + +LKLDG WR ELN QK K+PL+F
Sbjct: 301 IDSAEIGKNKLPHASICADIKLALQGLNSILEGKEGKLKLDGSAWRQELNEQKVYPLNF 360

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGF 515
KTFGEAIPPQYAI+VLDELTDG AIISTGVGQHQMWAQFY YKKPRQWL+SGGLGAMGF
Sbjct: 361 KTFGEAIPPQYAIQVLDELTDGKAIISTGVGQHQMWAQFYKYKKPRQWLSSGGLGAMGF 420

Query: 516 GLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
GLPAA+GA+V P IVVDIDGDSF+MNVQELATI+VENLPVK++LLNNQHLGMV+QWE
Sbjct: 421 GLPAAMGAAGVGRPEIVVDIDGDSFMMNVQELATIKVENLPVKIMLLNNQHLGMVVQWE 480

Query: 576 DRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPY 635
DRFYKANRAHT+LGDP A E+EIFPNML FA ACG+PAARVT + +LR AIQ MLDTPGPY
Sbjct: 481 DRFYKANRAHTYLGDPANEEEIFPNMLKFAEACGVPAARVTHRDELRAAIQKMLDTPGPY 540

Query: 636 LLDVICPHQEHVLPMPNGGTFNDV 660
LLDVI PHQEHVLPMP+GG F DV
Sbjct: 541 LLDVIVPHQEHVLPMPSGGAFKDV 565

>gb|ABR68866.1| acetohydroxyacid synthase [Solanum ptychanthum]
Length = 565

Score = 999 bits (2582), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 474/565 (83%), Positives = 516/565 (91%)

Query: 96 PRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYA 155
PRKG D+LVEALER+GV VFAYPPGGASMEIHQALTRS+ IRNVLPHEQGGVFAAEGYA
Sbjct: 1 PRKGCVDLVEALEREVDVVFAYPPGGASMEIHQALTRSNIIRNVLPHEQGGVFAAEGYA 60

Query: 156 RSSGKPGICIATSGPGATNLVSGLDALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVT 215
R++G PG+CIATSGPGATNLVSGLDALLDS+P+VAITGQVPRRMIGTD FQETPIVEVT
Sbjct: 61 RATGFPVCIATSGPGATNLVSGLDALLDSIPVVAITGQVPRRMIGTDVDFQETPIVEVT 120

Query: 216 RSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLP 275
RSITKHNLYLMDVEDIPRI+ EAFFLA SGRPGPVL+DVPKDIQQQL IPNW+Q M+LPG
Sbjct: 121 RSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLVIPNWDQPMRLPG 180

Query: 276 YMSRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCLNSSDELGRFVELTGIPVASTLMGL 335
YMSR+PK P + LEQIVRLISESKKPVLVYGGGC SS+EL RFVELTGIPVASTLMGL
Sbjct: 181 YMSRLPKLPNEMLLEQIVRLISESKKPVLVYGGGCSSEELRRFVELTGIPVASTLMGL 240

Query: 336 GSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAKIVHID 395
G++P DELSL MLGMHGTVYANYAV+ SDLLAFGVRFDRTVGKLEAFASRAKIVHID
Sbjct: 241 GAFPTGDELSQLMLGMHGTVYANYAVDSSDLLAFGVRFDRTVGKLEAFASRAKIVHID 300

Query: 396 IDSAEIGKNKTPHVSVCQDVKLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQKPLSF 455
IDSAEIGKNK PH S+C D+KLALQG+N +LE + +LKLDG WR ELN QK K+PL+F
Sbjct: 301 IDSAEIGKNKLPHASICADIKLALQGLNSILEGKEGKLKLDGSAWRQELNEQKVYPLNF 360

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGF 515
KTFGEAIPPQYAI+VLDELTDG AIISTGVGQHQMWAQFY YKKPRQWL+SGGLGAMGF
Sbjct: 361 KTFGEAIPPQYAIQVLDELTDGKAIISTGVGQHQMWAQFYKYKKPRQWLSSGGLGAMGF 420

Query: 516 GLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
GLPAA+GA+V P IVVDIDGDSF+MNVQELATI+VENLPVK++LLNNQHLGMV+QWE
Sbjct: 421 GLPAAMGAAGVGRPEIVVDIDGDSFMMNVQELATIKVENLPVKIMLLNNQHLGMVVQWE 480

Query: 576 DRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPY 635
DRFYKANRAHT+LGDP A E+EIFPNML FA ACG+PAARVT + +LR AIQ MLDTPGPY
Sbjct: 481 DRFYKANRAHTYLGDPANEEEIFPNMLKFAEACGVPAARVTHRDELRAAIQKMLDTPGPY 540

Query: 636 LLDVICPHQEHVLPMPNGGTFNDV 660
LLDVI PHQEHVLPMP+GG F DV
Sbjct: 541 LLDVIVPHQEHVLPMPSGGAFKDV 565

>gb|AAT07329.1| acetohydroxyacid synthase 3 [Helianthus annuus]
Length = 646

Score = 990 bits (2559), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 462/585 (78%), Positives = 527/585 (90%), Gaps = 4/585 (0%)

Query: 88 ISRFPADQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHEQGG 147
+SRF PD+PRKG+D+LVEALER+GV VFAYPGGA++EIHQALTRS+ IRN+LPRHEQGG
Sbjct: 63 VSRFGPDEPRKGSDDLVEALEREQGVTVNFAYPGGATLEIHQALTRSTIIRNVLPRHEQGG 122

Query: 148 VFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQ 207
VFAAEGYAR+SG G+CI+TSGPGATNLVSLADALLDSVP+VAITGQVPR MIGTDAFQ
Sbjct: 123 VFAAEGYARASGLTGCISTSGPGATNLVSLADALLDSVPIVAITGQVPRNMIGTDAFQ 182

Query: 208 ETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNW 267
ETPIVEV+RSITKHNYLV++V+DIPRI+ EAFFLA+SGRPGPVL+D+PKDIQQQL +PNW
Sbjct: 183 ETPIVEVRSITKHNYLVNVQDIPRIVHEAFLASSGRPGPVLIDIPKDIQQQLVVPNW 242

Query: 268 ---EQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELT 324
+Q M+L GY+SR+PKPP ++HL QIVR I ESK+PVLYVGGGC+NSSDELGRFVELT
Sbjct: 243 DEQQQPMRLDGYISRLPKPPNETHLRQIVRFIKESKRPVLYVGGGCMNSSDELGRFVELT 302

Query: 325 GIPVASTLMGLGSYPCCDELHMLGMHGT VYANYAVEHSDLLAFGVRFDRTVGKLEA 384
GIPVA+TLMGLG+YP +LSLHMLGMHGT VYANYA++ SDLLAFGVRFDRTVGK+EA
Sbjct: 303 GIPVANTLMGLGTYPGSHDLHMLGMHGT VYANYAIDKSDLLAFGVRFDRTVGKIEA 362

Query: 385 FASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWVRNEL 444
FASRAKIVHIDID AEIGKNK PH S+CGD+K ALQG+NK+LE R E+L DF W+ E+
Sbjct: 363 FASRAKIVHIDIDPAEIGKNKQPHFSICGDIKAALQGLNKILE-RGEDLDFDFSPWKEEV 421

Query: 445 NVQKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQAQFYNYKKPRQW 504
QK PLS+KTFG+AIPPQYAI+VL+E+T G AII+TGVGQHQMWAQAQFY Y +PRQW
Sbjct: 422 MNQKASNPLSYKTFGDAIPPQYAIQVLNEVTGGNAIITGVGQHQMWAQAQFYKYNRPRQW 481

Query: 505 LSSGGLGAMGFGLPAAIGASVANPD AIVVDIDGDGSFIMNVQELATIRVENLPVKVLLN 564
L+S GLGAMGFGLPAAIGA+VA PDA+VVDIDGDGSF+MNVQELATIRVENLPVK+++LN
Sbjct: 482 LTSAGLGAMGFGLPAAIGA AAVRPDAVVDIDGDGSFMMNVQELATIRVENLPVKMMVLN 541

Query: 565 NQHLGMVQWEDRFYKANRAHTFLGDPAQEDEIFPNMMLFAAACGIPAARVTKKADLREA 624
NQHLGMV+QWEDRFYKANRAHT+LG+P E IFPNML FA AC IPAARVTKK D+R A
Sbjct: 542 NQHLGMVVQWEDRFYKANRAHTYLGNTNESGIFPNMLKFAEACDIPAARVTKKGDVRTA 601

Query: 625 IQTMLDTPGPYLLDVICPHQEHVLPMPINGGT FNDVITEGDGRIK 669
IQ MLDTPGPYLLDVI PHQEHVLPMP GG FND+IT+GDGR +
Sbjct: 602 IQKMLDTPGPYLLDVIVPHQEHVLPMPAGGGFNDIITDGDGRTQ 646

>gb|ABR68867.1| acetohydroxyacid synthase [Solanum ptychanthum]
Length = 554

Score = 980 bits (2533), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 465/554 (83%), Positives = 506/554 (91%)

Query: 107 LERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHEQGGVFAAEGYARSSGKPGICIA 166
LER+GV VFAYPGG SMEIHQALTRS+ IRNVLPRHEQGGVFAAEGYAR++G PG+CIA
Sbjct: 1 LEREGVTDVFAYPGGTSMEIHQALTRSNIIIRNVLPRHEQGGVFAAEGYARATGFPGVCIA 60

Query: 167 TSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVM 226
TSGPGATNLVSLADALLDS+P+VAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVM
Sbjct: 61 TSGPGATNLVSLADALLDSIPIVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVM 120

Query: 227 DVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMSRMPKPPED 286
DVEDIPRI+ EAFFLA SGRPGPVL+DVPKDIQQQL IPNW+Q M+LPGYMSR+PK P +
Sbjct: 121 DVEDIPRIVREAFFLAKSGRPGPVLIDVPKDIQQQLVIPNWDQPMRLPGYMSRLPKLPNE 180

Query: 287 SHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSYPCCDELSL 346
LEQIVRLISESKKPVLYVGGGC SS+EL RFVELTGIPVASTLMGLG++P DELSL
Sbjct: 181 MLLEQIVRLISESKKPVLYVGGGCSQSSEELRRFVELTGIPVASTLMGLGAFPTGDELSL 240

Query: 347 HMLGMHGT VYANYAVEHSDLLAFGVRFDDRV TGKLEAFASRAKIVHIDIDSAEIGKNKT 406
MLGMHGT VYANYAV+ SDLLAFGVRFDDRV TGKLEAFASRAKIVHIDIDSAEIGKNK
Sbjct: 241 QMLGMHGT VYANYAVDSSDLLAFGVRFDDRV TGKLEAFASRAKIVHIDIDSAEIGKNKL 300

Query: 407 PHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKFPLSFKTFGEAIPPQY 466
PH S+C D+KLALQG+N +LE + +LKLD F WR ELN QK K+PL+FKTFGEAIPPQY
Sbjct: 301 PHASICADIKLALQGLNSILEGKEGKLKLD FSAWRQELNEQKVYPLNFKTFGEAIPPQY 360

Query: 467 AIKVLDEL TDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGLGAMGFGLPAAIGASVA 526
AI+VLDEL T+G AIISTGVGQHQMWA AQFY YKKPRQWL+SGGLGAMGFGLPAA+GA+V
Sbjct: 361 AIQVLDEL TNGNAIISTGVGQHQMWA AQFYKYKKPRQWL TSGGLGAMGFGLPAA MGAAVG 420

Query: 527 NPDAIVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWEDRFYKANRAHT 586
P IVVDIDGDSF+MNVQELATI+VENLPVK++LNNQHLGMV+QWEDRFYKANRAHT
Sbjct: 421 RPGEIVDIDGDSFMMNVQELATIKVENLPVKIMLLNNQHLGMVVQWEDRFYKANRAHT 480

Query: 587 FLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPYLLDVICPHQE 646
+LGDP A E+EIFPNML FA ACG+PAARVT + +LR AIQ MLDTPGPYLLDVI PHQE
Sbjct: 481 YLGDPANEEEEIFPNMLKFAEACGVPAARVTHRDELRAAIQKMLDTPGPYLLDVIVPHQE 540

Query: 647 VLPMPNGGTFNDV 660
VLPMP+GG F DV
Sbjct: 541 VLPMPISGGAFKDV 554

>dbj|BAF57909.1| acetolactate synthase [Sagittaria trifolia]
Length = 684

Score = 968 bits (2502), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 454/584 (77%), Positives = 517/584 (88%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
I F PD+PRKGADILVEALER+GV+ VFAYPGGASMEIHQALTRS SI N L RHEQG
Sbjct: 101 LIRNFGPDEPRKGADILVEALEREKVDFVAYPGGASMEIHQALTRSPSIVNHLFRHEQG 160

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
+FAAEGYAR++G+PG+CIATSGPGATNLVSLADALLDS PLVAITGQVPRRMIGTDAF
Sbjct: 161 EIFAAEGYARATGRPGVCIATSGPGATNLVSLADALLDSTPLVAITGQVPRRMIGTDAF 220

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTRSITKHNYLV+ V+DIPRI+ EAF+LATSGRPGPVL+D+PKDIQQQLAIP
Sbjct: 221 QETPIVEVTRSITKHNYLVLSVDDIPRIVHEAFYLATSGRPGPVLIDIPKDIQQQLAIP 280

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W MKL GYMSR+PKPP+ S LEQIVRL+ ES+KPVLY GGG LN+SDEL RFVELTG+
Sbjct: 281 WRTTMKLHGYSRLPKPPQQSQLEQIVRLLLLESRKPVLYTGGGSLNASDELRRFVELTGV 340

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRV TGKLEAFA 386
PVASTLMGLGS+P +LSL MLGMHGT VYANYAVEHSDLLAFGVRFDDRV TGKLEAFA
Sbjct: 341 PVASTLMGLGSFPTSSDSLKMLGMHGT VYANYAVEHSDLLAFGVRFDDRV TGKLEAFA 400

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRAKIVHIDID AEIGKNK PHVS+CGD+KLAL+G+N++LE +LDF WR EL+
Sbjct: 401 SRAKIVHIDIDPAEIGKNKQPHVSICGDLKLALEGINELLEETKIHEQLDFSSWRGELDE 460

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDEL TDGKAIISTGVGQHQMWA AQFYNYKKPRQWLS 506
QK+KFPLS+K FG+AIPPQYAI VLDEL T+G+A+ISTGVGQHQMWA AQ+Y+YKKPR WLS
Sbjct: 461 QKRKFPLSYKKFGDAIPPQYAIHVDEL TNGEAVISTGVGQHQMWA AQWYSYKKPRNWLS 520

Query: 507 SGGLGAMGFGLPAAIGASVANPDAIVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
S GLGAMGFGLPAA GA+V P++IVVDIDGDSF+MN+QELA +R+ENLPVK+++LNNQ
Sbjct: 521 SAGLGAMGFGLPAAAGAAVGRPESIVDIDGDSFIMNIQELAVLRIENLPVKIMVLNNQ 580

Query: 567 HLGVMVQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFY ANRAHT+LGDP A+E +I+P+++ A IPAAR+TK ++R AI
Sbjct: 581 HLGMMVQWEDRFYHANRAHTYLGDPARESDIYPLVSIAGFNIPARITKIGEVRAAIT 640

Query: 627 TMLDTPGPYLLDVICPHQEHLVLPMPNGGTFNDVITEGDGRIKY 670
ML+TPGPYLLD+I PHQEHLVLPMP+GG F D+I EGDGR Y
Sbjct: 641 KMLETPGPYLLDIIVPHQEHLVLPMPISGGAFKDLIVEGDGRSSY 684

>dbj|BAE97677.1| acetolactate synthase [Schoenoplectus juncooides]
dbj|BAE97678.1| acetolactate synthase [Schoenoplectus juncooides]
Length = 645

Score = 950 bits (2455), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 443/580 (76%), Positives = 510/580 (87%)

Query: 88 ISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGG 147
I +P PRKGADILVEALER+GV VFAYPGGASMEIHQALTRS I N L RHEQG
Sbjct: 60 IRNLSPTDPRKGADILVEALEREGVTDVFAYPGGASMEIHQALTRSPIIENHLLRHEQGE 119

Query: 148 VFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQ 207
FAA GYARS+GK G+C+ATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQ
Sbjct: 120 SFAASGYARSTGKAGVCVATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQ 179

Query: 208 ETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNW 267
ETPIVEVTRSITKHNYLV+D++DIPRII+EAFFLATSGRPGPVLVD+PKDIQQQLA+P W
Sbjct: 180 ETPIVEVTRSITKHNYLVLDIDDIPRIIKEAFLATSGRPGPVLVDIPKDIQQQLAVPAW 239

Query: 268 EQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGCLNSSDELGRFVELTGIP 327
+ M+LPGY SR+PK P L+QI RL+SESK+PVLYVGGGC NS EL RFVELTGIP
Sbjct: 240 DLPMLRPGYTSRLPKPEAHLLDQITRLVSESKRPVLYVGGGCANSGAELKRFVELTGIP 299

Query: 328 VASTLMGLGSYPCCDELHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTKLEAFAS 387
V +TLMGLG+YP +DELSL MLGMHGTVYANYAV+ +DLLLAFGVRFDDRVTKLEAFAS
Sbjct: 300 VTTTLMGLGNYPNSDELRLMLGMHGTVYANYAVDKADLLAFGVRFDDRVTKLEAFAS 359

Query: 388 RAKIVHIDIDSAEIGKNKTPHVSVCGDVKLALQGMNKVLENRAEELKLDGFWRNELNVQ 447
R+KIVHIDIDSAEIGKNK PH+S+C DVK +LQGMNK+LE+ KLDF WR EL+ Q
Sbjct: 360 RSKIVHIDIDSAEIGKNKQPHLSICADV KPSLQGMNKILESTGLHRKLD FSSWRAELEQ 419

Query: 448 KQKFPFLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSS 507
K+ +PL++KTGFE IPPQYAI+VLDELTD G+AIISTGVGQHQMWAQ+YNYK+PRQWLSS
Sbjct: 420 KKAYPLNYKTFGEEIPPQYAIQVLDELTKGEAIISTGVGQHQMWAQYNYKRPRQWLSS 479

Query: 508 GGLGAMGFGLPAAIGASVANPDIAVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQH 567
GLGAMGFGLPAA GA+V NP V+DIDGDSF+MN+QELA I++ENLPVK ++LNNQH
Sbjct: 480 SGLGAMGFGLPAAAGAAVGNPGVTVIDIDGDSFLMNIQELAMIKIENLPVKTMVLNNQH 539

Query: 568 LGMVMQWEDRFYKANRAHTFLGDPQAQDEIFPNMLLFAAACGIPAARVTKADLREAIQT 627
LGMV+QWEDRFYKANRAHT+LG+PA E++I+P+ + + G+PAARVT+++++REA++
Sbjct: 540 LGMVVQWEDRFYKANRAHTYLGNDPADEEQIYPDFVKISEGFGVPAARVTRRSEVREAVRK 599

Query: 628 MLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGR 667
ML+TPGPYLLDVI PHQEHVLPMP+GG F D+I +GDGR
Sbjct: 600 MLETPGPYLLDVIVPHQEHVLPMPISGGAFQDMILDGDGR 639

>dbj|BAE97675.1| acetolactate synthase [Schoenoplectus juncooides]
dbj|BAE97676.1| acetolactate synthase [Schoenoplectus juncooides]
Length = 645

Score = 948 bits (2450), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 443/580 (76%), Positives = 510/580 (87%)

Query: 88 ISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGG 147
I +P PRKGADILVEALER+GV VFAYPGGASMEIHQALTRS I N L RHEQG
Sbjct: 63 IRNLSPTDPRKGADILVEALEREGVTDVFAYPGGASMEIHQALTRSPIIENHLLRHEQGE 122

Query: 148 VFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQ 207
FAA GYARS+GK G+C+ATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQ
Sbjct: 123 SFAASGYARSTGKAGVCVATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQ 182

Query: 208 ETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNW 267
ETPIVEVTRSITKHNYLV+D++DIPRII+EAFFLATSGRPGPVLVD+PKDIQQQLA+P W
Sbjct: 183 ETPIVEVTRSITKHNYLVLDIDDIPRIIKEAFLATSGRPGPVLVDIPKDIQQQLAVPAW 242

Query: 268 EQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIP 327
+ M+LPGY SR+PK P L+QI RL+SESK+PVLYVGGGC NS EL RFVELTGIP
Sbjct: 243 DLPMLRLPGYTSRLPKPEPAHLLDQITRLVSESKRPVLYVGGGCANSGAELKRFVELTGIP 302

Query: 328 VASTLMGLGSYPDCDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKLEAFAS 387
V +TLMGLG+YP +DELSL MLGMHGTVYANYAV+ +DLLLLAFGVRFDDRVTGKLEAFAS
Sbjct: 303 VTTTLMGLGNYPNSDELRLMLGMHGTVYANYAVDKADLLAFGVRFDDRVTGKLEAFAS 362

Query: 388 RAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWVRNENLVQ 447
R+KIVHIDIDSAEIGKNK PH+S+C DVK +LQGMN++LE+ KLDF WR EL+ Q
Sbjct: 363 RSKIVHIDIDSAEIGKNKQPHLSICADV KPSLQGMNEILESTGLHRKLD FSSWRAELDEQ 422

Query: 448 KQKFPLSFKTFGEAIPPQYAIKVDELDTGKAIISTGVGQHQMWAQFYNYKKPRQWLSS 507
++ +PLSG+KTFGE IPPQYAI+VLDEL T G+AIISTGVGQHQMWAQ+YNYK+PRQWLSS
Sbjct: 423 RKAYPLSYKTFGEEIPPQYAIQVDELTKGEAIISTGVGQHQMWAQYNYKRPRQWLSS 482

Query: 508 GGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQH 567
GLGAMGFGLPAA GA+V NP VVDIDGDSF+MN+QELA I++ENLPVK ++LNNQH
Sbjct: 483 SGLGAMGFGLPAAAGAVGNPGVTVDIDGDSFLMNIQELAMIKIENLPVKAMVLLNNQH 542

Query: 568 LGMVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQT 627
LGMV+QWEDRFYKANRAHT+LG+PA E++I+P+ + + G+PAARVT++++RE++
Sbjct: 543 LGMVVQWEDRFYKANRAHTYLGPNAD EEQIYPDFVKISEGFGVPAARVTRRSEVREAVRK 602

Query: 628 MLDTPGPYLLDVICPHQEHVLP MIPNGGTFNDVITEGDGR 667
ML+TPGPYLLDVI PHQEHVLP MIP+GG F D+I +GDGR
Sbjct: 603 MLETPGPYLLDVIVPHQEHVLP MIPSGGAFQDMILDGDGR 642

>gb|AAM03119.1|AF488771_1 acetolactate synthase [Bromus tectorum]
Length = 583

Score = 941 bits (2432), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 439/580 (75%), Positives = 505/580 (87%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
+ P +PRKGADILVEALER G+ VFAYPGGASMEIHQALTRS I N L RHEQ FA
Sbjct: 4 WGPSEPRKGADILVEALERCGIVDV FAYPGGASMEIHQALTRSPVITNHLFRHEQVEAFA 63

Query: 151 AEGYARSSGKPGICIA TSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYAR+SG+ G+C+ATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAFQETP
Sbjct: 64 ASGYARASGRVGVCVATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAFQETP 123

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEAFLATSGRPGPVLVDV PKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+
Sbjct: 124 IVEVTRSITKHNYLVLDVEDIPRVIQEAFFLASSGRPGPVLVDIPKDIQQQMAVPAWDTP 183

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ E+K+P+LYVGGGC S +EL RFVELTGIPV +
Sbjct: 184 MSLPGYIARLPKPPSTESLEQVRLVGEAKRPILYVGGGCAASGEELRRFVELTGIPVTT 243

Query: 331 TLMGLGSYPDCDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGTVYANYAV+ +DLLLLAFGVRFDDRVTGK+EAFA SR+K
Sbjct: 244 TLMGLGNFSD DPLSLRMLGMHGTVYANYAVDKADLLAFGVRFDDRVTGKIEAFASRSK 303

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWVRNENLVQKQK 450
IVHIDID AEIGKNK PHVS+C DVKLALQG+N +L + LDFG W+ EL QK+
Sbjct: 304 IVHIDIDPAEIGKNKQPHVSI CADVKLALQGLNDLLNGSKAQKSLDFGPWQEELQKQRT 363

Query: 451 FPLSFKTFGEAIPPQYAIKVDELDTGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
FPL +KTFGEAIPPQYAI+VLDEL T G+AI I+TGVGQHQMWAQ+Y+YK+PRQWLSS GL
Sbjct: 364 FPLGYKTFGEAIPPQYAIQVDELTKGEAI IATGVGQHQMWAQYYSYKRPRQWLSSAGL 423

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA GASVANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGM
Sbjct: 424 GAMGFGLPAAAGASVANPGVTVDIDGDSFLMNIQELALIRIENLPVKVMILNNQHLGM 483

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFYKANRAHT+LG+P E EI+P+ + A +PA RVTKK+++R AIQ MLD
Sbjct: 484 VVQWEDRFYKANRAHTYLGPNENESEIYPDFVTIAKGFNVPVRVTKKSEVR AAIQKMLD 543

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
TPGPYLLD+I PHQEHVLPMP+GG F D+I EGDGRI+Y
Sbjct: 544 TPGPYLLDIIIVPHQEHVLPMPSSGGAFFKDIIMEGDGRIEY 583

>gb|AA14281.1| acetolactate synthase [Oryza sativa]
gb|ABF66050.1| acetolactate synthase [Oryza sativa (indica cultivar-group)]
gb|ACD74787.1| acetolactate synthase [Oryza sativa Indica Group]
gb|ACD74788.1| acetolactate synthase [Oryza sativa Indica Group]
Length = 644

Score = 939 bits (2426), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 440/580 (75%), Positives = 504/580 (86%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPRHEQGGVFA 150
+ P +PRKGADILVEALER GV VFAYPPGGASMEIHQALTRS I N L RHEQG FA
Sbjct: 65 WGPAPRKGADILVEALERCGVSDVFAYPPGGASMEIHQALTRSPVITNHLFRHEQGEAFA 124

Query: 151 AEGYARSSGKPGICIASGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYAR+SG+ G+C+ATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQETP
Sbjct: 125 ASGYARASGRVGVCVATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQETP 184

Query: 211 IVEVTRSTITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQA 270
IVEVTRSTITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+ +
Sbjct: 185 IVEVTRSTITKHNYLVLDVEDIPRVIQEAFFLASSGRPGPVLVDIPKDIQQQMAVPVWDT 244

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ ES++P+LYVGGGC S DEL RFVELTGIPV +
Sbjct: 245 MNLPGYIARLPKPPATELLEQVLRVLGESSRPILYVGGGCSASGDELRFRFVELTGIPVTT 304

Query: 331 TLMGLSGSPCDDLSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGTVYANYAV+ +DLLAFGVRFDRTVGK+EAFAASRAK
Sbjct: 305 TLMGLGNFSDPLSLRMLGMHGTVYANYAVDKADLLAFGVRFDRTVGKIEAFASRAK 364

Query: 391 IVHIDIDSAEIGKNKTPHVSVCVDKLLALQGMNKVLENRAEELKLDGFWVRNENLVQKQK 450
IVHIDID AEIGKNK PHVS+C DVKLLALQG+N +L+ + DF W NEL+ QK++
Sbjct: 365 IVHIDIDPAEIGKNKQPHVSICADVKLLALQGLNALLDQSTTKTSSDFSAAHNELDQKRE 424

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
FPL +KTFGE IPPQYAI+VLDELTD G+AI+TGVGQHQMWAQ+Y YK+PRQWLSS GL
Sbjct: 425 FPLGYKTFGEAIPPQYAIQVLDELTDGKAIATGVGQHQMWAQYTYKPRQWLSSAGL 484

Query: 511 GAMGFGLPAAAGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA GASVANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGM
Sbjct: 485 GAMGFGLPAAAGASVANPVGTVVDIDGDSFLMNIQELALIRIENLPVKVMVLNNQHLGM 544

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFPMNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFYKANRAHT+LG+P E EI+P+ + A IPA RVTKK+++R AI+ MLD
Sbjct: 545 VVQWEDRFYKANRAHTYLGNPCESEIYPDFVTIAKGFNIPAVRVTKKSEVRRAIKKMLD 604

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
TPGPYLLD+I PHQEHVLPMP+GG F D+I +GDGR Y
Sbjct: 605 TPGPYLLDIIIVPHQEHVLPMPSSGGAFFKDMILDGDGRTVY 644

>gb|AAL93207.1|AF487459_1 acetolactate synthase [Bromus tectorum]
Length = 583

Score = 939 bits (2426), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 438/580 (75%), Positives = 504/580 (86%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPRHEQGGVFA 150
+ P +PRKGADILVEALER G+ VFAYPPGGASMEIHQALTRS I N L RHEQ FA
Sbjct: 4 WGPSEPRKGADILVEALERCGIVDVVFAYPPGGASMEIHQALTRSPVITNHLFRHEQVEAFA 63

Query: 151 AEGYARSSGKPGICIASGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYAR+SG+ G+C+ATSGPGATNLVS LADALLDS+P+VAITGQV RRMIGTDAFQETP
Sbjct: 64 ASGYARASGRVGVCVATSGPGATNLVSALADALLDSIPMVAITGQVSRRMIGTDAFQETP 123

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEAFLATSGRPGPVLVDVPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+
Sbjct: 124 IVEVTRSITKHNYLVLDVEDIPRVIQEAFLASSGRPGPVLVDIPKDIQQQMAVPWADTP 183

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M LPGA++R+PKPP LEQ++RL+ E+K+P+LYVGGG S +EL RFVELTGIPV +
Sbjct: 184 MSLPGAIRARLPKPPSTESLEQVRLVGEAKRPILYVGGGCAASGEELRRFVELTGIPVTT 243

Query: 331 TLMGLGSYPCDELHMLGMHGTIVYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGTIVYANYAV+ +DLLLLAFGVRFDRTVGK+EAFAASR+K
Sbjct: 244 TLMGLGNFSDPLSLRMLGMHGTIVYANYAVDKADLLLLAFGVRFDRTVGKIEAFASRSK 303

Query: 391 IVHIDIDSAEIGKNKTPHVSVCADVCLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQK 450
IVHIDID AEIGKNK PHVS+C DVKLALQG+N +L + LDFG W+ EL QK+
Sbjct: 304 IVHIDIDPAEIGKNKQPHVSICADVCLALQGLNDLLNGSKAQKSLDFGPWQEELEQQKRT 363

Query: 451 FPLSFKTFGEAIPPQYAIKVDELDTGKAIISTGVGQHQMWAQQFYNYKKPRQWLSSGGL 510
FPL +KTFGEAIPPQYAI+VLDELDT G+AII+TGVGQHQMWAQQ+Y+YK+PRQWLSS GL
Sbjct: 364 FPLGYKTFGEAIPPQYAIQVDELDTGKAIISTGVGQHQMWAQQYYSYKPRQWLSSAGL 423

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA GASVANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGM
Sbjct: 424 GAMGFGLPAAAGASVANPGVTVDIDGDSFLMNIQELALIRIENLPVKVMILNNQHLGM 483

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFYKANRAHT+LG+P E EI+P+ + A +PA RVTKK+++R AIQ MLD
Sbjct: 484 VVQWEDRFYKANRAHTYLGPNENESEIYPDFVTIAKGFNPVAVRVTKKSEVRAAIQKMLD 543

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
TPGPYLLD+I PHQEHVLPMP+GG F D+I EGDGRI+Y
Sbjct: 544 TPGPYLLDIIIVPHQEHVLPMPSGGAFKDIIMEGDGRIEY 583

>gb|AA14282.1| acetolactate synthase [Oryza sativa (japonica cultivar-group)]
Length = 644

Score = 937 bits (2422), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 439/580 (75%), Positives = 504/580 (86%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPREHQQGVFA 150
+ P +PRKGADILVEALER GV VFAYPGGASMEIHQALTRS I N L RHEQG FA
Sbjct: 65 WGAEPKRGADILVEALERCGVSDVFAYPGGASMEIHQALTRSPVITNHLFRHEQGEAFA 124

Query: 151 AEGYARSSGKPGICATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYAR+SG+ G+C+ATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQETP
Sbjct: 125 ASGYARASGRVGVCVATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQETP 184

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEAFLATSGRPGPVLVDVPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+ +
Sbjct: 185 IVEVTRSITKHNYLVLDVEDIPRVIQEAFLASSGRPGPVLVDIPKDIQQQMAVPVWDTS 244

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M LPGA++R+PKPP LEQ++RL+ ES++P+LYVGGG S DEL RFVELTGIPV +
Sbjct: 245 MNLPGAIRARLPKPPATELLEQVRLVGESRRPILYVGGGCSASGDELRRFVELTGIPVTT 304

Query: 331 TLMGLGSYPCDELHMLGMHGTIVYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGTIVYANYAV+ +DLLLLAFGVRFDRTVGK+EAFAASRAK
Sbjct: 305 TLMGLGNFSDPLSLRMLGMHGTIVYANYAVDKADLLLLAFGVRFDRTVGKIEAFASRAK 364

Query: 391 IVHIDIDSAEIGKNKTPHVSVCADVCLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQK 450
IVHIDID AEIGKNK PHVS+C DVKLALQG+N +L+ + DF W NEL+ QK++
Sbjct: 365 IVHIDIDPAEIGKNKQPHVSICADVCLALQGLNALLDQSTTKTSSDFSAAWNELDQQKRE 424

Query: 451 FPLSFKTFGEAIPPQYAIKVDELDTGKAIISTGVGQHQMWAQQFYNYKKPRQWLSSGGL 510
FPL +KTFGE IPPQYAI+VLDELDT G+AII+TGVGQHQMWAQQ+Y YK+PRQWLSS GL
Sbjct: 425 FPLGYKTFGEEIPPQYAIQVDELDTGKAIISTGVGQHQMWAQQYYSYKPRQWLSSAGL 484

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA GASVANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGM
Sbjct: 485 GAMGFGLPAAAGASVANPGVTVDIDGDSFLMNIQELALIRIENLPVKVMVLLNNQHLGM 544

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFYKANRAHT+LG+P E EI+P+ + A IPA RVTKK+++R AI+ ML+
Sbjct: 545 VVQWEDRFYKANRAHTYLGNEPECESEIYPDFVTIAKGFNIPAVRVTKKSEVRAAIKKMLE 604

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
TPGPYLLD+I PHQEHVLPMP+GG F D+I +GDGR Y
Sbjct: 605 TPGPYLLDIIIVPHQEHVLPMPSSGGAFAKMDILDGDGRTVY 644

>gb|ABM92357.2| acetolactate synthase [Cyperus difformis]
Length = 569

Score = 937 bits (2422), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 438/567 (77%), Positives = 504/567 (88%)

Query: 101 DILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSSGK 160
D+LVE LERQGV VFAYPPGGASMEIHQALTRS I N L RH QG FAA GYARS+GK
Sbjct: 1 DVLVEVLERQGVTDVFAYPPGGASMEIHQALTRSPVIDNHLRHQGESFAASGYARSTGK 60

Query: 161 PGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITK 220
G+C+ATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGT+AFQETPIVEVTRSITK
Sbjct: 61 AGVCVATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTEAFQETPIVEVTRSITK 120

Query: 221 HNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMSRM 280
HNYLV+DV+DIPRII+EAFFLATSGRPGPVLVD+PKDIQQQLA+P W+ M+LPGY SR+
Sbjct: 121 HNYLVLDVDDIPRIIEEAFFLATSGRPGPVLVDIPKDIQQQLAVPVWDTMRLPGYTSRL 180

Query: 281 PKPPEDSHLEQIVRLISESKKPVLYVGGCLNSSDELGRFVELTGIPVASTLMGLGSYPC 340
PK PED+ L+QI+RL+SESK+PVLYVGGC NS EL RFVELTGIPV +TLMGLG++PC
Sbjct: 181 PKQPEDNQLDQIIRLVSESKRPVLYVGGCANSGAELKRFVELTGIPVTTTLMGLGNFPC 240

Query: 341 DDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVHIDIDSAE 400
D+ L L +LGMHGTVYANYAV+ +DLLAFGVRFDRTGKLEAFASR+KIVHIDID AE
Sbjct: 241 DEPLCLRLGMHGTVYANYAVDKADLLAFGVRFDRTGKLEAFASRSKIVHIDIDPAE 300

Query: 401 IGKNKTPHVSVCADVCLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQKFLSFKTFGE 460
IGKNK PHVS DVK ALQGMN++LE+ KLDF WR EL+ QK+ +PLS+KTFGE
Sbjct: 301 IGKNKQPHVSIKADVKPALQGMNQILESSGVHKKLDFSSWRAELDEQKKTYPKSYKTFGE 360

Query: 461 AIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGFLPAA 520
IPPQYAI+VLDELTDG+AIISTGVGQHQMWAQ+YNYK+PRQWLSS GLGAMGFLPAA
Sbjct: 361 EIPPQYAIQVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGFLPAA 420

Query: 521 IGASVANPDIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWEDRFYK 580
GA+V NP VVDI+GDGSF+MN+QELA I+VENLPVK ++LNNQHLGMV+QWEDRFYK
Sbjct: 421 AGAAVGNPGVTVDINDGDSFLMNIQELAMIKVENLPVKTMVLLNNQHLGMVQWEDRFYK 480

Query: 581 ANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPYLLDVI 640
ANRAHT+LG+PA E++I+P+ + A G+PAARV+++++REA++ MLDTPGPYLLDVI
Sbjct: 481 ANRAHTYLGNPANEEQIYPDFVKIAEGFGVPAARVTRRSEVREAVRIMLDTPGPYLLDVI 540

Query: 641 CPHQEHVLPMPNGGTFNDVITEGDGR 667
PHQEHVLPMP+GG F D+IT+GDGR
Sbjct: 541 VPHQEHVLPMPSSGGAFAKMDITDGDGR 567

>gb|EAY86003.1| hypothetical protein OsI_007236 [Oryza sativa (indica
cultivar-group)]
Length = 644

Score = 937 bits (2421), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 439/580 (75%), Positives = 503/580 (86%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVF 150
+ P +PRKGADILVEALER GV VFAYPPGGASMEIHQALTRS I L RHEQG FA
Sbjct: 65 WGPAEPRKGADILVEALERCVDVFAVPPGGASMEIHQALTRSPVITXQLFRHEQGEAFA 124

Query: 151 AEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYAR+SG+ G+C+ATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQETP
Sbjct: 125 ASGYARASGRVGVCVATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQETP 184

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+ +
Sbjct: 185 IVEVTRSITKHNYLVLDVEDIPRVIQEAFFLASSGRPGPVLVDIPKDIQQQMAVPVWDTS 244

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ ES++P+LYVGGGC S DEL RFVELTGIPV +
Sbjct: 245 MNLPGYIARLPKPPATELLEQVLRVLVGESRRPILYVGGGCSASGDELRRFVELTGIPVTT 304

Query: 331 TLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGT VYANYAV+ +DLLAFGVRFDRTGK+EAFAASRAK
Sbjct: 305 TLMGLGNFSDPLSLRMLGMHGT VYANYAVDKADLLAFGVRFDRTGKIEAFASRAK 364

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQK 450
IVHIDID AEIGKNK PHVS+C DVKLALQG+N +L+ + DF W NEL+ QK++
Sbjct: 365 IVHIDIDPAEIGKNKQPHVSICADVKLALQGLNALLDQSTTKTSSDFS AWHNELDQKRE 424

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
FPL +KTFGE IPPQYAI+VLDEL T G+AII+TGVGQHQMWAQ+Y YK+PRQWLSS GL
Sbjct: 425 FPLGYKTFGEEIPPQYAIQVLDELTKGEAIIATGVGQHQMWAQYTYTKRPRQWLSSAGL 484

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA GASVANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGM
Sbjct: 485 GAMGFGLPAAAGASVANPGVTVDIDGDSFLMNIQELALIRIENLPVKVMVLNNQHLGM 544

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAAVTKKADLREAIQTMLD 630
V+QWEDRFYKANRAHT+LG+P E EI+P+ + A IPA RVTKK+++R AI+ MLD
Sbjct: 545 VVQWEDRFYKANRAHTYLGNECESEIYPDFVTIAKGFNIPAVRVTKKSEVRAAIKKMLD 604

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGT FNDVITEGDGRIKY 670
TPGPYLLD+I PHQEHLVPMIP+GG F D+I +GDGR Y
Sbjct: 605 TPGPYLLDIIVPHQEHLVPMIPSGGAFKDMILDGDGRVTY 644

>ref|NP_001046931.1| Os02g0510200 [Oryza sativa (japonica cultivar-group)]
sp|Q6K2E8|ILV1_ORYSJ Acetolactate synthase 1, chloroplast precursor (Acetohydroxy-acid
synthase 1)
dbj|BAB20812.1| acetolactate synthase [Oryza sativa (japonica cultivar-group)]
dbj|BAD23668.1| acetolactate synthase [Oryza sativa Japonica Group]
dbj|BAF08845.1| Os02g0510200 [Oryza sativa (japonica cultivar-group)]
Length = 644

Score = 935 bits (2416), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 438/580 (75%), Positives = 503/580 (86%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
+ P +PRKGADILVEALER GV VFAYPPGGASMEIHQALTRS I N L RHEQG FA
Sbjct: 65 WGPAEPRKGADILVEALERCGVSDVFAYPPGGASMEIHQALTRSPVITNHLFRHEQGEAFA 124

Query: 151 AEGYARSSGKPGICATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYAR+SG+ G+C+ATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQETP
Sbjct: 125 ASGYARASGRVGVCVATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQETP 184

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+ +
Sbjct: 185 IVEVTRSITKHNYLVLDVEDIPRVIQEAFFLASSGRPGPVLVDIPKDIQQQMAVPVWDTS 244

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ ES++P+LYVGGGC S DEL FVELTGIPV +
Sbjct: 245 MNLPGYIARLPKPPATELLEQVLRVLVGESRRPILYVGGGCSASGDELRFVELTGIPVTT 304

Query: 331 TLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGT VYANYAV+ +DLLAFGVRFDRTGK+EAFAASRAK
Sbjct: 305 TLMGLGNFSDPLSLRMLGMHGT VYANYAVDKADLLAFGVRFDRTGKIEAFASRAK 364

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQK 450
IVHIDID AEIGKNK PHVS+C DVKLALQG+N +L+ + DF W NEL+ QK++
Sbjct: 365 IVHIDIDPAEIGKNKQPHVSICADVKLALQGLNALLQSTTKTSSDFS AWHNELDQKRE 424

Query: 451 FPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
FPL +KTFGE IPPQYAI+VLDELTD G+AII+TGVGQHQMWAQ+Y YK+PRQWLSS GL
Sbjct: 425 FPLGYKTFGEEIPPQYAIQVDELTDKGEAIIATGVGQHQMWAQYYTYKRPRQWLSSAGL 484

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA GASVANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGM
Sbjct: 485 GAMGFGLPAAAGASVANPGVTVDIDGDSFLMNIQELALIRIENLPVKVMVLNNQHLGM 544

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFPMNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFYKANRAHT+LG+P E EI+P+ + A IPA RVTKK+++R AI+ ML+
Sbjct: 545 VVQWEDRFYKANRAHTYLGNPCESEIYPDFVTIAKGFNIPAVRVTKKSEVRAAIKKMLE 604

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
TPGPYLLD+I PHQEHVLPMP+GG F D+I +GDGR Y
Sbjct: 605 TPGPYLLDIIIVPHQEHVLPMPISGGAFKDMILDGDGRTVY 644

>gb|ACD74789.1| acetolactate synthase [Oryza sativa Indica Group]
gb|ACD74790.1| acetolactate synthase [Oryza sativa Indica Group]
Length = 644

Score = 935 bits (2416), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 438/580 (75%), Positives = 503/580 (86%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPRHEQGGVFA 150
+ P +PRKGADILVEALER GV VFAYPPGGASMEIHQALTRS I N L RHEQG FA
Sbjct: 65 WGAPEPRKGADILVEALERCGVSDVFAYPPGGASMEIHQALTRSPVITNHLFRHEQGEAFA 124

Query: 151 AEGYARSSGKPGICATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYAR+SG+ G+C+ATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQETP
Sbjct: 125 ASGYARASGRVGCVCATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQETP 184

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+ +
Sbjct: 185 IVEVTRSITKHNYLVLDVEDIPRVIQEAFFLASSGRPGPVLVDIPKDIQQQMAVPVWDT 244

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ ES++P+LYVGGC S DEL RFVELTGIPV +
Sbjct: 245 MNLPGYIARLPKPPATELLEQVLRVLGESRRPILYVGGCSASGDELRRFVELTGIPVTT 304

Query: 331 TLMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGTVYANYAV+ +DLLAFGVRFDDRVTK+EAFAASRAK
Sbjct: 305 TLMGLGNFSDPLSLRMLGMHGTVYANYAVDKADLLAFGVRFDDRVTKIEAFASRAK 364

Query: 391 IVHIDIDSAEIGKNKTPHVSVCADVKLALQGMNVLENRAEELKLDGFWVRNELNVQKQK 450
IVHIDID AEIGKNK PHVS+C DVKLALQG+N +L+ + DF W NEL+ QK++
Sbjct: 365 IVHIDIDPAEIGKNKQPHVSICADVKLALQGLNALLDQSTTKTSSDFSAWNELDQKQRE 424

Query: 451 FPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
FPL +KTFGE IPPQYAI+VLDELTD G+AII+TGVGQHQMWAQ+Y YK+PRQWLSS GL
Sbjct: 425 FPLGYKTFGEEIPPQYAIQVDELTDKGEAIIATGVGQHQMWAQYYTYKRPRQWLSSAGL 484

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA GASVANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGM
Sbjct: 485 GAMGFGLPAAAGASVANPGVTVDIDGDSFLMNIQELALIRIENLPVKVMVLNNQHLGM 544

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFPMNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFYKANRAHT+LG+P E EI+P+ + A IPA RVTKK+++R AI+ ML+
Sbjct: 545 VVQWEDRFYKANRAHTYLGNPCESEIYPDFVTIAKGFNIPAVRVTKKSEVRAAIKKMLE 604

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
TPGPYLLD+I PHQEHVLPMP+ G F D+I +GDGR Y
Sbjct: 605 TPGPYLLDIIIVPHQEHVLPMPSEGAFKDMILDGDGRTMY 644

>gb|AAx14283.1| acetolactate synthase [Oryza sativa]
Length = 644

Score = 935 bits (2416), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 438/580 (75%), Positives = 503/580 (86%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
+ P +PRKGADILVEALER GV VFAYPPGGASMEIHQALTRS I N L RHEQG FA
Sbjct: 65 WGAEPKRGADILVEALERCGVSDVFAYPPGGASMEIHQALTRSPVITNHLFRHEQGEAFA 124

Query: 151 AEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYAR+SG+ G+C+ATSGPGATNLVS LADALLD VP+VAITGQVPRRMIGTDAFQETP
Sbjct: 125 ASGYARASGRVGVCVATSGPGATNLVSALADALLDPVPMVAITGQVPRRMIGTDAFQETP 184

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+ +
Sbjct: 185 IVEVTRSITKHNYLVLDVEDIPRVIQEAFFLASSGRPGPVLVDIPKDIQQQMAVPVWDT 244

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ ES++P+LYVGGG S DEL RFVELTGIPV +
Sbjct: 245 MNLPGYIARLPKPPATELLEQVLRVLGESRRPILYVGGGCSASGDELRRFVELTGIPVTT 304

Query: 331 TLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGT VYANYAV+ +DLLAFGVRFDDRVTK+EAFAASRAK
Sbjct: 305 TLMGLGNFSDPLSLRMLGMHGT VYANYAVDKADLLAFGVRFDDRVTKIEAFASRAK 364

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWVRNENLVQKQK 450
IVHIDID AEIGKNK PHVS+C DV+LALQG+N +L+ + DF W NEL+ QK++
Sbjct: 365 IVHIDIDPAEIGKNKQPHVSI CADVELALQGLNALLDQSTTKTSSDFS AWHNELDQKQKRE 424

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
FPL +KTFGE IPPQYAI+VLDEL T G+AII+TGVGQHQMWAQ+Y YK+PRQWLSS GL
Sbjct: 425 FPLGYKTFGEEIPPQYAIQVLDELTKGEAIIATGVGQHQMWAQYYYTYKRPRQWLSSAGL 484

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA GASVANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGM
Sbjct: 485 GAMGFGLPAAAGASVANPGVTVDIDGDSFIMNIQELALIRIENLPVKVMVLNNQHLGM 544

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFPMNMLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFYKANRAHT+LG+P E EI+P+ + A IPA RVTKK+++R AI+ ML+
Sbjct: 545 VVQWEDRFYKANRAHTYLGNEPECESEIYPDFVTIAKGFNIPAVRVTKKSEVRAAIKKMLE 604

Query: 631 TPGPYLLDVICPHQEHVLP MIPNGGT FNDVITEGDGRIKY 670
TPGPYLLD+I PHQEHVLP MIPNGG F D+I +GDGR Y
Sbjct: 605 TPGPYLLDIIVPHQEHVLP MIPNGGAFKDMIPDGDGRVY 644

>gb|ABF66052.1| acetolactate synthase [Oryza sativa (indica cultivar-group)]
Length = 644

Score = 932 bits (2409), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 437/580 (75%), Positives = 503/580 (86%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
+ P +PRKGADILVEALER GV VFAYPPGGASMEIHQALTRS I N L RHEQG FA
Sbjct: 65 WGAEPKRGADILVEALERCGVSDVFAYPPGGASMEIHQALTRSPVITNHLFRHEQGEAFA 124

Query: 151 AEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYAR+SG+ G+C+ATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQETP
Sbjct: 125 ASGYARASGRVGVCVATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQETP 184

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQA 270
IVEVTRSITKH+YLV+DVEDIPR+I+EAFFLA+SG PGPVLVD+PKDIQQQ+A+P W+ +
Sbjct: 185 IVEVTRSITKHSYLVLDVEDIPRVIQEAFFLASSGGPGPVLVDIPKDIQQQMAVPVWDT 244

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ ES++P+LYVGGG S DEL RFVELTGIPV +
Sbjct: 245 MDLPGYIARLPKPPATELLEQVLRVLGESRRPILYVGGGCSASGDELRRFVELTGIPVTT 304

Query: 331 TLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGT VYANYAV+ +DLLAFGVRFDDRVTK+EAFAASRAK
Sbjct: 305 TLMGLGNFSDPLSLRMLGMHGT VYANYAVDKADLLAFGVRFDDRVTKIEAFASRAK 364

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWVRNENLVQKQK 450
IVHIDID AEIGKNK PHVS+C DVKLALQG+N +L+ + DF W NEL+ QK++
Sbjct: 365 IVHIDIDPAEIGKNKQPHVSI CADVKLALQGLNALLDQSTTKTSSDFS AWHNELDQKQKRE 424

Query: 451 FPLSFKTFGEAIPPQYAIKVDELDTGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
FPL +KTFGE IPPQYAI+VLDELDT G+AI+TGVGQHQMWAQ+Y YK+PRQWLSS GL
Sbjct: 425 FPLGYKTFGEEIPPQYAIQVDELDTGKAIATGVGQHQMWAQYYTYKRPRQWLSSAGL 484

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA GASVANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGM
Sbjct: 485 GAMGFGLPAAAGASVANPGVTVVDIDGDSFLMNIQELALIRIENLPVKVMVLNNQHLGM 544

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFYKANRAHT+LG+P E EI+P+ + A IPA RVT+K+++R AI+ MLD
Sbjct: 545 VVQWEDRFYKANRAHTYLGNEPECESEIYPDFVTIAKGFNIPAVRVTRKSEVRAAIKKMLD 604

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
TPGPYLLD+I PHQEHVLPMP+GG F D+I +GDGR Y
Sbjct: 605 TPGPYLLDIIVPHQEHVLPMPISGGAFKDMILDGDGRTVY 644

>gb|ABF66048.1| acetolactate synthase [Oryza sativa (indica cultivar-group)]
Length = 644

Score = 931 bits (2407), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 436/576 (75%), Positives = 500/576 (86%)

Query: 95 QPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGY 154
+PRKGADILVEALER GV VFAYPGGASMEIHQALTRS I N L RHEQG F A GY
Sbjct: 69 EPRKGADILVEALERCVSDFAYPGGASMEIHQALTRSPVITNHLFRHEQGEAFVASGY 128

Query: 155 ARSSGKPGICIASGPGATNLVSGDALDLSVPLVAITGQVPRRMIGTDAFQETPIVEV 214
AR+SG+ G+C+ATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQETPIVEV
Sbjct: 129 ARASGRVGVCVATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQETPIVEV 188

Query: 215 TRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLP 274
TRSITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+ +M LP
Sbjct: 189 TRSITKHNYLVLDVEDIPRVIQEAFFLASSGRPGPVLVDIPKDIQQQMAVPAWDTSMNLP 248

Query: 275 GYMSRMPKPPEDSHLEQIVRLISESKPVLYVGGGCLNSSDELGRFVELTGIPVASTLMG 334
GY++R+PKPP LEQ++RL+ ES++P+LYVGGGC S DEL RFVELTGIPV +TLMG
Sbjct: 249 GYIARLPKPPATELLEQVLRVLVGESRRPILYVGGGCSASGDELRRFVELTGIPVTTLMG 308

Query: 335 LGSYPCDEDESLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVHI 394
LG++P DD LSL MLGMHGTVYANYAV+ +DLLAFGVRFDRTGK+EAFAASRAKIVHI
Sbjct: 309 LGNFPSDDPLSLRMLGMHGTVYANYAVDKADLLAFGVRFDRTGKIEAFASRAKIVHI 368

Query: 395 DIDS AEIGKKNTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWVRNELNVQKQKFPPLS 454
DID AEIGKKN PHVS+C DVKLALQG+N +L+ + DF W NEL+ QK++FPL
Sbjct: 369 DIDPAEIGKKNQPHVSI CADVKLALQGLNALLDQSTTKTSSDFS AWHNELDQKREFPLG 428

Query: 455 FKTFGEAIPPQYAIKVDELDTGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMG 514
+KTFGE IPPQYAI+VLDELDT G+AI+TGVGQHQMWAQ+Y YK+PRQWLSS GLGAMG
Sbjct: 429 YKTFGEEIPPQYAIQVDELDTGKAIATGVGQHQMWAQYYTYKRPRQWLSSAGLQAG 488

Query: 515 FGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQW 574
FGLPAA GASVANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGMV+QW
Sbjct: 489 FGLPAAAGASVANPGVTVVDIDGDSFLMNIQELALIRIENLPVKVMVLNNQHLGMVVQW 548

Query: 575 EDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGP 634
EDRFYKANRAHT+LG+P E EI+P+ + A IPA RVT++R AI+ ML+TPGP
Sbjct: 549 EDRFYKANRAHTYLGNEPECESEIYPDFVTIAKGFNIPAVRVTKKSEVRAAIKKMLETPGP 608

Query: 635 YLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
YLLD+I PHQEHVLPMP+GG D+I +GDGR Y
Sbjct: 609 YLLDIIVPHQEHVLPMPISGGALKDMILDGDGRTVY 644

>gb|ABF66051.1| acetolactate synthase [Oryza sativa (indica cultivar-group)]
Length = 644

Score = 931 bits (2407), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 437/576 (75%), Positives = 500/576 (86%)

Query: 95 QPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGY 154
+P KGADILVEALER GV VFAYPPGGASMEIHQALTRS I N L RHEQG FAA GY
Sbjct: 69 EPHKGADILVEALERCVSDFVAYPPGGASMEIHQALTRSPVITNHLFRHEQGEAFAASGY 128

Query: 155 ARSSGKPGICIAATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEV 214
AR+SG+ G+C+ATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQETPIVEV
Sbjct: 129 ARASGRVGVCVATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQETPIVEV 188

Query: 215 TRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDV PKDIQQQLAIPNWEQAMKLP 274
TRSITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQ Q+A+P W+ +M LP
Sbjct: 189 TRSITKHNYLVLDVEDIPRVIQEAFFLASSGRPGPVLVDIPKDIQLQMAVPVWDTSMNLP 248

Query: 275 GYMSRMPKPPEDSHLEQIVRLISESKKPVLVVG GGCNLSDELGRFVELTGIPVASTLMG 334
GY++R+PKPP LEQ++RL+ ES++P+LYVGGGC S DEL RFVELTGIPV +TLMG
Sbjct: 249 GYIARLPKPPATELLEQVRLVVGESRRPILYVGGGCASGDELRRFVELTGIPVTTTLMG 308

Query: 335 LGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIVHI 394
LG++P DD LSL MLGMHGT VYANYAV+ +DLLAFGVRFDDRVTGK+EAFASRAKIVHI
Sbjct: 309 LGNFPSDDPLSLRMLGMHGT VYANYAVDKADLLAFGVRFDDRVTGKIEAFASRAKIVHI 368

Query: 395 DIDS AEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKFPLS 454
DID AEIGKNK PHVS+C DVKLALQG+N +L+ + DF W NEL+ QK++FPL
Sbjct: 369 DIDPAEIGKNKQPHVSICADV KLALQGLNALLDQSTTKTSSDFS AWHNELDQQKREFPLG 428

Query: 455 FKTGFEAIPPQYAIKVLDELTDGKAIISTGVGQHQM WAAQFYNYKKPRQWLSSGGLGAMG 514
+KTGFE IPPQYAI+VLDELTD G+AII+TGVGQHQM WAAQ+Y YK+PRQWLSS GLGAMG
Sbjct: 429 YKTGFEAIPPQYAIQVLDELTDGKAIISTGVGQHQM WAAQYTYKRPQWLSSAGLGAMG 488

Query: 515 FGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQW 574
FGLPAA GASVANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGMV+QW
Sbjct: 489 FGLPAAAGASVANPGVTVDIDGDSFIMNIQELALIRIENLPVKVMVLNNQHLGMVVQW 548

Query: 575 EDRFYKANRAHTFLGDP AQEDEFIPNM L LFAAACGIPAARVTKKADLREAIQTMLDTPGP 634
EDRFYKANRAHT+LG+P E EI+P+ + A IPA RVTKK+++R AI+ MLDTPGP
Sbjct: 549 EDRFYKANRAHTYLG NPECESEIYPDFVTIAGFNIPAVRVTKKSEVR AAIKKMLDTPGP 608

Query: 635 YLLDVICPHQEHVLP MIPNGGTFNDVITEGDGRIKY 670
YLLD+I PHQEHVLP MIP+GG F D+I +GDGR Y
Sbjct: 609 YLLDIIVPHQEHVLP MIPSGGAFKDMILDGDGRTVY 644

>dbj|BAE53597.1| acetolactate synthase [Monochoria vaginalis]
dbj|BAE53599.1| acetolactate synthase [Monochoria vaginalis]
dbj|BAE53600.1| acetolactate synthase [Monochoria vaginalis]
dbj|BAE53603.1| acetolactate synthase [Monochoria vaginalis]
Length = 604

Score = 931 bits (2405), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 434/577 (75%), Positives = 507/577 (87%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
FA D+PRKGADILVEALER+GV +FAYPPGGASMEIHQALTRS SI N L RHEQG FA
Sbjct: 25 FASDEPRKGADILVEALERE GVTDLFAYPPGGASMEIHQALTRSPSITNHLRHEQGEAFA 84

Query: 151 AEGYARSSGKPGICIAATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYARS+G+PG+CIATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAFQETP
Sbjct: 85 ASGYARSTGRPGVCIATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAFQETP 144

Query: 211 IVEVTRTSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDV PKDIQQQLAIPNWEQA 270
IVEVTRTSITKHNYLV+DV+DIPRII+EAFF+ATSGRPGPVLVD+PKDIQQQLA+P W+Q
Sbjct: 145 IVEVTRTSITKHNYLVLDVDDIPRIIEEAFFIATSGRPGPVLVDIPKDIQQQLAVPVWDQP 204

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVVG GGCNLSDELGRFVELTGIPVAS 330
++LPGY+SR+PKPP LE+I+RL+S S PVLYVGGGCL++S+EL RF +LTGIP+AS
Sbjct: 205 VRLPGYVSR LKPPALHLLERIIRLVSASSHPVLVVG GGCCLHASEELRRFADLTGIPIAS 264

Query: 331 TLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAK 390
TLMGLG YP D LSL MLGMHGT VYANY+++ +DLLAFGVRFDDRVTGKLEAFASRAK
Sbjct: 265 TLMGLGVYPLDAHLSL KMLGMHGT VYANYSIDKADLLAFGVRFDDRVTGKLEAFASRAK 324

Query: 391 IVHIDIDSAEIGKNKTPHVSVCQDVKLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQK 450
IVHIDID AEIGKNK PHVS+C D+KLALQ MNK++E KL+F WR EL+ K+
Sbjct: 325 IVHIDIDPAEIGKNKQPHVSIKADIKLALQEMNKIIIESGIIYNKLNFSAWREELDQHKKN 384

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
+PL++KTFG+ IPPQYAI+VLDELTDG AII+TGVGQHQMWAQ+YNYK+PRQWL+S GL
Sbjct: 385 YPLNYKTFGDLIPPQYAIKVLDELTDGDAIITGVGQHQMWAQYNYKPRQWLTSAGL 444

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA+GA+V NP VVDIDGDSF MN QELA IR+ENL VK+L+LNNQHLGM
Sbjct: 445 GAMGFGLPAAVGAAGNPGVTVDIDGDSFQMNQELAVIRIENLDVKMLILNNQHLGM 504

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFPMNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFY++NRAHT+LG+PA E ++FP+ + A + IPA+RV+KK+ +R+AI+ ML
Sbjct: 505 VVQWEDRFYQSNRAHTYLGPNANESKVFDPFVKLADSYDIPASRVSKKSQVRDAIRKMLQ 564

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGR 667
TPGPYLLDVI PH+EHVLPMP+GG F D+I +GDGR
Sbjct: 565 TPGPYLLDVIVPHEEHVLPMPISGGAFKDMILDGDGR 601

>dbj|BAE53591.1| acetolactate synthase [Monochoria vaginalis]
dbj|BAE53592.1| acetolactate synthase [Monochoria vaginalis]
Length = 642

Score = 929 bits (2402), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 433/577 (75%), Positives = 511/577 (88%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPREHQQGVFA 150
FAPD+PRKGADILVEALER+GV +FAYPGGASMEIHQALTRS SI N L RHEQG FA
Sbjct: 63 FAPDEPRKGADILVEALEREVTDLFAYPGGASMEIHQALTRSPSITNHLRHEQGEAFA 122

Query: 151 AEGYARSSGKPGICIAATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYARS+G+PG+CIATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAFQETP
Sbjct: 123 ASGYARSTGRPGVCIATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAFQETP 182

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLV+DV+DIPRII+EAFF+ATSGRPGPVLVD+PKDIQQQLA+P W
Sbjct: 183 IVEVTRSITKHNYLVLDVDDIPRIIEEAFFIATSGRPGPVLVDIPKDIQQQLAVPVWNPP 242

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
++LPGY+SR+PKPP L+QIVR++SES +PVLYVGGG L++S+EL RF +LTGIP+AS
Sbjct: 243 VRLPGYVSRPKPPALHLLQIVRIVSESSRPVLYVGGGSLHASEELRRFADLTGIPIAS 302

Query: 331 TLMGLGSYPCDDELSLHMLGMHGTIVYANYAVEHSDLLAFGVRFDRTVTGKLEAFASRAK 390
TLMG+G YP D LSL MLGMHGTIVYANYA++ +DLLAFGVRFDRTVTGKLEAFASRAK
Sbjct: 303 TLMGIGVYPLDGPLSLKMLGMHGTIVYANYAIDKADLLAFGVRFDRTVTGKLEAFASRAK 362

Query: 391 IVHIDIDSAEIGKNKTPHVSVCQDVKLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQK 450
IVHIDID AEIGKNK PHVS+CGD+KLALQ MN+++E KLDF WR EL+ QK+
Sbjct: 363 IVHIDIDPAEIGKNKQPHVSIKADIKLALQEMNEMIEESGIIHNKLDFAWREELDQKKN 422

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
+PL +KTFG+ IPPQ+AI++L+ELT+G+AII+TGVGQHQMWAQ+Y+YK+PRQWL+S GL
Sbjct: 423 YPLEYKTFGDLIPPQHAIELLEELTNGEAIITGVGQHQMWAQYYSYKPRQWLTSAGL 482

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA+GA+V NP +VVDIDGDSF MN QELA IR+ENL VK+L+LNNQHLGM
Sbjct: 483 GAMGFGLPAAVGAAGNPGVMVVDIDGDSFQMNQELAIIRIENLDVKMLILNNQHLGM 542

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFPMNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFYK+NRAHT+LG+PA E ++FP+ + A + IPAARV+KK+++R+AI+ M+
Sbjct: 543 VVQWEDRFYKSNRAHTYLGPNANESKVFDPFVKLAESYDIPAARVSKKSEVRDAIRKMIQ 602

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGR 667
TPGPYLLDVI PH+EHVLPMP+GG F D+I +GDGR
Sbjct: 603 TPGPYLLDVIVPHEEHVLPMPISGGAFKDMILDGDGR 639

```
>dbj|BAE53587.1| acetolactate synthase [Monochoria vaginalis]
dbj|BAE53589.1| acetolactate synthase [Monochoria vaginalis]
dbj|BAE53590.1| acetolactate synthase [Monochoria vaginalis]
dbj|BAE53594.1| acetolactate synthase [Monochoria vaginalis]
Length = 642
```

Score = 928 bits (2399), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 432/577 (74%), Positives = 511/577 (88%)

```
Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
F+PD+PRKGADILVEALER+GV +FAYPPGGASMEIHQALTRS SI N L RHEQG FA
Sbjct: 63 FSPDEPRKGADILVEALEREGVTDLFAYPPGGASMEIHQALTRSPSITNHLRHEQGEAFA 122

Query: 151 AEGYARSSGKPGICIAATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYARS+G+PG+CIATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAFQETP
Sbjct: 123 ASGYARSTGRPGVCIATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAFQETP 182

Query: 211 IVEVTRSTITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDV PKDIQQQLAIPNWEQA 270
IVEVTRSTITKHNYLV+DV+DIPRII+EAFF+ATSGRPGPVLVD+PKDIQQQLA+P W
Sbjct: 183 IVEVTRSTITKHNYLVLDVDDIPRIIKEAFFIATSGRPGPVLVDIPKDIQQQLAVPVWNPP 242

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
++LPGY+SR+PKPP L+QIVR++SES +PVLYVGGG L++S+EL RF +LTGIP+AS
Sbjct: 243 VRLPGYVSRLPKPPALHLLQQIVRIVSESSRPVLYVGGGSLHASEELRRFADLTGIPIAS 302

Query: 331 TLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRTVGKLEAFASRAK 390
TLMG+G YP D LSL MLGMHGT VYANYA++ +DLLAFGVRFDDRTVGKLEAFASRAK
Sbjct: 303 TLMGIGVYPLDGPLSLKMLGMHGT VYANYAIDKADLLAFGVRFDDRTVGKLEAFASRAK 362

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQK 450
IVHIDID AEIGKNK PHVS+CGD+KLALQ MN+++E KLDF WR EL+ QK+
Sbjct: 363 IVHIDIDPAEIGKNKQPHVSI CGDIKLALQEMNEMIEESGIHNKLD FSAWREELDQQKKN 422

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGL 510
+PL +KTFG+ IPPQ+AI++L+ELT+G+AI+TGVGQHQMWA AQ+Y+YK+PRQWL+S GL
Sbjct: 423 YPLEYKTFGDLIPPQHAIELLEELTNGEAIITGVGQHQMWA AQYYSYKRPRQWLSAGL 482

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLLNQHLGM 570
GAMGFGLPAA+GA+V NP +VVDIDGDSF MN QELA IR+ENL VK+L+LNNQHLGM
Sbjct: 483 GAMGFGLPAAVGAAGNPGVMVVDIDGDSFQMNAQELAIIRIENLDVKMLILNNQHLGM 542

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFPNMMLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFYK+NRAHT+LG+PA E ++FP+ + A + IPAARV+KK+++R+AI+ M+
Sbjct: 543 VVQWEDRFYKSNRAHTYLGPNANESKVFDPFVKLAESYDIPAARVSKKSEVRDAIRKMIQ 602

Query: 631 TPGPYLLDVICPHQEHVLPMPINGGT FNDVITEGDGR 667
TPGPYLLDVI PH+EHVLPMP+GG F D+I +GDGR
Sbjct: 603 TPGPYLLDVIVPHEEHVLPMPISGGAFKDMILDGDGR 639
```

```
>dbj|BAB20813.1| acetolactate synthase [Oryza sativa (japonica cultivar-group)]
Length = 644
```

Score = 928 bits (2398), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 437/580 (75%), Positives = 501/580 (86%)

```
Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
+ P +PRKGADILVEALER GV VFAYPPGGASMEIHQALTRS I N L RHEQG FA
Sbjct: 65 WGPAEPRKGADILVEALERCVS DVFAYPPGGASMEIHQALTRSPVITNHLRHEQGEAFA 124

Query: 151 AEGYARSSGKPGICIAATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYAR+SG+ G+C+ATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQETP
Sbjct: 125 ASGYARASGRVGVCVATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQETP 184

Query: 211 IVEVTRSTITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDV PKDIQQQLAIPNWEQA 270
IVEVTRSTITKHNYLV+DV+DIPRII+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+ +
Sbjct: 185 IVEVTRSTITKHNYLVLDVEDIPRVIQEAFFLASSGRPGPVLVDIPKDIQQQMAVPVWDT 244

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ ES++P+LYVGGG S DEL FVELTGIPV +
Sbjct: 245 MNLPGYIARLPKPPATELLEQVLRVLGESSRRPILYVGGGCSASGDELRFVELTGIPVTT 304
```

Query: 331 TLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGT VYANYAV+ +DLLAFGVRFDDRVTK+EAFAASRAK
Sbjct: 305 TLMGLGNFSDPLSLRMLGMHGT VYANYAVDKADLLAFGVRFDDRVTKIEAFASRAK 364

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNENLVQKQK 450
IVHIDID AEIGKNK PHVS+C DVKLALQG+N +L+ + DF W NEL+ QK++
Sbjct: 365 IVHIDIDPAEIGKNKQPHVSICADV KLALQGLNALLQQSTTKTSSDFS AWHNELDQQKRE 424

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGL 510
FPL +KTFGE IPPQYAI+VLDELTD G+AII+TGVGQHQMWA AQ+Y YK+PRQWLSS GL
Sbjct: 425 FPLGYKTFGEEIPPQYAIQVLDELTDGKAIATGVGQHQMWA AQYYTYKRPRQWLSSAGL 484

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA GASVANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGM
Sbjct: 485 GAMGFGLPAAAGASVANPGVTVDIDGDSFLMNIQELALIRIENLPVKVMVLNNQHLGM 544

Query: 571 VMQWEDRFYKANRAHTFLGDP AQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+Q EDRFYKANRAHT+LG+P E EI+P+ + A IPA RVTKK+++R AI+ ML+
Sbjct: 545 VVQLED RFYKANRAHTYLG NPECESEIYPDFVTIAKGFNIPAVRVTKKSEVR AAIKKMLE 604

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGT FNDVITEGDGRIKY 670
TPGPYLLD+I PHQEHLVPMIP GG F D+I +GDGR Y
Sbjct: 605 TPGPYLLDIIIVPHQEHLVPMIPIGGAFKDMILDGDGR TVY 644

>dbj|BAE53596.1| acetolactate synthase [Monochoria vaginalis]
Length = 604

Score = 927 bits (2397), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 433/577 (75%), Positives = 506/577 (87%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
FA D+PRKGADILVEAL R+GV +FAYPGGASMEIHQALTRS SI N L RHEQG FA
Sbjct: 25 FASDEPRKGADILVEALGREGVTDLFAYPGGASMEIHQALTRSPSITNHLRHEQGEAFA 84

Query: 151 AEGYARSSGKPGICIA TSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYARS+G+PG+CIATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAFQETP
Sbjct: 85 ASGYARSTGRPGVCIATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAFQETP 144

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLV+DV+DIPRII+EAFF+ATSGRPGPVLVD+PKDIQQQLA+P W+Q
Sbjct: 145 IVEVTRSITKHNYLVLDVDDIPRIIEEAFFIATSGRPGPVLVDIPKDIQQQLAVPVWDQP 204

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
++LPGY+SR+PKPP LE+I+RL+S S PVLYVGGGCL++S+EL RF +LTGIP+AS
Sbjct: 205 VRLPGYVSR LKPPALHLLERIIRLVSASSHPVLYVGGGCLHASEELRRFADLTGIPIAS 264

Query: 331 TLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAK 390
TLMGLG YP D LSL MLGMHGT VYANY+++ +DLLAFGVRFDDRVTKLEAFASRAK
Sbjct: 265 TLMGLGVYPLDAHLSLKMGMHGT VYANYSIDKADLLAFGVRFDDRVTKLEAFASRAK 324

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNENLVQKQK 450
IVHIDID AEIGKNK PHVS+C D+KLALQ MNK++E KL+F WR EL+ K+
Sbjct: 325 IVHIDIDPAEIGKNKQPHVSICADIKLALQEMNKIIIEESGIYNKLNFS AWRRELDQHKKN 384

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGL 510
+PL++KTFG+ IPPQYAI+VLDELTD G AII+TGVGQHQMWA AQ+YNYK+PRQWL+S GL
Sbjct: 385 YPLNYKTFGDLIPPQYAI EVLDELTDNGDAIITTG VGQHQMWA AQYYNYKRPRQWLTSAGL 444

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA+GA+V NP VVDIDGDSF MN QELA IR+ENL VK+L+LNNQHLGM
Sbjct: 445 GAMGFGLPAAVGA AVGNPGVTVDIDGDSFQMNAQELAVIRIENLDVKMLILNNQHLGM 504

Query: 571 VMQWEDRFYKANRAHTFLGDP AQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFY++NRAHT+LG+PA E ++FP+ + A + IPA+RV+KK+ +R+AI+ ML
Sbjct: 505 VVQWEDRFYQSNRAHTYLG N PANESKVFDPFVKLADSYDIPASRVSKKSQVRDAIRKMLQ 564

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGT FNDVITEGDGR 667
TPGPYLLDVI PH+EHVLP MIP+GG F D+I +GDGR
Sbjct: 565 TPGPYLLDVIVPHEEHVLP MIPSGGAFKDMILDGDGR 601

>dbj|BAE53598.1| acetolactate synthase [Monochoria vaginalis]
dbj|BAE53601.1| acetolactate synthase [Monochoria vaginalis]
Length = 604

Score = 927 bits (2397), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 433/577 (75%), Positives = 506/577 (87%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
FA D+PRKGADILVEALER+GV +FAYPPGGASMEIHQALTRS SI N L RHEQG FA
Sbjct: 25 FASDEPRKGADILVEALEREVTDLFAYPPGGASMEIHQALTRSPSITNHLRHEQGEAFA 84

Query: 151 AEGYARSSGKPGICIAATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYARS+G+PG+CIATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAFQETP
Sbjct: 85 ASGYARSTGRPGVCIATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAFQETP 144

Query: 211 IVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNLYL+DV+DIPRII+EAFF+ATSGRPGPVLVD+PKDIQQQLA+P W+Q
Sbjct: 145 IVEVTRSITKHNLYLVDVDDIPRIIEEAFFIATSGRPGPVLVDIPKDIQQQLAVPVWDQP 204

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
++LPGY+SR+PKPP LE+I+RL+S S PVLYVGGGCL++S+ L RF +LTGIP+AS
Sbjct: 205 VRLPGYVSRLPKPPALHLLERIIRLVSASSHPVLYVGGGCLHASEGLRRFADLTGIPIAS 264

Query: 331 TLMGLGSYPCDELDSLHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFASRAK 390
TLMGLG YP D LSL MLGMHGT VYANY+++ +DLLAFGVRFDRTGKLEAFASRAK
Sbjct: 265 TLMGLGVYPLDAHLSLKMGMHGT VYANYSIDKADLLAFGVRFDRTGKLEAFASRAK 324

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQK 450
IVHIDID AEIGKNK PHVS+C D+KLALQ MNK++E KL+F WR EL+ K+
Sbjct: 325 IVHIDIDPAEIGKNKQPHVSI CADIKLALQEMNKII EESGIYNKLNFSAWREELDQHKKN 384

Query: 451 FPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGL 510
+PL++KTFG+ IPPQYAI+VDELTD+G AII+TGVGQHQMWA AQ+YNYK+PRQWL+S GL
Sbjct: 385 YPLNYKTFGDLIPPQYAEVLDELTDNGDAIITGVGQHQMWA AQYNYKPRQWLTSAGL 444

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA+GA+V NP VVDIDGDSF MN QELA IR+ENL VK+L+LNNQHLGM
Sbjct: 445 GAMGFGLPAAVGAAGVNP GVTVDIDGDSFQMNAQELAVIRIENLDVKMLILNNQHLGM 504

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTM LD 630
V+QWEDRFY++NRAHT+LG+PA E ++FP+ + A + IPA+RV+KK+ +R+AI+ ML
Sbjct: 505 VVQWEDRFYQSNRAHTYLGNPANESKVFPDFVKLADSYDIPASRVSKKSQVRDAIRKMLQ 564

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGTFNDVITEGDGR 667
TPGPYLLDVI PH+EHVLP MIP+GG F D+I +GDGR
Sbjct: 565 TPGPYLLDVIVPHEEHLVPMIPSGGA FKMILDGDGR 601

>dbj|BAE53602.1| acetolactate synthase [Monochoria vaginalis]
Length = 604

Score = 927 bits (2396), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 433/577 (75%), Positives = 506/577 (87%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
FA D+PRKGADILVEALER+GV +FAYPPGGASMEIHQALTRS SI N L RHEQG FA
Sbjct: 25 FASDEPRKGADILVEALEREVTDLFAYPPGGASMEIHQALTRSPSITNHLRHEQGEAFA 84

Query: 151 AEGYARSSGKPGICIAATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYARS+G+PG+CIATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAFQETP
Sbjct: 85 ASGYARSTGRPGVCIATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAFQETP 144

Query: 211 IVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNLYL+DV+DIPRII+EAFF+ATSGRPGPVLVD+PKDIQQQLA+P W+Q
Sbjct: 145 IVEVTRSITKHNLYLVDVDDIPRIIEEAFFIATSGRPGPVLVDIPKDIQQQLAVPVWDQP 204

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
++LPGY+SR+PKPP LE+I+RL+S S PVLYVGGGCL++S+ L RF +LTGIP+AS
Sbjct: 205 VRLPGYVSRLPKPPALHLLERIIRLVSASSHPVLYVGGGCLHASEGLRRFADLTGIPIAS 264

Query: 331 TLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRVTKLEAFASRAK 390
TLMGLG YP D LSL MLGMHGT VYANY+++ +DLLLLAFGVRFDDRVTKLEAFASRAK
Sbjct: 265 TLMGLGVYPLDAHL SLKMLGMHGT VYANYSIDKADLLLAFGVRFDDRVTKLEAFASRAK 324

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNENLVQKQK 450
IVHIDID AEIGKNK PHVS+C D+KLALQ MNK++E KL+F WR EL+ K+
Sbjct: 325 IVHIDIDPAEIGKNKQPHVSI CADIKLALQEMNKII EESGIYNKLNFSAWREELDQHKKN 384

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGL 510
+PL++KTFG+ IPPQYAI+VLDELTDG AII+TGVGQHQMWA AQ+YNYK+PRQWL+S GL
Sbjct: 385 YPLNYKTFGDLIPPQYAEVLDELTDGDAIITGVGQHQMWA AQYNYKRPRQWLT SAGL 444

Query: 511 GAMGFGLPAAIGASVANPD AIVVDIDGDGSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA+GA+V NP VVDIDGDGSF MN QELA IR+ENL VK+L+LNNQHLGM
Sbjct: 445 GAMGFGLPAAVGA AVGNPGVT VVDIDGDGSFQMNAQELAVIRIENLDVKMLILNNQHLGM 504

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAA RVTKKADLREAIQTMLD 630
V+QWEDRFY++NRAHT+LG+PA E ++FP+ + A + IPA+RV+KK+ +R+AI+ ML
Sbjct: 505 VVQWEDRFYQSNRAHTYLGPNANESKVFPDFVKLADSYDIPASRVSKKSQVRDAIRKMLQ 564

Query: 631 TPGPYLLDVICPHQEHVLP MIPNGGTFNDVITEGDGR 667
TPGPYLLDVI PH+EHVLP MIP+GG F D+I +GDGR
Sbjct: 565 TPGPYLLDVIVPHEEHVLP MIPSGGAFKDMILDGDGR 601

>emb|CAD24801.2| acetolactate synthase [Alopecurus myosuroides]
Length = 640

Score = 927 bits (2395), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 438/581 (75%), Positives = 507/581 (87%), Gaps = 1/581 (0%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
+ P +PRKGADILVEALER GV VFAYPGGASMEIHQALTRS +I N L RHEQG FA
Sbjct: 60 WGFSEPRKGADILVEALERC VSDVFAYPGGASMEIHQALTRSPAITNHLFRHEQGEAFA 119

Query: 151 AEGYARSSGKPGIC IATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYAR+SG+ G+C+ATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAFQETP
Sbjct: 120 ASGYARASGRVGV CVATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAFQETP 179

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEAFLATSGRPGPVLVDVPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+
Sbjct: 180 IVEVTRSITKHNYLVLDVEDIPRVIQEAFLASSGRPGPVLVDIPKDIQQQMAVPVWDAP 239

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ ES++P+LYVGGC S +EL RFVELTGIPV +
Sbjct: 240 MSLPGYIARLPKPPATELLEQVLRVLGESRRPILYVGGCSASGEELRRFVELTGIPVTT 299

Query: 331 TLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRVTKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGT VYANYAV+ +DLLLLAFGVRFDDRVTK+EAFA SR+K
Sbjct: 300 TLMGLGNFSSDDPLSLRMLGMHGT VYANYAVDRADLLLAFGVRFDDRVTKIEAFASRSK 359

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKL-DFGVWRNENLVQKQ 449
IVHIDID AEIGKNK PHVS+C DVK+ALQG+N +L N ++ K DF W EL+ QK+
Sbjct: 360 IVHIDIDPAEIGKNKQPHVSI CADVKIALQGLNTLLNLSKTRKCSDFSSWHEELDQQR 419

Query: 450 KFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSG 509
+FPL +KTFGEAIPPQYAIKVLDELTDG AII+TGVGQHQMWA AQ+Y YK+PRQWLSS G
Sbjct: 420 EFPLGYKTFGEAIPPQYAIKVLDELTDGDAIATGVGQHQMWA AQYYTYKRPRQWLSSG 479

Query: 510 LGAMGFGLPAAIGASVANPD AIVVDIDGDGSFIMNVQELATIRVENLPVKVLLNNQHLG 569
LGAMGFGLPAA GA+VANP VVDIDGDGSF+MN+QELA IR+ENLPVKV++LNNQHLG
Sbjct: 480 LGAMGFGLPAAAGAAVANPGVT VVDIDGDGSFLMNIQELALIRIENLPVKVMILNNQHLG 539

Query: 570 MVMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAA RVTKKADLREAIQTML 629
MV+QWEDRFYKANRAHT+LG+P E EI+P+ + A +PA RVTKK+++R AI+ ML
Sbjct: 540 MVMQWEDRFYKANRAHTYLGPNENESIYPDFVTIAGFNVPVAVRVTKKSEVRAAIKML 599

Query: 630 DTPGPYLLDVICPHQEHVLP MIPNGGTFNDVITEGDGRIKY 670
+TPGPYLLD+I PHQEHVLP MIP+GG F D+I EGDGRI Y
Sbjct: 600 ETPGPYLLDII VPHQEHVLP MIPSGGAFKDIIMEGDGRISY 640

>dbj|BAE53593.1| acetolactate synthase [Monochoria vaginalis]
Length = 642

Score = 926 bits (2394), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 432/577 (74%), Positives = 510/577 (88%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
FAPD+PRKGADILVEALER+GV +FAYPPGGASMEIHQALTRS I N L RHEQG FA
Sbjct: 63 FAPDEPRKGADILVEALEREVTDLFAYPPGGASMEIHQALTRSPSITNHLRHEQGEAFA 122

Query: 151 AEGYARSSGKPGICIAATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYARS+G+PG+CIATSGPGATNLVS LADALLDS+P+VAITGQV RRMIGTDAFQETP
Sbjct: 123 ASGYARSTGRPGVCIATSGPGATNLVSALADALLDSIPMVAITGQVSRRMIGTDAFQETP 182

Query: 211 IVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNLYL+DV+DIPRII+EAFF+ATSGRPGPVLVD+PKDIQQQLA+P W
Sbjct: 183 IVEVTRSITKHNLYLVDVDDIPRIIEEAFFIATSGRPGPVLVDIPKDIQQQLAVPVWNP 242

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
++LPGY+SR+PKPP L+QIVR++SES +PVLYVGGG L++S+EL RF +LTGIP+AS
Sbjct: 243 VRLPGYVSRPLPKPPALHLLQIVRIVSESSRPVLYVGGGSLHASEELRRFADLTGIPIAS 302

Query: 331 TLMGLGSYPCDDELSTHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFASRAK 390
TLMG+G YP D LSL MLGMHGT VYANYA++ +DLLAFGVRFDRTGKLEAFASRAK
Sbjct: 303 TLMGIGVYPLDGPLSLKMLGMHGT VYANYAIDKADLLAFGVRFDRTGKLEAFASRAK 362

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQK 450
IVHIDID AEIGKNK PHVS+CGD+KLALQ MN+++E KLDF WR EL+ QK+
Sbjct: 363 IVHIDIDPAEIGKNKQPHVSICGDIKALQEMNEMIEESGIHNKLD FSAWREELDQKKN 422

Query: 451 FPLSFKTFGEAIPPQYAIKVLELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
+PL +KTFG+ IPPQ+AI++L+ELT+G+AI+TG VGQHQMWAQ+Y+YK+PRQWL+S GL
Sbjct: 423 YPLEYKTFGDLIPPQHAIELEELTNGEAIITGVGQHQMWAQYYSYKPRQWLTSAGL 482

Query: 511 GAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA+GA+V NP +VVDIDGDSF MN QELA IR+ENL VK+L+LNNQHLGM
Sbjct: 483 GAMGFGLPAAVGAAGVGNPGVMVVDIDGDSFQMNAQELAIIRIENLDVKMLILNNQHLGM 542

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFYK+NRAHT+LG+PA E ++FP+ + A + IPAARV+KK+++R+AI+ M+
Sbjct: 543 VVQWEDRFYKSNRAHTYLGNPANESKVFPDFVLAESYDIPAARVSKKSEVRDAIRKMIQ 602

