

SUMMARY

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STUDY TITLE

Sequence Similarity Assessment of AAD-12 Protein to Known Toxins by Bioinformatics
Analysis
(Update, February, 2011)

DATA REQUIREMENTS

N/A

AUTHOR(S)

P. Song

STUDY COMPLETED ON

20 – April – 2011

PERFORMING LABORATORY

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LABORATORY STUDY ID

110327

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Sequence Similarity Assessment of AAD-12 Protein to Known Toxins by Bioinformatics
Analysis
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SUMMARY

Aryloxyalkanoate dioxygenase-12 (AAD-12) protein, encoded by a plant-optimized *aad-12* gene originally from soil bacterium *Delftia acidovorans*, was expressed in soybean (*Glycine max* L.) events DAS-68416-4 and DAS-44406-6. AAD-12 provides tolerance to 2,4-dichlorophenoxyacetic acid (2,4-D), fluroxypyr, and triclopyr-based herbicides. In this study, the amino acid sequence of the AAD-12 protein was evaluated for sequence similarity to known protein toxins using a BLASTp search against an up-to-date GenBank non-redundant protein database (update to February 18, 2011). All the sequence alignments returned by the search were associated with dioxygenase or similar proteins. The results indicated that the AAD-12 protein expressed in soybean events DAS-68416-4 and DAS-44406-6 contains no significant sequence similarity with any known toxic protein that is harmful to humans or animals.

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N/A

AUTHOR(S)

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Compound: AAD-12 Protein

Title: Sequence Similarity Assessment of AAD-12 Protein to Known Toxins by
Bioinformatics Analysis
(Update, February, 2011)

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Company: Dow AgroSciences LLC

Company Agent: M. Krieger

Title: Regulatory Manager

Signature: 

Date: 19 April 2011

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Title: Sequence Similarity Assessment of AAD-12 Protein to Known Toxins by
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(Update, February, 2011)

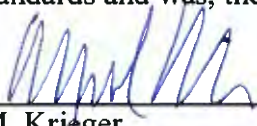
Study Initiation Date: 02/16/2011

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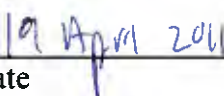
United States Environmental Protection Agency
Title 40 Code of Federal Regulations Part 160
FEDERAL REGISTER, August 17, 1989

Organisation for Economic Co-Operation and Development
ENV/MC/CHEM(98)17, Paris January 26, 1998

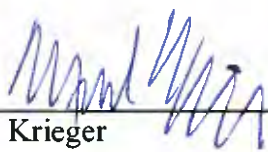
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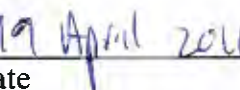
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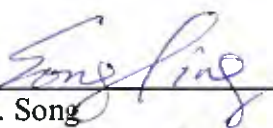
Date




M. Krieger
Submitter
Dow AgroSciences LLC



Date



P. Song
Study Director/Author
Dow AgroSciences LLC



Study Completion Date

QUALITY ASSURANCE STATEMENT

Compound: AAD-12 Protein

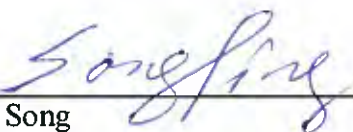
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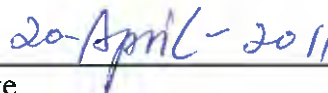
Study Completion Date: 20 – April – 2011

NON-GLP STUDY

SIGNATURE PAGE



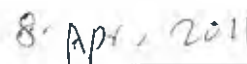
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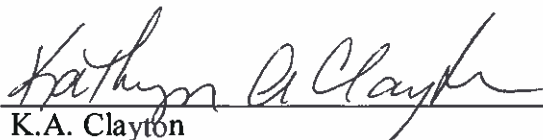
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STUDY PERSONNEL

Title: Sequence Similarity Assessment of AAD-12 Protein to Known Toxins by
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Principal Analyst: N/A
(Principle Investigator)

Analysts: N/A

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Sequence Similarity Assessment of AAD-12 Protein to Known Toxins by Bioinformatics
Analysis
(Update, February, 2011)

ABSTRACT

Aryloxyalkanoate dioxygenase-12 (AAD-12) protein, encoded by a plant-optimized aad-12 gene originally from soil bacterium *Delftia acidovorans*, was expressed in soybean (*Glycine max* L.) event DAS-68416-4 and DAS-44406-6. AAD-12 provides tolerance to 2,4-dichlorophenoxyacetic acid (2,4-D), fluroxypyr, and triclopyr-based herbicides. In this study, the amino acid sequence of the AAD-12 protein was evaluated for sequence similarity to known protein toxins using a BLASTp search against an up-to-date GenBank non-redundant protein database (update to February 18, 2011). All the sequence alignments returned by the search were associated with dioxygenase or similar proteins. The results indicated that the AAD-12 protein expressed in soybean events, DAS-68416-4 and DAS-44406-6, contains no significant sequence similarity with any known toxic protein that is harmful to humans or animals.

INTRODUCTION

Aryloxyalkanoate dioxygenase-12 (AAD-12) protein, encoded by a plant-optimized aad-12 gene originally from soil bacterium *Delftia acidovorans*, was expressed in soybean (*Glycine max* L.) events DAS-68416-4 and DAS-44406-6. AAD-12 provides tolerance to 2,4-dichlorophenoxyacetic acid (2,4-D), fluroxypyr, and triclopyr-based herbicides.

The safety assessment of proteins expressed in transgenic plants may include an evaluation of whether or not the protein can function as a potential toxin when present in the human diet. It has been reported that assessing the potential toxicity of a protein may include comparison of the protein sequence to known protein toxin sequences (¹). Since there is no commonly recognized definition of a protein toxin based on its sequence, a comparison should be made to a database of all available protein sequences as a conservative approach. Proteins identified with statistically significant similarity using a local alignment algorithm should then be evaluated for their relevance as potential toxins. For small-scale analyses, such as a single search of a query protein against a large database, a statistically significant similarity that ensures avoidance of false positives (labeling a sequence as related to something in the database when it is not) typically employs an expectation value (E-value) threshold between 0.001 and 0.01. The E-value corresponds to the frequency one would expect to see a match of equal or greater quality by chance (false positive) in a search of the database. For E-values of 0.001 or 0.01, one would expect to find a false positive result once in 1000 or 100 searches, respectively (²). For $E() = 1$, there is a statistically equal chance of a hit occurring due to homology or by random chance in a search of a given database. Although little can be done to avoid false negatives (labeling a sequence as unrelated to something in the database when in fact a homolog is present), visual inspection of the quality