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGR 667
TPGPYLLDVI PH+EHVLPMP+GG F D+I +GDGR
Sbjct: 603 TPGPYLLDVIVPHEEHVLPMPSGGAFKDMILDGDGR 639

>gb|AAO53551.1| acetohydroxyacid synthase [Triticum aestivum]
Length = 598

Score = 926 bits (2393), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 437/580 (75%), Positives = 503/580 (86%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
+ P +PRKGADILVEALER G+ VFAYPPGGASMEIHQALTRS I N L RHEQG FA
Sbjct: 19 WGPSEPRKGADILVEALERCIVDVFAYPGGASMEIHQALTRSPVITNHLRHEQGEAFA 78

Query: 151 AEGYARSSGKPGICIAATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYAR+SG+ G+C+ATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAFQETP
Sbjct: 79 ASGYARASGRVGVCVATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAFQETP 138

Query: 211 IVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNLYL+DV+DIPRII+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+
Sbjct: 139 IVEVTRSITKHNLYLVDVEDIPRVIQEAFFLASSGRPGPVLVDIPKDIQQQMAVPVWDTP 198

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ ES++P+LYVGGG S +EL RFVELTGIPV +
Sbjct: 199 MSLPGYIARLPKPPSTESLEQVLRVLGESRRPILYVGGGCAASGEELRRFVELTGIPVTT 258

Query: 331 TLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTVGKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGT VYANYAV+ +DLLAFGVRFD DRTVGK+EAFASR+K
Sbjct: 259 TLMGLGNFSD DPLSLRMLGMHGT VYANYAVDKADLLAFGVRFD DRTVGKIEAFASRSK 318

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNENLVQKQK 450
IVHIDID AEIGKNK PHVS+C DVKLALQG+N +L + LDFG W EL+ QK++
Sbjct: 319 IVHIDIDPAEIGKNKQPHVSICADVKLALQGLNALLNGSKAQQGLDFGPW HKELDQQKRE 378

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGL 510
FPL FKTGFEAIPPQYAI+VLDEL T G+AII+TGVGQHQMWA AQ+Y YK+PRQWLSS GL
Sbjct: 379 FPLGFKTFGEAIPPQYAIQVLDELTKGEAIIATGVGQHQMWA AQYYTYKRPRQWLSSGGL 438

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA GA+VANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGM
Sbjct: 439 GAMGFGLPAAAGAAVANP GVTVDIDGDSFLMNIQELALIRIENLPVKVMILNNQHLGM 498

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFYKANRAHT+LG+P E EI+P+ + A +PA RVTKK+++ AI+ ML+
Sbjct: 499 VVQWEDRFYKANRAHTYLGPNENESEIYPDFVTIAKGFNPVAVRVTKKSEVTAAIKKMLE 558

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGT FNDVITEGDGRIKY 670
TPGPYLLD+I PHQEHLVPMIPNGG F D+I EGDGR Y
Sbjct: 559 TPGPYLLDIIIVPHQEHLVPMIPNGGAFKDMIMEGDGR TSY 598

>dbj|BAE53588.1| acetolactate synthase [Monochoria vaginalis]
Length = 642

Score = 926 bits (2392), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 432/577 (74%), Positives = 510/577 (88%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
FAPD+PRKGADILVEALER+GV +FAYPGGASMEIHQALTRS SI N L RHEQG FA
Sbjct: 63 FAPDEPRKGADILVEALEREGVTDLFAYPGGASMEIHQALTRSPSITNHL LRHEQGEAFA 122

Query: 151 AEGYARSSGKPGICIA TSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYARS+G+PG+CIATSGPGATNLVS LADALLDS+P+VAITGQV RRMIGTDAFQETP
Sbjct: 123 ASGYARSTGRPGVCIATSGPGATNLVSALADALLDSIPMVAITGQVLR RMIGTDAFQETP 182

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLV+DV+DIPRII+EAFF+ATSGRPGPVLVD+PKDIQQQLA+P W
Sbjct: 183 IVEVTRSITKHNYLVLDVDDIPRIIEEAFFIATSGRPGPVLVDIPKDIQQQLAVPVWNPP 242

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
++LPGY+SR+PKPP L+QIVR++SES +PVLYVGGG L++S+EL RF +LTGIP+AS
Sbjct: 243 VRLPGYVSR LKPPALHLLQQIVRIVSESSRPVLYVGGGSLHASEELRRFADLTGIPIAS 302

Query: 331 TLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTVGKLEAFASRAK 390
TLMG+G YP D LSL MLGMHGT VYANYA++ +DLLAFGVRFD DRTVGKLEAFASRAK
Sbjct: 303 TLMGIGVYPLDGPLSLKMLGMHGT VYANYAIDKADLLAFGVRFD DRTVGKLEAFASRAK 362

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNENLVQKQK 450
IVHIDID AEIGKNK PHVS+CGD+KLALQ MN+++E KLDF WR EL+ QK+
Sbjct: 363 IVHIDIDPAEIGKNKQPHVSICGDIKALQEMNEMIEESGIHNKLD FSAWREELDQQKKN 422

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGL 510
+PL +KTFG+ IPPQ+AI++L+ELT+G+AII+TGVGQHQMWA AQ+Y+YK+PRQWL+S GL
Sbjct: 423 YPLEYKTFGDLIPPQHAIELLEELTNGEAIITTGVGQHQMWA AQYYSYKRPRQWLTSAGL 482

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA+GA+V NP +VVDIDGDSF MN QELA IR+ENL VK+L+LNNQHLGM
Sbjct: 483 GAMGFGLPAAVGA AVGNPGVMVVDIDGDSFQMNAQELAIIRIENLDVKMLILNNQHLGM 542

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFYK+NRAHT+LG+PA E ++FP+ + A + IPAARV+KK+++R+AI+ M+
Sbjct: 543 VVQWEDRFYKSNRAHTYLGPNANESKVFDFVKLAESYDIPAARVSKKSEVRDAIRKMIQ 602

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGT FNDVITEGDGR 667
TPGPYLLDVI PH+EHVLPMP+GG F D+I +GDGR
Sbjct: 603 TPGPYLLDVIVPHEEHVLPMPISGGAFKDMILDGDGR 639

>sp|Q41768|ILV1_MAIZE Acetolactate synthase 1, chloroplast precursor (Acetohydroxy-acid synthase 1)
emb|CAA45116.1| acetohydroxyacid synthase [Zea mays]
Length = 638

Score = 925 bits (2391), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 436/580 (75%), Positives = 497/580 (85%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
+ P PRKGADILVE+LER GV VFAYPPGGASMEIHQALTRS I N L RHEQG FA
Sbjct: 59 WGPTDPRKGADILVESLERCGVRDVFAYPGGASMEIHQALTRSPVIANHLFRHEQGEAFA 118

Query: 151 AEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYARSSG+ G+CIATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQETP
Sbjct: 119 ASGYARSSGRVGVCIATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQETP 178

Query: 211 IVEVTRSTITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDV PKDIQQQLAIPNWEQA 270
IVEVTRSTITKHNYLV+DV+DIPR+++EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W++
Sbjct: 179 IVEVTRSTITKHNYLVLDVDDIPRVVQEAFFLASSGRPGPVLVDIPKDIQQQMAVPVWDKP 238

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ ES++PVLYVGGGC S +EL RFVELTGIPV +
Sbjct: 239 MSLPGYIARLPKPPATELLEQVLRVLGESRRPVLYVGGGCAASGEELRRFVELTGIPVTT 298

Query: 331 TLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLALF GVRFDDRVTGKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGT VYANYAV+ +DLLA GVRFDDRVTGK+EAFA SRAK
Sbjct: 299 TLMGLGNFSDPLSLRMLGMHGT VYANYAVDKADLLALGVRFDDRVTGKIEAFASRAK 358

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQK 450
IVH+DID AEIGKNK PHVS+C DVKLALQGMN +LE + DFG W +EL+ QK++
Sbjct: 359 IVHVIDPAEIGKNKQPHVSI CADVKLALQGMNALLEGSTSKSFDG SWNDEL DQQKRE 418

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQM WAAQFYNYKKPRQWLSSGGL 510
FPL +KT E I PQYAI+VLDEL T G+AI TGVGQHQM WAAQ+Y YK+PRQWLSS GL
Sbjct: 419 FPLGYKTSNEEQPQYAIQVDELTKGEAIIIGTGVGQHQM WAAQYYTYKRPRQWLSSAGL 478

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLLNQHLGM 570
GAMGFGLPAA GASVANP VVDIDGDSF+MNVQELA IR+ENLPVKV +LNNQHLGM
Sbjct: 479 GAMGFGLPAAAGASVANPGVTVDIDGDSFLMNVQELAMIRIENLPVKVFLNNQHLGM 538

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFPNMMLFAAACGIPAA RVTKKADLREAIQTMLD 630
V+QWEDRFYKANRAHT+LG+P E EI+P+ + A IPA RVTKK ++R AI+ ML+
Sbjct: 539 VVQWEDRFYKANRAHTYLGPNENESEIYPDFVTIAKGFNIPAVRVTKKNEVRAAIKKMLE 598

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGTFNDVITEGDGRIKY 670
TPGPYLLD+I PHQEHLVPMIP+GG F D+I +GDGR Y
Sbjct: 599 TPGPYLLDIIIVPHQEHLVPMIPSGGAFKDMILDGDGRTVY 638

>gb|AA053549.1| acetohydroxyacid synthase [Triticum aestivum]
Length = 598

Score = 924 bits (2389), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 436/580 (75%), Positives = 503/580 (86%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
+ P +PRKGADILVEALER G+ VFAYPPGGASMEIHQALTRS I N L RHEQG FA
Sbjct: 19 WGPSEPRKGADILVEALERCGIVDVFAYPGGASMEIHQALTRSPVITNHLFRHEQGEAFA 78

Query: 151 AEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYAR+SG+ G+C+ATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAFQETP
Sbjct: 79 ASGYARASGRVGVCVATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAFQETP 138

Query: 211 IVEVTRSTITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDV PKDIQQQLAIPNWEQA 270
IVEVTRSTITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+
Sbjct: 139 IVEVTRSTITKHNYLVLDVEDIPRVIQEAFFLASSGRPGPVLVDIPKDIQQQMAVPVWDTP 198

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ ES++P+LYVGGGC S +EL RFVELTGIPV +
Sbjct: 199 MSLPGYIARLPKPPSTESLEQVLRVLGESRRPILYVGGGCAASGEELRRFVELTGIPVTT 258

```

Query: 331 TLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAK 390
          TLMGLG++P DD LSL MLGMHGT VYANYAV+ +DLLAFGVRFDDRVTK+EAFASR+K
Sbjct: 259 TLMGLGNFSDDDLRLMLGMHGT VYANYAVDKADLLAFGVRFDDRVTKIEAFASRSK 318

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNENLVQKQK 450
          IVHIDID AEIGKNK PHVS+C DVKLALQG+N +L + LDFG W EL+ QK++
Sbjct: 319 IVHIDIDPAEIGKNKQPHVSI CADVKLALQGLNALLNGSKAQQGLDFGPWHKELDQKRE 378

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGL 510
          FPL FKTTFGEAIPPQYAI+VLDEL T G+AI+TGVGQHQMWA AQ+Y YK+PRQWLSS GL
Sbjct: 379 FPLGFKTFGEAIPPQYAIQVDELTKGEAIIATGVGQHQMWA AQYYTYKRPRQWLSSSGL 438

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
          GAMGFGLPAA GA+VANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGM
Sbjct: 439 GAMGFGLPAAAGAAVANPGVTVDIDGDSFLMNIQELALIRIENLPVKVMILNNQHLGM 498

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
          V+QWEDRFYKANRAHT+LG+P E EI+P+ + A +PA RVTKK+++ AI+ ML+
Sbjct: 499 VVQWEDRFYKANRAHTYLGPNENESEIYPDFVTIAKGFNPAVRVTKKSEVTAAIKKMLE 558

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGT FNDVITEGDGRIKY 670
          TPGPYLLD+I PHQEHLVPMIP+GG F D+I EGDGR Y
Sbjct: 559 TPGPYLLDIIIVPHQEHLVPMIPSGGAFKDMIMEGDGRTSY 598

>gb|AA053550.1| acetohydroxyacid synthase [Triticum aestivum]
          Length = 598

Score = 924 bits (2389), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 437/580 (75%), Positives = 503/580 (86%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
          + P +PRKGADILVEALER G+ VFAYPGGASMEIHQALTRS I N L RHEQG FA
Sbjct: 19 WGFSEPRKGADILVEALERCGIVDVFA YPGGASMEIHQALTRSPVITNHLFRHEQGEAFA 78

Query: 151 AEGYARSSGKPGICIA TSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
          A GYAR+SG+ G+C+ATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAFQETP
Sbjct: 79 ASGYARASGRVGC VATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAFQETP 138

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEAFLATSGRPGPVLVDVPKDIQQQLAIPNWEQA 270
          IVEVTRSITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+
Sbjct: 139 IVEVTRSITKHNYLVLDVEDIPRVIQEAFFLASSGRPGPVLVDIPKDIQQQMAVPVWDTP 198

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
          M LPGY++R+PKPP LEQ++RL+ ES++P+LYVGGG C S +EL RFVELTGIPV +
Sbjct: 199 MSLPGYIARLPKPPSTESLEQVLRVLGESRRPILYVGGGCAASGEELRRFVELTGIPVTT 258

Query: 331 TLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAK 390
          TLMGLG++P DD LSL MLGMHGT VYANYAV+ +DLLAFGVRFDDRVTK+EAFASR+K
Sbjct: 259 TLMGLGNFSDDDLRLMLGMHGT VYANYAVDKADLLAFGVRFDDRVTKIEAFASRSK 318

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNENLVQKQK 450
          IVHIDID AEIGKNK PHVS+C DVKLALQG+N +L + LDFG W EL+ QK++
Sbjct: 319 IVHIDIDPAEIGKNKQPHVSI CADVKLALQGLNLLNGSKAQQGLDFGPWHKELDQKRE 378

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGL 510
          FPL FKTTFGEAIPPQYAI+VLDEL T G+AI+TGVGQHQMWA AQ+Y YK+PRQWLSS GL
Sbjct: 379 FPLGFKTFGEAIPPQYAIQVDELTKGEAIIATGVGQHQMWA AQYYTYKRPRQWLSSSGL 438

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
          GAMGFGLPAA GA+VANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGM
Sbjct: 439 GAMGFGLPAAAGAAVANPGVTVDIDGDSFLMNIQELALIRIENLPVKVMILNNQHLGM 498

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
          V+QWEDRFYKANRAHT+LG+P E EI+P+ + A +PA RVTKK+++ AI+ ML+
Sbjct: 499 VVQWEDRFYKANRAHTYLGPNENESEIYPDFVTIAKGFNPAVRVTKKSEVTAAIKKMLE 558

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGT FNDVITEGDGRIKY 670
          TPGPYLLD+I PHQEHLVPMIPNGG F D+I EGDGR Y
Sbjct: 559 TPGPYLLDIIIVPHQEHLVPMIPNGGAFKDMIMEGDGRTSY 598

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>dbj|BAE53610.1| acetolactate synthase [Monochoria vaginalis]
Length = 614

Score = 923 bits (2386), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 430/575 (74%), Positives = 509/575 (88%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
FAPD+PRKGADILVEALER+GV +FAYPPGGASMEIHQALTRS SI N L RHEQG FA
Sbjct: 40 FAPDEPRKGADILVEALEREVTDLFAYPPGGASMEIHQALTRSPSITNHLRHEQGEAFA 99

Query: 151 AEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYARS+G+PG+CIATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAFQETP
Sbjct: 100 ASGYARSTGRPGVCIATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAFQETP 159

Query: 211 IVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDV PKDIQQQLAIPNWEQA 270
IVEVTRSITKHNLYL+DV+DIPRII+EAFF+ATSGRPGPVLVD+PKDIQQQLA+P W+
Sbjct: 160 IVEVTRSITKHNLYLVDVDDIPRIIEEAFFIATSGRPGPVLVDIPKDIQQQLAVPVWDPP 219

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGCLNSSDELGRFVELTGIPVAS 330
+LPGY+SR+PKPP L+QI+R++SES +PVLYVGGG L++S+EL F +LTGIP+AS
Sbjct: 220 VRLPGYVSRPKPPALHLLQIIRILSESSRPVLYVGGSLHASEELRGFADLTGIPIAS 279

Query: 331 TLMGLSGSPCDELDSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRTVGKLEAFASRAK 390
TLMGLG YP D LSL MLGMHGT VYANYA++ +DLLAFGVRFDDRTVGKLEAFASRAK
Sbjct: 280 TLMGLGVYPLDGPLSLKMLGMHGT VYANYAIDKADLLAFGVRFDDRTVGKLEAFASRAK 339

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQK 450
IVHIDID AEIGKNK PHVS+CGD+KLALQ MN+++E KLDF WR EL+ QK+
Sbjct: 340 IVHIDIDPAEIGKNKQPHVSI CGDIKLALQEMNEMIEENG IHSKLD FSAWREELDQKKN 399

Query: 451 FPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGL 510
+PL +KTFG+ IPPQ+AI++L+ELT+G+AI I+TGVGQHQMWA AQ+YNYK+PRQWL+S GL
Sbjct: 400 YPLKYKTFGD LIPPQHAIELLEELTNGEAIIT TGVGQHQMWA AQYNYKPRQWLTSAGL 459

Query: 511 GAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA+GA+V NP +VVDIDGDSF MN QELA IR+ENL VK+L+LNNQHLGM
Sbjct: 460 GAMGFGLPAAVGAAGNPGVVVDIDGDSFQMNAQELAIIRIENLDVKMLILNNQHLGM 519

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKADLREAIQTM LD 630
V+QWEDRFY++NRAHT+LG+PA E ++FP+ + A + IPAARV+KK+++R+AI+ M+
Sbjct: 520 VVQWEDRFYQSNRAHTYLGNPANESKVF PDKLAESYDIPAARVSKKSEVRDAIRKMIQ 579

Query: 631 TPGPYLLDVICPHQEHVLP MIPNGGTFNDVITEGD 665
TPGPYLLDVI PH+EHVLP MIP+GG F D+I +GD
Sbjct: 580 TPGPYLLDVIVPHEEHVLP MIPSGGAFKDMILDGD 614

>dbj|BAE53605.1| acetolactate synthase [Monochoria vaginalis]
dbj|BAE53606.1| acetolactate synthase [Monochoria vaginalis]
dbj|BAE53607.1| acetolactate synthase [Monochoria vaginalis]
dbj|BAE53609.1| acetolactate synthase [Monochoria vaginalis]
Length = 614

Score = 923 bits (2385), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 430/575 (74%), Positives = 509/575 (88%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
FAPD+PRKGADILVEALER+GV +FAYPPGGASMEIHQALTRS SI N L RHEQG FA
Sbjct: 40 FAPDEPRKGADILVEALEREVTDLFAYPPGGASMEIHQALTRSPSITNHLRHEQGEAFA 99

Query: 151 AEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYARS+G+PG+CIATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAFQETP
Sbjct: 100 ASGYARSTGRPGVCIATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAFQETP 159

Query: 211 IVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDV PKDIQQQLAIPNWEQA 270
IVEVTRSITKHNLYL+DV+DIPRII+EAFF+ATSGRPGPVLVD+PKDIQQQLA+P W+
Sbjct: 160 IVEVTRSITKHNLYLVDVDDIPRIIEEAFFIATSGRPGPVLVDIPKDIQQQLAVPVWDPP 219

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
++LPGY+SR+PKPP L+QI+R++SES +PVLYVGGG L++S+EL RF +LTGIP+AS
Sbjct: 220 VRLPGYVSRPKPPALHLLQIIRILSESSRPVLYVGGGSLHASEELRRFADLTGIPIAS 279

Query: 331 TLMGLGSYPCDDELSTHMLGMHGTIVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAK 390
TLMGLG YP D LSL MLGMHGTIVYANYA++ +DLLLLAFGVRFDDRVTGKLEAFASRAK
Sbjct: 280 TLMGLGVYPLDGPLSLKMLGMHGTIVYANYAIDKADLLAFGVRFDDRVTGKLEAFASRAK 339

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQK 450
IVHIDID AEIGKNK PHVS+CGD+KLALQ MN+++E KLDF WR EL+ QK+
Sbjct: 340 IVHIDIDPAEIGKNKQPHVSI CDIKLALQEMNEMIEENGIH SKLDFS AWEELDQKKN 399

Query: 451 FPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
+PL +KTFG+ IPPQ+AI++L+ELT+G+AI+TGVGQHQMWAQ+YNYK+PRQWL+S GL
Sbjct: 400 YPLKYKTFGDLIPPQHAIELLEELTNGEAIITGVGQHQMWAQYNYKPRQWLTSAGL 459

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA+GA+V NP +VVDIDGDSF MN QELA IR+ENL VK+L+LNNQHLGM
Sbjct: 460 GAMGFGLPAAVGAAGVNPVVDIDGDSFQMNAQELAIIRIENLDVKMLILNNQHLGM 519

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFY++NRAHT+LG+PA E ++FP+ + A + IPAA V+KK+++R+AI+ M+
Sbjct: 520 VVQWEDRFYQSNRAHTYLGPNANESKVFDPFKLAESYDIPAAACVSKKSEVRDAIRKMIQ 579

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGTFNDVITEGD 665
TPGPYLLDVI PH+EHVLPMP+GG F D+I +GD
Sbjct: 580 TPGPYLLDVIVPHEEHVLPMPISGGAFKDMILDGD 614

>gb|AA053548.1| acetohydroxyacid synthase [Triticum aestivum]
Length = 598

Score = 922 bits (2384), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 436/580 (75%), Positives = 503/580 (86%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
+ P +PRKGADILVEALER G+ VFAYPGGASMEIHQALTRS I N L RHEQG FA
Sbjct: 19 WGPSEPRKGADILVEALERCIVDVFAYPGGASMEIHQALTRSPVITNHLFRHEQGEAFA 78

Query: 151 AEGYARSSGKPGICIAATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYAR+SG+ G+C+ATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAFQETP
Sbjct: 79 ASGYARASGRVGVCVATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAFQETP 138

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDV PKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+
Sbjct: 139 IVEVTRSITKHNYLVLDVEDIPRVIQEAFFLASSGRPGPVLVDIPKDIQQQMAVPVWDTP 198

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ ES++P+LYVGGG S +EL RFVELTGIPV +
Sbjct: 199 MSLPGYIARLPKPPSTESLEQVRLVGE SRRPILYVGGGCAASGEELRRFVELTGIPVTT 258

Query: 331 TLMGLGSYPCDDELSTHMLGMHGTIVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGTIVYANYAV+ +DLLLLAFGVRFDDRVTGK+EAFASR+K
Sbjct: 259 TLMGLGNFSDPLSLRMLGMHGTIVYANYAVDKADLLAFGVRFDDRVTGKIEAFASRSK 318

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQK 450
IVHIDID AEIGKNK PHVS+C DVKLALQG+N +L + LDFG W EL+ QK++
Sbjct: 319 IVHIDIDPAEIGKNKQPHVSI CADVKLALQGLNDLLNGSKAQGLDFGPWHKELDQKKRE 378

Query: 451 FPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
FPL FKTGFEAIPPQYAI+VLDELTD G+AI+TGVGQHQMWAQ+Y YK+PRQWLSS GL
Sbjct: 379 FPLGFKTFGEAIPPQYAIQVDELTDKGEAIATGVGQHQMWAQYYYTKRPRQWLSSSGGL 438

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA GA+VANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGM
Sbjct: 439 GAMGFGLPAAAGAAVANPGVTVDIDGDSFLMNIQELALIRIENLPVKVMILNNQHLGM 498

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFYKANRAHT+LG+P E EI+P+ + A +PA RVTKK+++ AI+ ML+
Sbjct: 499 VVQWEDRFYKANRAHTYLGPNENESEIYPDFVTIAKGFNVPVRVTKKSEVTAAIKKMLE 558

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGTFNDVITEGDGRIKY 670
TPGPYLLD+I PHQEHLVPMIP+GG F D+I EGDGR Y
Sbjct: 559 TPGPYLLDIIIVPHQEHLVPMIPSGGAFKDMIMEGDGRYSY 598

>dbj|BAE53612.1| acetolactate synthase [Monochoria vaginalis]
Length = 614

Score = 922 bits (2383), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 429/575 (74%), Positives = 509/575 (88%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVFA 150
FAPD+PRKGADILVEALER+GV +FAYPPGGASMEIHQALTRS SI N L RHEQG FA
Sbjct: 40 FAPDEPRKGADILVEALEREVTDLFAYPPGGASMEIHQALTRSPSITNHLRHEQGEAFA 99

Query: 151 AEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYARS+G+PG+CIATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAFQETP
Sbjct: 100 ASGYARSTGRPGVCIATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAFQETP 159

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQA 270
IVEVTRSIT+HNYLV+DV+DIPRII+EAFF+ATSGRPGPVLVD+PKDIQQQLA+P W+
Sbjct: 160 IVEVTRSITQHNYLVLDVDDIPRIIEEAFFIATSGRPGPVLVDIPKDIQQQLAVPVWDPP 219

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
+LPGY+SR+PKPP L+QI+R++SES +PVLVYVGGG L++S+EL F +LTGIP+AS
Sbjct: 220 VRLPGYVSRLPKPPALHLLQIIRILSESSRPVLYVGGGSLHASEELRGFADLTGIPIAS 279

Query: 331 TLMGLGSPYPCDELHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAK 390
TLMGLG YP D LSL MLGMHGTVYANYA++ +DLLAFGVRFDDRVTKLEAFASRAK
Sbjct: 280 TLMGLGVYPLDGPLSLKMLGMHGTVYANYAIDKADLLAFGVRFDDRVTKLEAFASRAK 339

Query: 391 IVHIDIDSAEIGKNKTPHVSVCGDVKLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQK 450
IVHIDID AEIGKNK PHVS+CGD+KLALQ MN+++E KLDF WR EL+ QK+
Sbjct: 340 IVHIDIDPAEIGKNKQPHVSI CGDIKALQEMNEMIEENGHISKLDFSAWREELDQKKN 399

Query: 451 FPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
+PL +KTFG+ IPPQ+AI++L+ELT+G+AI+TGVGQHQMWAQ+YNYK+PRQWL+S GL
Sbjct: 400 YPLKYKTFGDLIPPQHAIEELLEELTNGEAIITGVGQHQMWAQYNYKPRQWLTSAAG 459

Query: 511 GAMGFGLPAAIGASVANPDAIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA+GA+V NP +VVDIDGDSF MN QELA IR+ENL VK+L+LNNQHLGM
Sbjct: 460 GAMGFGLPAAVGAAGVGNPGVVVDIDGDSFQMAQELAIIRIENLDVKMLILNNQHLGM 519

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNPMMLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFY++NRAHT+LG+PA E ++FP+ + A + IPAARV+KK+++R+AI+ M+
Sbjct: 520 VVQWEDRFYQSNRAHTYLGPNANESKVFPDFVKLAESYDIPAARVSKKSEVRDAIRKMIQ 579

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGTFNDVITEGD 665
TPGPYLLDVI PH+EHVLPMP+GG F D+I +GD
Sbjct: 580 TPGPYLLDVIVPHEEHVLPMPISGGAFKDMILDGD 614

>gb|ABF66049.1| acetolactate synthase [Oryza sativa (indica cultivar-group)]
Length = 644

Score = 922 bits (2382), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 432/576 (75%), Positives = 497/576 (86%)

Query: 95 QPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGY 154
+PRKGADILVEALER GV VFAYPPGGASMEIHQALTRS I N L RHEQG F A GY
Sbjct: 69 EPRKGADILVEALERCVSDFVAYPPGGASMEIHQALTRSPVITNHLRHEQGEAFVAGSY 128

Query: 155 ARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEV 214
AR+SG+ G+C+ATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQETPIVEV
Sbjct: 129 ARASGRVGVCVATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQETPIVEV 188

Query: 215 TRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLP 274
TRSITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+ +M LP
Sbjct: 189 TRSITKHNYLVLDVEDIPRVIQEAFFLASSGRPGPVLVDIPKDIQQQMAVPVWDTSMNLP 248

Query: 275 GYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVASTLMG 334
 GY++R+PKPP LEQ++RL+ ES++P+LYVGGG S DEL RFVELTGIPV +TLMG
 Sbjct: 249 GYIARLPKPPATELLEQVLRVVGESRRPILYVGGGCSASGDELRRFVELTGIPVTTTLMG 308

Query: 335 LGSYPCDDELSLHMLGMHGTIVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIVHI 394
 LG++P DD LSL MLGMHGTIVYANYAV+ +DLLAFGVRFDDRVTGK+EAFASRAK +
 Sbjct: 309 LGNFPSDDPLSLRMLGMHGTIVYANYAVDKADLLAFGVRFDDRVTGKIEAFASRAKSLV 368

Query: 395 DIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWVRNENLVQKQKFPLS 454
 DID AEIGKNK PHVS+C DVKLALQG+N +L+ + DF W NEL+ QK++FPL
 Sbjct: 369 DIDPAEIGKNKQPHVSICADVKLALQGLNALLDQSTTKTSSDFSAAHNELDQKQKREFPLG 428

Query: 455 FKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMG 514
 +KTFGE IPPQYAI+VLDELTDG+AI+TGVGQHQMWAQ+Y YK+PRQWLSS GLGAMG
 Sbjct: 429 YKTFGEEIPPQYAIQVLDELTDGKAIISTGVGQHQMWAQYYTYKRPRQWLSSAGLGAMG 488

Query: 515 FGLPAAIGASVANPDIAIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQW 574
 FGLPAA GASVANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGMV+QW
 Sbjct: 489 FGLPAAAGASVANPGVTVDIDGDSFIMNVQELALIRIENLPVKVMVLNNQHLGMVVQW 548

Query: 575 EDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGP 634
 EDRFYKANRAHT+LG+P E EI+P+ + A IPA RVTKK+++R AI+ ML+TPGP
 Sbjct: 549 EDRFYKANRAHTYLGNDPECESEIYPDFVTIAKGFNIPAVRVTKKSEVRAAIKKMLETPGP 608

Query: 635 YLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
 YLLD+I PHQEHVLPMP+GG D+I +GDGR Y
 Sbjct: 609 YLLDIIIVPHQEHVLPMPISGGALKDMILDGDGRTVY 644

>dbj|BAE53611.1| acetolactate synthase [Monochoria vaginalis]
 Length = 614

Score = 920 bits (2378), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 429/575 (74%), Positives = 508/575 (88%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPREHQQGVFA 150
 FAPD+PRKGADILVEALER+GV +FAYPGGASMEIHQALTRS SI N L RHEQG FA
 Sbjct: 40 FAPDEPRKGADILVEALEREVTDLFAYPGGASMEIHQALTRSPSITNHLRHEQGEAFA 99

Query: 151 AEGYARSSGKPGICIAATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
 A GYARS+G+PG+CIATSGPGATNLVS LADALLDS+P+VAITGQV RRMIGTDAFQETP
 Sbjct: 100 ASGYARSTGRPGVCIATSGPGATNLVSALADALLDSIPMVAITGQVSRRMIGTDAFQETP 159

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQA 270
 IVEVTRSITKHNYLV+DV+DIPRII+EAFF+ATSGRPGPVLVD+PKDIQQQLA+P W+
 Sbjct: 160 IVEVTRSITKHNYLVLDVDDIPRIIEEAFFIATSGRPGPVLVDIPKDIQQQLAVPVWDPP 219

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
 ++LPGY+SR+PKPP L+QI+R++SES +PVLYVGGG L++S+EL RF +LTGIP+AS
 Sbjct: 220 VRLPGYVSRPLPKPPALHLLQIIRILSESSRPVLYVGGGSLHASEELRRFADLTGIPIAS 279

Query: 331 TLMGLSGSYPCDDELSLHMLGMHGTIVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAK 390
 TLMGLG YP D LSL MLGMHGTIVYANYA++ +DLLAFGVRFDDRVTGKLEAFASRAK
 Sbjct: 280 TLMGLGVYPLDGPLSLKMLGMHGTIVYANYAIDKADLLAFGVRFDDRVTGKLEAFASRAK 339

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWVRNENLVQKQK 450
 IVHIDID AEIGKNK PHVS+CGD+KLALQ MN+++E KLDF WR EL+ QK+
 Sbjct: 340 IVHIDIDPAEIGKNKQPHVSICGDIKALQEMNEMIEENGIHSKLDFSAAWRELDQKQKN 399

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
 +PL +KTFG+ IPPQ+AI++L+ELT+G+AI+TGVGQHQMWAQ+YNYK+PRQWL+S GL
 Sbjct: 400 YPLKYKTFGDLPQHAIELLEELTNGEAIITTVGVGQHQMWAQYYNYKRPRQWLSAGL 459

Query: 511 GAMGFLPAAIGASVANPDIAIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
 GAMGFLPAA+GA+V NP +VVDIDGDSF MN QELA IR+ENL VK+L+LNNQHLGM
 Sbjct: 460 GAMGFLPAAVGAAGVNPVVVDIDGDSFQMAQELAIIRIENLDVKMLILNNQHLGM 519

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
 V+QWEDRFY++NRAHT+LG+PA E ++FP+ + A + IPAA V+KK+++R+AI+ M+
 Sbjct: 520 VVQWEDRFYQSNRAHTYLGNDPANESKVFDFVLAESYDIPAAVSKKSEVRDAIRKMIQ 579

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGTFNDVITEGD 665
TPGPYLLDVI PH+EHVLPMP+GG F D+I +GD
Sbjct: 580 TPGPYLLDVIVPHEEHVLPMPISGGAFKDMILDGD 614

>gb|AAG30931.1|AF310684_1 acetolactate synthase precursor [Lolium multiflorum]
Length = 640

Score = 920 bits (2378), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 428/580 (73%), Positives = 498/580 (85%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPRHEQGGVFA 150
+ P +PRKGADILVEALER G+ VFAYPPGGASMEIHQALT S I N L RHEQG FA
Sbjct: 61 WGPSEPRKGADILVEALERCGISDVFAYPGGASMEIHQALTSSPLITNHLFRHEQGEAFA 120

Query: 151 AEGYARSSGKPGICCIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYAR+SG+ G+C+ATSGPGATNLVS LADALLDS+P+VAITGQV RRMIGTDAFQETP
Sbjct: 121 ASGYARASGRVGVCVATSGPGATNLVSALADALLDSIPMVAITGQVQRRMIGTDAFQETP 180

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+
Sbjct: 181 IVEVTRSITKHNYLVLDVEDIPRVIQEAFFLASSGRPGPVLVDIPKDIQQQMAVPVWDAP 240

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ E ++P+LYVGGC S +++ RFVELTGIPV +
Sbjct: 241 MSLPGYIARLPKPPATELLEQVLRVLGEERRPILYVGGCSASGEDVRRFVELTGIPVTT 300

Query: 331 TLMGLGSYPCDELSTHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGTVYANYAV+ +DLLAFGVRFDRTGK+EAFASR+K
Sbjct: 301 TLMGLGNFSDPLSLRMLGMHGTVYANYAVDKADLLAFGVRFDRTGKIEAFASRSK 360

Query: 391 IVHIDIDSAEIGKNKTPHVSVCGDVKLALQGMNVLENRAEELKLDGFWVRNENLVQKQK 450
IVHIDID AEIGKNK PHVS+C DVKLALQG+N VL + DF W +EL QK++
Sbjct: 361 IVHIDIDPAEIGKNKQPHVSIADVKLALQGLNAVLTGSKCDKSFDFASWHDELEQQKRE 420

Query: 451 FPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
FPL +KTFGEAIPPQYAI+VLDELTD G+AII+TGVGQHQMWAQ+Y YK+PRQ LSS GL
Sbjct: 421 FPLGYKTFGEAIPPQYAIQVDELTDGKAIATGVGQHQMWAQYYTYKRPRQVLSAGL 480

Query: 511 GAMGFGLPAAIGASVANPDAIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA G +VANP VVDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGM
Sbjct: 481 GAMGFGLPAAAGTAVANPGVTVDIDGDSFLMNIQELALIRIENLPVKVMILNNQHLGM 540

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNPMMLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFYKANRAHT+LG+P E EI+P+ + A +PA RVTK++++R AI+ ML+
Sbjct: 541 VVQWEDRFYKANRAHTYLGPNENESEIYPDFVTIAKGFNPAVRVTKRSEVRRAAIKMLE 600

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGTFNDVITEGDGRIKY 670
TPGPYLLD+I PHQEHLVPMIP+GG F D+I EGDGRI Y
Sbjct: 601 TPGPYLLDIIVPHQEHLVPMIPSGGAFKDIIMEGDGRISY 640

>dbj|BAE53608.1| acetolactate synthase [Monochoria vaginalis]
Length = 614

Score = 917 bits (2370), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 428/575 (74%), Positives = 507/575 (88%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPRHEQGGVFA 150
FAPD+PRKGADILVEALER+GV +FAYPPGGASMEIHQALTRS SI N L RHEQG FA
Sbjct: 40 FAPDEPRKGADILVEALEREGVTDLFAYPPGGASMEIHQALTRSPSITNHLRHEQGEAFA 99

Query: 151 AEGYARSSGKPGICCIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYARS+G+PG+CIATSGPGATNLVS LADALLDS+P+VAITGQV RRMIGTDAFQETP
Sbjct: 100 ASGYARSTGRPGVCIATSGPGATNLVSALADALLDSIPMVAITGQVSRRMIGTDAFQETP 159

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLV+DV+DIPRII+EAFF+ATSGRPGPVLVD+PKDIQQQLA+P W+
Sbjct: 160 IVEVTRSITKHNYLVLDVDDIPRIIEAFAFIATSGRPGPVLVDIPKDIQQQLAVPVWDPP 219

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
++LPGY+SR+PKPP L+QI+R++SES +PVLYVGGG L++S+EL RF +LTGIP+AS
Sbjct: 220 VRLPGYVSRLPKPPALHLLQIIRILSESSRPVLYVGGGSLHASEELRRFADLTGIIPIAS 279

Query: 331 TLMGLGSYPCCDELSLHMLGMHGTIVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAK 390
TLMGLG YP D LSL MLGMHGTIVYANYA++ +DLLAFGVRFDDRVTGKLEAFASRAK
Sbjct: 280 TLMGLGVYPLDGPLSLKMLGMHGTIVYANYAIDKADLLAFGVRFDDRVTGKLEAFASRAK 339

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFGVWRNENLVQKQK 450
IVHIDID AEIGKNK PHVS+CGD+KLALQ MN+++E KLDF WR EL+ QK+
Sbjct: 340 IVHIDIDPAEIGKNKQPHVSICGDIKALQEMNEMIEENGIHSKLDFSAWREELDQKQKN 399

Query: 451 FPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
+PL +KTFG+ IPPQ+AI++L+ELT+G+AII+TGVGQHQMWAQ+YNYK+ RQWL+S GL
Sbjct: 400 YPLKYKTFGDLIPPQHAIELLEELTNGEAIITGVGQHQMWAQYNYKRRARQWLTSAGL 459

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA+GA+V NP +VVDIDGDSF MN QELA IR+ENL VK+L+LNNQHLGM
Sbjct: 460 GAMGFGLPAAVGAAGNPGVVDIDGDSFQMNAQELAIIRIENLDVKMLILNNQHLGM 519

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFY++NRAHT+LG+PA E ++FP+ + A + IPAA V+KK+++R+AI+ M+
Sbjct: 520 VVQWEDRFYQSNRAHTYLGPNANESKVFPDFVKLAESYDIPAAVSKKSEVRDAIRKMIQ 579

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGTNDVITEGD 665
TPGPYLLDVI PH+EHVLPMP+GG F D+I +GD
Sbjct: 580 TPGPYLLDVIVPHEEHVLPMPISGGAFKDMILDGD 614

>dbj|BAE53604.1| acetolactate synthase [Monochoria vaginalis]
Length = 614

Score = 915 bits (2364), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 428/575 (74%), Positives = 506/575 (88%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFA 150
FAPD+PRKGADILVEALER+GV +FAYPGGASMEIHQALTRS SI N L RHEQG FA
Sbjct: 40 FAPDEPRKGADILVEALEREVTDLFAYPGGASMEIHQALTRSPSITNHLRHEQGEAFA 99

Query: 151 AEGYARSSGKPGICIASGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYARS+G+PG+CIATSGPGATNLVS LADALLDS+P+VAITGQV RRMIGTDAFQETP
Sbjct: 100 ASGYARSTGRPGVCIATSGPGATNLVSALADALLDSIPMVAITGQVLRMMIGTDAFQETP 159

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNYLV+DV+DIPRII+EAFF+ATSGRPGPVLVD+PKDIQQQLA+P W+
Sbjct: 160 IVEVTRSITKHNYLVLDVDDIPRIIEEAFFIATSGRPGPVLVDIPKDIQQQLAVPVWDPP 219

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
++LPGY+SR+PKPP L+QI+R++SES +PVLYVGGG L++S+EL F +LTGIP+AS
Sbjct: 220 VRLPGYVSRLPKPPALHLLQIIRILSESSRPVLYVGGGSLHASEELRGFADLTGIIPIAS 279

Query: 331 TLMGLGSYPCCDELSLHMLGMHGTIVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAK 390
TLMGLG YP D LSL M GMHGTIVYANYA++ +DLLAFGVRFDDRVTGKLEAFASRAK
Sbjct: 280 TLMGLGVYPLDGPLSLKMWGMHGTIVYANYAIDKADLLAFGVRFDDRVTGKLEAFASRAK 339

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFGVWRNENLVQKQK 450
IVHIDID AEIGKNK PHVS+CGD+KLALQ MN+++E KLDF WR EL+ QK+
Sbjct: 340 IVHIDIDPAEIGKNKQPHVSICGDIKALQEMNEMIEENGIHSKLDFSAWREELDQKQKN 399

Query: 451 FPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
PL +KTFG+ IPPQ+AI++L+ELT+G+AII+TGVGQHQMWAQ+YNYK+PRQWL+S GL
Sbjct: 400 NPLKYKTFGDLIPPQHAIELLEELTNGEAIITGVGQHQMWAQYNYKRRARQWLTSAGL 459

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA+GA+V NP +VVDIDGDSF MN QELA IR+ENL VK+L+LNNQHLGM
Sbjct: 460 GAMGFGLPAAVGAAGNPGVVDIDGDSFQMNAQELAIIRIENLDVKMLILNNQHLGM 519

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFY++NRAHT+LG+PA E ++FP+ + A + IPAAV+KK+++R+AI+ M+
Sbjct: 520 VVQWEDRFYQSNRAHTYLGPNANESKVFPDFVKLAESYDIPAAVSKKSEVRDAIRKMIQ 579

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGD 665
TPGPYLLDVI PH+EHVLPMP+GG F D+I +GD
Sbjct: 580 TPGPYLLDVIVPHEEHVLPMPSSGGAFFKDMILDGD 614

>gb|ACF87819.1| unknown [Zea mays]
Length = 638

Score = 911 bits (2354), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 434/580 (74%), Positives = 497/580 (85%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVFA 150
+ P++PRKG+DILVEALER GV VFAYPPGGASMEIHQALTRS I N L RHEQG FA
Sbjct: 59 WGPNEPRKGS DILVEALERCGVRDVFAYPGGASMEIHQALTRSPVIANHLFRHEQGEAFA 118

Query: 151 AEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYARSSG+ G+CIATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQETP
Sbjct: 119 ASGYARSSGRVGVCIATSGPGATNLVSALADALLDSVP+VAITGQVPRRMIGTDAFQETP 178

Query: 211 IVEVTRISITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQA 270
IVEVTRISITKHNYLV+DV+DIPR+++EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+
Sbjct: 179 IVEVTRISITKHNYLVLDVDDIPRVVQEAFFLASSGRPGPVLVDIPKDIQQQMAVPAWDTP 238

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ ES++PVLYVGGGC S +EL RFVELTGIPV +
Sbjct: 239 MSLPGYIARLPKPPATEFLEQVLRVLGESSRPPVLYVGGGCAASGEELCRFVELTGIPVTT 298

Query: 331 TLMGLGSPYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGTVYANYAV+ +DLLAFGVRFDRTVGK+EAFA RAK
Sbjct: 299 TLMGLGNFPDDPLSLRMLGMHGTVYANYAVDKADLLAFGVRFDRTVGKIEAFAGRAK 358

Query: 391 IVHIDIDSAEIGKNKTPHVSVCDDVKKLALQGMNVLENRAEELKLDGFWVRNENLVQKQK 450
IVHIDID AEIGKNK PHVS+C DVKKLALQGMN +LE + DFG W +EL+ QK++
Sbjct: 359 IVHIDIDPAEIGKNKQPHVSIADVKLALQGMNTLLEGSTSKSFDGFSWHDELQKQKRE 418

Query: 451 FPLSFKTFGEAIPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
FPL +K F E I PQYAI+VLDELTD GKAI+TGVGQHQMWAQ+Y YK+PRQWLSS GL
Sbjct: 419 FPLGYKIFNEEIQPYAIQVDELTDGKAI+ATGVGQHQMWAQYTYKPRQWLSSAGL 478

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA GA+VANP VVDIDGDSF+MN+QELA IR+ENLPVKV +LNNQHLGM
Sbjct: 479 GAMGFGLPAAAGAAVANPVTVDIDGDSFLMNIQELAMIRIENLPVKVFLNNQHLGM 538

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFPMNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V+QWEDRFYKANRAHTFLG+P E EI+P+ + A IPA RVTKK+++ AI+ ML+
Sbjct: 539 VVQWEDRFYKANRAHTFLGNPENESIEYPDFVAIAKGFNIPAVRVTKKSEVHAAIKKMLE 598

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
PG YLLD+I PHQEHVLPMP+GG F D+I +GDGR Y
Sbjct: 599 APGQYLLDIIVPHQEHVLPMPSSGGAFFKDMILDGDGRTVY 638

>sp|Q41769|ILV2_MAIZE Acetolactate synthase 2, chloroplast precursor (Acetohydroxy-acid
synthase 2)
emb|CAA45117.1| acetohydroxyacid synthase [Zea mays]
Length = 638

Score = 910 bits (2353), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 433/580 (74%), Positives = 497/580 (85%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVFA 150
+ P++PRKG+DILVEALER GV VFAYPPGGASMEIHQALTRS I N L RHEQG FA
Sbjct: 59 WGPNEPRKGS DILVEALERCGVRDVFAYPGGASMEIHQALTRSPVIANHLFRHEQGEAFA 118

Query: 151 AEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A YARSSG+ G+CIATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQETP
Sbjct: 119 ASAYARSSGRVGVCIATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQETP 178

Query: 211 IVEVTRISITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQA 270
IVEVTRISITKHNYLV+DV+DIPR+++EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+
Sbjct: 179 IVEVTRISITKHNYLVLDVDDIPRVVQEAFFLASSGRPGPVLVDIPKDIQQQMAVPAWDTP 238

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ ES++PVLYVGGG S +EL RFVELTGIPV +
Sbjct: 239 MSLLPGYIARLPKPPATEFLEQVLRVLVGGESRRPVLYVGGGCAASGEELCRFVELTGIPVTT 298

Query: 331 TLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGT VYANYAV+ +DLLAFGVRFDDRVTK+EAFA RAK
Sbjct: 299 TLMGLGNFSDDPLSLRMLGMHGT VYANYAVDKADLLAFGVRFDDRVTKIEAFAGRAK 358

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNVLENRAEELKLD FGVWRNENLVQKQK 450
IVHIDID AEIGKNK PHVS+C DVKALQGMN +LE + DFG W +EL+ QK++
Sbjct: 359 IVHIDIDPAEIGKNKQPHVSICADV KALQGMNTLEGSTSKSFDFGSWHDEL DQKQRE 418

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
FPL +K F E I PQYAI+VLDEL T G+AII+TGVGQHQMWAQ+Y YK+PRQWLSS GL
Sbjct: 419 FPLGYKIFNEEIQPQYAIQVDELTKGEAIIATGVGQHQMWAQYIYTYKRPRQWLSSAGL 478

Query: 511 GAMGFGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGFLPAA GA+VANP VVDIDGDSF+MN+QELA IR+ENLPVKV +LNNQHLGM
Sbjct: 479 GAMGFGFLPAAAGAAVANP GVTVDIDGDSFLMNIQELAMIRIENLPVKVFLNNQHLGM 538

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFPMMLLFAAACGIPAAVTKKADLREAIQTMLD 630
V+QWEDRFYKANRAHTFLG+P E EI+P+ + A IPA RVTKK+++ AI+ ML+
Sbjct: 539 VVQWEDRFYKANRAHTFLGNPENES E IYPDFVAIAKGFNIPAVRVTKKSEVHAAIKKMLE 598

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGT FNDVITEGDGRIKY 670
PGPYLLD+I PHQEHLVPMIP+GG F D+I +GDGR Y
Sbjct: 599 APGPYLLDIIVPHQEHLVPMIPSGGAFKDMILDGDGRVY 638

>ref|XP_001759950.1| predicted protein [Physcomitrella patens subsp. patens]
gb|EDQ75075.1| predicted protein [Physcomitrella patens subsp. patens]
Length = 583

Score = 894 bits (2310), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 423/584 (72%), Positives = 498/584 (85%), Gaps = 2/584 (0%)

Query: 88 ISRFPADQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGG 147
+SR+A D+PRKG+DILVEALER+GV T FAYPGGASMEIHQALTRS+ IRNVLP RHEQGG
Sbjct: 1 MSRYADDEPRKGS DILVEALERE GVRTTFAYPGGASMEIHQALTRSNVIRNVLCRHEQGE 60

Query: 148 VFAAEGYARSSGKPGICIATSGPGATNLVSG LADALLDSVPLVAITGQVPRRMIGTDAFQ 207
+FAAEGYA+SSG+ G+CIATSGPGATNLV+G ADALLDSVPLVAITGQVPRR IGTDAFQ
Sbjct: 61 IFAAEGYAKSSGRVGVCIATSGPGATNLVTGFADALLDSVPLVAITGQVPRRFIGTDAFQ 120

Query: 208 ETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNW 267
ETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNW
Sbjct: 121 ETPIVEVTRSITKHNYLVMTVEDIPRVIREAFLAASGRPGPVLVDIPKDIQQQMAIPDW 180

Query: 268 EQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIP 327
Q MKL Y+SR+P PP+ S ++QI+RL++ +KKPV+Y GGGCL++S EL FVELTGIP
Sbjct: 181 NQPMKLQSYLSRLPPPPQISLMQQIIRLLATAKKPVIYSGGGCLHASKELREFVELTGIP 240

Query: 328 VASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFAS 387
V STLMLGLG++P D+ L MLGMHGT VYANYAV+++D+LLAFGVRFDDRVTKLE+FAFAS
Sbjct: 241 VTSTLMGLGTFPASDKRYLSMLGMHGT VYANYAVDNADMLLAFGVRFDDRVTKLESFAS 300

Query: 388 RAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNVLENRAEELKLD FGVWRNENLVQK 447
RA IVHIDID AEIGKNK PH+S+C DV+LAL G+NK+++ E + DF WR EL+
Sbjct: 301 RASIVHIDIDPAEIGKNKQPHISICADVQLALAGLNKLIKEGP AE-RPDFSAWRAELDGV 359

Query: 448 KQKFPPLSFKTFGEA-IPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
K K+P+ F F + I PQ AI+ L ELT G AIIISTGVGQHQMWAQ+Y Y++PR+WL+
Sbjct: 360 KLKWPMPKPKFDNSVIVPQLAIQTLCELTGGNAIISTGVGQHQMWAQWY EYEQPRRWLT 419

Query: 507 SGGLGAMGFGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLGAMGFGFLP+A+GA+ +PD VVDIDGDSFIMN+QELATI VE LPVK+++LNNQ
Sbjct: 420 SGGLGAMGFGFLPSALGAAATHPDIPVDIDGDSFIMNIQELATIHVEKLPVKIMILNNQ 479

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGMV+QWEDRFYKANRAHT+LGDP E +I+P+ A C +P+ARVT++ LR+AI
Sbjct: 480 HLGMMVQWEDRFYKANRAHTYLGDPEAEADIYPDFCKIAEGCKVPSARVTRREHLRDAIT 539

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
ML+TPGPYLLDVI PHQEHVLPMP G +F ++ITEGDGR Y
Sbjct: 540 KMLETPGPYLLDVIVPHQEHVLPMPGGASFKEIITEGDGRQIY 583

>gb|EAZ23185.1| hypothetical protein OsJ_006668 [Oryza sativa (japonica
cultivar-group)]
Length = 628

Score = 891 bits (2303), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 423/580 (72%), Positives = 488/580 (84%), Gaps = 16/580 (2%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPREHQQGVFA 150
+ P +PRKG DILVEA PG IHQALTRS I N L RHEQG FA
Sbjct: 65 WGAEPKRGPDILVEA-----PGA----IHQALTRSPVITNHLFRHEQGEAFA 108

Query: 151 AEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYAR+SG+ G+C+ATSGPGATNLVS LADALLDSVP+VAITGQVPRRMIGTDAFQETP
Sbjct: 109 ASGYARASGRVGVCVATSGPGATNLVSALADALLDSVPMVAITGQVPRRMIGTDAFQETP 168

Query: 211 IVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQA 270
IVEVTRSITKHNLYL+DVEDIPR+I+EAFFLA+SGRPGPVLVD+PKDIQQQ+A+P W+ +
Sbjct: 169 IVEVTRSITKHNLYLMDVEDIPRVIQEAFGLASSGRPGPVLVDIPKDIQQQMAVPVWDT 228

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAS 330
M LPGY++R+PKPP LEQ++RL+ ES++P+LYVGGG S DEL FVELTGIPV +
Sbjct: 229 MNLPGYIARLPKPPATELLEQVLRVGESESRPILYVGGGCSASGDELRFVELTGIPVTT 288

Query: 331 TLMGLGSYPCDELSSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASRAK 390
TLMGLG++P DD LSL MLGMHGTVYANYAV+ +DLLAFGVRFDRTGK+EAFAASRAK
Sbjct: 289 TLMGLGNFSDPLSLRMLGMHGTVYANYAVDKADLLAFGVRFDRTGKLEAFASRAK 348

Query: 391 IVHIDIDSAEIGKNKTPHVSVCADVGLALQGMNVLENRAEELKLDGFWVRNENLVQKQK 450
IVHIDID AEIGKNK PHVS+C DVKLALQG+N +L+ + DF W NEL+ QK++
Sbjct: 349 IVHIDIDPAEIGKNKQPHVSIKADVGLALQGLNALLQQSTTKTSSDFSAWHNELDQKRE 408

Query: 451 FPLSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
FPL +KTFGE IPPQYAI+VLDELTDG+AI+TGVGQHQMWAQ+Y YK+PRQWLSS GL
Sbjct: 409 FPLGYKTFGEAIPPQYAIQVDELTDGKAIISTGVGQHQMWAQYTYKPRQWLSSAGL 468

Query: 511 GAMGFGLPAAAGASVANPDAIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
GAMGFGLPAA GASVANP VDDIDGDSF+MN+QELA IR+ENLPVKV++LNNQHLGM
Sbjct: 469 GAMGFGLPAAAGASVANPVGTVDDIDGDSFIMNIQELALIRIENLPVKVMVLNNQHLGM 528

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTM 630
V+QWEDRFYKANRAHT+LG+P E EI+P+ + A IPA RVTKK+++R AI+ ML+
Sbjct: 529 VVQWEDRFYKANRAHTYLGNEPECESEIYPDFVTIAKGFNIPAVRVTKKSEVRAAIKMLE 588

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
TPGPYLLD+I PHQEHVLPMP+GG F D+I +GDGR Y
Sbjct: 589 TPGPYLLDIIIVPHQEHVLPMPSGGAFKDMILDGDGRTVY 628

>ref|XP_001758473.1| predicted protein [Physcomitrella patens subsp. patens]
gb|EDQ76875.1| predicted protein [Physcomitrella patens subsp. patens]
Length = 618

Score = 890 bits (2299), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 429/585 (73%), Positives = 501/585 (85%), Gaps = 2/585 (0%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPREHQQ 146
F+SR+A D+PRKG+DILVEALER+GV T FAYPGGASMEIHQALTRS+ IRNVLP RHEQG
Sbjct: 35 FVSRYAEDEPRKGS DILVEALEREGVRTTFAYPGGASMEIHQALTRSNVIRNVLCRHEQG 94

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
+FAAEGYA+SSG+ G+CIATSGPGATNLV+GLADALLDSVPLVAITGQVPRR IGTDAF
Sbjct: 95 EIFAAEGYAKSSGRVGVCIATSGPGATNLVTGLADALLDSVPLVAITGQVPRRFIGTDAF 154

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPN 266
QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPN
Sbjct: 155 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPN 214

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W Q MKL Y++R+P PP+ S ++QI+RL+S +KKPV+Y GGGCL++S EL FVELTGI
Sbjct: 215 WNQPMKLQSYLNRLPPPPQVSLMQQIIRLLSTAKKPVIIYSGGGCLHASKELREFVELTGI 274

Query: 327 PVASTLMGLGSGPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTGKLEAFA 386
PV STLMGLG++P DE L MLGMHGT VYANYA+++SD+LLAFGVRFD DRTGKLE+FA
Sbjct: 275 PVTSTLMGLGTFPASDERYLSMLGMHGT VYANYAIDNSDMLAFGVRFD DRTGKLESFA 334

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMN KVLNRAEELKLD FGVWRNELNV 446
SRA IVHIDID AEIGKNK PH+S+C DV+LAL G+NK+++ + F WR EL+
Sbjct: 335 SRASIVHIDIDPAEIGKNKQPHISICADVQLALAGLNKLIKE-GPATRPSFSAWRKELDG 393

Query: 447 QKQKFP LSF-KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWL 505
K+K+P+ F K + I PQ+AI+ L ELT G AIISTGVGQHQMWA AQ+Y Y++PR+WL
Sbjct: 394 VKEKWPMPKFPKLD SQVIVPQFAIQTLC ELTGNAIISTGVGQHQMWA AQWYEQPRRWL 453

Query: 506 SSGGLGAMGFLPAAIGASVANPD AIVVDIDGDGSFIMNVQELATIRVENLPVKVLLNN 565
+SSGGLGAMGFLPAA+GA+ NP D VVDIDGDGSFIMN+QELATI VE LPVK+++LNN
Sbjct: 454 TSGGLGAMGFLPAAAGAAATNP DIPVVDIDGDGSFIMNIQELATIHVEKLPVKIMVLLNN 513

Query: 566 QHLGMVMQWEDRFYKANRAHTFLGDP AQEDEFNMLLFAAACGIPAA RVTKKADLREAI 625
QHLGMV+QWEDRFYKANRAHT+LGDP E EI+P+ A C +P+ARVT+K DLR+AI
Sbjct: 514 QHLGMVVQWEDRFYKANRAHTYLGDP EAEAEIYPDFCKIAEGCKVPSARVTRKEDLRDAI 573

Query: 626 QTMLDTPGPYLLDVICPHQEHLVPMIPNGGT FNDVITEGDGRIKY 670
+ ML TPGPYLLDVI PHQEHLVPMIP G +F ++ITEGDGR Y
Sbjct: 574 KKMLQTPGPYLLDVIVPHQEHLVPMIPGGASFKEIITEGDGRQIY 618

>emb|CAH66432.1| OSIGBa0096P03.6 [Oryza sativa (indica cultivar-group)]
Length = 663

Score = 877 bits (2265), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 419/584 (71%), Positives = 500/584 (85%), Gaps = 5/584 (0%)

Query: 92 APDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVF 151
AP RKGADI+VEALER GV VF YPGGASMEIHQALTRS IRN L RHEQG FAA
Sbjct: 80 APMGQRRKGADIVVEALERCGVRDVFEYPPGGASMEIHQALTRSPVIRNHLRHEQGEAF 139

Query: 152 EGYARSSGKPGICIA TSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPI 211
GYARSSG+PG+C+ATSGPGATNLVS LADA LDSVPLVAITGQVPRRMIGTDAFQETPI
Sbjct: 140 SGYARSSGRPGVCVATSGPGATNLVSALADAHLD SVPLVAITGQVPRRMIGTDAFQETPI 199

Query: 212 VEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQAM 271
VE+TRSITKHNLYL++D++DIPR+I EAFFLA++GRPGPVLVD+PKDIQQQ+A+P+W+ M
Sbjct: 200 VELTRSITKHNLYLIDIDDIPRVINEAFLASTGRPGPVLVDIPKDIQQQMAVPSWDAPM 259

Query: 272 KLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAST 331
+LPGY+SR+PKPP + L++++RL+ ++++PVLYVGGGC S DEL RFVELTGIPV +T
Sbjct: 260 RLPGYISRLPKPPAANLLDEVIRLVGDAERPVLVYVGGGCSASGDELRRFVELTGIPVTTT 319

Query: 332 LMGLGSGPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTGKLEAFASRAKI 391
LMG+G++P DD LSL MLGMHGT VYANYAV+++DLLA GVRFD DRTGK+EAFASRAKI
Sbjct: 320 LMGIGNFSPDDPLSLRMLGMHGT VYANYAVDNADLLALGVRFDDRTGKVEAFASRAKI 379

Query: 392 VHIDIDSAEIGKNKTPHVSVC GDVKLALQGMN KVLNRAEELKLD FGVWRNELNVQK 448
VH+DID +E+GKNK PHVS+C DVKALQGMN +LE + A LDF WR+EL +K
Sbjct: 380 VHVDIDPSELGKNKQPHVSICADVKLALQGMNAMLEEQSAAAARKNLDFS AWRSELEKKK 439

Query: 449 QKFP LSF-KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSG 508
+FPL ++TFGE IPPQYAI+VLDE+T+G+AI++TGVGQHQMWA Q Y Y++PRQWLSS
Sbjct: 440 VEFPLGYRTFGEEIPPQYAIQVLDEVNTGEAIVATGVGQHQMWA TQHYTYRRPRQWLSSA 499

Query: 509 GLGAMGFLPAAIGASVANPD AIVVDIDGDGSFIMNVQELATIRVENLPVKVLLNNQHL 568
GLGAMGFLPAA GA+VANP A VVDIDGDGS +MN+QELA +RVE+LPVKV++LNNQHL
Sbjct: 500 GLGAMGFLPAAAGAAVANPGATVVDIDGDGSLLMNIQELAMVRVEDLPVKVMVLLNNQHL 559

Query: 569 GMVMQWEDRFYKANRAHTFLGDPAQE--DEIFPNMLLFAAACGIPAARVTKKADLREAIQ 626
GMV+QWEDRFY ANRAHT+LG+PA E++P+ + A GIPAARVT+K ++R A++
Sbjct: 560 GMVVQWEDRFYDANRAHTYLGNAANGGGEVYPDFVTIAGGFGIPAARVTRKGEVRAAVE 619

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
M+ PGPYLLDV+ PHQEHVLPMP+ G F D+I +GDGR Y
Sbjct: 620 EMMAAPGPYLLDVVVPHQEHVLPMPISNGAFKDIIVDGDGRSSY 663

>gb|EAY93888.1| hypothetical protein OsI_015121 [Oryza sativa (indica
cultivar-group)]
Length = 662

Score = 874 bits (2259), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 418/580 (72%), Positives = 498/580 (85%), Gaps = 3/580 (0%)

Query: 90 RFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVF 149
R+ P + RKGADILVEAL R GV VF YPGGASMEIHQALTRS +IRN L RHEQG F
Sbjct: 82 RWGPTERRKGADILVEALGRCGVRDVFYPPGGASMEIHQALTRSPAIRNHLRHEQGEAF 141

Query: 150 AAEGYARSSGKPGICIAATSGPGATNLVSLDALDLSVPLVAITGQVPRRMIGTDAFQET 209
AA GYARSSG+PG+C+ATSGPGATNLVS LADA LDSVPLVAITGQVPRRMIGTDAFQET
Sbjct: 142 AASGYARSSGRPGVCVATSGPGATNLVSALADAHLSVPLVAITGQVPRRMIGTDAFQET 201

Query: 210 PIVEVTRSITKHNYLVMDEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQ 269
PIVE+TRSITKHNYLV+DV+DIPR+I EAFFLAT+GRPGPVLVD+PKDIQQQ+A+P+W+
Sbjct: 202 PIVELTRSITKHNYLVLDVDDIPRVINEAFLATTGRPGPVLVDIPKDIQQQMAVPSWDA 261

Query: 270 AMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVA 329
M+LPGY+SR+PKPP + L++++RL+ ++++PVLYVGGGC S DEL RFVELTGIPV
Sbjct: 262 PMRLPGYISRLPKPPSANLLDEVIRLVGDAERPVLVYVGGGCSASGDELRRFVELTGIPVT 321

Query: 330 STLMLGLSGYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASRA 389
+TLMG+G++P DD LSL MLGMHGTVYANYAV++DLLA GVRFDRTGK+EAFAASRA
Sbjct: 322 TLMGIGNFPDDPLSLRMLGMHGTVYANYAVDNADLLALGVRFDRTGKVEAFASRA 381

Query: 390 KIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWRNELNVQKQ 449
KIVH+DID +E+GKNK PHVS+C DVKLALQGMN LE + + LDF WR+EL +K
Sbjct: 382 KIVHVIDIDPSELGKNKQPHVSICADVKLALQGMNATLEQQQRK-NLDFSARWSELEKKKA 440

Query: 450 KFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGG 509
+FPL ++TFGE IPPQYAI+VLDE+T+G+AI++TGVGQHQMWA Q Y +++PRQWLSS G
Sbjct: 441 EFPLGYRTFGEEIPPQYAIQVLDEVNTEAIVATGVGQHQMWAQHYTFRRPRQWLSSAG 500

Query: 510 LGAMGFGLPAAIGASVANPDIVVDIDGDGSFIMNVQELATIRVENLPVKVLLNNQHLG 569
LGAMGFGLPAA GA+VANP A VVDIDGDGS +MN+QELA +RVENLPVKV++LNNQHLG
Sbjct: 501 LGAMGFGLPAAAGAAVANPGATVVDIDGDGSLLMNQELAMVRVENLPVKVMVLNNQHLG 560

Query: 570 MVMQWEDRFYKANRAHTFLGDPAQE--DEIFPNMLLFAAACGIPAARVTKKADLREAIQT 627
MV+QWEDRFY ANRAHT+LG+PA E++P+ + A GIPAARVT+K ++R A++
Sbjct: 561 MVVQWEDRFYDANRAHTYLGNAANGGGEVYPDFVAIAGGFGIPAARVTRKGEVRAAVEE 620

Query: 628 MLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGR 667
M+ PGPYLLDV+ PHQEHV PMIP+ G F D+I +G GR
Sbjct: 621 MMAAPGPYLLDVVVPHQEHVQPMIPISNGAFKDIIVDGGGR 660

>gb|AAC14572.1| acetohydroxyacid synthase [Hordeum vulgare]
Length = 541

Score = 872 bits (2254), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 404/541 (74%), Positives = 469/541 (86%)

Query: 130 LTRSSSIRNVLPHEQGGVFAAEGYARSSGKPGICIAATSGPGATNLVSLDALDLSVPL 189
LTRS I N L RHEQG FAA GYAR+SG+ G+C+ATSGPGATNLVS LADALDS+P+
Sbjct: 1 LTRSPVITNHLFRHEQGEAFAASGYARASGRVGVCVATSGPGATNLVSALADALDSIPM 60

Query: 190 VAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMDEDIPRIIEEAFFLATSGRPGP 249
VAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGP
Sbjct: 61 VAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVLDVEDIPRVIQEAFFLASSGRPGP 120

Query: 250 VLVDVPKDIQQQLAIPNWEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGG 309
VLVD+PKDIQQQ+A+P W+ M LPGA++R+PKPP LEQ++RL+ E+++P+LYVGGG
Sbjct: 121 VLVDIPKDIQQQMAVPVWDTPMSLPGYIARLPKPPSTESLEQVLRVVGEARRPILYVGGG 180

Query: 310 CLNSSDELGRFVELTGIPVASTLMGLGSYPDCDELHMLGMHGT VYANYAVEHSDLLLA 369
C S +EL RFVELTGIPV +TLMGLG++P DD LSL MLGMHGT VYANYAV+ +DLLLA
Sbjct: 181 CAASGEELRRFVELTGIPVTTTLMGLGNFSDPLSLRMLGMHGT VYANYAVDKADLLLA 240

Query: 370 FGVRFD DVRTGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENR 429
FGVRFD DVRTGK+EAFASR+KIVHIDID AEIGKNK PHVS+C DVKLALQG+N +L
Sbjct: 241 FGVRFD DVRTGKIEAFASRSKIVHIDIDPAEIGKNKQPHVSI CADVKLALQGLNGLSGS 300

Query: 430 AEELKLD FGVWRNELNVQKQKFLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQH 489
+ LDFG W EL+ QK++FPL +KTFGEAIPPQYAI+VLDELTDG+AI+TGVGQH
Sbjct: 301 KAQQGLDFGFWHKELDQKREFPLGYKTFGEAIPPQYAIQVLDELTDGKAIISTGVGQH 360

Query: 490 MWAAQFYNYKKPRQWLSSGGLGAMGFLPAAIGASVANPD AIVVDIDGDSFIMNVQELA 549
MWAAQ+Y YK+PRQWLSS GLGAMGFLPAA GASVANP VVDIDGDSF+MN+QELA
Sbjct: 361 MWAAQYYTYKRPRQWLSSGGLGAMGFLPAAAGASVANPGVT VVDIDGDSFLMNIQELA 420

Query: 550 TIRVENLPVKVLLNNQHLGMVQWEDRFYKANRAHTFLGDP AQEDEFPNMMLFAAACG 609
IR+ENLPVKV++LNNQHLGMV+QWEDRFYKANRAHT+LG+P E EI+P+ + A
Sbjct: 421 LIRIENLPVKVMILNNQHLGMVQWEDRFYKANRAHTYLG N PENESIYPDFVTIAGFN 480

Query: 610 IPAARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLP MIPNGGTFNDVITEGDGRIK 669
+PA RVTKK+++ AI+ ML+TPGPYLLD+I PHQEHVLP MIP+GG F D+I EGDGR
Sbjct: 481 VPAVRVTKKSEVSAAIKMLETGPYLLDIIVPHQEHVLP MIPSGGAFKDMIMEGDGRS 540

Query: 670 Y 670
Y
Sbjct: 541 Y 541

>sp|Q7XKQ8|ILV2_ORYSJ Probable acetolactate synthase 2, chloroplast precursor
(Acetohydroxy-acid synthase 2)
emb|CAE05539.2| OSJNBa0053B21.13 [Oryza sativa (japonica cultivar-group)]
gb|EAY93893.1| hypothetical protein OsI_015126 [Oryza sativa (indica
cultivar-group)]
Length = 663

Score = 872 bits (2252), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 418/584 (71%), Positives = 497/584 (85%), Gaps = 5/584 (0%)

Query: 92 APDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVF 151
AP RKGADI+VEALER GV VF YPGGASMEIHQALTRS IRN L RHEQG FAA
Sbjct: 80 APMGQRKGADIVVEALERCGVRDVFEYPPGGASMEIHQALTRSPVIRNHLRHEQGEAF 139

Query: 152 EGYARSSGKPGICIAITSGPGATNLVSLGLADALLDSVPLVAITGQVPRRMIGTDAFQETPI 211
GYARSSG+PG+C+ATSGPGATNLVS LADA LDSVPLVAITGQ PRRMIGTDAFQETPI
Sbjct: 140 SGYARSSGRPGVCVATSGPGATNLVSALADAHLDVPLVAITGQAPRRMIGTDAFQETPI 199

Query: 212 VEVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAM 271
VE TRSIKHNLYL++DV+DIPR+I EAFFLA++GRPGPVLVD+PKDIQQQ+A+P+W+ M
Sbjct: 200 VEFTRSIKHNLYLILDVDDIPRVINEAFASTGRPGPVLVDIPKDIQQQMAVPSWDAPM 259

Query: 272 KLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAST 331
+LPGA+SR+PKPP + L++++RL+ ++++PVLYVGGGC S EL RFVELTGIPV +T
Sbjct: 260 RLPGYISRLPKPPAANLLDEVIRLVGDAERPVLVYVGGGCSASGYELRRFVELTGIPVTTT 319

Query: 332 LMGLGSYPDCDELHMLGMHGT VYANYAVEHSDLLLA FGVRFD DVRTGKLEAFASRAKI 391
LMG+G++P DD LSL MLGMHGT VYANYAV+++DLLLA GVRFD DVRTGK+EAFASRAKI
Sbjct: 320 LMGIGNFSDPLSLRMLGMHGT VYANYAVDNADLLALGVRFD DVRTGKVEAFASRAKI 379

Query: 392 VHIDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENR---AEELKLD FGVWRNELNVQK 448
VH+DID +E+GKNK PHVS+C DVKLALQGMN +LE + A LDF WR+EL +K
Sbjct: 380 VHVDIDPSELGKNKQPHVSI CADVKLALQGMNAMLEEQSAAAARKNLDFS AWRSELEKKK 439

Query: 449 QKFLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSG 508
+FPL ++TFGE IPPQYAI+VLDE+T+G+AI++TGVGQHQMWA Q Y Y++PRQWLSS
Sbjct: 440 VEFPLGYRTFGEEIPPQYAIQVLDEVNTGEAIVATGVGQHQMWAQHYTYRRPRQWLSSA 499

Query: 509 GLGAMGFGLPAAIGASVANPDIAVVDIDGDGSFIMNVQELATIRVENLPVKVLLNNQHL 568
 GLGAMGFGLPAA GA+VANP A VVDIDGDGS +MN+QELA +RVE+LPVKV++LNNQHL
 Sbjct: 500 GLGAMGFGLPAAAGAAVANPGATVVDIDGDGSLLMNIQELAMVRVEDLPVKVMVLLNNQHL 559

Query: 569 GMVMQWEDRFYKANRAHTFLGDPAQE--DEIFPNMLLFAAACGIPAARVTTKADLREAIQ 626
 GMV+QWEDRFY ANRAHT+LG+PA E++P+ + A GIPAARVT+K ++R A++
 Sbjct: 560 GMVVQWEDRFYDANRAHTYLGNPAAANGGGEVYPDFVTIAGGFGIPAARVTRKGEVRAAVE 619

Query: 627 TMLTPGPYLLDVCIPHQEHVLMIPNGGTFNDVITEGDGRIKY 670
M+ PGPYLLDV+ PHQEHVLMIP+ G F D+I +GDGR Y
Sbjct: 620 EMMAAPGPYLLDVVPHQEHVLMIPNSGAFKDIIVDGDGRSSY 663

```
>emb|CAN73760.1| hypothetical protein [Vitis vinifera]
      Length = 586
```

Score = 858 bits (2217), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 398/580 (68%), Positives = 484/580 (83%), Gaps = 13/580 (2%)

Query: 95 QPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPREHQQGVFAAEGY 154
PRKG+DILVEALER+GV VF YPGGASMEIH+AL RSS IRNVLPREHQQG+FAA+GY
Sbjct: 3 NPRKGS DILVEALERE GVTHVFGYPGGASMEIHEALRSSMIRNVLPREHQQGIFAADGY 62

Query: 155 ARSSGKPGICIAATSGPGATNLVSLGADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEV 214
AR+SG+PG+C+ +SGPGATN++SG+ADA DS+P+VA TG VPR ++GTDAFQE P++++
Sbjct: 63 ARASGRPGVCLTSSGPGATNIISSIADANFDSIPIVAXTGXVPRGLMGTDAPFOEVLPLIDI 122

Query: 215 TRSITKHNYLVMDVEDIPRIIEEAFFLATSGRGPVLVDVPKDIQQQLAIPNWEQAMKLP 274
 TR ITK NYLV+DVEDIPR ++EAF LATSGRGPVL+D+P+DIQ++L +PNW + + LP
 Sbjct: 123 TRPITKFNYLVLDVEDIPRTVKEAFLLATSGRGPVLIDIPRDIQKELVVPNWNKPIMLP 182

Query: 275 GYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVASTLMG 334
 G SR+PK PE +HLE+IVRLIS SK+PV+Y GGGC+N S+EL RFV LTGIPVASTLMG
 Sbjct: 183 GNASRLPKLPEKAHLEEIVRLISVSKRPVYAGGGCMNCSEELRRFVLTGIPVASTLMG 242

Query: 335 LGSYPCDDELSDLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRVTKGLEAFASRAKIVHI 394
 LG + C D+LSLHMLGMHGT+ ANYAV+ SDLLLAFGVRFDDRVTKG+EAF A IVHI
 Sbjct: 243 LGIFACTDDLSDLHMLGMHGTIQANYAVDRSDLLLAFGVRFDDRVTKGVEAFARNATIVHI 302

Query: 395 DIDS AEIGKNKTPHVS VCGDVKLALQGMNKVLENRA-----EELKLDGFWWR 441
 DID AEIGKNK PH+S+C DVKLAL+G+N +LE A + + W
 Sbjct: 303 DIDPAEIGKNKKPHLSICTDVKLALLEGINTILEKNAAKOPTAENKRKGKTFKFNNDVNSAWI 362

Query: 442 NELNVQKQKFLPSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWWAAQFYNYKKP 501
E++ QK+K+P S+KTFGEAIPPQYAI++LDELTDG AII TGVGQHQMWWAAQ+Y +K P
Sbjct: 363 EEIDEQEKYPASYKTFGEAIPPQYAIQLLDELTDNGNAICTGVGQHQMWWAAQYYKHKNP 422

Query: 502 RQWLSSGGLGAMGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVL 561
R WLSS GLGAMGFLPAA+GA++A PDAIVVDIDGDSF+MN+QELATIRVENLPVK++
Sbjct: 423 RHWLSSSGGLGAMGFLPAAMGAALAKPDAIVVDIDGDSFMMNIQELATIRVENLPVKIM 482

Query: 562 LLNNQHLMVMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAACGIPAARVTKKADL 621
 LLNNQHLMGV Q+E + + H+++G+P+ + ++FP+ML+FA AC I AARVTKKA+L
 Sbjct: 483 LLNNQHLMVYQYQEYEGDGSLSHSYMGNPSNQAQVFPDMLMFAEACNITAARVTKKAEL 542

Query: 622 REAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
 REAI+ ML TPGPYLLDV+ PHQ VL +IP+GGTF D I
 Sbjct: 543 REAIEKMLKTGPYLLDVMVPHOAQVLQIPDGGTFKDAI 582

```
>emb|CA017032.1| unnamed protein product [Vitis vinifera]
      Length = 866
```

Score = 834 bits (2155), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 394/568 (69%), Positives = 475/568 (83%), Gaps = 12/568 (2%)

Query: 99 GADILVEALERQGVETVFAYPPGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSS 158
G+DILVEALER+GV VF YPPGASM IH+AL RSS IRNVLP RHEQGG+FAA+GYAR+S
Sbjct: 302 GSDILVEALERE GVTHVFGYPGGASMG IHEALRSSMIRNVLP RHEQGGIFAADGYARAS 361

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
G+PG+C+ +SGPGATN++SG+ADA DS+P+VAITGQVPR ++GTDAFQE P++++TR I
Sbjct: 362 GRPGVCLTSSGPGATNIISGIADANFDSIPIVAITGQVPRGLMGTDADFQEVPLIDITRPI 421

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TK NYLV+DVEDIPRI++EAF LATSGRPGPVL+D+P+DIQ++L +PNW + + LPG S
Sbjct: 422 TKFNYLVLDVEDIPRIVKEAFLLATSGRPGPVLIDIPRDIQKELVVPNNWKPIMLPGNAS 481

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSY 338
R+PK E +HLE+IVRLIS SK+PV+Y GGGC+N S+EL RFV LTGIPVASTLMGLG +
Sbjct: 482 RLPKLQKAHLEEIIVRLISVSKRPVVYAGGGCMNCSEELRRFVGLTGIPVASTLMGLGIF 541

Query: 339 PCDDDELSLHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTKLEAFASRAKIVHIDIDS 398
PC D LSLHMLGMHGT+ ANYAV+ SDLLLAFGVRFDDRVTKG+EAF A IVHIDID
Sbjct: 542 PCTDGLSLHMLGMHGTIQANYAVDRSDLLLAFGVRFDDRVTKVEAFARNATIVHIDIDP 601

Query: 399 AEIGKNKTPHVSVCADVGLALQGMNKVLENRA-----EELKLDGFWRNELNVQKQKFP 453
AEIGKNK PH+S+C DVKLAL+G+N +LE A E K G N+ P
Sbjct: 602 AEIGKNKKPHLSICTDVKLALLEGINTILEKNAKQPTAENKRGKGTGFND-----NPP 654

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAM 513
S++TFGEAIPPQYAI++LDELTDG AII TGVGQHQMWAAQ+Y +K PR WLSS GLGAM
Sbjct: 655 SYRTFGEAIPPQYAIQLDELTDGNAICTGVGQHQMWAAQYKHKNPRLWLSSSGGLGAM 714

Query: 514 GFGLPAAIGASVANPDAIVVDIDGDGSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQ 573
GFGLPAA+GA++A PDAIVVDIDGDGSF+MN+QELATIRVENLPVK++LLNNQHLGMV Q
Sbjct: 715 GFGLPAAAMGAALAKPDAIVVDIDGDGSFMMNIQELATIRVENLPVKIMLLNNQHLGMVYQ 774

Query: 574 WEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDTPG 633
+E + + H+++G+P+ + ++FP+ML+FA AC I AARVTKK +LREAI+ ML TPG
Sbjct: 775 FEYEYGDGDSLHSYMGNPSNQAVFPDMLMFAEACNITAARVTKKVELREAIKMLKTPG 834

Query: 634 PYLLDVICPHQEHVLPMPINGGTFNDVI 661
PYLLDV+ PHQ VL +IP+GGTF D I
Sbjct: 835 PYLLDVMVPHQAQVLQLIPDGGTFKDAI 862

>gb|AAB88296.1| acetolactate synthase [Volvox carteri]
Length = 681

Score = 832 bits (2150), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 399/597 (66%), Positives = 486/597 (81%), Gaps = 16/597 (2%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQG 146
++ RF +PRKGADILV+ LER+GV+ VFAYPPGGASMEIHQALTRS I NVL RHEQG
Sbjct: 88 WVDRFG-SEPRKGADILVQCLEREGVDNVFAYPPGGASMEIHQALTRSDRITNVLCRHEQG 146

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
+FAAEGYA++SG+ G+CIATSGPGATNLV+GLADA++DS+PLVAITGQVPRRMIGTDAF
Sbjct: 147 EIFAAEGYAKASGRVGVCIATSGPGATNLVTGLADAMMDSIPLVAITGQVPRRMIGTDAF 206

Query: 207 QETPIVEVTRITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTR+ITKHNYLV+D++D+PR+I+EAF+LA +GRPGPVLVDVPKDIQQQLA+P+
Sbjct: 207 QETPIVEVTRAITKHNYLVLDIKDLPRVIKEAFYLARTGRPGPVLVDVPKDIQQQLAVPD 266

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W+ M + GY+SR+P P E+S + ++R I + KPV+Y GGGCL++ DEL F TGI
Sbjct: 267 WDSPPMSITGYISRLPPPVEESQMIPVLRAIQSASKPVIYGGGCLDARDELREFAARTGI 326

Query: 327 PVASTLMGLGSYPCDDDELSLHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTKLEAFA 386
P+AST MGLG P +D L MLGMHGTV ANYAV+ +DLL+A GVRFDDRVTG+L+AFA
Sbjct: 327 PLASTFMGLGVPAEDPNHLQMLGMHGTVAANYAVDQADLLVALGVRFDDRVTRGLDAFA 386

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVCADVGLALQGMNKVLENRAEELKLDGFWRNELNV 446
SRA+IVH+DID+AEI KNKT HV VCGDVK AL+ +N++LE AE L F WR EL
Sbjct: 387 SRARIVHVDIDAAEISKNTAHVPVCGDVKQALRHLNRMLE--AEPLSDRFVAWRAELAA 444

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLS 506
++ +FPL + +AI PQYAI+VL E T G+ II+TGVGQHQMWAAQ+Y YK+PR+W+S
Sbjct: 445 KRAEFPLRYPQRDDAIVPQYAIQVLGEETKGEVIITGVGQHQMWAAQWYPYKEPRRWIS 504

Query: 507 SGGGLGAMGFGLPAAIGASVA-----NPDAIVVDIDGDSFIMNVQELATIRVENLPVKV 560
SGGLG+MGFGLPAA+GA+VA IVVDIDGDSF+MNVQELAT+ +E L VKV
Sbjct: 505 SGGLGSMGFGLPAAALGAFAVDGKQGREKRIVVDIDGDSFLMNVQELATVFIEKLDVKV 564

Query: 561 LLLNNQHLGMVMQWEDRFYKANRAHTFLGD-----PAQEDEFIPNMLLFAAACGIPAA 613
++LNNQHLGMV+QWEDRFYKANRAHT+LG E++I+PN + A + G+P+
Sbjct: 565 MILNNQHLGMVVQWEDRFYKANRAHTYLGKREAEWHATGDEEDIYPNFVGMARSFGVPSM 624

Query: 614 RVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGRIKY 670
RV +K DLR AI+TMLDTPGPYLL+V+ PH EHVLPMP G TF D+ITEGDG +KY
Sbjct: 625 RVIRKEDLRGAIRTMMLDTPGPYLLLEVMPVPHIEHVLPMPGGATFKDIITEGDGSVKY 681

>emb|CAO42659.1| unnamed protein product [Vitis vinifera]
Length = 616

Score = 829 bits (2141), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 390/575 (67%), Positives = 474/575 (82%), Gaps = 27/575 (4%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
F+SRFA DQPRKG+DILVEALER+GV VF YPGGASMEIH+AL RSS IRNVLPHEQG
Sbjct: 65 FVSRFAADQPRKGSILVEALEREVTHVFGYPGGASMEIHEALARSSMIRNVLPHEQG 124

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAF 206
G+FAA+GYAR+SG+PG+C+ +SGPGATN++SG+ADA DS+P+VAITGQVPR ++GTDAF
Sbjct: 125 GIFAADGYARASGRPGVCLTSSGPGATNIISGIADANFDSIPIVAITGQVPRGLMGTDFAF 184

Query: 207 QETPIVEVTRISITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLDVDPKDIQQQLAIPN 266
QE P+++++TR ITK NYLV+DVEDIPR ++EAF LATSGRPGPVLD+P+DIQ++L +PN
Sbjct: 185 QEVLIDITRPIITKFNLYLMDVEDIPRTVKEAFLATSGRPGPVLDIPRDIQKELVVPN 244

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSLDELGRFVELTGI 326
W + + LPG SR+PK PE +HLE+IVRLIS SK+PV+Y GGGC+N S+EL RFV LTGI
Sbjct: 245 WNKPIMLPGNASRLPKLPEKAHLEEVRLISVSKRPVYAGGGCMNCSEELRRFVGLTGI 304

Query: 327 PVASTLMGLGSGPCDDDESLHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRTVGKLEAFA 386
PVASTLMGLG +PC D+LSLHMLGMHGT+ ANYAV+ SDLLLAFGVRFDDRTVGK+E+FA
Sbjct: 305 PVASTLMGLGIFPCTDDSLHMLGMHGTIQANYAVDRSDLLLAFGVRFDDRTVGKVESFA 364

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVCQDVKLALQGMNVLENRAEELKLDGFGVWRNELNV 446
A IVHIDID AEIGKNK PH+S+C D A EN
Sbjct: 365 RNATIVHIDIDPAEIGKNKKPHLSICTDQPTA-----EN----- 398

Query: 447 QKQKFLPSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
K+ +++TFGEAIPPQYAI++LDELTDG +II TGVGQHQMWAQ+ +K PR WLS
Sbjct: 399 -KRKGKGTNYRTFGEAIPPQYAIQLDELTDGNSIICTGVGQHQMWAQYCKHKNPRHWLS 457

Query: 507 SGGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
S GLGAMGFGLPAA+GA++A PDAIVVDIDGDSF+MN+QELATIRVENLPVK++LNNQ
Sbjct: 458 SSGGLGAMGFGLPAAAMGAALAKPDAIVVDIDGDSFMMNIQELATIRVENLPVKIMLLNNQ 517

Query: 567 HLGVMVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQ 626
HLGMV Q+E + + H+++G+P+ + ++FP+ML+FA AC I AARVTKKA+LREAI+
Sbjct: 518 HLGVMVQYQYEGDGSLSHSGMGNPSNQAQVFPDMLMFAEACNITAARVTKKAELREAI 577

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVI 661
ML TPGP+LLDV+ PHQ VL +IP+GGTF D I
Sbjct: 578 KMLKTPGPFLLDVMVPHQAQVQLQLIPDGGTFKDAI 612

>emb|CAL58226.1| acetolactate synthase 1 (ISS) [Ostreococcus tauri]
Length = 679

Score = 829 bits (2141), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 396/590 (67%), Positives = 478/590 (81%), Gaps = 10/590 (1%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRS-SSIRNVLPHEQG 145
F SRFA D+PRKGADILVEALER+GV+ VFAYPGGASMEIHQ+LT+S + IRNVLPHEQG
Sbjct: 81 FQSRFADDEPRKGADILVEALEREVDVCFAYPGGASMEIHQSLTKSVTGIRNVLPHEQG 140

Query: 146 GGVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDA 205
G VFAAEGYA+S+GK G+CIATSGPGATNLV+GLADALLDSVP+VAITGQVPR MIGTDA
Sbjct: 141 GEVFAAEGYAKSTGKVGVCIATSGPGATNLVTGLADALLDSVPMVAITGQVPRPMIGTDA 200

Query: 206 FQETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIP 265
FQETPIVE+TR ITKHNLYLVM+VE+IPRI+ EAFFLA+SGRPGPVL+D+PKD+QQQLA+P
Sbjct: 201 FQETPIVEITRQITKHNLYLVMNVEEIPRIVREAFFLASSGRPGPVLIDIPKDVQQQLAVP 260

Query: 266 NWEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTG 325
WE + L GY+SR+P PP + ++Q+V LI +SKKP++Y GGGCL++S EL F TG
Sbjct: 261 YWEPKVS LHGYLSRLPGPPTNPQIQQVVDLIKSSKKPIVYAGGGCLDASKELVEFCRATG 320

Query: 326 IPVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVGTGKLEAF 385
IPV +TLMGLG++P D+LSL MLGMHG VYANYA++ +DLLAFGVRFDDRVGTGKL F
Sbjct: 321 IPVVTNTLMGLGTFPQSDDLSSLMLGMHGA VYANYAIDSADLLAFGVRFDDRVGTGKLEAF 380

Query: 386 ASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELN 445
A RA IVHIDID AE+GKNK P S+ ++K AL+ +NK++ A L DF WR E+
Sbjct: 381 AKRAAIVHIDIDPAELGKNKPFCSIFSNIKPALRSLNKLI ALDAANLP-DFS DWRAEIE 439

Query: 446 VQKQKFLPSF-KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQW 504
V++++FP K G+ I PQ AI++L +LT+GKAIISTGVGQHQMWAQ Y + +PR W
Sbjct: 440 VKRKEFFFPPIPKQQGDVIAPQAIE LLCKL TEGKAIISTGVGQHQMWAQHYKFDEPRNW 499

Query: 505 LSSGGLGAMGFLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLN 564
LSSGGLG+MGFGLPAAIGA A PD +V+DIDGDSF+MN+QELAT+ E LPVK +LN
Sbjct: 500 LSSGGLGSMGFLPAAIGAQAARPD ELVIDIDGDSFVMNIQELATLHAEELPVKCFILN 559

Query: 565 NQHLGMVMQWEDRFYKANRAHTFLGDP-----AQEDEFNMLLFAAACGIPAARVTK 617
NQ+LGMV+QWEDRFYKANR HT+LG P +E IFP+ + + +PA RVT+
Sbjct: 560 NQYLGMMVQWEDRFYKANRGHTYLGSPNDYQVSKEEAHIFPDFVTISNGFRVPAERVTR 619

Query: 618 KADLREAIQTMLDTPGPYLLDVICPHQEHVLP MIPNGGTFNDVITEGDGR 667
++L AI+ M++TPGPYLLDV+ PH EHVLP M+P GGTF D I GDGR
Sbjct: 620 MSELEGAIKRMIETPGPYLLDVMVPHVEHVLP M+VPGGGTFADTIVTGDGR 669

>gb|ABQ85870.1| acetolactate synthase [Lolium rigidum]
Length = 516

Score = 823 bits (2125), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 386/516 (74%), Positives = 449/516 (87%)

Query: 136 IRNVLP RHEQG GGVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQ 195
I N L RHEQG FAA GYAR+SG+ G+C+ATSGPGATNLVS LADALLDS+P+VAITGQ
Sbjct: 1 ITNHLFRHEQGEAFAASGYARASGRVGVCVATSGPGATNLVSALADALLDSIPMVAITGQ 60

Query: 196 VPRRMIGTDAFQETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVP 255
VPRRMIGTDAFQETPIVEVTRSITKHNLYLMDVEDIPR+I+EAFFLA+SGRPGPVLVD+P
Sbjct: 61 VPRRMIGTDAFQETPIVEVTRSITKHNLYLMDVEDIPRVIQEAFFLASSGRPGPVLVDIP 120

Query: 256 KDIQQQLAIPNWEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSD 315
KDIQQQ+A+P W+ M LPGA++R+PKPP LEQ++RL+ E+++P+LYVGGGC S +
Sbjct: 121 KDIQQQMAVPVWDAPMSLPGYIARLPKPPATELLEQVLRVGEARRPILYVGGGCSASGE 180

Query: 316 ELGRFVELTGIPVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD 375
EL RFVELTGIPV +TLMGLG++P DD LSL MLGMHGT VYANYAV+ +DLLAFGVRFD
Sbjct: 181 ELRRFVELTGIPVTTTLMGLGNFSSDDPLSLRMLGMHGT VYANYAVDKADLLAFGVRFD 240

Query: 376 DRVTGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKL 435
DRVTGK+EAFA SR+KIVHIDID AEIGKNK PHVS+C DVKLALQG+N +L
Sbjct: 241 DRVTGKIEAFASRSKIVHIDIDPAEIGKNKQPHVSICADV KLALQGLNALLTGTKAHKSF 300

Query: 436 DFGVWRNELNVQKQKFLPSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQF 495
DFG W EL QK++FPL +KTFGEAIPPQYAI+VLDEL T G+AI I+TGVGQHQMWAQ+
Sbjct: 301 DFGSWHEELEQQKREFPLGYKTFGEAIPPQYAIQVLD ELTKGEAIIATGVGQHQMWAQY 360

Query: 496 YNYKKPRQWLSSGGLGAMGFLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVEN 555
Y YK+PRQWLSS GLGAMGFLPAA GA+VANP VVDIDGDSF+MN+QELA IR+EN
Sbjct: 361 YTYKRPRQWLSSAGLGAMGFLPAAAGAAVANPGVTVVDIDGDSFLMNIQELALIRIEN 420

Query: 556 LPVKVLLNNQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARV 615
LPVKV++LNNQHLGMV+QWEDRFYKANRAHT+LG+P E EI+P+ + A +PA RV
Sbjct: 421 LPVKVMILNNQHLGMVVQWEDRFYKANRAHTYLGPNPENESIEYPDFVTIAKGFNPAVRV 480

Query: 616 TKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMI 651
TK++++R AI+ ML+TPGPYLLD+I PHQEHVLPMI
Sbjct: 481 TKRSEVRAAIKKMLETPGPYLLDIIVPHQEHVLPMI 516

>gb|AAB88292.1| acetolactate synthase [Chlamydomonas reinhardtii]
Length = 683

Score = 819 bits (2116), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 396/598 (66%), Positives = 484/598 (80%), Gaps = 17/598 (2%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPREHQQ 146
++ R+ +PRKGADILV+ALER+GV++VFAYPGGASMEIHQALTRS I NVL RHEQQ
Sbjct: 89 WVDRYG-SEPRKGADILVQALEREVDVSFAYPGGASMEIHQALTRSDRITNVLCRHEQQ 147

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
+FAAEGYA+++G+ G+CIATSGPGATNLV+GLADA++DS+PLVAITGQVPRRMIGTDAF
Sbjct: 148 EIFAAEGYAKAAGRVGVCIATSGPGATNLVTLGLADAMDSIPLVAITGQVPRRMIGTDAF 207

Query: 207 QETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTR+ITKHNLYL+D++D+PR+I+EAF+LA +GRPGPVLVDVPKDIQQQLA+P+
Sbjct: 208 QETPIVEVTRAITKHNLYLVDIKDLPRVIKEAFYLARTGRPGPVLVDVPKDIQQQLAVPD 267

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
WE M + GY+SR+P P E+S + ++R + + KPV+Y GGGCL++ EL F TGI
Sbjct: 268 WEAPMSITGYISRLPPPVEESQVLPVLRALQGAAPVIYYGGGCLDAQAELREFAAARTGI 327

Query: 327 PVASTLMGLGSGPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFA 386
P+AST MGLG P D L MLGMHGTV+ANYAV+ +DLL+A GVRFDRTGKLEAFA
Sbjct: 328 PLASTFMGLGVVPSTDPNHLQMLGMHGTVFANYAVDQADLLVALGVRFDRTGKLEAFA 387

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVCGDVKLALQGMNKVLENRAEELKLD-FGVWRNELN 445
+RA+IVHIDID+AEI KNKT HV VCGDVK AL +N++L AE L D + WR EL
Sbjct: 388 ARARIVHIDIDAAEISKNTAHVPVCGDVKQALSHLNRLLA--AEPLPADKWAGWRAELA 445

Query: 446 VQKQKFLPSFKTFGEAIPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWL 505
++ +FP+ + +AI PQ+AI+VL E T G+AIITGVGQHQMWAQ+Y YK+ R+W+
Sbjct: 446 AKRAEFPMRYPQRDDAIVPQHAIQVLGEETQGEAIIITGVGQHQMWAQWYPYKETRRWI 505

Query: 506 SSGGLGAMGFLPAAIGASVA-----NPDAIVVDIDGDGSFIMNVQELATIRVENLPVK 559
SSGGLG+MGFLPAA+GA+VA P VVDIDGDGSF+MNVQELATI +E L VK
Sbjct: 506 SSGGLGSMGFLPAAIGAFAFDGKNRPPKTVVDIDGDGSFLMNVQELATIFIEKLDVK 565

Query: 560 VLLNNQHLGMVMQWEDRFYKANRAHTFLGD-----PAQEDEFNMLLFAAACGIPA 612
V+LLNNQHLGMV+QWEDRFYKANRAHT+LG E++I+PN + A A G+P+
Sbjct: 566 VMLNNQHLGMVVQWEDRFYKANRAHTYLGKRESEWHATQDEEDIYPNFVNMAQAFGVPS 625

Query: 613 ARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMIIPNGGTFNDVITEGDGRIKY 670
RV K LR AI+TMLDTPGPYLL+V+ PH EHVLPMIIP G +F D+ITEGDG +KY
Sbjct: 626 RRIVIVKEQLRGAIRTMLDTPGPYLLVEMVPHIEHVLPMIIPGGASFKDIITEGDGTVKY 683

>gb|AAC03784.1| acetolactate synthase [Chlamydomonas reinhardtii]
Length = 683

Score = 818 bits (2114), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 396/598 (66%), Positives = 483/598 (80%), Gaps = 17/598 (2%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPREHQQ 146
++ R+ +PRKGADILV+ALER+GV++VFAYPGGASMEIHQALTRS I NVL RHEQQ
Sbjct: 89 WVDRYG-SEPRKGADILVQALEREVDVSFAYPGGASMEIHQALTRSDRITNVLCRHEQQ 147

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
+FAAEGYA+++G+ G+CIATSGPGATNLV+GLADA++DS+PLVAITGQVPRRMIGTDAF
Sbjct: 148 EIFAAEGYAKAAGRVGVCIATSGPGATNLVTLGLADAMDSIPLVAITGQVPRRMIGTDAF 207

Query: 207 QETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
QETPIVEVTR+ITKHNYLV+D++D+PR+I+EAF+LA +GRPGPVLVDVP DIQQQLA+P+

Sbjct: 208 QETPIVEVTRAITKHNYLVLDIKDLPRVIKEAFYLARTGRPGPVLVDVPTDIQQQLAVPD 267

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
WE M + GY+SR+P P E+S + +VR + + KPV+Y GGGCL++ EL F TGI

Sbjct: 268 WEAPMSITGYISRLPPVEESQVLPVVRALQGAAPVIYYGGGCLDAQAELREFAARTGI 327

Query: 327 PVASTLMGLGSPCDDELHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTGKLEAFA 386
P+AST MGLG P D L MLGMHGT V+ANYAV+ +DLL+A GVRFD DRTGKL+AFA

Sbjct: 328 PLASTFMGLGVVPSTDPNHLQMLGMHGT V FANYAVDQADLLVALGVRFD DRTGKLDAFA 387

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD-FGVWRNELN 445
+RA+IVHIDID+AEI KNKT HV VCGDVK AL +N++L AE L D + WR EL

Sbjct: 388 ARARIVHIDIDAAEISKNTAHVPVCGDVKQALSHLNRLLA--AEPLPADKWAGWRAELA 445

Query: 446 VQKQKFLPSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWL 505
++ +FP+ + +AI PQ+AI+VL E T G+AI+TGVGQHQMWAQ+Y YK+ R+W+

Sbjct: 446 AKRAEFPMPYRQDDAIVPQHAIQVLGEETQGEAIITGVGQHQMWAQWYPYKETRRWI 505

Query: 506 SSGGLGAMGFLPAAIGASVA-----NPDAIVVDIDGGSFIMNVQELATIRVENLPVK 559
SSGGLG+MGFLPAA+GA+VA P VVDIDGGSF+MNVQELATI +E L VK

Sbjct: 506 SSGGLGSMGFLPAAALGA AVAFDGNRPPKTVVDIDGGSFLMNVQELATIFIEKLDVK 565

Query: 560 VLLNNQHLGMVMQWEDRFYKANRAHTFLGD-----PAQEDEFNMLLFAAACGIPA 612
V+LLNNQHLGMV+QWEDRFYKANRAHT+LG E++I+PN + A A G+P+

Sbjct: 566 VMLNNQHLGMVVQWEDRFYKANRAHTYLGKRESEWHATQDEEDIYPNFVNMAQAFGVPS 625

Query: 613 ARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
RV K LR AI+TMLDTPGPYLL+V+ PH EHVLPMP G +F D+ITEGDG +KY

Sbjct: 626 RRVIVKEQLRGAIRTMLDTPGPYLLVEMVPHIEHVLPMPGGASFKDIIITEGDGTVKY 683

>gb|ABQ85869.1| acetolactate synthase [Lolium rigidum]
Length = 516

Score = 818 bits (2114), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 385/516 (74%), Positives = 448/516 (86%)

Query: 136 IRNVLPREHQQGVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQ 195
I N L RHEQG FAA GYAR+SG+ G+C+ATSGPGATNLVS LADALLDS+P+VAITGQ

Sbjct: 1 ITNHLFRHEQGEAFAASGYARASGRVGVCVATSGPGATNLVSALADALLDSIPMVAITGQ 60

Query: 196 VPRRMIGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVP 255
VPRRMIGTDAFQETPIVEVTRSITKHNYLV+DVEDIPR+I+EAFFLA+SGRPGPVLVD+P

Sbjct: 61 VPRRMIGTDAFQETPIVEVTRSITKHNYLVLDVEDIPRVIQEAFFLASSGRPGPVLVDIP 120

Query: 256 KDIQQQLAIPNWEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSD 315
KDIQQQ+A+P W+ M LPGA++R+PKPP LEQ++RL+ E+++P+LYVGGG S +

Sbjct: 121 KDIQQQMAVPVWDAPMSLPGYIARLPKPPATELLEQVLRVGEARRPILYVGGGCSASGE 180

Query: 316 ELGRFVELTGIPVASTLMGLGSPCDDELHMLGMHGT VYANYAVEHSDLLAFGVRFD 375
EL RFVELTGIPV +TLMGLG++P DD LSL MLGMHGT VYANYAV+ +DLLAFGVRFD

Sbjct: 181 ELRRFVELTGIPVTTTLMGLGNFSPDDPLSLRMLGMHGT VYANYAVDKADLLAFGVRFD 240

Query: 376 DRVTGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKL 435
DRVTGK+EAFASR+KIVHIDID AEIGKNK PHVS+C DVKLALQG+N +L

Sbjct: 241 DRVTGKIEAFASRSKIVHIDIDPAEIGKNKQPHVSICADVKLALQGLNALLTGTHAKHSF 300

Query: 436 DFGVWRNELNVQKQKFLPSFKTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQF 495
DFG W EL QK++FPL +KTFGEAIPPQYAI+VLDELTD G+AI+TGVGQHQMWAQ+

Sbjct: 301 DFGSWHEELEQKREFPLGYKTFGEAIPPQYAIQVDELTDKGEAIATGVGQHQMWAQY 360

Query: 496 YNYKKPRQWLSSGGLGAMGFLPAAIGASVANPDAIVVDIDGGSFIMNVQELATIRVEN 555
Y YK+PRQWLSS GLGAMGFLPAA GA+VANP VVDIDGGSF+MN+QELA IR+EN

Sbjct: 361 YTYKPRQWLSSAGLGAMGFLPAAAGAAVANPGVTVDIDGGSFLMNIQELALIRIEN 420

Query: 556 LPVKVLLNNQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARV 615
LPVKV++LNNQHLGMV+Q EDRFYKANRAHT+LG+P E EI+P+ + A +PA RV

Sbjct: 421 LPVKVMILNNQHLGMVVQLEDRFYKANRAHTYLGPNENESEIYPDFVTIAKGFNVPVRV 480

Query: 616 TKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMP 651
TK++++R AI+ ML+TPGPYLLD+I PHQEHVLPMP
Sbjct: 481 TKRSEVRAAIKKMLETPGPYLLDIIVPHQEHVLPMP 516

>gb|AAC04854.1| acetolactate synthase [Volvox carterii]
Length = 681

Score = 812 bits (2097), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 388/597 (64%), Positives = 480/597 (80%), Gaps = 16/597 (2%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
++ RF +PRKGADIL++ LER+GV+ VFAYPGGASMEIHQALTRS I NVL RHEQG
Sbjct: 88 WVDRFG-SEPRKGADILIQCLEREGVDNVFAYPGGASMEIHQALTRSDRITNVLCRHEQG 146

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
+F+AEGYA++SG+ G+CIATSGPGATNLV+ L DA++DS+ L+AITGQVPRRMIGTDAF
Sbjct: 147 EIFSAEGYAKASGRVGVCIATSGPGATNLVTRLDDAMMDSITLIAITGQVPRRMIGTDAF 206

Query: 207 QETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPN 266
QETPIVEVTR+ITKHNLYLVD++D+PR+I+EAF+LA +GRPGPVLVDVDPKDIQQQLA+P+
Sbjct: 207 QETPIVEVTRAITKHNLYLVDIKDLPRVIKEAFYLARTGRPGPVLVDVDPKDIQQQLAVPD 266

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
W+ M + GY+SR+P P E+ + ++R I + KP++Y GGGCL++ +EL F TGI
Sbjct: 267 WDSPPSITGYISRLPPPVEEYKMIPVLRAIQSATKPIIYGGGCLDARNELREFAAARTGI 326

Query: 327 PVASTLMGLGSPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRTVGKLEAFA 386
P+AS MGLG P +D L MLGMHGT V ANYAV+ +DLL+A GVRFDDRTVG+L+AFA
Sbjct: 327 PLASKFMGLGVVPAEDPNHLQMLGMHGTVAANYAVDQADLLVALGVRFDDRTVGRLD AFA 386

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNV 446
SRA+IVH+DID+AEI KNKT HV VCGDVK AL+ +N++LE AE L F WR EL
Sbjct: 387 SRARIVHVDIDAAEISKNKTAHVPCGDVKQALRHLNRMLE--AEPLSDRFVAWRAELAA 444

Query: 447 QKQKFPLSFKTFGEAIPPQYAIKVDELDTGKAIISTGVGQHQMWAQQFYNYKKPRQWLS 506
++ +FPL + +AI PQYAI+VL E T G+ II+TGVGQHQMWAQQ+Y YK+PR+W+S
Sbjct: 445 KRAEFPLRYPQRDDAIVPQYAIQVLGEETKGEVIITGVGQHQMWAQQWYPYKEPRRWIS 504

Query: 507 SGGLGAMGFGLPAAIGASVA-----NPDAIVVDIDGDSFIMNVQELATIRVENLPVKV 560
SGGLG+MGFGLPAA+GA+VA IVVDIDGDSF+MNVQELAT+ +E L VKV
Sbjct: 505 SGGLGSMGFGLPAAALGA AVADGKQGREKRI VVDIDGDSFIMNVQELATVFIEKLDVKV 564

Query: 561 LLLNNQHLGMVMQWEDRFYKANRAHTFLGD-----PAQEDEFIPNMLLFAAACGIPAA 613
++LNNQHLGMV+QWEDRFYKANRAHT+LG E++I+PN + A + G+P+
Sbjct: 565 MILNNQHLGMVVQWEDRFYKANRAHTYLGKREAEWHATGDEEDIYPNFVGMARSFVGPSM 624

Query: 614 RVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
RV +K DLR A +TMLDTPGPYLL+V+ PH EHVLPMP G TF D+ITEGDG +KY
Sbjct: 625 RVIRKEDLRGANRTMLDTPGPYLLVMVPHIEHVLPMPGGATFKDIITEGDGSKY 681

>ref|XP_001421626.1| predicted protein [Ostreococcus lucimarinus CCE9901]
gb|ABO99919.1| predicted protein [Ostreococcus lucimarinus CCE9901]
Length = 610

Score = 801 bits (2068), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 390/590 (66%), Positives = 475/590 (80%), Gaps = 11/590 (1%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSS-IRNVLP RHEQ 145
F SRFA D+PRKG+DILVEALER+GV+ VFAYPGGASMEIHQ+LT+S++ IRNVL RHEQ
Sbjct: 13 FASRFADDEPRKGS DILVEALEREVDVCFAYPGGASMEIHQSLTKSATGIRNVLCRHEQ 72

Query: 146 GGVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDA 205
G VFAAEGYA+++GK G+CIATSGPGATNLV+GLADALLDSVP+VAITGQVPR MIGTDA
Sbjct: 73 GEVFAAEGYAKATGKVGVC IATSGPGATNLVTGLADALLDSVPMVAITGQVPRRMIGTDA 132

Query: 206 FQETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIP 265
FQETPIVE+TR ITKHNLYLVM+VE+IPRI+ EAFFLA SGRPGPVL+D+PKD+QQQLA+P
Sbjct: 133 FQETPIVEITRQITKHNLYLVMNVEEIPRIVREAFFLAASGRPGPVLIDIPKDVQQQLAVP 192

Query: 266 NWEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTG 325
WE + L GY+SR+P PP L+Q++ LI +SK+PV+Y GGGCL++ EL F TG
Sbjct: 193 YWEPKVSINGYLSRLPAPPTSPQLQQVLDLIKDSKRPVYAGGGCLDADLELVEFCRATG 252

Query: 326 IPVASTLMGLGSYPCDELHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKLEAF 385
IPV +TLMGLG++P D+LSL MLGMHG VYANYA++ +DLLAFGVRFDDRVTGKL F
Sbjct: 253 IPVTNTLMGLGTFPQSDDLSLMLGMHGAUYANYAIDSADLLAFGVRFDDRVTGKLAEF 312

Query: 386 ASRAKIVHIDIDSAEIGKNKTPHVSVCADVCLALQGMNKVLENRAEELKLDGFGVWRNENL 445
A RA IVHIDID AE+GKNK P S+ ++K AL+ +NK++ E+ DF WR ++
Sbjct: 313 AKRAAIVHIDIDPAELGKNKKPFCISFNSNIKPAK'TLNKLI--LEKDMPDFSEWRAAID 370

Query: 446 VQKQKFLPSF-KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQAQFYNYKKPRQW 504
VQ++KFP + G+ I PQ AI++L ++T+GKAIISTGVGQHQMWAQAQ Y + +PR W
Sbjct: 371 VQRKKFFPPIPEQVGDVIAPQAAIELLCKMTEGKAIISTGVGQHQMWAQAQHYKFDPRNW 430

Query: 505 LSSGGLGAMGFLPAAIGASVANPDIAVVDIDGDSFIMNVQELATIRVENLPVKVLLLN 564
L+SGGLG+MGFGLPAAIGA+ A P +VVDIDGDSF+MN+QELAT+ ENLPVK +LN
Sbjct: 431 LTSGGLGSMGFLPAAIGAAAARPGDLVVDIDGDSFVMNIQELATLHAENLPVKCFILN 490

Query: 565 NQHLGMVMQWEDRFYKANRAHTFLGDP-----AQEDEFNMLLFAAACGIPAARVTK 617
NQ+LGMV+QWEDRFYKANR HT+LG P +E IFP+ + + +PA RV +
Sbjct: 491 NQYLGMMVQWEDRFYKANRGHTYLGSPNDDFQVSKEEAHIFPDFVTISQGRFVPAERVMR 550

Query: 618 KADLREAIQTMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVITEGDGR 667
+DL AI+ M++ GPYLLDV+ PH EHVLPMP+P GGTF D IT GDGR
Sbjct: 551 MSDLEGAIKRMIEADGPYLLDVMVPHVEHVLPMPVGGGTFADTITITGDGR 600

>dbj|BAE53595.1| acetolactate synthase [Monochoria vaginalis]
Length = 566

Score = 792 bits (2046), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 382/563 (67%), Positives = 448/563 (79%)

Query: 105 EALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFABEGYARSSSGKPGIC 164
EALER+GV +FAYPGGASMEIHQALTRS SI N L RHE GYARS+G+PG+C
Sbjct: 1 EALEREQVTDLFAYPGGASMEIHQALTRSPSITNHLRHEXXXXXXXXXXGYARSTGRPGVC 60

Query: 165 IATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYL 224
IATSGPGATNLVS VAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYL
Sbjct: 61 IATSGPGATNLVXXXXXXXXXXXXVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYL 120

Query: 225 VMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMSRMPKPP 284
V+DV+DIPRII+EAFF+ATSGRPGPVLVD+PKDIQQQLA+P W ++LPGY+SR+PKPP
Sbjct: 121 VLDVDDIPRIIEEAFFIATSGRPGPVLVDIPKDIQQQLAVPVWNNPPVRLPGYVSRPKPP 180

Query: 285 EDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSYPCDEL 344
L+QIVR++SES +PVLYVGGG L++S+EL RF +LTGIP+ASTLMG+G YP D L
Sbjct: 181 ALHLLQIVRIVSESSRPVLYVGGGSLHASEELRRFADLTGIPIASTLMGIGVYPLDGPL 240

Query: 345 SLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSAEIGKN 404
SL MLGMHGTVYANYA++ +DLLAFGVRFDDRVTGKLEAFASRAKIVHIDID AEIGKN
Sbjct: 241 SLKMLGMHGTVYANYAIDKADLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDPAEIGKN 300

Query: 405 KTPHVSVCADVCLALQGMNKVLENRAEELKLDGFGVWRNENLVQKQKFLPSFKTFGEAIPP 464
K PHVS+CGD+KLALQ MN+++E KLD
Sbjct: 301 KQPHVSI CGDIKLALQEMNEMIEESGIHNKLDXXXXXXXXXXXXXXXXXXXXXXXXXXXX 360

Query: 465 QYAIKVLDELTDGKAIISTGVGQHQMWAQAQFYNYKKPRQWLSSGGLGAMGFLPAAIGAS 524
+G+AII+TGVGQHQMWAQAQ+Y+YK+PRQWL+S GLGAMGFLPAA+GA+
Sbjct: 361 XXXXXXXXXXXXNGEAIITTGVGQHQMWAQAQYYSYKRPRQWLTSAGLGAMGFLPAAVGAA 420

Query: 525 VANPDIAVVDIDGDSFIMNVQELATIRVENLPVKVLLLNQHLGMVMQWEDRFYKANRA 584
V NP +VVDIDGDSF MN QELA IR+ENL VK+L+LNNQHLGMV+QWEDRFYK+NRA
Sbjct: 421 VGNPGVMVVDIDGDSFQMNAQELAIIRIENLDVKMLILNNQHLGMVVQWEDRFYKSNRA 480

Query: 585 HTFLGDPAQEDEFNMLLFAAACGIPAARVTKADLREAIQTMLDTPGPYLLDVICPHQ 644
HT+LG+PA E ++FP+ + A + IPAARV+KK+++R+AI+ M+ TPGPYL DVI PH+
Sbjct: 481 HTYLGPNANESKVFDPFVKLAESYDIPAARVSKKSEVRDAIKMKIQTGPYLLWDVIVPHE 540

Query: 645 EHVLPMPNGGTFNDVITEGDGR 667
EHVLPMP+GG F D+I +GDGR
Sbjct: 541 EHVLPMPSSGAFKDMILDGDGR 563

>emb|CAC86697.1| putative acetolactate synthase [Raphanus raphanistrum]
Length = 409

Score = 788 bits (2036), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 375/409 (91%), Positives = 391/409 (95%)

Query: 262 LAIPNWEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFV 321
LAIP W+Q M+LPGYMSR+P+PP S L QIVRLISESK+PVLYVGGG LNSS+ELGRFV
Sbjct: 1 LAIPXWDQPMRLPGYMSRLPQPPXVSLRQIVRLISESKRPVLYVGGGSLNSSEELGRFV 60

Query: 322 ELTGIPVASTLMGLGSYPCCDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRTGK 381
ELTGIPVASTLMGLGSYPC+DELSL MLGMHGTVYANYAVEHSDLLAFGVRFDDRTGK
Sbjct: 61 ELTGIPVASTLMGLGSYPCNDELSLQMLGMHGTVYANYAVEHSDLLAFGVRFDDRTGK 120

Query: 382 LEAFASRAKIVHIDIDSAEIGKNKTPHVSVCQDVKLALQGMNKVLENRAEELKLDGFWVR 441
LEAFASRAKIVHIDIDSAEIGKNKTPHVSVCQDVKLALQGMNK+LENRAEELKLDGFWVR
Sbjct: 121 LEAFASRAKIVHIDIDSAEIGKNKTPHVSVCQDVKLALQGMNKILENRAEELKLDGFWVR 180

Query: 442 NELNVQKQKFPPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKP 501
+EL QKQKFPPLSFKTFGEAIPPQYAI+VLDELTDGKAIISTGVGQHQMWAQFY Y+KP
Sbjct: 181 SELKEQKQKFPPLSFKTFGEAIPPQYAIQVLDELTDGKAIISTGVGQHQMWAQFYKVRKP 240

Query: 502 RQWLSSSGLGAMGFGLPAAIGASVANPDIAVVDIDGDSFIMNVQELATIRVENLPVKVL 561
RQWLSS GLGAMGFGLPAAIGASVANPDIAVVDIDGDSFIMNVQELATIRVENLPVK+L
Sbjct: 241 RQWLSSSGLGAMGFGLPAAIGASVANPDIAVVDIDGDSFIMNVQELATIRVENLPVKIL 300

Query: 562 LLNNQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLFAACGIPAARVTKKADL 621
LLNNQHLGMVMQWEDRFYKANRAHT+LGDPA+E EIFPNML FA ACGIPAARVTKK +L
Sbjct: 301 LLNNQHLGMVMQWEDRFYKANRAHTYLGDPARESEIFPNMLQFAGACGIPAARVTKKEEL 360

Query: 622 REAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRKY 670
REAIQTMLDTPGPYLLDVICPHQEHVLPMP+GGTF DVITEGDGR KY
Sbjct: 361 REAIQTMLDTPGPYLLDVICPHQEHVLPMPSSGTFKDVITEGDGRKY 409

>gb|EAZ30535.1| hypothetical protein OsJ_014018 [Oryza sativa (japonica
cultivar-group)]
Length = 610

Score = 758 bits (1956), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 370/584 (63%), Positives = 445/584 (76%), Gaps = 58/584 (9%)

Query: 92 APDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVF 151
AP RKGADI+VEALER GV G FAA
Sbjct: 80 APMGQRKGADIVVEALERCGVR-----DGEAF 108

Query: 152 EGYARSSGKPGICATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPI 211
GYARSSG+PG+C+ATSGPGATNLVS LADA LDSVPLVAITGQ PRRMIGTDAFQETPI
Sbjct: 109 SGYARSSGRPGVCVATSGPGATNLVSALADAHLDVPLVAITGQAPRRMIGTDAFQETPI 168

Query: 212 VEVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAM 271
VE TRSITKHNLYL++DV+DIPR+I EAFFLA++GRPGPVLVD+PKDIQQQ+A+P+W+ M
Sbjct: 169 VEFTRSIKHNLYLILDVDDIPRVINEAFLASTGRPGPVLVDIPKDIQQQMAVPSWDAPM 228

Query: 272 KLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAST 331
+LPGY+SR+PKPP + L++++RL+ +++++PVLYVGGGC S EL RFVELTGIPV +T
Sbjct: 229 RLPGYISRLPKPPAANLLDEVIRLVGDAERPVLVYVGGGCSASGYELRRFVELTGIPVTTT 288

Query: 332 LMGLGSYPCCDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRTGKLEAFASRAKI 391
LMG+G++P DD LSL MLGMHGTVYANYAV+++DLLA GVRFDDRTGK+EAFASRAKI
Sbjct: 289 LMGIGNFSPDDPLSLRMLGMHGTVYANYAVDNADLLALGVRFDDRTGKVEAFASRAKI 348

Query: 392 VHIDIDSAEIGKNKTPHVSVCQDVKLALQGMNKVLENR---AEELKLDGFWVRNELNVQK 448
VH+DID +E+GKNK PHVS+C DVKLALQGMN +LE + A LDF WR+EL +K
Sbjct: 349 VHVDIDPSELGKNKQPHVSICADVKLALQGMNAMLEEQSAAAARKNLDFSARWSELEKKK 408

Query: 449 QKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSG 508
+FPL ++TFGE IPPQYAI+VLDE+T+G AI++TGVGQHQMWA Q Y Y++PRQWLSS
Sbjct: 409 VEFPLGYRTFGEEIPPQYAIQVLDEVINGVAIVATGVGQHQMWATQHYTYRRPRQWLSSA 468

Query: 509 GLGAMGFGLPAAIGASVANPDAIVVDIDGDGGSFIMNVQELATIRVENLPVKVLLNNQHL 568
GLGAMGFGL ELA +RVE+LPVKV++LNNQHL
Sbjct: 469 GLGAMGFGL-----PAAAGAAELAMVRVEDLPVKVMVLNNQHL 506

Query: 569 GMVMQWEDRFYKANRAHTFLGDPAQE--DEIFPNMLLFAAACGIPAARVTKADLREAIQ 626
GMV+QWEDRFY ANRAHT+LG+PA E++P+ + A GIPAARVT+K ++R A++
Sbjct: 507 GMVVQWEDRFYDANRAHTYLGNPAANGGGEVYPDFVTIAGGFGIPAARVTRKGEVRAAVE 566

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPINGGTENDVITEGDGRIKY 670
M+ PGPYLLDV+ PHQEHVLPMP+ G F D+I +GDGR Y
Sbjct: 567 EMMAAPGPYLLDVVVPQEHVLPMPISNGAFKDIIVDGDGRSSY 610

>gb|EAZ30530.1| hypothetical protein OsJ_014013 [Oryza sativa (japonica
cultivar-group)]
Length = 620

Score = 726 bits (1874), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 363/580 (62%), Positives = 444/580 (76%), Gaps = 45/580 (7%)

Query: 90 RFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVF 149
R+ P + RKGADILVEAL R GV VF YPG R G
Sbjct: 82 RWGPTERRKGADILVEALGRCGVRDVFYYPG-----RRVDGDP 120

Query: 150 AAEGYARSSGKPGICIAITSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQET 209
A+ A P + P A + G+ +VPRRMIGTDAFQET
Sbjct: 121 GADAVAGHPQPP-----APPRAGGGLRGV-----RVPRRMIGTDAFQET 159

Query: 210 PIVEVTRSITKHNYLVMDEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQ 269
PIVE+TRSITKHNYLV+DV+DIPR+I EAAFFLAT+GRPGPVLVD+PKDIQQQ+A+P+W+
Sbjct: 160 PIVELTRSITKHNYLVLDVDDIPRVINEAFLATTGRPGPVLVDIPKDIQQQMAVPSWDA 219

Query: 270 AMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVA 329
M+LPGY+SR+PKPP + L++++RL+ +++PVLYVGGGC S DEL RFVELTGIPV
Sbjct: 220 PMRLPGYISRLPKPPSANLLDEVIRLVGDAERPVLVYVGGGCSASGDELRRFVELTGIPVT 279

Query: 330 STLMLGLSGYPCDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRA 389
+TLMG+G+++P DD LSL MLGMHGTVYANYAV+++DLLLA GVRFDDRVTGK+EAFAFASRA
Sbjct: 280 TTLMGIGNFSDPLSLRMLGMHGTVYANYAVDNADLLALGVRFDDRVTGKVEAFASRA 339

Query: 390 KIVHIDIDSAEIGKNKTPHVSVCADVKLALQGMNKVLENRAEELKLDGFWVRNENLVQKQ 449
KIVH+DID +E+GKNK PHVS+C DVKLALQGMN LE + + LDF WR+EL +K
Sbjct: 340 KIVHVIDIDPSELGKNKQPHVSICADVKLALQGMNATLEQQQRK-NLDFSARWSELEKKKA 398

Query: 450 KFLPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSG 509
+FPL ++TFGE IPPQYAI+VLDE+T+G+AI++TGVGQHQMWA Q Y +++PRQWLSS G
Sbjct: 399 EFPLGYRTFGEEIPPQYAIQVLDEVINGEIVATGVGQHQMWATQHYTFRRPRQWLSSAG 458

Query: 510 LGAMGFGLPAAIGASVANPDAIVVDIDGDGGSFIMNVQELATIRVENLPVKVLLNNQHLG 569
LGAMGFGLPAA GA+VANP A VVDIDGDGS +MN+QELA +RVENLPVKV++LNNQHLG
Sbjct: 459 LGAMGFGLPAAAGAAVANPGATVVDIDGDGSLMNIQELAMVRVENLPVKVMVLNNQHLG 518

Query: 570 MVMQWEDRFYKANRAHTFLGDPAQE--DEIFPNMLLFAAACGIPAARVTKADLREAIQT 627
MV+QWEDRFY ANRAHT+LG+PA E++P+ + A GIPAARVT+K ++R A++
Sbjct: 519 MVVQWEDRFYDANRAHTYLGNPAANGGGEVYPDFVAIAGGFGIPAARVTRKGEVRAAVEE 578

Query: 628 MLDTPGPYLLDVICPHQEHVLPMPINGGTENDVITEGDGR 667
M+ PGPYLLDV+ PHQEHV PMIP+ G F D+I +G GR
Sbjct: 579 MMAAPGPYLLDVVVPQEHVPMIPISNGAFKDIIVDGGGR 618

>gb|AAT72502.1| AT3G48560 [Arabidopsis lyrata subsp. lyrata]
Length = 344

Score = 706 bits (1821), Expect = 0.0, Method: Compositional matrix adjust.

Identities = 341/344 (99%), Positives = 344/344 (100%)

```
Query: 152 EGYARSSGKPGICIAITSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPI 211
          EGYARSSGKPGICIAITSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPI
Sbjct: 1   EGYARSSGKPGICIAITSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPI 60

Query: 212 VEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQAM 271
          VEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQAM
Sbjct: 61  VEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQAM 120

Query: 272 KLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAST 331
          +LPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAST
Sbjct: 121 RLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVAST 180

Query: 332 LMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDVRTGKLEAFASRAKI 391
          LMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDVRTGKLEAFASRAKI
Sbjct: 181 LMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDVRTGKLEAFASRAKI 240

Query: 392 VHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKF 451
          VHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKF
Sbjct: 241 VHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKF 300

Query: 452 PLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQF 495
          PLSFKTFGEAIPPQYAI++LDELTDGKAIISTGVGQHQMWAQF
Sbjct: 301 PLSFKTFGEAIPPQYAIQLDELTDGKAIISTGVGQHQMWAQF 344
```

>emb|CAP09635.1| acetolactate-synthase-N-DnaE intein-N fusion protein
[Transformation Vector pICH13688]
Length = 558

Score = 701 bits (1808), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 344/355 (96%), Positives = 346/355 (97%), Gaps = 2/355 (0%)

```
Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
          FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG
Sbjct: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146

Query: 147 GVFAAEGYARSSGKPGICIAITSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
          GVFAAEGYARSSGKPGICIAITSGPGATNLVSLADALLDSVPLVAITGQV RRMIGTDAF
Sbjct: 147 GVFAAEGYARSSGKPGICIAITSGPGATNLVSLADALLDSVPLVAITGQVSRRMIGTDAF 206

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPN 266
          QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPN
Sbjct: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPN 266

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326
          WEQAM+LPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI
Sbjct: 267 WEQAMRLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI 326

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDVRTGKLEAFA 386
          PVASTLMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDVRTGKLEAFA
Sbjct: 327 PVASTLMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDVRTGKLEAFA 386

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLEN--RAEELKLD FGV 439
          SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLEN + E L FG
Sbjct: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENDVKFAEYCLSFSGT 441
```

>ref|XP_001695168.1| acetolactate synthase, large subunit [Chlamydomonas reinhardtii]
gb|EDP01876.1| acetolactate synthase, large subunit [Chlamydomonas reinhardtii]
Length = 640

Score = 701 bits (1808), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 355/598 (59%), Positives = 434/598 (72%), Gaps = 60/598 (10%)

```
Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQG 146
          ++ R+ +PRKGADILV+ALER+GV++VFAYPGGASMEIHQALTRS I NVL RHEQG
Sbjct: 89 WVDTRYG-SEPRKGADILVQALEREGVDSVFAYPGGASMEIHQALTRSDRITNVLCRHEQG 147
```

```

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
      +FAAEGYA+++G+ G+CIATSGPGATNLV+GLADA++DS+PLVAITGQVPRRMIGTDAF
Sbjct: 148 EIFAAEGYAKAAGRVGVCIAATSGPGATNLVTGLADAMMDSIPLVAITGQVPRRMIGTDAF 207

Query: 207 QETPIVEVTRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPN 266
      QETPI PR ++ T P
Sbjct: 208 QETPI-----PRTSSSSWRCRTGSAP----- 228

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCLNSSDELGRFVELTGI 326
      M + GY+SR+P P E+S + ++R + + KP+Y GGGCL++ EL F TGI
Sbjct: 229 ----MSITGYISRLPPPVEESQVLPVLRALQGAAPVIYGGGCLDAQAELREFAARTGI 284

Query: 327 PVASTLMGLSGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFA 386
      P+AST MGLG P D L MLGMHGTV+ANYAV+ +DLL+A GVRFDDRVTKL+AFA
Sbjct: 285 PLASTFMGLGVVPSTDPNHLQMLGMHGTVFANYAVDQADLLVALGVRFDDRVTKLDafa 344

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVCADVKLALQGMNKVLENRAEELKLD-FGVWRNELN 445
      +RA+IVHIDID+AEI KNKT HV VCGDVK AL +N++L AE L D + WR EL
Sbjct: 345 ARARIVHIDIDAAEISKNTAHVPVCGDVKQALSHLNRLLA--AEPLPADKWAGWRAELA 402

Query: 446 VQKQKFLPSFKTFGEAIPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWL 505
      ++ +F+P + +AI PQ+AI+VL E T G+AII+TGVGQHQMWAQ+Y YK+ R+W+
Sbjct: 403 AKRAEFPMRYPQRDDAIVPQHAIQVLGEETQGEAIIITGVGQHQMWAQWYPYKETRRWI 462

Query: 506 SSGGLGAMGFLPAAIGASVA-----NPDAIVVDIDGDSFIMNVQELATIRVENLPVK 559
      SSGGLG+MGFGLPAA+GA+VA P VVDIDGDSF+MNVQELATI +E L VK
Sbjct: 463 SSGGLGSMGFLPAAALGAFAVDGKNGRPKKTVDIDGDSFLMNVQELATIFIEKLDVK 522

Query: 560 VLLNNQHLGMVMQWEDRFYKANRAHTFLGD-----PAQEDEFIPNMLLFAAACGIPA 612
      V+LLNNQHLGMV+QWEDRFYKANRAHT+LG E++I+PN + A A G+P+
Sbjct: 523 VMLNNQHLGMVVQWEDRFYKANRAHTYLGKRESEWHATQDEEDIYPNFVNMAQAFGVPS 582

Query: 613 ARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIKY 670
      RV K LR AI+TMLDTPGPYLL+V+ PH EHVLPMP G +F D+ITEGDG +KY
Sbjct: 583 RRVIVKEQLRGAIARTMLDTPGPYLLVEMVPHIEHVLPMPGGASFKDIIITEGDGTVKY 640

>ref|ZP_03129981.1| acetolactate synthase, large subunit, biosynthetic type
      [Chthoniobacter flavus Ellin428]
gb|EDY19461.1| acetolactate synthase, large subunit, biosynthetic type
      [Chthoniobacter flavus Ellin428]
      Length = 591

Score = 675 bits (1741), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 344/586 (58%), Positives = 421/586 (71%), Gaps = 17/586 (2%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALT-RSSSIRNVLPHEQGGVFAAEGYARS 157
      GA+ILVE L R+GV+T+FAYPGGASM +HQALT R IR LPRHEQGGVFAAEGYAR+
Sbjct: 3 GAEILVECLIREGVDTFAYPGGASMHMHQALTREKIRTYLPRHEQGGVFAAEGYARA 62

Query: 158 SGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
      +GK G+ +ATSGPGATNLV+G+ADA LDS PLVAITGQVP+ MIG AFQET + VT
Sbjct: 63 TGKAGVVMATSGPGATNLVTGIADAYLDSTPLVAITGQVPQAMIGKGAFTQDVFVSVAQ 122

Query: 218 ITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYM 277
      I KHNLYLMDV DIPRI++EAF++A +GRPGPVL+D+PK+IQ P + + L GY
Sbjct: 123 IVKHNLYLMDVNDIPRIVKEAFYIAQTGRPGPVLIDIPKNIQLATTQPVFPAEINLRGYD 182

Query: 278 SRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCLN--SSDELGRFVELTGIPVASTLMGL 335
      K +D L ++V LI ++K P++Y GGG ++ +S EL FVE TGIPVA+TLMG+
Sbjct: 183 PI--KHADDVALNEVGLIKQAKCPMIYCGGIIISGEASGELLEFVERTGIPVATTLMGI 240

Query: 336 GSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIVHID 395
      G +P ELSL LGMHGTVYAN AV +DLLA GVRFDDRVTKL+ FA IVHID
Sbjct: 241 GCFPETHELKWLGMHGTVYANNAVNEADLLAIGVRFDDRVTKISEFAKHGTIVHID 300

Query: 396 IDSAEIGKNKTPHVSVCADVKLALQGMNKVLE---NRAEELKLDGFWWRNELNVQKQKF 451
      ID++EI KNK + + DVK AL +N++LE R + F W ++N ++ F
Sbjct: 301 IDNSEINKNKVVKLPILSDVKYALGRNLQLEESGAKRVQSGFKAFPDWYVKINAWREAF 360

```

Query: 452 PLSFKTFGEAIPPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLG 511
P +F + I PQYAIK+L ELT G AII+TGVGQHQMWAQFY+Y KPR L+S GLG
Sbjct: 361 PFTFNDTEDVIQPPQYAIKLLCELTKGDALITITGVGQHQMWAQFYDYTKPRTLTSAGLG 420

Query: 512 AMGFGLPAAIGASVANPDIAIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMV 571
+MGFG PAA+GA VA PD V+DIDGDSF+MNVQELA VE + KV++LNNQ LGMV
Sbjct: 421 SMGFGYPALGAKVAFDPKEVIDIDGDSFLMNVQELALAHVEGVNAKVMILNNQWLGMV 480

Query: 572 MQWEDRFYKANRAHTFLGDPAQEDE-----IFPNMLLFAAACGIPAARVTKKADLRE 623
MQWEDRFYK+NR HTFLG+P + E I+P+ + + RV K DL
Sbjct: 481 MQWEDRFYKSNRGHTFLGNPKKVYEGSLEDPTGIYPDYVKMCEGFAVKCERVMHKKDLAA 540

Query: 624 AIQTMMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGRIK 669
A+Q MLD PY+LDV+ P+ EHVLPMP+GGT+ DVI EG +K
Sbjct: 541 AMQRMLDAKEPYVLDVMVPYTEHVLPMPISGGTYKDVIEYGRQTLK 586

>emb|CAO45071.1| unnamed protein product [Vitis vinifera]
Length = 463

Score = 673 bits (1736), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 315/461 (68%), Positives = 382/461 (82%), Gaps = 2/461 (0%)

Query: 201 IGTDAFQETPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQ 260
+GTDAFQE P++++TR ITK NYLV+DVEDIPR ++EAF LATSGRPGPVL+D+P+DIQ+
Sbjct: 1 MGTDAFQEVPLIDITRPITKFNLYLVLDVEDIPRTVKEAFLLATSGRPGPVLIDIPRDIQK 60

Query: 261 QLAIPNWEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGCLNSSDELGRF 320
+L +PNW + + LPG SR+PK PE +HLE+IVRLIS SK+PV+Y GGGC+N S+EL RF
Sbjct: 61 ELVVPNWNKPIMLPGNASRLPKLPEKAHLEEIVRLISVSKRPVYAGGGCMNCSEELRRF 120

Query: 321 VELTGIPVASTLMGLGSYPCDDELSLHLMGMHGTVYANYAVEHSDLLAFGVRFDDRVTVG 380
V LTGIPVASTLMGLG + C D+LSLHLMGMHGT+ ANYAV+ SDLLAFGVRFDDRVTVG
Sbjct: 121 VGLTGIPVASTLMGLGIFACTDDLSLHLMGMHGTIQANYAVDRSDLLAFGVRFDDRVTVG 180

Query: 381 KLEAFASRAKIVHIDIDSAEIGKNKTPHVSVCQDVKLALQGMNKVLENRAEELKLDGFWV 440
K+EAF A IVHIDID AEIGKNK PH+S+C DVKLAL+G+N +LE A K
Sbjct: 181 KVEAFARNATIVHIDIDPAEIGKNKKPHLSICTDVKLALLEGINTILEKNAA--KQPTAEN 238

Query: 441 RNELNVQKQKFPPLSFKTFGEAIPPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKK 500
+ + P S++TFGEAIPPPQYAI++LDELTDG AII TGVGQHQMWAQ+Y +K
Sbjct: 239 KRKGKTKFNDNPPSYRTFGEAIPPPQYAIQLDELTDGNAIICTGVGQHQMWAQYQYKHKN 298

Query: 501 PRQWLSSGGLGAMGFLPAAIGASVANPDIAIVDDIDGDSFIMNVQELATIRVENLPVKV 560
PR WLSS GLGAMGFLPAA+GA++A PDAIVDDIDGDSF+MN+QELATIRVENLPVK+
Sbjct: 299 PRHWLSSSGLGAMGFLPAAAMGAALAKPDAIVDDIDGDSFMMNIQELATIRVENLPVKI 358

Query: 561 LLLNNQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKAD 620
+LLNNQHLGMV Q+E + + H+++G+P+ + ++FP+ML+FA AC I AARVTKKA+
Sbjct: 359 MLLNNQHLGMVYQYEEYEGDGLSHSYMGNPSNQAQVFPDMLMAEACNITAARVTKKAE 418

Query: 621 LREAIQTMMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
LREAI+ ML TPGPYLLDV+ PHQ VL +IP+GGTF D I
Sbjct: 419 LREAIKMLKTPGPYLLDVMVPHQAQVLQLIPDGGTFKDAI 459

>ref|ZP_01089063.1| acetolactate synthase III (Precursor) [Blastopirellula marina DSM
3645]
gb|EAQ82178.1| acetolactate synthase III (Precursor) [Blastopirellula marina DSM
3645]
Length = 590

Score = 669 bits (1726), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 333/582 (57%), Positives = 424/582 (72%), Gaps = 25/582 (4%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTR-SSSIRNVLPHEQGGVFAAEGYARS 157
GADI++E+L R GV+ +FAYPGG SM +HQALTR IR +LPRHEQGG FAA+G AR+
Sbjct: 17 GADIMIESLVRHGVDFVIFAYPGGCSMPLHQALTRYKDKIRTILPRHEQGGGFAAQGVART 76

Query: 158 SGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
+GK G+C+ATSGPGATNLV+ +ADA LDS+P+VAIT QVPR +IG+DAFQETPIVEV R
Sbjct: 77 TGKVGVCMATSGPGATNLVTAIDAKLDSIPMAITAQVPRVIGSDAFQETPIVEVCRG 136

Query: 218 ITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPG-- 275
ITKH+YLV D+ D+ RI++EAF +A++GRPGPVL+D+PKD+Q + +P+W+ AM LPG
Sbjct: 137 ITKHHYLVTDIADLTRIMKEAFHIASTGRPGPVLIDIPKDVQLEQIVPDWDACAMNLPGYN 196

Query: 276 YMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLM 333
Y +R KP + ++QI I +K+P++Y GGG + S S+EL VE TGIP+ +T+M
Sbjct: 197 YEARTAKPEQ---IKQIAAAIKRAKRPMIYSGGGIITSGASEELRELVEKTGIPITTTVM 253

Query: 334 GLGSPCDDELSTHMLGMHGTIVYANYAVEHSDLLAFGVRFDDRTVGKLEAFASRAKIVH 393
GLGS+P DD LSL MLGMHGTIVYANYAV++ DLL++ GVRFDDRTVGKL FA AKI+H
Sbjct: 254 GLGSFPDGDPLSLDMLGMHGTIVYANYAVQNCDDLISLGVRFDDRTVGKLAFAKHAKIIH 313

Query: 394 IDIDSAEIGKNKTPHVSVCADVKLALQGMNVLENRAEELKLDGFWRNELNVQKQKFP 453
IDID +EI KNK H V D+K AL+ + ++E D W + K+ PL
Sbjct: 314 IDIDPSEINKKLAHFPVVDLKPALRMLCDIVEKPE-----DISEWVAQCAKWKDEPL 368

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGK-AIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGA 512
+ T E I Q+AI L+++ + IIS GVGQHQMWAAQFY +KKPR WLSS GLG
Sbjct: 369 KYDTSFEGILQQAIAELNDICKERDTIISVGVGQHQMWAAQFYKFKKPRTWLSSSGLGT 428

Query: 513 MGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVM 572
MGFGLPAA+GA VA PDA+ +DI+GDGSF MN+QELAT E LPVKV+LLNNQHLGMV+
Sbjct: 429 MGFGLPAAMGAQVAFPDALCIDIEGDSFTMNIQELATCFCEKLPVKVMLNNQHLGMVV 488

Query: 573 QWEDRFYKANRAHTFL-----GDPAQEDEFIFNMMLFAAACGIPAARVTKADL 621
QWEDRF NRAHT+L G+ E +P+ ++ A G A V++K++L
Sbjct: 489 QWEDRFMSGNRAHTYLGPHVHPEATGDGNERYAAERYPDFVMIAGFGCGGATVSRKSEL 548

Query: 622 REAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITE 663
R AI+ M++ GPY+LDV P+QE VLPMP+G T ND+I E
Sbjct: 549 RAAIEEMINYDGPYVLDVQVPYQEQVLPMPISGMTVNDIIE 590

>ref|YP_001941018.1| Acetolactate synthase large subunit or other thiamine
pyrophosphate-requiring enzyme [Methylokorus inferorum
V4]
gb|ACD84421.1| Acetolactate synthase large subunit or other thiamine
pyrophosphate-requiring enzyme [Methylococcus inferorum V4]
Length = 589

Score = 667 bits (1721), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 319/570 (55%), Positives = 431/570 (75%), Gaps = 7/570 (1%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFMAEGYARSS 158
GAD ++ ALE++GV +FAYPGGASM +HQ+LTR+ +R VLPHEQGGVF AEGYARS+
Sbjct: 24 GADCVIAALEKEGVGILFAYPGGASMPMHQSLTRAKILRTVLPHEQGGVFMAEGYARST 83

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+C++TSGPGATNL++G+ADA +DSVPLVAITGQV + MIG AFQET + +T I
Sbjct: 84 GKVGVCMSTSGPGATNLITGIADAYMDSVPLVAITGQVKEMIGKGAQFQETDVFGITLPI 143

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
KH+YLV+D +IP+II+EA +A SGRPGPV++D+PKD+QQ + P + + G S
Sbjct: 144 VKHSYLVDPREIPQIIKEALLIARSGRPGPVVIDIPKDVQAVFKPFFPHST---GLES 200

Query: 279 RMPKPPED-SHLEQIVRLISESKKPVLYVGGGCLNS--DELGRFVELTGIPVASTLMGL 335
++ PP D S LE ++ I ++K+PV+YVGGG ++S EL F + T IPVA+TLMG+
Sbjct: 201 KLAPPPIDISALETVLDWIEKAKRPVMYVGGGISSGAYHELLEFAQKTAIPVATTLMGI 260

Query: 336 GSYPCDDELSTHMLGMHGTIVYANYAVEHSDLLAFGVRFDDRTVGKLEAFASRAKIVHID 395
GS+P + LSL LGMHG+VY+N+AV+ SDLLAFGVRFDDRTVG ++AFA +A+IVHID
Sbjct: 261 GSFPENHPSLKLWLMHGSVYSNFAVDQSDLLAFGVRFDDRTVGNVQAFQAKARIVHID 320

Query: 396 IDSAEIGKNKTPHVSVCADVKLALQGMNVLENRAEELKLDGFWRNELNVQKQKFP 455
ID++E+ KNK + + GD+K AL+ +N+++E R + + +W+ E+ K K+P +
Sbjct: 321 IDNSELNKNKRVLDLPILGDIKEALRLNRLIEERKFQ-SPGYSLWQEEIQAWKIKYPFRY 379

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGF 515
K F I PQ I+ L +LT G+AIITGVGQHQMWAQFYNY+ +PR +L+SGGLGAMGF
Sbjct: 380 KKFEGVIMPQMVIEELYKLTRGEAIITGVGQHQMWAQFYNFHRPRTFLTSGGLGAMGF 439

Query: 516 GLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
G PAA+GA +A+P+A V+D+DGDGSF+MN+QELAT E +PVK ++LNNQHLGMV+QWE
Sbjct: 440 GYPAAIGAKIAHPEATVIDVDGDSFLMNIQELATAVTEKIPVKAVILNNQHLGMVQWE 499

Query: 576 DRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPY 635
DRFY +NRAHTFLG P ++ ++P+ G+ + R++K +L A++ MLD+ PY
Sbjct: 500 DRFYDSNRAHTFLGLPDNKNMVYPDPFQICKGFGVKSERISKPHLVPALKRMLDSEEPY 559

Query: 636 LLDVICPHQEHVLPMPINGGTNDVITEGD 665
+LDVI P+ EHVLPMP G T D+I + D
Sbjct: 560 VLDVIVPYTEHVLPMPAGMTVKDIIIDND 589

>ref|ZP_02966895.1| acetolactate synthase, large subunit, biosynthetic type [bacterium
Ellin514]
gb|EDU04401.1| acetolactate synthase, large subunit, biosynthetic type [bacterium
Ellin514]
Length = 622

Score = 653 bits (1685), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 333/600 (55%), Positives = 418/600 (69%), Gaps = 42/600 (7%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
G++IL+ LER+GV+T+FAYPGGASME HQAL+RS IR +LPRHEQGGVFAAEGYAR++
Sbjct: 25 GSEILIACLEREGVDITIFAYPGGASMEFHQALSRK-IRITLPRHEQGGVFAAEGYARAT 83

Query: 159 GKPGICIATSGPGATNLVSGADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+C+ATSGPGATNLVSG+ADA +DS+PLV+ITGQVP+ MIG AFQET +T I
Sbjct: 84 GKAGVCMATSGPGATNLVSGIADAYMDSIPLVSITGQVPQAMIGRAFQETDFFGTMPLPI 143

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
KH+YLV DV DIPRII+EAF++ATSGRPGPV+VDVPK+IQQ P + + + GY
Sbjct: 144 VKHSYLVTDVNDIPRIIEEAFYVATSGRPGPVVDVPKNIQAKTQPVFPSEVLVRGY-- 201

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLN--SSDELGRFVELTGIPVASTLMGLG 336
+ + D L +IV LI +S++P+LYVGGG ++ +S+EL +F E IPV +TLMG+G
Sbjct: 202 DVDRRASDIELNEIVGLIEKSERPLLYVGGGIISGEASEELKFAEAAQIPVTTTLMGIG 261

Query: 337 SYPCDDELSLHMLGMHGTVYANYAVEH-----SDLLAFGVRFD DRV 378
++P LSL LGMHG YAN+AV +DLLAFGVRFD DRV
Sbjct: 262 AFPESHPLSLRWLGMHGAAYANWAVSGEFEPKKEFTDPSVQIAPGADLLAFGVRFD DRV 321

Query: 379 TGKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKLLENRAEELKLD FG 438
TGK+E F IVH+DID +EI KNK ++ V DVK AL+ +N++L RA + F
Sbjct: 322 TGKVEKCFEHGTIVHLDIDPSEINKNKPANLPVVS DVKALRRLNQLNRA--IAKKFT 379

Query: 439 VWRNELNVQKQKFPLSFKT-----FGEAIPPQYAIKVLDELTDGKAI 481
W ++ K K P ++ E I PQ AI++L ELT G AII
Sbjct: 380 AWHKQVADWKAKAPFGYRVTEEVVKSQHMRDHLEGQVSEVILPQMAIEMLYELTGGDAII 439

Query: 482 STGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSF 541
+TGVGQHQMWAQ+Y YK PRQ L+S GLGAMG+G PAA+GA VA PD VVDIDGDSF
Sbjct: 440 TTGVGQHQMWAQYYKYKFPRQLLTSAGLGAMGYGYPAAMGAKVACPDQVVDIDGDSF 499

Query: 542 IMNVQELATIRVENLPVKVLLNNQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEFIPNM 601
+MN+QELAT +E + K L+LNNQHLGMVMQWEDRFYK NR +T+LGDP +I+P+
Sbjct: 500 LMNIQELATAHIEKIAAKALVLNNQHLGMVMQWEDRFYKGNRGNTYLGDPENMKKIYDPY 559

Query: 602 LLFAAACGIPAARVTKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMPINGGTNDVI 661
+ A +P RV + DLR A+Q MLD+ PY+LDVI P+ EHVLP IP G T ++I
Sbjct: 560 VAMAKGFSVPCERVMFRKDLRAAMQRMMLDSKEPYVLDVIVPYTEHVLPFIPAGKTVAEMI 619

>ref|ZP_01857674.1| acetolactate synthase III (Precursor) [Planctomyces maris DSM 8797]
gb|EDL56438.1| acetolactate synthase III (Precursor) [Planctomyces maris DSM 8797]
Length = 593

Score = 653 bits (1685), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 333/585 (56%), Positives = 423/585 (72%), Gaps = 27/585 (4%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTR-SSSIRNVLP RHEQGGVFAAEGYARS 157
GA+ILV+AL RQGV+T+FAYPGG SM +HQAL + IR +LPRHEQGG FAA+G AR+
Sbjct: 16 GAEILVQALVRQGVKTIFAYPGGCSMPLHQALMKYKDDIRTLPRHEQGGGFAAQGIART 75

Query: 158 SGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
+G+ G+C+ATSGPGATNLV+ LADA LDS+PLVAITGQVP+ +IG+DAFQETP+VE++R+
Sbjct: 76 TGEVGVCMATSGPGATNLVTALADAKLDSIPLVAITGQVQAVIGSDAFQETPMVEISRA 135

Query: 218 ITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAI----PNWEQAMKL 273
ITKH+Y+V DV+D+ RI++EAF+ A +GRPGPVL+D PKD QLA P++ L
Sbjct: 136 ITKHHYMTVDKDVARIKVEAFFIANTGRPGPVLIDFPKDC--QLATLDEEPDYNPDYTL 193

Query: 274 PGYMSRMPK-PPEDSHLEQIVRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVAS 330
PGY M K PE ++QI+ I SKKP+LYVGGG + ++S+EL +F T IPV +
Sbjct: 194 PGYRPEMRKAAPE--QIKQILAAIKRSKKPILYVGGGAIISDASEELVKFARRTNIPVTT 251

Query: 331 TLMGLSGYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRTVGKLEAFASRAK 390
T+MGLG +P +D LSL MLGMHGT VYANYAV +DLLAFGVRFDDRTVGKLE FA K
Sbjct: 252 TVMGLGVFPGEDPLSLDMLGMHGT VYANYAVNEADLLAFGVRFDDRTVGKLEFAKHGK 311

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMKNVLENRAEELKLDGFWVRNENLVQKQK 450
IVH+DID +E+ KNK H+ + D+K L +N+ + + ++L W + K+K
Sbjct: 312 IVHVDIDPSELQKNKEAHIPINADLKHVLTLENAITD--DDL P-QVDSWLAQCKEWEK 368

Query: 451 FPLSFKTFGEAIPPQYAIKVL-DELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGG 509
FPL + G+ + QYAI L + + I+ GVGQHQMWAQFY + KPR WLSS G
Sbjct: 369 FPLKYPELGDMVMSQQYAIHELWQQSKERDPYITVGVGQHQMWAQFYKFNKPRHWLSSSG 428

Query: 510 LGAMGFGLPAAIGASVANPDIAIVVDIDGDGSFIMNVQELATIRVENLPVKVLLNNQHLG 569
LG MGFGLPAA+G P+ +VVDIDGDGS +MN+QELAT+ ENLPVK+LLNNQHLG
Sbjct: 429 LGTMGFGLPAAAMGVQAQFPNDLVVDIDGDGSMLMNIQELATLHTENLPVKILLNNQHLG 488

Query: 570 MVMQWEDRFYKANRAHTFLG---DPAQE-----DEIFPNMLLFAAACGIPAARVTCK 618
MV+QWEDRF + RAHT+LG P E + +P+ + A G+ A +V K
Sbjct: 489 MVMQWEDRFMEGRRAHTYLGPHVHPEWEGKSGEHAETYPDFVSIAGKFGQLQARQVRSK 548

Query: 619 ADLREAIQTMLDTPGPYLLDVICPHQEHLVLPMPNGGTFNDVITE 663
A+ A+ ML + PYLLDVIC +QEHVLPMP+GGT ND+ITE
Sbjct: 549 AEYPAALAEMLASDQPYLLDVICTYQEHVLPMPISGGTVNDIITE 593

>ref|ZP_02737021.1| acetolactate synthase III [Gemmata obscuriglobus UQM 2246]
Length = 590

Score = 650 bits (1678), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 328/580 (56%), Positives = 411/580 (70%), Gaps = 22/580 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTR-SSSIRNVLP RHEQGGVFAAEGYARS 157
GADILV+AL R GV+TVFAYPGGASM IHQALTR +R +LPRHEQGG F A GY R+
Sbjct: 18 GADILVQALIRHGVDTVFAYPGGASMPHQAALTRVQKGLRITLPRHEQGGGFMAHGYCRT 77

Query: 158 SGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
+GK +C++TSGPGATN V+ +ADA +DS+P + ITGQV ++G DAFQETP+VE+ R
Sbjct: 78 TGKASVCVSTSGPGATNFVTCTADAKMDSIPAIFITGQVSTNVLGNDAFQETPMVEICRG 137

Query: 218 ITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYM 277
ITKH+YL+ EDI R+++EAF +AT+GRPGPVL+DV KD+Q + +P+W+ AM LPGY
Sbjct: 138 ITKHHYLLTRTEDITRMKEAFHIAITGRPGPVLIDVCKDVQTKSVVPDWDVAMDLPGY- 196

Query: 278 SRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGL 335
R + + LE ++ I SKKP +Y GGG +S + EL F EL G PV T+ GL
Sbjct: 197 -RPVRKAPRAELEPVIAAIRASKKPFYAGGGVTHSDAAAELEKFAELVGAPVGLTVHGL 255

Query: 336 GSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRTVGKLEAFASRAKIVHID 395
G++P D L L MLGMHGT VY+NYA+ +DLLAFGVRFDDRTVGKL FA KIVH+D
Sbjct: 256 GNFPADHYLCLQMLGMHGT VYSNYAINDADLLAFGVRFDDRTVGKLEAFKHGKIVHVD 315

Query: 396 IDSAEIGKNKTPHVSVCADVKLALQGMNVLENRAEELKLD-----FGVWRNELNVQKQ 449
ID +EI KNK HV V D+K AL G+N +L+ EE D + W +++ +
Sbjct: 316 IDKSEIHKNKFAHVPVHSDLKHALHGLNALLK---EEKNADLTAGGRYTDWWRQVDAWRD 372

Query: 450 KFPLSFKTFGEAIPQYAIKVLDELTDGK-----AIISTGVGQHQMWAAQFYNYKKPRQW 504
PL F I PQYAIK L E+ + II+TGVGQHQMWAAQF+++ KPR+W
Sbjct: 373 AEPLKFAEPDNFIIPQYAIKRLWEILRDRNQLDDTIITTGVGQHQMWAAQFFHFNKPRKW 432

Query: 505 LSSGGLGAMGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLLN 564
++SGGLG MGFGLP+A+GA VA P+ +V+DIDGDSF+MNVQELAT E +P KVLLLN
Sbjct: 433 ITSGGLGTMGFGLPSALGAKVAFPNNLVIDIDGDSFLMNVQELATAYAEEKIPAKVLLLN 492

Query: 565 NQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEI-FPNMLLFAAACGIPAARVTKKADLRE 623
NQHLGMVMQWEDRF+ +NR HT+LG A ED +P+ A G+ A V KADL
Sbjct: 493 NQHLGMVMQWEDRFFGSNRGHTYLG--AGEDHAPYPDFCKIAEGFGVTAKSVIDKADLDA 550

Query: 624 AIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITE 663
A+ M++ PGP+LL+V PHQEHVLPMP G T D+I E
Sbjct: 551 ALIEMIEAPGPFLNVHVPHEHVLPMPAGSTVKDIKE 590

>ref|NP_870771.1| acetolactate synthase III [precursor] [Rhodopirellula baltica SH 1]
emb|CAD77848.1| acetolactate synthase III [Precursor] [Rhodopirellula baltica SH 1]
Length = 619

Score = 642 bits (1655), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/588 (55%), Positives = 414/588 (70%), Gaps = 27/588 (4%)

Query: 95 QPRKGADILVEALERQGVETVFAYPGGASMEIHQALTR-SSSIRNVLPHEQGGVFAAEG 153
QP GAD+LV++L GVE +FAYPGG SM +HQALTR SIR +LPRHEQGG FAA+G
Sbjct: 40 QPMNGADVLVKSLVDHGEVLFAYPGGCSMPMHQALTRYGDSIRTILPRHEQGGAFAAQG 99

Query: 154 YARSSGKPGICIATSGPGATNLVSGADALLDSVPLVAITGQVPRRMIGTDAFQETPIVE 213
Y+RS+GK G+ +ATSGPGATNLV+ +ADA LDS+P++ ITGQVP IGTDFAFQETP+VE
Sbjct: 100 YSRSTGKIGVVMATSGPGATNLVTAIADAKLDSIPMLCITGQVPTGAIGTDAFQETPMVE 159

Query: 214 VTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKL 273
+ R ITKH+YLV D+ D+PR+++EAF +ATSGRPGPVLVD+PKD+Q + + M L
Sbjct: 160 ICRGITKHNYLVTDLADLPRVMKEAFHIATSGRPGPVLVDMPKDVQLGNFPIDMDPEMDL 219

Query: 274 PGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGCLN--SSDELGRFVELTGIPVAST 331
PGY PK ++ ++Q+ I +++PV+Y GGG ++ +S+EL ++ TGIP +T
Sbjct: 220 PGYSPEAPKVAGET- IKQMAAAIKLARRPVIYAGGGIISGEASEELRELIKKTGIPTVTT 278

Query: 332 LMGLGSYPCCDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKI 391
+MGLG+ DD SL LGMHG YANYAV DLL+A GVRFDDRVTKG+EAF A KI
Sbjct: 279 IMGLGAVSPDDPRSLDWLGMHGAAYANYAVRDCDLLIALGVRFDDRVTKVEAFADAKI 338

Query: 392 VHIDIDSAEIGKNKTPHVSVCADVKLALQGMNVLENRAEELKLDGFGVWRNELNVQKQKF 451
+H+DIDS+E+ KNK H+ V GDVK L +NK+++ E W+ K K+
Sbjct: 339 IHVDIDSSSELNKNKAHIPVRGDVLDVLQNLKIVQPPEIE-----AWQKTCTDLKAKY 392

Query: 452 PLSFKTFGEAIPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGL 510
PL + + I Q+AI L ++T D + +S GVGQHQMWAAQF+ ++ PR W+SS GL
Sbjct: 393 PLKYDNSFQDILQQAIAITLSKITADRETYVSVGVGQHQMWAAQFFKFRNPRTWMSSSGL 452

Query: 511 GAMGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLLNQHLGM 570
G MGFGLPAA+G A+PDA+V+DIDGDSF MN+QELAT E LPVKVLLLNQHLGM
Sbjct: 453 GTMGFLPAAAGVQAHPDALVIDIDGDSFQMNQELATCFCEKLPVKVLLLNQHLGM 512

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEI-----FPNMLLFAAACGIPAARV 615
V+QWEDRF NRAHT+LG P DE +PN + A G AA V
Sbjct: 513 VVQWEDRFMDRNRAHTYLG-PIDHDEAKGKSTADRFEYASDRYPNFVQIAKGYGCGAATV 571

Query: 616 TKKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITE 663
KKADL A+Q M+D GP+LLDV P+QEHVLPMP G T +D++ +
Sbjct: 572 KKKADLEGALQEMIDHKGPFLLDVEVPYQEHVLPMPGGMTVDDMLLD 619

>gb|EDY84597.1| acetolactate synthase, large subunit, biosynthetic type
[Verrucomicrobiae bacterium DG1235]
Length = 592

Score = 629 bits (1622), Expect = e-178, Method: Compositional matrix adjust.
Identities = 307/572 (53%), Positives = 410/572 (71%), Gaps = 11/572 (1%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALT-RSSSIRNVLP RHEQGGVFAAEGYARS 157
GADI+VE+L R+GV+ +FAYPGGAS+E+HQ+L R IR +LPRHEQGG FAAEGYAR
Sbjct: 21 GADIVVESLIREGVDVIFAYPGGASLEMHQSLAKRKDDIRTILPRHEQGGSF A AEGYARV 80

Query: 158 SGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
+GK G+C+ATSGPGATNL++ +ADA +DS PLV ITGQV + IG AFQET +T
Sbjct: 81 TGKAGVCMATSGPGATNLMTAIDAFMDSTPLVCITGQVYSKFIGKAAFQETDFFGMTIP 140

Query: 218 ITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYM 277
+ KH+YLV+DV D+PR+++EAF +AT+GRPGPV+VD+PKD+QQ L P W +P
Sbjct: 141 VVKHSYLVLDVNDLPRVMKEAFKIAATTGRPGPVVDIPKDVQQTLTTPVWPTDADVPYRE 200

Query: 278 SRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLN--SSDELGRFVELTGIPVASTLMGL 335
S++P D LE ++RLI ++K+PV+Y GGG ++ +S EL F E GIPVASTLMG
Sbjct: 201 SKLPAKASDRDLENVRLIEDAKRPVIYFGGGVVSAEASKELTEFAERIGIPVASTLMGA 260

Query: 336 GSYPCDDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRV TGKLEAFASRAKIVHID 395
GS+P ELSL GMHG+ + N+AV SDLLL G RFDDR+TG + FA +A+IVHID
Sbjct: 261 GSFPETHELKSLKWFHGMHSAFGNWAHVHQSDDLTLGARFDDRITGDVSKFAPQAEIVHID 320

Query: 396 IDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQKPLSF 455
+D++E KNK H + D+K AL M ++++ + + K + W+ + K+ +P S+
Sbjct: 321 VDASEHNKNIHVHPISVDIKHALGRMIELMDQKGFK-KPNLEAWQQQCAEWKRDYPFSY 379

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQAQFYNYKKPRQWLSSGGLGAMGF 515
+ I PQ+A++ L ELT G+AII+TGVGQHQM+AAQFY++ PR +SS GLG+MG+
Sbjct: 380 NE-SDHIIPQHAVQTLCELTKEAIIITGVGQHQMFAAQFYDFNHRSLISSLGLGSMGY 438

Query: 516 GLPAAIGASVANPD AIVVDIDGDGSGFIMNVQELATIRVENLPVKVLLLNQHLGMVMQWE 575
G PAA+GA VA PD VVDIDGDGSGF+MNVQELAT ++E + K ++LNNQHLGMV+QWE
Sbjct: 439 GYPALGAKVARPDRQVVDIDGDGSGFMMNVQELATAKIEKIAAKAMILNNQHLGMVVQWE 498

Query: 576 DRFYKANRAHTFLGD-----PAQEDEFIPNMLLFAAACGIPAARVTKADLREAIQTML 629
DRFY + R +T LGD P ++P+ + A G+P RV KK++L++AIQ ML
Sbjct: 499 DRFYNSVRGNTILGDENNIGTPENLTGLYPDYVKIAEGFGLPGRRVHKKSELKDAIQEML 558

Query: 630 DTPGPYLLDVICPHQEHLVPMIPNGGTFNDVI 661
D+ +LLDVI P+ EHVLP MIP G T + +I
Sbjct: 559 DSEEAFLLDVITPYDEHLVPMIPAGKTVDQMI 590

>ref|ZP_02013682.1| acetolactate synthase, large subunit, biosynthetic type
[Opitutaceae bacterium TAV2]
gb|EDN44799.1| acetolactate synthase, large subunit, biosynthetic type
[Opitutaceae bacterium TAV2]
Length = 601

Score = 611 bits (1575), Expect = e-173, Method: Compositional matrix adjust.
Identities = 299/573 (52%), Positives = 397/573 (69%), Gaps = 11/573 (1%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSS 158
GAD++VEAL +GVE +FAYPGGAS E+HQA RS +R +LPRHEQGG FAAEGYAR+S
Sbjct: 28 GADVVEALAHAGVEVIFAYPGGASQELHQAFAARSDKVRVILPRHEQGGSF A AEGYARAS 87

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+C+ATSGPGATNLVS +ADA +DS PL+AITGQV + IG AFQET +T I
Sbjct: 88 GKVGVCMATSGPGATNLVSAIADAFMDSTPLIAITGQVFSKFIGKSAFQETDFFGMTLPI 147

Query: 219 TKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
KH+YLV++ D+PR+ +EAF LA +GRPGPV++D+PKD+QQ P + + ++
Sbjct: 148 VKHSYLVLNADHLPRVFKEAFHLARTGRPGPVVIDIPKDVQQAKLTPVFPETVEFANPTL 207

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGCLNSS--DELGRFVELTGIPVASTLMGLG 336
D L +++ LI+++++PV+Y GGG +++ +L +F ELT IPVA+TLMG+G
Sbjct: 208 NALPHATDEELNEVLDLIAKAERPVIYAGGGVISAEAHGDLKKFAELTHIPVATTLMGVG 267

Query: 337 SYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIVHIDI 396
++P LS+ GMHG+ Y N+AV+ +DL+L G RFDDR+TG FAS A+IVHIDI
Sbjct: 268 AFPETHPLSMQWFGMHGSAYGNWAVDQADLVLCGARFDDRITGDTSKFASHARIVHIDI 327

Query: 397 DSAEIGKNKTPHVSVCADVCLALQGMNKVLENR--AEELKLDGFWVRNENLVQKQKFPLS 454
D +E KNK H + D+K AL +N++ A+ D W ++N K+ +P +
Sbjct: 328 DPSEHNKNKRHHPIVSDLKHALSRLNELAAGAGGAKFTAPDTKSWHTQINAWKRDYPFA 387

Query: 455 FKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAMG 514
+ I PQ A++ L +LT G AII TGVGQHQMWAAQFY + +PR+++SS GLGAMG
Sbjct: 388 YDE-SRHIIPQEAVETLYQLTQGDAAIIVTGVGQHQMWAAQFYRFNEPRRYISSLGLGAMG 446

Query: 515 FGLPAAIGASVANPDIAVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQW 574
+G PAA+GA +A PD V+DIDGDSF+MN+QELAT VE + KV++LNNQHLGMV+QW
Sbjct: 447 YGYPAALGAKIARPDQVIDIDGDSFLMNIQELATAAVEKIAAKVMILNNQHLGMVVQW 506

Query: 575 EDRFYKANRAHTFLGD-----PAQEDEFIPNMLLFAAACGIPAAARVTKKADLREAIQTM 628
EDRFY + R +T LG P ++P+ + A G+ RV KK +LREAIQ M
Sbjct: 507 EDRFYGVSVRGNTILGHHDNIGGPDNPGGLYPDFVKIAEGFGVKGRRVIKKEELREAIQEM 566

Query: 629 LDTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
L GPYLLDV+ P+ EHVLPMP G T D+I
Sbjct: 567 LAHDGPYLLDVVPYTEHVLPMPAGRTVKDMI 599

>ref|YP_001818911.1| acetolactate synthase, large subunit, biosynthetic type [Opitutus
terrae PB90-1]
gb|ACB75311.1| acetolactate synthase, large subunit, biosynthetic type [Opitutus
terrae PB90-1]
Length = 591

Score = 606 bits (1563), Expect = e-171, Method: Compositional matrix adjust.
Identities = 312/573 (54%), Positives = 406/573 (70%), Gaps = 12/573 (2%)

Query: 98 KGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARS 157
KGA+ +VE L R+GV+ +FAYPGGAS E+HQAL R+ IR +LPRHEQGG FAA GYAR+
Sbjct: 20 KGAEAVVECLIREGVDVIFAYPGGASQELHQALARTEKIRITILPRHEQGGFAAGGYARA 79

Query: 158 SGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
+GK G+C+ATSGPGATNLVSG+ADA +DS+PLVAITGQV + IG AFQET I +T
Sbjct: 80 TGKVGVCMATSGPGATNLVSGIADAFMDSIPLVAITGQVYSKYIGKMAFQETDIYGMTLP 139

Query: 218 ITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYM 277
+ KH+YLVLM+V+D+PR+ +EAF LA SGRPGPVL+D+PKD+QQ P + A++
Sbjct: 140 VVKHSYLVMMVQDLPRVFKEAFQLARSGRPGPVLIDLKDVQQTRFTPVFPFAIEFRNSY 199

Query: 278 SRMPKPPEDSHLEQIVRLISESKKPVLYVGGCL--NSSDELGRFVELTGIPVASTLMGL 335
+ + D L+Q++ L++E+K+PVLYVGGG + N+ EL F E T IPVA+TLMG+
Sbjct: 200 ASGAQHATDEQLKQVLGLVAEAKRPVLYVGGGIISANAHAELKAFAEKTNIPIVATTLMGV 259

Query: 336 GSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIVHIDI 395
G++P LS+ GMHG+ Y N+AV+ +DL+L FG RFDDR+TG FA AKIVHIDI
Sbjct: 260 GAFPETHPLSMQWFGMHGSAYGNWAVDEADLVLCGARFDDRITGDTSKFAGGAKIVHIDI 319

Query: 396 IDSAEIGKNKTPHVSVCADVCLALQGMNKV--LENRAEELKLDGFWVRNENLVQKQKFPLS 454
ID++E KNK H+ + D+K AL +N++ + NR D W ++ K++ P
Sbjct: 320 IDASEHNKNKRHHPIVSDIKFALTRLNELAVANRFT--APDTAAWHAQITKWKKEHPFR 377

Query: 455 FKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAMG 514
F+ + I PQ A+ L ELT G A+I TGVGQHQMWAAQFY + +PR ++SS GLGAMG
Sbjct: 378 FEA-SKHIVPQEAVAALYELTKGDAVIVTGVGQHQMWAAQFYRFQPRHYISSLGLGAMG 436

Query: 515 FGLPAAIGASVANPDIAVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQW 574
FG PAA+GA VA PD VVDIDGDSF+MN+QELAT ++E + K ++LNNQHLGMV+QW
Sbjct: 437 FGYPAAALGAKVARPDQVVDIDGDSFLMNIQELATAKIEKIHAKAMILNNQHLGMVVQW 496

Query: 575 EDRFYKANRAHTFLGD-----PAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTM 628
EDRFY + R +T LGD P ++PN + A G+ RV K+DL+ AIQ M
Sbjct: 497 EDRFYGVSVRGNTILGDETNVGSFDNLGGLYPNFVQIAEGFGVKGRVHLKSDLKPAIQEM 556

Query: 629 LDTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
LD GPY+LDVI P+ EHVLPMP G T D++
Sbjct: 557 LDHDGPYVLDVIVPYTEHVLPMPAGKTVKDML 589

>ref|YP_001878250.1| acetolactate synthase, large subunit, biosynthetic type
[Akkermansia muciniphila ATCC BAA-835]
gb|ACD05469.1| acetolactate synthase, large subunit, biosynthetic type
[Akkermansia muciniphila ATCC BAA-835]
Length = 617

Score = 598 bits (1543), Expect = e-169, Method: Compositional matrix adjust.
Identities = 308/597 (51%), Positives = 408/597 (68%), Gaps = 21/597 (3%)

Query: 92 APDQPR-KGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFA 150
AP + R GA++LVE L R+GV+ VFAYPGGASM IHQAL+ IR +LPRHEQGG F
Sbjct: 10 APTKTRMTGAEVLVECLVREGVDVVFAYPGGASMPHIALSHQPKIRTLPRHEQGGAFG 69

Query: 151 AEGYARSSGKPGICIAITSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
AEGY R +GK G+CI+TSGPGATN+++ +ADA LDS PLVAIT QV R +IG AFQET
Sbjct: 70 AEGYGRVTGKVGVCISTSGPGATNMITSIADAYLDSTPLVAITAQVMRSLIGRGAFQETD 129

Query: 211 IVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVVKDIQQQLAIPNWEQA 270
+ +T I KH+YLV + E++PRII+EAF++A++GRPGPVL+D+PKD+Q+ + P+++
Sbjct: 130 VFGMTAPIVKHSYLVTEPEELPRIIEAFYIASTGRPGPVLIDMPKDVQEAVFTPDFDME 189

Query: 271 MKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLN--SDELGRFVELTGIPV 328
M +PGY +P P + LE+++ LI +++PV+Y GGG ++ +S +L F E + IPV
Sbjct: 190 MDIPGYNPVLVPAD--KLEELIPLIENARRPVIYAGGGIISAEASGDLLEFAERSQIPV 247

Query: 329 ASTLMGLSGYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASR 388
A+TLMG+G+ P LSL LGMHG V+AN AV +DL++A G RFDDRTG + F
Sbjct: 248 ATTLMGIGAMPETHPLSLRWLGMHGAFFANNAVNEADLVIALGARFDDRTGAVNMFCE 307

Query: 389 AKIVHIDIDSAEIGKNKTPHVSVCVDKLLAQGMNKVLENRAEELKLDGFGV---WRNEL 444
+ IVHIDID++EI KNK + +VK ALQ +N L + E K W +
Sbjct: 308 STIVHIDIDASEINKKKVAYPIRANVKDALQVLNSALAAKGERKSSGYTRTPWFVGVI 367

Query: 445 NVQKQKFPPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQ 503
+ K+++P S++ I PQ I+ L T D II TGVGQHQM+AAQF+ + KPR+
Sbjct: 368 DSWKKQYFPFSEYEDRKYIAPQAVIEELYRQTADKDPICITGVGQHQMFAAQFFKFDKPRR 427

Query: 504 WLSSGGLGAMGFLPAAIGASVANPDIVDIDGDSFIMNVQELATIRVENLPVKVLLL 563
+SGGLG MG+GLPA++GA +A PD +VV+IDGDGS +MN+QELATI VE LPVK ++L
Sbjct: 428 LATSGGLGTMGYGLPASMGLAYPDRLLVNIDGDSMLMNIQELATIHVERLPVKCIIL 487

Query: 564 NNQHLGMVMQWEDRFYKANRAHTFLGDP-----AQEDEFIPNMLLFAAACGIPAARV 615
NNQHLGMV+QWED Y +NRA TFL DP ED I+PN L A G+ RV
Sbjct: 488 NNQHLGMVQWEDLKYSNRAQTFLADPHDNDPHTKTEDVIYPNYPLICAGFGVKCERV 547

Query: 616 TKKADLREAIQTM LDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITE--GDGRIK 669
+ +L AI M+++P Y+LDV+ PH HVLPMI G ++ DVI E GDG K
Sbjct: 548 LRIEELPAAITRMIESPEAYVLDVMPHVDHVLPMILGMSYKDVILERIAGDGS AK 604

>dbj|BAF37288.1| acetolactate synthase [Monochoria vaginalis]
Length = 614

Score = 597 bits (1540), Expect = e-169, Method: Compositional matrix adjust.
Identities = 273/387 (70%), Positives = 334/387 (86%)

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGIPVASTLMGLGSY 338
R+PKPP L+QI+R++SES +PVLVGGG L++S+EL RF +LTGIP+ASTLMGLG Y
Sbjct: 228 RLKPPALHLLQQIIRILSESRPVLYVGGGSLHASEELRRFADLTGIPIASTLMGLGVY 287

Query: 339 PCDDLSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVHIDIDS 398
P D LSL MLGMHGTVYANYA++ +DLLLLAFGVRFDRTGKLEAFASRAKIVHIDID
Sbjct: 288 PLDGPLSLKMLGMHGTVYANYAIDKADLLLLAFGVRFDRTGKLEAFASRAKIVHIDIDP 347

Query: 399 AEIGKNKTPHVSVCQDVKLALQGMNKLLENRAEELKLDGFGVWRNELNVQKQKPLSFKTF 458
AEIGKNK PHVS+CGD+KLALQ MN+++E KLDF WR EL+ QK+ +PL +KTF
Sbjct: 348 AEIGKNKQPHVSICGDIKLALQEMNEMIEENGHISKLDGSAWREELDQKKNYPLKYKTF 407

Query: 459 GEAIIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGFGLP 518
G+ IPPQ+AI++L+ELT+G+AI+TGVGQHQMWAAQ+YNYK+PRQWL+S GLGAMGFGLP
Sbjct: 408 GDLIPPQHAIEELLEELTNGEAIITTVGVGQHQMWAAQYNYKKPRQWLTSAGLGAMGFGLP 467

Query: 519 AAIGASVANPDIAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWEDRF 578
AA+GA+V NP +VVDIDGDSF MN QELA IR+ENL VK+L+LNNQHLGMV+QWEDRF
Sbjct: 468 AAVGAAVGNPGVGVVDIDGDSFQMNQELAIIRIENLDVKMLILNNQHLGMVVQWEDRF 527

Query: 579 YKANRAHTFLGDPAQDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPYLLD 638
Y++NRAHT+LG+PA E ++FP+ + A + IPAA V+KK+++R+AI+ M+ TPGPYLLD
Sbjct: 528 YQSNRAHTYLGPNANESKVFDFVKLAESYDIPAAVSKKSEVRDAIRKMIQTTPGPYLLD 587

Query: 639 VICPHQEHVLPMPNGGTFNDVITEGD 665
VI PH+EHVLPMP+GG F D+I +GD
Sbjct: 588 VIVPHEEHVLPMPISGGAFAKDMILDGD 614

Score = 212 bits (539), Expect = 1e-52, Method: Compositional matrix adjust.
Identities = 102/120 (85%), Positives = 110/120 (91%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFA 150
FAPD+PRKGADILVEALER+GV +FAYPGGASMEIHQALTRS SI N L RHEQG FA
Sbjct: 40 FAPDEPRKGADILVEALEREVTDLFAYPGGASMEIHQALTRSPSITNHLRHEQGEAFA 99

Query: 151 AEGYARSSGKPGICIAITSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETP 210
A GYARS+G+PG+CIATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAFQETP
Sbjct: 100 ASGYARSTGRPGVCIATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAFQETP 159

>ref|ZP_01922597.1| acetolactate synthase, large subunit, biosynthetic type
[Victivallis vadensis ATCC BAA-548]
gb|EDM96972.1| acetolactate synthase, large subunit, biosynthetic type
[Victivallis vadensis ATCC BAA-548]
Length = 586

Score = 574 bits (1480), Expect = e-162, Method: Compositional matrix adjust.
Identities = 304/587 (51%), Positives = 404/587 (68%), Gaps = 31/587 (5%)

Query: 98 KGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARS 157
KG++I ++ LE GV+ VFAYPGG ++E+HQAL+RS +R VLPHEQGG FAA GYAR+
Sbjct: 10 KGSEITIKCLELLGVVDVVFAYPGGQAIELHQALSRSG-MRVVLPHEQGGFAAGGYARA 68

Query: 158 SGKPGICIAITSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
SG+ G+C+ATSGPGATNLVSG+ADA +DS+P V ITGQVP MIG + FQET I+ VTR
Sbjct: 69 SGRVGVCMATSGPGATNLVSGIADAYMDSIPTVFITGQVPSSMIGKNVFQETDIIGVTRP 128

Query: 218 ITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLDVDPKDIQQQLAIPNWEQAMKLPGYM 277
I KH++LV+D DIPRI+ EAF++A SGRPGPV+VD+PK++QQQ +++QA +L Y
Sbjct: 129 IVKHSFLVLDANDIPRIMREAFYIAQSGRPGPVVDIPKNVQQQCKVDFDQAPELKYYH 188

Query: 278 SRMPKPPED-SHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMG 334
P P D + + +I +I+ SK+P +Y GGG +++ S+EL +F E IPV +TLMG
Sbjct: 189 ---PDPALDPAAVGKIKAMIAASKRPCIYAGGGIISAGASEELVKFAESYNIPVVTTLMG 245

Query: 335 LGSYPCCDELSDLHMLGMHGTIVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIVHI 394
+G+ P LSL LGMHGTIVYANYA DLLAFG RFDDRVTG ++FA AKIVH+
Sbjct: 246 IGAIPDSHPLSLRWLGMHGTIVYANYAANECDDLLAFGARFDDRVTGNPKSFAVGAKIVHV 305

Query: 395 DIDS AEIGKNKTPHVSVCQDVKLALQGMNKLLENRAEELKLDGFGVWRNELNVQKQKPLS 454
DID +EI KNK + V D++ L +N+ E + ++ W + K+K+P
Sbjct: 306 DIDDSEINKNKPADLGLADIREVLTKLNEAPEPQ-----EYAEWFARIREWKKKYPFH 359

Query: 455 FKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAMG 514
++ + + PQ+ ++ L LT G+A+I GVGQHQMWAAQ+Y+Y PRQ L+SGGLGAMG
Sbjct: 360 YRNKPDHVQPQFVMTLSRLTRGQAVIVPGVQHQMWAAQYDYNYPRQLLTSGLGAMG 419

Query: 515 FGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQW 574
FGLPAA+GA VA P+ V++IDGDSF MN+QEL T+ VE +PVK+++L+NQHLGMV QW
Sbjct: 420 FGLPAAMGAKVACPEKTVINIDGDSFQMNQELGTLFVEEIPVKMIILDNQHLGMVAQW 479

Query: 575 EDRFYKANRAHTFLGDPAQEDEI-----FPNMLLFAAACGIPAARVT 616
EDRFY NR +T LG + +P+ ++ A GIP V
Sbjct: 480 EDRFYHNHNRGNTVLGRCKSGNGCGSAKNCDDCDGTRCTGRPYPDFVMIANGYGIPGRNVF 539

Query: 617 KKADLREAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITE 663
+ +L AI+ ML GP+LLDV ++EHVLPMP GG + +I E
Sbjct: 540 TREELVPAIEEMLAADGPFLLDVHTGYEEHVLPMPGGDYTAIIME 586

>ref|YP_001930430.1| acetolactate synthase, large subunit, biosynthetic type
[Sulfurihydrogenibium sp. YO3AOP1]
gb|ACD65876.1| acetolactate synthase, large subunit, biosynthetic type
[Sulfurihydrogenibium sp. YO3AOP1]
Length = 582

Score = 556 bits (1432), Expect = e-156, Method: Compositional matrix adjust.
Identities = 287/572 (50%), Positives = 385/572 (67%), Gaps = 17/572 (2%)

Query: 97 RKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSIRNVLPHEQGGVFAAEGYAR 156
++GADI+V+ L ++GV+TVF PGGA ME++ AL + RNVL RHEQ A+GYAR
Sbjct: 5 KRGADIVVDVLIKEGVDTVFGLPGGAIMEVYDALF-DAPFRNVLPTRHEQAACHMADGYAR 63

Query: 157 SSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTR 216
++GK G+ IATSGPGATNLV+GLA A +DS+PLVAITGQVPR IGTDFAQE ++ +TR
Sbjct: 64 ATGKVGVIATSGPGATNLVTGLATAYMDSIPLVAITGQVPRHYIGTDAFQEADVIGITR 123

Query: 217 SITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQ---LAIPNWEQAMK- 272
ITKHN+LV D++D+P I+ +AF++A +GRPGPVLVD+PKDI QQ +P E+ +
Sbjct: 124 PITKHNFLVTDIKDLPLILRQAFYIARTGRPGPVLVDIPKIDITQQKTTYKMPTDEEVRES 183

Query: 273 LPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVAS 330
LPGY P +++ LI ++ +PVLYVGGG + ++++E+ + L IPV +
Sbjct: 184 LPGYNPHTEGNP--VQIKKAAELIRKATRPVLYVGGGAILSDAAEEIYKLAHLAQIPVTT 241

Query: 331 TLMGLSGSPCDELSELHMLGMHGTVYANYAVEHSDLLAFGVRFDRTVTGKLEAFASRAK 390
T MG G++P D LSLHMLGMHGT YAN AV HSDLL+A G RFDDRTVTGK+ FA AK
Sbjct: 242 TNMGKGAFFETDPLSLHMLGMHGTYYANMAVYHSDLLIAGGARFDDRTVTGKINEFAPEAK 301

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWVRNENLVQKQK 450
I+HIDID A I K T V + GDVK L+ + K LE + E W ++N K+K
Sbjct: 302 IIVHIDIDPASISKTITVDVPIVGDVKNVLRKLIKEEKPIEWIAAREQWLKQINWEKEK 361

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
PL+++ + I PQ I+ + +T+G+AIIS GVGQHQMWAQ FY YK PRQ+L+SGGL
Sbjct: 362 HPLNYRKSDKIIKPQAVIEEIYNITNGEAIISAGVGQHQMWAAMFYKYKPRQFLNSGGL 421

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
G MGFG PAA+GA + PD V I+GDGDSFIMNVQ+LAT +PVK+ ++NN LGM
Sbjct: 422 GTMGFGFPAAGAKIGRPDKTVFAIEGDGDSFIMNVQDLATAVQYRVPVKIAIINNGFLGM 481

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREA-IQTML 629
V QW+ FY + A L + P+ + A + G R TK +++RE ++ M
Sbjct: 482 VRQWQQFFYDSRYASVCL-----SVQPDFVKLAESFGAVGLRATKPSEVREVLLKAME 534

Query: 630 DTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
P L+D + +E+VLPM+P G ++ ++I
Sbjct: 535 INDRPVLMDVFVDKEENVLPMPVAGKSYREMI 566

>ref|ZP_01923625.1| acetolactate synthase, large subunit, biosynthetic type
[Victivallis vadensis ATCC BAA-548]
gb|EDM95893.1| acetolactate synthase, large subunit, biosynthetic type
[Victivallis vadensis ATCC BAA-548]
Length = 561

Score = 549 bits (1415), Expect = e-154, Method: Compositional matrix adjust.
Identities = 280/568 (49%), Positives = 386/568 (67%), Gaps = 14/568 (2%)

Query: 98 KGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARS 157
KGA+I + LER G+E VFAYPGG+++E HQAL S IR +LPRHEQGG FAA GYAR+
Sbjct: 6 KGAEITIRTLERLGIELVFAYPGGSAIEFHQALA-DSPIRVILPRHEQGGGAFAACGYARA 64

Query: 158 SGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
+G+ G+C+ATSGPGATNL++G+ADA +DSVPLV ITGQV ++IG +AFQET I+ +TR
Sbjct: 65 TGRTGVCMATSGPGATNLLTGADAYMDSVPLVIITGQVESKLIGRNAFQETDIIGMTRP 124

Query: 218 ITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYM 277
I KH+YLV M E++ + + +AF+LA SGRPGPV +D+PKD+QQ+ + + +
Sbjct: 125 IVKHSYLVMPKEELSQTVTDAFYLANSGRPGPVWIDIPKDVQQRRL--EFRFCPEPSPSEL 182

Query: 278 SRMPKPPEDSHLEQIVRLISESKKPVLY--VGGGCLNSSDELGRFVELTGIPVASTLMGL 335
R P + E ++ I+ S++P +Y G +++EL RF E IPVA++LMG+
Sbjct: 183 IRKPPAVTEQDCEAVLAAIARSRRRCIYAGGGVIAAGAAEELTRFAEGFNIPVATSLMGI 242

Query: 336 GSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIVHID 395
G++P D LSL LGMHG+ YANYA DLLAFG RF DR TG + FA A+I+HID
Sbjct: 243 GAFPEDHPLSLKWLGMHGSYYANYAANECDLLAFGARFADRSTGNPDEFARPARIIHID 302

Query: 396 IDSAEIGKNKTPHVSVCVDVKLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQKPLSF 455
ID +EI KN + + D++ L+ +N+ R ++ W N + K+ PL++
Sbjct: 303 IDPSEINKNVRADLGITADIREFLERLNRTPRFR-----EYAEWHNRIAGWKRAHPLAY 356

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQAQFYNYKKPRQWLSSGGLGAMGF 515
+ + PQ I+ + + G A+I GVGQHQMWAQAQFY + +PRQ L+SGGLG+MGF
Sbjct: 357 RDEPGKVQPQRVIETICRMA-GDAVIVPGVGQHQMWSAQFYTFQPRQLTSGGLGSMGF 415

Query: 516 GLPAAIGASVANPDIAIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
GLPAA+GA +A P+A V++IDGDSF MN+QEL TI E + VK+++LNNQHLGMV Q E
Sbjct: 416 GLPAAMGAKLARPEATVINIDGDSFQMNIQELGTIATEEIAVKMVLNNQHLGMVAQLE 475

Query: 576 DRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPY 635
DRFY + R +T L + + FP+ A GIP+ V A+L +AI+ ML+TPGP+
Sbjct: 476 DRFYHSRRGNNTDLR--VRGERPFPDFAGIARCYGIPSREVYDPAELEDIAIREMLETPGPF 533

Query: 636 LLDVICPHQEHVLPMPNGGTFNDVITE 663
LLD + +HVLPMIP G ++ ++ITE
Sbjct: 534 LLDCHTVYLDHVLPMIPGGKSYREIITE 561

>ref|ZP_01188450.1| Acetolactate synthase, large subunit, biosynthetic type
[Halothermothrix orenii H 168]
gb|EAR80052.1| Acetolactate synthase, large subunit, biosynthetic type
[Halothermothrix orenii H 168]
Length = 555

Score = 548 bits (1413), Expect = e-154, Method: Compositional matrix adjust.
Identities = 283/568 (49%), Positives = 384/568 (67%), Gaps = 25/568 (4%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA+I+V++L ++ V+ +F YPGGA + I+ L S I + L RHEQG + AA+GYARS+
Sbjct: 6 GAEIVVQSLLEKVKDIFGYPGGAVLPIDVL-YDSPINHYLTRHEQGAIIHAADGYARST 64

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
G+ G+CIATSGPG+TNLV+GLA A +DSVP+VA TGQV IG DAFQE I +T I
Sbjct: 65 GEVGVCIATSGPGSTNLVTGLATAYMDSVPVVAFTGQVTTNFIGKDAFQEADIRGITIPI 124

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNYLV D++D+ R I+EAF+LA +GRPGPVL+D+PKDI + + ++LPGY
Sbjct: 125 TKHNYLVTDIQLARTIKEAFYLARTGRPGPVLIDIPKDITRDKCEFYVPDKVELPGY-- 182

Query: 279 RMPKPPEDSHLEQIVRL--ISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLM 333
P H QI + I++++KPV++ GGG + S S EL + V+ + IP+ ++LM
Sbjct: 183 ---DPTYRGHKLQINKAAHEINKAEKPVIFAGGGVIASEASTELRKLKVKSSIPITSLM 239

Query: 334 GLGSPYCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIVH 393
GLG YP +D LSL M GMHGT YANYA+ +DLL+A GVRFDDRVTKG+E FA AKI+H
Sbjct: 240 GLGIYPENDFLSLGMPGMHGTTRYANYAISEADLLVAVGVRFDDRVTKIEEFAPDAKIIH 299

Query: 394 IDIDSAEIGKNKTPHVSVCVDVKLALQGMNKVLENRAEELKLDGFWRNELNVQKQKFP 453
IDID AEI KN H+ + GD + L+ + ++E++ + G W ++ K+K PL
Sbjct: 300 IDIDPAEICKNVEAHIPIVGDARNILKELLPLIEHK-----ERGAWLQQIKWEKEKNPL 353

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAM 513
++ I PQY I+ L ELT G+AIIST VGQ+QMWAAQ+Y Y PR +LSSGGLG M
Sbjct: 354 KYEQSETNIKPYVIEKLYELTGGEAIISTEVGQNQMWAAYYKYSHPRTFLSSGGLGTM 413

Query: 514 GFGLPAAIGASVANPDIAIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQ 573
G+G PAAIGA V NPD +V+DI GDGS MN+QELAT+ NLPVK+++LNN +LGMV Q
Sbjct: 414 GYGFPAAIGAQVGNPDRVVIDIAGDGSIQMNIQELATVSNNYLPVKIILNNSYLMVMRQ 473

Query: 574 WEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPG 633
W++ FY + T L + P+ + A A G+ A ++ KK +++ A++ +L G
Sbjct: 474 WQELFYDKRYSSTGLKN-----PDFIKLAEAYGVYALKIDKKDEVKPALEKILSVNG 525

Query: 634 PYLLDVICPHQEHVLPMPNGGTFNDVI 661
P LLDV +E+V PM+P G +I
Sbjct: 526 PALLDVRIEEENVFPMVPQGAGIKMI 553

>ref|ZP_02177150.1| acetolactate synthase large subunit [Hydrogenivirga sp. 128-5-R1-1]
gb|EDP76188.1| acetolactate synthase large subunit [Hydrogenivirga sp. 128-5-R1-1]
Length = 583

Score = 548 bits (1412), Expect = e-154, Method: Compositional matrix adjust.
Identities = 281/583 (48%), Positives = 392/583 (67%), Gaps = 25/583 (4%)

Query: 97 RKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPREHQQGVFAAEGYAR 156
RKGADI++E L+ +GVE +F PGGA ME++ AL R SI+++L RHEQG AEGYA+
Sbjct: 3 RKGADIVITLKEEGVEVIFGLPGGAIMEVYDALYRDSIKHILARHEQGAGHMAEGYAK 62

Query: 157 SSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTR 216
++GK G+ + TSGPGATN+V+ +ADA +DSVP+V ITGQVP MIG DAFQE IV +TR
Sbjct: 63 ATGKVGAMTTSGPGATNIVTPIADAYMDSVPMVVITGQVPTHMIGNDAFQEVDIVGITR 122

Query: 217 SITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLA---IPNWEQAMK- 272
ITKHN+LV D++++P +I +AF++A++GRPGPVLVD+PKDI QQL+ IP+ ++ +
Sbjct: 123 PITKHNFVLRDIDELPLVIRKAFYIASTGRPGPVLVDIPKDIQQQLSDVKIPSMDEVKRS 182

Query: 273 LPGYMSRMPKPPEDSHLEQI---VRLISESKKPVLYVGGGCLNSS--DELGRFVELTGIP 327
LPGY KP + +++QI +LI E+K+PVLYVGGG +NS +EL EL IP
Sbjct: 183 LPGY-----KPHVEGNIQIKKAAKLIMEAKRPVLYVGGGAVNSEAQEELIELAELMKIP 237

Query: 328 VASTLMGLGSPYCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFAS 387
V +T G G++P D L+L MLGMHGT YAN AV +SDLL+A G RFDDRVTKG++ FA
Sbjct: 238 VTTTQKQGAFFEDHPLALRLMLGMHGTYYANMAVYNSDLLIAVGARFDDRVTKGIDEFAP 297

Query: 388 RAKIVHIDIDSAEIGKNKTPHVSVCVDVKLALQGMNKVLENRAEELKL--DFGVWRNELN 445
AKI+HIDID A I KN V + GDVK+ L+ + L+ + ++ + W ++
Sbjct: 298 DAKIIHIDIDPASISKNIIVDVPVIGDVKIVLRKLINELKRKGAKIAYPEERERWIEQIE 357

Query: 446 VQKQKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWL 505
K+ PL+++ + I PQY I+ + ++T+G AII GVGQHQMWAA F+ Y PRQ+L
Sbjct: 358 KWKKLHPLTYRNSKKVIKPYVIEQIHKVTNGDAIIVPGVGQHQMWAAAMFFKYSYPRQFL 417

Query: 506 SSGGLGAMGFGLPAAIGASVANPDIAIVDDIDGDSFIMNVQELATIRVENLPVKVLLNN 565
+SGGLG MGFGLPA IGA V P+ V +DGDGSF+M +QE+ T +PVKV ++NN
Sbjct: 418 NSGGLGTMGFGLPAGIGAKVGRPEKEVFVVDGDSFVMTMQEIITAVQYRIPVKVAIINN 477

Query: 566 QHLGMVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAI 625
+LGMV QW++ FY + L + P+ + A + G R K ++RE +
Sbjct: 478 AYLGMVRQWQELFYDKRYSEVDLS-----LQPDFVKLAESMGAVGFRAEKPKEVREIL 530

Query: 626 QTMLDT-PGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGR 667
+ + P ++D + +E+VLPM+P G ++ D+I E DG+
Sbjct: 531 EEAMKIDDKPIMDFVVDREENVLPMPVPGKSYKDMILE-DGK 572

>ref|NP_213319.1| acetolactate synthase large subunit [Aquifex aeolicus VF5]
gb|AAC06706.1| acetolactate synthase large subunit [Aquifex aeolicus VF5]
Length = 585

Score = 542 bits (1396), Expect = e-152, Method: Compositional matrix adjust.
Identities = 285/583 (48%), Positives = 386/583 (66%), Gaps = 19/583 (3%)

Query: 97 RKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVF AAEGYAR 156
+KGADI++E L+ +GVE VF PGGA ME++ AL R I+++L RHEQG AEGYA+
Sbjct: 4 KKGADIVIETLKAEGVEVVFGLPGGAIMEVVDALYRLGGIKHILARHEQAGHMAEGYAK 63

Query: 157 SSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTR 216
++GK G+ + TSGPGATNLV+ +ADA +DSVPLVAITGQVP +IG DAFQE IV +TR
Sbjct: 64 ATGKVGVMVMTSGPGATNLVTPIADAYMDSVPLVAITGQVPTH LIGNDAFQEVDIVGITR 123

Query: 217 SITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLA---IPNWEQA-MK 272
ITKHN+LV +E++P I+ EAF++A +GRPGPVLVD+PKD+ QQ+A IP+ E+
Sbjct: 124 PITKHNFLVKSIEELPLILREAFYIARTGRPGPVLVDLPKDVTTQIADVKIPSDEEVKAA 183

Query: 273 LPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVAS 330
LPGY + P+ +++ LI +K+PVLYVGGG +NS +EL EL IPV +
Sbjct: 184 LPGYKPHVEGNPQ--QIKKAAELIMSAKRFPVLYVGGGAVNSEAQEELIELAELMQIPVTT 241

Query: 331 TLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRV TKGLEAFASRAK 390
T G G++P LSL MLGMHGT YAN AV +SDLL+A G RFDDRV TKG++ FA AK
Sbjct: 242 TTQKGGAFFPETHPLSLRMLGMHGTYYANMAVYNSDLLIAVGARFDDRV TKGIDEFAPGAK 301

Query: 391 IVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKL--DFGVWRNELNVQK 448
I+HIDID A I KN T V + GDVK+ L+ + ++ R ++ + W ++ K
Sbjct: 302 IIHIDIDPASISKNITVDVPIVGDVKIVLRKLINEIKKRGAKILYPEERKKWLEQIEKWK 361

Query: 449 QKFPLSPKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSG 508
+ PL+++ + I PQY I+ L E T+G+AI GVGQHQMWA FY +K PRQ+++SG
Sbjct: 362 KLHPLTYRNSDKVIKQYVIEQLWEATNGEAIIVPGVGQHQMWAAMFYKFKYPRQFINSG 421

Query: 509 GLGAMGFLPAAIGASVANPD AIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQHL 568
GLG MGFGLPA IGA + PD V +DGDGSF+M +QE+ T +PVKV ++NN +L
Sbjct: 422 GLGTMGFLPAGIGAKIGRPDREVWVDGDSFVMTMQEVITAVQYKVPVKVAIINNAYL 481

Query: 569 GMVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTM 628
GMV QW++ FY + L + P+ + A A G R K ++RE I+
Sbjct: 482 GMVRQWQELFYDKRYSEVDL-----SVQPDFVKLAEMGAVGMRAKKPKREVREVEEA 534

Query: 629 LDTPG-PYLLDVICPHQEHVLP MIPNGGTFNDVITEGDGRIKY 670
P ++D +E+VLP M+P G ++ D+I E DG+ K+
Sbjct: 535 RKIDDRPVIIDFWVDREENVLP MVPAGKSYKDMILE-DGKGKH 576

>ref|ZP_03135286.1| acetolactate synthase, large subunit, biosynthetic type [Thermus
aquaticus Y51MC23]
gb|EDY14029.1| acetolactate synthase, large subunit, biosynthetic type [Thermus
aquaticus Y51MC23]
Length = 561

Score = 538 bits (1385), Expect = e-151, Method: Compositional matrix adjust.
Identities = 281/570 (49%), Positives = 382/570 (67%), Gaps = 23/570 (4%)

Query: 98 KGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVF AAEGYARS 157
KGA+ L++ALER+GVE +F +PGGA M + AL S IR++L RHEQGG+ AA YAR+
Sbjct: 2 KGAEALLKALEREVEVIFGHPGGAIMPTYDALY-DSPIRHILVRHEQGGIHAATAYARA 60

Query: 158 SGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
SG+ G+ +ATSGPGA NLV+GLADA++DS P+VAITG VPR +IGTDAFQE + VT
Sbjct: 61 SGRVGVVMATSGPGALNLVTGLADAMMDSTPVVAITGNVPRALIGTDAFQEADV TGV TMP 120

Query: 218 ITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQAMKLPGYM 277
ITKHNLYL DV +IPR+++EAF +A++GRPGPVL+D+PKD+Q ++ + LPGY
Sbjct: 121 ITKHNLYLQDVNEIPRVVKEAFHIASTGRPGPVLIDL PKDVQLAEFTGEFVDLDPGY- 179

Query: 278 SRMPKPPEDSHLEQIVR---LISESKKPVLYVGGGCLNSSDELGRFVELTGIPVASTLMG 334
 KP H +QI R + +++P+L VGGG ++ EL F E TG+PV +TLMG
 Sbjct: 180 ----KPTLRGHPKQIERALDALEKAERPILMVGGGAQHAAHALLAFAEKTGLPVITITLMG 235

Query: 335 LGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAK-IVH 393
 LG++P+ L L M GMHGTV AN A+ H+D++LA G+RFDDRVTGK+ FA A I+H
 Sbjct: 236 LGAFPGNHPLWLGMPPGMHGTVAANRAIHADVILAIGLRFDDRVTGKVSFAPHAHTIIH 295

Query: 394 IDIDSAEIGKNKTPHVSVCVGDVKLALQGMNKLLENRAEELKLDGFWRNELNVQKQKFP 453
 +DID AEIGK H+ + GD +L L+ M K A+ L+L W EL + ++PL
 Sbjct: 296 VDIDPAEIGKVVRTHIPVIGDSRLVLKEMLK----GAKPLRL--AAWWRELEEWRTYPL 349

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAM 513
 ++ P+ I+ E T G AI++TGVGQHQM+AAQ++ +PR +L+SSGGLG M
 Sbjct: 350 RYRPRPHLQAPE-VIRAFHEATGGNAIVTTGVGQHQMFAAQYFTVTRPRSF LTSGGLGTM 408

Query: 514 GFGLPAAIGASVANPDAIVVDIDGDGSGFIMNVQELATIRVENLPVKVLLNNQHLGMVMQ 573
 G GLP AIGA +A P+ +V+D DGDGSGF M +QELAT+ LPVKV++LNN +LGMV Q
 Sbjct: 409 GVGLPFAIGAQIARPEELVIDFDGDGSGFQMTLQELATVVKYRLPVKVILNNGYLGVMVRQ 468

Query: 574 WEDRFYKANRAHTFLGDPAQEDEFPMNMLLFAAACGIPAAARVTKKADLREAIQTMLDTPG 633
 W+D F+ + +L D P+ A A GI RV +K DL++ ++ +L+ G
 Sbjct: 469 WQDLFHAKRYSEVYLADSN-----PDFAKLAEAYGIKGVVERKEDLKKGVEAVLNADG 522

Query: 634 PYLLDVICPHQEHVLPMPNGGTFNDVITE 663
 P + + H+E V PMIP GG D+I E
 Sbjct: 523 PVVAEFKVYHEEGVFPMPAGGAAEDMILE 552

>ref|YP_001111655.1| acetolactate synthase, large subunit, biosynthetic type
 [Desulfotomaculum reducens MI-1]
 gb|ABO48830.1| acetolactate synthase, large subunit [Desulfotomaculum reducens
 MI-1]
 Length = 554

Score = 538 bits (1385), Expect = e-151, Method: Compositional matrix adjust.
 Identities = 276/568 (48%), Positives = 385/568 (67%), Gaps = 25/568 (4%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
 GA IL+++L+ GV+T+F YPGG+++ I+ AL S IR++L RHEQG V AA+GYAR+S
 Sbjct: 6 GAKILLDSLKEMGVDTIFGYPGGSAPIYDALY-DSDIRHILCRHEQGAVHAADGYARAS 64

Query: 159 GKPICIAITSGPGATNLVSLGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
 GK G+C+ATSGPGATNLV+G+A+A +DS+PLVAITGQVP M+G D+FQE I +T I
 Sbjct: 65 GKVGVCLATSGPGATNLVTGIANAYMDSIPLVAITGQVPTSMGLRDSFQEADITGITLPI 124

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
 TKHNY+V D+ ++ +++++EAF +A SGRPGPVL+D+PKDI + LPGY
 Sbjct: 125 TKHNYIVKDINELGKVVEAFHIAASGRPGPVLIDIPKDISAGEMDYQPNGPVDLPGY-- 182

Query: 279 RMPKPP---EDSHLEQIVRLISESKKPVLYVGGGCLNSS--DELGRFVELTGIPVASTLM 333
 KPP + + Q RLI+ S++PV+Y GGG +++ +EL + E PVA+TLM
 Sbjct: 183 ---KPPGMAREDLVNQAFRLIAVSRPVIYAGGGIISAGAHEELKKLAETILAPVATITLM 239

Query: 334 GLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIVH 393
 GLG +P D L+L MLGMHGT YAN+A+ DLL+A GVRFDDRVTGK+E+FA AKI+H
 Sbjct: 240 GLGGFPGDHALALGMLGMHGTKYANFAICDCDLLIAVGVRFDDRVTGKVESFAPNAKIIH 299

Query: 394 IDIDSAEIGKNKTPHVSVCVGDVKLALQGMNKLLENRAEELKLDGFWRNELNVQKQKFP 453
 IDID AE+GKN V + G+VKL LQ + + ++ R E W++++ K+++PL
 Sbjct: 300 IDIDPAELGKNVRVDVPIAGNVKLVLLQQLLERVQTRIFE-----AWQHKVAQWKKEYPL 353

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAM 513
 F GE + PQY I+ + T G+A I+T VGQHQMWAA +Y Y KPR ++SSGGLG M
 Sbjct: 354 DFDENGEGLTPQYVIREIYRQTGGEARIEVVGQHQMWAAHYTYTKPRSFISSGGLGTM 413

Query: 514 GFGLPAAIGASVANPDAIVVDIDGDGSGFIMNVQELATIRVENLPVKVLLNNQHLGMVMQ 573
 G+G PAAIG VA P+ V DI GDGS MN+QELAT +LPV + ++NN +LGMV Q
 Sbjct: 414 GYGFPAAIGVQVACPEETVFVDIAGDGSIQMNIQELATAVDYDLPVNIAMNNGYLGVMVRQ 473

Query: 574 WEDRFYKANRAHTFLGDPAQEDEFIFPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPG 633
W++ FY NR ++++ + PN + A A G +VT+K ++ E +Q + +
Sbjct: 474 WQELFY--NRRYSYV-----EMKSPNFVKLAAYGAEGYQVTRKDEVAEVMQAAVQSRK 525

Query: 634 PYLLDVICPHQEHVLPMPNGGTFNDVI 661
P L+D + + +VLP +P G N+++
Sbjct: 526 PVLMDVFVEREGNVLPFVPPGKALNEML 553

>ref|YP_001568611.1| acetolactate synthase, large subunit, biosynthetic type [Petroto-
mobilis SJ95]
gb|ABX32288.1| acetolactate synthase, large subunit, biosynthetic type [Petroto-
mobilis SJ95]
Length = 569

Score = 538 bits (1385), Expect = e-151, Method: Compositional matrix adjust.
Identities = 271/567 (47%), Positives = 381/567 (67%), Gaps = 25/567 (4%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA I VE+L R+ VE VF YPGG + ++ L + I+++L RHEQG AA+GYARS+
Sbjct: 6 GARIFVESLLREKVEVVFYGGKVIPLYDEL-YDAPIKHILVRHEQGAHAADGYARST 64

Query: 159 GKGPGICIATSGPGATNLVSLGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+CIATSGPGATNLV+GLA A +DSVP+VA TGQ P +IGTD+FQE I +T +
Sbjct: 65 GKVGVCIATSGPGATNLVTGLATAYMDSVPVVAFTGQAPTSIGTDSFQEIDIRGITLPV 124

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY+V +V+D+ + I+EAF++A +GRPGPVL+D+P D+ + A + +++ LPGY
Sbjct: 125 TKHNYMVTNVKDLAKTIKEAFYIARTGRPGPVLIDLVDVLKSHADFMYPESVHLPGY-- 182

Query: 279 RMPKPPEDSHLEQI---VRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLM 333
+P + + QI I+ S++PV++ GGG +NS S+EL IPV ++LM
Sbjct: 183 ---QPTYEGNYMQIKLAAETINTSQRPFVIFAGGGVINSNASEELTNMAIKGRIPVVTSLM 239

Query: 334 GLGSPCDDELSDLHMLGMHGTVYANYAVEHSDLLAFGVRFRDVRTGKLEAFASRAKIVH 393
GLG +P D ELSL MLGMHGT+YANYA+ +DL++ GVRFRDVRTGKLE FA AKI+H
Sbjct: 240 GLGVFPEDHESLKMMLGMHGTMYANYAISEADLIIGVGRFRDVRTGKLETAFPHAKIIH 299

Query: 394 IDIDSAEIGKNKTPHVSVCQDVKLALQGMNKLLENRAEELKLDGFWRNELNVQKQKFPL 453
IDID AEI KN + + G+ K L + +++ ++ W ++ K++FPL
Sbjct: 300 IDIDPAEINKNVKVDIPIVGNKLVLDKLIPLIKT-----IERKEWLEQIKWKRRFPL 353

Query: 454 SFKTFGEAIPPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAM 513
+++ +I PQY I+ LDELTD +I T VGQ+QMWAAQ++ + KPR +++SGGLG M
Sbjct: 354 NYEYDDNSIKPQYLIEKLDELTDENTVIVTEVGQNQMWAQYFRFSKPRSFITSGGLGTM 413

Query: 514 GFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQ 573
G+GLPA++G V NP+ V++I GDGSF MN+QELATI LPVK++LNN LGMV Q
Sbjct: 414 GYGLPASVGVQVGNPNKTVINISGDGSFQMLNQLATISSNRLPVKIIILNNGTLGMVRQ 473

Query: 574 WEDRFYKANRAHTFLGDPAQEDEFIFPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPG 633
W++ F+ + T L + P+ + A A GI + R+ + D+ A++ L+ G
Sbjct: 474 WQELFFDERYSVTILEN-----PDFVKLAQAYGIKSLRIDQTNDVEMALKEALNYDG 525

Query: 634 PYLLDVICPHQEHVLPMPNGGTFNDV 660
P LLDVI P E+V PM+P G + N++
Sbjct: 526 PVLLDVIIPQDENVFMVPEGASINEM 552

>ref|NP_952960.1| acetolactate synthase, large subunit, biosynthetic type [Geobacter
sulfurreducens PCA]
gb|AAR35287.1| acetolactate synthase, large subunit, biosynthetic type [Geobacter
sulfurreducens PCA]
Length = 566

Score = 536 bits (1382), Expect = e-150, Method: Compositional matrix adjust.
Identities = 275/571 (48%), Positives = 376/571 (65%), Gaps = 20/571 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA IL+E L+ +GV+TVF YPGG + I+ L IR++LPRHEQ GV AA+G+AR++
Sbjct: 5 GARILLECLKLEGVDTVFGYPPGTVINIYDELFSFKEIRHILPRHEQAGVHAADGFARAT 64

Query: 159 GKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
G+ G+ IATSGPGATN V+G+A A +DS+P+V ITGQVP +IG DAFQE IV +TR
Sbjct: 65 GRVGVAIATSGPGATNTVTGTIATAYMDSIPVVITGQVPTALIGNDAFQEVDIVGITRPC 124

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHN+LV DV+DIP II++AF++A +GRPGPVLVD+PKD+Q A ++ +++L Y
Sbjct: 125 TKHNFLVKDVKDIPSIKKAFYIARTGRPGPVLVDLPKDVQIATAEFHYPDSEIELRSY-- 182

Query: 279 RMPKPPEDSHLEQI---VRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLM 333
KP + H +QI V L+ E+KKPV+YVGGG + +++ EL F + +PV +TLM
Sbjct: 183 ---KPTVEGHKQIEKAVSLMLEAKKPVIIYVGGGVISGDAAGELYDFAKKLNMPVTTTLM 239

Query: 334 GLGSGPCDDELSTHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVH 393
GLGS+P DD +L +LGMHGT YAN AV + D+L A G RFDDRTGK+ FA AKI+H
Sbjct: 240 GLGSFPEDDHQALRLMLGMHGTYYANMAVTNCDMLFAVGARFDDRTGKVATFAPHAKEI 299

Query: 394 IDIDSAEIGKNKTPHVSVCGLKALQGMNKLVE---NRAEELKLDGFWVRNENLVQKQK 450
+D+D I KN + + G+VK L M KVLE ++ E + W E+ KQK
Sbjct: 300 VDVDPSTIRKNVRVDLPVIGEVKKVLSQMLKVLEEQGDKVERFRTGIEPWWAEIEGWKQK 359

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGHQMWAAQFYNYKKPRQWLSSGGL 510
P+++K I PQY I+ L EL++ AII+T VGHQMW AQF+ + K R LSSGGL
Sbjct: 360 HPMTYKQTTSTVIKQYVIQKRELSEPDIIATDVGQHMWTAQFFTTKARTLLSSGGL 419

Query: 511 GAMGFGLPAAIGASVANPDIVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
G MG+GLPAA+GA A PD V+ I GDG F MN+QELAT+ LPVK+ +LNN LGM
Sbjct: 420 GTMGYGLPAAMGAQAAYPDRQVIAICGDDGGFQMNMQELATLVQNRPLVKICILNNNPLGM 479

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V QW++ F+ + T + P + + A A G + +K ++ I+ +
Sbjct: 480 VRQWQELFFDRYSQTCMELPI-----DFIKLAEAFGATGLQASKVDEVEGTIKKAFE 532

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTNDVI 661
TPGP +++ +E VLPM+P G + N+++
Sbjct: 533 TPGPVIMEFKIAREEKVLPMPAGASLNEMV 563

>ref|YP_001046985.1| acetolactate synthase, large subunit, biosynthetic type
[Methanoculleus marisnigri JR1]
gb|ABN57003.1| acetolactate synthase, large subunit [Methanoculleus marisnigri
JR1]
Length = 558

Score = 536 bits (1380), Expect = e-150, Method: Compositional matrix adjust.
Identities = 278/573 (48%), Positives = 381/573 (66%), Gaps = 29/573 (5%)

Query: 97 RKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYAR 156
+ GA L+EAL+R+GV+T+F YPGG + I+ L SSIR++L RHEQ AA+GYAR
Sbjct: 2 KTGARTLIEALQREGVDTIFGYPGGVVLPYDEL-YDSSIRHILVRHEQAAAAHAADGYAR 60

Query: 157 SSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTR 216
+SG+ G+C+ATSGPGA NLV+G+A A +DS+P+VA+TGQVP ++G DAFQE+ I +T
Sbjct: 61 ASGRVGVCLATSGPGACNLVTGTIATAYMDSIPIVALTGQVPTALLGNDAFQESDITGITM 120

Query: 217 SITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQ--QQLAIPNWEQAMKLP 274
+TKHNYLV D D+ R+++EAF++A +GRPGPVLVD+PKD+ Q L + + L
Sbjct: 121 PVTKHNYLVKDAGDLDRVVQEAFFVARTGRPGPVLVDIPKDVSTGQVLEKGPVPETVSLR 180

Query: 275 GYMSRMPKPPEDSHLEQIVR---LISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVA 329
GY +P H+ QI + LI+ +++P++Y GGG + +S EL FVE IPV
Sbjct: 181 GY-----QPTYQGHVRQIEKALDLIATAERPLVYAGGGVVLGASAELEFVEAAAIPVT 235

Query: 330 STLMLGLSGYPCDDELSTHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFASRA 389
+TLMGLG+ P D L L MLGMHGT ANYAV DLL+A GVRFDRTGK+E FA A
Sbjct: 236 TTLMLGLGAVPGDHPLCLGMLGMHGTQSANYAVTECDLLVAVGVRFDRTGKIETFAPNA 295

Query: 390 KIVHIDIDSAEIGKNKTPHVSVCGLKALQGMNKLVENRAEELKLDGFWVRNENLVQKQ 449
++HIDID AEIGKNK V + GDVK LQ ++ R D W + + K
Sbjct: 296 AVIHIDIDPAEIGKNKKVDVPIVDVKAVLQAFLSRMQKRG-----DTAAWVSRIKAWKA 350

Query: 450 KFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGG 509
++PL ++ + + PQY ++ L E+ G+ I+ + VGQ+QMW A +Y +KKPR W++SGG
Sbjct: 351 QYPLGYRD-DDHLRPQYVVEQLSEILKGEIVVSEVGQNQMWTALYYCFKKPRTWITSGG 409

Query: 510 LGAMGFGLPAAIGASVANPDIAIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLG 569
LG MG+G PAAIGA A PD VVDI GDGSF MN+QEL T+ +PVKV++LNN +LG
Sbjct: 410 LGTMGYGFPAAGAHYARPDMPVVDIAGDGSFQMNIIQELGTVAQYKIPVKVILNNMYLG 469

Query: 570 MVMQWEDRFYKANRAHTFLGDPAQEDEIFP-NMLLFAAACGIPAARVTKKADLREAIQTM 628
MV QW++ FY ++T E+ P + + A A G+ +V +KA +REA++T
Sbjct: 470 MVRQWQELFYDRRYSY-----ELPPVDFVKIANAYGVEGLQVDEKAGVREALETA 520

Query: 629 LDTGPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
L T GP++LD +E+V PM+P G N++I
Sbjct: 521 LATDGPVFLDFRVEREENVFPMVPAGAAINEMI 553

>ref|YP_002249089.1| acetolactate synthase, large subunit, biosynthetic type
[Thermodesulfovibrio yellowstonii DSM 11347]
gb|ACI21111.1| acetolactate synthase, large subunit, biosynthetic type
[Thermodesulfovibrio yellowstonii DSM 11347]
Length = 576

Score = 536 bits (1380), Expect = e-150, Method: Compositional matrix adjust.
Identities = 274/570 (48%), Positives = 375/570 (65%), Gaps = 18/570 (3%)

Query: 98 KGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARS 157
KGA+IL+E L+R+GV+ +F YPGG ++I L I+ +L RHEQG AA+GYAR
Sbjct: 5 KGAEILIECLKREGVKHIFGYPGGVILDIFDLLYDDPDIKLILTRHEQGATHAADGYARV 64

Query: 158 SGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
SGKPG+ + TSGPGATN V+G+A+A +DSVPLV TGQVP +IG DAFQE IV +TR
Sbjct: 65 SGKPGVVLVTSGPGATNTVTGIANAYMDSVPLVVFTGQVPTFLIGNDAFQEADIVGITRP 124

Query: 218 ITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYM 277
TK+N LV DV+D+ + + EAF++AT+GRPGPVL+D+PKD+ Q W + + + Y
Sbjct: 125 CTKYNILVKDVKDLAKQVREAFYIATGRPGPVLIDLPKDVTQKTEFIWPEKIHRSY- 183

Query: 278 SRMPKPPEDSHLEQIVRL---ISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTL 332
P + ++ I + I+++KKPV+ GGGC+ N+ + L E T IPVA+TL
Sbjct: 184 ---NPTYEGNVYMIKKAQEIAKAKKPVIAGGGCIISNAHEYKELAEFTQIPVANTL 239

Query: 333 MGLGSYPCDDELHMLGMHGTYYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIV 392
MGLGS+P ELSL MLGMHGT YAN AV++SDL++A G+RFDDRVTGK +AFA AKI+
Sbjct: 240 MGLGSFPGTHELSLGMHGTYYANMAVQNSDLIVAIGMRFDDRVTGKTDAFAPNAKII 299

Query: 393 HIDIDSAEIGKNKTPHVSVCADVKLALQGMNVLENRAE-ELKLDGFWVRNELNVQKQKF 451
HIDID I KN + + GDV LQ +NK+L+ + + K W ++N K++
Sbjct: 300 HIDIDPTSIRKNVRVDIPIVGDVSRVLQVLNKLKEEVKQWKEIRQAWLKQINQWKKER 359

Query: 452 PLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLG 511
PL+++ I PQY I+ + E+T G AII+T VGQ+QMWAAQFY + KPR+ ++SGGLG
Sbjct: 360 PLTYEFDEAVIKPQYVIEKIYEVTKGDAIITTEVGQNQMWAQFYKFDKPRRLVTSGLG 419

Query: 512 AMGFGFLPAAIGASVANPDIAIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMV 571
MG+G PAAIGA +A PD V+DI GDGS MN+QELAT + NLPVKV ++NN +LGMV
Sbjct: 420 TMGYGFPAAGIQLAFPDMTVIDIAGDSIQMNIQELATAVIYNLPVKVAIINNSYLG 479

Query: 572 MQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTM 631
QW++ FY +HT+L P+ + A + G R TK +++ I+ L
Sbjct: 480 RQWQEIFYGERYSHTYLSA-----PDFVKVAESYGAVGLRATKPSVEPEVIKEALSI 532

Query: 632 PGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
P +D + +E V PM+P G + +I
Sbjct: 533 RKPVFMDVVDWKEKVPMVPPGAPIDQMI 562

>gb|ABV24338.1| indole-3-pyruvate decarboxylase [Paenibacillus polymyxa]
Length = 581

Score = 533 bits (1374), Expect = e-149, Method: Compositional matrix adjust.
Identities = 271/567 (47%), Positives = 374/567 (65%), Gaps = 19/567 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSS 158
G++IL+ +L +GV+ VF YPGA + I+ A+ ++VL RHEQG + AA+GYAR+S
Sbjct: 26 GSEILLRSLLEGVDCVFGYPGGAVLYIDAMYGFKDFKHVLRHEQGAIIHAADGYARAS 85

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+CIATSGPGATNLV+G+A A +DSVPLV ITG V +IGTDAFQE I +T I
Sbjct: 86 GKVGVCIATSGPGATNLVTGIATAFMDSVPLVVITGNVISSLIGTDAFQEADITGITMPI 145

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQ--QQLAIPNWEQAMKLPGY 276
TKH+YL V DVED+PRII EAF +A +GR GPVL+D+PKDI Q L +P + + GY
Sbjct: 146 TKHSYLVRDVEDLPRIIEAFHIAANTGRKGPVLIDIPKDISAAQTLFVPQ-TGPVTRMGY 204

Query: 277 MSRMPPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSS--DELGRFVELTGIPVASTLMG 334
++ P L+++ + ISE+++P + GGG + S + L FV T IP+ +TL+G
Sbjct: 205 NPKV--LPNKIQLDKLTQAISEAERPFILAGGGVYSGGHEALYEFVRKTEIPITTTLLG 262

Query: 335 LGSYPCDDELHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIVHI 394
LG +P EL M GMHGT +N A++ SDDL+ G RFDDRVTGKL+ FA +AKIVHI
Sbjct: 263 LGGFPSGHELWTGMPGMHGTYSNQAIQQSDLLICIGARFDDRVTGKLDGFAPQAKIVHI 322

Query: 395 DIDS AEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKFP LS 454
DID AEIGKN + + GDVK L+ +N+ ++ RA+ WR ++ K + P S
Sbjct: 323 DIDPAEIGKNVAADIPIVGDVKAVLELLNQDVK-RADRAD----AWRAQIQHWKNEKPYS 377

Query: 455 FKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMG 514
+K + PQ+ +++LDE T G AI++T VGQHQMWAQ+Y + +PR W++SGGLG MG
Sbjct: 378 YKDSETVLKPQWVVELLDET TKGAIVTTDVGQHQMWAQYKFNQPRSWVTSGLGTMG 437

Query: 515 FGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQW 574
FG P+AIGA +ANPD +V+ I+GDG M QELA + N+PVK++++NNQ LGMV QW
Sbjct: 438 FGFPSAIGAQMNPDR LVISINGDGMQMCQELAICAINNIPVKIVIIINNQLGMVVRQW 497

Query: 575 EDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKADLREAIQTMLDTPGP 634
++ Y +H L P+ + A A G+ R T K + R A Q LDTPGP
Sbjct: 498 QELIYNNRYSHIDL A G S-----PDFVKLA EAYGVKGLRATNKEEARRAQEALDTPGP 550

Query: 635 YLLDVICPHQEHVLP MIPNGGTFNDVI 661
+++ + +E+V PM+ G T + ++
Sbjct: 551 VVVEFVVSKEENVYPMVTQGSTIDQML 577

>ref|YP_004823.1| acetolactate synthase large subunit [Thermus thermophilus HB27]
gb|AAS81196.1| acetolactate synthase large subunit [Thermus thermophilus HB27]
Length = 562

Score = 533 bits (1374), Expect = e-149, Method: Compositional matrix adjust.
Identities = 283/570 (49%), Positives = 378/570 (66%), Gaps = 23/570 (4%)

Query: 98 KGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARS 157
KGA+ L+ ALER+GVE +F +PGA M + AL S IR++L RHEQGGV AA YAR+
Sbjct: 2 KGAEALLRALERE GVEVIFGHPGGAIMPTYDALY-DSPIRHILVRHEQGGVHAATAYARA 60

Query: 158 SGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 217
SG+ G+ +ATSGPGA NLV+GLADA++DS P+VAITG VPR +IGTDAFQE + VT
Sbjct: 61 SGRVGVMMATSGPGALNLVTGLADAMMDSTPVVAITGNVPRALIGTDAFQEADVTGVTMP 120

Query: 218 ITKHNLYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYM 277
ITKHNLYLV DV +IPR+++EAF +A +GRPGPVL+D+PKD+Q +++ + LPGA
Sbjct: 121 ITKHNLYLVQDVNEIPRVVKEAFHIAATGRPGPVLIDIPKDVQLAEFTGSFVDVKLDLPGY- 179

Query: 278 SRMPKPPEDSHLEQIVR---LISESKKPVLYVGGGCLNSSDELGRFVELTGIPVASTLMG 334
KP H +QI R + ++++PVL VGGG ++ EL F E TG+PV +TLMG
Sbjct: 180 ----KPTLKGHKQIERALDALEKAERPVL MVGGGAQHAAELLAFAEKTGLPVITTLMG 235

Query: 335 LGSYPCDDELHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAK-IVH 393
LG++P + L L M GMHGTV AN A+ H+D++LA G+RFDDRVTGK+ FA A I+H
Sbjct: 236 LGAFPGNHPLWLGMPMHGTVAANRAIHADVILAIGLRFDDRVTGKVS RFAPHAHTIIH 295

Query: 394 IDIDS AEIGK NKT PHV SVCGDVKLALQGMNKVLENRAEELKLDGFWRNELNVQKQKFPL 453
+DID AEIGK H+ + GD +L L K L A+ L+L W EL + ++PL
Sbjct: 296 VDIDPAEIGKVVRTHIPVIGDSRLVL----KELLKGAKALRL--AAWWRELEEWTRYPL 349

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAM 513
++ + Q I+ E T G AI++TGVGQHQMWAAQF+ +PR +L+SGGLG M
Sbjct: 350 RYRP-KPHLQSQEVIRAFYEATGGHAIVTTGVGQHQMFQAQFFPVTRPRSLTSGGLGTM 408

Query: 514 GFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQ 573
G GLP AIGA +A P+ +V+D DGDGSF M +QELAT+ L VKV++LNN +LGMV Q
Sbjct: 409 GVGLPFAIGAKIARPEELVIDFDGDSFQMTLQELATVVKYKLDVKVILNNGYLGVMVQ 468

Query: 574 WEDRFYKANRAHTFLGDPAQEDEFPMNMLLFAAACGIPAARVTKKADLREAIQTMLDTPG 633
W+D F+ + +L D P+ A A GI RV +K DL + ++ +L+ G
Sbjct: 469 WQDLFHAKRYSEVYLADSN-----PDFARLAEAYGIKGVVERKEDLMKGVAVLNADG 522

Query: 634 PYLLDVICPHQEHVLPMPNGGTFNDVITE 663
P + + H+E V PMIP GG D+I E
Sbjct: 523 PVVAEFKVYHEEGVFPMPAGGAAEDMILE 552

>ref|NP_831551.1| acetolactate synthase 3 catalytic subunit [Bacillus cereus ATCC
14579]
gb|AAP08752.1| Acetolactate synthase large subunit [Bacillus cereus ATCC 14579]
Length = 573

Score = 532 bits (1370), Expect = e-149, Method: Compositional matrix adjust.
Identities = 272/566 (48%), Positives = 370/566 (65%), Gaps = 21/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA +++ L++ GV TVF YPGA + ++ AL S +++VL RHEQ + AAEGYAR+S
Sbjct: 20 GAGHVIQCLKKLGVTTFVFGYPGGAILPVYDALYESG-LKHVLTRHEQAIIHAAEGYARAS 78

Query: 159 GKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ ATSGPGATNLV+GLADA +DS+PLV ITGQV +IG D FQE +V +T +
Sbjct: 79 GKVGVPVATSGPGATNLVTGLADAYMDSIPLVVITGQVATPLIGKDFQEADVVGITVPV 138

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V DV + RI++EAF++A SGRPGPVL+D+PKD+Q + + + +PGY
Sbjct: 139 TKHNYQVRDVNHVSRIVQEAFYIAKSGRPGPVLIDIPKDVQNAKVTSFFNEEVDIPGYKP 198

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLG 336
P+ L ++ + IS+SK+P+LY+GGG ++S SDEL F IPV STLMGLG
Sbjct: 199 EF--VPDSMKLREVAKAISKSKRPLLYIGGGVIHSGGSDELFEFARENRIIPVSTLMGLG 256

Query: 337 SYPCDDELSLHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDI 396
+YP DD L L MLGMHGT AN AV DLLLA GVRFDDRVTGKLE F+ +K VHIDI
Sbjct: 257 AYPPDDSLFLGMLGMHGTYAANMAVTECDLLALGVRFDDRVTGKLELFSPNSKKVHIDI 316

Query: 397 DSAEIGK NKT PHV SVCGDVKLALQG-MNKVLENRAEELKLDGFWRNELNVQKQKFPLSF 455
DS+E KN T + GDVK AL ++ + + +E W ++ K+++PLS+
Sbjct: 317 DSSEFHKNVTVHEPIVGDVKKALHMLLHMSIYTQTDE-----WLQKVKTWKEEYPLSY 369

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGF 515
K + PQ+ I ++ ELT+G+AI++T VGQHQMWAA FY +KPR +L+SGGLG MGF
Sbjct: 370 KQKESELKPQHVINLVSELTNGEAIVTTEVGQHQMWAAHFYKARKPRTFLTSGGLGTMGF 429

Query: 516 GLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
G PAAIGA +A + +V+ I GD SF MN+QEL TI N+PVKV ++NN+ LGMV QW+
Sbjct: 430 GFPAAIGAQLAKKEELVICIAGDASFQMNIEQLQTAENNIIPVKVFIINNKFGLGMVQWQ 489

Query: 576 DRFYKANRAHTFLGDPAQEDEFPMNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPY 635
+ FY+ + + +G P+ + A A G+ R T + ++ + GP
Sbjct: 490 EMFYENRLSESKIGS-----PDFVKVAEAYGVKGLRATNSTEAKQVMLEAFAYEGPV 541

Query: 636 LLDVICPHQEHVLPMPNGGTFNDVI 661
++D E+V PM+P N++I
Sbjct: 542 VVDFCVEEENVFPMVPPNKGNNEMI 567

>ref|ZP_02179310.1| acetolactate synthase large subunit [Hydrogenivirga sp. 128-5-R1-1]
gb|EDP73924.1| acetolactate synthase large subunit [Hydrogenivirga sp. 128-5-R1-1]
Length = 567

Score = 531 bits (1369), Expect = e-149, Method: Compositional matrix adjust.
Identities = 276/577 (47%), Positives = 384/577 (66%), Gaps = 27/577 (4%)

Query: 97 RKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHEQGGVFAAEGYAR 156
++GADI+V+ L + V+TVF PGGA ME++ AL ++ +N+L RHE A+GYAR
Sbjct: 4 KRGADIVVDVLEEKVDTVFGLPGGAIMEVYDALF-NAPFKNILARHELAACHMADGYAR 62

Query: 157 SSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTR 216
++GK G+ +ATSGPGATNLV+GLA A +DSVPLVAITGQVP IGTDAFQE + +TR
Sbjct: 63 ATGKVGVMATSGPGATNLVTLATAHMDSVPLVAITGQVPTHYIGTDAFQEADVTGTR 122

Query: 217 SITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQL-----AIPNWEQA 270
+TKHN+LV D++D+ I+ EAF++A +GRPGPVLVD+PKDI QQ+ + + E+A
Sbjct: 123 PVTKHNFLVTDIKDLALILREAFYIARTGRPGPVLVDIPKDIQQVYDYKMPKLDVVEA 182

Query: 271 MKLPGYMSRMPKPPEDSHLEQI---VRLISESKKPVLYVGGGCL--NSSDELGRFVELTG 325
LPGY KP + ++ QI + + + +LI ++K+PVLYVGGG + + +EL + E+
Sbjct: 183 --LPGY-----KPHYEGNIAQIKKAAKLIRQAKRPVLYVGGGAVAAEAQEELVKLAEMAK 235

Query: 326 IPVASTLMGLSGSYPCDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRTVGKLEAF 385
IPV +TLMG G++P D L+LHMLGMHGT YAN AV +SDLL+A G RFDDRTVGK++ F
Sbjct: 236 IPVTTTLMGKGAFFPEDHPLALHMLGMHGTYYANMAVNSDLLIAVGSRFDDRTVGKIDEF 295

Query: 386 ASRAKIVHIDIDSAEIGKNKTPHVSVCGDVKLALQGMNKVLENRAEELKLDGFWVRNELN 445
A AKI+HIDID A I K V + GDVK LQ + K LE + E W +
Sbjct: 296 APEAKIHHIDIDPASISKTINVDVPIVGDVKVLQKLIKELEKRPVEWDEARESWIKLIE 355

Query: 446 VQKQKFPLSFKTFGEAIPPQYAIKVLELTDGKAIISTGVGQHQMWAQFYNYKKPRQWL 505
K + PL++ + I P+Y ++ + +T G+AII+ GVGQHQMWAQ FY YK PRQ++
Sbjct: 356 KWKIEHPLTYDRKSKIIPKPEYVVEEYINITGAEIITAGVGQHQMWAAMFYKYKPRQFI 415

Query: 506 SSGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNN 565
+SGGLG MGFG PAA+GA +A PD V+ I+GDGSF+MN+Q++AT +PVKV +LNN
Sbjct: 416 NSGGLGTMGFGFPAAVGAIAIPDKIEVIAIEGDGSFLMNIQDIATAVQYRVPVKVAILNN 475

Query: 566 QHLMVMQWEDRFYKANRAHTFLGDPAQEDEFPMNLLFAAACGIPAARVTKKADLREAI 625
+ LGMV QW++ FY + + L P+ + A + G R TK +++++ +
Sbjct: 476 EFLGMVRQWQELFYDSRYSSVCLSTQ-----PDFVKLAESFGAVGLRATKPSEVKKVL 528

Query: 626 -QTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
+ M P ++D +E+VLPMP+P G ++ ++I
Sbjct: 529 KEAMSINDRPVIMDFAVDREENVLPMPVAGKSYREMI 565

>ref|YP_144479.1| acetolactate synthase, large subunit [Thermus thermophilus HB8]
dbj|BAD71036.1| acetolactate synthase, large subunit [Thermus thermophilus HB8]
Length = 562

Score = 531 bits (1367), Expect = e-148, Method: Compositional matrix adjust.
Identities = 282/570 (49%), Positives = 377/570 (66%), Gaps = 23/570 (4%)

Query: 98 KGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHEQGGVFAAEGYARS 157
KGA+ L+ ALER+GVE +F +PGGA M + AL S IR++L RHEQGGV AA YAR+
Sbjct: 2 KGAEALLRALEREGVEVIFGHPGGAIMPTYDALY-DSPIRHILVRHEQGGVHAATAYARA 60

Query: 158 SGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
SG+ G+ +ATSGPGA NLV+GLADA++DS P+VAITG VPR +IGTDAFQE + VT
Sbjct: 61 SGRVGVVMATSGPGALNLVTGLADAMMDSTPVVAITGNVPRALIGTDAFQEADVTGVTMP 120

Query: 218 ITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYM 277
ITKHNLYL DV +IPR+++EAF +A +GRPGPVL+D+PKD+Q +++ + LPGY
Sbjct: 121 ITKHNLYLQDVNEIPRVVKEAFHIAATGRPGPVLIDIPKDVQLAEFTGSFVVKLDLPGY- 179

Query: 278 SRMPKPPEDSHLEQIVR---LISESKKPVLYVGGGCLNSSDELGRFVELTGIPVASTLMG 334
KP H +QI R + ++++PVL VGGG ++ EL F E TG+PV +TLMG
Sbjct: 180 ----KPTLKGHKQIERALDALEKAERPVLMMVGGGAQHAAELLAFAEKTGLPVITTLMG 235

Query: 335 LGSYPCEDELSLHMLGMHGT VYANYAVEHSDLLLA FGVRFDDRVTGKLEAFASRAK-IVH 393
LG++P + L L M GMHGT V AN A+ H+D++LA G+RFDDRVTGK+ FA A I+H
Sbjct: 236 LGAFPGNHPLWLGMPGMHGTVAANRAIHADVILAIGLRFDDRVTGKVS RFAPHAHTIIH 295

Query: 394 IDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKFPL 453
+DID AEIGK H+ + GD +L L K L A+ L+L W EL + ++PL
Sbjct: 296 V D I D P A E I G K V V R T H I P I V G D S R L V L ---K E L L K G A K A L R L --A A W W R E L E E W R T R Y P L 349

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGLGAM 513
++ + Q I+ E T G AI++TGVGQHQM+AAQF+ +PR +L+SGGLG M
Sbjct: 350 RYRP-KPHLQSQEVIRAFYEATGGHAIVTTGVGQHQMFAAQFFPVTRPRSLTSGGLGTM 408

Query: 514 GFGLPAAIGASVANPD AIVVDIDGDGSFIMNVQELATIRVENLPVKVLLLNQHLGMVMQ 573
G GLP AIGA +A P+ +V+D DGDGSF M +QELAT+ L VKV++LNN +LGMV Q
Sbjct: 409 GVGLPFAIGAKIARPEELVIDFDGDGSFQMTLQELATVVVKYKLDVKVVLNNGYLGVMVRQ 468

Query: 574 WEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPG 633
W+D F+ + +L D P+ A A GI RV +K DL + ++ +L+ G
Sbjct: 469 WQDLFHAKRYSEVYLADSN-----PDFARLAEAYGIKGV RVERKEDLMKGV EAVLNADG 522

Query: 634 PYLLDVICPHQEHVLP MIPNGGTFNDVITE 663
P + + +E V PMIP GG D+I E
Sbjct: 523 PVVAEFKVYQEEGVFPMIPAGGAAEDMILE 552

>ref|YP_502706.1| acetolactate synthase, large subunit, biosynthetic type
[Methanospirillum hungatei JF-1]
gb|ABD40987.1| acetolactate synthase, large subunit [Methanospirillum hungatei
JF-1]
Length = 563

Score = 530 bits (1364), Expect = e-148, Method: Compositional matrix adjust.
Identities = 277/572 (48%), Positives = 376/572 (65%), Gaps = 27/572 (4%)

Query: 97 RKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYAR 156
+ GA IL+E L+ QGV+ +F YPGG + I+ L + IR++L RHEQ + AA+GYAR
Sbjct: 2 KSGAQILIEGLKEQGVDIIFGYPGGVLPIDELY-DADIRHILVRHEQA AIIHAADGYAR 60

Query: 157 SSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTR 216
+SGK G+C+ATSGPGA NLV+GLA A +DS+P+VAITGQVP ++G DAFQE+ I +T
Sbjct: 61 ASGKTGVCLATSGPGACNLVTGLATAYMDSIPVVAITGQVPTSLLGNDAFQESDITGITM 120

Query: 217 SITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDV PKDIQQQLA--IPNWEQAMKLP 274
+TKHNLYLV D D+ RII EAF +A++GR GPVL+D+PKD+ + + ++ +L
Sbjct: 121 PVTKHNLYLVT DARDLRRRIIEAFHIASTGRKGPVLIDL PKDVCTSMVPD VDPDEQPRLR 180

Query: 275 GYMSRMPKPPEDSHLEQIVR---LISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVA 329
GY KP H + I R L+ ++K+PV+Y GGG + N+S EL E +PV
Sbjct: 181 GY-----KPKYQGHSKMIQRAVDLLLQAKRPVIYAGGGVISSNASAE LVALAEKMCMPVT 235

Query: 330 STLMLGLSYPCEDELSLHMLGMHGT VYANYAVEHSDLLLA FGVRFDDRVTGKLEAFASRA 389
+TLMGLG P D L+L MLGMHGT YANYA+ SDLL + GVRFDDRVTGK+EAFA +A
Sbjct: 236 TTLMLGLCIPTDHLNLGMLGMHGT EYANYAITESDLLFSIGVRFDDRVTGKIEAFAPQA 295

Query: 390 KIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQ 449
KI+HIDID AEIGKNK P V + GD K L + K + + W ++ + K+
Sbjct: 296 KIIHIDIDPAEIGKNKQPDVPIVGDAKSVLS DILKKIPESCPHPE-----WSEKVAMWKK 350

Query: 450 KFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGG 509
PL +++ G+ + PQ+ IK L ++ K II + VGQ+QMW AQ++ + +PRQW+SSGG
Sbjct: 351 NHPLRYRSDGK-LYPQFVIKTLADILGEKGIIVSEVGQNQM WTAQWFKFTRPRQWISSGG 409

Query: 510 LGAMGFGLPAAIGASVANPD AIVVDIDGDGSFIMNVQELATIRVENLPVKVLLLNQHLG 569
LG MG+G PA++G A PD V + GDGSF MN+QEL T+ N+PVKV++LNNQ LG
Sbjct: 410 LGTMGYGFPA SMGVHFACPDQPVFVL AGDGSFQMNIQELGTVAQYNIPVKVIVLNNQFLG 469

Query: 570 MVMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTML 629
MV QW+ FY+ ++T L + E A A GI AA V +D+ AI+T L
Sbjct: 470 MVRQWQQLFYERRYSTELPEVHFER-----IAKAYGIEAATVRNASDVEAAIR TAL 521

Query: 630 DTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
PGPY+LDV +E+V PM+P G +++I
Sbjct: 522 AHPGPYVLDVRVEREENVFPMVPAGANISEMI 553

>ref|ZP_01389342.1| acetolactate synthase, large subunit, biosynthetic type [Geobacter
sp. FRC-32]
gb|EAT61366.1| acetolactate synthase, large subunit, biosynthetic type [Geobacter
sp. FRC-32]
Length = 566

Score = 529 bits (1363), Expect = e-148, Method: Compositional matrix adjust.
Identities = 264/568 (46%), Positives = 373/568 (65%), Gaps = 14/568 (2%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHEQGGVFAAEGYARSS 158
GA IL+E L+ +GV+TVF YPGG + ++ + IR++LPRHEQ GV AA+GYAR++
Sbjct: 5 GARILLECLKLEGVDTVFGYPGGTVINLYDEIFSFKEIRHILPRHEQAGVHAADGYARAT 64

Query: 159 GKPATICATSGPGATNLVSGADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ IATSGPGATN ++G+A A +DS+P+V ITGQVP +IG DAFQE I+ +TR
Sbjct: 65 GKVGVAIATSGPGATNTITGIATAYMDSIPMVIITGQVPTGLIGNDAFQEADIIGITRPC 124

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHN+LV DV+D+ I+++AF++A +GRPGPVL+D+PKD+Q + + + + GY
Sbjct: 125 TKHNFVLKDVKDLATIVKKAIFYIARTGRPGPVLIDLPKDVQIATTEFKYPETVDIRGYKP 184

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLMGLG 336
+ P+ +E+ + L+ E+KKPV+YVGGG + N+++EL + +L PV +TLMGLG
Sbjct: 185 TVGGHPK--QVEKAITLLLEAKKPVIVVGGGVLGNAAEELTKLAQLLNAPVTTTLMGLG 242

Query: 337 SYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIVHIDI 396
++P D+ LSL +LGMHGT YAN AV H DLL+A G RFDDRVTKG+ +FA A+I+HID+
Sbjct: 243 AFPEDNPLSLGLGMHGTYYANMAVSHCDLLIAVGARFDDRVTKIASFAPHAQIIHIDV 302

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEE---LKLDFGVWRNELNVQKQKFPL 453
D I KN + + GDVK L+ + KVL +AE+ + W E+ K K P+
Sbjct: 303 DPTSIKKNVRVDLPVIGDVKDVLKQLLKVLAGQAQKATFQKQIVPWSQEIEAWKAKHPM 362

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAM 513
++K+ I PQ I+ L EL+ AI+ST VGQHQMW AQF+ + +PR LSSGGLG M
Sbjct: 363 TYKSSASVIKPLVIQKLRELSKPDIAVSTDVGQHQMWTAQFFKFNRPRTLLSSGGLGTM 422

Query: 514 GFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQ 573
GFGLPAA+GA A P V+ + GDG F MN+QELAT+ LPVK+ +LNN LGMV Q
Sbjct: 423 GFGLPAAAGAAAFPKRQVIVVCGDGGFQMNQELATLVQNRLPVKICILNNFLGMVRQ 482

Query: 574 WEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPG 633
W++ F+ + T + P + + A A G + TK ++ I+ TPG
Sbjct: 483 WQELFFDKRYSQTCMELPI-----DFIKLAEAFGAKGFQATKPEEVEAVIKKGFATPG 535

Query: 634 PYLLDVICPHQEHVLPMPNGGTFNDVI 661
P +++ +E VLPMP+P G + +++
Sbjct: 536 PVIMEFKVAREEKVLPMPVAGASLTEMV 563

>ref|ZP_03038955.1| acetolactate synthase, large subunit, biosynthetic type
[Geobacillus sp. Y412MC10]
gb|EDV77081.1| acetolactate synthase, large subunit, biosynthetic type
[Geobacillus sp. Y412MC10]
Length = 580

Score = 528 bits (1361), Expect = e-148, Method: Compositional matrix adjust.
Identities = 262/565 (46%), Positives = 373/565 (66%), Gaps = 16/565 (2%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPRHEQGGVFAAEGYARSS 158
G++IL+ +L +GVE VF YPGGA + I+ A+ +VL RHEQG + AA+GYAR+S
Sbjct: 26 GSEILLRSLLEGVCEVFGYPGGAVLYIYDAMYGFKDFNHVLRHEQGAIHAADGYARAS 85

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+CIATSGPGATNLV+G+A A +DSVPLV ITG V +IGTDAFQE I +T I
Sbjct: 86 GKVGVCIATSGPGATNLVTGIATAYMDSVPLVVTITGNVATTLLIGTDAFQEADITGITMPI 145

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKH+YLV DV+D+PR+I EAF +A++GR GPVL+D+PKD+ + E+ ++L GY
Sbjct: 146 TKHSYLVDRDVKDLPRVIEAFHIASTGRKGPVLIDIPKDVSAATTLFQPEERIQLRGYNP 205

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELG--RFVELTGIPVASTLMGLG 336
R P L+++ R I E+++P++ GGG + S G FV TGIP+ +TL+GLG
Sbjct: 206 R--TVPNKLQDLKLARAIEEAERPMILAGGGVIYSGAHEGLYEFVNKTGIPITTTLLGLG 263

Query: 337 SYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIVHIDI 396
++P ++L M GMHGT +N+ ++ SDLL+ G RFDDRVTGKL+ FA AKIVHIDI
Sbjct: 264 AFPTGNDLWTGMPGMHGTYSNHGIQQSDLLINIGARFDDRVTGKLDGFAPHAKIVHIDI 323

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWVRNENLVQKQKFPPLSF 456
D AEIGKN + + GDVK L+ +N ++ A K D WR++++ K ++P +
Sbjct: 324 DPAEIGKNVPTDIPVGDVKTVLEMLNPLVPYAA---KAD--AWRDQISKWKAEPFRYV 378

Query: 457 TFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGFG 516
+ PQ+ I++L++ T G+AI++T VQGHQMWAQ+Y + +PR W++SGGLG MGFG
Sbjct: 379 DSDTVLKPQWVIEMLNDTTKGEAIVTTDVGQHQMWAQYKFNQPRSWITSGGLGTMGFG 438

Query: 517 LPAAIGASVANPDIAIVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWED 576
P+AIGA +A+PD +V+ I+GDG M QELA + N+PVK++++NNQ LGMV QW++
Sbjct: 439 FPSAIGAQMAHPDRLVISINGDGMQMSQELAICAINNIPVKIVINNQLGMVQRWQE 498

Query: 577 RFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPYL 636
Y +H L P+ + A A G+ R T K + + A ++TPGP L
Sbjct: 499 IIYDNRYSHIDLGS-----PDFVKLAEAYGVKGLRATTKEEAQRAWAEAMETPGPVL 551

Query: 637 LDVICPHQEHVLPMPNGGTFNDVI 661
++ + E+V PM+ G T + ++
Sbjct: 552 VEFVVEKGENVYPMVTQGSTIDQML 576

>ref|ZP_03024969.1| acetolactate synthase, large subunit, biosynthetic type [Geobacter
sp. M21]
gb|EDV71326.1| acetolactate synthase, large subunit, biosynthetic type [Geobacter
sp. M21]
Length = 566

Score = 528 bits (1360), Expect = e-148, Method: Compositional matrix adjust.
Identities = 268/568 (47%), Positives = 373/568 (65%), Gaps = 14/568 (2%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA IL+E L+R+GV+T+F YPGG + ++ L IR++LPRHEQ GV AA+GYAR++
Sbjct: 5 GARILLECLKREGVDITFGYPGGTVINLYDELFSFKEIRHILPRHEQAGVHAADGYARAT 64

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ IATSGPGATN ++G+A A +DS+P+V ITGQVP +IG DAFQE I+ +TR
Sbjct: 65 GKVGVAIATSGPGATNTITGIATAYMDSIPMVIITGQVPTALIGNDAFQEADIIGITRPC 124

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHN+LV DV+D+P I+++AF+++A +GRPGPVLVD+PKD+Q A + + +++ GY
Sbjct: 125 TKHNFLVKDVKDLPTIMKAFYIARTGRPGPVLVDLPKDVQMAQAEFKYPETVEIRGYKP 184

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLMGLG 336
+ P+ +E+ V +I+++K+PVLYVGGG + N++ EL F + IPV +TLMGLG
Sbjct: 185 NLEGHPK--QVEKAVAMITQAKRPVLYVGGGVILGNAAELTAFAKRLAIPVTTTLMGLG 242

Query: 337 SYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIVHIDI 396
++P +D SL +LGMHGT YAN AV H D+L+A G RFDDRVTGK+ +FA AKIVH+D+
Sbjct: 243 AFPENDPQSLGLLGMHGTYYANMAVSHCDVLAIGARFDDRVTGKIASFAPHAKIVHVDV 302

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKL---DFGVVRNENLVQKQKFPPL 453
D I KN + + GDV+ L M K E + K W E+ K K P+
Sbjct: 303 DPTSIKKNVVRDLPVIGDVRDVLAKMLKASEQVCPDAKACQDAIAPWTAIEGWKAKHPM 362

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAM 513
S+K G I PQY I+ L L+D AI++T VGQHQMW AQF+ + PR LSSGGLG M
Sbjct: 363 SYKQSGTVIKPQYVIQRLRLSDPDIAIVATDVGQHQMWTAQFFGFTTPTLLSSGGLGTM 422

Query: 514 GFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQ 573
G+GLPAA+GA A P+ V+ + GDG F MN+QELATI L VK+++LNN LGMV Q
Sbjct: 423 GYGLPAAAGAAAFPERQVMVVCDDGGFQMNQELATIVQNRLNVKIVILNNFLGMVRQ 482

Query: 574 WEDRFYKANRAHTFLGDPAQEDEIFPNMMLFAAACGIPAARVTKKADLREAIQTMLDTPG 633
W++ F+ + T+ + E+ + + A A G + TK ++ E I+ T G
Sbjct: 483 WQELFFDKRYSSTCM-----ELPIDFIKLAEAFGATGLQATKVDEVDEVIKKGFATNG 535

Query: 634 PYLLDVICPHQEHVLPMPNGGTFNDVI 661
P L++ +E VLP+P G + +++
Sbjct: 536 PVLMEFKVAREEKVLPMPAGASLTEMV 563

>ref|YP_002121866.1| acetolactate synthase, large subunit, biosynthetic type
[Hydrogenobaculum sp. Y04AAS1]
gb|ACG57888.1| acetolactate synthase, large subunit, biosynthetic type
[Hydrogenobaculum sp. Y04AAS1]
Length = 584

Score = 528 bits (1359), Expect = e-148, Method: Compositional matrix adjust.
Identities = 276/580 (47%), Positives = 388/580 (66%), Gaps = 19/580 (3%)

Query: 97 RKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYAR 156
RKGAD+++E L ++GV+ +F PGGA+MEI+ AL R + I+++L RHEQG AEGYA+
Sbjct: 4 RKGADVVIETLLKEGVDVIFGIPGGANMEIYDALYRINKIKHILARHEQGAGHMAEGYAK 63

Query: 157 SSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTR 216
+SGK G+ +ATSGPGATNL++ +ADA +DSVP+V +TGQVP +IG DAFQE IV +TR
Sbjct: 64 ASGKVGVALATSGPGATNLITAIADAYMDSVPVFLTGQVPTFLIGNDAFQEVDIVGMTR 123

Query: 217 SITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLA---IPNWEQAMK- 272
+TKHN+LV VED+P II +AF+++A +GRPGPVLVD+PKDI Q + IP+ E+ +
Sbjct: 124 PVTKNHFLVKRVEDLPLIIRQAFYIAKTGRPGPVLVDIPKDIQTMTDVEIPSDEEVINS 183

Query: 273 LPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGG--CLNSSDELGRFVELTGIPVAS 330
LPGY + P+ +++ +LI E+K+PVLYVGGG ++ E+ EL IPV +
Sbjct: 184 LPGYKPHIEGNPQ--QIKRAQLILEAKRPVLYVGGGAVAAEANAELAEELMKIPVTT 241

Query: 331 TLMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAK 390
T MG G++ LSL MLGMHGT YAN AV HSDLL+A G RFDDRVTKG++ FA AK
Sbjct: 242 TNMGKGAFFDERHPLSLRMLGMHGTYYANMAVYHSDLLIAGVSRFDDRVTKVDEFAPFAK 301

Query: 391 IVHIDIDSAEIGKNKTPHVSVCDDVKLALQGMNKVLENRAEEL--KLDFGVWRNELNVQK 448
I+HIDID A I KN T V + GD++ L + + ++ + ++ + + W +++ K
Sbjct: 302 IIHIDIDPASISKNITVDVPIVGDIVSVLRLIEEIKGKNSKIVHEEERKTWLEQIDAWK 361

Query: 449 QKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSG 508
+ +PLS+K + + PQ+ I+ + ++T+G AII+TGVGQHQMW+A FY Y PRQ+++SG
Sbjct: 362 KAYPLSYKPSDKVVKPQFLIETIYDVTENAIITTGVGQHQMWSAMFYKYSFPRQFINSG 421

Query: 509 GLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHL 568
GLG MGFGLPA IGA VA PD V IDGDGSF+M +QEL T N+P+KV++LNN +
Sbjct: 422 GLGTMGFGLPAGIGAKVAKPKDVFIIIDGDSFMTMQELITAAHYNIPIKVIIILNNAYY 481

Query: 569 GMVMQWEDRFYKANRAHTFLGDPAQEDEIFPNMMLFAAACGIPAARVTKKADLREAIQTM 628
GMV QW++ FY + L P+ A ACG R +L++ +
Sbjct: 482 GMVRQWQELFYNKRYSEVDL-----SFQPDFGKLAEACGAVGMRTDNPKEKLDVLLKA 534

Query: 629 LD-TPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDGR 667
+ P L++VI +E+ LPM+P G ++ D++ DG+
Sbjct: 535 KNVNDKPVLVVEVIVDREENCLPMVPAGKSYKDMLLS-DGK 573

>ref|NP_693544.1| acetolactate synthase large subunit [Oceanobacillus iheyensis
HTE831]
dbj|BAC14579.1| acetolactate synthase large subunit [Oceanobacillus iheyensis
HTE831]

Length = 573

Score = 527 bits (1357), Expect = e-147, Method: Compositional matrix adjust.
Identities = 263/566 (46%), Positives = 375/566 (66%), Gaps = 17/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRS-SSIRNVLPHEQGGVFAAEGYARS 157
GAD+ V+ALER VE VF YPGA + I+ AL R+ +S +VL RHEQG + AAEGYAR
Sbjct: 18 GADLFVQALERANVEVVFYGGAVLPIYDALHRNQTSFEHVLRSHEQGSIHAAEGYARV 77

Query: 158 SGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
SGKPG+ IATSGPGATNL++G+ DA++DS+PLV TGQV + +IGTDAFQE ++ +T
Sbjct: 78 SGKPGVVIATSGPGATNLITGITDAMMDSIPLVIFTGQVAKGVIGTDAFQEADVMGITTP 137

Query: 218 ITKHNLYVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYM 277
ITK+NY V ++ ++PRI+ EAF +AT+GRPGPV+VD+PK+I + + ++E LPGY
Sbjct: 138 ITKYNQVNEIAELPRIVNEAFHIAITGRPGPVVDIPKNISSTVTVNDYEDFHLPGYQ 197

Query: 278 SRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCL--NSSDELGRFVELTGIPVASTLMGL 335
+ P + ++ + ++KPVL G G L ++S+EL +F + +PV +TL+GL
Sbjct: 198 PTI--TPNPLQITKVNEALKRAEKPVLLAGAGILISDASNELKQFAQHYQLPVVTTLLGL 255

Query: 336 GSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRTVGKLEAFASRAKIVHID 395
GSYP + LSL M GMHGT AN A+ DLL+ G RFDDR+TG ++ FA AKIVHID
Sbjct: 256 GSYPGKESLSLGMAGMHGTAAANMAIYECDLLINIGARFDDRLTGNIKHFAFNAKIVHID 315

Query: 396 IDSAEIGKNKTPHVSVCADVKLALQGMNKVLENRAEELKLDGFWVRNELNVQKQKPLSF 455
ID AEIGKN ++ V D K AL + L+N E K D W ++L + FPL +
Sbjct: 316 IDPAEIGKNITNIPVADAKRALTA---LKNTE--KCDHQNLWHLQKHNQLDFPLWY 370

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSGGGLGAMGF 515
+ I PQ+ ++ + EL+ G+A+++T VGQHQMWAQ+Y++K P W++SGGLG MGF
Sbjct: 371 DRSDQEISPQWLMEQIYELSKGEAVVTVDVGQHQMWAQYYSFKDPHNWVTSGGGLGTMGF 430

Query: 516 GLPAAIGASVANPDIAIVVDIDGDSFIMNVQELATIRVENLPVKVLLLNQHLGMVMQWE 575
G PAAIGA +A P+++V+ + GDG F M +QEL+ ++ +NLPVKV++LNN+ LGMV QW+
Sbjct: 431 GFPAAIGAQMKNPSLVAVVGDGGFQMTLQELSILKSQNLVVKVILNNEALGMVRQWQ 490

Query: 576 DRFYKANRAHTFLGDPAQEDEFPMMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPY 635
+ FY+ +H+ + P+ + A + G+ RV K+AD+ + + GP
Sbjct: 491 ESFYEERYSHSLFSEN-----PDFVKLAESYGVGRMRVEKEADVPNILSEVFTYDGPV 543

Query: 636 LLDVICPHQEHVLPMPINGGTNDVI 661
++D + V PMI G ++I
Sbjct: 544 VIDCRVQKTSVYPMIAPGTGIQEMI 569

>ref|YP_388660.1| acetolactate synthase, large subunit [Desulfovibrio desulfuricans
subsp. desulfuricans str. G20]
gb|ABB38965.1| acetolactate synthase, large subunit [Desulfovibrio desulfuricans
G20]
Length = 562

Score = 527 bits (1357), Expect = e-147, Method: Compositional matrix adjust.
Identities = 277/568 (48%), Positives = 370/568 (65%), Gaps = 15/568 (2%)

Query: 98 KGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARS 157
GA IL+E L+++GV+ +F YPGA ++I+ L R +R+VL RHEQ V AA+GYAR+
Sbjct: 4 SGARILLECLKKEGVDFVIFGYPGGAVIDIYDELPRHD-LRHVLVRHEQAAVHAADGYARA 62

Query: 158 SGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
SG+ G+C+ TSGPGATN V+G+A A DS+PLV +TGQVPR +IG DAFQE IV +TR
Sbjct: 63 SGRVGVCLVTSFGPGATNTVTGIATAYCDSIPLVLTGQVPRALIGNDAFQEVDIVGITRP 122

Query: 218 ITKHNLYVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYM 277
TKHNLYV ++ D+PRII EAF+LA SGRPGPVLVD+PKDI A + +KL Y
Sbjct: 123 CTKHNLYVKELSDLPRIIREAFYLARSGRPGPVLVDLPKDIMVARAEFQIPEEVKLRYSN 182

Query: 278 SRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCLNS--SDELGRFVELTGIPVASTLMGL 335
P + L + L+ +++P+L+ GGG + S S+ELG IPV S+LMGL
Sbjct: 183 PTY--RPNLNQLRRAELVLSARRPLLFAGGGVVGSDASEELGWLARTLQIPVTSSLMGL 240

Query: 336 GSYPCDELHSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRV TGKLEAFASRAKIVHID 395
GS+P DD L L MLGMHGT AN AV D+L+A G RFDDRV TGKL AFA+ AKI+HID
Sbjct: 241 GSFPGDDPLFLGMLGMHGTFAANKAVNSCDVLI AAGARFDDRV TGKLSAFAAGAKIIHID 300

Query: 396 IDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEE--LKLD FGVWRNELNVQKQKFPL 453
ID I KN V V GD ++AL GM ++L R EE + W ++ Q PL
Sbjct: 301 IDPTSIRKNVGVVEPVVGD CRMALAGMREILSARFEENIPVPRWTEWLATVHDWAQSHPL 360

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGLGAM 513
+ E I PQ ++ + +T G+ I++T VGQ+QMWA AQF+ Y+KPR L+SGGLG M
Sbjct: 361 GYVP-SEGIKPQQVETVFGITRGECIVTTEVGQNMWA AQFFKYRKPRTLTSGGLGTM 419

Query: 514 GFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLLNQHLGMVMQ 573
G+G PAAIGA +A P +V+D GDGS MN+QELAT LPVK+++LNN +LGMV Q
Sbjct: 420 GYGFPAAIGAQM AFGHLVIDFAGDGSIQMNIQELATAVCNKLPVKIIILNNGYLMVRQ 479

Query: 574 WEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPG 633
W++ FY+ N T + E P+ + A A G R+T +ADL ++ L +P
Sbjct: 480 WQELFYQRNYCSTCM-----EAQPDFVKLA EAYGAEGYRITAQADLEPVL RQALQSPA 532

Query: 634 PYLLDVICPHQEHVLP MIPNGGTFNDVI 661
P ++DV +E+V PM+P G ++++
Sbjct: 533 PAIVDVRVEREENVYPMVPAGAALDEML 560

>ref|YP_894460.1| acetolactate synthase 3 catalytic subunit [Bacillus thuringiensis str. Al Hakam]
ref|ZP_03112221.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus cereus 03BB108]
gb|ABK84953.1| acetolactate synthase, large subunit [Bacillus thuringiensis str. Al Hakam]
gb|EDX62664.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus cereus 03BB108]
Length = 570

Score = 526 bits (1356), Expect = e-147, Method: Compositional matrix adjust.
Identities = 268/566 (47%), Positives = 375/566 (66%), Gaps = 21/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGQGVFAAEGYARSS 158
GA +++ L++ GV TVF YPGA + ++ AL S +++L RHEQ + AAEGYAR+S
Sbjct: 17 GAGHVIQCLKKLGVTTFVGYPGGAILPVYDAL-YESGLKHILTRHEQA AIIHAAEGYARAS 75

Query: 159 GKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ ATSGPGATNLV+GLADA +DS+PLV ITGQV +IG D FQE +V +T +
Sbjct: 76 GKVGVVFATSGPGATNLVTGLADAYMDSIPLVVITGQVATPLIGKDFQEADVVGITVPV 135

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V DV + RI++EAF++A SGRPGPVL+D+PKD+Q + + + ++PGY
Sbjct: 136 TKHNYQVRDVNQLSRIVQEAFYIAESGRPGPVLIDIPKDVQIEKVSFYNEVIEIPGY-- 193

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLG 336
++ P+ L+++ + IS++K+P+LY+GGG ++S SDEL +F IPV STLMLGLG
Sbjct: 194 KIEDMPDSMKLKEVAKEISKAKRPLLYIGGGVIHSGGSDELKFAREHRIPVSTLMGLG 253

Query: 337 SYPCDELHSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRV TGKLEAFASRAKIVHIDI 396
+YP D L L MLGMHGT AN AV DLLLA GVRFDDRV TGKLE F+ ++K VHIDI
Sbjct: 254 AYPPGDSLFLGMLGMHGTAAANMAVTECDLLALGVRFDDRV TGKLELFSPQSKKVHIDI 313

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQGMNKV-LENRAEELKLD FGVWRNELNVQKQKFPLSF 455
DS+E KN T V GDVK AL + + ++ + +E W ++ K+++PLS+
Sbjct: 314 DSSEFHKNVTVVEYPVVG DVKNALHMLLHMPIDTQTDE-----WLT KIEGWKEEYPLSY 366

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGLGAMGF 515
+ PQ+ I ++ ELT+G+AI++T VGQHQMWA FY K PR +L+SGGLG MGF
Sbjct: 367 NQKERELKPQHVISLSELTNGEAIVTTEVGQHQMWA AHFYKAKNPRTFLTSGGLGTMGF 426

Query: 516 GLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLLNQHLGMVMQWE 575
G PAAIGA +A + +V+ I GD SF MN+QEL T+ N+PVKV ++NN+ LGMV QW+
Sbjct: 427 GFPAAGAQLAKEEQLVICIAGDASFQMNIQELQTVAENNIPVKVFI INNKFLGMVRQWQ 486

Query: 576 DRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKADLREAIQTMLDTPGPY 635
+ FY+ + + +G P+ + A A G+ R T + ++ + GP
Sbjct: 487 EMFYENRLSESKIGS-----PDFVKVAEAYGVKGLRATNSTEAKQVMLEAFAHEGPV 538

Query: 636 LLDVICPHQEHVLPMPNGGTFNDVI 661
++D E+V PM+P N++I
Sbjct: 539 VVDFCVEEGENVFPMVPPNKGNNEMI 564

>ref|YP_384221.1| acetolactate synthase, large subunit [Geobacter metallireducens
GS-15]
gb|ABB31496.1| acetolactate synthase, large subunit [Geobacter metallireducens
GS-15]
Length = 566

Score = 526 bits (1355), Expect = e-147, Method: Compositional matrix adjust.
Identities = 269/571 (47%), Positives = 375/571 (65%), Gaps = 20/571 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA IL+E L+R+GV+TVF YPGG + ++ L IR++LPRHEQ GV AA+G+AR++
Sbjct: 5 GARILLECLKREGVDTVFGYPGGTVINLYDELFSFKDIRHILPRHEQAGVHAADGFARAT 64

Query: 159 GKPICICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
G+ G+ IATSGPGATN V+G+A A +DS+PLV ITGQVP +IG DAFQE I+ +TR
Sbjct: 65 GRVGVAIATSGPGATNTVTGTIATAYMDSIPLVVITGQVPTALIGNDAFQEVDIIGITRPC 124

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHN+LV DV+DI II++AF++A +GRPGPVLVD+PKD+Q A + +A++L Y
Sbjct: 125 TKHNFVLKDVKDIAITIIKKAFYIARTGRPGPVLVDLPKDVQIATAEFYEPAEIELRSY-- 182

Query: 279 RMPKPPEDSHLEQIVRLIS---ESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLM 333
KP + H +QI + +S +KKPV+YVGGG + +++ EL IPV +TLM
Sbjct: 183 ---KPTVEGHKPKIEKAVSMLLAAKKPVMYVGGGAISGDAAGELTALATRLHIPVTTTLM 239

Query: 334 GLGSPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIVH 393
GLGS+P D+ LSL +LGMHGT +AN AV + DLL+A G RFDDRVTKG+ FA AKI+H
Sbjct: 240 GLGSFPEDNPLSLKLLGMHGTYFANMAVTNCDLLVAVGARFDDRVTKIATFAPHAKIIH 299

Query: 394 IDIDSAEIGKNKTPHVSVCVDKLLALQGMNKVLENRAEELKLDGCV---WRNELNVQKQK 450
+D+D I KN + + G VK L M K L+ +++ W E+ KQK
Sbjct: 300 MDVDPTSIRKNVRVDLPVIGQVKEVLGRMLKSLDESGDKVAAFHTAIEPWLAEIEGWKQK 359

Query: 451 FPLSFKTFGEAIPPQYAIKVDELDTGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
P+++K I PQ+ I+ L EL+D AI++T VGGHQMWA AQF+ +++PR LSSGGL
Sbjct: 360 HPITYKQASTVIKQPQVFIQKRELSDPDAIVATDVGGHQMWTAQFFGFREPRTLSSGGL 419

Query: 511 GAMGFLPAAIGASVANPDIAIVDDIDGGSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
G MGFLPAA+GA A P+ V+ + GDG F MN+QE+AT+ LPVK+++LNN LGM
Sbjct: 420 GTMGFLPAAAGAAAFPNRQVIAVCGDGGFQMNLEQVATLVQNRLPVKIVILNNNFLGM 479

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKADLREAIQTMLD 630
V QW++ F+ + T + P + + A A G + TK ++ I+ +
Sbjct: 480 VRQWQELFFDKRYSQTCMELPI-----DFIKLAEAFGAKGFQATKSDEVEATIKKAFE 532

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
TPGP +++ +E VLPM+P G + N+++
Sbjct: 533 TPGPVIMEFKIAREEKVLPMPAGASLNEMV 563

>ref|ZP_02585109.1| acetolactate synthase 3 catalytic subunit [Bacillus cereus G9842]
Length = 571

Score = 526 bits (1354), Expect = e-147, Method: Compositional matrix adjust.
Identities = 270/566 (47%), Positives = 369/566 (65%), Gaps = 21/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA +++ L++ GV TVF YPGGA + ++ AL S +++VL RHEQ + AAEGYAR+S
Sbjct: 18 GAGHVIQCLKKLGVTTVFGYPGGAILPVYNALYESG-LKHLVTRHEQAIIHAAEGYARAS 76

Query: 159 GKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ ATSGPGATNLV+GLADA +DS+PLV ITGQV +IG D FQE +V +T +
Sbjct: 77 GKVGVVFATSGPGATNLVTGLADAYMDSIPLVVITGQVATPLIGKDGFEADVVGITVPV 136

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V DV + RI++EAF++A SGRPGPVL+D+PKD+Q + + + +PGY
Sbjct: 137 TKHNYQVRDENVHVSRIQEAIFYIAESGRPGPVLIDIPKDVQNAKVTSTFFNEEVDIPGYKP 196

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLG 336
+ P+ L ++ + IS+SK+P+LY+GGG ++S SDEL F IPV STLMGLG
Sbjct: 197 EL--VPDSMKLREVAKAISKSRPLLYIGGGVIHSGGSDELFEFARENRIIPVSTLMGLG 254

Query: 337 SYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAKIVHIDI 396
+XP D L L MLGMHT AN AV DLLLA GVRFDRTVGKLE F+ +K VHIDI
Sbjct: 255 AYPPGDPLFLGMLGMHGTAAANMAVTECDLLALGVRFDRTVGKLELFSPHSKKVHIDI 314

Query: 397 DSAEIGKNKTPHVSVCQDVKLALQG-MNKVLENRAEELKLDGVRNRELNVQKQKFPPLSF 455
D +E KN T + GDVK AL ++ + + +E W ++ K+++PLS+
Sbjct: 315 DPSEFHNKVTVEHPVIGDVKALHMLLHMSIYTQTDE-----WLQKVKAWKEEYPLSY 367

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGF 515
K + PQ+ I ++ ELT+G+AI++T VGQHQMWAA FY +KPR +L+SGGLG MGF
Sbjct: 368 KQKESELKPKQHVINLVSELTNGEAIIVTEVGVGQHQMWAAHFYKARKPRFTLTSGGLGTMGF 427

Query: 516 GLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
G PAAIGA +A + +V+ I GD SF MN+QEL TI N+PVKV ++NN+ LGMV QW+
Sbjct: 428 GFPAAGAQLAKKEELVICIAGDASQFQMNQELQTIENNIPVKVFIINNKLGMVRQWQ 487

Query: 576 DRFYKANRAHTFLGDPAQEDEFPPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPY 635
+ FY+ + + +G P+ + A A G+ R T + ++ + GP
Sbjct: 488 EMFYENRLSESKIGS-----PDFVKVAEAYGVKGLRATNSTEAKQVMLEAFAHEGPA 539

Query: 636 LLDVICPHQEHVLPMPNGGTFNDVI 661
++D E+V PM+P N++I
Sbjct: 540 VVDFCVEEENVFPMVPPNKGNNEMI 565

>gb|EDZ37939.1| acetolactate synthase, large subunit [Leptospirillum sp. Group II
'5-way CG']
Length = 587

Score = 525 bits (1353), Expect = e-147, Method: Compositional matrix adjust.
Identities = 269/571 (47%), Positives = 374/571 (65%), Gaps = 18/571 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA++++E L+ + V +F YPGG + I AL + + +L RHEQG V AAEGYAR++
Sbjct: 6 GAEMILECLKTEKVSQIFGYPGGLVLPIDFALYKDPGLSVILTRHEQGAVHAAEGYARTT 65

Query: 159 GKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
G+ G+ + TSGPGATN V+GLADA +DS+PLV ITGQV +MIG DAFQE IV ++RS
Sbjct: 66 GEVGVVLVTSGPGATNTVTGLADAHMDSIPLVVITGQVPTKMIGNDAFQEADIVGISRSC 125

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHN+LV + ++PRI++EAF++A SGRPGPVLVD+PKD+ A ++ + + L GY
Sbjct: 126 TKHNFVLSRIGELPRILKEAFYIARSGRPGPVLVDIPKDVITDRADFHYPETLTTLRGY-- 183

Query: 279 RMPKPPEDSHLEQI---VRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLM 333
P + QI +L+S++KKPVLYVGGG + +S +EL V L+ IPV TLM
Sbjct: 184 ---NPTVQGNRWQIRKAAQLMSKAKKPVLYVGGGVIASDSHEELAELVSLSQIPVTLTLM 240

Query: 334 GLGSPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAKIVH 393
GLG++P + L + MLGMHT AN AV + DLL+A G RFDDRTVGK+ F+ +K++H
Sbjct: 241 GLGAFPGNHSLFMGMLGMHGTAAANMAVHNCDLLIAVGARFDDRTVGKVAEFSPHSKVH 300

Query: 394 IDIDSAEIGKNKTPHVSVCQDVKLALQGMNKVLEN-RAEELKLDGVRNRELNVQKQKFP 452
IDID I KN + V + GD +L L + + L R EE + W ++ K++ P
Sbjct: 301 IDIDPTSIRKNFSVDVPIVGDARLILSDLLEDLRKIRDEEGLVSLAEAWHRQIEFWKEEHP 360

Query: 453 LSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGA 512
LS+K E I PQ+ I+ +LT G IIST VGQHQMW AQF+ + PR WL+SGGLG
Sbjct: 361 LSYKKDPEVIKPKQFVIEKTFDLTGDCIISTDVGQHQMWTAQFFKFLTPRTWLTSGGLGT 420

Query: 513 MGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVM 572
MG+G PAAIGA A P V+ + G+GSF+MN+QELAT+ +PVK+++LNNQ+LGMV
Sbjct: 421 MGYGFPAAGAQRAPFKRVIAVTGEGSFMMNIQELATVASLEIPVKIIVLNNQYLGMR 480

Query: 573 QWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDTP 632
QW++ FY + +F+G P+ + A A G+ R TK + + + L T
Sbjct: 481 QWQEFFYGGYSSSFIGQS-----PDFVKLAFAFGVAGFRATKTDQVEDILLKGLSTN 533

Query: 633 GPYLLDVICPHQEHVLPMPNGGTFNDVITE 663
GP L++ + +E+V PM+P GG+ ++I E
Sbjct: 534 GPVLMFEMVDPEENVFPMVPAGGSNIEMIFE 564

>ref|YP_001232446.1| acetolactate synthase, large subunit, biosynthetic type [Geobacter
uraniireducens Rf4]
gb|ABQ27873.1| acetolactate synthase, large subunit [Geobacter uraniireducens Rf4]
Length = 566

Score = 525 bits (1353), Expect = e-147, Method: Compositional matrix adjust.
Identities = 267/568 (47%), Positives = 372/568 (65%), Gaps = 14/568 (2%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA IL+E L+ +GV+TVF YPGG + ++ L IR++LPRHEQ GV AA+GYAR++
Sbjct: 5 GAKILLECLKLEGVDTVFYPGGTVINLYDELFSFKEIRHILPRHEQAGVHAADGYARAT 64

Query: 159 GKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ IATSGPGATN ++G+A A +DS+P+V ITGQVP +IG DAFQE I+ +TR
Sbjct: 65 GKVGVAIATSGPGATNTITGIATAYMDSIPMVIITGQVPTALIGNDAFQEADIIGITRPC 124

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHN+LV DV+D+ I+++AF++A +GRPGPVL+D+PKD+Q A + +++ GY
Sbjct: 125 TKHNFLVKDVKDLALIVKKAIFYIARTGRPGPVLIDLPKDVQIATAEFKYPDTVEIRGYKP 184

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLMGLG 336
+ P+ +E+ + L+ +K+PV+YVGGG + N+++EL + PV +TLMGLG
Sbjct: 185 TIEGHPK--QVEKAMSLLLGAKRPVIVYVGGGVILGNAAEELTALSKKLEAPVTTTLMGLG 242

Query: 337 SYPCDDELSLHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDI 396
S+P DD LSL +LGMHGT YAN AV + DLL+A G RFDDRVTGK+ +FA AKI+HID+
Sbjct: 243 SFPEDDPLSLGLLGMHGTYYANMAVSNCDLLVAVGARFDDRVTGKIASFAPHAKI IHIDV 302

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEEL---KLDGFGVWRNELNVQKQKFP 453
D I KN + + GDVK L M KVLE + ++L K W E+ K K P+
Sbjct: 303 DPTSIKKNVRVDLPVIGDVKDLTQMLKVLEEQQGDKLDDFKKSIVPWTEIEGWKAKHPM 362

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAM 513
S+K I PQ+ I+ L EL+D AI++T VGQHQMW AQF+ + +PR LSSGGLG M
Sbjct: 363 SYKQSATVIKPFVIQKLRELSDDPAIVATDVGQHQMWTAQFFKFNRPRTLSSGGLGTM 422

Query: 514 GFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQ 573
G+GLPAA+GA A PD V+ I GDG F MN+QELAT+ L VK+ ++NN LGMV Q
Sbjct: 423 GYGLPAAMGAQAAPDRQVIVICGDGGFQMNQELATVQNRALAVKICIINNINFLGMVRQ 482

Query: 574 WEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDTPG 633
W++ F+ + T + P + + A A G + TK ++ I+ TPG
Sbjct: 483 WQELFFDKRYSQTCMELPI-----DFIKLAFAFGAKGFQATKPDEVEAVIKKGFATPG 535

Query: 634 PYLLDVICPHQEHVLPMPNGGTFNDVI 661
P +++ +E VLPM+P G + +++
Sbjct: 536 PVIMEFKVAREEKVLPMPAGASLTEMV 563

>ref|ZP_00740942.1| Acetolactate synthase large subunit [Bacillus thuringiensis serovar
israelensis ATCC 35646]
gb|EA054777.1| Acetolactate synthase large subunit [Bacillus thuringiensis serovar
israelensis ATCC 35646]
Length = 571

Score = 525 bits (1353), Expect = e-147, Method: Compositional matrix adjust.

Identities = 270/566 (47%), Positives = 369/566 (65%), Gaps = 21/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA +++ L++ GV TVF YPGA + ++ AL S +++VL RHEQ + AAEGYAR+S
Sbjct: 18 GAGHVIQCLKKLGVTTFVGYPGGAILPVYDALYESG-LKHVLTREHQAIIHAAEGYARAS 76

Query: 159 GKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ ATSGPGATNLV+GLADA +DS+PLV ITGQV +IG D FQE +V +T +
Sbjct: 77 GKVGVVFATSGPGATNLVTGLADAYMDSIPLVVITGQVATPLIGKDFQEADVVGITVPV 136

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V DV + RI++EAF++A SGRPGPVL+D+PKD+Q + + + +PGY
Sbjct: 137 TKHNYQVRDVNVHSRIVQEAIFYIAESGRPGPVLIDIPKDVQNAKVTSSFFNEEVDIPGYKP 196

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLG 336
+ P+ L ++ + IS+SK+P+LY+GGG ++S SDEL F IPV STLMLGLG
Sbjct: 197 EL--VPDSMKLREVAKAISKSRPLLYIGGGVIHSGGSDLEFEFARENRIPIVSTLMGLG 254

Query: 337 SYPCDDELSLHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTKLEAFASRAKIVHIDI 396
+YP D L L MLGMHGT AN AV DLLLA GVRFDDRVTKLE F+ +K VHIDI
Sbjct: 255 AYPPGDPLFLGMLGMHGTAAANMAVTECDLLALGVRFDDRVTKLELFSPHSKKVHIDI 314

Query: 397 DSAEIGKNKTPHVSVCQDVKLALQG-MNKVLENRAEELKLDGFWVRNENLVQKQKPLSF 455
D +E KN T + GDVK AL ++ + + +E W ++ K+++PLS+
Sbjct: 315 DPSEFHNKVTVEHPIVGDVKKALHMLHMSIYTQTDE-----WLQKVKAWEKPYPLSY 367

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGF 515
K + PQ+ I ++ ELT+G+AI++T VGGQHQMWAA FY +KPR +L+SGGLG MGF
Sbjct: 368 KQKESELKPKQHVINLVSELTNGEAIIVTEVGGQHQMWAAHFYKARKPRTFLTSGGLGTMGF 427

Query: 516 GLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
G PAAIGA +A + +V+ I GD SF MN+QEL TI N+PVKV ++NN+ LGMV QW+
Sbjct: 428 GFPAAGAQLAKKEELVICIAGDASQFQNIQELQTAENNIIPVKVFIINNKLGMVRQWQ 487

Query: 576 DRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKADLREAIQTMLDTPGPY 635
+ FY+ + + +G P+ + A A G+ R T + ++ + GP
Sbjct: 488 EMFYENRLSESKIGS-----PDFVKVAEAYGVKGLRATNSTEAKQVMLEAFAHEGPA 539

Query: 636 LLDVICPHQEHVLPMPNGGTFNDVI 661
++D E+V PM+P N++I
Sbjct: 540 VVDFCVEEENVFPMVPPNKGNNEMI 565

>ref|YP_036023.1| acetolactate synthase 3 catalytic subunit [Bacillus thuringiensis
serovar konkukian str. 97-27]
gb|AAT63317.1| acetolactate synthase [Bacillus thuringiensis serovar konkukian
str. 97-27]
Length = 570

Score = 525 bits (1352), Expect = e-147, Method: Compositional matrix adjust.
Identities = 268/566 (47%), Positives = 371/566 (65%), Gaps = 21/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA +++ L++ GV TVF YPGA + ++ AL S +++L RHEQ + AAEGYAR+S
Sbjct: 17 GAGHVIQCLKKLGVTTFVGYPGGAILPVYDAL-YESGLKHILTRHEQAIIHAAEGYARAS 75

Query: 159 GKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ ATSGPGATNLV+GLADA +DS+PLV ITGQV +IG D FQE IV +T +
Sbjct: 76 GKVGVVFATSGPGATNLVTGLADAYMDSIPLVVITGQVATPLIGKDFQEADIVGITVPV 135

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V DV + RI++EAF++A SGRPGPVL+D+PKD+Q + + + +PGY
Sbjct: 136 TKHNYQVRDVNQLSRIVQEAIFYIAESGRPGPVLIDIPKDVQIKKVTSSFYNEVIEIPGY-- 193

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLG 336
++ P+ L ++ + ISE+K+P+LY+GGG +++ S+EL +F GIPV STLMLGLG
Sbjct: 194 KLEPRPDSMKLREVAKAISEAKRPLLYIGGGIIHADGSEELIQFARKKGIPVSTLMGLG 253

Query: 337 SYPCDDELSLHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTKLEAFASRAKIVHIDI 396
+YP D L L MLGMHGT AN AV DLLLA GVRFDDRVTKLE F+ +K VHIDI
Sbjct: 254 AYPPGDPLFLGMLGMHGTAAANMAVTECDLLALGVRFDDRVTKLELFSPHSKKVHIDI 313

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQG-MNKVLENRAEELKLD FGVWRNELNVQKQKFLSF 455
D +E KN V GDVK AL ++ + + +E W ++ K+++ LS+
Sbjct: 314 DPSEFQKNVAVEYPVVG DVKKALHMLLHMSIHTQTDE-----WLQKVKTWKEEYQLSY 366

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGF 515
K + PQ+ I ++ ELT+G+AI++T VGQHQMWA FY K PR +L+SGGLG MGF
Sbjct: 367 KQKESELKPQHVINLVSELTNGEAIIVTTEVGVGQHQMWAHAFYKAKNPRTFLTSGGLGTMGF 426

Query: 516 GLPAAIGASVANPDAIVVDIDGDG SFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
G PAAIGA +A + +V+ I GD SF MN+QEL TI N+PVKV ++NN+ LGMV QW+
Sbjct: 427 GFPAAGAQLAKEEELVICIAGDASFQMNIEQLQTAENNIPVKVFIINNKLGMVQRQW 486

Query: 576 DRFYKANRAHTFLGDPAQEDEFNPMMLFAAACGIPAAARVTKKADLREAIQTMLDTPGPY 635
+ FY+ + + +G P+ + A A G+ R T + ++ + GP
Sbjct: 487 EMFYENRLSESKIGS-----PDFVKVAEAYGVKGLRATNATEAKQVMLEAFHAKGPV 538

Query: 636 LLDVICPHQEHVLPMPNGGTFNDVI 661
++D E+V PM+P N++I
Sbjct: 539 VVDFCVEEGENVFPMVPPNKGNNEMI 564

>ref|YP_002139546.1| acetolactate synthase, large subunit, biosynthetic type [Geobacter
bemidjensis Bem]
gb|ACH39750.1| acetolactate synthase, large subunit, biosynthetic type [Geobacter
bemidjensis Bem]
Length = 566

Score = 525 bits (1351), Expect = e-147, Method: Compositional matrix adjust.
Identities = 266/568 (46%), Positives = 374/568 (65%), Gaps = 14/568 (2%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSS 158
GA IL+E L+R+GV+T+F YPGG + ++ L IR++LPRHEQ GV AA+GYAR++
Sbjct: 5 GARILLECLKREGVD TIFGYPGGTVINLYDELFSFKEIRHILPRHEQAGVHAADGYARAT 64

Query: 159 GKPGICIATSGPGATNLVSG LADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ IATSGPGATN ++G+A A +DS+P+V +TGQVP +IG DAFQE I+ +TR
Sbjct: 65 GKVGVAIATSGPGATNTITGIATAYMDSIPMVI VTGQVPTALIGNDAFQEADIIGITRPC 124

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHN+LV DV+D+P I+++AF+++A +GRPGPVLVD+PKD+Q A ++ + +++ GY
Sbjct: 125 TKHNFVLKDVKDLPTIMKKAFYIARTGRPGPVLVDLPKDQMAQAEFHYPETVEIRGYKP 184

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLMGLG 336
+ P+ +E+ V +I+++K+PVLVGGG + N++ EL F + IPV +TLMGLG
Sbjct: 185 NLEGHPK--QVEKAVTMITQAKRPVLYVGGGVILGNAAELTAFAKRLAIPVTTTLMGLG 242

Query: 337 SYPCDEL SLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIVHIDI 396
++P +D LSL +LGMHGT YAN AV + D+L+A G RFDDRVTGK+ +FA AKIVH+D+
Sbjct: 243 AFPENDTSLGLLGMHGTYYANMAVSNCDVLAIGARFDDRVTGKIASFAPHAKIVHVDV 302

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKL--DFGVWRNELNVQKQKFLP 453
D I KN + + GDV+ L M K E + K+ W E+ K K P+
Sbjct: 303 DPTSIKKNVRVDLP IVGDVRDVLAKMLKAAELVCPDAKVCQDAIAPWTAIEGWKAKHPM 362

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAM 513
S+K I PQY I+ L L+D AI++T VGQHQMWA AQF+ + PR LSSGGLG M
Sbjct: 363 SYKQSTTTIKPQYVIQRLRLSDPD AIVATDVGVGQHQMWAQFFGFTTPTLLSSGGLGTM 422

Query: 514 GFGLPAAIGASVANPDAIVVDIDGDG SFIMNVQELATIRVENLPVKVLLNNQHLGMVMQ 573
G+GLPAA+GA A P+ V+ + GDG F MN+QELATI L VK+ +LNN LGMV Q
Sbjct: 423 GYGLPAAAGQAAPPERQVMVVC GGGFQMNQLQELATIVQNRLNVKICILNNFLGMVRQ 482

Query: 574 WEDRFYKANRAHTFLGDPAQEDEFNPMMLFAAACGIPAAARVTKKADLREAIQTMLDTPG 633
W++ F+ + T + E+ + + A A G + TK ++ E I+ T G
Sbjct: 483 WQELFFDKRYSSTCM-----ELPIDFIKLAEAFGATGLQATKVDEVDEVIKKGFATNG 535

Query: 634 PYLLDVICPHQEHVLPMPNGGTFNDVI 661
P L++ +E VLPMP+P G + +++
Sbjct: 536 PVLMEFKVAREKVLPMVPAGASLTEMV 563

>ref|ZP_03231724.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus cereus AH1134]
gb|EDZ51578.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus cereus AH1134]
Length = 571

Score = 525 bits (1351), Expect = e-147, Method: Compositional matrix adjust.
Identities = 270/566 (47%), Positives = 369/566 (65%), Gaps = 21/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA +++ L++ GV TVF YPGGA + ++ AL S +++VL RHEQ + AAEYAR+S
Sbjct: 18 GAGHVIQGLKKLGVTTFVGYPGGAILPVYDALYESG-LKHVLTREQAIIHAAEGYARAS 76

Query: 159 GKP GICATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ ATSGPG TNLV+GLADA +DS+PLV ITGQV +IG D FQE +V +T +
Sbjct: 77 GKVG VVFATSGPGVTNLVLTGLADAYMDSIPLVVITGQVATPLIGKDFQEADVVGITVPV 136

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V DV + RI++EAF++A SGRPGPVL+D+PKD+Q + + + +PGY
Sbjct: 137 TKHNYQVRDVNHVSRIVQEAFYIAKSGRPGPVLIDIPKDVQNAKVTSSFFNEEVDIPGYKP 196

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLG 336
+ P+ L ++ + IS+SK+P+LY+GGG ++S SDEL F IPV STLMLGLG
Sbjct: 197 EL--VPDSMKLREVAKAISKSRPLLYIGGGVIHSGGSDELFEFARENRIPIVSTLMGLG 254

Query: 337 SYPCDDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRTVGKLEAFASRAKIVHIDI 396
+YP D L L MLGMHGT AN AV DLLLA GVRFDDRTVGKLE F+ ++K VHIDI
Sbjct: 255 AYPPGDPLFLGMLGMHGTAAANMAVTECDLLALGVRFDDRTVGKLELFSPQSKKVHIDI 314

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQG-MNKVLENRAEELKLDGFGVWRNENLVQKQKPLSF 455
D +E KN T + GDVK AL ++ + + +E W ++ K+++PLS+
Sbjct: 315 DPSEFHKNVTVEHPIVGDVKALYMLLHMSIYTQTDE-----WLQKV KAWKEEYPLSY 367

Query: 456 KTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGF 515
K + PQ+ I ++ ELT+G+AI++T VGQHQMWAQ FY +KPR +L+SGGLG MGF
Sbjct: 368 KQKESELKPQHVINLVSELTNGEAIIVTEVGVGQHQMWAHAFYKARKPRTFLTSGGLGTMGF 427

Query: 516 GLPAAIGASVANPDIAIVVDIDGDSFIMNVQELATIRVENLPVKVLLLNQHLGMVMQWE 575
G PAAIGA +A + +VV I GD SF MN+QEL TI N+PVKV ++NN+ LGMV QW+
Sbjct: 428 GFPAAGAQLAKEEELVVCIAGDASFQMNIELQTIENNIPVKVFIINNRFGLGMVRQWQ 487

Query: 576 DRFYKANRAHTFLGDPAQEDEFPPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPY 635
+ FY+ + + +G P+ + A A G+ R T + ++ + GP
Sbjct: 488 EMFYENRLSESKIGS-----PDFVKVAEAYGVKGLRATNSTEAKQVVLEAFAHEGPV 539

Query: 636 LLDVICPHQEHVLPMPNGGTNDVI 661
++D E+V PM+P N++I
Sbjct: 540 VVDFCVEEGENVFPMPNPKGNNEI 565

>ref|NP_844268.1| acetolactate synthase 3 catalytic subunit [Bacillus anthracis str. Ames]
ref|YP_018490.1| acetolactate synthase 3 catalytic subunit [Bacillus anthracis str. 'Ames Ancestor']
ref|YP_027979.1| acetolactate synthase 3 catalytic subunit [Bacillus anthracis str. Sterne]
ref|ZP_00392128.1| COG0028: Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase] [Bacillus anthracis str. A2012]
ref|ZP_02213936.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis str. A0488]
ref|ZP_02258927.1| acetolactate synthase 3 catalytic subunit [Bacillus cereus AH820]
ref|ZP_02391592.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis str. A0442]
ref|ZP_02397134.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis str. A0193]
ref|ZP_02877432.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis str. A0465]

ref|ZP_02897759.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis str. A0389]
ref|ZP_02933574.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis str. A0174]
ref|ZP_03019259.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis Tsiankovskii-I]
gb|AAP25754.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis str. Ames]
gb|AAT30965.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis str. 'Ames Ancestor']
gb|AAT54030.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis str. Sterne]
gb|EDR20235.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis str. A0488]
gb|EDR88694.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis str. A0193]
gb|EDR93983.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis str. A0442]
gb|EDS96675.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis str. A0389]
gb|EDT20648.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis str. A0465]
gb|EDT68811.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis str. A0174]
gb|EDV16443.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus anthracis Tsiankovskii-I]
Length = 570

Score = 524 bits (1350), Expect = e-147, Method: Compositional matrix adjust.
Identities = 267/566 (47%), Positives = 371/566 (65%), Gaps = 21/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA +++ L++ GV TVF YPGGA + ++ AL S +++L RHEQ + AAEYAR+S
Sbjct: 17 GAGHVIQCLKKLGVTTFVGYPGGAILPVYDAL-YESGLKHILTRHEQAIIHAAEGYARAS 75

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ ATSGPGATNLV+GLADA +DS+PLV ITGQV +IG D FQE +V +T +
Sbjct: 76 GKVGVVFATSGPGATNLVTGLADAYMDSIPLVVITGQVATPLIGKDFQEADVVGITVPV 135

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V DV + RI++EAF++A SGRPGPVL+D+PKD+Q + + + +PGY
Sbjct: 136 TKHNYQVRDVNQLSRIVQEAFYIAESGRPGPVLIDIPKDVQIEKVSFYNEVIEIPGY-- 193

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLG 336
++ P+ L ++ + ISE+K+P+LY+GGG +++ S+EL +F GIPV STLMLGLG
Sbjct: 194 KLEPRPDMSMKLREVAKAISEAKRPLLYIGGGI IHADGSEELIQFARKKGIPVSTLMGLG 253

Query: 337 SYPCDELDSLHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDI 396
+YP D L L MLGMHGT AN AV DLLLA GVRFDDRVTGKLE F+ +K VHIDI
Sbjct: 254 AYPPGDPLFLGMLGMHGTAAANMAVTECDLLALGVRFDDRVTGKLELFSPHSKKVHIDI 313

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQG-MNKVLENRAEELKLDGFGVWRNELNVQKQKFPLSF 455
D +E KN V GDVK AL ++ + + +E W ++ K+++ LS+
Sbjct: 314 DPSEFQKNVAVEYPVVG DVKKALHMLLHMSIHTQTDE-----WLQKVKTWKEEYQLSY 366

Query: 456 KTFGEAIPPQYAIKVDELDTGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGF 515
K + PQ+ I ++ ELT+G+AI++T VGQHQMWAA FY K PR +L+SGGLG MGF
Sbjct: 367 KQKESELKPQHVINLVSELTNGEAIIVTEVGVGQHQMWAAHFYKAKNPRTFLTSGGLGTMGF 426

Query: 516 GLPAAIGASVANPDAIVVDIDGGSFIMNVQELATIRVENLPVKVLLLNQHLGMVMQWE 575
G PAAIGA +A + +V+ I GD SF MN+QEL TI N+PVKV ++NN+ LGMV QW+
Sbjct: 427 GFPAAGAQLAKEEELVICIAGDASFGQMNQELQTIENNIPVKVFIINNKLGMVRQWQ 486

Query: 576 DRFYKANRAHTFLGDPQAEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPY 635
+ FY+ + + +G P+ + A A G+ R T + ++ + GP
Sbjct: 487 EMFYENRLSESKIGS-----PDFVKVAEAYGVKGLRATNATEAKQVMLEAFAHKGPV 538

Query: 636 LLDVICPHQEHVLPMPINGGTFNDVI 661
++D E+V PM+P N++I
Sbjct: 539 VVDFCVEEGENVFPMVPPNKGNNEMI 564

>ref|ZP_03100840.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus cereus W]
gb|EDX57818.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus cereus W]
Length = 570

Score = 524 bits (1350), Expect = e-147, Method: Compositional matrix adjust.
Identities = 267/566 (47%), Positives = 371/566 (65%), Gaps = 21/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVF AAEGYARSS 158
GA +++ L++ GV TVF YPGA + ++ AL S ++++L RHEQ + AAEGYAR+S
Sbjct: 17 GAGHVIQCLKKLGVTTVFGYPGGAILPVYDAL-YESGLKHILTRHEQA AIHAAEGYARAS 75

Query: 159 GKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ ATSGPGATNLV+GLADA +DS+PLV ITGQV +IG D FQE +V +T +
Sbjct: 76 GKVG VVFATSGPGATNLVTGLADAYMDSIPLVVITGQVATPLIGKDFQEADVVGITVPV 135

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V DV + RI++EAF++A SGRPGPVL+D+PKD+Q + + + +PGY
Sbjct: 136 TKHNYQVRDVNQLSRIVQEAFYIAESGRPGPVLIDIPKDVQIEKVT SFYNEVIEIPGY-- 193

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLG 336
++ P+ L ++ + ISE+K+P+LY+GGG +++ S+EL +F GIPV STLMLGLG
Sbjct: 194 KLEPRPD SMKLR EVAKAISEAKRPLLYIGGGI IHADGSEELIQFARKKGIPV VSTLMGLG 253

Query: 337 SYPCDDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRVTGKLEAFASRAKIVHIDI 396
+YP D L L MLGMHGT AN AV DLLLA GVRFDDRVTGKLE F+ +K VHIDI
Sbjct: 254 AYPPGDPLFLGMLGMHGT Y AANMAVTECDLLALGVRFDDRVTGKLELFSPHSKKVHIDI 313

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQG-MNKVLENRAEELKLDGFWVRNENLVQKQKFP LSF 455
D +E KN V GDVK AL ++ + + +E W ++ K+++ LS+
Sbjct: 314 DPSEFQKNVAVEYPVVG DVKKALHMLLHMSIHTQTDE-----WLQKVKTWKEEYQLSY 366

Query: 456 KTFGEAIPPQYAIKVDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGLGAMGF 515
K + PQ+ I ++ ELT+G+AI++T VGQHQMWA FY K PR +L+SGGLG MGF
Sbjct: 367 KQKESELKPQHVINLVSELTNGEAI VTEVGQHQMWA AHFYKAKNPRTFLTSGGLGTMGF 426

Query: 516 GLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLLNNQHLGMVMQWE 575
G PAAIGA +A + +V+ I GD SF MN+QEL TI N+PVKV ++NN+ LGMV QW+
Sbjct: 427 GFPA AIGAQLAKEEQLVICIAGDASFQMN IQLQTI AENNIPVKVFIINNKF LGMVRQWQ 486

Query: 576 DRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAA RVTKKADLREAIQTMLDTPGPY 635
+ FY+ + + +G P+ + A A G+ R T + ++ + GP
Sbjct: 487 EMFYENRLSESKIGS-----PDFVKVAEAYGVKGLRATNATEAKQVMLEAFAHKGPV 538

Query: 636 LLDVICPHQEHLVPMIPNGGTFNDVI 661
++D E+V PM+P N++I
Sbjct: 539 VVDFC VEEGENVFPMVPPNKGNNEMI 564

>ref|ZP_03108556.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus cereus NVH0597-99]
gb|EDX66581.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus cereus NVH0597-99]
Length = 570

Score = 524 bits (1350), Expect = e-147, Method: Compositional matrix adjust.
Identities = 267/566 (47%), Positives = 370/566 (65%), Gaps = 21/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVF AAEGYARSS 158
GA +++ L++ GV TVF YPGA + ++ AL S ++++L RHEQ + AAEGYAR+S
Sbjct: 17 GAGHVIQCLKKLGVTTVFGYPGGAILPVYDAL-YESGLKHILTRHEQA AIHAAEGYARAS 75

Query: 159 GKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ ATSGPGATNLV+GLADA +DS+PLV ITGQV +IG D FQE +V +T +
Sbjct: 76 GKVG VVFATSGPGATNLVTGLADAYMDSIPLVVITGQVATPLIGKDFQEADVVGITVPV 135

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V DV + RI++EAF++A SGRPGPVL+D+PKDIQ + + + +++PGY
Sbjct: 136 TKHNYQVRDVNQLSRIVQEAFYIAESGRPGPVLIDIPKDIQNEKVTSTFYNEVIEIPGY-- 193

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLG 336
++ P+ L ++ + ISE+K+P+LY+GGG +++ S+EL +F GIPV STLMGLG
Sbjct: 194 KLEPMPDSMKLREVAKAISEAKRPLLYIGGGIHHADGSEELIQFARKKGIPVSTLMGLG 253

Query: 337 SYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DVRTGKLEAFASRAKIVHIDI 396
+YP D L L MLGMHGT AN AV DLLLA GVRFD DVRTGKLE F+ +K VHIDI
Sbjct: 254 AYPPGDPLFLGMLGMHGT YVANMAVTECDLLALGVRFDDRTGKLELFSPHSKKVHIDI 313

Query: 397 DSAEIGKNKTPHVSVC G DVKLALQG-MNKVLENRAEELKLD FGVWRNELNVQKQKFPLSF 455
D +E KN V GDVK AL ++ + + +E W ++ K+++ LS+
Sbjct: 314 DPSEFQKNVAVEYPVVG DVKKALHMLLHMSIHTQTDE-----WLQKVKTWKEEYQLSY 366

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGLGAMGF 515
K + PQ+ I ++ ELT+G+AI++T VGQHQMWA FY K PR +L+SGGLG MGF
Sbjct: 367 KQKESELKPQHVINLVSELTNGEAIVTTEVGQHQMWA AHFYKAKNPRFTLTSGGLGTMGF 426

Query: 516 GLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLLNQHLGMVMQWE 575
G PAAIGA +A + +V+ I GD SF MN+QEL TI N+PVKV ++NN+ LGMV QW+
Sbjct: 427 GFPAAGAQLAKEEQLVICIAGDASFQMN IQELQTIAENNIPVKVFIINNKF LGMVQRWQ 486

Query: 576 DRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPY 635
+ FY+ + + +G P+ + A A G+ R T + ++ + P
Sbjct: 487 EMFYENRLSESKIGS-----PDFVKVAEAYGVKGLRATNATEAKQVMLEAF AHKAPV 538

Query: 636 LLDVICPHQEHVLPMPNGGTFNDVI 661
++D E+V PM+P N++I
Sbjct: 539 VVDFCVEEGENVFPMVPPNKGNNEMI 564

>ref|NP_978250.1| acetolactate synthase 3 catalytic subunit [Bacillus cereus ATCC 10987]
gb|AAS40858.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus cereus ATCC 10987]
Length = 571

Score = 524 bits (1350), Expect = e-147, Method: Compositional matrix adjust.
Identities = 269/566 (47%), Positives = 372/566 (65%), Gaps = 21/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSS 158
GA +++ L++ GV TVF YPGGA + ++ AL S +++VL RHEQ + AAEGYAR+S
Sbjct: 18 GAGHVQICLKKLGVTTFVFGYPGGAILPVYDAL-YGSGLKHVLRHEQA AIIHAAEGYARAS 76

Query: 159 GKPGICIATSGPGATNLVSG LADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ ATSGPGATNLV+GLADA +DS+PLV ITGQV + +IG D FQE +V +T +
Sbjct: 77 GKVG VVFATSGPGATNLVTGLADAYMDSIPLVITGQVAKSLIGKDG FQEADVVGITVPV 136

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY + DV + RI++EAF++A SGRPGPVL+D+PKDIQ + + + +++PGY
Sbjct: 137 TKHNYQIRDVNHL SRIVQEAFYIAESGRPGPVLIDIPKDIQNE NVTSFYNEVIEIPGY-- 194

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLG 336
++ P+ L+++ + IS++K+P+LY+GGG ++S SDEL +F IPV STLMGLG
Sbjct: 195 KLEPMPDSMKLKEVAKEISKAKRPLLYIGGGVIHSGGSDEL IKFARENRI PVVSTLMGLG 254

Query: 337 SYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DVRTGKLEAFASRAKIVHIDI 396
+YP D L L MLGMHGT AN AV DLLLA GVRFD DVRTGKLE F+ +K VHIDI
Sbjct: 255 AYPPGDSLFLGMLGMHGT YANMAVTECDLLALGVRFDDRTGKLELFS PYSKKVHIDI 314

Query: 397 DSAEIGKNKTPHVSVC G DVKLALQGMNKV-LENRAEELKLD FGVWRNELNVQKQKFPLSF 455
D +E KN T V GDVK AL + + + + +E W + K ++PLS+
Sbjct: 315 DPSEFHKNVTV EYPVVG DVKKALHMLLHMP ICTQTDE-----WLTKTEEWKA EYPLSY 367

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGLGAMGF 515
+ PQ+ I ++ ELT+G+AI++T VGQHQMWA FY K PR +L+SGGLG MGF
Sbjct: 368 NQKESDLKPQHVISLVSELTNGEAIVTTEVGQHQMWA AHFYKAKNPRFTLTSGGLGTMGF 427

Query: 516 GLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
G PAAIGA +A + +V+ I GD SF MN+QEL TI N+PVKV ++NN+ LGMV QW+
Sbjct: 428 GFPAAGAQLAKEEELVICIAGDASFQMNQELQTIENNIPVKVFIINNKFVLMVQRWQ 487

Query: 576 DRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPY 635
+ FY+ + + +G P+ + A A G+ R T + + + + + GP
Sbjct: 488 EMFYENRLSESKIGS-----PDFVKVAEAYGVKGLRATNSIEAKQVMLEAIAHEGPV 539

Query: 636 LLDVICPHQEHVLPMPNGGTFNDVI 661
++D E+V PM+P N++I
Sbjct: 540 VVDFCVEEGENVFPMVPPNKGNNEMI 565

>ref|YP_359378.1| acetolactate synthase, large subunit, biosynthetic type
[Carboxydotherrmus hydrogenoformans Z-2901]
gb|AB14028.1| acetolactate synthase, large subunit, biosynthetic type
[Carboxydotherrmus hydrogenoformans Z-2901]
Length = 554

Score = 522 bits (1345), Expect = e-146, Method: Compositional matrix adjust.
Identities = 279/567 (49%), Positives = 375/567 (66%), Gaps = 23/567 (4%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA LV+ALE +GV T+F YPGGA + ++ AL+RS I++VL RHE G + AA GYAR+S
Sbjct: 5 GAQALVKALELEGVTTIFGYPGGAVVPLYDALSRK-IQHVLVRHEPGAIIHAANGYARAS 63

Query: 159 GKPICIAITSGPGATNLVSLGADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+C+ATSGPGATNLV+G+A A +DSVP+V ITGQVP M+GTDAFQE I +T I
Sbjct: 64 GKVGVCVATSGPGATNLVTGIATAYMDSVPVVTITGQVPTTMVGTDAFQEVDITGITMPI 123

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHN+LV + DIP +++++AF++A +GRPGPVL+D+PKD+ + + + + + GY
Sbjct: 124 TKHNFVKNPADIPAVVKKAFYIAATGRPGPVLIDLKPKDVAARTIDFQYPEKVEIRGYKP 183

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLMGLG 336
+ P+ + + V+LI E+K+PV+ GGG L N+S EL F IPV +TLMGL
Sbjct: 184 NLKGHPQ--KIAEAVKLIREAKRPVVIAGGGVLAANASQELYEFVAVRAEIPVTNTLMGLT 241

Query: 337 SYPCDDELSLHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRVTKLEAFASRAKIVHIDI 396
S+P D L L MLG+HGT YAN AV D+L+ GVRV DRVTVG+L FA +AKI+HID+
Sbjct: 242 SFPQDSPLFLGMLGLHGTTRYANLAVTECDVLI GLGVRFADRVTVGELSGFAPKAKI IHIDV 301

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQGMNKVLE--NRAEELKLDGFWVRNENLVQKQKFPLS 454
D AEIGKN V + GDVK LQ M K +E NR E W +++N KQ+FPL
Sbjct: 302 DPAEIGKNVRADVPIVGDVKNVLQEMLKQIEPQNRQE-----WLSQINTWKQEFPLK 353

Query: 455 FKTFGAIPQYAIKVLDELTDGKAIISTGVGHQHMWAAQFYNYKKPRQWLSSGGLGAMG 514
++ + I PQ IK+L E T II+T VGQHQM W AQFY +KKPR +L+SGGLG MG
Sbjct: 354 YEK-DDFIKPQETIKLLGEKTADTIIATDVGHQHMWTAQFYFPKKPRFTLTSGLGCMG 412

Query: 515 FGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQW 574
+GLPAAIGA+VA D V+ I GDGSF MN+ ELAT R +NL +K++L N+ LGMV Q
Sbjct: 413 YGLPAAIGA AVAFRDQVILITGDGSFQMMNGELATAREQNLSLKIILFVNKKLGMVKQL 472

Query: 575 EDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGP 634
++ + N LG P+ + A A GIP ++T+ ++ A+ ML G
Sbjct: 473 QEYYANKNYFVDLG-----FVPDFVALAKAYGIPGRKITRPEEVDGALDEMLAHKGM 525

Query: 635 YLLDVICPHQEHVLPMPNGGTFNDVI 661
YLL++ +E VLP+ +G + +
Sbjct: 526 YLLEIEISPEEKVLPVLSGAPIGEAV 552

>dbj|BAF37287.1| acetolactate synthase [Monochoria vaginalis]
Length = 642

Score = 521 bits (1343), Expect = e-146, Method: Compositional matrix adjust.
Identities = 237/332 (71%), Positives = 288/332 (86%)

Query: 336 GSYPCDELSTHMLGMHGTIVYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAKIVHID 395
G YP D LSL MLGMHGTIVYANYA++ +DLLAFGVRFD+RVTGKLEAFASRAKIVHID
Sbjct: 308 GVPYLDGPLSLKMLGMHGTIVYANYAIDKADLLAFGVRFDRTVGKLEAFASRAKIVHID 367

Query: 396 IDSAEIGKNKTPHVSVCADVCLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQKFLPSF 455
ID AEIGKNK PHVS+CGD+KLALQ MN+++E KLDF WR EL+ QK+ +PL +
Sbjct: 368 IDPAEIGKNKQPHVSICGDIKLALQEMNEMIEESGIHNKLDFAWREELDQKKKNYPLEY 427

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGF 515
KTFG+ IPPQ+AI++L+ELT+G+AI+I+TGVGQHQMWAQ+Y+YK+PRQWL+S GLGAMGF
Sbjct: 428 KTFGDLIPPQHAIELLEELTNGEAIITTGVGQHQMWAQYYSYKPRQWLTSAGLGAMGF 487

Query: 516 GLPAAIGASVANPDIAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
GLPAA+GA+V NP +VVDIDGDSF MN QELA IR+ENL VK+L+LNNQHLGMV+QWE
Sbjct: 488 GLPAAVGAAGVGNPGVMVVDIDGDSFQMNAQELAIIRIENLDVKMLILNNQHLGMVVQWE 547

Query: 576 DRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKADLREAIQTMLDTPGPY 635
DRFYK+NRHT+LG+PA E ++FP+ + A + IPAARV+KK+++R+AI+ M+ TPGPY
Sbjct: 548 DRFYKSNRAHTYLGPNANESKVFDPFVKLAESYDIPAARVSKKSEVRDAIRKMIQTGPY 607

Query: 636 LLDVICPHQEHVLPMPINGGTNDVITEGDGR 667
LLDVI PH+EHVLPMP+GG F D+I +GDGR
Sbjct: 608 LLDVIVPHEEHVLPMPISGGAFKDMILDGDGR 639

Score = 202 bits (514), Expect = 8e-50, Method: Compositional matrix adjust.
Identities = 97/116 (83%), Positives = 106/116 (91%)

Query: 91 FAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPREHQQGVFA 150
F+PD+PRKGADILVEALER+GV +FAYPGGASMEIHQALTRS SI N L RHEQG FA
Sbjct: 63 FSPDEPRKGADILVEALEREVTDLFAYPGGASMEIHQALTRSPSITNHLRHEQGEAFA 122

Query: 151 AEGYARSSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAF 206
A GYARS+G+PG+CIATSGPGATNLVS LADALLDS+P+VAITGQVPRRMIGTDAF
Sbjct: 123 ASGYARSTGRPGVCIATSGPGATNLVSALADALLDSIPMVAITGQVPRRMIGTDAF 178

>ref|ZP_02850743.1| acetolactate synthase, large subunit, biosynthetic type
[Paenibacillus sp. JDR-2]
gb|EDS49383.1| acetolactate synthase, large subunit, biosynthetic type
[Paenibacillus sp. JDR-2]
Length = 581

Score = 521 bits (1343), Expect = e-146, Method: Compositional matrix adjust.
Identities = 264/565 (46%), Positives = 366/565 (64%), Gaps = 16/565 (2%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPREHQQGVFAAEGYARSS 158
G++IL+ +L +GV+ VF YPGA + I+ A+ S +VL RHEQG + AA+GYAR+S
Sbjct: 26 GSEILLRSLVLEGVDCVFGYPGGAVLYIDAMHGFSDFNHVLTRHEQGAIAHADGYARAS 85

Query: 159 GKGPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
G G+CIATSGPGATNLV+G+A A +DSVPLV ITG V +IGTDAFQE I +T I
Sbjct: 86 GNVGVCATSGPGATNLVTGIATAYMDSVPLVVITGNVISSLIGTDAFQEADITGITMPI 145

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKH+Y+V DVED+PRII EAF +A +GR GPVL+D+PKD+ + + + GY
Sbjct: 146 TKHSYMRDVEDLPRIIEAFHIANTRKGPVLIDIPKDVSAAKTLFKPVTEVNIIRGYNP 205

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSS--DELGRFVELTGIPVASTLMGLG 336
M P +++++ I S++P++ GGG + S +EL FV T IP+ +TL+GLG
Sbjct: 206 TM--SPNKLQVDKLIKAEASERPLILAGGGVYSGAHEELLEFTKTIDIPITTTLLGLG 263

Query: 337 SYPCDELSTHMLGMHGTIVYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAKIVHIDI 396
+P ++L L M GMHGT AN +++ +DLL+ G RFDDRTVGKL FA AKIVHIDI
Sbjct: 264 GFPSGNDLWLGMPGMHGTYTANKSIQADLLINIGARFDDRTVGKLAGFAPLAKIVHIDI 323

Query: 397 DSAEIGKNKTPHVSVCADVCLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQKFLPSFK 456
D AEIGKN + + GDVK LQ +N+ L RA++ WR E+ K ++P S+K
Sbjct: 324 DPAEIGKNVPTDIPVIGDVKTVLQVQVQ--LAKRADKAD---AWRQEIQESKAQYPPFSYK 378

Query: 457 TFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGFG 516
+ PQ+ ++++ E T G AI++T VGQHQMWAQ+Y + KPR W++SGGLG MGFG
Sbjct: 379 DSDVELKPQWVVEMIHETTGGDAIVTTDVGQHQMWAQYYKFNKPRSWVTSGGLGTMGFG 438

Query: 517 LPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWED 576
P+AIGA +ANPD VV I+GDG M QELA + N+PVKV++LNNQ LGMV QW++
Sbjct: 439 FPSAIGAQMNPDRTPVVSINGDGMQCAQELAICAINNIPVKVILNNQVLGMVRQWQE 498

Query: 577 RFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKADLREAIQTMLDTPGPYL 636
++ +H L P+ + A A G+ R + K + + + L PGP +
Sbjct: 499 LIHENRFSHIDLAGE-----PDFVKLAAYGVKGFASRNKEEAKAVWEEALRHPGPAV 551

Query: 637 LDVICPHQEHVLPMPNGGTFNDVI 661
++ + E+V PM+ G T + +I
Sbjct: 552 VEFVVRDENVPMPVAGSTIDQMI 576

>ref|YP_001833518.1| acetolactate synthase, large subunit, biosynthetic type
[Beijerinckia indica subsp. indica ATCC 9039]
gb|ACB96029.1| acetolactate synthase, large subunit, biosynthetic type
[Beijerinckia indica subsp. indica ATCC 9039]
Length = 586

Score = 521 bits (1342), Expect = e-146, Method: Compositional matrix adjust.
Identities = 268/575 (46%), Positives = 370/575 (64%), Gaps = 27/575 (4%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA ++V AL+ QGV+T+F YPGGA + I+ AL +S+++VL RHEQG V AAEYARSS
Sbjct: 7 GAQMVVLTALKDQGVDTIFGYPGGAVLPIDALFHQNSVKHVLVRHEQGAHVHAAEGYARSS 66

Query: 159 GKPICATISGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ + TSGPGATN V+GL DALLDS+PLV ITGQVP +IG+DAFQE V +TR
Sbjct: 67 GKIGVVLVTSGPGATNAVTGLTDALLDSIPLVCITGQVPTHLIGSDAFQECDTVGITRHC 126

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAI----PNWEQAMKLP 274
TKHNYLV VED+PRI+ EAF++A GRPGPV++D+PKD+Q L + N E P
Sbjct: 127 TKHNYLVQRVEDLPRILHEAFYVAQHGRPGPVVIDIPKDVQFALGLYAGPENIEHKTYKP 186

Query: 275 GYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDE----LGRFVELTGIPVAS 330
+ + + +++ + I+ +K+P+ Y GGG +NS E L V+LTG P+ S
Sbjct: 187 AFKGDGLGR-----IDEALSWIAAKRPIFYTGCGIINSGEASALLRELVDLTGAPITS 240

Query: 331 TLMGLGSYPCDELDELHMLGMHGTIVYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAK 390
TLMGLG+YP L MLGMHGT AN A+ DL++A G RFDDR+TG+++AF+ ++
Sbjct: 241 TLMGLGAYPASSPRWLGMLGMHGTYEANNAMHDCDLMAIGARFDDRITGRIDAFSPGSR 300

Query: 391 IVHIDIDSAEIGKNKTPHVSVCVDKALQGMNKVLENRAEELKLDGFGV---WRNELNVQ 447
+HIDID + I K + + GD L+ M V + L D V W E++
Sbjct: 301 KIHIDIDPSSINKTVKVDLGIIVGDCITAVLRDM--VARWKRHLACDAAVLQKWWQEIHW 358

Query: 448 KQKFPLSFKTFGEAIPPQYAIKVLDELTDGK-AIISTGVGQHQMWAQFYNYKKPRQWLS 506
+ + L+++ + I PQYAI+ L ELT G+ IST VGQHQMWAQ Y++ +P +W++
Sbjct: 359 RARKSLAYRASNKVIKPYAIQRLFELTRGRDITYISTEVGQHQMWAQHYHFDEPNRWMT 418

Query: 507 SGGLGAMGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLG MG+GLPAAIGA +A+P ++VVDI G+ S +MN+QEL+T LPVK+ +LNNQ
Sbjct: 419 SGGLGTMGYGLPAAIGAQAHPGSLVVDIAGEASILMNIQELSTAVQFRLPVKIFILNNQ 478

Query: 567 HLGVMVMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKADLREAIQ 626
++GMV QW++ + + ++ E P+ + A A G R L AI
Sbjct: 479 YMGVMVRQWQELHGGRYSESY-----SEALPDFVKLAAYGCHGIRCADPNTLDAAIL 531

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
M++TP P L D I +E+ LPMIP+G N++I
Sbjct: 532 EMETPKPVLFDCIVDRENCPLMIPSGKAHNEMI 566

>ref|ZP_02577817.1| acetolactate synthase 3 catalytic subunit [Bacillus cereus B4264]
Length = 573

Score = 520 bits (1340), Expect = e-145, Method: Compositional matrix adjust.
Identities = 267/566 (47%), Positives = 368/566 (65%), Gaps = 21/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSS 158
GA +++ L++ GV TVF YPGA + ++ AL S +++VL RHEQ + AAEGYAR+S
Sbjct: 20 GAGHVIQCLKKLGVTTFVGYPGGAILPVYDALYESG-LKHVLRHEQAIIHAAEGYARAS 78

Query: 159 GKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
K G+ ATSGPGATNLV+GLADA +DS+PLV ITGQV +IG D FQE +V +T +
Sbjct: 79 RKGVGVFATSGPGATNLVTGLADAYMDSIPLVVITGQVATPLIGKDFQEADVVGITVPV 138

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V DV + +++EAF++A SGRPGPVL+D+PKD+Q + + + +PGY
Sbjct: 139 TKHNYQVRDVNHVSQVQEA FYIAKSGRPGPVLIDIPKDVQNAKVTSSFFNEEVDIPGYKP 198

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLG 336
+ P+ L ++ + IS+SK+P+LY+GGG ++S SDEL F IPV STLMLGLG
Sbjct: 199 EL--VPDSMKLREVAKAISKSKRPLLYIGGGVIHSGGSDELFEFARENRI PVVSTLMGLG 256

Query: 337 SYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTVGKLEAFASRAKIVHIDI 396
+YP D L L MLGMHGT AN AV D LLA GVRFD DRTVGKLE F+ +K VHIDI
Sbjct: 257 AYPPGDPLFLGMLGMHGTAAANMAVTECDLLALGVRFD DRTVGKLELFSPHSKKVHIDI 316

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQG-MNKVLENRAEELKLD FGVWRNELNVQKQKFPLSF 455
D +E KN T + GDVK AL ++ + + +E W ++ K+++PLS+
Sbjct: 317 DPSEFHKNITVEHPIVGDVKALHMLLHMSIYTQTDE-----WLQKV KAWKEEYPLSY 369

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGLGAMGF 515
K + PQ+ I ++ ELT+G+AI++T VGQHQMWA FY +KPR +L+SGGLG MGF
Sbjct: 370 KQKESELKPQHVINLVSELTNGEAI VTEVGVGQHQMWA AHFYKARKPRTFLTSGGLGTMGF 429

Query: 516 GLPAAIGASVANPDAIVVDIDGDGSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
G PAAIGA +A + +V+ I GD SF MN+QEL TI N+PVKV ++NN+ LGMV QW+
Sbjct: 430 GPAAIGAQLAKKEELVICIAGDASFQMN IQELQTAENNIPVKVFIINNKF LGMVRQWQ 489

Query: 576 DRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKADLREAIQTMLDTPGPY 635
+ FY+ + + +G P+ + A A G+ R T + ++ + GP
Sbjct: 490 EMFYENRLSESKIGS-----PDFVKVAEAYGVKGLRATNSTEAKQVMLEAFAHEGPV 541

Query: 636 LLDVICPHQEHLVPMIPNGGTFNDVI 661
++D E+V PM+P N++I
Sbjct: 542 VVDFCVEEGENVFPMVPPNKGNNEMI 567

>ref|YP_357321.1| acetolactate synthase, large subunit, biosynthetic type [Pelobacter
carbinolicus DSM 2380]
gb|ABA89151.1| acetolactate synthase, large subunit [Pelobacter carbinolicus DSM
2380]
Length = 565

Score = 520 bits (1340), Expect = e-145, Method: Compositional matrix adjust.
Identities = 267/573 (46%), Positives = 379/573 (66%), Gaps = 21/573 (3%)

Query: 97 RKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYAR 156
+ G+ IL+E+L ++GV+TVF YPGG + I+ L I+++L RHEQ V AA+GYAR
Sbjct: 3 KTGSQILLESLLQEGVDTVFGYPGGTVINIYNDLP-DYPIKHILTRHEQA AVHAADGYAR 61

Query: 157 SSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTR 216
+SGK G+ IATSGPGATN V+G+A A +DS P+V ITGQVP +IG DAFQE IV +TR
Sbjct: 62 ASGKVGVAIATSGPGATNTVTGIATAYMDSTPMVVITGQVPTPLIGNDAFQEADIVG ITR 121

Query: 217 SITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGY 276
SITKHNYLV DV+D+ RI+++AF++A +GRPGPVL+D+PKD+Q + + ++L GY
Sbjct: 122 SITKHNYLVKDVKDLARIVKQAFYIARTGRPGPVLIDL PKDVQLASTKFVYPENVELRGY 181

Query: 277 MSRMPPKPPEDSHLEQI---VRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVAST 331
KP ++ Q+ ++I +++PVLYVGGG S S++L F EL PV +T
Sbjct: 182 -----KPTYSGNVRQVDKAAKMILAAARRPVLYVGGGATASDASEDLVAFSELIQAPVVTT 236

Query: 332 LMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKI 391
LMG+ ++P LSL MLGMHGT YAN AV ++DLL+A G RFDDRVTG++ AFA +AKI
Sbjct: 237 LMGMAAFPTAHPLSLGMLGMHGTYYANMAVTNADLLVAVGARFDDRVTGRIAAAFAPKAKI 296

Query: 392 VHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGV--WRNELNVQK 448
+HIDID I KN + + G+++ + + L+ +E++K + WR++++ +
Sbjct: 297 IHIDIDPTSIKKNVRVDLPVIGELRDVMGKIVAKLKEDSEKVKELSEISAPWRSQIDSWR 356

Query: 449 QKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSG 508
++P+++K+ I PQY I+ + ELT AII+T VGQHQMWAQF+N+ PR +L+SG
Sbjct: 357 AQYPMYTKSSDVIKPYVIEKIRELTRKD AIIATEVGQHQMWAQFFNFSPRTFLTSG 416

Query: 509 GLGAMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHL 568
GLG MGFGLPAA+GA V PD V+DI GDGSF MN QELAT+ LPVK+ +LNN L
Sbjct: 417 GLGTMGFGLPALGAQVGCPRQVIDISGDGSFQMNSQELATLVQYQLPVKIAILNNNFL 476

Query: 569 GMVMQWEDRFYKANRAHFTLGDPAQEDEIFPNMLLFAAACGIPAA RVTKKADLREAIQTM 628
GMV QW+ F+ + T L P + + A A G + + + I+
Sbjct: 477 GMVRQWQQLFFDRYSQTPLDLPI-----DFVKLAEAYGATGLQASSPDQVEGVIRKA 529

Query: 629 LDTPGPYLLDVICPHQEHVLPMPINGGTFNDVI 661
L+TPGP L++ +E+V+PM+P G ++++
Sbjct: 530 LETPGPVLMEFKVDREENVMPMPAGAAIDEMV 562

>ref|YP_001126680.1| acetolactate synthase catalytic subunit [Geobacillus
thermodenitrificans NG80-2]
ref|ZP_03148878.1| acetolactate synthase, large subunit, biosynthetic type
[Geobacillus sp. G11MC16]
gb|ABO67935.1| Acetohydroxy acid synthase large subunit, acetolactate synthase
large subunit [Geobacillus thermodenitrificans NG80-2]
gb|EDY05133.1| acetolactate synthase, large subunit, biosynthetic type
[Geobacillus sp. G11MC16]
Length = 577

Score = 520 bits (1339), Expect = e-145, Method: Compositional matrix adjust.
Identities = 266/565 (47%), Positives = 372/565 (65%), Gaps = 17/565 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSS 158
G+ +L+EAL+ + VE +F YPGGA + ++ L ++ + +VL RHEQG + AAEGYAR S
Sbjct: 18 GSLMLIEALKAENVEVIFGYPGGAVLPLYDELYKAG-VFHVLT RHEQGAIHAAEGYARIS 76

Query: 159 GKPGICIATSGPGATNLVSG LADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GKPG+ IATSGPGATN+V+GL DA++DS+PLV TGQV +IG+DAFQE +V +T I
Sbjct: 77 GKPGVVIATSGPGATNIVTGLTDAMMDSLPLVVFTGQVATNVIGSDAFQEADVVGITMPI 136

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V D+ ++P+II+EAF +AT+GRPGPVL+D+PKD+ ++ Q + LPGY
Sbjct: 137 TKHNYQVRDISELPKIIKEAFHIATTGRPGPVLIDIPKDVITAEGEFDYNQDVHLPGYQP 196

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLMGLG 336
P + ++V +S+SK+PV+ G G L N++DEL ++ E IPVA TL+GLG
Sbjct: 197 T--TQPNHWQIRRLVEAVSQSKRPVILAGAGVLHANAADLQQYAEQQNIPVAHTLLGLG 254

Query: 337 SYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIVHIDI 396
+P D L L M GMHGT AN A+ DLL+ G RFDDRVTG L+ FA +A + HIDI
Sbjct: 255 GFPADHPLFLGMAGMHGTAAANMALYECDLLINIGARFDDRVTG NLKYFAPKATVAHIDI 314

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKFPLSFK 456
D AEIGKN + + D K ALQ +++E + + D W +LN K++FPL ++
Sbjct: 315 DPAEIGKNVPTKIPIVSDAKAALQ---ELIEQQGK--PADNAAWLAQLNEWKRRFPLHYE 369

Query: 457 TFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGFG 516
AI PQ I+++ E+T G+AI++T VGQHQMWAQY+ + +P +W++SGGLG MGFG
Sbjct: 370 PEAGAIKPQKLIEMIYEVTTGGEAIVTTDVGQHQMWAQYKFNRPNRWVTS GGLGTMGFG 429

Query: 517 LPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWED 576
LPAAIGA +A+ A VV I GDG F M QEL+ I+ LP+KV+++NNQ LGMV QW++
Sbjct: 430 LPAAIGAQLADQSATVVSIVGDGGFQMTQCQLSVIQELQLPIKVIVNNQALGMVRQWQE 489

Query: 577 RFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPYL 636
FY +H+ + P Q P+ + A A G+P R +A+ E ++ GP L
Sbjct: 490 LFYDKRYSHSLI--PNQ-----PDFVKLAAYGMPGLRAKTEAEAAEVLKQAFIDGPVL 542

Query: 637 LDVICPHQEHVLPMPNGGTFNDVI 661
LD E+V PM+ G ++++
Sbjct: 543 LDFHVCADENVPMVAPGKGLHEMV 567

>ref|YP_001413730.1| acetolactate synthase, large subunit, biosynthetic type
[Parvibaculum lavamentivorans DS-1]
gb|ABS64073.1| acetolactate synthase, large subunit, biosynthetic type
[Parvibaculum lavamentivorans DS-1]
Length = 585

Score = 520 bits (1338), Expect = e-145, Method: Compositional matrix adjust.
Identities = 264/578 (45%), Positives = 379/578 (65%), Gaps = 17/578 (2%)

Query: 95 QPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGY 154
Q GA+I+++AL QGV+T+F YPGGA + I+ AL + + IR++L RHEQG V AAEGY
Sbjct: 4 QELTGAEIVIKALVDQGVDTIFGYPGGAVLPYDALFQQNKIRHILVRHEQGAVHAAEGY 63

Query: 155 ARSSGKPGICIAATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEV 214
ARS+GKPG+ + TSGPGATN V+GL DAL+DS+PLV +TGQV +IG+DAFQE V +
Sbjct: 64 ARSTGKPGVVLVTSGPGATNAVLTGLTALMDSIPLVCLTGQVATHLIGSDAFQECDTVGI 123

Query: 215 TRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLP 274
TR TKHN+LV ++ R++ EAF++AT+GRPGPV++D+PKD+Q Q A Q +
Sbjct: 124 TRHCTKHNWLKSAPELSRVMEAFYVATNGRPGPVVIDIPKDVQFQRAEYAGPQNVVHR 183

Query: 275 GYMSRMPKPPED-SHLEQIVRLISESKKPVLYVGGGCLNS----SDELGRFVELTGIPVA 329
Y PK D +++ V LI+ +KKPV Y GGG +NS S L FV LTG P+
Sbjct: 184 TY---RPKVKGDIDKIKEAVDLIANAKKPVFYTGGGIINSGNLASQLLREFVRLTGYPI 240

Query: 330 STLMLGSGYPCDELHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRA 389
STLMGLG+YP D+ L MLGMHGT AN A+ D+L+ G RFDDRVTG+L+AF+ +
Sbjct: 241 STLMLGAYPASDKQWLGMMLGMHGTFEANNAMHDCDVLINIGARFDDRVTGRLDAFSPNS 300

Query: 390 KIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD-FGVWRNELNVQK 448
K +H+DID++ + KN V + GD L+ M ++ +++A D W ++ +
Sbjct: 301 KKIHVVIDASSLNKNVRIDVGIIGDCAHVLEMLRIWKSARRPDKDALADWWKQIETWR 360

Query: 449 QKFPLSFKTFGEAIPPQYAIKVLDELTDGK-AIISTGVGHQMWAQFYNYKKPRQWLSS 507
+ LSFKT + I PQ AI+ L EL+ + I+T VGHQMWAQ + +++P+ W++S
Sbjct: 361 GRKSLSFKTNDVIKQQAIRLYELSKHRDITYITTEVGHQMWAQHFPFEEPKEHWM 420

Query: 508 GGLGAMGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQH 567
GGLG MG+GLPAA+G +A+PDA+V+DI G+ S M +QE++T LPVK+ +LNN++
Sbjct: 421 GGLGTMGYGLPAAVGVQIAHPDALVIDIAGEASVQMCMEISTAVQFMLPVKIFILNNEY 480

Query: 568 LGMVMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQT 627
+GMV QW++ ++ +H++ + P+ + A A G R K ++L AI+
Sbjct: 481 MGMVRQWQELLHEGRYSY-----SDSLPDFVKLAAYGATGIRAEKPSELDAAIKK 533

Query: 628 MLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGD 665
M++TPGP + D + E+ PMIP+G N++I D
Sbjct: 534 MIETPGPVIFDCLVDKFENCYPMIPSGAAHNEMILGDD 571

>ref|YP_010595.1| acetolactate synthase, large subunit, biosynthetic type
[Desulfovibrio vulgaris subsp. vulgaris str.
Hildenborough]
gb|AAS95854.1| acetolactate synthase, large subunit, biosynthetic type
[Desulfovibrio vulgaris subsp. vulgaris str.
Hildenborough]
Length = 563

Score = 519 bits (1336), Expect = e-145, Method: Compositional matrix adjust.
Identities = 272/573 (47%), Positives = 373/573 (65%), Gaps = 24/573 (4%)

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Query: 98  KGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARS 157
          GA IL+E L+++GV+  F YPGA ++I+  + R  + +VL RHEQ  V AA+GYAR+
Sbjct: 4   NGAQILLECLKKEGVDVFFGYPGGAVIDIYDEIPRHPHLLHVLVRHEQAAVHAADGYARA 63

Query: 158  SGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
          SGK G+C+ TSGPGATN V+G+A A  DS+P+V +TGQVP  +IG DAFQE  IV +TR
Sbjct: 64  SGKVGCLVLTSGPGATNTVTGIATAYSDSIPVVILTQVPTPLIGNDAFQEVDIVGITRP 123

Query: 218  ITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYM 277
          TKHNYLV DV+++  ++ +AF+LA +GRPGPVLVD+PKD+ Q      W + + +  Y
Sbjct: 124  CTKHNYLVDRVKELATVVRQAFYLARTGRPGPVLVDLPKDVMAKTDVFWPEVDVSMRSY- 182

Query: 278  SRMPKPPEDSHLEQIVRLIS---ESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTL 332
          P      +L QI R      E+++P+L+VGGG +  ++S+ELG F      IPVASTL
Sbjct: 183  ----NPTYKPNLNQIRRAADAFFEAERPLLFGGGVMSDASEELGWFAFTRIPVASTL 238

Query: 333  MGLGSYPCDDELHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIV 392
          MGLG++P DD L L MLGMHGT  AN AV ++DL++A G RFDDRVTG+L AFAS+A+I+
Sbjct: 239  MGLGAFFGDDPLWGLMGMHGTAAANKAVNNADLIVAVGARFDDRVTGRLSAFASKARII 298

Query: 393  HIDIDSAEIGKNKTPHVSVCADVKLALQGMNVLENRAEELKLDGFGV---WRNELNVQK 448
          HIDID  I KN  + V GD + +L  + ++L R EE  D+G  W +L  +
Sbjct: 299  HIDIDPTSIRKNVQGVIPVVGDCRQSLANIREILVPRLEE--KDWGAHARWLEQLASWR 356

Query: 449  QKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSG 508
          + PL F  G I PQ  I+ L  +T G AII+T VGQ+QMW AQFY ++KPR  ++SG
Sbjct: 357  VEQPLGFSREG-GIKPQQVIEQLFAITRGDAIITTEVGQNQMWAQFYFTRKPRTLITSG 415

Query: 509  GLGAMGFGLPAAIGASVANPDIAIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQHL 568
          GLG MG+G PAAIGA  A PD +VVD+ GDGS  MN+QELAT  LPVK+L+LNN +L
Sbjct: 416  GLGTMGYGFPAAIGAQAFAFPDKLVVDVAGDGSIQMNIQELATAVCNKLPVKILILNNGYL 475

Query: 569  GMVMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTM 628
          GMV QW++ FY+ N  T +      + P+ + A A G  R+T+  L  ++
Sbjct: 476  GMVRQWQELFYQRNYCSTCM-----DAQPDFVKLAEAYGAEGYRITEVESLESTLREA 528

Query: 629  LDTPGPYLLDVICPHQEHLVPMIPNGGTFNDVI 661
          L +P P ++DV  +E+V PM+P G  ++++
Sbjct: 529  LASPHPAIIDVRVEREENVYPMVPAGAALDEML 561

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>ref|YP_967136.1| acetolactate synthase, large subunit, biosynthetic type
  [Desulfovibrio vulgaris subsp. vulgaris DP4]
gb|ABM28709.1| acetolactate synthase, large subunit [Desulfovibrio vulgaris subsp.
  vulgaris DP4]
  Length = 563

```

Score = 519 bits (1336), Expect = e-145, Method: Compositional matrix adjust.
Identities = 272/573 (47%), Positives = 373/573 (65%), Gaps = 24/573 (4%)

```

Query: 98  KGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARS 157
          GA IL+E L+++GV+  F YPGA ++I+  + R  + +VL RHEQ  V AA+GYAR+
Sbjct: 4   NGAQILLECLKKEGVDVFFGYPGGAVIDIYDEIPRHPHLLHVLVRHEQAAVHAADGYARA 63

Query: 158  SGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
          SGK G+C+ TSGPGATN V+G+A A  DS+P+V +TGQVP  +IG DAFQE  IV +TR
Sbjct: 64  SGKVGCLVLTSGPGATNTVTGIATAYSDSIPVVILTQVPTPLIGNDAFQEVDIVGITRP 123

Query: 218  ITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYM 277
          TKHNYLV DV+++  ++ +AF+LA +GRPGPVLVD+PKD+ Q      W + + +  Y
Sbjct: 124  CTKHNYLVDRVKELATVVRQAFYLARTGRPGPVLVDLPKDVMAKTEFVWPEVDVSMRSY- 182

Query: 278  SRMPKPPEDSHLEQIVRLIS---ESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTL 332
          P      +L QI R      E+++P+L+VGGG +  ++S+ELG F      IPVASTL
Sbjct: 183  ----NPTYKPNLNQIRRAADAFFEAERPLLFGGGVMSDASEELGWFAFTRIPVASTL 238

Query: 333  MGLGSYPCDDELHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIV 392
          MGLG++P DD L L MLGMHGT  AN AV ++DL++A G RFDDRVTG+L AFAS+A+I+
Sbjct: 239  MGLGAFFGDDPLWGLMGMHGTAAANKAVNNADLIVAVGARFDDRVTGRLSAFASKARII 298

```

Query: 393 HIDIDSAEIGKNKTPHVSVCADVKKALQGMNKLLENRAEELKLDGFGV---WRNELNVQK 448
HIDID I KN + V GD + +L + ++L R EE D+G W +L +
Sbjct: 299 HIDIDPTSIRKNVQVGPVVGDCRQSLANIREILVPRLEE--KDWGAHARWLEQLASWR 356

Query: 449 QKFPPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSG 508
+ PL F G I PQ I+ L +T G AII+T VGQ+QMW AQFY ++KPR ++SG
Sbjct: 357 VEQPLGFSREG-GIKPQQVIEQLFAITRGDAIITTEVGQNMWTAQFYTFRKPRTLITSG 415

Query: 509 GLGAMGFLPAAIGASVANPDIAIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQHL 568
GLG MG+G PAAIGA A PD +VVD+ GDGS MN+QELAT LPVK+L+LNN +L
Sbjct: 416 GLGTMGYGFPAAGAQAFAFDPKLVVDVAGDSIQMNIQELATAVCNKLPVKILILNNGYL 475

Query: 569 GMVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTM 628
GMV QW++ FY+ N T + + P+ + A A G R+T+ L ++
Sbjct: 476 GMVRQWQELFYQRNYCSTCM-----DAQPDFVKLAEAYGAEGYRITEVESLESTLREA 528

Query: 629 LDTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
L +P P ++DV +E+V PM+P G ++++
Sbjct: 529 LASPHPAIIDVRVEREENVYPMVPAGAALDEML 561

>ref|YP_864823.1| acetolactate synthase, large subunit [Magnetococcus sp. MC-1]
gb|ABK43417.1| acetolactate synthase, large subunit [Magnetococcus sp. MC-1]
Length = 564

Score = 519 bits (1336), Expect = e-145, Method: Compositional matrix adjust.
Identities = 270/570 (47%), Positives = 370/570 (64%), Gaps = 19/570 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA+I+V+ L QGV+TVF YPGA + I+ + + +++VL RHEQG + AA+GYAR +
Sbjct: 5 GAEIIVQCLLEQGVKTVFGYPGGAVLNIYDEIYCKDLQHVLRHEQGLLHAADGYARVT 64

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
G+ G+ + TSGPGATN V+GLA A +DS+P+V ITGQVP +IG DAFQE V +TRS
Sbjct: 65 GEVGVALTSGPGATNAVTLATAYMDSIPMVCITGQVPVALIGNDAFQEADTVGITRSC 124

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNYLV DV+D+ R++ EAF++A +GRPGPVLVD+PKDI +A + A G +S
Sbjct: 125 TKHNYLVKDVKDLARVLEAFYIARTGRPGPVLVDIPKDI--TIAATEYSPA---KGEVS 179

Query: 279 -RMPKPPEDSHLEQIVR---LISESKPVLYVGGGCL--NSSDELGRFVELTGIPVASTL 332
R KP H QI + L+++K+P+ Y GGG + N+++EL + V G P+ +TL
Sbjct: 180 IRSYKPSISGHTGQIRKAAGLMAKAKRPLFYTGGGVILSNAAEELTQLVRKLGAPITNTL 239

Query: 333 MGLGSPYPCDELSDLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIV 392
MGLG +PC D+ + MLGMHGT AN AV DLL+A G RFDDRVTKG+ FA AKI+
Sbjct: 240 MGLGGFPCDQFVGMGLGMHGTYEANMAVSRCDLLVAIGARFDDRVTKISQFAPEAKII 299

Query: 393 HIDIDSAEIGKNKTPHVSVCADVKKALQGMNKLLENRAEELKL-DFGVWRNELNVQKQKF 451
H+D+D I KN V + GD+K L M ++E+ + +L D G W E+ ++K
Sbjct: 300 HLDVDPSTISKNVEVDPIVGDIKTVLGKMLAMMEDGKYQSELPDLGDWWAEIEQWRRKE 359

Query: 452 PLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLG 511
L F E I QY I+ L ELT G AI++T VGQHQMWAAQFY ++KPR+WL+SGGLG
Sbjct: 360 CLKFTQGEVIEAQYVIQKLYELTKGNAIVATDVGQHQMWAAQFYGFEPKPRWLTSGLG 419

Query: 512 AMGFGFLPAAIGASVANPDIAIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMV 571
MG+GLPAAIGA +A P VV I G+ S MN+QELAT++ NLPVK+ +LNN LGMV
Sbjct: 420 TMGYGLPAAIGAQAFAFPHETVVLITGESSIQMNIQELATLKQYNLPVKIAILNNSFLGMV 479

Query: 572 MQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTM 631
QW++ FY+ + + + + P+ + A A G + A++ I+ L
Sbjct: 480 RQWQELFYERRYSESDM-----TVHPDFVQLAQAYGATGMMTARPAEVSGLIEKALAI 532

Query: 632 PGYLLDVICPHQEHVLPMPNGGTFNDVI 661
GP L+D + +V PM+P G N++I
Sbjct: 533 DGPVLMDFRVNREANVYPMVPAGAALNEMI 562

>ref|ZP_02956061.1| acetolactate synthase, large subunit, biosynthetic type
[Methylocella silvestris BL2]
gb|EDT53522.1| acetolactate synthase, large subunit, biosynthetic type
[Methylocella silvestris BL2]
Length = 585

Score = 519 bits (1336), Expect = e-145, Method: Compositional matrix adjust.
Identities = 266/571 (46%), Positives = 368/571 (64%), Gaps = 19/571 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA+++V AL+ QGV+++F YPGGA + I+ AL + I +VL RHEQG AAEGYARSS
Sbjct: 7 GAEMVVRALQDQGVDSIFGYPGGAVLPIYDALFHQNQIVHVLVRHEQGAHAHAEGYARSS 66

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ + TSGPGATN ++GL DAL+DS+PLV ITGQVP +IG+DAFQE V +TR
Sbjct: 67 GKVGVVLVTSVSGPGATNAITGLTDALMDSIPLVCITGQVPTHLIGSDAFQECDTVGITRHC 126

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNYLV +ED+PR++ EAF++A +GRPGPV++D+PKD+Q L ++ Y
Sbjct: 127 TKHNYLVRSIEDLPRVLHEAFYVAQTGRPGPVVIDIPKDVQFALGDYFGPHKIEHKTYKP 186

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGR----FVELTGIPVASTLMG 334
R+ E +E V ++ +++PV Y GGG +NS E R VELTG P+ STLMG
Sbjct: 187 RLDGDAEK--IEHAVTMMLAARRPVFTYGGGVINSNGPEASRLRELVELTGFPITSTLMG 244

Query: 335 LGSYPCDDELSTHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIVHI 394
LGSYP + L MLGMHGT AN A+ DL++A G RFDDR+TG+L+AF+ +K +HI
Sbjct: 245 LGSYPASGDKWLGMHGMHGTFEANNAMHDCDLMIAGSRFDDRITGRDLDAFSPGSKKIHI 304

Query: 395 DIDSAEIGKNKTPHVSVCQGVKLLALQGMNKLLENRA---EELKLDGFWVRNENLVQKQKF 451
DID + I KN + + GD L+ M R +E L W E+N + +
Sbjct: 305 DIDPSSINKNVKIDLGIIGDCAHVLRLQMLDAYRARKSAPDEAALTR--WWQEINKWRARK 362

Query: 452 PLSFKTFGEAIPPQYAIKVLDELTDGK-AIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
LSFK I PQYA++ L ELT + I+T VGGHQMWAQ Y++++P +W++SGGL
Sbjct: 363 SLSFKQSSAVIKPQYAVQRLYELTKNRDITYITTEVGGHQMWAQHYHFEEPNRWMTSGGL 422

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLLNQHLGM 570
G MG+GLPAAIGA +A+P A+VVDI G+ S +MN+QEL+T LPVK+ +LNN+++GM
Sbjct: 423 GTMGYGLPAAIGAIAHPGALVVDIAGEASILMNIQELSTAIQFRLPVKIFILNNEYMG 482

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V QW++ + + ++ E P+ + A A G R + A L +AI M+D
Sbjct: 483 VRQWQELLHGRLSQSY-----SEALPDFVKLAAYGAQGIRCSDFASLDDAIEMID 535

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFFNDVI 661
+P + D I E+ LPMIP+G N+++
Sbjct: 536 SPRTTVFDCIVDKTENCLPMIPSGKAHNEML 566

>ref|YP_002250909.1| acetolactate synthase, large subunit, biosynthetic type
[Dictyoglomus thermophilum H-6-12]
gb|ACI19136.1| acetolactate synthase, large subunit, biosynthetic type
[Dictyoglomus thermophilum H-6-12]
Length = 557

Score = 518 bits (1335), Expect = e-145, Method: Compositional matrix adjust.
Identities = 272/565 (48%), Positives = 370/565 (65%), Gaps = 31/565 (5%)

Query: 108 ERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSSGKPGICIAT 167
E +G+E +F YPGGA + + AL +SS+++VL RHEQG AA+GYARS+GK G+C+AT
Sbjct: 15 EEEGIEVIFGYPGGAVIGFYDAL-YNSSLKHVLVRHEQGAHAADGYARSTGKVGVCVAT 73

Query: 168 SGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSIKHNLYLMD 227
SGPGATNL +G+A A +DSVP+VAITGQV IG D+FQE +T ITKHNLY+ D
Sbjct: 74 SGPGATNLTTGIATAYMDSVPIVAITGQVKTSAGKDSFQEVDRGITMPITKHNLYLTD 133

Query: 228 VEDIPRIIEEAFFLATSGRPGPVLVDVPKDI---QQQLAIPNWEQAMKLPGYMSRMPKPP 284
+ RI++EAF++A +GR GPVL+D+P DI + + ++P+ ++L GY KP
Sbjct: 134 PHEALRIVKEAFYIAKTGRKGPVLIDIPSDIFLSKIEYSVPS---KVELLGY-----KPN 185

Query: 285 EDSHLEQIVR---LISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLGSYP 339
+ H QI R LI ES+KP++ GGG + S S EL +F E PV +TLMG G+ P
Sbjct: 186 YEPHPLQIKRAAQLIKESEKPIILAGGGVIASEASQELIKFAERINAPVVTLMGKGAIP 245

Query: 340 CDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTGKLEAFASRAKIVHIDIDSA 399
ELS +GMHG YANYA+ SDL++A GVRF DR TGK+E FA AKI+HIDID A
Sbjct: 246 ETHELSCGFIGMHGAAYANYAINSDLI IAIGVRFSDRSTGKVETFAPNAKIIHIDIDPA 305

Query: 400 EIGKNKTPHVSVC GVDVKLALQGMNKVLENRAEELKLD FGVWRNENLVQKQKFP LSFKTFG 459
EIGKN P+V + D K AL+ + +V+E + +W ++ K K+PL ++
Sbjct: 306 EIGKNVQPYVPIVADAKRALEKLI EVVEPKTNP-----IWWEKIKDWKNKYPLRYRMSN 359

Query: 460 EAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLS SGG LGAMGFLPA 519
E I PQY I+ + ELT G+AI+ T VGQ+QMWA AQ+Y K+PRQ+++SGGLG MGFG PA
Sbjct: 360 EVIKPQVIERIYELTKGEAIVVTEVGQNQMWA AQYKVKRPRQFITSGGLGTMGFGFPA 419

Query: 520 AIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLL LNNQHLGMVMQWEDRFY 579
AIGA + N D +V+DI GDGS MN+QELAT E LPVK+ +LNN LGMV QW++ FY
Sbjct: 420 AIGAQIGNKDKVVIDIAGDSIQMNIQELATAASEKLPVKIFILNNSCLGMVRQWQELFY 479

Query: 580 KANRAHTFLGDP AQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLD-TPGPYLLD 638
+ + T L ++ P+ A A G RV K +L EAI+ L+ P ++D
Sbjct: 480 ERRYSTLL-----DVAPDFEKLAEAYGAYGRRVEKIEELDEAIEWALNINDSPVIVD 532

Query: 639 VICPHQEHVLP MIPNGGTFNDVITE 663
+ +E+V PMIP GG+ + ++ +
Sbjct: 533 IKVNREENVFP MIPAGGSIDKMLID 557

>ref|YP_001030046.1| acetolactate synthase, large subunit [Methanocorpusculum labreanum
Z]
gb|ABN06779.1| acetolactate synthase, large subunit [Methanocorpusculum labreanum
Z]
Length = 567

Score = 518 bits (1333), Expect = e-145, Method: Compositional matrix adjust.
Identities = 285/586 (48%), Positives = 379/586 (64%), Gaps = 37/586 (6%)

Query: 97 RKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYAR 156
+ GA IL+E+L+ +GV+ +F YPGG+ + I+ L + + ++L RHEQ V AA+GYAR
Sbjct: 4 KTGAAILIESLKEEGVDIIFGYPGGSVLPIYDEL-YDAELTHILVRHEQA AVHAADGYAR 62

Query: 157 SSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTR 216
+SG+ G+C++TSGPGA NL+SG+A A +DSVP+VA+TGQVP M+G DAFQE+ I +T
Sbjct: 63 ASGRVGVCLSTSGPGACNLISGIATANMDSVP IVALTGQVPTGMLGNDAFQESDITGITL 122

Query: 217 SITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAM----- 271
ITKHNYLV D DI ++ AF++A +GR GPVL+D+PKD+ L E+ +
Sbjct: 123 PITKHNYLVKDARDIKMTVKAIFYIAGTGRNGPVLIDL PKDV--LTAKVAEEEVLSGEP 179

Query: 272 KLPGYMSRMPKPPEDSHLEQIVR---LISESKKPVLYVGGGCLNS--SDELGRFVELTGI 326
+L GY KP H +QI + LI ++KKPVLYVGGG + S S+EL + EL +
Sbjct: 180 ELRGY-----KPTLKGHSKQIKKALDLIYKAKKPVLYVGGGVITSGASEELVKLAELFCL 234

Query: 327 PVASTLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTGKLEAFA 386
PV +T+MGLG+ P D L+L MLGMHGT YANYAV +DLL+A G RFDDRTGK L FA
Sbjct: 235 PVT TMMGLGAIPADHPLNLGMLGMHGT EYANYAVSEADLLI AVGARFDDRTGKLSHFA 294

Query: 387 SRAKIVHIDIDSAEIGKNKTPHVSVC GVDVKLALQGMNKVLENRAEELKLD FGVWRNENLV 446
+ AK++HIDID AEIGKN P V + GD K L M + EN + W ++ +
Sbjct: 295 THAKVIHIDIDPAEIGKNVNPDPVIVGDAKSVLADMICLAENNGCISE----PWLEQVKL 350

Query: 447 QKQKFP LSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLS 506
+ PL G+ + PQ IK L EL DG II + VGQ+QMWA AQ Y +KKPRQW+S
Sbjct: 351 WRTNHPLRVVEDGK-VHPQNIKKLSELDDGGGIIVSEVGQNQMWA AQHYGFKKPRQWIS 409

Query: 507 SGGLGAMGFLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLL LNNQ 566
SGGLG MG+G PAAIGA A P+ VV I GDGSF MN+QELAT+ +PVK+++LNN
Sbjct: 410 SGGLGTMGYGFPA AIGAWFAKPEETVVL IAGDSFQMNIQELATVAQYKIPVKIVILNNM 469

Query: 567 HLGVMVQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKADLREAIQ 626
+LGMV QW++ FY +R +++ PA + + A A GI +V + A+Q
Sbjct: 470 YLGMVRQWQELFY--DRRYSYTELPAVD-----FVGIAKAYGIQGMKVSVDQIDAALQ 521

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITE-----GDGR 667
T LD GPYLLD E+V PM+P G +D+I + G GR
Sbjct: 522 TALDYNGPYLLDFQIERGENVPMVPAGAAISDMIGKHCHNGGSGR 567

>ref|ZP_00236615.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus cereus G9241]
gb|EAL15891.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus cereus G9241]
Length = 571

Score = 517 bits (1332), Expect = e-144, Method: Compositional matrix adjust.
Identities = 268/566 (47%), Positives = 365/566 (64%), Gaps = 21/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA +++ L+ GV TVF YPGGA + ++ AL S +++L RHEQ + AAEGYAR+S
Sbjct: 18 GAGHVIQCLKNLGVTTVFGYPGAILPVYDAL-YGSLKHLITRHEQAIIHAAEGYARAS 76

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ ATSGPGATNLV+GLADA +DS+PLV ITGQV +IG D FQE +V +T +
Sbjct: 77 GKVGVVFATSGPGATNLVTGLADAYMDSIPLVVITGQVATPLIGKDFQEADVVGITVPV 136

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V DV + RI++EAF++A SGRPGPVL+D+PKD+Q + + + +PGY
Sbjct: 137 TKHNYQVRDVNHVSRIVQEAFYIAKSGRPGPVLIDIPKDVQNAKVTSSFFNEEVDIPGYKP 196

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLG 336
+ P+ L ++ + IS+SK+P+LY+GGG ++S SDEL +F IPV STLMLGLG
Sbjct: 197 EL--VPDSMKLREVAKAISKSRPLLYIGGGVIHSDGSELIKFARENRIPIVSTLMGLG 254

Query: 337 SYPCDDELSLHMLGMHGTVYANYAVEHSDLLLAFGVRFDDRTVGKLEAFASRAKIVHIDI 396
+YP D L L MLGMHGT AN AV DLLLA GVRFDDRTVGKLE F+ +K VHIDI
Sbjct: 255 AYPPGDSLFLGMLGMHGTAAANMAVTECDLLALGVRFDDRTVGKLELFSFYSSKKVHIDI 314

Query: 397 DSAEIGKNKTPHVSVCVDVKLALQGMNKV--LENRAEELKLDGFGVWRNENLVQKQKPLSF 455
D +E KN T V GDVK AL + + + +E W + K ++PLS+
Sbjct: 315 DPSEFHKNVTVVEYPVVGVDVKALHMLLHMPICQTDE-----WITKTEEWKAEPYLSY 367

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGF 515
+ PQ+ I ++ ELT+G+AI++T VGQHQMWAA FY K PR +L+SGGLG MGF
Sbjct: 368 IQKESELKPQHVISLVSELTNGEAIIVTEVGVGQHQMWAAHFYKAKNPRTFLTSGGLGTMGF 427

Query: 516 GLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLLNQHLGMVMQWE 575
G PAA+GA +A + +V+ I GD SF MN+QEL TI N+PVKV ++NN+ LGMV QW+
Sbjct: 428 GFPAAVGAQLAKEEELVICIAGDASFQMNQELQTIENNIPVKVFIINNKFGLGMVRQWQ 487

Query: 576 DRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKADLREAIQTMLDTPGPY 635
+ FY+ + + +G P+ + A A G+ R T + + + + GP
Sbjct: 488 EMFYENRLSESKIGS-----PDFVKVAEAYGVKGLRATNSTEAKQVMLEAFAHEGPV 539

Query: 636 LLDVICPHQEHVLPMPNGGTFNDVI 661
++D E+V PM+P N++I
Sbjct: 540 VVDFCVEEGENVFPMVPPNKGNNEMI 565

>ref|ZP_02326419.1| acetolactate synthase catalytic subunit [Paenibacillus larvae subsp. larvae BRL-230010]
Length = 581

Score = 517 bits (1331), Expect = e-144, Method: Compositional matrix adjust.
Identities = 260/579 (44%), Positives = 376/579 (64%), Gaps = 20/579 (3%)

Query: 87 FISRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQG 146
+ +F + G++IL+ +L +GVE VF YPGG+ + I+ A+ ++L RHEQG
Sbjct: 14 LMEKFQKPELITGSEILLRSLVLEGVECVFYPGGSVLYIYDAMHGFKDFDHLTRHEQG 73

Query: 147 GVFAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAF 206
+ AA+GYARS+GK G+CIATSGPGATNLV+G+A A +DSVPLV ITG V IGTDAF
Sbjct: 74 AIHAADGYARSTGKVGVCIAATSGPGATNLVTGIATAYMDSVPLVVITGNVATNFIGTDAF 133

Query: 207 QETPIVEVTRSIKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPN 266
QE I +T ITKHNLYL DV D+PRII EAF +A++GR GPVL+D+PKD+ Q A+ +
Sbjct: 134 QEADITGITMPITKHNLYLVRDVNDLPRIIHEAFHIASTGRKGPVLIDIPKDVSAQQAVFH 193

Query: 267 WEQAMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLVYGGGCL--NSSDELGRFVELT 324
+ + GY + P +E++++ I ES++PV+ GGG + +++D+L FVE T
Sbjct: 194 PAGGINIRGYNPTV--HPNKLQVERLLKAIEESERPVIAGGGVVYADAADQLIEFVEKT 251

Query: 325 GIPVASTLMGLGSYPDCDELHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEA 384
IPV +TL+GLG +P +L + M GMHGT AN A++++DLL++ G RFDDRVT KL+
Sbjct: 252 RIPVTTTLLGLGGFSAHDLWMGMGMHGTYTANNAIQNADLLISIGSRFDDRVTMKLDG 311

Query: 385 FASRA-KIVHIDIDSAEIGKNKTPHVSVCADVGLALQGMN-KVLENRAEELKLDGFWRN 442
FA +A KI HIDID AEIGKN + GD+K L+ N K + R++ VW
Sbjct: 312 FAPKAKKIAHIDIDPAEIGKNVKTIDPCVGDIKTVLEHANQKAMPARSD-----VWIK 364

Query: 443 ELNVQKQKFPKSFKTGFAIPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPR 502
++ K+ +PL +K + + PQY I +++E T G+AI++T VGQHQMW AQFY ++ PR
Sbjct: 365 QIQENKKNYPLKYKDSKELKPQYVIGMINETTKGEAIVTTDVGQHQMWVAQFYKFQHPR 424

Query: 503 QWLSSGGLGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLL 562
++SSGGLG MG+G P+AIGA + N D +V+ I+GDG M QELA + N+PVK+++
Sbjct: 425 SMITSGGLGTMGYGFPSAIGAQIGNKDMVISINGDGMQMCQELAICAINNIPVKIVV 484

Query: 563 LNNQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLR 622
+NN+ LGMV QW++ Y + +H L E P+ + A A G+ R K +
Sbjct: 485 INNRVLGMVRQWQELIYGSRYSHIDL-----EGSPDFVKLAEAYGVKGLRAANKEEAH 537

Query: 623 EAIQTMLDTPGPYLLDVICPHQEHVLPMPINNGTFNDVI 661
+ Q ++TPGP L++ + E+V PM+ G T ++++
Sbjct: 538 QVWQEAMNTPGPVLVEFVVSKHENVPMTQGSTISEMM 576

>ref|ZP_02912696.1| acetolactate synthase, large subunit, biosynthetic type
[Geobacillus sp. WCH70]
gb|EDT36143.1| acetolactate synthase, large subunit, biosynthetic type
[Geobacillus sp. WCH70]
Length = 577

Score = 517 bits (1331), Expect = e-144, Method: Compositional matrix adjust.
Identities = 265/565 (46%), Positives = 373/565 (66%), Gaps = 17/565 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA +L+EAL+ + VE +F YPGGA + ++ L +S + +VL RHEQG + AAEGYAR S
Sbjct: 18 GALMLIEALKAKEKVEVIFGYPGGAVLPLYDKLYQSG-VFHVLTREQGAIHAAEGYARIS 76

Query: 159 GKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GKPG+ IATSGPGATN+V+GL DA++DS+P+V TGQV +IG+DAFQE ++ +T I
Sbjct: 77 GKPGVVIATSGPGATNIVTGLTDAMMDSLPIVVFTGQVATSVIGSDAFQEADVLTGIMPI 136

Query: 219 TKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V D+ ++P+II+EAF +AT+GRPGPVL+D+PKDI ++EQ + LPGY
Sbjct: 137 TKHNYQVRDISELPKIIKEAFHIATTGRPGPVLIDIPKIDITIAEGEFDYEQEVHLPGYQP 196

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLVYGGGCL--NSSDELGRFVELTGIPVASTLMGLG 336
P + ++V +S+SK+PV+ G G L N+S+EL ++ E IPV TL+GLG
Sbjct: 197 T--THPNHLQIRRLVETVSQSKRPVILAGAGVLHANASNELRQYAEQQNIPVVHTLLGLG 254

Query: 337 SYPCDELHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVHIDI 396
+P D L L M GMHGT AN A+ DLL+ G RFDDRVTG L+ FA +A + HIDI
Sbjct: 255 GFPADHPLFLGMAGMHGTYTANMALYECDLLINIGARFDDRVTGNLKYFAPKATVAHIDI 314

Query: 397 DSAEIGKNKTPHVSVCADVGLALQGMNKLLENRAEELKLDGFWRNELNVQKQKFPPLSFK 456
D AEIGKN + + D K ALQ +++ + + D W +LN K++FPL ++
Sbjct: 315 DPAEIGKNVPTKIPIVSDAKAALQ---ELIHQQGK--PADTSAWLAQLNEWKRQFPYYE 369

Query: 457 TFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGFG 516
+ I PQ ++++ ELT+G+AIIT VGQHQMWAQ+Y + +P +W++SGGLG MGFG
Sbjct: 370 DDEQTIKPKQLVEMIELTNGEAIITDVGQHQMWAQYYKFNPRHRWVTSGLGTMGFG 429

Query: 517 LPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWED 576
LPAAIGA +A+ +A VV I GDG F M QEL+ I+ LP+KV+++NNQ LGMV QW++
Sbjct: 430 LPAAIGAQLADRNAAVSIVGDGGFQMTFQELSVIQELQLPIKVVIVNNQALGMVRQWQE 489

Query: 577 RFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPYL 636
FY+ +H+ + P Q P+ + A A IP + +A+ E ++ GP L
Sbjct: 490 LFYEKRYSHSLI--PNQ-----PDFVKLAEAYNIPGFQAKTEAEAMEVLKKAFAIDGPVL 542

Query: 637 LDVICPHQEHVLPMPNGGTFNDVI 661
LD E+V PM+ G ++++
Sbjct: 543 LDFHVKADENVYPMVAPGKGLHEMV 567

>ref|YP_148514.1| acetolactate synthase catalytic subunit [Geobacillus kaustophilus
HTA426]
dbj|BAD76946.1| acetolactate synthase large subunit [Geobacillus kaustophilus
HTA426]
Length = 596

Score = 517 bits (1331), Expect = e-144, Method: Compositional matrix adjust.
Identities = 266/566 (46%), Positives = 371/566 (65%), Gaps = 19/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
G+ +L+EAL+ + VE +F YPGGA + ++ L ++ + +VL RHEQG + AAEGYAR S
Sbjct: 37 GSLMLIEALKEEKVEVIFGYPGGAVLPLYDELYKAG-VFHVLTREHQAIAHAAEGYARIS 95

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GKPG+ IATSGPGATN+V+GL DA++DS+PLV TGQV +IG+DAFQE +V +T I
Sbjct: 96 GKPGVIATSGPGATNIVTGLTDAMDSLPLVVFTGQVATSVIGSDAFQEADVVGITMPI 155

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V D+ ++PRII+EAF +AT+GRPGPVL+D+PKDI +++Q + LPGA
Sbjct: 156 TKHNYQVRDISELPRIIEAFHIATTGRPGPVLIDIPKDIITAEGEFDYDQDVHLPGYQP 215

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGCL--NSSDELGRFVELTGIPVASTLMGLG 336
P + ++V +S+SK+PV+ G G L N+S+EL ++ E IPV TL+GLG
Sbjct: 216 T--TQPNHWQIRRLVEAVSQSKRPVILAGAGILHANASNELQYAEQQNIPVIHTLLGLG 273

Query: 337 SYPCDELDSLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIVHIDI 396
+P D L L M GMHGT AN A+ DLL+ G RFDDRVTG L+ FA +A + HIDI
Sbjct: 274 GFPADHPLFLGMAGMHGTYTANMALCECDLLINIGARFDDRVTKNLKYFAPKATVAHIDI 333

Query: 397 DSAEIGKNKTPHVSVCVDVKLALQGMNKLLENRAEELK-LDFGVWRNELNVQKQKFLPLSF 455
D AEIGKN + + D K ALQ E A++ K D W +L+ K++FPL +
Sbjct: 334 DPAEIGKNVPTKIPIVSDAKAALQ-----ELIAQQGKPADTAAWLTQLDEWKRRFPLHY 387

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGF 515
+ I PQ I+++ E+T+G+AIIT VGQHQMWAQ+Y + +P +W++SGGLG MGF
Sbjct: 388 EPEAGTIKPKQLIEMIYEMTNGEAIITDVGQHQMWAQYYKFNPRHRWVTSGLGTMGF 447

Query: 516 GLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
GLPAAIGA +A+ +A VV I GDG F M QEL+ I+ LP+K++++NNQ LGMV QW+
Sbjct: 448 GLPAAIGAQLADRSATVVSIVGDGGFQMTFQELSVIQELRLPIKIVIVNNQALGMVRQWQ 507

Query: 576 DRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPY 635
+ FY +H+ + P Q P+ + A A G+P R +A+ E ++ GP
Sbjct: 508 ELFYDKRYSHSLI--PNQ-----PDFVKLAEAYGMPGLRAKTEAEAAEVLKQAFAMDPV 560

Query: 636 LLDVICPHQEHVLPMPNGGTFNDVI 661
LLD E+V PM+ G ++++
Sbjct: 561 LLDHVRADENVYPMVAPGKGLHEMV 586

>ref|YP_083261.1| acetolactate synthase 3 catalytic subunit [Bacillus cereus E33L]
gb|AAU1857.1| acetolactate synthase [Bacillus cereus E33L]
Length = 570

Score = 516 bits (1329), Expect = e-144, Method: Compositional matrix adjust.
Identities = 267/566 (47%), Positives = 368/566 (65%), Gaps = 21/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSS 158
G +++ L++ GV TVF YPGA + ++ AL S ++++L RHEQ + AAEYAR+S
Sbjct: 17 GTGHVQLCKLGVTTTVFGYPGGAILPVYDAL-YESGLKHILTRHEQAIIHAAEGYARAS 75

Query: 159 GKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ ATSGPGATNLV+GLADA +DS+PLV ITGQV +IG D FQE +V +T +
Sbjct: 76 GKVGVVFATSGPGATNLVTGLADAYMDSIPLVVITGQVATPLIGKDFQEADVVGITVPV 135

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V DV + RI+++EAF++A SGRPGPVL+D+PKD+Q + + + ++PGY
Sbjct: 136 TKHNYQVRDVNQLSRIVQEAFYIAESGRPGPVLIDIPKDVQIEKVTsfyNEVIEIPGY-- 193

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLG 336
++ P+ L+++V+ IS++K+P+LY+GG ++S SDEL +F IPV STLMLGL
Sbjct: 194 KIEAMPDSMKLKEVVKEISKAKRPLLYIGGGVIHSGGSELIKFARENRIPVVSTLMGLG 253

Query: 337 SYPCDDESLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVHIDI 396
+YP D L L MLGMHGT AN AV DLLA GVRFDRTGKLE F+ +K VHIDI
Sbjct: 254 AYPPGDPLFLGMLGMHGTAAANMAVTECDLLALGVRFDRTGKLELFSPHSKKVHIDI 313

Query: 397 DSAEIGKNKTPHVSVCVDVKLALQGMNKV-LENRAEELKLDGFWVRNENLVQKQKFPPLSF 455
D +E KN V GDVK AL + + + +E W + K ++PLS+
Sbjct: 314 DPSEFQKNVVVKYPVVGVDVKALHMLLHMPICQTDE-----WLTKEEWKA EYPLSY 366

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGF 515
+ PQ+ I ++ ELT+G+AI++T VGQHQMWA FY K PR +L+SGGLG MGF
Sbjct: 367 IQKESKLKPQHVISLVSELTNGEAIIVTEVGVGQHQMWAHFKAKNPRFTLTSGGLGTMGF 426

Query: 516 GLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
G PAAIGA +A + +V+ I GD SF MN+QEL TI N+PVKV ++NN+ LGMV QW+
Sbjct: 427 GPPAAIGAQLAKEEELVICIAGDASQMNQELQTAENNIIPVKVFIINNKF LGMVRQWQ 486

Query: 576 DRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKADLREAIQTMLDTPGPY 635
+ FY+ + + +G P+ + A A G+ R T + + + GP
Sbjct: 487 EMFYENRLSESKIGS-----PDFVKVAEAYGVKGLRATNSTEAKLVMIEAFAHEGPV 538

Query: 636 LLDVICPHQEHVLPMPNGGTTFNDVI 661
++D E+V PM+P N++I
Sbjct: 539 IVDFCVEEGENVFPMVPPNKGNNEMI 564

>ref|ZP_01695377.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus
coagulans 36D1]
gb|EAY45391.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus
coagulans 36D1]
Length = 571

Score = 516 bits (1329), Expect = e-144, Method: Compositional matrix adjust.
Identities = 267/565 (47%), Positives = 368/565 (65%), Gaps = 17/565 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSS 158
GA+ LV+ L R+GV+ +F YPGA + I+ AL + IR++L RHEQ + AAEYAR S
Sbjct: 18 GAEALVQLLVREGVDVMFGYPGGAVLPIYDAL-YNQPIRHILARHEQGAIHAAEGYARVS 76

Query: 159 GKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GKPG+ IATSGPGATNL++G+ADA++DS+PLV TGQV +IG+DAFQE ++ +T I
Sbjct: 77 GKPGVIATSGPGATNLITGIADAMDSLPLVFTGQVGTSGVIGSDAFQEADVIGMTAPI 136

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V D+ D+PR+++EAF +A SGRPGPV+VD+PKDIQQ + + LPGY
Sbjct: 137 TKHNYQVRDLRDLPRVKEAFHIAKSGRPGPVVVDIPKDIQQGTVMGESREVYLPYGP 196

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLN--SSDELGRFVELTGIPVASTLMGLG 336
P ++++V +S S+KPV+ G G L+ +SD L +F E IPV +TL+GLG
Sbjct: 197 N--TSPNPLQIKKLVEAVSYSEKPVILAGAGILHAKASDLLKFAEKCQIPVVNTLLGLG 254

Query: 337 SYPCDELHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTGKLEAFASRAKIVHIDI 396
S+P L L M GMHGT AN A+ DLL+ G RFDDR+TG L FA A +VHIDI
Sbjct: 255 SFFFRHPLFLGMGMHGT YAA NMAICECDLLINIGARFDDRLTGNLAHFAPNAMVVHIDI 314

Query: 397 DSAEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKFPLSFK 456
D AEIGKN ++ D K ALQ K+ + D W L + FPL ++
Sbjct: 315 DPAEIGKNVKT DIPIVADAKEALQ---KICSED LQ NAGTD--EWVRHLKKAENFPLWYE 369

Query: 457 TFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQM WAAQFYNYKKPRQWLSSGGLGAMGFG 516
GE + PQ+ I+ + T+G AIIST VGQHQM WAAQ+Y ++KP +W++SGGLG MGFG
Sbjct: 370 DDGEELSPQHVIQRIHHTYNGDAIISTDVGQHQM WAAQYYGFEPKHKWITSGLGTMGFG 429

Query: 517 LPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWED 576
PAAIGA +A PD +VV I GDG F M +QELA ++ NLP+K+ ++NNQ+LGMV QW++
Sbjct: 430 FPAAIGA QIAYPDQLVVSISGDGGFQMTLQELAVVKELNLP LKIFIVNNQYLG MVRQWQE 489

Query: 577 RFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIP AARVTKKADLREAIQTMLDTPGPYL 636
FY+ +++ + P Q P+ + A + GI R T +L + ++T+ + GP +
Sbjct: 490 SFYEERYSYSTI--PVQ-----PDFVKLAESY GIRGCRATNNEELDKVLKTVFEDDGPV 542

Query: 637 LDVICPHQEHVLP MIPNGGTFNDVI 661
+D E V PM+ G ++++
Sbjct: 543 VDCRVKRL EAVFPMVAPGKGLHEMM 567

>ref|YP_565425.1| acetolactate synthase 3 catalytic subunit [Methanococcoides
burtonii DSM 6242]
gb|ABE51675.1| acetolactate synthase, large subunit [Methanococcoides burtonii DSM
6242]
Length = 563

Score = 516 bits (1329), Expect = e-144, Method: Compositional matrix adjust.
Identities = 269/568 (47%), Positives = 373/568 (65%), Gaps = 25/568 (4%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVF AAEGYARSS 158
GA VE L R+ VE +F YPGG + I+ L + + ++L RHEQ V AAEGYAR++
Sbjct: 10 GARAFVECLYRENVEVIFGYPGGVLLHIYDEL-YDAHLHLLV RHEQA AVHAAEGYARAT 68

Query: 159 GKPGICIATSGPGATNLVSG LADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+C+ATSGPGATNLV+G+A+A +DSVP+VA TGQVP MIG DAFQE I +T I
Sbjct: 69 GKVGVC LATS GPGATNLVTGIANAYMDSVPMVAFTGQVPSSMIGNDAFQEANITGITMPI 128

Query: 219 TKHNYLVMDVEDIPRIIEEAF FLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNYLV DV+D+PRII+EAF +A++GRPGPVL+D+PKDI + ++L GY
Sbjct: 129 TKHNYLVQDV KDLPRIIEAFHIASTGRPGPVLIDL PKDITTEIDFVYPDTVELRGY-- 186

Query: 279 RMPKPPEDSHLEQIVR---LISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLM 333
KP + +QI R ++ ++K+PV+Y GGG + S S EL F E PV +TL
Sbjct: 187 ---KPTFKGNAQQIKRAA AVLKDAKRPIYAGGGVIGSEGSKELLAF AEK LKAPVTTTLT 243

Query: 334 GLGSPCDELHMLGMHGT VYANYAVEHSDLLAFGVRFD DRTGKLEAFASRAKIVH 393
G+G +P D+EL L M GMHGT YANYA++ SD+L+A GVRFD DRTGK +FA A ++H
Sbjct: 244 GIGGFNDNELYLGM PMGHGTYANYAIQESDVLIAGVRFD DRTGKTTSFAPNATVIH 303

Query: 394 IDIDSAEIGKNKTPHVSVC G DVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKFPL 453
IDID AEI K V + GD K Q + +L++ +E D W +++ K+ FPL
Sbjct: 304 IDIDPAEISKI IKVDVPIVGDAK---QILGALLKHVSE---CDTKEWLDKIATWK RDFPL 357

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQM WAAQFYNYKKPRQWLSSGGLGAM 513
+ + I PQY ++ ++E+ AII T VGQHQM WAAQ++NY +PR ++SSGGLG M
Sbjct: 358 FVVRDDVIKPYILEQINEVCP-D AIIIVTEVGQHQM WAAQYFNYTEPRTFIS SGLGTM 416

Query: 514 GFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQ 573
G+G PAAIGA + PD +V D+ GDGSF MN QE+ATI N+P+ + + NN +LGMV Q
Sbjct: 417 GYGFPAAIGAKIGRPDKVVDVSGDGSFQMNSQEMATIVQNNIPIIIAIFNNGYLG MVRQ 476

Query: 574 WEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIP AARVTKKADLREAIQTMLDTPG 633
W+ F++ +HT + E+ + + + A A G RVTK ++++ AI+ ++
Sbjct: 477 WQALFFEHRYSHTTI-----ENSV--DFVKLA EAYGAMGIRVTKPSEVKA AIEKAVEANA 529

Query: 634 PYLLDVICPHQEHVLPMPNGGTFNDVI 661
P L+D I +E+V PM+P G N+++
Sbjct: 530 PVLIDFIIEREENVSPMPAGAAINEIL 557

>ref|YP_754808.1| acetolactate synthase large subunit [Syntrophomonas wolfei subsp.
wolfei str. Goettingen]
gb|ABI69437.1| acetolactate synthase, large subunit [Syntrophomonas wolfei subsp.
wolfei str. Goettingen]
Length = 562

Score = 516 bits (1328), Expect = e-144, Method: Compositional matrix adjust.
Identities = 269/569 (47%), Positives = 376/569 (66%), Gaps = 18/569 (3%)

Query: 98 KGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARS 157
KGA+IL++ L+++GV+TVF YPGA + I+ AL +S IR++L RHEQG AA+GYAR+
Sbjct: 4 KGAEILLQCLQKEGVDTVFGYPGGAVLPIDYALYKSE-IRHILSRHEQGAHAADGYARA 62

Query: 158 SGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
+G+ G+CIATSGPGATNLV+G+A A +DS+PLV TGQV +IG DAFQE I +T
Sbjct: 63 TGRVGVCIATSGPGATNLVTGIATAYMDSIPLVCFQTGQVGTSLIGRDAFQEADITGITLP 122

Query: 218 ITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDI-QQQLAIPNWEQAMKLPY 276
ITKHNYLV ED+ RI++EAF++A + RGPV+VD+PKD+ ++++ E+A+ + GY
Sbjct: 123 ITKHNYLVEKTEDLARIVKEAFYIARTNRPGPVVVDLPKDVMEKEIDFEYPEEAINIRGY 182

Query: 277 MSRMPPKPEDSHLEQIVRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLMG 334
R+ K + + V I ++++PV+Y GGG + N+++EL E IPV +TLMG
Sbjct: 183 --RVVKGYSNSQVITAVDYIQKARRPVIYAGGGVISSNAEELRELAEKRIKIPVTTTLMG 240

Query: 335 LGSYPCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVHI 394
+G + + LSL MLGMHGT YANYA+ DLL+A GVRFDRTGK++ FA A+++HI
Sbjct: 241 MGGFLGNSYLSLGMMLGMHGT RYANYAIGECDLLIAVGVRFDRTGKIDTFAPHARVIHI 300

Query: 395 DIDS AEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKFP LS 454
DID+AEIGKN V + G VK L +N+ LE E + W ++ K+++PL
Sbjct: 301 DIDAAEIGKNVEVEVPIVGQVKEVLA AINQRLEAIESE---ELNEWHETIHRWKEEYPLR 357

Query: 455 FKTFGEA-IPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAM 513
+ E I PQ+ I+ + LT G+AI I T VGQ+QMWAAQ+Y+YK PR +LSSGGLG M
Sbjct: 358 YGDSSEGRIMPQHVIEEVYSLTQGEAIICTEVGQNMWAAQYHYHKHRSFLSSGGLGTM 417

Query: 514 GFGLPAAIGASVANPDAIVDDIDGDSGIFMNVQELATIRVENLPVKVLLNNQHLGMVMQ 573
G+G PAAIGA +A P+ VVDI GDGS MN+QEL T LP+ + +LNN LGMV Q
Sbjct: 418 GYGFPAAIGAKIACPELPVVDIAGDGSIQMNIQELGTAVQYRLPIIICILNNHFLGMVRQ 477

Query: 574 WEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAAARVTKKADLREAIQTMLDTPG 633
W+ FY ++T + P+ + A A G R+ + + +REA++ L
Sbjct: 478 WQGLFYGGRYSYTDMHQ-----PDFVKIAEAYGAIGRIKEASQVREALEEALKVKD 530

Query: 634 -PYLLDVICPHQEHVLPMPNGGTFNDVI 661
P +LD + V PM+P GG+ +++
Sbjct: 531 RPVVLDFWVEREADVPMVPPGSLMNM 559

>ref|YP_821479.1| acetolactate synthase, large subunit [Solibacter usitatus
Ellin6076]
gb|ABJ81194.1| acetolactate synthase, large subunit [Solibacter usitatus
Ellin6076]
Length = 577

Score = 515 bits (1327), Expect = e-144, Method: Compositional matrix adjust.
Identities = 269/577 (46%), Positives = 369/577 (63%), Gaps = 30/577 (5%)

Query: 98 KGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARS 157
GA +L E L R+GV+ +F YPGG ++ + L IR+VL RHE+ FAAEGYARS
Sbjct: 6 SGARMLAECLAREGVDCMFGYPGGVTLPPFYDVL-YDQIRHVLVRHEENAAFAAEGYARS 64

Query: 158 SGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRS 217
+GK G+C ATSGPGATNL +GL DA++DS+P+VAITGQV ++IG+DAFQE +TR
Sbjct: 65 TGKVGCCATSGPGATNLTTGLVDAMMDSIPIVAITGQVTSKLIGSDAFQEADTFGITRP 124

Query: 218 ITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYM 277
TKHNYLV ++++P+II EAF++A +GRPGPVLVD+ KD+ Q + ++ LPGY
Sbjct: 125 CTKHNYLVKKLDELPIIIEAFYIAATGRPGPVLVDITKDLVQGMGHYQPVTSIHLPGY- 183

Query: 278 SRMPKPPEDSHLEQIVR---LISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTL 332
K + H QI R LI ES++P++Y GGG + N+SDEL FV+LT P +TL
Sbjct: 184 ----KVFTGHTGQIRRALQLIQESERPLVYAGGGIVAANASDELREFVQLTDAPAVNTL 239

Query: 333 MGLGSYPCDDELSDLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIV 392
MGLG+ P D + M GMHG+ AN A+ ++DLL+A GVRFDDRVTG+L AFA AK++
Sbjct: 240 MGLGAMPSSDPNFISMFGMSYAAANMAMSNADLLIALGVRFDDRVTGRLAFAFAPHAQVI 299

Query: 393 HIDIDSAEIGKNTKPHVSVCGDVKLALQGMNKVL-----ENRAEELKLDGFWVRNEL 444
H+DID AE+GK + P V + GDVK L +NK++ E R+ + W +++
Sbjct: 300 HVDIDPAEVLGKIRNPEVPIVGDVVKRLAKLNKMMVETPAEPDEKRSAAARR---AWWHQI 355

Query: 445 NVQKQKFLPSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQW 504
K + P T I PQ+ + +D L+ G+AII++ VGQHQMWAAQ + +PR W
Sbjct: 356 REWKAHEPHYDTPSTTEIKPQHLMAEIDRLSGGEAIITSDVGQHQMWAAQLCRFNEPRLW 415

Query: 505 LSSGGLGAMGFLPAAIGASVANPDIVVDIDGDSFIMNVQELATIRVENLPVKVLLN 564
++SGGLG+MGFGLP+AIGA A PD +V I GDG F M + ELATI LP+K++++N
Sbjct: 416 INSGGLGSMGFLPSAIGAQAQFARPDKLVFSICGDDGFQMAIPELATIASHALPIKIIVMN 475

Query: 565 NQHLGMVMQWEDRFYKANRAHTFLGDPAQEDEIFPNMMLFAAACGIPAARVTKKADLREA 624
N +LGMV QW+ FY + E + FP+ A A G + K +L A
Sbjct: 476 NGYLGVMVRQWQTLFYNDRLSSV-----ELDAFPDAEKLGAAYGFKGRTIDKPWELAAA 528

Query: 625 IQTMLDTPGPYLLDVICPHQEHVLPMPINGGTFNDVI 661
++ + PGPYLL+V E V PM+P GG N+++
Sbjct: 529 LEEAVREPGPYLLNVKVTPEFCVYPMVPAGGAINEMV 565

>ref|ZP_03286153.1| acetolactate synthase, large subunit, biosynthetic type
[Dictyoglomus turgidum DSM 6724]
gb|EEA17352.1| acetolactate synthase, large subunit, biosynthetic type
[Dictyoglomus turgidum DSM 6724]
Length = 557

Score = 515 bits (1327), Expect = e-144, Method: Compositional matrix adjust.
Identities = 271/565 (47%), Positives = 368/565 (65%), Gaps = 31/565 (5%)

Query: 108 ERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSSGKPGICIAT 167
E +G+E +F YPGA + + AL +S+++VL RHEQG AA+GYARS+GK G+CIAT
Sbjct: 15 EEGIEVIFGYPGGAVIGFYDAL-HNSTLKHVLRHEQGAHAADGYARSTGKVGVCIAAT 73

Query: 168 SGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSITKHNYLVMD 227
SGPGATNL +G+A A +DS+P+VAITGQV IG D+FQE +T ITKHNYL+ +
Sbjct: 74 SGPGATNLTTGIATAYMDSIPIVAITGQVKTSAIGKDSFQEVDRGITMPITKHNYLITN 133

Query: 228 VEDIPRIIEEAFFLATSGRPGPVLVDVPKDI---QQQLAIPNWEQAMKLPGYMSRMPKPP 284
+ RII+EAF++A +GR GPVLVD+P D+ + + ++P+ + L GY KP
Sbjct: 134 PHEALRIIEAFYIAKTGRKGPVLVDIPSDVFLSKIEYSVPS---KVDLLGY-----KPN 185

Query: 285 EDHLEQIVR---LISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLGSYP 339
D H QI R LI E+++P++ GGG + S S EL +F E PV +TLMG GS P
Sbjct: 186 YDPHPLQIKRAAQLIKEAERPIILAGGGVIASEASQELIKFAEKINAPVVTTLMGKSIP 245

Query: 340 CDDELSDLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIVHIDIDSA 399
ELS +GMHG YANYA+ SDL++A GVRF DR TGK+E FA AKI+HIDID A
Sbjct: 246 ETHELSCGFIGMHGAAYANYAINDSDLIIAIGVRFSDRSTGKVETFAPNAKIIHIDIDPA 305

Query: 400 EIGKNTKPHVSVCGDVKLALQGMNKVLENRAEELKLDGFWVRNELNVQKQKFLPSFKTFG 459
EIGKN P+V + D K AL+ + +V+E + + W ++ K K+PL ++
Sbjct: 306 EIGKNVNPYVPIVADAKRALERLVEVVEPKINAM-----WWEKIKEWKTKYPLRYMSN 359

Query: 460 EAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAMGFLPA 519
+ I PQY I+ + ELT G+AI+ T VGQ+QMWWAAQ+Y K+PRQ+++SGGLG MGFG PA
Sbjct: 360 DIKPKQYVIERIYELTKGEAIVVTEVGQNQMWWAAQYKVKRPRQFITSGGLGTMGFGFPA 419

Query: 520 AIGASVANPDIAVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWEDRFY 579
AIGA + N D IV+DI GDGS MN+QELAT E LPVK+ +LNN LGMV QW++ FY
Sbjct: 420 AIGAQIGNRDKIVIDIAGDGSIQMNIQELATAASERLPVKIFILNNSCLGMVRQWQELFY 479

Query: 580 KANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLD-TPGPYLLD 638
+ + T L ++ PN A G RV K +L EAI+ L+ P ++D
Sbjct: 480 EKRYSTLL-----DVAPNFEKLAEVYGGYGRVVEKIEELDEAIEWALNINDSPVIVD 532

Query: 639 VICPHQEHVLPMPNGGTFNDVITE 663
+ +E+V PMIP GG+ + ++ +
Sbjct: 533 IQVNREENVFPMPAGGSIDKMLID 557

>ref|YP_001644574.1| acetolactate synthase 3 catalytic subunit [Bacillus
weihenstephanensis KBAB4]
gb|ABY42946.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus
weihenstephanensis KBAB4]
Length = 571

Score = 515 bits (1326), Expect = e-144, Method: Compositional matrix adjust.
Identities = 268/567 (47%), Positives = 371/567 (65%), Gaps = 23/567 (4%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA +++ L++ GV TVF YPGA + I+ AL S +++VL RHEQ + AAEGYAR+S
Sbjct: 18 GAGHVIQCLKKLGVTTVFGYPGGAILPIYDALYESG-LKHVLTREHQAIIHAAEGYARAS 76

Query: 159 GKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ ATSGPGATNLV+GLADA +DS+PLV ITGQV +IG D FQE +V +T +
Sbjct: 77 GKVGVVFATSGPGATNLVTGLADAYMDSIPLVVITGQVATPLIGKDFQEADVVGITVPV 136

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V DV + R ++EAF++A SGRPGPVL+D+PKD+Q + + +++ GY
Sbjct: 137 TKHNYQVRDVNHLSTVQEAIFYIAESGRPGPVLIDIPKDVQNAVTSFFNEEVEILGY-- 194

Query: 279 RMPKP-PEDSHLEQIVRLISESKKPVLYVGGCLNS--SDELGRFVELTGPIVASTLMGL 335
P+P P+ L ++ + IS++K+P+LY+GGG ++S S+EL +F IPV STLMGL
Sbjct: 195 -KPEFPDLSKLREVAKSISKAKRPLLYIGGGVIHSGGSEELIKFARENRIPVVSTLMGL 253

Query: 336 GSYPCDELSELHMLGMHGTVYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAKIVHID 395
G+YP D L L MLGMHGT AN AV DLLLA GVRFDRTVGKLE F+ +K VHID
Sbjct: 254 GAYPPGDPLFLGMLGMHGTAAANMAVTECDLLALGVRFDRTVGKLELFSKPHSKVHID 313

Query: 396 IDSAEIGKNKTPHVSVC GDVKALQG-MNKVLENRAEELKLDGFWVRNELNVQKQKPLS 454
ID +E KN T + GDVK AL ++ + + +E W ++ ++++PLS
Sbjct: 314 IDPSEFHKNVTVEHPIVGDVKALHMLLHMSIYTQTDE-----WLQKVKKQWEEYPLS 366

Query: 455 FKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAMG 514
+K + PQ+ I ++ ELT+G+AI++T VGQHQMWAA FY +KPR +L+SGGLG MG
Sbjct: 367 YKQKEFELKQPQHVINLVSELTNGEAIVTTEVGQHQMWAAHFYKARKPRTFLTSGGLGTMG 426

Query: 515 FGLPAAIGASVANPDIAVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQW 574
FG PAAIGA +A + +V+ I GD SF MN+QEL TI N+PVKV ++NN+ LGMV QW
Sbjct: 427 FGFPAAIGAQLAKEEELVICIAGDASFQMNQELQTIANNIPVKVFIINNKLGMVRQW 486

Query: 575 EDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGP 634
++ FY+ + + +G P+ + A A G+ R T + ++ + GP
Sbjct: 487 QEMFYENRLSESRIGS-----PDFVKVAEAYGVKGLRATNSFEAKKVMLEAFSHEGP 538

Query: 635 YLLDVICPHQEHVLPMPNGGTFNDVI 661
++D E+V PM+P N++I
Sbjct: 539 VVVDVFCVEEENVFPMVPPNKGNNEMI 565

>ref|ZP_01104189.1| Acetolactate synthase [gamma proteobacterium KT 71]
gb|EAQ96312.1| Acetolactate synthase [Congregibacter litoralis KT71]
Length = 619

Score = 515 bits (1326), Expect = e-144, Method: Compositional matrix adjust.
Identities = 286/592 (48%), Positives = 377/592 (63%), Gaps = 25/592 (4%)

Query: 89 SRFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGV 148
SR + +GA IL + L +GV+T+F YPGGA++EI L + IR + HEQG V
Sbjct: 24 SRGGEVALRGAQILAKCLVAEGVDTLFGYPGGANLEIFDVLQFG-IRCIRTEHEQGAV 82

Query: 149 FAAEGYARSSGKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQE 208
AA+GYAR +G+PG+C+ATSGPGATNLV+G+ADA DS PLVAITG VP ++G +AFQE
Sbjct: 83 HAAQGYARVTGRPGVCLATSGPGATNLVTGIADANSSTPLVAITGNVPSHLLGKNAFQE 142

Query: 209 TPIVEVTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIP--- 265
IV VT +ITK NYLV V IP ++ EAF LA RPPVLD+D+PKDIQQQ
Sbjct: 143 VDIVAVTDAITKRNLYVKRVGAIPEVVREAFALAGGNRPGPVLIDIPKDIQQQYPKDPEG 202

Query: 266 NWEQAMKLPGYMSRMPKPP----EDSHLEQIVRLISESKKPVLY--VGGGCLNSSDELGR 319
N+ +A ++P + P+P E LE+ +RL+ ES++PV+Y G G D L
Sbjct: 203 NY-KAPRIPAVID-TPEPAMTGMEQQGLEECMRLRESERPVIYAGGGIGVAAGEDSLLA 260

Query: 320 FVELTGIPVASTLMGLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDRT 379
F E IPV T+MG+G +P D LSL +LGMHG YAN A+ +DL+LA GVRFDRT
Sbjct: 261 FAEKAQIPVTWTIMGVGCFPPDHSLDVLGMHGAKYANRAIYADLVLALGVRFDRT 320

Query: 380 GKLEAFASRAKIVHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFGV 439
G + FA +A+I+HIDID +E+ KNKT + + D+K AL M E ++
Sbjct: 321 GNVAEFAKQARIHIDIDRSELNKNKT VTLPIRADLKPALLQMLGACE-----PVESRP 374

Query: 440 WRNELNVQKQKFLSFKTFGEAIPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYK 499
W +N KQ +P ++ E + PQ+ I+ L T G A++S GVGQHQMWA QFY K
Sbjct: 375 WVETVNGWKQDYPYP-ESDSEGLKPQH VIRALCAATLGDAVSLGVGQHQMWAMQFYRSK 433

Query: 500 KPRQWLSGGLGAMGFLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVK 559
+PR +LSS G G MG+GLPAAIGA +A PD V+DIDGDS M + EL+T + VK
Sbjct: 434 QPRSFLSSSGFGTMGYGLPAAIGAKIAAPDRQVIDIDGDSLNTIHELSTCHRYGIGVK 493

Query: 560 VLLNNQHLGMVMQWEDRFYKANRAHTFLGDP-----AQEDEIFPNMLLFAAACGIPAAR 614
+++NNQ LGMV QW+D Y ++RA + L DP + + +I+P+ L A + A R
Sbjct: 494 TVVINNQWLMVRQWQDMIYDSHRAGSDLSDPMAVKSSDDADIYPDFLSIAKGYRVTAER 553

Query: 615 VTKKADLREAIQTMLDTP-GPYLLDVICPHQEHVLP MIPNGGTFNDVITEGD 665
V + DL AI+ ML P PYLLDVI +E+V PMIP GGT+ D+I D
Sbjct: 554 VRAEDLPAAIERMLADPEEPYLLDVIVEAEENVYP MIPAGGTYRDIIMSAD 605

>ref|ZP_02118763.1| acetolactate synthase, large subunit, biosynthetic type
[Methylobacterium nodulans ORS 2060]
gb|EDQ44363.1| acetolactate synthase, large subunit, biosynthetic type
[Methylobacterium nodulans ORS 2060]
Length = 592

Score = 514 bits (1325), Expect = e-144, Method: Compositional matrix adjust.
Identities = 266/572 (46%), Positives = 372/572 (65%), Gaps = 21/572 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA++++ AL+ QGV+T+F YPGGA + I+ AL S+++VL RHEQG V AAEGYARSS
Sbjct: 9 GAEMVIRALQDQGVDTLFGYPGGAVLPIDALFHQDSVKHVLVRHEQGAVHAAEGYARSS 68

Query: 159 GKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G + TSGPGATN+++GL DALLDS+PLV ITGQVP +IG+DAFQE V +TRS
Sbjct: 69 GKVGCVLVTSGPGATNVITGLTDALLDSIPLVCITGQVPTHLIGSDAFQECDTVGITRSC 128

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNYLV +ED+PRI+ EAF+++A GRPGPV+VD+PKDI Q A + + ++ G+ +
Sbjct: 129 TKHNYLVKSIEDLPRILHEAFYVASHGRPGPVVDLPKDI--QFASGLYRRPVE-NGHKT 185

Query: 279 RMPKPPED-SHLEQIVRLISESKKPVLYVGGGCLNSSDELGR----FVELTGIPVASTLM 333
P D + + V L++ +++PV Y GGG +NS E R V TG P+ STLM
Sbjct: 186 YRPTIHGDLAKIRAAVALMAGARRPVFYTG GGVINSPEASRLRELVRATGFPITSTLM 245

Query: 334 GLGSYPCCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVH 393
GLG+YP D L MLGMHGT AN A+ DL++ G RFDDR+TG+L+AF+ +K +H
Sbjct: 246 GLGAYPGSDPQFLGMLGMHGT YEANLAMHECDLMICIGARFDDRITGRLDAFSPFSKKIH 305

Query: 394 IDIDSAEIGKNKTPHVSVCADVGLALQGMNKLLENRAEELKLDGFGV---WRNELNVQKQK 450
+DID++ I KN + + GD L M K E RA + D G W +++N K +
Sbjct: 306 VDIDASSINKNVKADIGILGDCASVLDMLK--EWRVAVTPEPDKGRLTEWLSKINGWKAR 363

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGK-AIISTGVGQHQMWAAQFYNYKKPRQWLSSGG 509
L + G I PQYA++ L E T + ++T VGQHQMWAAQ+Y +++P +W++SGG
Sbjct: 364 ECLGYWPSGTTIKPQYAVQRLYEATKNRETYVTTEVGQHQMWAAQYKFEENRWMTSSGG 423

Query: 510 LGAMGFGLPAAIGASVANPDIAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLG 569
LG MG+GLPAAIG +A+P A+V+DI G+ S +MN+QE++T LPVK+ +LNN+++G
Sbjct: 424 LGTMGYGLPAAIGTQLAHPGALVIDIAGEASILNMNMQEMSTAVQYRLPVKIFILNNEYMG 483

Query: 570 MVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTML 629
MV QW++ + + + ++ P+ + A A G R K DL AIQ ML
Sbjct: 484 MVRQWQELLHGSRYSESYSAS-----LPDFVKLAAYGAKGIRCEKPGDLDAAIQEML 536

Query: 630 DTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
D GP + D I E+ PMIP+G N+++
Sbjct: 537 DYDGPVIFDCIVDKTENCFFMIPSGKAHNEML 568

>ref|YP_001952737.1| acetolactate synthase, large subunit, biosynthetic type [Geobacter
lovleyi SZ]
gb|ACD96217.1| acetolactate synthase, large subunit, biosynthetic type [Geobacter
lovleyi SZ]
Length = 566

Score = 514 bits (1325), Expect = e-144, Method: Compositional matrix adjust.
Identities = 259/571 (45%), Positives = 368/571 (64%), Gaps = 20/571 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA IL+E+L+R+GV+ VF YPGG + ++ L IR++LPRHEQGG AA+GYAR++
Sbjct: 5 GARILLESRLKREGVDLVFGYPGGTVINLYDELMNVREIRHILPRHEQGGTHAADGYARAT 64

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ IATSGPGATN ++G+A A +DS+P+V ITGQVP +IG DAFQE I+ +TR I
Sbjct: 65 GKVGVAIATSGPGATNTITGIATAYMDSIPMVIITGQVPTPLIGNDAFQEVDIIGITRPI 124

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKH++L+ +DIP I+ +AF+++A SGRPGPVL+D PKD+Q A W +++++ GY
Sbjct: 125 TKHSFLIRHAKDIPTIVRKAFYIARSGRPGPVLIDFPKDVQISQAEFKWPESIEIRGY-- 182

Query: 279 RMPKPPEDSHLEQI---VRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLM 333
KP + H +Q+ V ++ +++PV+YVGGG + N+++EL PV +TLM
Sbjct: 183 ---KPNLEGHQKQVEKAVDMLLVARRPVMYVGGGVILANAAEELTELARTLQFPVTTTLM 239

Query: 334 GLGSPCDDESLHMLGMHGTVYANYAVEHSDLLAFGVFRDDRVTGKLEAFASRAKIVH 393
GLG++P +D LSL MLGMHG AN A+ HSDL+LA G RFDDRVTGK+ FA AKI+H
Sbjct: 240 GLGAFPENDPLSLKMLGMHGAYAANMAMTHSDLILAVGARFDDRVTGKIATFAPHAKIIH 299

Query: 394 IDIDSAEIGKNKTPHVSVCADVGLALQGMNKLLENRAEELKLDGFG---VWRNELNVQKQK 450
ID+D I KN + + GD K L M + L+ + E++ W +++ K K
Sbjct: 300 IDVDPTSIRKNVRVDLPVGDTKDVLVKMIECLKGQTEKVSQAHSAMEAWHEDISGWKAK 359

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGL 510
P+++K I PQY I+ L EL++ AI++T VGQHQMW AQF+ + +PR L+SGGL
Sbjct: 360 HPIAYKQSSSVIKPQYVIQKRELSEDDAIMATDVGQHQMWTAQFFEFNQPRTLTSSGGL 419

Query: 511 GAMGFGLPAAIGASVANPDIAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
G MGFGLPAA+GA A P V+ + GDG MN+QELAT+ LPVK+++LNN LGM
Sbjct: 420 GTMGFGLPAAAGAAAYPKRQVICVCGDGGVQMMNQELATLVQHRLPVKIVLNNNFLGM 479

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V QW++ F+ + T L P I A A G + K +++ + I+
Sbjct: 480 VRQWQELFFDKRYSQTCLLPMDFARI-----AEAYGAKGLKADKPSEVEQVIKEGFA 532

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
GP +++ +E VLPM+P G + N+++
Sbjct: 533 HDGPVIMEFKIAREEKVLPMPVAGASLNEMV 563

>ref|NP_632694.1| acetolactate synthase 3 catalytic subunit [Methanosarcina mazei
Gol]
gb|AAM30366.1| Acetolactate synthase large subunit [Methanosarcina mazei Gol]
Length = 564

Score = 514 bits (1325), Expect = e-144, Method: Compositional matrix adjust.
Identities = 262/569 (46%), Positives = 380/569 (66%), Gaps = 27/569 (4%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSS 158
GA L++ LE++GV+T+F YPGG + + L S +R++L RHEQ AA+GYAR++
Sbjct: 11 GAKALIKCLEKEGVDTLFGYPGGQIIPFYNEL-YDSDLRHILVRHEQAAAAHAADGYARAT 69

Query: 159 GKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+C++TSGPGATNLV+G+A A +DSVP+VA+TGQVPR +IG DAFQE I +T I
Sbjct: 70 GKTGVCVSTSGPGATNLVTGIATAYMDSVPIVALTGQVPRSLIGNDAFQEADITGITMPI 129

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNYLV D ++IPRI++EAF +A++GRPGPVL+D+PKD+Q ++ + ++L GY
Sbjct: 130 TKHNYLVQDPQEIPRIVKEAFHIASTGRPGPVLIDLKDVQNEIDLHYPERVELRGY-- 187

Query: 279 RMPKPPEDSHLEQIVRL---ISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLM 333
KP + +QI R I+ S +P++Y GGG + N+S EL F E PV +TLM
Sbjct: 188 ---KPTYKGNTQQIKRAAEEIANSRPIIYAGGGVISSNASAEELVEFAETIKAPVTTTLM 244

Query: 334 GLGSPYCDDELHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRVTKLEAFASRAKIVH 393
G+ S P + L + MLGMHG YANYA++ SDL++A G RFDDRVTKLE+FA A+++H
Sbjct: 245 GISSIPTEHPLYVGMMLGMHGCKYANYAIQESDLIIAVGARFDDRVTKLESFAPNARVIH 304

Query: 394 IDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLE-NRAEELKLDFGVWRNELNVQKQKFP 452
ID+D AEI KN H+ + GD K L+ + + ++ R+ E W ++N+ K+++P
Sbjct: 305 IDVDPAEISKNVKVHPIVGDQKQLSLIRYVQCCRSAE-----WIEKVNLWKKEYP 357

Query: 453 LSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQLWSSGGLGA 512
L+++ + I PQ+ I+ + E+ AII T VGQHQMWAAQF+ Y KPR +L+SGGLG
Sbjct: 358 LNYRECRDTIMPQFVIEQISEVCR-DAIIVTEVGQHQMWAAQFFKYSKPRFTLTSGGLGT 416

Query: 513 MGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLLNQHLMVM 572
MG+G PAA+GA V PD V++I GDGSF MN QELAT+ ++PV ++LNN +LGMV
Sbjct: 417 MGYGFPAAMGAKVGRPDKTVINIAGDSFQMNQELATVVQNDIPVVSILNNGYLGMVR 476

Query: 573 QWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLDTP 632
QW++ FY ++TF+ + + A A G R + +++R AI+ +++
Sbjct: 477 QWQELFYDRRYSYTFIKGSV-----DFVKLAEEYAGLGLRAERPSEVRPAIEEAVNSG 529

Query: 633 GPYLLDVICPHQEHVLP MIPNGGTFNDVI 661
P +++VI + +V PM+P G N++I
Sbjct: 530 RPTVVEVIVECEANVYPMVPAGAAINEII 558

>ref|ZP_02257502.1| acetolactate synthase 3 catalytic subunit [Bacillus cereus AH187]
ref|ZP_03235733.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus
cereus H3081.97]
gb|EDZ58229.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus
cereus H3081.97]
Length = 571

Score = 513 bits (1322), Expect = e-143, Method: Compositional matrix adjust.
Identities = 266/566 (46%), Positives = 364/566 (64%), Gaps = 21/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSS 158
GA +++ L+ GV TVF YPGGA + ++ AL S ++++L RHEQ + AAEGYAR+S
Sbjct: 18 GAGHVIQCLKNLGVTTVFYPGGAILPVYDAL-YGSGLKHILTRHEQAAIHAAEGYARAS 76

Query: 159 GKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ ATSGPGATNLV+GLADA +DS+PLV ITGQV +IG D FQE +V +T +
Sbjct: 77 GKVGVVFATSGPGATNLVTGLADAYMDSIPLVVITGQVATPLIGKDGFEADVVGITVPV 136

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V DV + RI++EAF++A SGRPGPVL+D+PKD+Q + + + +PGY
Sbjct: 137 TKHNYQVRDYNHVSRIVQEAFYIAKSGRPGPVLIDIPKDVQNAKVTSTFFNEEVDIPGYKP 196

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLG 336
+ P+ L ++ + IS++K+P+LY+GGG ++S SDEL +F IPV STLMLGLG
Sbjct: 197 EL--VPDSMKLREVAKEISKAKRPLLYIGGGVIHSDGSELIKFARENRIIPVSTLMGLG 254

Query: 337 SYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVHIDI 396
+YP D L L MLGMHGT AN AV DLLLA GVRFDRTGKLE F+ +K VHIDI
Sbjct: 255 AYPPGDSLFLGMLGMHGTAAANMAVTECDLLALGVRFDRTGKLELFSHSPKSKVHIDI 314

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQGMNKV--LENRAEELKLDGVRNRELNVQKQKFLPSF 455
D +E KN T V GDVK AL + + + + +E W + K ++PLS+
Sbjct: 315 DPSEFHKNVTVVEYPVGDVKALHMLLHMPICQTDE-----WITKTEEWKAEYPLSY 367

Query: 456 KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGF 515
+ PQ+ I ++ ELT+G+AI++T VGQHQMWAQ FY K PR +L+SGGLG MGF
Sbjct: 368 IQKESELKPQHVISLVSELTNGEAIIVTEVGVGQHQMWAHFKAKNPRFTLSTGGLGTMGF 427

Query: 516 GLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
G PAA+GA +A + +V+ I GD SF MN+QEL TI N+PVKV ++NN+ LGMV QW+
Sbjct: 428 GFPAAGAQLAKEEELVICIAGDASFQMNQELQTIENNIPVKVFIINNKLGMVQRWQ 487

Query: 576 DRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPY 635
+ FY+ + + +G P+ + A A G+ R + + + + GP
Sbjct: 488 EMFYENRLSESKIGS-----PDFVKVAEAYGVKGLRAINSTEAKQVMLEAFAHEGPV 539

Query: 636 LLDVICPHQEHVLPMPNGGTFNDVI 661
++D E+V PM+P N++I
Sbjct: 540 VVDFCVEEENVFPMVPPNKGNNEMI 565

>gb|EDZ60585.1| acetolactate synthase, large subunit, biosynthetic type [Candidatus
Pelagibacter sp. HTCC7211]
Length = 588

Score = 513 bits (1322), Expect = e-143, Method: Compositional matrix adjust.
Identities = 258/572 (45%), Positives = 363/572 (63%), Gaps = 18/572 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA+I+ + LE Q VE +F YPGGA + I+ L SSI+++L RHEQG AAEYARSS
Sbjct: 7 GAEIVFKCLEDQKVEHIFGYPGGAVLPIYDELKNHSSIKHILVRHEQGAGHAAEGYARSS 66

Query: 159 GKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GKPG+ + TSGPGATN+V+ L DA +DSVPLV I+GQVP +IGTDAFQE +TR
Sbjct: 67 GKPGVVLVTSVPGATNVVTALTDAYMDSVPLVCISGQVPTHLIGTDAFQECDDTGTITRPC 126

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHN+LV D+ D+ ++ EAF +AT+GRPGPVL+D+PKDI Q A +++
Sbjct: 127 TKHNWLKVDINDLSNMHEAFKVATTGRPGPVLIDIPKDI--QFAKAKYKKPKIEKKLNG 184

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS---SDELGRFVELTGIPVASTLMG 334
++ + +E+++L S++KKPV+Y GGG +NS S+ L LTG P+ STL G
Sbjct: 185 KIQNKFSQNDIEELIKLFSKAKKPVYISGGGVINS GPKASEALRELASLTGFPTSTLQG 244

Query: 335 LGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVHI 394
LG++P DD L MLGMHGT AN A+ DLL+ G RFDDR+TGK++ F+ ++K VHI
Sbjct: 245 LGAFPDDNQFLGMLGMHGTYEANNAMHDCDLLINIGARFDDRITGKIDFSPKSKKVHI 304

Query: 395 DIDSIEIGKNKTPHVSVC GDVKLALQGMNKV----ENRAEELKLDGVRNRELNVQKQK 450
DID + I K +++ GDV L +NK + + K + W ++ ++K
Sbjct: 305 DIDPSSINKIIKVDLAIVGDVSSVLNRINKTIVKSKNGKSNKSNIAKWWQIEKWRKK 364

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGK-AIISTGVGQHQMWAQFYNYKKPRQWLSSGG 509
L+F E I PQYA++ L ELT K ++T VGQHQMWAQ Y + KP +W++SGG
Sbjct: 365 DSLNFINSDETIKPQYAVQRLYELTKNKDITYTTEVGVGQHQMWAQHYKFNKPNRWMTSGG 424

Query: 510 LGAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLG 569
LG MG+GLPAA+G +A+P+ +VVDI G+ S +M +QE++T NLP+K+ +LNNQ++G
Sbjct: 425 LGTMGYGLPAAVGVQIAHPEKLVDIAGEASVLMTQMESTAIQYNLPKIFILNNQYMG 484

Query: 570 MVMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKADLREAIQTML 629
MV QW++ ++ N + ++ E P+ + A A G + DL E IQ M+
Sbjct: 485 MVRQWQELLHEKNYSESY-----SEALPDFMKMAEAYGCKGIKAVNPLDLDEKIQEMI 537

Query: 630 DTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
D GP + D E+ PMIP+G N +I
Sbjct: 538 DYDGPVIFDCHVDPNENCFPMIPSGKPHNQMI 569

>ref|NP_618663.1| acetolactate synthase 3 catalytic subunit [Methanosarcina
acetivorans C2A]
gb|AAM07143.1| acetolactate synthase, large subunit [Methanosarcina acetivorans
C2A]
Length = 564

Score = 512 bits (1319), Expect = e-143, Method: Compositional matrix adjust.
Identities = 266/571 (46%), Positives = 377/571 (66%), Gaps = 30/571 (5%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA L++ LE++GV+T+F YPGG + + L S +R++L RHEQ AA+GYAR++
Sbjct: 11 GAKALIKCLEKEGVDTLFGYPGGQIIPFYNEL-YSDLRHILVRHEQAAAAHAADGYARAT 69

Query: 159 GKPGICIATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+C++TSGPGATNLV+G+A A +DSVP+VA+TGQVPR +IG DAFQE I +T I
Sbjct: 70 GKTGVCVSTSGPGATNLVTGIATAYMDSVPIVALTGQVPRPLIGNDAFQEADITGITLPI 129

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVDPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNYLV D E+IPRI++EAF +A++GRPGPVL+D+PKD+Q + ++L GY
Sbjct: 130 TKHNYLVQDAEEIPRIVKEAFHIASTGRPGPVLIDLPKDVQNIIDLQYDPKVELRGY-- 187

Query: 279 RMPKPPEDSHLEQIVRL---ISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLM 333
KP + +QI R I+ S +P++Y GGG + N+S EL E PV +TLM
Sbjct: 188 ---KPTYKGNTQQIKRAAEEIANSRPIIYAGGGVISSNASAELEVELAETLMAPVTTTLM 244

Query: 334 GLGSPCDDESLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIVH 393
G+ + P + L + MLGMHG YANYAV+ SDL++A G RFDDRVTKLE+FA A+++H
Sbjct: 245 GISAIPTEHPLYVGMGMHGCKYANYAVQESDLIIAVGARFDDRVTKLESFAPNARVIH 304

Query: 394 IDIDSAEIGKNTKPHVSVCGDVKLALQGMNKVLE--NRAEELKLDGFWVRNENLVQKQKF 451
ID+D AEI KN HV + GD K L+ + K ++ N AE W ++N K+++
Sbjct: 305 IDVDPAEISKNVHVPIVGDAKQILKSLIKYIQRCSAE-----WIEKINQWKKEY 356

Query: 452 PLSFKTF-GEAIPPQYAIKVDELDTGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGL 510
PL+++ + I PQ+ ++ + E+ AII T VGQHQMWAQ++ Y+KPR +L+SGGL
Sbjct: 357 PLAYRYVSSDTIMPQFVVEQISEVCK-DAIIVTEVGQHQMWAQYFYKRPRTFLTSGGL 415

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLLNQHLGM 570
G MG+GLPAA+GA V PD V++I GDGSF MN QELAT+ ++PV ++LNN +LGM
Sbjct: 416 GTMGYGLPAAAGAKVGKPKDVTVINIAGDSFQMNSQELATLVQNDIPVVSILNNGYLGM 475

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKADLREAIQTMLD 630
V QW++ FY +HTF+ + + A A G R K +++R AI+ +
Sbjct: 476 VRQWQELFYDRRYSHTFIKGSV-----DFVKLAAYGALGLRAEKPSEVRPAIEEAVG 528

Query: 631 TPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
+ P +++VI + +V PM+P G N++I
Sbjct: 529 SGRPAVEVIVECEANVYPMVPAGAAINEII 559

>ref|ZP_03039219.1| acetolactate synthase, large subunit, biosynthetic type
[Geobacillus sp. Y412MC10]
gb|EDV77345.1| acetolactate synthase, large subunit, biosynthetic type
[Geobacillus sp. Y412MC10]
Length = 576

Score = 511 bits (1317), Expect = e-143, Method: Compositional matrix adjust.
Identities = 266/567 (46%), Positives = 365/567 (64%), Gaps = 20/567 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
G+++L+ L ++GVE VF YPGG + I+ A+ +++L RHEQG + AA+GYARS+
Sbjct: 21 GSEVLLRGLLQEGVECVFGYPGGNVLYIYDAMVHQPDFKHILTRHEQGAIIHAADGYARST 80

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+CIATSGPGATNLV+G+A A +DSVPLV ITG V ++GTDAFQE I+ +T I
Sbjct: 81 GKVGVCIATSGPGATNLVTGIATAYMDSVPLVVITGNVSTNVMGTDAFQEADIISITMPI 140

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYM- 277
TKH+Y+V DV D+PRII EAF++A +GR GPVL+D+PKD+ Q ++L GY
Sbjct: 141 TKHSYMRDVLDPRIIEEAFYIANTGRKGPVLIDIPKDVNTQRMAYRPADTVRLRGYHG 200

Query: 278 SRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLMGL 335
+ P P E ++ +++ I+E++KPV+ GGG + NSS EL +FV T IPVA+TL+GL
Sbjct: 201 APEPNPAE---MDALLQAIAEARKPVIIAGGGVYANSSQELIKFVHTTRIPVATTLGL 257

Query: 336 GSYPCDELHMLGMHGT VYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAK-IVHI 394
G +P DDE+ L MLG HG AN AV+++DL+++ G RFDDRVT KL+ FA +AK I HI
Sbjct: 258 GGFPDDEMWLGMLGHGVYANMAVQNADLIISIGSRFDDRVTMKGDFAPQAKRIAH 317

Query: 395 DIDSAEIGKNKTPHVSVCADVKLALQGMNVLENRAEELKLDGFWRNELNVQKQKPLS 454
DID AEIGKN ++ GD+K L N +A+ + G W +L K + PL
Sbjct: 318 DIDPAEIGKNVKTDLACIGDIKNVLAYAN---TKAQAAQT--GTWLEQLQEYKVQHPLR 371

Query: 455 FKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMG 514
+ I PQY ++++ E T G+AI+T VGQHQMWAQFY +K PR ++SGGLG MG
Sbjct: 372 YTDSDTVIKPQYVLEMISETTQGEAIITTDVGQHQMWAQFYRFKHPRSLITSGGLGTMG 431

Query: 515 FGLPAAIGASVANPDIAVVDIDGGSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQW 574
FG PAAIGA V NPD +VV I+GDG M QE+A + +PVK+++LNNQ LGMV Q
Sbjct: 432 FGFPAAIGAKVGNPDRLVVSINGDGMQMAQEMAICAIHQIPVKIVLNNQVLGMVKQQ 491

Query: 575 EDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGP 634
++ Y+ + L P+ + A A GI R T K + + L T GP
Sbjct: 492 QELMYERRYSDIDLSGS-----PDFVKLAAYGIKGLRATNKDEASKVWLEALQTTGP 544

Query: 635 YLLDVICPHQEHVLPMPNGGTFNDVI 661
L++ + P E+V PM+ G + +I
Sbjct: 545 VLVEFVIPTNENVYPMVLAGTPLDQMI 571

>ref|YP_001642303.1| acetolactate synthase, large subunit, biosynthetic type
[Methylobacterium extorquens PA1]
gb|ABY33232.1| acetolactate synthase, large subunit, biosynthetic type
[Methylobacterium extorquens PA1]
Length = 591

Score = 511 bits (1317), Expect = e-143, Method: Compositional matrix adjust.
Identities = 259/572 (45%), Positives = 374/572 (65%), Gaps = 21/572 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA +++ A + QGV+T+F YPGGA + I+ AL + I++VL RHEQG V AAEYARSS
Sbjct: 8 GAQMVIRAFQDQGVDTLFGYPGGAVLPIYDALFNETKIQHVLVRHEQGAVHAAEGYARSS 67

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ + TSGPGATN+V+GL DA+LDS+PLVA+TGQVP +IG+DAFQE V +TR
Sbjct: 68 GKVGVLVTSGPGATNIVTGLTDAMLDIPLVAVTGQVPTHLIGSDAFQECDTVGITRHC 127

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNYLV +ED+PRI+ EAF++A+ GRPGPV++D+PKDI Q A + + + G+ +
Sbjct: 128 TKHNYLVKSIEDLPRILHEAFYVASHGRPGPVVIDLPKDI--QFASGVYSRPAQ-DGHKT 184

Query: 279 RMPKPPEDS-HLEQIVRLISESKKPVLYVGGGCLNSSDELGR---FVELTGIPVASTLM 333
P DS + V L++ +++PV Y GGG +NS E R V TG PV STLM
Sbjct: 185 YNPPVKGDSKIRAAVELMASARRPVFYTTGGGVINSGEASRLRLRELVAETGFPVSTLM 244

Query: 334 GLGSYPCDELHMLGMHGT VYANYAVEHSDLLAFGVRFDRTVGKLEAFASRAKIVH 393
GLG++P D+ L MLGMHGT AN A+ D+++ G RFDDR+TG+L+AFA +K +H
Sbjct: 245 GLGAFPASDDKFLGMLGMHGTYEANLAMHDCDVMINIGARFDDRITGRDLDAFAPFSKKIH 304

Query: 394 IDIDSAEIGKNKTPHVSVCQDVKLALQGM---NKVLENRAEELKLDGFGVWRNELNVQKQK 450
+D+D++ I K V + GD L+ M + L + ++ +++ W N+++ K +
Sbjct: 305 VDVDASSINKVVKVDVGILGDCAAVLEEMLAQWRALPKQPKDRME--DWFNKISRWKS 362

Query: 451 FPLSFKTFGEAIPPQYAIKVLDE-LTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGG 509
L++ G I PQYA++ L E D K ++T VGQHQMWAAQ++ + +P +W++SGG
Sbjct: 363 DCLAYWPSGTIIKPQYAVQRLYEACKDRKTFVTTEVGQHQMWAAQYFKFDEPNRWMTSGG 422

Query: 510 LGAMGFGLPAAIGASVANPDIAIVVDIDGGSFIMNVQELATIRVENLPVKVLLNNQHLG 569
LG MG+GLPAAIG +ANPD +V+DI G+ S +MN+QE++T LPVK+ +LNN+++G
Sbjct: 423 LGTMGYGLPAAIGTQLANPDGLVIDIAGEASILNMNMQEMSTAVQYRLPVKIFILNNEYMG 482

Query: 570 MVMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTML 629
MV QW++ + + + ++ E P+ + A A G R K +L AIQ ML
Sbjct: 483 MVRQWQELLHGSRYSSQSY-----SESLPDFVKLA EAYGAKGIRCEKPGELDAAIQEML 535

Query: 630 DTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
D GP + D I +E+ PMIP+G N+++
Sbjct: 536 DYDGPVIFDCIVDKKENCFFPMIPSGKAHNEML 567

>ref|YP_001404604.1| acetolactate synthase, large subunit, biosynthetic type [Candidatus
Methanoregula boonei 6A8]
gb|ABS55961.1| acetolactate synthase, large subunit, biosynthetic type [Candidatus
Methanoregula boonei 6A8]
Length = 559

Score = 511 bits (1317), Expect = e-143, Method: Compositional matrix adjust.
Identities = 266/572 (46%), Positives = 371/572 (64%), Gaps = 27/572 (4%)

Query: 97 RKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYAR 156
+ GA +LVE+L+R+GV+T+F YPGG+ + I+ L S +R++L RHEQ AA+GYAR
Sbjct: 2 KTGAKLLVESLQREGVDTLFGYPGGSVLPIYDEL-YDSPLRHILVRHEQAAAHAAADGYAR 60

Query: 157 SSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTR 216
+SG+ G+C+ATSGPGA NLV+G+A A +DSVP+VAITGQVP M+G DAFQE+ I +T
Sbjct: 61 ASGRVGVCLATSGPGACNLVTGIATAYMDSVPVVAITGQVPTTMLGNDAFQESDIQGITM 120

Query: 217 SITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQ-QQLAIPNWEQAMKLP 275
ITKHNLYLV + DIPR+++EAF+++A +GR GPVL+D+PKD+ + + P + + L G
Sbjct: 121 PITKHNLYLVKETSDIPRVVQEAIFYIAGTGRQGPVLIDLPKDVNTRSVKEPIVPEKVVLRG 180

Query: 276 YMSRMPKPPEDSHLEQI---VRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVAS 330
Y P H QI + LI+ +++P+++Y GGG + N+S EL F GIPV +
Sbjct: 181 Y-----NPTYKGHQRIDKAIELITTAERPLIYAGGVISSNASPELVAFASTHGIPVTT 235

Query: 331 TLMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVGTGKLEAFASRAK 390
TLMG+G PCD L++ MLGMHGT YAN+AV DLL+A G RFDDRVGTGK++ FA AK
Sbjct: 236 TLMGIGCIPCDHPLNMGLGMHGT EYANFAVTECDLLIAIGARFDDRVGTGKIDTFAPNAK 295

Query: 391 IVHIDIDSAEIGKNKTPHVSVCQDVKLALQGMNKVLENR-AEELKLDGFGVWRNELNVQKQ 449
++HIDID AEIGKNK V + GD K L + L + A E W+ + KQ
Sbjct: 296 VIHIDIDPAEIGKNKRVDPIVGDTKAVLTDIIAGLAKKNASE-----AWQKRIKHWKQ 349

Query: 450 KFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGG 509
PL + + PQ+ ++ ++EL G A+I + VGQ+QMW AQ++ ++ PR W++SGG
Sbjct: 350 NHPLRYGKDNGLHPQFILQQMNELLKGDVAVIVSEVGQNMWTAQYFCFRHPRTWITSGG 409

Query: 510 LGAMGFGLPAAIGASVANPDIAIVVDIDGGSFIMNVQELATIRVENLPVKVLLNNQHLG 569
LG MG+G PAAIGA A PD V D+ GDGS MN+QE+ T+ N+PVK+ +LNN +LG
Sbjct: 410 LGTMGYGFPAAGAHFARPDVPVFDVAGDSIQMNIQEMGTVAQYNIPVKIAILNNMYLG 469

Query: 570 MVMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTML 629
MV QW++ FY A+T L P E + A GI +V ++ A++ +
Sbjct: 470 MVRQWQELFYDRRYAYTEL--PPVE-----FVRIGQAYGIEGKVESCEVMPALKA 521

Query: 630 DTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
D GP++LD +E+V PM+P G N++I
Sbjct: 522 DHGDPFVLDRIEREENVFPMVPAGAAINEMI 553

>ref|ZP_01311443.1| acetolactate synthase, large subunit, biosynthetic type
[Desulfuromonas acetoxidans DSM 684]
gb|EAT16695.1| acetolactate synthase, large subunit, biosynthetic type
[Desulfuromonas acetoxidans DSM 684]
Length = 565

Score = 511 bits (1316), Expect = e-143, Method: Compositional matrix adjust.
Identities = 264/570 (46%), Positives = 375/570 (65%), Gaps = 15/570 (2%)

Query: 97 RKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYAR 156
+ G+ IL+E L +GV+TVF YPGG + I+ L S I+++L RHEQ V AA+ YAR
Sbjct: 3 KTGSQILLECLRLLEGVDTVFGYPGGTVINIYDDLMDSPIKHILNRHEQA AVHAADAYAR 61

Query: 157 SSGKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTR 216
+G G+ IATSGPGATN ++G+A A +DS+P+V I+GQVP +IG DAFQE ++ +TR
Sbjct: 62 VTGNVGVAIATSGPGATNTITGIATAYMDSIPMVIISGQVPTPLIGNDAFQEADMIGITR 121

Query: 217 SITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGY 276
ITKHNLYLV DV+D+ RI+++AF++A +GRPGPVL+D+PKD+Q ++ ++++L GY
Sbjct: 122 PITKHNLYLVRDVKDLARIVKQAFYIARTGRPGPVLIDLPKDVQVDSTTFSTPESVELRGY 181

Query: 277 MSRMPPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMG 334
+ P LE+ ++I ++KPV+YVGGG S S++L +F E PV +TLMG
Sbjct: 182 KPTVNANPR--QLEKATKMILAARKPVIYVGGGATLSDVSEDLKFAETIQAPVTTTLMG 239

Query: 335 LGSYPCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIVHI 394
+ S+P LS+ MLGMHGT YAN AV +SDLL+A G RFDDRVTGK+ FA AKI+H+
Sbjct: 240 MASFPKTHPLSVGMLGMHGT FANMAVTNSDLLIALGARFDDRVTGKIATFAPHAKIIHV 299

Query: 395 DIDS AEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDLDF---GVWRNELNVQKQKF 451
D+D I KN + V G + L + + ++ +ELK WR +++ K++
Sbjct: 300 DVDPTS IKKNVRVDLPVVGMLDDVLPRLTEKVQRDQDELKETIEATDAWRAQVDEWKEQH 359

Query: 452 PLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLG 511
P+S+K I PQY I+ L ELTD AII+T VGQHQMW AQF+++ +PR +++SGGLG
Sbjct: 360 PMSYKQTKSTIKPQYVIEKLRELTDDAIIITEVGQHQMWTAQFFDFSQPRTFVTSSGGLG 419

Query: 512 AMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMV 571
MGFGLPAA+GA A P+ V+DI GDGSF MN QELAT+ LPVK+++LNN LGMV
Sbjct: 420 TMGFGLPAALGAQA AAFPERQVIDISGDGSFQMNSQELATLVQYRLPVKIVILNNNPLGMV 479

Query: 572 MQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLDT 631
QW+ F+ + T + P + + A A G R TK ++ + I+ L+T
Sbjct: 480 RQWQQLFFDKRYSQTCMELPI-----DFIKLAEAYGATGLRATKVEEVGDVIKKALET 532

Query: 632 GPGYLLDVICPHQEHVLPMPINGGTFNDVI 661
PGP +++ +E+VLPM+P G N+++
Sbjct: 533 GPGVIMEFKVSREENVLPMPVAGAGLNEMV 562

>ref|ZP_02059000.1| acetolactate synthase, large subunit, biosynthetic type
[Methylobacterium chloromethanicum CM4]
gb|EDO20756.1| acetolactate synthase, large subunit, biosynthetic type
[Methylobacterium chloromethanicum CM4]
Length = 591

Score = 510 bits (1314), Expect = e-142, Method: Compositional matrix adjust.
Identities = 259/572 (45%), Positives = 374/572 (65%), Gaps = 21/572 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA +++ A + QGV+T+F YPGGA + I+ AL + I++VL RHEQG V AAEGYARSS
Sbjct: 8 GAQMVIRAFQDQGVDTLFGYPGGA VLPYDALFNETKIQHVLVRHEQGA VHA AEGYARSS 67

Query: 159 GKPGICIATSGPGATNLVSLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ + TSGPGATN+V+GL DA+LDS+PLVA+TGQVP +IG+DAFQE V +TR
Sbjct: 68 GKVGVVLVTSGPGATNIVTGLTDAMLDSIPLVAVTGQVPTHLIGSDAFQECDTVGITRHC 127

Query: 219 TKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNLYLV +ED+PRI+ EAF+++A GRPGPV++D+PKDI Q A + + + G+ +
Sbjct: 128 TKHNLYLVKSIEDLPRILHEAFYVASHGRPGPVVIDLPKDI--QFASGVYSRPAQ-DGHKT 184

Query: 279 RMPKPPEDS-HLEQIVRLISESKKPVLYVGGGCLNSSDELGR----FVELTGIPVASTLM 333
P DS + V L++ +++PV Y GGG +NS E R V TG PV STLM
Sbjct: 185 YNPPVKGSDKIRAAVELMAGARRPVFTYGGGVINSGPEASRLRLRELVAETGFPVSTLM 244

Query: 334 GLGSPYPCDDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRVTGKLEAFASRAKIVH 393
GLG++P D+ L MLGMHGT AN A+ D+++ G RFDDR+TG+L+AFA +K +H
Sbjct: 245 GLGAFFASDDKFLGMLGMHGT YEANLAMHDCDVMINIGARFDDRITGRLDAFAPFSKKIH 304

Query: 394 IDIDSAEIGKNKTPHVSVC GDVKLALQGM---NKVLENRAEELKLD FGVWRNENLVQKQK 450
+D+D++ I K V + GD L+ M + L + ++ +++ W N+++ K +
Sbjct: 305 VDVDASSINKVVKVDVGILGDCAAVLEEMLAQWRALPKQPKDRME--DWFNKISRWKS R 362

Query: 451 FPLSFKTFGEAIPPQYAIKVLDE-LTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGG 509
L++ G I PQYA++ L E D K ++T VGQHQMWAQ++ + +P +W++SGG
Sbjct: 363 DCLAYWPSGTIIKPQYAVQRLYEACKDRKTFVTTEVGQHQMWAQYFKFDEPNRWMTSGG 422

Query: 510 LGAMGFGLPAAIGASVANPD AIVVDIDGGSFIMNVQELATIRVENLPVKVLLNNQHLG 569
LG MG+GLPAAIG +ANPD +V+DI G+ S +MN+QE++T LPVK+ +LNN+++G
Sbjct: 423 LGTMGYGLPAAIGTQLANPDGLVIDIAGEASILNMNMQEMSTAVQYRLPVKIFILNNEYMG 482

Query: 570 MVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTML 629
MV QW++ + + + ++ E P+ + A A G R K +L AIQ ML
Sbjct: 483 MVRQWQELLHGSRYSQSY-----SESLPDFVKLAEAYGAKGIRCEKPGELDAAIQEML 535

Query: 630 DTPGPYLLDVICPHQEHVLPMPINGGTFNDVI 661
D GP + D I +E+ PMIP+G N+++
Sbjct: 536 DYDGPVIFDCIVDKKENC FPMIPSGKAHNEML 567

>ref|YP_706419.1| acetolactate synthase 1 catalytic subunit [Rhodococcus sp. RHA1]
gb|ABG98261.1| acetolactate synthase large subunit [Rhodococcus sp. RHA1]
Length = 647

Score = 510 bits (1314), Expect = e-142, Method: Compositional matrix adjust.
Identities = 283/584 (48%), Positives = 371/584 (63%), Gaps = 15/584 (2%)

Query: 90 RFAPDQPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVF 149
+ AP++ GA +V ALE V+TVF PGGA + ++ L S +R+VL RHEQG
Sbjct: 34 QLAPER-VSGAQSVVRALEELEVDTVFGIPGGAVLPVYDPLFDSKKVRHVLVRHEQGAGH 92

Query: 150 AAEGYARSSGKPGICIA TSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQET 209
AA GYA+++GK G+C+ATSGPGATNLV+ LADA +DSVP+VAITGQV R +IGTDAFQE
Sbjct: 93 AATGYAQTGKVGVC MATSGPGATNLVTPLADAQMDSVPVVAITGQVGRSLIGTDAFQEA 152

Query: 210 PIVEVTRSITKHNYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQ 269
I +T ITKHN+L+ D DIPRII EAF+LA+SGRPG VLVD+PKD+ Q +W
Sbjct: 153 DISGITMPITKHNF LITDGV DIPRIIAEAFYLASSGRPGAVLVDIPKDVLAQTTF SWPP 212

Query: 270 AMKLPGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLN--SSDELGRFVELTGIP 327
M+LPGY R P + + RLI+++K PVLYVGGG + SS EL ELTGIP
Sbjct: 213 EMRLPGY--RPVTKPHGKQVREAA RLIADAKHPVLYVGGGVKSESSPELLELAELTGIP 270

Query: 328 VASTLMGLGSPYPCDDELSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRVTGKLEAFAS 387
V +TLM G++P L+ M GMHGT V A A++ SDLL+ G RFDDRVTG+L++FA
Sbjct: 271 VVTTLMARGAFPSHTLNC GMPGMHGTVA AVALQRSDLLITL GARFDDRVTGQLDSFAP 330

Query: 388 RAKIVHIDIDSAEIGKNKTPHVSVC GDVK-LALQGMNKVLENRAEELKLD FGVWRNENLV 446
AK++H DID AEIGKN+ V + GD K + ++ + + + A LD W L+
Sbjct: 331 DAKVIHADIDPAEIGKNRYADVP IVDGCKEIVELIEAIKADLATGTTLDL TEWWAYLDG 390

Query: 447 QKQKFPLSFKTFGE-AIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWL 505
++ +PLS+ + A+ P+Y I+ + +L AI GVGQHQMWAQF NY+KPR WL
Sbjct: 391 IRRTYPLSYDRPSDGAL SPEYVIQAVGKLAGPD AYCAGVGQHQMWAQFVNYEKPRTWL 450

Query: 506 SSGGLGAMGFGLPAAIGASVANPD AIVVDIDGGSFIMNVQELATIRVENLPVKVLLNN 565
+SGGLG MG+ +PAA+GA + PD V IDGDG F M QELAT +E +P+KV L+NN
Sbjct: 451 NSGGLGTMGYAVPAAMGAKMGPDPTEVWAIDGDCFQMTNQELATCALEGIPKVALINN 510

Query: 566 QHGLMVMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAI 625
+LGMV QW+ FY ++T LG P+ + A A G RV ++ D+ AI
Sbjct: 511 GNLGMVRQWQTLFYDERYSNTNLGTHGAIR--IPDFVKLAEALGCHGIRVEREEDVEAAI 568

Query: 626 ---QTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVITEGDG 666
Q + D P ++D I V PM+ GT ND I G
Sbjct: 569 REAQAINDK--PVVIDFIVGADAQVWPMV-AAGTSNDEIMAARG 609

>gb|AAL99356.1| acetohydroxy acid synthase large subunit; acetolactate synthase
large subunit [Geobacillus stearothermophilus]
Length = 572

Score = 510 bits (1313), Expect = e-142, Method: Compositional matrix adjust.
Identities = 262/566 (46%), Positives = 369/566 (65%), Gaps = 19/566 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
G+ +L+EAL+ + VE +F YPGA + ++ L ++ + +VL RHEQG + AAEGYAR S
Sbjct: 16 GSMMLIEALKAEQVEVIFGYPGGAVLPLYDELYKAG-VFHVLTREQGAIAHAAEGYARIS 74

Query: 159 GKPGICATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GKPG IATSGPGATN+V+GL DA++DS+PLV TGQV +IG+DAFQE +V +T I
Sbjct: 75 GKPGFVIATSGPGATNIVTGLTDAMMDSLPLVVFTGQVATSVIGSDAFQEADVVGITMPI 134

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNY V D+ ++P+II+EAF +AT+GRPGPVL+D+PKDI +++++ + LPGA
Sbjct: 135 TKHNYQVRDISELPKIIKEAFHIATTGRPGPVLIDIPKDIITTAEGEFYDEEVCLPGYQP 194

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLMGLG 336
P + ++V +S+SK+PV+ G G L +++++EL ++ E IPV TL+GLG
Sbjct: 195 T--TQPNHWQIRRLVEAVSQSRPVLILAGAGVLHADAANELRQYAEQQNIPVVHTLLGLG 252

Query: 337 SYPCDDESLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVHIDI 396
+P D L L M GMHGT AN A+ DLL+ G RF DRVGT L+ FA +A + HIDI
Sbjct: 253 GFPADHPLFLGMAGMHTYTANMALYECDDLINIGARFADRVGTNLKYFAPKATVAHIDI 312

Query: 397 DSAEIGKNKTPHVSVCGDVKLALQGMNKVLENRAEELK-LDFGVWRNELNVQKQKFLPLSF 455
D AEIGKN + + D K ALQ E A++ K D W +LN K++FPL +
Sbjct: 313 DPAEIGKNVPTKIPIVSDAKALQ-----ELIAQQGKPADNAAWLEQLNEWKRRFPLHY 366

Query: 456 KTFGEAIPPQYAIKVLDLTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGF 515
+ I PQ I+++ ELT+G+AI++T VGQHQMWAQ+Y + +P +W++SGGLG MGF
Sbjct: 367 EPEAGTIKPKLIEMIYELTNGEAIVTVDVGQHQMWAQYYKFNRPNRWVTSGLGTMGF 426

Query: 516 GLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWE 575
GLPAAIGA +A+ A VV I GDG F M +QEL+ IR LP+K++++NNQ LGMV QW+
Sbjct: 427 GLPAAIGAQLADRSATVVSIVDGGFQMTLQELSVIRELGLPIKIVVNNQALGMVRQWQ 486

Query: 576 DRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPY 635
+ FY+ +H+ + + P+ + A GIP R +A+ E ++ GP
Sbjct: 487 ELFYEKRYSHSLIPN-----HPDFVKLAEPYGIPGLRAKTEAESAEVLKQAFAMDGPV 539

Query: 636 LLDVICPHQEHVLPMPNGGTFNDVI 661
LLD E+V PM+ G ++++
Sbjct: 540 LLDHFVRADENVYPMVSPGKGLHEMV 565

>ref|YP_001211077.1| thiamine pyrophosphate-requiring enzymes [Pelotomaculum
thermopropionicum SI]
dbj|BAF58708.1| thiamine pyrophosphate-requiring enzymes [Pelotomaculum
thermopropionicum SI]
Length = 555

Score = 510 bits (1313), Expect = e-142, Method: Compositional matrix adjust.
Identities = 270/567 (47%), Positives = 374/567 (65%), Gaps = 24/567 (4%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA +L+++LE V+T+F YPGG ++ I+ AL S +R++L RHEQG AA+GYAR++
Sbjct: 8 GAQVLIKSLEAANVDITFGYPGGQALPIYDALY-DSEVRHILTRHEQGAHAADGYARAT 66

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GKPG+C+ATSGPGATNLV+G+A+A +DSVPLVAITGQVPRR++G D+FQE IV +T I
Sbjct: 67 GKPGVCLATSGPGATNLVTGIANAYMDSVPLVAITGQVPRRLGRDSFQEADIVGITMPI 126

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQ--AMKLPGY 276
TKH+Y V D ++ R+++EAF +AT+GRPGPVL+DVP DI LA +E+ + LPGY
Sbjct: 127 TKHSYHVEDPSELARVVKEAFHIATTGRPGPVLIDVPSDI--SLAKVEYEEPEGELFLPGY 184

Query: 277 MSRMPPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFVELTGI--PVASTLMG 334
+ P + R I+ES++P++Y GGG + S + PV +TLMG
Sbjct: 185 RPLVDGDP--VQVAAAAAIAESERPLIYAGGGVVTSGAHEELLRLAELLMAPVCTTLMG 242

Query: 335 LGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIVHI 394
L +P + LSL MLGMHGT YAN+AV DLL+A G RFDDRVTGKLE FA A+I+HI
Sbjct: 243 LSGFPNGHPLSLGMLGMHGT KYANFVCECDLLIAGGARFDDRVTGKLETFAPPEARIIHI 302

Query: 395 DIDS AEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKFP LS 454
DID AEIGKN + + GDVK L + ++L E WR ++ K+++PL+
Sbjct: 303 DIDPAEIGKNVRVDIPIVGDVKRVLSQLLEILRPGLRE-----AWREKIEAWKEYPLT 356

Query: 455 FKTFGEAIP PQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMG 514
+ G + PQ I+ + LT+GKA I+T VGGHQMWA AQ+Y + +PR +++SGGLG MG
Sbjct: 357 YCEQGR-LKPQAIIREIYRLTEGKARITTEVGQHQMWAQYYTFTPRPSFITSGGLGTMG 415

Query: 515 FGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQW 574
FG+PAAIG V PD V DI GDGS MN+QEL T LP+ V ++NN LGMV QW
Sbjct: 416 FGMPAAIGVQVGPDETVFDIAGDGSIQMNIQELCTAVNYELPINVAIINNGLGMVRQW 475

Query: 575 EDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGP 634
++ FY NR ++ Q + P+ + A A G RVTKKA++ A++ + + P
Sbjct: 476 QEFFY--NRRYS-----QSELRNPDFVKLA EAYGAEGIRVTKKAEVAPALEQAIRSAKP 527

Query: 635 YLLDVICPHQEHVLP MIPNGGTFNDVI 661
++D + +++VLPM+P GG+ + +I
Sbjct: 528 VMIDFVVDREDNVLPMPVPPGSLDKMI 554

>ref|YP_431088.1| acetolactate synthase, large subunit [Moorella thermoacetica ATCC
39073]
gb|ABC20545.1| acetolactate synthase, large subunit [Moorella thermoacetica ATCC
39073]
Length = 569

Score = 510 bits (1313), Expect = e-142, Method: Compositional matrix adjust.
Identities = 272/571 (47%), Positives = 381/571 (66%), Gaps = 21/571 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSS 158
GA+I+V+AL+ +GV+TVF PGG+ + ++ L +SIR++L RHEQ AA+GYAR+S
Sbjct: 16 GAEIIVQALQAEGVDTVFGIPGGSVLPYHELA-VASIRHILTRHEQAAAAHADGYARAS 74

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GKPG+CIATSGPGATNLV+G+A+A +DS+PLVAITGQV MIG D+FQE I +T I
Sbjct: 75 GKPGVCIATSGPGATNLVTGIANAYMDSIPLVAITGQVSPMIGHDSFQEADITGITLPI 134

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TK NYLV +V D+ I EAF++AT+GRPGPVL+D+PKDI Q A+ + + LPGY
Sbjct: 135 TKANYLVKNVHDLAATIHEAFYIATTGRPGPVLIDIPKDIITQRALFRYPRLHLPGYRC 194

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSS--DELGRFVELTGIPVASTLMGLG 336
++ P + Q I ++KP+L++GGG + S +E+ + E IPV ++MG G
Sbjct: 195 KV--QPHALQVAQAAAAIGAAEKPLLFIGGGVITSEAHEEVRQLAEGQDIPVVMSSMMGKG 252

Query: 337 SYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIVHIDI 396
+P L + M+GMHGT ANYA+ +DL++ GVRFDDRVTGK+EAFA +AKI+HIDI
Sbjct: 253 GFPETHPLFVGMVGMHGTAAANYAMCETDLIIIGVGVRFDDRVTGKVEAFAPKAKI+HIDI 312

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLD FGVWRNELNVQKQKFP LSF 456
D+AEIGK H+ + D + QG+ +LE + K D WR ++ +++ PL ++
Sbjct: 313 DAAEIGKVQAHIPIVSDAR---QGLAAILEKLSG--KGDHQAQRQIRRWQEENPLRYE 367

Query: 457 TFGEAIPPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLGAMGFG 516
G + PQY ++ L LT G+AI T VGQHQMWA Q+Y +PR +LSS GLG MGFG
Sbjct: 368 KSG--LKPQYVLEELYNLTGQAIICTDVGQHQMWAQYYPPLSRPRAFLSSCGLGTMGFG 425

Query: 517 LPAAIGASVANPDIAIVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQWED 576
+PAA+GA+VA P +V I GDGSF MN+QELATI LP+K++++NN +LGMV QW++
Sbjct: 426 VPAAMGAAVARPGEPIVVITGDGSFQMNIQELATISHYQLPLKIIIMNGYLGMVRQWQE 485

Query: 577 RFYKANRAHT-FLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPGPY 635
F+ A++ LG+ P+ + A A IP V + ++ A++ L GP+
Sbjct: 486 FFFNRRYAYSEMLGN-----PDFVKVAEAYRIPGRLVNESREVPALAEALAAEGPF 537

Query: 636 LLDVICPHQEHVLPMPINGGTTFNDVITEGDG 666
L+DV +E+V PM+P GGT N ++T G G
Sbjct: 538 LVDVRIDREENVFPMPVPPGTLNKMVTGGKG 568

>ref|YP_001487695.1| acetolactate synthase catalytic subunit [Bacillus pumilus SAFR-032]
gb|ABV63135.1| acetolactate synthase large subunit [Bacillus pumilus SAFR-032]
Length = 574

Score = 510 bits (1313), Expect = e-142, Method: Compositional matrix adjust.
Identities = 267/570 (46%), Positives = 374/570 (65%), Gaps = 18/570 (3%)

Query: 95 QPRKGADILVEALERQGVETVFAYPPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGY 154
Q GA +L+EAL+R+ VE +F YPGA + I+ + S + +VLPHEQG + AAEGY
Sbjct: 16 QTMNGALMLIEALKREKVEVIFGYPGGAVLPIYDKI-YDSGLFHVLPHEQGAIHAAEGY 74

Query: 155 ARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEV 214
AR SGKPG+ IATSGPGATNLV+G+ADA++DS+PLV TGQV +IG+DAFQE ++ +
Sbjct: 75 ARVSGKPGVVIATSGPGATNLVTGIADAMIDSLPLVFTGQVATSVIGSDAFQEADVGLGI 134

Query: 215 TRSITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLP 274
T ITKH+Y V + E++P +I+EAF +AT+GRPGPVL+D+PKD+ ++Q + LP
Sbjct: 135 TMPITKHSYQVRNPEELPGVIKEAFHIATTGRPGPVLIDIPKDVAGIEGTFEYDQPIDLP 194

Query: 275 GYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLN--SSDELGRFVELTGIPVASTL 332
GY ++ P + ++V +S +KKPV+ G G L+ +S+EL ++VE IPVA TL
Sbjct: 195 GYQPKV--EPNYLQIRKLVEAVSRAKPKVILAGAGVLHGKASEELRQYVEQQQIPVAHTL 252

Query: 333 MGLGSYPCDDELSDLHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKIV 392
+GLG +P L L M GMHGT AN A+ DLL++ G RFDDRVTG L FA AK+
Sbjct: 253 LGLGGFPAKHPLFLGMAGMHGTAAANMALHQCDDLISIGARFDDRVTGNLHFAKHAKVA 312

Query: 393 HIDIDSAEIGKNKTPHVSVCDDVKKLQGMNKVLENRAEELKLDGFWVRNELNVQKQKFP 452
HIDID AEIGKN H+ V GD KL LQ + K + E + W+N+L+ K+++P
Sbjct: 313 HIDIDPAEIGKNITHIPVVGDSKLVQELIKQDQKQGESDE-----WKNQLDQWKEEYP 367

Query: 453 LSF-KTFGEAIPPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLG 511
L + + E PQ I+ + + T G+AI++T VGQHQMWAQFY ++ +W++SGGLG
Sbjct: 368 LWYVNEAEAGFKPKLIEYIHQFTKGEAIVATDVGQHQMWAQFYPFENADKQVTSGLG 427

Query: 512 AMGFGLPAAIGASVANPDIAIVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMV 571
MGFGLPAAIGA +A+ +A VV I GDG F M +QELA IR NLPVKV++LNN LGMV
Sbjct: 428 TMGFGLPAAIGAQLADQEATVVAILGDGGFQMTLQELAVIRELNLPVKVIVLNNHSLGMV 487

Query: 572 MQWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLDT 631
QW++ FY+ +++ + P+ + + A GI R++ + +E ++ L +
Sbjct: 488 RQWQEIFYEERYSYSKFSEQ-----PDFVKLSEAYGIKIRISSDEEAKKLEALTS 540

Query: 632 PGPYLLDVICPHQEHVLPMPINGGTTFNDVI 661
P +DV E V PM+ G ++++
Sbjct: 541 REPVFIDVNVARDEKVFPMVAPGKGLHEMV 570

>ref|YP_001416393.1| acetolactate synthase, large subunit, biosynthetic type
[Xanthobacter autotrophicus Py2]
gb|ABS66736.1| acetolactate synthase, large subunit, biosynthetic type
[Xanthobacter autotrophicus Py2]
Length = 601

Score = 509 bits (1312), Expect = e-142, Method: Compositional matrix adjust.
Identities = 259/571 (45%), Positives = 366/571 (64%), Gaps = 19/571 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA++++ A QGVE F YPGA + I+ AL + ++I ++L RHEQ V AAEGYARSS
Sbjct: 22 GAEMVMRAFADQGVHEFFGYPGGAVLPIYDALFQQNAIEHILVRHEQA AVHAAEGYARSS 81

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ + TSGPGATN V+GL DAL+DS+PLV ITGQV +IG DAFQE V +TR
Sbjct: 82 GKVGVVLVTSGPGATNAVTLTDLMDSIPLVCITGQVATHLIGNDAFQECDTVGITRPC 141

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNYLV DV D+ R++ EAF++A +GRPGPV+VD+PKD+Q + ++ Y
Sbjct: 142 TKHNYLVDRVNDLARVLHEAFYVAQNGRPGPVVDIPKDVQFATGTIYIGRENIQHKTYP 201

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDELGRFV---ELTGIPVASTLMG 334
++ ED+ + V +I+ +KKP+ Y GGG +NS E R + LTG+PV STLMG
Sbjct: 202 KLKA--EDAQISAAVEMIAGAKKPIFYTGGGVINSGPEASRLRELARLTGVPVTSTLMG 259

Query: 335 LGSYPCDELDELHMLGMHGTVYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIVHI 394
LG++P + L MLGMHGT AN A+ D+++ G RFDDR+TG+L+AFA +K +HI
Sbjct: 260 LGAFPAANRQWLGMMLGMHGTYEANMAMHDCDVMVCIGARFDDRITGRDLAFAPGSKKIHI 319

Query: 395 DIDSAEIGKNKTPHVSVCGLDALQGMNKVLENRAEELKLD---FGVWRNELNVQKQKF 451
DID + I KN + + GD L M + R+ LK+D W ++ + +
Sbjct: 320 DIDPSSINKNVKVDLPIIGDCTRVLADMVEAWNARS--LKIDQPALAAWWTQIERWRSRN 377

Query: 452 PLSFKTFGEAIPQYAIKVLDELTDGKAI-ISTGVGHQMWAQFYNYKKPRQWLSSGGL 510
L+++ E I PQ+AI+ L E T K + IST VGHQMWAQF+ +++P +W++SGGL
Sbjct: 378 CLAYRPSDEIIPQFAIERLYEATKDKDVYISTEVGHQMWAQFFRFEENRWMTSGGL 437

Query: 511 GAMGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
G MG+GLPAAIGA A+P+A+ +DI G+ S +MN+QE++T +LPVK+ +LNN+++GM
Sbjct: 438 GTMGYGLPAAIGAQAHPNALCIDIAGEASILNMNMQEMSTAVQFDLPVKIFILNNRYMGM 497

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKADLREAIQTMLD 630
V QW++ + +H++ E P+ + A A G R K DL AIQ M++
Sbjct: 498 VRQWQELLHGGYSHSY-----SEALPDFVKLADAYGGVGIRCEKPGDLDAAIQEMIN 550

Query: 631 TPGPYLLDVICPHQEHLVPMIPNGGTNDVI 661
P + D I QE+ PMIP+G N++I
Sbjct: 551 VKRPVIFDCIVDQEQENCFFMIPSGRAHNEMI 581

>ref|YP_902220.1| acetolactate synthase, large subunit, biosynthetic type [Pelobacter
propionicus DSM 2379]
gb|ABL00163.1| acetolactate synthase, large subunit [Pelobacter propionicus DSM
2379]
Length = 566

Score = 509 bits (1312), Expect = e-142, Method: Compositional matrix adjust.
Identities = 263/571 (46%), Positives = 365/571 (63%), Gaps = 20/571 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA IL+E L ++GV+TVF YPGG + ++ L IR+++PRHEQ G AA+GYAR++
Sbjct: 5 GARILLECLMKEGVDTVFGYPGGTVLNVYDELFGCKEIRHIMPRHEQAGTHAADGYARAT 64

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ IATSGPGATN V+G+A A +DS+P+V ITGQVP +IG DAFQE IV +TRS
Sbjct: 65 GKVGVVAIATSGPGATNTVTGIATAYMDSIPMVIITGQVPTALIGNDAFQEVDIVGITRSC 124

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHN+LV DV DI II++AF++A +GRPGPVLVD+PKD+Q + +++L Y
Sbjct: 125 TKHNFLVKDVNDIAPIIKKAFYIARTGRPGPVLVDLPKDVQIAKTEFCYPESELRSY-- 182

Query: 279 RMPKPPEDSHLEQIVRLIS---ESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLM 333
KP H Q+ + +S S +PV+YVGGG + N++ EL L IPV +TLM
Sbjct: 183 ---KPTTGGHPRQVSKAVSMLLASHRPVMYVGGGVILSNAAPELTALSRLSIPVTTTLM 239

Query: 334 GLGSPCDDELSDLHMLGMHGTVYANYAVEHSDLLAFGVFRFDDRVTKLEAFASRAKIV 393
GLG++P DD SL MLGMHG AN A+ HSDL++A G RFDDRVTKG++ FA AKI+H
Sbjct: 240 GLGAFFGDDVNSLGMMLGMHGAYCANMAMTHSDLIVAVGARFDDRVTKGVDTFAPHAKIIH 299

Query: 394 IDIDSAEIGKNKTPHVSVCADVKLALQGMNVLENRAEE---LKLDGFWVRNENLVQKQK 450
ID+D I KN + + GDV+ L M K +E + + W ++ K+K
Sbjct: 300 IDVDPTSIKNNVRVDLPVGDVDRDLTKMIKKVEKSEGDQAAYRESLAPWHEQIAGWKEK 359

Query: 451 FPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGL 510
P+SF I PQ+ I+ L EL+D AI+ST VGQHQMW AQF+++ PR L+SGGL
Sbjct: 360 HPVSFTRSSAVIKPQFVIQKRELSDRDAIVSTDVGVGQHQMWTAQFFSFTGPRTLLTSGGL 419

Query: 511 GAMGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGM 570
G MGFLPAA+GA A P V+ I GDG MN+QE+AT+ LPVK++++NN LGM
Sbjct: 420 GTMGFLPAAAGAAAFPRQVIAICGDDGQIMNIQEMATLVQNRLPVKIVIINNQLGM 479

Query: 571 VMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLD 630
V QW++ F+ + + L E+ + + A A G +K +++ I+
Sbjct: 480 VRQWQEMFFDKRYSQSCL-----ELPIDYIKLADAYGAKGFVASKPSEVETVIRQGFA 532

Query: 631 TPGPYLLDVICPHQEHVLPMPINGGTFNDVI 661
PGP +++ +E VLPMP+P+G + N+++
Sbjct: 533 EPGPVIMEFRVAREEKVLPMPVPSGASLNEML 563

>ref|YP_080105.1| acetolactate synthase catalytic subunit [Bacillus licheniformis
ATCC 14580]
ref|YP_092522.1| acetolactate synthase catalytic subunit [Bacillus licheniformis
ATCC 14580]
gb|AAU24467.1| acetolactate synthase IlvB [Bacillus licheniformis ATCC 14580]
gb|AAU41829.1| IlvB [Bacillus licheniformis DSM 13]
Length = 574

Score = 509 bits (1311), Expect = e-142, Method: Compositional matrix adjust.
Identities = 270/570 (47%), Positives = 370/570 (64%), Gaps = 18/570 (3%)

Query: 95 QPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGY 154
Q GA +L+EAL+++ VE ++ YPGA + I+ L S + +VL RHEQG + AAEY
Sbjct: 16 QTMAGASMLIEALKQENVEVIYGYPGGAVLPYDKL-YGSGMFHVLTRHEQGAIHAAEGY 74

Query: 155 ARSSGKPGICIAATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEV 214
AR SGKPG+ IATSGPGATNLV+GLADA++DS+PLV TGQV +IG+DAFQE ++ +
Sbjct: 75 ARISGKPGVVIATSGPGATNLVTGLADAMIDSLPLVFTGQVATSVIGSDAFQEADVIGI 134

Query: 215 TRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLP 274
T ITKH+Y V + ED+PRII+EAF +AT+GRPGPVL+D+PKDI ++ + LP
Sbjct: 135 TMPITKHSYQVRNAEDLPRIIEAFHIAATTGRPGPVLIDIPKDIADVVEGEFRYDHDHILP 194

Query: 275 GYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLN--SSDELGRFVELTGIPVASTL 332
GY K P + ++V +S +KKPV+ G G L+ +S+EL +VE IPVA TL
Sbjct: 195 GYQPT--KEPNYLQIRKLVEAVSAKKPVILAGAGVLHGKASEELKNYVEQQQIPVAHTL 252

Query: 333 MGLGSPCDDELSDLHMLGMHGTVYANYAVEHSDLLAFGVFRFDDRVTKLEAFASRAKIV 392
+GLG +P D L L M GMHG AN A+ SDLL++ G RFDDRVTK L+ FA AK+
Sbjct: 253 LGLGGFPADHPLFLGMAGMHGTYAANMALYESDLLISIGARFDDRVTKNLKHFAYAKVA 312

Query: 393 HIDIDSAEIGKNKTPHVSVCADVKLALQGMNVLENRAEELKLDGFWVRNENLVQKQKFP 452
HIDID AEIGKN H+ V GD KL L +++++ + D W+ +L K ++P
Sbjct: 313 HIDIDPAEIGKNVHTHIPVVGDSKLVL---TELKQNGKPSASD--EWKKQLAAWTEYP 367

Query: 453 LSF-KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLG 511
L + + E PQ I+ + T G+AI++T VGQHQMWAAQFY ++K +W++SGGLG
Sbjct: 368 LWYEENETEGFKPKLIEYIHYRTKGEAIVTTDVGQHQMWAAQFYQFKADRWTSGGLG 427

Query: 512 AMGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMV 571
MGFLPAAIGA +A+ DA VV I GDG F M +QEL+ I NLP+KV++LNN+ LGMV
Sbjct: 428 TMGFLPAAIGAQLADKDATVVSILGDGGFQMTLQELSVIHDNLNLPKVVVLNNRCLGMV 487

Query: 572 MQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDT 631
QW++ FY +H+ P+ + + A GI R+T + + E ++ L +
Sbjct: 488 RQWQEIFYDERYSKFTSQ-----PDFIKLSEAYGIKVRITSEEEAEKLEAALTS 540

Query: 632 GPGYLLDVICPHQEHVLPMPNGGTFNDVI 661
P ++DV E V PM+ G ++++
Sbjct: 541 NEPMVIDVQVAQAEKVFPMPVAPGKGLHEMV 570

>ref|YP_066505.1| acetolactate synthase isozyme III, large subunit (IlvI)
[Desulfotalea psychrophila LSv54]
emb|CAG37498.1| probable acetolactate synthase isozyme III, large subunit (IlvI)
[Desulfotalea psychrophila LSv54]
Length = 612

Score = 509 bits (1310), Expect = e-142, Method: Compositional matrix adjust.
Identities = 267/562 (47%), Positives = 360/562 (64%), Gaps = 15/562 (2%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSS 158
G+ +V+ L+ +GV+T+F YPGGA ++++ AL S+ I +VL RHEQG V AA+ +AR +
Sbjct: 51 GSRAIVQCLKEEGVQTIFGYPGGAVIDLYDALMDSTDIEHVLVRHEQGAVHAADAFARVT 110

Query: 159 GKP GICATSGPGATNLVSG LADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
G+ G+ + TSGPGATN V+G+A A LDS+PLV +TGQVPR +IG DAFQE IV +TR
Sbjct: 111 GEVGVALLTSGPGATNGVTGIATAYLDSIPLVVL TGQVPRALIGNDAFQEVDIVGITRPC 170

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDV PKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNYLV ED+ ++ EAF +A +GRPGPVLVD+PKDI L +KL Y
Sbjct: 171 TKHNYLVSKPEDLVPVLREAFHVAKTGRPGPVLVDLPKDILATLIDYPQIAPIKLDSYQP 230

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLMGLG 336
P + + +L+ ++K KPVLYVGGG + NS EL E IPV TLMGLG
Sbjct: 231 NY--KPHQGQITKACKLLMQAKKPVLYVGGGVILSN SHKELSALAEKLQIPVTMTLMGLG 288

Query: 337 SYPCDDELSLHMLGMHGT VYANYAVEHSDLLLA FGVRFD DRTVGKLEAFASRAKIVHIDI 396
++P +LS+ MLGMHG+ AN AV SDLL+A G RFDDRVTGKLE FAS+AKI+H+DI
Sbjct: 289 AFGSHDL SMGMLGMHGSYTANMAVAESDLLIAVGARFDDRVTGKLEDFASKAKIIHVDI 348

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAE---ELKLD FGVRNRELNVQKQKFP 452
D I KN V + D AL +N LE E E + W + ++ ++ P
Sbjct: 349 DPTSISKNVKVDVPIVADCLALTAINDWLEKCP EEEIAERRDAHKPWIDTVHNWTK EHP 408

Query: 453 LSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGLGA 512
+ + + G I PQ+ ++ +D LT G+AIIT VGQ+QMWA AQFY + PR +++SGGLG
Sbjct: 409 MRYNSNGSEIKPQFV VETIDRLTKGEAIIITTEVGQNMWA AQFYKFNHPRHFVTS GGLGT 468

Query: 513 MGFGLPAAIGASVANPDAIVVDIDGDGSFIMNVQELATIRVENLPVKVLLLNQHLGMVM 572
MGFGLPAAIGA +A PD IV+DI GDGS MN+QELAT R N VK+++LNN +LGMV
Sbjct: 469 MGFGLPAAIGA QMAFPDKIVIDIAGDSIQMNIQELATARQNNCNVKIVILNNGYLG MVR 528

Query: 573 QWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLDTP 632
QW++ FY A T + ++ P+ + A A G R TTK ++ + L T
Sbjct: 529 QWQELFYDKRYASTVM-----DVAPDFVKLA EAYGAVGLRATKKEEVESVLA EGLATD 581

Query: 633 GPYLLDVICPHQEHVLPMPNG 654
+++ + +E V PM+P G
Sbjct: 582 NVVIMEFLVAPEEGVYPMVPAG 603

>ref|ZP_00051726.2| COG0028: Thiamine pyrophosphate-requiring enzymes [acetolactate
synthase, pyruvate dehydrogenase (cytochrome),
glyoxylate carboligase, phosphonopyruvate decarboxylase]
[Magnetospirillum magnetotacticum MS-1]
Length = 595

Score = 508 bits (1308), Expect = e-142, Method: Compositional matrix adjust.
Identities = 258/572 (45%), Positives = 372/572 (65%), Gaps = 21/572 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSS 158
GA +++ A + QGV+T+F YPGGA + I+ AL ++I++VL RHEQG V AAEGYARSS
Sbjct: 12 GAQM VIRAFQDQGVDTLFGYPGGAVLP IYDALFDETTIQHVLVRHEQGAVHAAEGYARSS 71

Query: 159 GKPGICATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ + TSGPGATN+++GL DA+LDS+PLVA+TGQVP +IG+DAFQE V +TR
Sbjct: 72 GKVGVLVLTSGPGATNIITGLTDAMLDSIPLVAVTGQVPTHLIGSDAFQECDTVGITRHC 131

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNYLV +ED+PRI+ EAF+++A+ GRPGPV++D+PKD+ Q A + + + G+ +
Sbjct: 132 TKHNYLVKSIEDLPRILHEAFYVASHGRPGPVVIDLPKDV--QFATGVYSRPTQ-NGHKT 188

Query: 279 RMPKPPEDSH-LEQIVRLISESKKPVLYVGGGCLNSSDELGR---FVELTGIPVASTLM 333
P DS + + L++ +++PV Y GGG +NS E R V TG PV STL
Sbjct: 189 YNPPVKGDSEKIRAAIELMAGARRPVFYTGGGVINSGPEASRLRELVAETGFPVTSTLM 248

Query: 334 GLGSPYCDDELSTHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIVH 393
GLG++P D+ L MLGMHGT AN A+ D+++ G RFDDR+TG+L+AFA +K +H
Sbjct: 249 GLGAFPASDDKFLGMLGMHGT YEANLAMHDCDVMICIGARFDDRITGRDLAFAPYSKKIH 308

Query: 394 IDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFGV---WRNELNVQKQK 450
+D+D++ I K V + GD L+ M + + RA + D G W N+++ K +
Sbjct: 309 VDVDASSINKVVKVDVGILGDCAAVLEEM--LAQWRALPKQPKGRMEDWFNKISRWKS 366

Query: 451 FPLSFKTFGEAIPQYAIKVLDE-LTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGG 509
L++ G I PQYA++ L E D K ++T VGQHQMWAQ++ + +P +W++SGG
Sbjct: 367 DCLAYWPSGTIIKPQYAVQRLYEACKDRKTFVTTEVGQHQMWAQYFKFDEPNRWMTSGG 426

Query: 510 LGAMGFLPAAIGASVANPDIAVVDIDGGSFIMNVQELATIRVENLPVKVLLNNQHLG 569
LG MG+GLPAAIG +ANPD +V+DI G+ S +MN+QEL+T LPVK+ +LNN+++G
Sbjct: 427 LGTMGYGLPAAIGTQLANPDGLVIDIAGEASILNMNQLSTAVQYRLPVKIFILNNEYMG 486

Query: 570 MVMQWEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTML 629
MV QW++ + + + ++ E P+ + A A G R K +L AIQ ML
Sbjct: 487 MVRQWQELLHGSRYQSQSY-----SESLPDFVKLA EAYGAKGIRCEKPGELDAAIQEML 539

Query: 630 DTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
GP + D + E+ PMIP+G N+++
Sbjct: 540 AYDGPVIFDCVVDKTENCFPMIPSGKAHNEML 571

>ref|ZP_03056016.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus
pumilus ATCC 7061]
gb|EDW20842.1| acetolactate synthase, large subunit, biosynthetic type [Bacillus
pumilus ATCC 7061]
Length = 574

Score = 508 bits (1308), Expect = e-142, Method: Compositional matrix adjust.
Identities = 266/570 (46%), Positives = 374/570 (65%), Gaps = 18/570 (3%)

Query: 95 QPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGY 154
Q GA +L+EAL+R+ VE +F YPGGA + I+ + S + +VLPRHEQG + AAEGY
Sbjct: 16 QTMNGALMLIEALKREKVEVIFGYPGGAVLPIYDKI-YDSGLFHVLP RHEQGAIHAAEGY 74

Query: 155 ARSSGKPGICATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEV 214
AR SGKPG+ IATSGPGATNLV+G+ADA++DS+PLV TGQV +IG+DAFQE ++ +
Sbjct: 75 ARVSGKPGVVIATSGPGATNLVTGIADAMIDSLPLVVTGQVATSVIGSDAFQEADVLGI 134

Query: 215 TRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLP 274
T ITKH+Y V + E++P +I+EAF +AT+GRPGPVL+D+PKD+ ++Q + LP
Sbjct: 135 TMPITKHSYQVRNPEELPGVIKEAFHIATTGRPGPVLIDIPKDVAGIEGTFEYDQPIDLP 194

Query: 275 GYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLN--SSDELGRFVELTGIPVASTL 332
GY ++ P + ++V +S +KKPV+ G G L+ +S+EL ++VE IPVA TL
Sbjct: 195 GYQPKV--EPNYLQIRKLVEAVSRAKPVILAGAGVLHGKASEELRQYVEQQQIPVAHTL 252

Query: 333 MGLGSPYCDDELSTHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIV 392
+GLG +P L L M GMHGT AN A+ DLL++ G RFDDRVTG L FA AK+
Sbjct: 253 LGLGGFPAKHPLFLGMAGMHGT YAAANMALHQCDLLISIGARFDDRVTGNLNFHFAKHAKVA 312

Query: 393 HIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFGVWRNELNVQKQKFP 452
HIDID AEIGKN H+ V GD KL L+ + K + E + W+N+L+ K+++P
Sbjct: 313 HIDIDPAEIGKNIHTHIPVVGDSKLVLEELIKQDGKQGESDE-----WKNQLDQWKEEYP 367

Query: 453 LSF-KTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLG 511
L + + E PQ I + + + T G+AI++T VGQHQMWAQFY ++ +W++SGGLG
Sbjct: 368 LWYVENEAEFGFKPQKLEIYIHQFTKGEAIVATDVGQHQMWAQFYFENADKWVTSGLG 427

Query: 512 AMGFGLPAAIGASVANPDAIVVDIDGGSFIMNVQELATIRVENLPVKVLLNNQHLMGV 571
MGFGLPAAIGA +A+ +A VV I GDG F M +QELA IR NLPVKV++LNN LGMV
Sbjct: 428 TMGFGLPAAIGAQLADQEATVVAI LGDGGFQMTLQELAVIRELNLPVKVIVLNNHSLGMV 487

Query: 572 MQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDT 631
QW++ FY+ +++ + P+ + + A GI R++ + +E ++ L +
Sbjct: 488 RQWQEIFYEERYSYSKFSEQ-----PDFVKLSEAYGIKIRISTDEEAKKLEALTS 540

Query: 632 PGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
P +DV E V PM+ G ++++
Sbjct: 541 REPVFIDVNVARDEKVFPMVAPGKGLHEMV 570

>ref|ZP_02169902.1| Acetolactate synthase [Bacillus selenitireducens MLS10]
gb|EDP83420.1| Acetolactate synthase [Bacillus selenitireducens MLS10]
Length = 579

Score = 508 bits (1307), Expect = e-142, Method: Compositional matrix adjust.
Identities = 260/570 (45%), Positives = 357/570 (62%), Gaps = 17/570 (2%)

Query: 95 QPRKGADILVEALERQGVETVFAYPGGASMEIHQALTRSS-SIRNVLP RHEQGGVFAAEG 153
QPR GADILVE+L +Q V+T+F YPGA + I+ AL RS ++L RHEQG + AEG
Sbjct: 19 QPRTGADILVESLLKQQVKTIFGYPGGAVLPIYDALYRSEGDHILTRHEQGAIIHAAEG 78

Query: 154 YARSSGKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVE 213
YAR + + + I TSGPGATNLV+G+ADA++DS+PLV ITGQV + GTDAFQE ++
Sbjct: 79 YARVTNEAAVIGTSGPGATNLVTGIADAMMDSLPLVITGQVATAVTGTDAFQEADVVMG 138

Query: 214 VTRSITKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKL 273
+T ITKHNY + D DIPRII EAF +A++GRPGPV+VD+PKDI + +A L
Sbjct: 139 ITTPIITKHNYQIQDAYDIPRIINEAFHIASTGRPGPVVDIPKDISAGIVTEKGPEAFHL 198

Query: 274 PGYMSRMPKPPEDSHLEQIVRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVAST 331
GY + P ++++ + +KKP++ G G L ++SD + +F E IPV ST
Sbjct: 199 QGYQPTI--KPNPMQIKKVAEALKHAKKPLILT GAGVLHGHASDAILQFAEACQIPVTST 256

Query: 332 LMGLGSYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTGKLEAFASRAKI 391
L+GLG++P D EL L M GMHGT +N A+ DLL+ G RFDDR+TG L FA A I
Sbjct: 257 LLGLGAFPGDHELFLGMAGMHGTYASNMAITECDLLINVGARFDDRLTG NLAHFAPEATI 316

Query: 392 VHIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWVRNELNVQKQKF 451
VH+DID AEIGKN + V D K A++ + K E D+ WR L +F
Sbjct: 317 VHVDIDPAEIGKNVPTDIPVSDSKAAVESIMKHTEATG-----DYSQWREHLQTYSAEF 371

Query: 452 PLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGGLG 511
PL F E + PQ+ I + ++T G AI++T VGQHQMWAQ+Y + +P +W++SGGLG
Sbjct: 372 PLWFNNPQEEMIPQWLISSIFDITKGDAIVTTDVGQHQMWSAQYYRFNRPRWVTSGLG 431

Query: 512 AMGFGLPAAIGASVANPDAIVVDIDGGSFIMNVQELATIRVENLPVKVLLNNQHLMGV 571
MGFG PAAIGA +A P+ V+ I GDG F M +QEL+ ++ LPVK++++NN LGMV
Sbjct: 432 TMGFGFPAAGAQLAKPEERVLAI VGDGGFQMTLQELSVLQERQLPVKIIIVNNGALGMV 491

Query: 572 MQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTMLDT 631
QW++ FY + + +G P+ + A + G+ ++ +A E L
Sbjct: 492 RQWQEAFYDKRYSESLGTQ-----PDFVKLADSYGVEGIKIESQAHFMEVAPEYLTN 544

Query: 632 PGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
P LLD QE+V PM+ G + ND+I
Sbjct: 545 DKPCLLDCRVLQQENVYPMVAPGKSINDMI 574

>ref|YP_001529918.1| acetolactate synthase, large subunit, biosynthetic type
[Desulfococcus oleovorans Hxd3]
gb|ABW67841.1| acetolactate synthase, large subunit, biosynthetic type
[Desulfococcus oleovorans Hxd3]
Length = 564

Score = 507 bits (1306), Expect = e-141, Method: Compositional matrix adjust.
Identities = 262/569 (46%), Positives = 366/569 (64%), Gaps = 17/569 (2%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA I+++ L+ + VET+F YPGGA ++++ L ++ ++L R EQG V AA+ YAR S
Sbjct: 5 GAQIMMKVLKEEKVETIFGYPGGAVLDVYNELL-NTDFAHILVRQEQGAVHAADAYARVS 63

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+C+ TSGPGATN ++G+A A DS+P+V TGQVP +IG DAFQE IV ++R
Sbjct: 64 GKTGVCLVTSFGPGATNTITGIASAYCDSIPVVIFTGQVPTPLIGNDAFQEVDIVGISRPC 123

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNYLV DV+D+ +I EAF++A SGRPGPVL+D+PKD+ + M L Y
Sbjct: 124 TKHNYLVKDVKDLAGVIREAFYIARSGRPGPVLIDMPKDVINAKTTYEPPKPMALKSYNP 183

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNS--SDELGRFVELTGIPVASTLMGLG 336
P L++++ L+ +KKPV++ GGG + S + EL RF + IPV STLMLGLG
Sbjct: 184 TY--EPNVKQLKKVIDLVKTAKKPVIFSGGGIIFSGAAKELTRFAKKARIPVTSTLMGLG 241

Query: 337 SYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKIVHIDI 396
++P D+L L M GMHGT AN ++ DLL+A GVRFDRTGK FA+ A IVHIDI
Sbjct: 242 AFPATDDLWLGMGMHGTYRANLSLSSCDLLIAGVRFDDRTGKTSEFAANATIVHIDI 301

Query: 397 DSAEIGKNKTPHVSVCGDVKLALQGMNKVLENR----AEELKLDGVRNENLVQKQKFP 452
D I KN + + GD K A+ +NK+ + +++K + W ++ K+ P
Sbjct: 302 DPTSIQKNVRVAIPVIGDCKAAMARLNKMADEDKDLLSDKVKKERTAWAKQIADWKKTKP 361

Query: 453 LSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGA 512
L++ T + I PQY ++ L ELT G+AIIT VGQ+QMWAAQ+Y+Y P Q+++SGGLG
Sbjct: 362 LAY-TQTDVIKQYVVEQLYELTKGQAIITTEVGQNMWAAQYHYHTWPGQFITSGGLGV 420

Query: 513 MGFGLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVM 572
MGFGLPAA+GA VA PD +V+DI GDGS MN+QE+ T NLPVK+ +LNN LGMV
Sbjct: 421 MGFGLPAAVGAQVAAPDKVVIDIAGDSIQMNIQEMMTAVSHNLPVKIAILNNGFLGMVR 480

Query: 573 QWEDRFYKANRAHTFLGDPAQEDEFIPNMLLFAAACGIPAARVTKKADLREAIQTMLDTP 632
QW++ FY A T + P+ + A A G R TK +++ + I+ L TP
Sbjct: 481 QWQELFYDRRYAWTDMAAA-----PDFVKLAAYGAVGLRATKPSSEVAKVIKKALATP 533

Query: 633 GPYLLDVICPHQEHVLPMPNGGTFNDVI 661
P ++D + +E+V PM+P G ++I
Sbjct: 534 KPVIIMDFVVEKEENVYPMVPAGSPITNMI 562

>ref|YP_359375.1| acetolactate synthase, large subunit, biosynthetic type
[Carboxydotherrmus hydrogenoformans Z-2901]
gb|ABB15575.1| acetolactate synthase, large subunit, biosynthetic type
[Carboxydotherrmus hydrogenoformans Z-2901]
Length = 552

Score = 507 bits (1305), Expect = e-141, Method: Compositional matrix adjust.
Identities = 275/567 (48%), Positives = 376/567 (66%), Gaps = 24/567 (4%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA IL++ LE GV+TVF YPGGA + I+ AL S I + L RHEQG AA+GYAR+S
Sbjct: 5 GAQILIKVLEDLGVDTVFGYPGGAVLPIYDAL-YDSKITHYLTRHEQGAHAADGYARAS 63

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+C ATSGPGATNLV+GLA A +DSVP+VAITGQV ++G D+EQE I +T I
Sbjct: 64 GKVGVCFATSGPGATNLVTGLATAYMDSVPVVAITGQVATSLGRDSFQEADITGITMPI 123

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNYLV D ++ + + EAF++A +GRPGPVL+D+PKD+ A + + ++LPGY
Sbjct: 124 TKHNYLVKDPGELAQTVEAFYIARTGRPGPVLIDIPKDVSAARARYEFPEKVELPGYKP 183

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLNSSDE--LGRFVELTGIPVASTLMGLG 336
+ P + + + + LI+ S++P+++ GGG +N+ E L F E PV ++LMGLG
Sbjct: 184 VL--TPGEEVNKAIALINSSERPLIFSGGGTVNAGAEQLLLAFAEKINAPVVASLMGLG 241

Query: 337 SYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFD DVRTGKLEAFASRAKIVHIDI 396
+P D L L MLGMHGT ANYAV D+L+A GVRFD DVRTG +++FA AKIVHIDI
Sbjct: 242 GFP GDHPLFLGMLGMHGT KPANYAVSECDVLI AVGVRFD DVRTG DVKS FAPNAKIVHIDI 301

Query: 397 DSAEIGKNKTPHVSVC GVDK LALQGMNKVLENRAEE--LKLD FGVWRNELNVQKQK FPLS 454
D AEI KN V + GDVK +L+ + K ++ + E LK FG+ K+K+PL+
Sbjct: 302 DPAEINKNVLEVPLVGDV KNSLELLIKGVKEKKPEKWLKYVFGL-----KEKYPLT 353

Query: 455 FKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGLGAMG 514
+ + PQ I+ L ++T G+AII T VGQHQMWA AQFY + KPR+++SSGGLG MG
Sbjct: 354 YNREC-GLKPQKVIETLYKITGGEAII VTDVGQHQMWA AQFYKFNKPRRFISSGGLGTMG 412

Query: 515 FGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLN NQHLGMVMQW 574
FGLPA IGA VA P+ V+ + GDGS MN QEL T+ N+PVKV++LNN +LGMV QW
Sbjct: 413 FGLPAGIGAQVARPEQQVIVVSGDGS IQMNSQELMTVAAYNIPVKV IILNNGYLG MVRQW 472

Query: 575 EDRFYKANRAHTFLGDPAQEDEFIPNM L LFAAACGIPAARVTKKADLREAIQTMLDTPGP 634
++ F++ +HT L + P+ + A A GI R+ K+ +L E + ++ GP
Sbjct: 473 QELFHQRRYSHTELKN-----PDFVKLADAYGIRGLRIKKEENLEEK LLEAINYAGP 524

Query: 635 YLLDVICPHQEHVLP MIPNGGTFNDVI 661
++DV +E+V PM+P GG + +I
Sbjct: 525 VVVDVWVDREENVFP MVPPGGAIHKMI 551

>ref|ZP_01288118.1| Acetolactate synthase, large subunit, biosynthetic type [delta
proteobacterium MLMS-1]
gb|EAT05501.1| Acetolactate synthase, large subunit, biosynthetic type [delta
proteobacterium MLMS-1]
Length = 553

Score = 506 bits (1304), Expect = e-141, Method: Compositional matrix adjust.
Identities = 261/557 (46%), Positives = 348/557 (62%), Gaps = 15/557 (2%)

Query: 111 GVETVFAYPPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSSGKPGICIATSGP 170
GVE +F +PGGA ++++ L R+ + +VL RHEQ + AA+ Y R G+ G+ + TSGP
Sbjct: 4 GVEVIFGFPGG AVIDLYDELLRTDKLTHVLVRHEQA AIIHAADAYGRV RGEVGVALVTSGP 63

Query: 171 GATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTR SITKHNYLVMDVED 230
GATN V+G+A A DS+PLV TGQVP +IG DAFQE IV +TR +TKHNYLV ED
Sbjct: 64 GATNTVTGIASAYCDSIPLVVF TGQVPTMLIGNDAFQEVDIVGITRPVTKHNYLVKKPED 123

Query: 231 IPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLP GYMSRMPKPPEDSHLE 290
+ I EAF LA SGRPGPVLVD+PKD+ + +K+ Y R P +E
Sbjct: 124 LIPTIREAFHLARSGRPGPVLVDLPKDVIGAMVKYTEPKPIKMRTY--RPTYEPHPGQIE 181

Query: 291 QIVRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVASTLMGLG SYPCDDELSLHM 348
+ + I ++KKPVLYVGGG + N+S+EL + IPV TLMGLG++P D LS+ M
Sbjct: 182 KACKTILKAKKPVLYVGGGVINANASEELTALAKKLDIPVTMTLMGLGAFFGT DPLSMGM 241

Query: 349 LGMHGT VYANYAVEHSDLLAFGVRFD DVRTGKLEAFASRAKIVHIDIDSDAEIGKNKTPH 408
LGMHGT YAN AV H DLL+A G RFDDRTG+++AFA AKI+HIDID + I KN
Sbjct: 242 LGMHGTYYANMAVAHCDLLI AVGARFD DVRTGRIDAFAPHAKIIHIDIDPSSISKNVKVD 301

Query: 409 VSVCGDVKLALQGMNKVLEN---RAEELKLD FGVWRNELNVQKQK FPLSFKTFGEAIPP 464
+ + D AL MN N EE + W ++ K K PL + I P
Sbjct: 302 IPIVADCNHALAAMNSWFNNSQEFNQEEARQRHRPWHEQIK EWKNKHPLGYIEETNVIKP 361

Query: 465 QYAIKVLDELTDGKAIISTGVGQHQMWA AQFYNYKKPRQWLSSGGLGAMG FGLPAAIGAS 524
Q+ ++ L ELT G AII+T VGQ+QMWA AQFY + KPR +++SSGGLG MG+G PAAIGA
Sbjct: 362 QFVVQKLHELTGGNAIITTEVGQNQMWA AQFYFYNKPRHFM TSGGLGVMGYGFPA AIGA Q 421

Query: 525 VANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLN NQHLGMVMQWEDRFYKANRA 584
+A P+ +V+D+ GDGS MN+QELAT R PVK+ +LNN +LGMV QW++ FY A
Sbjct: 422 MAAPNEVVVIDVAGDGS IQMNIQELATARQYKCPVKIAILN NNYLG MVRQWQELFYDKQYA 481

Query: 585 HTFLGDPAQEDEFIPNM L LFAAACGIPAARVTKKADLREAIQTMLDTPGP YLLDVICPHQ 644
HT L ++ P+ + A A G R TK +++ I+ L T L+D + +
Sbjct: 482 HTTL-----DVAPDFVKLA EAYGAVGLRATKPSVEVPVKEALKTNNTVLMDFVISRE 534

Query: 645 EHVLPMPNGGTFNDVI 661
E V PM+P G +++
Sbjct: 535 EGVYPMVPAGKATTEML 551

>ref|YP_001261115.1| acetolactate synthase, large subunit [Sphingomonas wittichii RW1]
gb|ABQ66977.1| acetolactate synthase, large subunit [Sphingomonas wittichii RW1]
Length = 584

Score = 506 bits (1304), Expect = e-141, Method: Compositional matrix adjust.
Identities = 265/574 (46%), Positives = 362/574 (63%), Gaps = 17/574 (2%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSS 158
GADIL++AL GVE VF YPGA + I+ AL + + IR++L RHE G V AAEYARS+
Sbjct: 7 GADILIQALNDLGVEVVFYGGAVLPIYDALFKQNRIRHILVRHEAGAVHAAEGYARST 66

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GKPG+ + TSGPGATN V+G+ADALLDS+PLV +TGQV +IG+DAFQE V +TR
Sbjct: 67 GKPGVVLVTSGPGATNAVGTGIADALLDSIPLVLTGQVGTPLIGSDAFQECDTVGITRHC 126

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLP--GY 276
TKHNYLV D + +I EAF +ATSGRPGPV+VD+PKD+Q A LP GY
Sbjct: 127 TKHNYLVKDPALLGDVIHEAFHIATSGRPGPVVDLPKDVQVASAAYRKPSVQALPHKGY 186

Query: 277 MSRMKPPEDSHLEQIVRLISESKKPVLYVGGGCLN----SSDELGRFVELTGIPVASTL 332
++ P + +EQ V +I+ +++P+LY GGG +N +S L +TG PV STL
Sbjct: 187 RPQVKADP--TLIEQAVAMIAAAERPILYTG GGIINAGPLASQVLRRELARVTGAPVTSTL 244

Query: 333 MGLGSYPDCDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIV 392
MGLG++P L MLGMHGT AN A+ +DL++ G RFDDRVTG+L+AFA +K +
Sbjct: 245 MGLGAPPASSGQWLGMGMHGTYEANMAMNKADLIVCLGARFDDRVTRLDAPHSKKI 304

Query: 393 HIDIDSAEIGKNKTPHVSVC GDVKLALQGMNKVLENRAEELKLDGFWVRNENLVQKQKFP 452
H+DID + I K + + GDV A++ M K+ + + + D W +++ + +
Sbjct: 305 HVDIDRSSINKIVRADIGIVGDVGRAMEDMVKIWKAGQHQR-DLAAWYEQIDAWRARKS 363

Query: 453 LSFKTFGEAIPPQYAIKVLDELTDG-KAIIISTGVGQHQMWAQFYNYKKPRQWLSSGGLG 511
L F + I PQ AI+ L E T K II+T VGQHQMWAQ +++ P +WL+SGGLG
Sbjct: 364 LKFPASTKEIMPQLAIRKLWEATHALKPIITTEVGQHQMWAQHFDFEGPNKWLTSGLG 423

Query: 512 AMGFGLPAAIGASVANPD AIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMV 571
MG+GLPAAIGA + NP+A+V+DI G+ S MN+QEL T LPVKV +LNN+++GMV
Sbjct: 424 TMGYGLPAAIGAQLGNPNALVIDIAGEASIQMNIQELGTATQYRLPVKFILNNEYMGV 483

Query: 572 MQWEDRFYKANRAHTFLGDPAQEDEIFPNMMLFAAACGIPAARVTKKADLREAIQTMLDT 631
QW+D Y + + + + P+ + A A G + K +L I ML+
Sbjct: 484 RQWQDLTYAGRYSQSY-----SDALPDFVKLA EAYGWKGVLIEKPEELDAGIAAMLEH 536

Query: 632 PGPYLLDVICPHQEHVLPMPNGGTFNDVITEGD 665
GP ++D + PMIP+G D+I E D
Sbjct: 537 DGPVIVDCRVAKLANCFPMIPSGAAHTDMILEAD 570

>ref|YP_001757953.1| acetolactate synthase, large subunit, biosynthetic type
[Methylobacterium radiotolerans JCM 2831]
gb|ACB27270.1| acetolactate synthase, large subunit, biosynthetic type
[Methylobacterium radiotolerans JCM 2831]
Length = 591

Score = 506 bits (1304), Expect = e-141, Method: Compositional matrix adjust.
Identities = 259/572 (45%), Positives = 369/572 (64%), Gaps = 21/572 (3%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLP RHEQGGVFAAEGYARSS 158
GA++++ A + QGV+T+F YPGA + I+ AL +++++L RHEQG V AAEYARSS
Sbjct: 8 GAEMVIRAFQDQGVDTLFGYPGGAVLPIYDALFHQNAVKHILVRHEQGAHVHAAEGYARSS 67

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G + TSGPGATN+V+GL DA+LDS+PLV ITGQVP +IGTDAFQE V +TR
Sbjct: 68 GKVGCVLVTSGPGATNIVTGLTDAMLDSIPLVCITGQVPTHLIGTDAFQECDTVGITRHC 127

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNYLV ++D+PRI+ EAF++A +GRPGPV+VD+PKDI Q A +E+ ++ + +
Sbjct: 128 TKHNYLVKSIDDLPRILHEAFYVAANGRPVGVVDLPKDI--QFASGLYERP-EIASHKT 184

Query: 279 RMPKPPEDS-HLEQIVRLISESKKPVLYVGGGCLNSSDELGR---FVELTGIPVASTLM 333
P D+ + V L++ +++PV Y GGG +NS E R V TG P+ STLM
Sbjct: 185 YRPAVKGDADRIRAAVELMATARRPVFYTTGGGVINSPEASRLRLRELVRGTGFPITSTLM 244

Query: 334 GLGSPYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAKIVH 393
GLG+YP DE L MLGMHGT AN A+ D+++ G RFDDR+TG+L+AF+ +K +H
Sbjct: 245 GLGAYPGTDEKFLGMLGMHGT YEANLAMHECDVMICVGARFDDRITGRDLAFSPFSKKIH 304

Query: 394 IDIDSAEIGKNKTPHVSVCADVKLALQGM---NKVLENRAEELKLDGFGVWRNELNVQKQK 450
ID+D++ I K V + GD L M + L +R + LD W ++N K +
Sbjct: 305 IDVDASSINKVVKVDVGIVGDCASVLADMLEAWRALPSRPDTSNLD--PWFQKINAWKAR 362

Query: 451 FPLSFKTFGEAIPQYAIKVLDE-LTDGKAIISTGVGQHQMWAQFYNYKKPRQWLSSGG 509
L++ G I PQYA++ L E D + I+T VGGHQMWAQ++ Y +P +W++SGG
Sbjct: 363 DCLAYWPSGTIIKPQYAVQRLYEACKDRETYITTEVGQHQMWAQYFKYDEPNRWMTSGG 422

Query: 510 LGAMGFLPAAIGASVANPDIAVVDIDGGSFIMNVQELATIRVENLPVKVLLNNQHLG 569
LG MG+GLPAAIG +A+P+ +V+DI G+ S +MN+QE++T LP+KV +LNN+++G
Sbjct: 423 LGTMGYGLPAAIGTQLAHPNGLVIDIAGEASILNMNQEMSTAVQYRLPIKVFILNNEYMG 482

Query: 570 MVMQWEDRFYKANRAHTFLGDPAQEDEFIPNMLFAAACGIPAARVTKKADLREAIQTML 629
MV QW++ + + + ++ E P+ + A A G R K DL AI ML
Sbjct: 483 MVRQWQELLHGSRYSSQSY-----SESPLDFVKLAEAYGAKGMRCEKPGDLDGAIAEML 535

Query: 630 DTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
GP + D I E+ PMIP+G N+++
Sbjct: 536 AHDGPVIFDCIVDKTENCFFMIPSGKAHNEML 567

>ref|YP_001928031.1| acetolactate synthase, large subunit, biosynthetic type
[Methylobacterium populi BJ001]
gb|ACB83496.1| acetolactate synthase, large subunit, biosynthetic type
[Methylobacterium populi BJ001]
Length = 591

Score = 506 bits (1303), Expect = e-141, Method: Compositional matrix adjust.
Identities = 255/575 (44%), Positives = 372/575 (64%), Gaps = 27/575 (4%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
GA +++ A + QGV+T+F YPGGA + I+ AL ++I++VL RHEQG V AAEYARSS
Sbjct: 8 GAQMVRIRAFQDQGVDTLFGYPGGAVLPIYDALFDETTIQHVLVRHEQGAVHAAEGYARSS 67

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
GK G+ + TSGPGATN+V+GL DA+LDS+PLVA+TGQVP +IG+DAFQE V +TR
Sbjct: 68 GKVGVLVTSGPGATNIVTGLTDAMLDSIPLVAVTGQVPTHLIGSDAFQECDTVIGITRHC 127

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHNYLV +ED+PRI+ EAF++A+ GRPGPV++D+PKD+Q + + P +
Sbjct: 128 TKHNYLVKSIEDLPRILHEAFYVASHGRPGPVVIDLPKDVQFATGV-----YQRPSHNG 181

Query: 279 -RMPKPPEDSHLEQI---VRLISESKKPVLYVGGGCLNSSDELGR---FVELTGIPVAS 330
+ PP E+I V L++ +++PV Y GGG +NS E R V TG PV S
Sbjct: 182 HKTYNPPVQGDAAEKIRAAVELMAGARRPVFYTTGGGVINSPEASRLRLRELVAETGFPVTS 241

Query: 331 TLMGLGSPYPCDDELSLHMLGMHGT VYANYAVEHSDLLAFGVRFDDRVTKLEAFASRAK 390
TLMGLG++P D+ L MLGMHGT AN A+ D+++ G RFDDR+TG+L+AF+ +K
Sbjct: 242 TLMGLGAFPASDDKFLGMLGMHGT YEANLAMHDCDVMICIGARFDDRITGRDLAFSPYSK 301

Query: 391 IVHIDIDSAEIGKNKTPHVSVCADVKLALQGM---NKVLENRAEELKLDGFGVWRNELNVQ 447
+H+D+D++ I K V + GD L+ M + L + ++ +++ W N+++
Sbjct: 302 KIHVDVDASSINKVVKVDVGILGDCAAVLEMLAQWRALPKQPDKARME--DWFNKISRW 359

Query: 448 KQKFLSFKTFGEAIPQYAIKVLDE-LTDGKAIISTGVGQHQMWAQFYNYKKPRQWLS 506
K + L++ G I PQYA++ L E + K ++T VGGHQMWAQ++ + +P +W++
Sbjct: 360 KSRDCLAYWPSGTIIKPQYAVQRLYEACKNRKTFVTTEVGQHQMWAQYFKFDEPNRWMT 419

Query: 507 SGGLGAMGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQ 566
SGGLG MG+GLPAAIG +ANPD +V+DI G+ S +MN+QEL+T LPVK+ +LNN+
Sbjct: 420 SGGLGTMGYGLPAAIGTQLANPDGLVIDIAGEASILMNMQELSTAVQYRLPVKIFILNNE 479

Query: 567 HLGMMVQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQ 626
++GMV QW++ + + + ++ E P+ + A A G R K +L AIQ
Sbjct: 480 YMGMVRQWQELHGSRYSSQSY-----SESLPDFVKLAEEYGAKGIRCEKPGELDGAIQ 532

Query: 627 TMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
ML GP + D + E+ PMIP+G N+++
Sbjct: 533 EMLAYDGPVIFDCVVDKTENCFFMIPSGKAHNEML 567

>emb|CAJ72436.1| strongly similar to acetohydroxy acid synthase IilvB [Candidatus
Kuenenia stuttgartiensis]
Length = 565

Score = 506 bits (1303), Expect = e-141, Method: Compositional matrix adjust.
Identities = 266/573 (46%), Positives = 369/573 (64%), Gaps = 30/573 (5%)

Query: 97 RKGADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYAR 156
+ G+ IL+ AL R+GVE VF PGGA + + AL S I+ +L RHEQG AA+G+AR
Sbjct: 11 KTGSHILINALIREGVEYVFGIPGGAVLPLFDAL-YESQIKFILTRHEQGAGHAADGFAR 69

Query: 157 SSGKPGICIAATSGPGATNLVSGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTR 216
++GK G+C+ATSGPGATNL + +A A +DSVP+VA+TGQV +IG DAFQE I+ +TR
Sbjct: 70 ATGKVGVLATSGPGATNLTTAATAYMDSVPMVALTGQVKTFLIGNDAFQEVDDIIGITR 129

Query: 217 SITKHNLYLMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGY 276
ITKH+YLV DV+D+ R+++EAF+LA SGR GPVL+D+P D+ + LPGA
Sbjct: 130 PITKHSYLVKDVKDLARVVKEAFYLANSGRQGPVLIDLVDVDTMAECEIIPPEIDLPGY 189

Query: 277 MSRMKPPEPDSHLEQI---VRLISESKKPVLYVGGGCL--NSSDELGRFVELTGIPVAST 331
KP + ++ QI +I+ +++PVLY GGG + +S+ EL E IPV +T
Sbjct: 190 -----KPTYEGNIRQIKIAAEVINNARRPVLYTGGGIIASDSAKELLELAEKGNIPVTTT 244

Query: 332 LMGLGSYPCDDELSLHMLGMHGTVYANYAVEHSDLLAFGVRFDRTGKLEAFASRAKI 391
LMGLG +P + LSL MLGMHGT YAN+AV D+L+A G RFDDR+TGK++ FA AKI
Sbjct: 245 LMGLGGFPENHNLSLGMHGTAYANFAVTTCDILIAIGARFDDRITGKIDEFAPNAKI 304

Query: 392 VHIDIDSAEIGKNKTPHVSVCQGVKLLALQGMNK---VLENRAEELKLDGVRNENLVQK 448
+HIDID + I KN + V G + L+ +NK +E R W +++ K
Sbjct: 305 IHIDIDPSSISKNIKVDIPVVGQAQNTLRELNKHISFVERRE-----WFDKIKQWK 355

Query: 449 QKFPLSFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSG 508
++ PL++ G+ I PQY I+ + E T+G+AII+T VGQ+QMWWAAQ+Y Y KPR +LSSG
Sbjct: 356 EQNPLTYNNSGDLIKPQYVIEQIYEATNGEAIITTEVGNQMWWAAQYTYTKPRTFLSSG 415

Query: 509 GLGAMGFLPAAIGASVANPDAIVVDIDGDSFIMNVQELATIRVENLPVKVLLNNQHL 568
GLG MG+G PAAIGA + PD IVVDI GDGS MN+QEL+T+ N+PVK+++LNN +L
Sbjct: 416 GLGTMGYGFPAIGAQLGCPDKIVVDIAGDSIQMNIQELSTVVRNLNIPVKIVILNNGYL 475

Query: 569 GMVMQWEDRFYKANRAHTFLGDPAQEDEFNMLLFAAACGIPAARVTKKADLREAIQTM 628
GMV QW++ FY + L P+ + A + G + KK D+R ++
Sbjct: 476 GMVRQWQELFYDKRYSSVSLNGN-----PDFVKLAESYGAKGFLIEKKEDVRPTLEKA 528

Query: 629 LDTPGPYLLDVICPHQEHVLPMPNGGTFNDVI 661
T P ++D E+V PM+P+G + +I
Sbjct: 529 FFTKQPVMDFRVDNENVFMVPSGKPIHQMI 561

>ref|YP_176141.1| acetolactate synthase large subunit [Bacillus clausii KSM-K16]
dbj|BAD65180.1| acetolactate synthase large subunit [Bacillus clausii KSM-K16]
Length = 576

Score = 506 bits (1302), Expect = e-141, Method: Compositional matrix adjust.
Identities = 262/561 (46%), Positives = 366/561 (65%), Gaps = 23/561 (4%)

Query: 99 GADILVEALERQGVETVFAYPGGASMEIHQALTRSSSIRNVLPHEQGGVFAAEGYARSS 158
G++IL++AL +GVE +F YPGGA + + + + + ++L RHEQG + AAEGYAR +
Sbjct: 22 GSEILLKALASEGVEVIFGYPGGAILPTYDEIYKLG-MNHILARHEQGAHAAEGYARIT 80

Query: 159 GKPGICIATSGPGATNLVSGGLADALLDSVPLVAITGQVPRRMIGTDAFQETPIVEVTRSI 218
KPG+CI TSGPGATN+V+G+ADA++DS+P+V ITGQV ++IGTDAFQE ++ +T I
Sbjct: 81 QKPGVCIVTSGPGATNVVTGIADAMMDSLPMVVITGQVATKVI GTDAFQEADMLGITMPI 140

Query: 219 TKHNYLVMDVEDIPRIIEEAFFLATSGRPGPVLVDVPKDIQQQLAIPNWEQAMKLPGYMS 278
TKHN+ + +E++ + ++EAF +A SGRPGPVL+D+PKDI ++L I ++E+ + LPGY
Sbjct: 141 TKHNFQIRSIIELAQTVKEAFHIAVSGRPGPVLIDL PKDISEKLGIFDYEEPVHLPGYQP 200

Query: 279 RMPKPPEDSHLEQIVRLISESKKPVLYVGGGCLN--SSDELGRFVELTGIPVASTLMGLG 336
+ P + +++ E+K+PVL VG G L+ +S+EL F IPVA TL+GLG
Sbjct: 201 TV--KPNKQQIRKLLDKFKKRPVLLVGAGVLHAQASEELTAFARKFQIPVAQTLLGLG 258

Query: 337 SYPCDDSLHMLGMHGT VYANYAVEHSDLLLAFGVRFDDRTGKLEAFASRAKIVHIDI 396
++P ++EL L M GMHGT AN A+ SD L+ G RFDDR+TG LE FA A I HIDI
Sbjct: 259 AFPGEELHLGMAGMHGTYAANMALHKSDFLINIGSRFDDRLTGALEHFAPEACIAHIDI 318

Query: 397 DSAEIGKNKTPHVSVC GDVKLALQGMNK---VLENRAEELKLDGFWRNELNVQKQKFP 453
D AEIGKN + V GD K AL + K ++ E WR +++ K+ +PL
Sbjct: 319 DPAEIGKNVHVEIPVVGDAKEALAMLVKSGAIDEHDE-----WRKQVSDWKRDYPL 370

Query: 454 SFKTFGEAIPPQYAIKVLDELTDGKAIISTGVGQHQMWAAQFYNYKKPRQWLSSGGLGAM 513
F GE I PQ I+ L E T G+AI++T VGQHQMW AQ + + KP +W++SGGLG M
Sbjct: 371 WFHRDGEVIKQELIQKLYEHTKGEAIVTTDVGQHQMWTAQHFKFNKPNRWITSGGLGTM 430

Query: 514 GFGLPAAIGASVANPDAIVDDIDGDSFIMNVQELATIRVENLPVKVLLNNQHLGMVMQ 573
GFG PAAIGA +A P+ V+ I GD F M +QE++ ++ +LPVK++++NN LGMV Q
Sbjct: 431 GFGFPAAIGAQIAEPELPVLAITGDAGFQMTLQEMSILQELDLPVKIVIVNNASLGMVRQ 490

Query: 574 WEDRFYKANRAHTFLGDPAQEDEIFPNMLLFAAACGIPAARVTKKADLREAIQTMLDTPG 633
W+ RF+ +H+ P Q PN A A I A +V K + L EAI L PG
Sbjct: 491 WQQRFGHGERYSLSL--PIQ-----PNFAKLAEAYNIKAVKVDKLSMLDEAIAETLAHPG 543

Query: 634 PYLLDVICPHQEHVLPMPNG 654
P LL+V +E+V PM+ G
Sbjct: 544 PVLLEVCVAKEENVYPMVCPG 564

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
from WGS projects
Posted date: Oct 26, 2008 5:54 PM
Number of letters in database: 2,468,333,968
Number of sequences in database: 7,155,275

Lambda	K	H
0.319	0.137	0.406

Gapped		
Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 7155275
Number of Hits to DB: 2,988,339,135
Number of extensions: 131465858
Number of successful extensions: 327324
Number of sequences better than 1.0: 4618
Number of HSP's gapped: 314312
Number of HSP's successfully gapped: 5204
Length of query: 670
Length of database: 2,468,333,968
Length adjustment: 142
Effective length of query: 528
Effective length of database: 1,452,284,918
Effective search space: 766806436704
Effective search space used: 766806436704
Neighboring words threshold: 11

Window for multiple hits: 40

X1: 16 (7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.8 bits)
S2: 91 (39.7 bits)

BLASTP 2.2.18 [Mar-02-2008]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Query= SEC61gamma
(69 letters)

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
from WGS projects
7,155,275 sequences; 2,468,333,968 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
ref NP_566909.1 protein transport protein SEC61 gamma subunit, ...	103	5e-21
ref NP_194222.1 protein transport protein SEC61 gamma subunit, ...	93	6e-18
ref NP_001046076.1 Os02g0178400 [Oryza sativa (japonica cultiva...	91	4e-17
ref NP_001058242.1 Os06g0653900 [Oryza sativa (japonica cultiva...	90	4e-17
gb ABK93099.1 unknown [Populus trichocarpa]	90	6e-17
gb ABK93166.1 unknown [Populus trichocarpa]	89	1e-16
emb CAN62208.1 hypothetical protein [Vitis vinifera]	88	2e-16
emb CAN67771.1 hypothetical protein [Vitis vinifera] >gi 157341...	88	2e-16
gb ABK21891.1 unknown [Picea sitchensis]	86	1e-15
gb ABK23495.1 unknown [Picea sitchensis]	86	1e-15
ref XP_001752211.1 predicted protein [Physcomitrella patens sub...	84	4e-15
ref XP_001783762.1 predicted protein [Physcomitrella patens sub...	83	6e-15
ref XP_001771807.1 predicted protein [Physcomitrella patens sub...	82	9e-15
ref XP_002116543.1 conserved hypothetical protein [Trichoplax a...	70	4e-11
sp Q7Z1B8.1 S61G1_GRYOR Protein transport protein Sec61 subunit ...	70	6e-11
ref XP_797211.1 PREDICTED: hypothetical protein [Strongylocentr...	70	7e-11
gb ABX75489.1 protein transport protein SEC61 subunit gamma [Ly...	69	8e-11
ref NP_001027676.1 sec61 protein [Ciona intestinalis] >gi 19843...	69	1e-10
ref XP_001606506.1 PREDICTED: similar to Sec61p gamma subunit [...	68	2e-10
ref XP_001892530.1 Protein transport protein SEC61 gamma subuni...	68	2e-10
ref NP_001037674.1 transport protein Sec61 gamma subunit [Bomby...	67	3e-10
sp Q962X7.1 SC61G_BRABE Protein transport protein Sec61 subunit ...	67	4e-10
ref XP_975621.1 PREDICTED: similar to Sec61p gamma subunit [Tri...	67	4e-10
gb ACG76276.1 mitochondrial import inner membrane translocase s...	67	4e-10
ref XP_001120892.1 PREDICTED: similar to CG14214-PA [Apis melli...	67	5e-10
sp Q66KU2.1 SC61G_XENLA Protein transport protein Sec61 subunit ...	67	6e-10
gb ACI68444.1 transport protein Sec61 subunit gamma [Salmo salar]	66	9e-10
ref XP_001650928.1 Sec61 protein complex gamma subunit, putativ...	66	9e-10
sp Q7SZU9.1 SC61G_GADMO Protein transport protein Sec61 subunit ...	66	9e-10
sp Q7T207.1 SC61G_HARAN Protein transport protein Sec61 subunit ...	66	9e-10
ref XP_001476947.1 PREDICTED: similar to Sec61-complex gamma-su...	65	1e-09
ref NP_505778.1 EndoMitotic Oocytes family member (emo-1) [Caen...	65	1e-09

emb CAF91108.1	unnamed protein product [Tetraodon nigroviridis]...	65	1e-09
ref NP_610738.1	CG8860 CG8860-PA [Drosophila melanogaster] >gi ...	65	1e-09
ref NP_055117.1	Sec61 gamma subunit [Homo sapiens] >gi 50979172...	65	1e-09
ref XP_001355499.1	GA12829 [Drosophila pseudoobscura pseudoobsc...	65	1e-09
ref NP_035473.2	SEC61, gamma subunit isoform 1 [Mus musculus] >...	65	1e-09
gb ABR23409.1	mitochondrial import inner membrane translocase s...	65	2e-09
ref NP_608337.1	Sec61gamma CG14214-PA [Drosophila melanogaster]...	65	2e-09
ref XP_001421202.1	predicted protein [Ostreococcus lucimarinus ...	65	2e-09
ref XP_001977803.1	GG19242 [Drosophila erecta] >gi 190649452 gb...	64	3e-09
ref XP_001949988.1	PREDICTED: similar to Sec61p gamma subunit [...	64	4e-09
ref XP_346041.3	PREDICTED: similar to Protein transport protein...	64	4e-09
ref XP_001634305.1	predicted protein [Nematostella vectensis] >...	64	5e-09
ref XP_001698939.1	SEC61-gamma subunit or ER translocon [Chlamy...	63	6e-09
ref XP_001367112.1	PREDICTED: similar to Sec61-complex gamma-su...	62	1e-08
gb AAI53755.1	LOC100127634 protein [Xenopus tropicalis]	62	1e-08
gb ACI64116.1	predicted protein [Thalassiosira pseudonana CCMP1...	62	2e-08
ref XP_637046.1	protein transport protein SEC61 gamma subunit [...	61	2e-08
gb EAZ37855.1	hypothetical protein OsJ_021338 [Oryza sativa (ja...	61	2e-08
ref XP_912247.1	PREDICTED: similar to SEC61 gamma [Mus musculus]	59	1e-07
gb AAR01761.1	putative transport protein [Oryza sativa (japonic...	59	1e-07
gb EDL03260.1	mCG1026143 [Mus musculus]	58	2e-07
gb EAY90536.1	hypothetical protein OsJ_011769 [Oryza sativa (in...	58	2e-07
gb AAX30649.1	SJCHGC06493 protein [Schistosoma japonicum]	55	1e-06
gb AAQ96232.1	LRRGT00019 [Rattus norvegicus]	55	1e-06
ref XP_001480688.1	PREDICTED: similar to Sec61-complex gamma-su...	55	2e-06
gb AAU93469.1	SEC61-gamma [Toxoplasma gondii]	54	5e-06
ref NP_001041386.1	hypothetical protein LOC100189555 [Rattus no...	53	8e-06
gb EDL06017.1	mCG140712 [Mus musculus]	52	1e-05
gb EDL36122.1	mCG1037623 [Mus musculus]	51	2e-05
gb ABV22148.1	Sec61-gamma subunit of protein translocation comp...	51	2e-05
ref XP_001473751.1	PREDICTED: similar to Sec61-complex gamma-su...	51	3e-05
ref XP_672204.1	Sec61-gamma subunit of protein translocation co...	49	1e-04
ref XP_001388404.1	Sec61-gamma subunit of protein translocation...	49	1e-04
ref XP_001432956.1	hypothetical protein GSPATT00035039001 [Para...	49	2e-04
ref XP_001451511.1	hypothetical protein GSPATT00018332001 [Para...	48	2e-04
gb AAW69344.1	protein transport protein SEC61 gamma subunit-lik...	48	2e-04
ref NP_001041402.1	hypothetical protein LOC499136 [Rattus norve...	48	2e-04
ref XP_001435064.1	hypothetical protein GSPATT00036447001 [Para...	48	2e-04
ref XP_366666.1	conserved hypothetical protein [Magnaporthe gri...	48	2e-04
ref XP_735829.1	Sec61-gamma subunit of protein translocation co...	48	2e-04
ref XP_001424615.1	hypothetical protein GSPATT00028252001 [Para...	48	3e-04
ref XP_001436648.1	hypothetical protein GSPATT00037690001 [Para...	48	3e-04
ref XP_001349608.1	Sec61-gamma subunit of protein translocation...	47	3e-04
ref XP_001742910.1	predicted protein [Monosiga brevicollis MX1]...	47	4e-04
emb CAQ38473.1	Sec61-gamma subunit of protein translocation, put...	47	4e-04
ref XP_001545872.1	hypothetical protein BCLG_15623 [Botryotinia...	47	5e-04
ref XP_001613029.1	transport protein SEC61 gamma subunit, putat...	47	5e-04
ref XP_002049604.1	GJ21688 [Drosophila virilis] >gi 194144401 g...	47	6e-04
ref XP_001937557.1	conserved hypothetical protein [Pyrenophora ...	47	6e-04
ref XP_001475587.1	PREDICTED: similar to SEC61 gamma [Mus muscu...	47	6e-04
ref XP_809106.1	protein transport protein Sec61 gamma subunit, ...	46	7e-04
ref XP_001586079.1	hypothetical protein SS1G_13172 [Sclerotinia...	46	8e-04
ref XP_001246613.1	hypothetical protein CIMG_00384 [Coccidioide...	46	0.001
ref XP_843692.1	protein transport protein Sec61 gamma subunit, ...	46	0.001
ref XP_002141107.1	protein translocation complex, SEC61 gamma s...	46	0.001
ref XP_001791442.1	hypothetical protein SNOG_00767 [Phaeosphaer...	46	0.001
ref XP_001565595.1	protein transport protein sec61 gamma subuni...	46	0.001
ref XP_001263761.1	protein translocase, putative [Neosartorya f...	45	0.001
ref XP_961283.1	hypothetical protein NCU04127 [Neurospora crass...	45	0.001
ref XP_001537820.1	predicted protein [Ajellomyces capsulatus NA...	44	0.003
ref XP_001911892.1	unnamed protein product [Podospira anserina]...	44	0.003
ref XP_001270709.1	protein translocase, putative [Aspergillus c...	44	0.003
ref NP_611482.1	CG13426 CG13426-PA [Drosophila melanogaster] >g...	44	0.003
ref XP_001466134.1	protein transport protein sec61 gamma subuni...	44	0.003
gb AAY85043.1	IP05558p [Drosophila melanogaster]	44	0.003
ref XP_001974909.1	GG20863 [Drosophila erecta] >gi 190658096 gb...	44	0.004
ref XP_001609442.1	protein transport protein SEC61 gamma subuni...	43	0.006
ref XP_001215615.1	conserved hypothetical protein [Aspergillus ...	43	0.006
ref XP_001959014.1	GF12667 [Drosophila ananassae] >gi 190620312...	43	0.007
ref XP_001022928.1	Protein transport protein SEC61 gamma-1 subu...	43	0.007

ref XP_001203964.1	PREDICTED: similar to Sec61 gamma subunit, p...	43	0.008
ref XP_763390.1	protein translocation complex, sec61 subunit ga...	43	0.009
ref XP_001829161.1	predicted protein [Coprinopsis cinerea okaya...	42	0.010
ref XP_955056.1	protein translocation complex subunit (SEC61 ga...	42	0.010
ref XP_002091685.1	GE13801 [Drosophila yakuba] >gi 194177786 gb...	42	0.014
ref XP_001874004.1	predicted protein [Laccaria bicolor S238N-H8...	42	0.019
ref XP_001522383.1	hypothetical protein MGCH7_ch7g490 [Magnapor...	41	0.022
ref XP_001300450.1	protein translocase gamma subunit, putative ...	41	0.022
ref XP_001389573.1	hypothetical protein An01gl1630 [Aspergillus...	41	0.025
ref XP_002006249.1	GI18672 [Drosophila sechellia] >gi 19391131...	41	0.028
ref XP_001224853.1	predicted protein [Chaetomium globosum CBS 1...	40	0.045
ref XP_002082332.1	GD25279 [Drosophila simulans] >gi 194194341 ...	40	0.046
ref NP_593061.1	translocon gamma subunit Sss1 [Schizosaccharomy...	40	0.048
ref XP_002034688.1	GM19788 [Drosophila sechellia] >gi 194126658...	40	0.062
ref XP_662193.1	hypothetical protein AN4589.2 [Aspergillus nidu...	40	0.080
gb EDL00527.1	mCG1042596 [Mus musculus]	39	0.081
ref XP_389047.1	hypothetical protein FG08871.1 [Gibberella zeae...	39	0.083
ref XP_001163709.1	PREDICTED: similar to SEC61 gamma, partial [...	39	0.14
ref XP_652711.1	Protein transport protein SEC61 gamma subunit,...	37	0.34
ref XP_567231.1	hypothetical protein [Cryptococcus neoformans v...	37	0.41
gb ACC54913.1	Sec61 gamma subunit beta [Xenopus borealis]	36	0.88

```
>ref|NP_566909.1| protein transport protein SEC61 gamma subunit, putative
[Arabidopsis thaliana]
sp|Q9SMP2.1|S61G3_ARATH Protein transport protein Sec61 subunit gamma-3
emb|CAB62346.1| protein translocation complex sec61 gamma chain-like protein
[Arabidopsis thaliana]
gb|AAM62573.1| protein translocation complex Sec61 gamma chain (pir T05513)
[Arabidopsis thaliana]
dbj|BAC42969.1| putative protein translocation complex sec61 gamma chain
[Arabidopsis thaliana]
gb|ABD38856.1| At3g48570 [Arabidopsis thaliana]
Length = 69
```

Score = 103 bits (256), Expect = 5e-21, Method: Compositional matrix adjust.
Identities = 53/69 (76%), Positives = 53/69 (76%)

```
Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAI IP
Sbjct: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIGFVVMGFVGFVVKLVFIP 60
```

```
Query: 61 INNIIVGSS 69
INNIIVGSS
Sbjct: 61 INNIIVGSS 69
```

```
>ref|NP_194222.1| protein transport protein SEC61 gamma subunit, putative
[Arabidopsis thaliana]
ref|NP_568728.1| protein transport protein SEC61 gamma subunit, putative
[Arabidopsis thaliana]
sp|Q9SW34.1|S61G1_ARATH Protein transport protein Sec61 subunit gamma-1
gb|AAK43984.1|AF370169_1 putative protein translocation complex Sec61 gamma chain
[Arabidopsis thaliana]
emb|CAB36734.1| PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis
thaliana]
emb|CAB79401.1| PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis
thaliana]
dbj|BAB09131.1| protein translocation complex Sec61 gamma chain [Arabidopsis
thaliana]
gb|AAL15237.1| putative protein translocation complex Sec61 gamma chain
[Arabidopsis thaliana]
gb|AAM20513.1| protein transport protein SEC61 gamma subunit-like [Arabidopsis
thaliana]
gb|AAM91250.1| protein transport protein SEC61 gamma subunit-like [Arabidopsis
thaliana]
Length = 69
```

Score = 93.2 bits (230), Expect = 6e-18, Method: Compositional matrix adjust.
Identities = 45/69 (65%), Positives = 51/69 (73%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+AIDS +DPLRDFAK S+RLV+RCHKPDRKEFTKVAVRTAI IP
Sbjct: 1 MDAIDSVVDPLRDFAKDSIRLVKRCHKPDRKEFTKVAVRTAIGFVVMGFVGFVFKLIFIP 60

Query: 61 INNIIVGSS 69
INNIIVG++
Sbjct: 61 INNIIVGAT 69

>ref|NP_001046076.1| Os02g0178400 [Oryza sativa (japonica cultivar-group)]
sp|P38385.1|SC61G_ORYSJ Protein transport protein Sec61 subunit gamma
dbj|BAD27997.1| transport protein SEC61 [Oryza sativa Japonica Group]
dbj|BAF07990.1| Os02g0178400 [Oryza sativa (japonica cultivar-group)]
gb|EAY84716.1| hypothetical protein OsI_005949 [Oryza sativa (indica
cultivar-group)]
gb|EAZ21956.1| hypothetical protein OsJ_005439 [Oryza sativa (japonica
cultivar-group)]
gb|ABR26051.1| protein transport protein sec61 gamma subunit [Oryza sativa
(indica cultivar-group)]
Length = 69

Score = 90.5 bits (223), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 44/69 (63%), Positives = 49/69 (71%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+A+DS +DPLR+FAK SVRLV+RCHKPDRKEFTKVA RTAI IP
Sbjct: 1 MDAVDSVVDPLREFAKDSVRLVKRCHKPDRKEFTKVAARTAIGFVVMGFVGFVFKLIFIP 60

Query: 61 INNIIVGSS 69
INNIIVGS
Sbjct: 61 INNIIVGSG 69

>ref|NP_001058242.1| Os06g0653900 [Oryza sativa (japonica cultivar-group)]
dbj|BAD37419.1| putative transport protein SEC61 [Oryza sativa Japonica Group]
dbj|BAD37541.1| putative transport protein SEC61 [Oryza sativa Japonica Group]
dbj|BAF20156.1| Os06g0653900 [Oryza sativa (japonica cultivar-group)]
gb|EAZ01925.1| hypothetical protein OsI_023157 [Oryza sativa (indica
cultivar-group)]
Length = 69

Score = 90.1 bits (222), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 44/69 (63%), Positives = 50/69 (72%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+AIDS +DPLR+FAK SVRLV+RCHKPDRKEFTKVA+RTAI IP
Sbjct: 1 MDAIDSVVDPLREFAKDSVRLVKRCHKPDRKEFTSKVALRTAIGFVVMGFVGFVFKLIFIP 60

Query: 61 INNIIVGSS 69
INNIIVGS
Sbjct: 61 INNIIVGSG 69

>gb|ABK93099.1| unknown [Populus trichocarpa]
Length = 69

Score = 89.7 bits (221), Expect = 6e-17, Method: Compositional matrix adjust.
Identities = 44/69 (63%), Positives = 50/69 (72%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+AIDS +DPLR+FAK SVRLV+RCHKPD+KEFTKVA RTAI IP
Sbjct: 1 MDAIDSVVDPLREFAKDSVRLVKRCHKPDQKEFTKVATRTAIGFVVMGFVGFVFKLIFIP 60

Query: 61 INNIIVGSS 69
INNIIVG+S
Sbjct: 61 INNIIVGAS 69

>gb|ABK93166.1| unknown [Populus trichocarpa]
Length = 69

Score = 89.0 bits (219), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 44/69 (63%), Positives = 50/69 (72%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+AIDS +DPLR+FAK SVRLV+RCHKPD+KEFTKVA RTAI IP
Sbjct: 1 MDAIDSVDPLREFAKDSVRLVKRCHKPDQKEFTKVASRTAIGFVVMGFVGFVVKLIFIP 60

Query: 61 INNIIVGSS 69
INNIIVG+S
Sbjct: 61 INNIIVGAS 69

>emb|CAN62208.1| hypothetical protein [Vitis vinifera]
Length = 69

Score = 88.2 bits (217), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 43/69 (62%), Positives = 49/69 (71%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+AIDSA+DPLR+F+K SVRLV+RCHKPDRKE+TKVA RTA IP
Sbjct: 1 MDAIDSAVDPLREFSKDSVRLVKRCHKPDRKEYTKVAFRTATGFVVMGFVGFVVKLIFIP 60

Query: 61 INNIIVGSS 69
INNIIVGS
Sbjct: 61 INNIIVGSG 69

>emb|CAN67771.1| hypothetical protein [Vitis vinifera]
emb|CA049023.1| unnamed protein product [Vitis vinifera]
Length = 69

Score = 88.2 bits (217), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 43/68 (63%), Positives = 48/68 (70%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+AID+ DP+R+FAK SVRLV+RCHKPDRKEFTKVA RTAI IP
Sbjct: 1 MDAIDNVFDPMREFAKDSVRLVKRCHKPDRKEFTKVAFRTAIGFVVMGFVGFVVKLIFIP 60

Query: 61 INNIIVGS 68
INNIIVGS
Sbjct: 61 INNIIVGS 68

>gb|ABK21891.1| unknown [Picea sitchensis]
Length = 69

Score = 85.5 bits (210), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 41/69 (59%), Positives = 48/69 (69%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+A+D+ + PL+DFAK SVRLV+RCHKPDRKEF+KVA RTAI IP
Sbjct: 1 MDAVDTVVRPLKDFAKDSVRLVKRCHKPDRKEFSKVAFRTAIGFVVMGFVGFVVKLIFIP 60

Query: 61 INNIIVGSS 69
INNIIVGS
Sbjct: 61 INNIIVGSG 69

>gb|ABK23495.1| unknown [Picea sitchensis]
Length = 69

Score = 85.5 bits (210), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 41/69 (59%), Positives = 48/69 (69%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
MEA+D+ + PL++FAK SVRLV+RCHKPDRKEF+KVA RTAI IP
Sbjct: 1 MEAVDAVVRPLQEFKDSVRLVKRCHKPDRKEFSKVAFRTAIGFVVMGFVGFVVKLIFIP 60

Query: 61 INNIIVGSS 69
INNIIVGS
Sbjct: 61 INNIIVGSG 69

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>ref|XP_001752211.1| predicted protein [Physcomitrella patens subsp. patens]
ref|XP_001769079.1| predicted protein [Physcomitrella patens subsp. patens]
gb|EDQ66157.1| predicted protein [Physcomitrella patens subsp. patens]
gb|EDQ82944.1| predicted protein [Physcomitrella patens subsp. patens]
      Length = 69

Score = 84.0 bits (206), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 38/69 (55%), Positives = 49/69 (71%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
      MEA+D+ + P++DFAK S+RLV+RCHKPDR+EF+KVA+RTA+ IP
Sbjct: 1 MEAVDTVVRPVKDFAKDSIRLVKRCHKPDRREFSKVAIRTAIGFIVMGFIGFFVKLIFIP 60

Query: 61 INNIIIVGSS 69
      INNIIIVGS
Sbjct: 61 INNIIIVGSG 69

>ref|XP_001783762.1| predicted protein [Physcomitrella patens subsp. patens]
gb|EDQ51414.1| predicted protein [Physcomitrella patens subsp. patens]
      Length = 69

Score = 83.2 bits (204), Expect = 6e-15, Method: Compositional matrix adjust.
Identities = 38/68 (55%), Positives = 48/68 (70%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
      MEA+D+ + P++DFAK SVRLV+RCHKPDRKEF+KVA+RT + IP
Sbjct: 1 MEAVDTVVRPVKDFAKDSVRLVKRCHKPDRKEFSKVAIRTGLGFIVMGFIGFFVKLIFIP 60

Query: 61 INNIIIVGS 68
      INNIIIVG+
Sbjct: 61 INNIIIVGA 68

>ref|XP_001771807.1| predicted protein [Physcomitrella patens subsp. patens]
gb|EDQ63415.1| predicted protein [Physcomitrella patens subsp. patens]
      Length = 69

Score = 82.4 bits (202), Expect = 9e-15, Method: Compositional matrix adjust.
Identities = 37/68 (54%), Positives = 48/68 (70%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
      MEA+D+ + P++DFAK S+RLV+RCHKPDRKEF+KVA+RT + IP
Sbjct: 1 MEAVDTVVRPVKDFAKDSIRLVKRCHKPDRKEFSKVALRTGLGFLVMGFIGFFVKLIFIP 60

Query: 61 INNIIIVGS 68
      INNIIIVG+
Sbjct: 61 INNIIIVGT 68

>ref|XP_002116543.1| conserved hypothetical protein [Trichoplax adhaerens]
gb|EDV20899.1| conserved hypothetical protein [Trichoplax adhaerens]
      Length = 68

Score = 70.1 bits (170), Expect = 4e-11, Method: Compositional matrix adjust.
Identities = 35/68 (51%), Positives = 42/68 (61%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
      M+ + + +DPL+ F K SVRLV+RC KPDRKEF K+A TAI IP
Sbjct: 1 MDQVTTLVDPLKVFKDSVRLVKRCKTPDRKEFQKIAFATAIGFGIMGFIGFFVKLIHIP 60

Query: 61 INNIIIVGS 68
      INNIIIVGS
Sbjct: 61 INNIIIVGS 68

>sp|Q7Z1B8.1|S61G1_GRYOR Protein transport protein Sec61 subunit gamma
gb|AAP47228.1| Sec61p gamma subunit [Gryllotalpa orientalis]
      Length = 68
```

Score = 69.7 bits (169), Expect = 6e-11, Method: Compositional matrix adjust.
Identities = 36/68 (52%), Positives = 42/68 (61%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + I+P R FAK S+RLV+RC KPDRKEF K+AV TAI IP
Sbjct: 1 MDQVTKFIEPGRQFAKDSIRLVKRCTKPDRKEFQKIAVATAIGFCIMGFIGFFVKLIHIP 60

Query: 61 INNIIIVGS 68
INNIIIVGS
Sbjct: 61 INNIIIVGS 68

>ref|XP_797211.1| PREDICTED: hypothetical protein [Strongylocentrotus purpuratus]
ref|XP_001176408.1| PREDICTED: hypothetical protein [Strongylocentrotus purpuratus]
Length = 68

Score = 69.7 bits (169), Expect = 7e-11, Method: Compositional matrix adjust.
Identities = 35/68 (51%), Positives = 42/68 (61%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ I I+P + FAK S+RLV+RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDQIQQTIEPAKQFAKDSIRLVKRCTKPDRKEFQKIAMATAIGFCIMGFIGFFVKLIHIP 60

Query: 61 INNIIIVGS 68
INNIIIVGS
Sbjct: 61 INNIIIVGS 68

>gb|ABX75489.1| protein transport protein SEC61 subunit gamma [Lycosa
singoriensis]
Length = 68

Score = 69.3 bits (168), Expect = 8e-11, Method: Compositional matrix adjust.
Identities = 36/68 (52%), Positives = 43/68 (63%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + S I+P R FAK S+RLV+RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDQVMSFIEPDRQFAKDSIRLVKRCTKPDRKEFQKIAMATAIGFAIMGFIGFFVKLIHIP 60

Query: 61 INNIIIVGS 68
INNIIIVGS
Sbjct: 61 INNIIIVGS 68

>ref|NP_001027676.1| sec61 protein [Ciona intestinalis]
ref|XP_002125574.1| PREDICTED: similar to putative transport protein sec61 gamma
subunit [Ciona intestinalis]
ref|XP_002119112.1| PREDICTED: hypothetical protein [Ciona intestinalis]
sp|Q8I7D9.1|SC61G_CIOIN Protein transport protein Sec61 subunit gamma
emb|CAC82549.1| putative transport protein sec61 gamma subunit [Ciona
intestinalis]
Length = 68

Score = 68.6 bits (166), Expect = 1e-10, Method: Compositional matrix adjust.
Identities = 34/68 (50%), Positives = 43/68 (63%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + + ++P + FAK S+RLV+RC KPDRKEF K+AV TAI IP
Sbjct: 1 MDQVMAWVEPGKQFAKDSIRLVKRCTKPDRKEFQKIAVATAIGFAIMGFIGFFVKLIHIP 60

Query: 61 INNIIIVGS 68
INNIIIVGS
Sbjct: 61 INNIIIVGS 68

>ref|XP_001606506.1| PREDICTED: similar to Sec61p gamma subunit [Nasonia vitripennis]
Length = 68

Score = 68.2 bits (165), Expect = 2e-10, Method: Compositional matrix adjust.

Identities = 35/68 (51%), Positives = 42/68 (61%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ I ++P R FAK S+RLV+RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDQIKMFVEPSRQFAKDSMRLVKRCKTPDRKEFQKIAIATAIGFCIMGFIGFFVKLIHIP 60

Query: 61 INNIIIVGS 68
INNIIIVGS
Sbjct: 61 INNIIIVGS 68

>ref|XP_001892530.1| Protein transport protein SEC61 gamma subunit [Brugia malayi]
gb|EDP38639.1| Protein transport protein SEC61 gamma subunit, putative [Brugia
malayi]
Length = 71

Score = 68.2 bits (165), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 33/68 (48%), Positives = 42/68 (61%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + + IDP + FAK S+RLV+RC KPDRKE+ K+AV TA+ IP
Sbjct: 4 MDHLQALIDPSKQFAKDSIRLVKRCKTPDRKEYQKIAVATAVGFAIMGFIGFFVKLIHIP 63

Query: 61 INNIIIVGS 68
INNIIIVG
Sbjct: 64 INNIIIVGG 71

>ref|NP_001037674.1| transport protein Sec61 gamma subunit [Bombyx mori]
gb|ABF51395.1| transport protein SEC61 [Bombyx mori]
gb|ABF85697.1| transport protein Sec61 gamma subunit [Bombyx mori]
Length = 68

Score = 67.4 bits (163), Expect = 3e-10, Method: Compositional matrix adjust.
Identities = 34/68 (50%), Positives = 42/68 (61%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ I ++P + FAK S+RLV+RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDQIAKFVEPGKQFAKDSIRLVRRCKTPDRKEFQKIAIATAIGFCIMGFIGFFVKLIHIP 60

Query: 61 INNIIIVGS 68
INNIIIVGS
Sbjct: 61 INNIIIVGS 68

>sp|Q962X7.1|SC61G_BRABE Protein transport protein Sec61 subunit gamma
gb|AAK72260.1|AF395915_1 SEC61 [Branchiostoma belcheri]
Length = 68

Score = 67.0 bits (162), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 34/68 (50%), Positives = 41/68 (60%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + ++P R FAK S RLV+RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDQLVQFVEPARQFAKDSYRLVKRCKTPDRKEFQKIAMATAIGFAIMGFIGFFVKLIHIP 60

Query: 61 INNIIIVGS 68
INNIIIVGS
Sbjct: 61 INNIIIVGS 68

>ref|XP_975621.1| PREDICTED: similar to Sec61p gamma subunit [Tribolium castaneum]
Length = 68

Score = 67.0 bits (162), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 34/68 (50%), Positives = 41/68 (60%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ I I+P R F K S+RLV+RC KPDR+EF K+A+ TAI IP
Sbjct: 1 MDQITKFIPEGRTKDSIRLVKRCKTPDRREFQKIAIATAIGFCIMGFIGFFVKLIHIP 60

Query: 61 INNIIIVGS 68
INNIIIVGS
Sbjct: 61 INNIIIVGS 68

>gb|ACG76276.1| mitochondrial import inner membrane translocase subunit TIM8
[Amblyomma americanum]
Length = 68

Score = 67.0 bits (162), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 32/68 (47%), Positives = 42/68 (61%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + + IDP + +K S+RL++RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDQVMAFIDPFKQLSKDSIRLIKRCTKPDRKEFQKIAMATAIGFAIMGFIGFFVKLIHIP 60

Query: 61 INNIIIVGS 68
INNIIIVGS
Sbjct: 61 INNIIIVGS 68

>ref|XP_001120892.1| PREDICTED: similar to CG14214-PA [Apis mellifera]
Length = 68

Score = 67.0 bits (162), Expect = 5e-10, Method: Compositional matrix adjust.
Identities = 33/68 (48%), Positives = 41/68 (60%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + +P R FAK S+RL++RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDQVKKLTPEGRQFAKDSIRLIKRCTKPDRKEFQKIAIATAIGFCIMGFIGFFVKLIHIP 60

Query: 61 INNIIIVGS 68
INNIIIVGS
Sbjct: 61 INNIIIVGS 68

>sp|Q66KU2.1|SC61G_XENLA Protein transport protein Sec61 subunit gamma
gb|AAH78558.1| Unknown (protein for MGC:85435) [Xenopus laevis]
Length = 68

Score = 66.6 bits (161), Expect = 6e-10, Method: Compositional matrix adjust.
Identities = 33/68 (48%), Positives = 41/68 (60%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + ++P R F K S+RLV+RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDQVMQFVEPSRQFVKDSIRLVKRCTKPDRKEFQKIAMATAIGFAIMGFIGFFVKLIHIP 60

Query: 61 INNIIIVGS 68
INNIIIVGS
Sbjct: 61 INNIIIVGS 68

>gb|ACI68444.1| transport protein Sec61 subunit gamma [Salmo salar]
Length = 68

Score = 65.9 bits (159), Expect = 9e-10, Method: Compositional matrix adjust.
Identities = 32/68 (47%), Positives = 41/68 (60%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + ++P R F K S+RLV+RC KPDRKEF+K+A+ TAI IP
Sbjct: 1 MDQVMQFVEPSRQFVKDSIRLVKRCTKPDRKEFSKIAMATAIGFAIMGFIGFFVKLIHIP 60

Query: 61 INNIIIVGS 68
INNIIIVG
Sbjct: 61 INNIIIVGG 68

>ref|XP_001650928.1| Sec61 protein complex gamma subunit, putative [Aedes aegypti]
ref|XP_001846718.1| Sec61 protein complex gamma subunit [Culex quinquefasciatus]

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gb|ABF18076.1| preprotein translocase gamma subunit [Aedes aegypti]
gb|EAT43047.1| Sec61 protein complex gamma subunit, putative [Aedes aegypti]
gb|EDS44447.1| Sec61 protein complex gamma subunit [Culex quinquefasciatus]
Length = 68

Score = 65.9 bits (159), Expect = 9e-10, Method: Compositional matrix adjust.
Identities = 33/68 (48%), Positives = 41/68 (60%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
      M+ I   ++P R FAK S+RL++RC KPDR+EF K+A+ TAI IP
Sbjct: 1 MDQIAKIYEPGRSFAKDSIRLIKRCTKPDRREFQKIAIATAIGFCIMGFIGFFVKLIHIP 60

Query: 61 INNIIVGS 68
      INNIIVGS
Sbjct: 61 INNIIVGS 68

>sp|Q7SZU9.1|SC61G_GADMO Protein transport protein Sec61 subunit gamma
gb|AAQ18693.1| Sec61 gamma subunit [Gadus morhua]
Length = 68

Score = 65.9 bits (159), Expect = 9e-10, Method: Compositional matrix adjust.
Identities = 33/68 (48%), Positives = 40/68 (58%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
      M+ I   ++P R F K S+RLV+RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDQIMQFVEPSRQFVKDSIRLVKRCTKPDRKEFQKIAMATAIGFAIMGFIGFFVKLIHIP 60

Query: 61 INNIIVGS 68
      INNIIVG
Sbjct: 61 INNIIVGG 68

>sp|Q7T207.1|SC61G_HARAN Protein transport protein Sec61 subunit gamma
gb|AAP74549.1| SEC61 gamma [Harpagifer antarcticus]
Length = 68

Score = 65.9 bits (159), Expect = 9e-10, Method: Compositional matrix adjust.
Identities = 33/68 (48%), Positives = 40/68 (58%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
      M+ +   ++P R F K S+RLV+RC KPDRKEF KVA+ TAI IP
Sbjct: 1 MDQVMQFVEPSRQFVKDSIRLVKRCTKPDRKEFQKVAMATAIGFAIMGFIGFFVKLIHIP 60

Query: 61 INNIIVGS 68
      INNIIVG
Sbjct: 61 INNIIVGG 68

>ref|XP_001476947.1| PREDICTED: similar to Sec61-complex gamma-subunit [Mus musculus]
ref|XP_001473383.1| PREDICTED: similar to Sec61-complex gamma-subunit [Mus musculus]
gb|EDL20549.1| mCG8406 [Mus musculus]
Length = 68

Score = 65.5 bits (158), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 32/68 (47%), Positives = 40/68 (58%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
      M+ +   ++P R F K S+RLV+RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDQVMQFVEPSRQFVKESIRLVKRCTKPDRKEFQKIAMATAIGFAIMGFIGFFVKLIHIP 60

Query: 61 INNIIVGS 68
      INNIIVG
Sbjct: 61 INNIIVGG 68

>ref|NP_505778.1| EndoMitotic Oocytes family member (emo-1) [Caenorhabditis
      elegans]
ref|XP_001673886.1| Hypothetical protein CBG09741 [Caenorhabditis briggsae AF16]
ref|XP_001673897.1| Hypothetical protein CBG09730 [Caenorhabditis briggsae AF16]
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sp|Q19967.1|SC61G_CAEL Protein transport protein Sec61 subunit gamma
gb|AAC47274.1| Sec61p gamma homolog
emb|CAA98458.1| C. elegans protein F32D8.6, confirmed by transcript evidence
[Caenorhabditis elegans]
emb|CAP28905.1| C. briggsae CBR-EMO-1 protein [Caenorhabditis briggsae]
Length = 68

Score = 65.5 bits (158), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 32/68 (47%), Positives = 41/68 (60%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + I+P R F+K S RLV+RC KPDRKE+ K+A+ TAI IP
Sbjct: 1 MDQFQALIEPARQFSKDSYRLVKRCKPDRKEYQKIAMATAIGFAIMGFIGFFVKLIHIP 60

Query: 61 INNIIVGS 68
INNIIVG+
Sbjct: 61 INNIIVGA 68

>emb|CAF91108.1| unnamed protein product [Tetraodon nigroviridis]
emb|CAF97954.1| unnamed protein product [Tetraodon nigroviridis]
Length = 68

Score = 65.5 bits (158), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 33/68 (48%), Positives = 40/68 (58%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + ++P R F K SVRLV+RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDQVMQFVEPGRQFIKDSVRLVKRCKPDRKEFQKIAMATAIGFAIMGFIGFFVKLIHIP 60

Query: 61 INNIIVGS 68
INNIIVG
Sbjct: 61 INNIIVGG 68

>ref|NP_610738.1| CG8860 CG8860-PA [Drosophila melanogaster]
ref|XP_001975973.1| GG22600 [Drosophila erecta]
ref|XP_002033494.1| GM20379 [Drosophila sechellia]
ref|XP_002091116.1| GE13468 [Drosophila yakuba]
ref|XP_002076308.1| GD15244 [Drosophila simulans]
sp|Q9V668.1|S61G1_DROME Protein transport protein Sec61 gamma-1 subunit
gb|AAF58563.1| CG8860-PA [Drosophila melanogaster]
gb|AAM50706.1| GM14157p [Drosophila melanogaster]
gb|EDV56373.1| GG22600 [Drosophila erecta]
gb|EDW47507.1| GM20379 [Drosophila sechellia]
gb|EDW90828.1| GE13468 [Drosophila yakuba]
gb|EDX15533.1| GD15244 [Drosophila simulans]
Length = 68

Score = 65.5 bits (158), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 33/68 (48%), Positives = 41/68 (60%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + +P R FAK S+RLV+RC KPDRKEF K+A+ TA+ IP
Sbjct: 1 MDKVVKFAEPGRAFAKDSIRLVKRCKPDRKEFQKIAIATAVGFAIMGFIGFFVKLIHIP 60

Query: 61 INNIIVGS 68
INNIIVGS
Sbjct: 61 INNIIVGS 68

>ref|NP_055117.1| Sec61 gamma subunit [Homo sapiens]
ref|NP_001003325.1| Sec61 gamma subunit [Canis lupus familiaris]
ref|NP_001012474.1| Sec61 gamma subunit [Homo sapiens]
ref|NP_001035676.1| Sec61 gamma subunit [Bos taurus]
ref|NP_001103441.1| SEC61, gamma subunit isoform 2 [Mus musculus]
ref|NP_001103442.1| SEC61, gamma subunit isoform 2 [Mus musculus]
ref|NP_001128492.1| SEC61, gamma subunit [Rattus norvegicus]
ref|XP_001107920.1| PREDICTED: similar to Protein transport protein SEC61 gamma
subunit [Macaca mulatta]

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ref|XP_001152525.1| PREDICTED: similar to SEC61 gamma [Pan troglodytes]
ref|XP_001236152.1| PREDICTED: similar to SEC61 gamma [Gallus gallus]
ref|XP_001479532.1| PREDICTED: similar to SEC61 gamma [Mus musculus]
ref|XP_001475666.1| PREDICTED: similar to SEC61 gamma [Mus musculus]
ref|XP_001478183.1| PREDICTED: similar to SEC61 gamma [Mus musculus]
ref|XP_001478570.1| PREDICTED: similar to SEC61 gamma [Mus musculus]
ref|XP_001480211.1| PREDICTED: similar to SEC61 gamma [Mus musculus]
sp|P60058.1|SC61G_CANFA Protein transport protein Sec61 subunit gamma
sp|P60059.1|SC61G_HUMAN Protein transport protein Sec61 subunit gamma
sp|P60060.1|SC61G_MOUSE RecName: Full=Protein transport protein Sec61 subunit gamma
sp|Q3T104.1|SC61G_BOVIN Protein transport protein Sec61 subunit gamma
gb|AAA19705.1| Sec61-complex gamma-subunit
gb|AAA19431.1| Sec61 protein complex gamma subunit
gb|AAC99401.1| Sec61 gamma [Homo sapiens]
dbj|BAB28210.1| unnamed protein product [Mus musculus]
dbj|BAB28376.1| unnamed protein product [Mus musculus]
gb|AAH09480.1| Sec61 gamma subunit [Homo sapiens]
gb|AAH19158.1| SEC61, gamma subunit [Mus musculus]
emb|CAG33260.1| SEC61G [Homo sapiens]
gb|AAH81456.1| SEC61, gamma subunit [Mus musculus]
gb|AAH51840.1| Sec61 gamma subunit [Homo sapiens]
emb|CAI24345.1| SEC61, gamma subunit (S. cerevisiae) [Mus musculus]
dbj|BAE35762.1| unnamed protein product [Mus musculus]
gb|AAI02187.1| Sec61 gamma subunit [Bos taurus]
emb|CAL38284.1| hypothetical protein [synthetic construct]
gb|EAW50960.1| Sec61 gamma subunit, isoform CRA_a [Homo sapiens]
gb|EAW50961.1| Sec61 gamma subunit, isoform CRA_a [Homo sapiens]
gb|EDL00154.1| mCG116534 [Mus musculus]
gb|EDL25421.1| mCG4124 [Mus musculus]
gb|EDL40660.1| mCG7641, isoform CRA_a [Mus musculus]
gb|EDL40661.1| mCG7641, isoform CRA_a [Mus musculus]
gb|EDL97891.1| rCG23282, isoform CRA_a [Rattus norvegicus]
gb|EDL97892.1| rCG23282, isoform CRA_a [Rattus norvegicus]
gb|EDL97893.1| rCG23282, isoform CRA_a [Rattus norvegicus]
dbj|BAG34787.1| unnamed protein product [Homo sapiens]
gb|AAI68720.1| Unknown (protein for MGC:188791) [Rattus norvegicus]
gb|AAI68779.1| Unknown (protein for MGC:188933) [Rattus norvegicus]
prf||2005371B Sec61 protein:SUBUNIT=gamma
      Length = 68

```

Score = 65.5 bits (158), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 32/68 (47%), Positives = 40/68 (58%)

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Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDREFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
      M+ + ++P R F K S+RLV+RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDQVMQFVEPSRQFVKDSIRLVKRC TKPDRKEFQKIAMATAIGFAIMGFIFVFKLIHIP 60

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Query: 61 INNIIVGS 68
      INNIIVG
Sbjct: 61 INNIIVGG 68

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>ref|XP_001355499.1| GA12829 [Drosophila pseudoobscura pseudoobscura]
ref|XP_001963467.1| GF20416 [Drosophila ananassae]
ref|XP_002010749.1| GI21533 [Drosophila mojavensis]
ref|XP_002027916.1| GL27062 [Drosophila persimilis]
ref|XP_002058289.1| GJ16006 [Drosophila virilis]
ref|XP_002067352.1| GK16225 [Drosophila willistoni]
gb|EAL32558.1| GA12829 [Drosophila pseudoobscura pseudoobscura]
gb|EDV44543.1| GF20416 [Drosophila ananassae]
gb|EDW06404.1| GI21533 [Drosophila mojavensis]
gb|EDW37648.1| GL27062 [Drosophila persimilis]
gb|EDW66397.1| GJ16006 [Drosophila virilis]
gb|EDW78338.1| GK16225 [Drosophila willistoni]
      Length = 68

```

Score = 65.1 bits (157), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 34/68 (50%), Positives = 41/68 (60%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + +P R FAK S+RLV+RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDKVVKFAEPGRAFAKDSIRLVKRCTKPDRKEFQKIAIATAIGFCIMGFIGFFVKLIHIP 60

Query: 61 INNIIIVGS 68
INNIIIVGS
Sbjct: 61 INNIIIVGS 68

>ref|NP_035473.2| SEC61, gamma subunit isoform 1 [Mus musculus]
gb|EDL40662.1| mCG7641, isoform CRA_b [Mus musculus]
Length = 100

Score = 65.1 bits (157), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 32/68 (47%), Positives = 40/68 (58%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + ++P R F K S+RLV+RC KPDRKEF K+A+ TAI IP
Sbjct: 33 MDQVMQFVEPSRQFVKDSIRLVKRCTKPDRKEFQKIAMATAIGFAIMGFIGFFVKLIHIP 92

Query: 61 INNIIIVGS 68
INNIIIVG
Sbjct: 93 INNIIIVGG 100

>gb|ABR23409.1| mitochondrial import inner membrane translocase subunit TIM8
[Ornithodoros parkeri]
Length = 68

Score = 64.7 bits (156), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 31/68 (45%), Positives = 42/68 (61%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + + +PL+ +K S+RLV+RC KPDRKE+ K+A+ TAI IP
Sbjct: 1 MDQVMAFFEPLKQLSKDSIRLVKRCTKPDRKEYQKIAMATAIGFAIMGFIGFFVKLIHIP 60

Query: 61 INNIIIVGS 68
INNIIIVGS
Sbjct: 61 INNIIIVGS 68

>ref|NP_608337.1| Sec61gamma CG14214-PA [Drosophila melanogaster]
ref|XP_002039446.1| GM22977 [Drosophila sechellia]
ref|XP_002100996.1| GE15861 [Drosophila yakuba]
sp|Q9VWE9.1|S61G2_DROME Protein transport protein Sec61 gamma-2 subunit
gb|AAF48993.1| CG14214-PA [Drosophila melanogaster]
gb|AAL48065.1| RE69515p [Drosophila melanogaster]
gb|EDW56188.1| GM22977 [Drosophila sechellia]
gb|EDX02104.1| GE15861 [Drosophila yakuba]
Length = 68

Score = 64.7 bits (156), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 33/68 (48%), Positives = 41/68 (60%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + +P R FAK S+RLV+RC KPDRKEF K+A+ TA+ IP
Sbjct: 1 MDKVVKFAEPGRAFAKDSIRLVKRCTKPDRKEFQKIAIATAVGFCIMGFIGFFVKLIHIP 60

Query: 61 INNIIIVGS 68
INNIIIVGS
Sbjct: 61 INNIIIVGS 68

>ref|XP_001421202.1| predicted protein [Ostreococcus lucimarinus CCE9901]
gb|ABO99495.1| predicted protein [Ostreococcus lucimarinus CCE9901]
Length = 68

Score = 64.7 bits (156), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 32/68 (47%), Positives = 40/68 (58%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
ME D A+ P+RDFA+ S RLV++C KPD +EF K+A RTA IP
Sbjct: 1 MEVADIAVKPVRDFARDSARLVKKCAKPDAREFWKIAARTATGFVIMGFVGFVVKLIHIP 60

Query: 61 INNIIVGS 68
INNII+ S
Sbjct: 61 INNIILSS 68

>ref|XP_001977803.1| GG19242 [Drosophila erecta]
gb|EDV46730.1| GG19242 [Drosophila erecta]
Length = 68

Score = 64.3 bits (155), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 33/68 (48%), Positives = 41/68 (60%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + +P R FAK S+RLV+RC KPDRKEF K+A+ TA+ IP
Sbjct: 1 MDKVVKFAEPGRVFAKDSIRLVKRCTKPDRKEFQKIAIATAVGFCIMGFIFGVVKLIHIP 60

Query: 61 INNIIVGS 68
INNIIVGS
Sbjct: 61 INNIIVGS 68

>ref|XP_001949988.1| PREDICTED: similar to Sec6lp gamma subunit [Acyrtosiphon pisum]
Length = 66

Score = 63.9 bits (154), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 32/66 (48%), Positives = 40/66 (60%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + ++P R F+K SVRLV+RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDQVTKVLEPGRQFSKDSVRLVKRCTKPDRKEFQKIAIATAIGFCIMGFIFGVVKLIHIP 60

Query: 61 INNIIV 66
INNIIV
Sbjct: 61 INNIIV 66

>ref|XP_346041.3| PREDICTED: similar to Protein transport protein SEC61 gamma
subunit [Rattus norvegicus]
Length = 68

Score = 63.9 bits (154), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 31/68 (45%), Positives = 40/68 (58%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + ++P + F K S+RLV+RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDQVMQFVEPSQQFVKDSIRLVKRCTKPDRKEFQKIAMATAIGFAIMGFIFGVVKLIHIP 60

Query: 61 INNIIVGS 68
INNIIVG
Sbjct: 61 INNIIVGG 68

>ref|XP_001634305.1| predicted protein [Nematostella vectensis]
gb|EDO42242.1| predicted protein [Nematostella vectensis]
Length = 67

Score = 63.5 bits (153), Expect = 5e-09, Method: Compositional matrix adjust.
Identities = 32/66 (48%), Positives = 41/66 (62%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ I + ++P + FAK S+RLV+RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDQIVNTLEPCKQFAKDSMRLVKRCTKPDRKEFQKIALATAIGFAIMGFIFGVVKLIHIP 60

Query: 61 INNIIV 66
INNIIV
Sbjct: 61 INNIIV 66

>ref|XP_001698939.1| SEC61-gamma subunit or ER translocon [Chlamydomonas reinhardtii]
dbj|BAF46295.1| putative protein transport protein SEC61 [Chlamydomonas
reinhardtii]
gb|EDO99221.1| SEC61-gamma subunit or ER translocon [Chlamydomonas reinhardtii]
Length = 68

Score = 63.2 bits (152), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 31/68 (45%), Positives = 40/68 (58%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ D + P++DFAK+S RLV+RC KPDRKEF KV RTA+ IP
Sbjct: 1 MDLGDVVVKPVKDFAKNSARLVKRC TKPDRKEFMKVC SRTAVGFIVMGFIGFFVKLLFIP 60

Query: 61 INNIIVGS 68
IN +I+ S
Sbjct: 61 INQVIMSS 68

>ref|XP_001367112.1| PREDICTED: similar to Sec61-complex gamma-subunit [Monodelphis
domestica]
ref|XP_001505526.1| PREDICTED: similar to Sec61-complex gamma-subunit
[Ornithorhynchus anatinus]
Length = 66

Score = 62.0 bits (149), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 31/66 (46%), Positives = 39/66 (59%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + ++P R F K S+RLV+RC KPDRKEF K+A+ TAI IP
Sbjct: 1 MDQVMQFVEPSRQFVKDSIRLVKRC TKPDRKEFQKIAMATAIGFAIMGFIGFFVKLIHIP 60

Query: 61 INNIIIV 66
INNIIIV
Sbjct: 61 INNIIIV 66

>gb|AAI53755.1| LOC100127634 protein [Xenopus tropicalis]
Length = 69

Score = 62.0 bits (149), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 29/68 (42%), Positives = 40/68 (58%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ ++ PL+DFAK+SVRL ++C KPD +EF K+A+ T I IP
Sbjct: 1 MDILEETAAPLKDFAKNSVRLFKCKTKPD AQEFQKIALATLIGFAIMGFIGFFVKLIHIP 60

Query: 61 INNIIVGS 68
INNI+VG
Sbjct: 61 INNILVGG 68

>gb|ACI64116.1| predicted protein [Thalassiosira pseudonana CCMP1335]
Length = 72

Score = 61.6 bits (148), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 30/61 (49%), Positives = 36/61 (59%)

Query: 8 IDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNIIVG 67
I PLR FAK S+ LV++C KPDRKEFT +A T I IPINNI+VG
Sbjct: 12 IQPLRQFAKDSIHLVKKCTKPDRKEFTAIKATGIGFLIMGFIGFFVKLVHIPINNILVG 71

Query: 68 S 68
+
Sbjct: 72 N 72

>ref|XP_637046.1| protein transport protein SEC61 gamma subunit [Dictyostelium
discoideum AX4]

sp|Q54JV6.1|SC61G_DICDI RecName: Full=Protein transport protein Sec61 subunit gamma
gb|EAL63535.1| protein transport protein SEC61 gamma subunit [Dictyostelium
discoideum AX4]
Length = 69

Score = 61.2 bits (147), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 28/68 (41%), Positives = 40/68 (58%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ ++ PL+DFAK+S+RL ++C KPD +EF K+A+ T I IP
Sbjct: 1 MDILEETAAPLKDFAKNSIRLFKKCTKPDAQEFQKIALATLIGFAIMGFIGFFVKLIHIP 60

Query: 61 INNIIVGS 68
INNI+VG
Sbjct: 61 INNILVGG 68

>gb|EAZ37855.1| hypothetical protein OsJ_021338 [Oryza sativa (japonica
cultivar-group)]
Length = 415

Score = 61.2 bits (147), Expect = 2e-08, Method: Composition-based stats.
Identities = 26/37 (70%), Positives = 32/37 (86%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVA 37
M+AIDS +DPLR+FAK SVRLV+RCHKPDRK ++A
Sbjct: 1 MDAIDSVVDPLREFAKDSVRLVKRCHKPDRKGRERLA 37

>ref|XP_912247.1| PREDICTED: similar to SEC61 gamma [Mus musculus]
Length = 68

Score = 58.9 bits (141), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 29/68 (42%), Positives = 38/68 (55%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + ++P + F K S+ LV+RC KP RKEF K+A+ TAI IP
Sbjct: 1 MDEVMQFVEPSQQFVKDSIWLVKRCSKPYRKEFQKIAMATAIGFAIIGFTGFFMKLIHIP 60

Query: 61 INNIIVGS 68
INNIIVG
Sbjct: 61 INNIIVGG 68

>gb|AAR01761.1| putative transport protein [Oryza sativa (japonica
cultivar-group)]
gb|ABF96729.1| Protein transport protein SEC61 gamma subunit, putative [Oryza
sativa (japonica cultivar-group)]
gb|EAZ27400.1| hypothetical protein OsJ_010883 [Oryza sativa (japonica
cultivar-group)]
Length = 71

Score = 58.9 bits (141), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 25/36 (69%), Positives = 31/36 (86%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKV 36
M+A+DS +D LR+FAK S+ LV+ CHKPDRKEFTKV
Sbjct: 1 MDAVDSVVDLSLREFAKDSICLVKHCHKPDRKEFTKV 36

>gb|EDL03260.1| mCG1026143 [Mus musculus]
Length = 68

Score = 57.8 bits (138), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 30/68 (44%), Positives = 38/68 (55%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + ++P R F K SV+LV+RC KPDRKEF K+A+ TAI I
Sbjct: 1 MDQVMQFVEPSRQFVKDSVQLVKRCKTPDRKEFQKIAMATAIGFSITRFIVFFVKRIHIC 60

Query: 61 INNIIVGS 68
INNI VG
Sbjct: 61 INNITVGG 68

>gb|EAY90536.1| hypothetical protein OsI_011769 [Oryza sativa (indica
cultivar-group)]
Length = 118

Score = 57.8 bits (138), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 25/36 (69%), Positives = 31/36 (86%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKV 36
M+A+DS +D LR+FAK S+ LV+ CHKPDRKEFTKV
Sbjct: 72 MDAVDSVVDLSREFAKDSICLVKHCHKPDRKEFTKV 107

>gb|AAX30649.1| SJCHGC06493 protein [Schistosoma japonicum]
Length = 68

Score = 55.5 bits (132), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 27/68 (39%), Positives = 38/68 (55%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + + +PL F+K SV + RC KPDRKEF K A+ TA+ +P
Sbjct: 1 MDRVSTLAEPVRFKSDSVHFINRCKTPDRKEFKKNAIATAVGFLAMGVLFIIKLIFVP 60

Query: 61 INNIIVGS 68
IN+IIVG+
Sbjct: 61 INSIIVGN 68

>gb|AAQ96232.1| LRRGT00019 [Rattus norvegicus]
Length = 353

Score = 55.5 bits (132), Expect = 1e-06, Method: Composition-based stats.
Identities = 28/58 (48%), Positives = 35/58 (60%)

Query: 8 IDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNII 65
++P + F K S+RLV+RC KPDRKEF K+A+ TAI IPINNII
Sbjct: 138 VEPSQQFVKDSIRLVKRCTKPDRKEFKIAMATAIGFAIMGFIGFVKLIHIPINNII 195

>ref|XP_001480688.1| PREDICTED: similar to Sec61-complex gamma-subunit [Mus musculus]
ref|XP_001476807.1| PREDICTED: similar to Sec61-complex gamma-subunit [Mus musculus]
Length = 68

Score = 55.1 bits (131), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 28/68 (41%), Positives = 38/68 (55%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
ME + + ++P R F K SVRLV+R KPDR+EF K+++ TA+ IP
Sbjct: 1 MEQVMNFVEPSRQFVKDSVRLVKRSTKPDRREFQKLSMATAVGFAIMGFIGFLMKLIHIP 60

Query: 61 INNIIVGS 68
INN VG
Sbjct: 61 INNNSVGG 68

>gb|AAU93469.1| SEC61-gamma [Toxoplasma gondii]
Length = 84

Score = 53.5 bits (127), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 29/64 (45%), Positives = 35/64 (54%)

Query: 4 IDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINN 63
I S + LR+F SVRLV+RC KPD+EF K+A AI IPINN
Sbjct: 18 IGSLLGLREFFFDSVRLVRRCTKPDAREFRKIAYACAIGFLLMGFIGYFIKLIFIPINN 77

Query: 64 IIVG 67
I+VG
Sbjct: 78 ILVG 81

>ref|NP_001041386.1| hypothetical protein LOC100189555 [Rattus norvegicus]
gb|AAP85375.1| Aa1027 [Rattus norvegicus]
Length = 135

Score = 52.8 bits (125), Expect = 8e-06, Method: Compositional matrix adjust.
Identities = 26/58 (44%), Positives = 34/58 (58%)

Query: 8 IDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNII 65
++P R F K S++LV+RC +P RKEF K+A+ TAI IPINNII
Sbjct: 4 VEPSRQFVKDSIQLVKRCCTEPARKEFQKIAMATAIGFAIMGFIGFFVKLIHIPINNII 61

>gb|EDL06017.1| mCG140712 [Mus musculus]
Length = 84

Score = 52.0 bits (123), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 22/42 (52%), Positives = 31/42 (73%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAI 42
M+ + ++P R F K S+R+V+RC KPDRKEF K+A+ TAI
Sbjct: 17 MDQVMQFVEPSRQFVKDSIRMVCRCTKPDRKEFQKIAMATAI 58

>gb|EDL36122.1| mCG1037623 [Mus musculus]
Length = 90

Score = 51.2 bits (121), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 27/68 (39%), Positives = 35/68 (51%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
++ + + P F K SV LV+RC KP R+EF K+A+ TAI IP
Sbjct: 23 LDQVMEFVKPSWQFVKDSVLLVKRCKPHRREFQKIAMATAIGFAIMGFIGFFEKLIHIP 82

Query: 61 INNIIIVGS 68
NNIIIVG
Sbjct: 83 NNNIIIVGG 90

>gb|ABV22148.1| Sec61-gamma subunit of protein translocation complex [Perkinsus
chesapeaki]
Length = 78

Score = 51.2 bits (121), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 27/58 (46%), Positives = 32/58 (55%)

Query: 11 LRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNIIIVGS 68
LR+FA S RL+Q+C KPD KEF K+A I IPINNII+GS
Sbjct: 21 LREFAIDSRRLIQKCEKPDKEFKKMASACFIGFCIMGFIGYTIKLVFIPINNIIIMGS 78

>ref|XP_001473751.1| PREDICTED: similar to Sec61-complex gamma-subunit [Mus musculus]
Length = 267

Score = 51.2 bits (121), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 28/66 (42%), Positives = 37/66 (56%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
M+ + ++P R F K SV+LV+RC KPDRKEF K+A+ TAI I
Sbjct: 1 MDQVMQFVEPSRQFVKDSVQLVKRCKPDRKEFQKIAMATAIGFSITRFIVFFVKRIHIC 60

Query: 61 INNIIIV 66
INNI +
Sbjct: 61 INNITM 66

>ref|XP_672204.1| Sec61-gamma subunit of protein translocation complex, [Plasmodium
berghei strain ANKA]
ref|XP_676321.1| hypothetical protein PB000994.03.0 [Plasmodium berghei strain
ANKA]

ref|XP_728579.1| protein translocase SEC61 complex subunit gamma [Plasmodium yoelii yoelii str. 17XNL]
gb|EAA20144.1| protein translocase SEC61 complex gamma subunit, archaeal and eukaryotic, putative [Plasmodium yoelii yoelii]
emb|CAI03977.1| Sec61-gamma subunit of protein translocation complex, putative [Plasmodium berghei]
emb|CAI00515.1| hypothetical protein PB000994.03.0 [Plasmodium berghei]
Length = 83

Score = 49.3 bits (116), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 24/65 (36%), Positives = 31/65 (47%)

Query: 4 IDSAIDPLRDFAKSSVRLVQRCHKPDREFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINN 63
I + + DF SVRLV++C KP +KE+T + I IPINN
Sbjct: 18 IGYIVTSIHDFVNDVRLVRKCTKPSKEYTNIVCACTIGFLIMGLIGYTIKLVFIPINN 77

Query: 64 IIVGS 68
I VGS
Sbjct: 78 IFVGS 82

>ref|XP_001388404.1| Sec61-gamma subunit of protein translocation complex, putative [Cryptosporidium parvum Iowa II]
gb|EAA51597.1| Sec61-gamma subunit of protein translocation complex, putative [Cryptosporidium parvum Iowa II]
Length = 87

Score = 48.5 bits (114), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 24/57 (42%), Positives = 30/57 (52%)

Query: 12 RDAKSSVRLVQRCHKPDREFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNIIVGS 68
++FA S+RLV+RC KPD KEF VA + IPINNI+G
Sbjct: 28 QEFALDSIRLVRRCTKPDACEFRNVAYACTVGFFLMGFIGYSVKLVFIPINNIIMGG 84

>ref|XP_001432956.1| hypothetical protein GSPATT00035039001 [Paramecium tetraurelia strain d4-2]
emb|CAK65559.1| unnamed protein product [Paramecium tetraurelia]
Length = 74

Score = 48.5 bits (114), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 20/69 (28%), Positives = 36/69 (52%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDREFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
+ I+ + ++ F + S R +++C KPD++E+ K+A AI IP
Sbjct: 6 LNGINGILQDVQGFGQESYRFIRKCTKPKDKREYIKIATSCAIGFAVMGAVGYFIKLVFIP 65

Query: 61 INNIIIVGSS 69
INNII+ ++
Sbjct: 66 INNIIILSAN 74

>ref|XP_001451511.1| hypothetical protein GSPATT00018332001 [Paramecium tetraurelia strain d4-2]
ref|XP_001451986.1| hypothetical protein GSPATT00018785001 [Paramecium tetraurelia strain d4-2]
emb|CAK84114.1| unnamed protein product [Paramecium tetraurelia]
emb|CAK84589.1| unnamed protein product [Paramecium tetraurelia]
Length = 74

Score = 48.1 bits (113), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 20/69 (28%), Positives = 36/69 (52%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDREFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
+ I+ + ++ F + S R +++C KPD++E+ K+A AI IP
Sbjct: 6 LNGINGILTQVQSFQESYRFIRKCTKPKDKREYIKIATSCAIGFAVMGAVGYFIKLVFIP 65

Query: 61 INNIIIVGSS 69
INNII+ ++
Sbjct: 66 INNIIILSAN 74

>gb|AAW69344.1| protein transport protein SEC61 gamma subunit-like protein
[Magnaporthe grisea]
Length = 70

Score = 48.1 bits (113), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 19/68 (27%), Positives = 34/68 (50%)

Query: 2 EAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 61
+++ +D R+F K ++ + RC KPD+KEF ++ + IP+
Sbjct: 3 DSVQEILDVPREFVKDGIQFLNRCQKPKKEFRQICQAVGVGFLIMGAVGYIVKLGHIP 62

Query: 62 NNIIVGSS 69
NNI+VG +
Sbjct: 63 NNILVGGA 70

>ref|NP_001041402.1| hypothetical protein LOC499136 [Rattus norvegicus]
gb|AAQ96234.1| LRRGT00021 [Rattus norvegicus]
Length = 233

Score = 48.1 bits (113), Expect = 2e-04, Method: Composition-based stats.
Identities = 22/42 (52%), Positives = 29/42 (69%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAI 42
M+ + ++P R F K S+RLV+R KPDRKEF K+A TAI
Sbjct: 173 MDQVMQFVEPSRQFVKDSIRLVKRRTPDRKEFQKIARATAI 214

>ref|XP_001435064.1| hypothetical protein GSPATT00036447001 [Paramecium tetraurelia
strain d4-2]
emb|CAK67667.1| unnamed protein product [Paramecium tetraurelia]
Length = 74

Score = 47.8 bits (112), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 20/69 (28%), Positives = 36/69 (52%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
+ I+ + ++ F + S R +++C KPD++E+ K+A AI IP
Sbjct: 6 LINGINGILSDVQGFGQESYRFLRKCTKPKREYIKIATSCAIGFAVMGAVGYFIKLVFIP 65

Query: 61 INNIIVGSS 69
INNII+ ++
Sbjct: 66 INNIIILSAN 74

>ref|XP_366666.1| conserved hypothetical protein [Magnaporthe grisea 70-15]
gb|EDK01811.1| conserved hypothetical protein [Magnaporthe grisea 70-15]
Length = 70

Score = 47.8 bits (112), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 19/68 (27%), Positives = 34/68 (50%)

Query: 2 EAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 61
+++ +D R+F K ++ + RC KPD+KEF ++ + IP+
Sbjct: 3 DSVQEILDVPREFVKDGIQFLNRCQKPKKEFRQICQAVGVGFLIMGAVGYIVKLHVIPL 62

Query: 62 NNIIVGSS 69
NNI+VG +
Sbjct: 63 NNILVGGA 70

>ref|XP_735829.1| Sec61-gamma subunit of protein translocation complex, [Plasmodium
chabaudi chabaudi]
emb|CAH85750.1| Sec61-gamma subunit of protein translocation complex, putative
[Plasmodium chabaudi]
Length = 83

Score = 47.8 bits (112), Expect = 2e-04, Method: Compositional matrix adjust.

Identities = 23/65 (35%), Positives = 31/65 (47%)

Query: 4 IDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINN 63
I + + +F SVRLV++C KP +KE+T + I IPINN
Sbjct: 18 IGYLVTSIHEFVNDSVRLVRKCTKPSKKEYTNIVCACTIGFLIMGLIGYTIKLVFIPINN 77

Query: 64 IIVGS 68
I VGS
Sbjct: 78 IFVGS 82

>ref|XP_001424615.1| hypothetical protein GSPATT00028252001 [Paramecium tetraurelia
strain d4-2]
emb|CAK57217.1| unnamed protein product [Paramecium tetraurelia]
Length = 74

Score = 47.8 bits (112), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 19/69 (27%), Positives = 36/69 (52%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
+ I+ + ++ F + S R +++C KPD++E+ K+A A+ IP
Sbjct: 6 LNGINGILQDVQSFQESYRFIRKCTKPKDKREYIKIATSCAVGFAVMGAVGYFIKLVFIP 65

Query: 61 INNIIIVGSS 69
INNII+ ++
Sbjct: 66 INNIIILSAN 74

>ref|XP_001436648.1| hypothetical protein GSPATT00037690001 [Paramecium tetraurelia
strain d4-2]
emb|CAK69251.1| unnamed protein product [Paramecium tetraurelia]
Length = 74

Score = 47.8 bits (112), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 20/69 (28%), Positives = 36/69 (52%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
+ I+ + ++ F + S R +++C KPD++E+ K+A AI IP
Sbjct: 6 LNGINGILSDVQSFQESYRFMRKCTKPKDKREYIKIATSCAIGFAVMGAVGYFIKLVFIP 65

Query: 61 INNIIIVGSS 69
INNII+ ++
Sbjct: 66 INNIIILSAN 74

>ref|XP_001349608.1| Sec61-gamma subunit of protein translocation complex, putative
[Plasmodium falciparum 3D7]
gb|AAC71879.1| Sec61-gamma subunit of protein translocation complex, putative
[Plasmodium falciparum 3D7]
Length = 81

Score = 47.4 bits (111), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 20/65 (30%), Positives = 34/65 (52%)

Query: 4 IDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINN 63
+ ++ ++ F + SVRL+++C KP++KE+T + + IPINN
Sbjct: 16 VGYCVNGIQTFVEDSVRLIRKCTKPNKKEYTNIVYACSFGLIMGFIGYIIKLVFIPINN 75

Query: 64 IIVGS 68
I VGS
Sbjct: 76 IFVGS 80

>ref|XP_001742910.1| predicted protein [Monosiga brevicollis MX1]
gb|EDQ93148.1| predicted protein [Monosiga brevicollis MX1]
Length = 67

Score = 47.4 bits (111), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 23/66 (34%), Positives = 34/66 (51%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXIP 60
M+ I ++ PL DF ++S + +C KP+ KEF K+A T + IP
Sbjct: 1 MDDIKDSVAPLNDFYRNSRMFLNKCDKPNTKEFMKIASATLVGFAIMGIGYAVKLIHIP 60

Query: 61 INNIIV 66
INNI+V
Sbjct: 61 INNILV 66

>emb|CAQ38473.1| Sec61-gamma subunit of protein translocation, putative [Plasmodium knowlesi strain H]
Length = 82

Score = 47.4 bits (111), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 22/65 (33%), Positives = 32/65 (49%)

Query: 4 IDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXIPINN 63
I I ++ F SVRL+++C KP++KE+T + + IPINN
Sbjct: 17 IGCIIISGIQTFVHDSVRLIRKCTKPNKKEYTNIVYACSFGLIMGFIGYTIKLVFIPINN 76

Query: 64 IIVGS 68
I VGS
Sbjct: 77 IFVGS 81

>ref|XP_001545872.1| hypothetical protein BC1G_15623 [Botryotinia fuckeliana B05.10]
gb|EDN22711.1| hypothetical protein BC1G_15623 [Botryotinia fuckeliana B05.10]
Length = 70

Score = 47.0 bits (110), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 21/58 (36%), Positives = 29/58 (50%)

Query: 12 RDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXIPINNIIVGSS 69
RDF K + V +C KPDR+EF +A A+ IP+NNI+VG +
Sbjct: 13 RDFIKDGTQFVNKCTKPDREFLNIAARAVAMGFLIMGAVGYIVKLIHIPLNNILVGGA 70

>ref|XP_001613029.1| transport protein SEC61 gamma subunit, putative [Plasmodium vivax Sal-1]
gb|EDL43302.1| transport protein SEC61 gamma subunit, putative [Plasmodium vivax]
Length = 82

Score = 46.6 bits (109), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 21/65 (32%), Positives = 32/65 (49%)

Query: 4 IDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXIPINN 63
I + ++ F SVRL+++C KP++KE+T + + IPINN
Sbjct: 17 IGYLVSSMQTFVHDSVRLIRKCTKPNKKEYTNIVYACSFGLIMGFIGYIIKLVFIPINN 76

Query: 64 IIVGS 68
I VGS
Sbjct: 77 IFVGS 81

>ref|XP_002049604.1| GJ21688 [Drosophila virilis]
gb|EDW60797.1| GJ21688 [Drosophila virilis]
Length = 107

Score = 46.6 bits (109), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 22/58 (37%), Positives = 31/58 (53%)

Query: 10 PLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXIPINNIIVG 67
PL F + SVR+++RC KPDR+EF + A+ + IPI NII+G
Sbjct: 50 PLLAFFRDSVRVIKCTKPDREQEFLRSALAITVGFLIMGFLGFIKLLHIPITNIIMG 107

>ref|XP_001937557.1| conserved hypothetical protein [Pyrenophora tritici-repentis Pt-1C-BFP]
gb|EDU50144.1| conserved hypothetical protein [Pyrenophora tritici-repentis]

Pt-1C-BFP]
Length = 69Score = 46.6 bits (109), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 23/69 (33%), Positives = 31/69 (44%)

```
Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
          ME I D +F K + RC KPD+KEF +++ I IP
Sbjct: 1 MENIKEFADMPAEFLKEGTLFMNRCTKPKKEFIRISQAVGIGFLIMGVIGYVVKLVHIP 60

Query: 61 INNIIVGSS 69
          +NNI+VG S
Sbjct: 61 VNNILVGGG 69
```

>ref|XP_001475587.1| PREDICTED: similar to SEC61 gamma [Mus musculus]
Length = 64Score = 46.6 bits (109), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 23/61 (37%), Positives = 32/61 (52%)

```
Query: 8 IDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNIIVG 67
          ++P + F K S+ LV+RC +P KEF K+A+ T I IPINNI +G
Sbjct: 4 VEPSQRFFVKDSIWLVRCTEPPIKEFKIAMATTIGFAIMEFIGFFVKLIHIPINNIITMG 63

Query: 68 S 68
Sbjct: 64 G 64
```

```
>ref|XP_809106.1| protein transport protein Sec61 gamma subunit, putative
[Trypanosoma cruzi strain CL Brener]
ref|XP_814770.1| protein transport protein Sec61 gamma subunit, putative
[Trypanosoma cruzi strain CL Brener]
gb|EAN87255.1| protein transport protein Sec61 gamma subunit, putative
[Trypanosoma cruzi]
gb|EAN92919.1| protein transport protein Sec61 gamma subunit, putative
[Trypanosoma cruzi]
Length = 69
```

Score = 46.2 bits (108), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 24/69 (34%), Positives = 37/69 (53%), Gaps = 1/69 (1%)

```
Query: 1 MEAIDSA-IDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXI 59
          M+ +D A I P+ F ++S LV++C KP+ EFT A+ T + I
Sbjct: 1 MDPLDEAVIYPVTAFIRNSRMLVRKCKQPNYSEFTTAAMATLMGFMVIMGFLGFFVKVIFI 60

Query: 60 PINNIIVGS 68
          PINN+I+G+
Sbjct: 61 PINNVILGA 69
```

```
>ref|XP_001586079.1| hypothetical protein SS1G_13172 [Sclerotinia sclerotiorum 1980]
gb|EDN98314.1| hypothetical protein SS1G_13172 [Sclerotinia sclerotiorum 1980]
Length = 70
```

Score = 46.2 bits (108), Expect = 8e-04, Method: Compositional matrix adjust.
Identities = 21/68 (30%), Positives = 33/68 (48%)

```
Query: 2 EAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPI 61
          + I +D +DF K + + +C KPDR+EF +A A+ IP+
Sbjct: 3 DQIQEFMDVPKDFIKDGTQFINKCTKPDREFINARAVAMGFVIMGAVGYIVKLIHIPL 62

Query: 62 NNIIVGSS 69
          NNI+VG +
Sbjct: 63 NNILVGGG 70
```

```
>ref|XP_001246613.1| hypothetical protein CIMG_00384 [Coccidioides immitis RS]
gb|EAS35030.1| hypothetical protein CIMG_00384 [Coccidioides immitis RS]
```

Length = 70

Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 21/68 (30%), Positives = 30/68 (44%)

```
Query: 2 EAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 61
          E      D  +DF K  +  V RC KPD++EF K++      IP+
Sbjct: 3 ETQELADIPKDFVKDGMFLFVNRCTKPKDKREFLKISQAVGFGFLIMGAIGYFIKLIHIPV 62
```

Query: 62 NNIIVGSS 69

NNI+VG +

Sbjct: 63 NNILVGGGA 70

```
>ref|XP_843692.1| protein transport protein Sec61 gamma subunit, putative
[Trypanosoma brucei]
gb|AA69889.1| protein transport protein Sec61 gamma subunit, putative
[Trypanosoma brucei]
gb|AAZ10133.1| protein transport protein Sec61 gamma subunit, putative
[Trypanosoma brucei]
Length = 69
```

Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 20/64 (31%), Positives = 34/64 (53%)

```
Query: 5 DSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNI 64
          ++ I P+  FA++S  LV++C KP+  EF  A+ T +      IPINN+
Sbjct: 6 ETVIHPMTAFARNSRMLVRKCKQKPNYSEFNASAMATLVGFVVMGLLGFFVKVVFIPINNV 65
```

Query: 65 IVGS 68

++G+

Sbjct: 66 VLGA 69

```
>ref|XP_002141107.1| protein translocation complex, SEC61 gamma subunit, putative
[Cryptosporidium muris RN66]
gb|EEA06758.1| protein translocation complex, SEC61 gamma subunit, putative
[Cryptosporidium muris RN66]
Length = 82
```

Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 24/66 (36%), Positives = 30/66 (45%)

```
Query: 4 IDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINN 63
          I      +++      S+RLV+RC KPD KEF  VA      I      IPINN
Sbjct: 15 IGYIFQGVQELTLDLSIRLVRRCTKPDACEFRNVAYACTIGFFLMGFIGYSVKLVFIPINN 74
```

Query: 64 IIVGSS 69

II+G

Sbjct: 75 IIMGQ 80

```
>ref|XP_001791442.1| hypothetical protein SNOG_00767 [Phaeosphaeria nodorum SN15]
gb|EAT92262.1| hypothetical protein SNOG_00767 [Phaeosphaeria nodorum SN15]
Length = 69
```

Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 22/69 (31%), Positives = 31/69 (44%)

```
Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
          ME +  D  +F K  +  RC KPD+KEF +++  I      IP
Sbjct: 1 MENVKEFADMPAEFLKEGTLFMNRCTKPKDKKEFIRISQAVGIGFLIMGVIGYIVKLVHIP 60
```

Query: 61 INNIIVGSS 69

+NNI+VG S

Sbjct: 61 VNNILVGGG 69

```
>ref|XP_001565595.1| protein transport protein sec61 gamma subunit, putative
[Leishmania braziliensis MHOM/BR/75/M2904]
```

emb|CAM39089.1| protein transport protein sec61 gamma subunit,putative
[Leishmania braziliensis]
Length = 69

Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 22/64 (34%), Positives = 31/64 (48%)

Query: 5 DSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNI 64
D P+ F K+S LV++C KP+ EFT + AI IPINN+
Sbjct: 6 DILFHPPIVAFTKNSRMLVRKCQKPNYNEFTTATMAAIGFLMMGFLGFFVKLVFIPINNV 65

Query: 65 IVGS 68
I+G+
Sbjct: 66 ILGA 69

>ref|XP_001263761.1| protein translocase, putative [Neosartorya fischeri NRRL 181]
gb|EAW21864.1| protein translocase, putative [Neosartorya fischeri NRRL 181]
Length = 70

Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 21/68 (30%), Positives = 33/68 (48%)

Query: 2 EAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPI 61
+ I D RDF + + V+RC KPD++EF K++ + IP+
Sbjct: 3 DTIQELADIPRDFLRDGMFLVRRCTKPKREFIKISQAVGMGFIIMGAIGYFIKLIHIPV 62

Query: 62 NNIIVGSS 69
NNI+VG +
Sbjct: 63 NNILVGGA 70

>ref|XP_961283.1| hypothetical protein NCU04127 [Neurospora crassa OR74A]
sp|Q9C2D4.2|SC61G_NEUCR RecName: Full=Probable protein transport protein Sec61 subunit
gamma
emb|CAC28779.2| putative protein [Neurospora crassa]
gb|EAA32047.1| hypothetical protein NCU04127 [Neurospora crassa OR74A]
Length = 70

Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 18/68 (26%), Positives = 33/68 (48%)

Query: 2 EAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPI 61
+ I +D R+F K ++ ++C KPDR+EF K++ IP+
Sbjct: 3 DQIQEILDVPREFLKDGIQFIKKCQKPKDRREFIKISQAVGTGFLIMGAVGYLVKLIHIPL 62

Query: 62 NNIIVGSS 69
N ++VG +
Sbjct: 63 NQVLVGGA 70

>ref|XP_001537820.1| predicted protein [Ajellomyces capsulatus NAm1]
gb|EDN10781.1| predicted protein [Ajellomyces capsulatus NAm1]
Length = 70

Score = 44.3 bits (103), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 18/58 (31%), Positives = 28/58 (48%)

Query: 12 RFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNIIVGSS 69
+DF K + + RC KPD++EF K++ IP+NNI+VG +
Sbjct: 13 KDFVKDGMFLFMNRCTKPKREFLKISQAVGFGFLIMGAIGYFIKLIHIPVNNILVGGA 70

>ref|XP_001911892.1| unnamed protein product [Podospira anserina]
emb|CAP73720.1| unnamed protein product [Podospira anserina]
Length = 70

Score = 44.3 bits (103), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 17/68 (25%), Positives = 33/68 (48%)

Query: 2 EAIDSAIDPLRDFAKSSVRLVQRCHKPDREFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 61
+ + +D R+F K + + + KPD+KEF K++ + +P+
Sbjct: 3 DQVQEILDVPREFLKDGIFHKAQKPDQKEFLKISQAVGVGFLIMGAVGYFVKLIHVPL 62

Query: 62 NNIIVGSS 69
NNI+VG +
Sbjct: 63 NNILVGA 70

>ref|XP_001270709.1| protein translocase, putative [Aspergillus clavatus NRRL 1]
gb|EAW09283.1| protein translocase, putative [Aspergillus clavatus NRRL 1]
Length = 70

Score = 44.3 bits (103), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 20/68 (29%), Positives = 33/68 (48%)

Query: 2 EAIDSAIDPLRDFAKSSVRLVQRCHKPDREFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 61
+ I D RDF + + V++C KPD++EF K++ + IP+
Sbjct: 3 DTIQELADIPRDFLRDGMFLVRKCTKPKREFIKISQAVGMGFIIMVSIGYFIKLIHIPV 62

Query: 62 NNIIVGSS 69
NNI+VG +
Sbjct: 63 NNILVGA 70

>ref|NP_611482.1| CG13426 CG13426-PA [Drosophila melanogaster]
gb|AAF57466.1| CG13426-PA [Drosophila melanogaster]
Length = 105

Score = 44.3 bits (103), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 20/57 (35%), Positives = 31/57 (54%)

Query: 10 PLRDFAKSSVRLVQRCHKPDREFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNIIV 66
P +DF K+S+R +RC KPDR+EF ++++ + IPI NII+
Sbjct: 48 PSKDFYKNSLRFYKRCTKPDREFQRISIGIGVGFLIMGLIGFVVKLMHIPIVNIIM 104

>ref|XP_001466134.1| protein transport protein sec61 gamma subunit [Leishmania
infantum JPCM5]
ref|XP_001683856.1| protein transport protein sec61 gamma subunit, putative
[Leishmania major]
emb|CAJ05099.1| protein transport protein sec61 gamma subunit, putative
[Leishmania major]
emb|CAM68573.1| protein transport protein sec61 gamma subunit, putative
[Leishmania infantum]
Length = 69

Score = 43.9 bits (102), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 22/64 (34%), Positives = 31/64 (48%)

Query: 5 DSAIDPLRDFAKSSVRLVQRCHKPDREFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNI 64
D P+ F K+S LV++C KP+ EFT A+ I IPINN+
Sbjct: 6 DILFHPHIVAFTKNSRMLVRKCKPKNYNEFTTAAIAALIGFFMMGFLGFFVKLVFIPINNV 65

Query: 65 IVGS 68
I+G+
Sbjct: 66 ILGA 69

>gb|AAV85043.1| IP05558p [Drosophila melanogaster]
Length = 124

Score = 43.9 bits (102), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 20/57 (35%), Positives = 31/57 (54%)

Query: 10 PLRDFAKSSVRLVQRCHKPDREFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNIIV 66
P +DF K+S+R +RC KPDR+EF ++++ + IPI NII+
Sbjct: 67 PSKDFYKNSLRFYKRCTKPDREFQRISIGIGVGFLIMGLIGFVVKLMHIPIVNIIM 123

>ref|XP_001974909.1| GG20863 [Drosophila erecta]
gb|EDV55309.1| GG20863 [Drosophila erecta]
Length = 105

Score = 43.9 bits (102), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 20/61 (32%), Positives = 32/61 (52%)

Query: 6 SAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNII 65
+++ P DF K+S+R +RC KPDR EF ++++ + IPI NII
Sbjct: 44 TSLLPSSDFYKNSLRFYKRC TKPDRHEFQRISIAIGVGFLIMGLIGFAVKLMHIPIVNII 103

Query: 66 V 66
+
Sbjct: 104 M 104

>ref|XP_001609442.1| protein transport protein SEC61 gamma subunit, putative [Babesia
bovis T2Bo]
gb|EDO05874.1| protein transport protein SEC61 gamma subunit, putative [Babesia
bovis]
Length = 82

Score = 43.1 bits (100), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 19/55 (34%), Positives = 29/55 (52%)

Query: 13 DFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNIIVG 67
DF S RLV++C KPD+KE+ ++ ++ IP+NNI+VG
Sbjct: 25 DFINDSTRLVKCTKPKDKKEYGRILRACSVGFFIMGFIGYMKVLMFIPVNNILVG 79

>ref|XP_001215615.1| conserved hypothetical protein [Aspergillus terreus NIH2624]
gb|EAU32981.1| conserved hypothetical protein [Aspergillus terreus NIH2624]
Length = 70

Score = 43.1 bits (100), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 17/58 (29%), Positives = 30/58 (51%)

Query: 12 RFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNIIVGSS 69
R+F K ++ + R KPDR+EF K++ + IP+NN++VG++
Sbjct: 13 REFFKDGMQFINRSQKPDREFFIKISQAVGVGFLVMGGIGFIVKLVHIPVNNVLVGAA 70

>ref|XP_001959014.1| GF12667 [Drosophila ananassae]
gb|EDV35836.1| GF12667 [Drosophila ananassae]
Length = 105

Score = 43.1 bits (100), Expect = 0.007, Method: Compositional matrix adjust.
Identities = 22/62 (35%), Positives = 31/62 (50%)

Query: 6 SAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNII 65
S I P F K S+R ++RC KP+R+EF + + A+ IPI NII
Sbjct: 44 SFIIPSSGFFKDSMRFMKRC TKPNRQEFRRTCMAIAGVFFIMGTIGFLVKLMHIPITNII 103

Query: 66 VG 67
+G
Sbjct: 104 MG 105

>ref|XP_001022928.1| Protein transport protein SEC61 gamma-1 subunit, putative
[Tetrahymena thermophila SB210]
gb|EAS02683.1| Protein transport protein SEC61 gamma-1 subunit, putative
[Tetrahymena thermophila SB210]
Length = 73

Score = 43.1 bits (100), Expect = 0.007, Method: Compositional matrix adjust.
Identities = 22/63 (34%), Positives = 31/63 (49%)

Query: 4 IDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINN 63
+ S + DFA+ S R V++C KP+ KE K A+ A+ IPINN
Sbjct: 9 VQSLVKSAIDFAEESKRFFVKKCTKPNAKELKKTAMYCAGFAVMGVVGYLIKLVFIPINN 68

Query: 64 IIV 66
II+
Sbjct: 69 IIL 71

>ref|XP_001203964.1| PREDICTED: similar to Sec61 gamma subunit, partial
[Strongylocentrotus purpuratus]
ref|XP_001199784.1| PREDICTED: similar to Sec61 gamma subunit, partial
[Strongylocentrotus purpuratus]
Length = 31

Score = 42.7 bits (99), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 18/31 (58%), Positives = 23/31 (74%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRK 31
M+ I I+P + FAK S+RLV+RC KPDRK
Sbjct: 1 MDQIQQTIEPAKQFAKDSIRLVKRCTKPDRK 31

>ref|XP_763390.1| protein translocation complex, sec61 subunit gamma [Theileria
parva strain Muguga]
gb|EAN31107.1| protein translocation complex, sec61 gamma chain, putative
[Theileria parva]
Length = 82

Score = 42.7 bits (99), Expect = 0.009, Method: Compositional matrix adjust.
Identities = 19/56 (33%), Positives = 29/56 (51%)

Query: 13 DFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNIIVGS 68
+F S RLV++C KPDRKE+ ++ A+ IP+NNI+V +
Sbjct: 25 EFVNGSTRLVKCTKPDRKEYMRILNACAVGFFVMGFIGYFVKLLFIPVNNILVAA 80

>ref|XP_001829161.1| predicted protein [Coprinosopsis cinerea okayama7#130]
gb|EAU92796.1| predicted protein [Coprinosopsis cinerea okayama7#130]
Length = 70

Score = 42.4 bits (98), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 20/68 (29%), Positives = 33/68 (48%)

Query: 2 EAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPI 61
E I ++ ++F + + + RC KP +KEFT++ A+ IPI
Sbjct: 3 EKIREFVEVPQEFFFQDGKQFLTRCTKPSKKEFTQICKAVAVGFAVMGFIGYFVKLIHIPI 62

Query: 62 NNIIVGSS 69
NNI+VG +
Sbjct: 63 NNILVGGA 70

>ref|XP_955056.1| protein translocation complex subunit (SEC61 gamma chain),
putative [Theileria annulata]
emb|CAI75580.1| protein translocation complex subunit (SEC61 gamma chain),
putative [Theileria annulata]
Length = 82

Score = 42.4 bits (98), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 19/56 (33%), Positives = 29/56 (51%)

Query: 13 DFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNIIVGS 68
+F S RLV++C KPDRKE+ ++ A+ IP+NNI+V +
Sbjct: 25 EFVNGSTRLVKCTKPDRKEYMRILNACAVGFFVMGFIGYFVKLLFIPVNNILVSA 80

>ref|XP_002091685.1| GE13801 [Drosophila yakuba]
gb|EDW91397.1| GE13801 [Drosophila yakuba]
Length = 105

Score = 42.0 bits (97), Expect = 0.014, Method: Compositional matrix adjust.
Identities = 20/61 (32%), Positives = 31/61 (50%)

Query: 6 SAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNII 65
S + P F K+S+R +RC KPDR+EF ++++ + IPI NII
Sbjct: 44 SLLLPSSHFYKNSLRFYKRCSPDRREFQRISLAIGVGFLIMGLIGFVVKLMHIPIVNII 103

Query: 66 V 66
+
Sbjct: 104 M 104

>ref|XP_001874004.1| predicted protein [Laccaria bicolor S238N-H82]
gb|EDR15796.1| predicted protein [Laccaria bicolor S238N-H82]
Length = 70

Score = 41.6 bits (96), Expect = 0.019, Method: Compositional matrix adjust.
Identities = 21/68 (30%), Positives = 32/68 (47%)

Query: 2 EAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 61
+ I ID + F + + + RC KP +KEFT++ A+ IPI
Sbjct: 3 DKIREFIDVPQQFIRDGNQFLTRCTKPSQKEFTQICKAVAVGFAVMGFIGYFVKLIHIPI 62

Query: 62 NNIIVGSS 69
NNI+VG +
Sbjct: 63 NNILVGGA 70

>ref|XP_001522383.1| hypothetical protein MGCH7_ch7g490 [Magnaporthe grisea 70-15]
gb|EAQ71083.1| hypothetical protein MGCH7_ch7g490 [Magnaporthe grisea 70-15]
Length = 601

Score = 41.2 bits (95), Expect = 0.022, Method: Composition-based stats.
Identities = 17/64 (26%), Positives = 31/64 (48%)

Query: 2 EAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 61
+++ +D R+F K ++ + RC KPD+KEF ++ + IP+
Sbjct: 3 DSVQEILDVPREFVKDGIQFLNRCQKPKKKEFRQICQAVGVGFLIMGAVGYIVKLVHIPL 62

Query: 62 NNII 65
NNI+
Sbjct: 63 NNIL 66

>ref|XP_001300450.1| protein translocase gamma subunit, putative [Trichomonas vaginalis G3]
ref|XP_001302120.1| protein translocase gamma subunit, putative [Trichomonas vaginalis G3]
ref|XP_001580487.1| protein translocase gamma subunit, putative [Trichomonas vaginalis G3]
gb|EAX87520.1| protein translocase gamma subunit, putative [Trichomonas vaginalis G3]
gb|EAX89190.1| protein translocase gamma subunit, putative [Trichomonas vaginalis G3]
gb|EAY19501.1| protein translocase gamma subunit, putative [Trichomonas vaginalis G3]
Length = 71

Score = 41.2 bits (95), Expect = 0.022, Method: Compositional matrix adjust.
Identities = 21/68 (30%), Positives = 31/68 (45%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 60
MEA+D P +F KS V++++RC P K A +A+ P
Sbjct: 1 MEALDIVAAPATNFVKSCVKVLKRCTLPSTKVLKDSASASAVGFLILGSVGFIFKVIAYP 60

Query: 61 INNIIVGS 68
INN+I+G
Sbjct: 61 INNVIIGG 68

>ref|XP_001389573.1| hypothetical protein An01g11630 [Aspergillus niger]
emb|CAK44065.1| unnamed protein product [Aspergillus niger]

Score = 39.7 bits (91), Expect = 0.062, Method: Compositional matrix adjust.
Identities = 19/61 (31%), Positives = 31/61 (50%)

Query: 6 SAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNII 65
+ + P F K+S+R +RC KPDR+EF +++++ + IPI NII
Sbjct: 44 TLLLPSSAFYKNSLRFYKRC TKPDRQEFQRISIAIGVGFLIMGLIGFVVKLMHIPIVNII 103

Query: 66 V 66
+
Sbjct: 104 M 104

>ref|XP_662193.1| hypothetical protein AN4589.2 [Aspergillus nidulans FGSC A4]
gb|EAA60932.1| hypothetical protein AN4589.2 [Aspergillus nidulans FGSC A4]
Length = 70

Score = 39.7 bits (91), Expect = 0.080, Method: Compositional matrix adjust.
Identities = 16/68 (23%), Positives = 32/68 (47%)

Query: 2 EAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIP 61
E + ++ ++F + ++ V R KPD++EF K++ IP+
Sbjct: 3 EQVQELLNIPQEFLRDGMQFVNRSQKPKDKREFIKISQAVGTGFLIMGFIGYIVKLIHIPV 62

Query: 62 NNIIVGSS 69
NN++VG +
Sbjct: 63 NNVLVGGA 70

>gb|EDL00527.1| mCG1042596 [Mus musculus]
Length = 62

Score = 39.3 bits (90), Expect = 0.081, Method: Compositional matrix adjust.
Identities = 19/42 (45%), Positives = 28/42 (66%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRKEFTKVAVRTAI 42
M+ + ++ R F+K+S+ LV+RC K RKEF K+A TAI
Sbjct: 1 MDQVIQFVELSRQFSKNSIHLVKRCKTIHRKEFQKIAKATAI 42

>ref|XP_389047.1| hypothetical protein FG08871.1 [Gibberella zeae PH-1]
Length = 70

Score = 39.3 bits (90), Expect = 0.083, Method: Compositional matrix adjust.
Identities = 16/57 (28%), Positives = 29/57 (50%)

Query: 13 DFAKSSVRLVQRCHKPDRKEFTKVAVRTAIXXXXXXXXXXXXXXXXXXIPINNIIIVGSS 69
+F + V+ ++RC KPD+KEF ++ + IP+N+ +VGS+
Sbjct: 14 EFVRDGVQFMRRCTKPDQKEFLRLCQAVGVGFLIMGAVGVVVKLVHIPLNHALVGSA 70

>ref|XP_001163709.1| PREDICTED: similar to SEC61 gamma, partial [Pan troglodytes]
Length = 31

Score = 38.5 bits (88), Expect = 0.14, Method: Compositional matrix adjust.
Identities = 16/31 (51%), Positives = 22/31 (70%)

Query: 1 MEAIDSAIDPLRDFAKSSVRLVQRCHKPDRK 31
M+ + ++P R F K S+RLV+RC KPDRK
Sbjct: 1 MDQVMQFVEPSRQFVKDSIRLVKRCTKPDRK 31

>ref|XP_652711.1| Protein transport protein SEC61 gamma subunit, putative
[Entamoeba histolytica HM-1:IMSS]
gb|EAL47328.1| Protein transport protein SEC61 gamma subunit, putative
[Entamoeba histolytica HM-1:IMSS]
Length = 69

Score = 37.4 bits (85), Expect = 0.34, Method: Compositional matrix adjust.
Identities = 13/28 (46%), Positives = 20/28 (71%)

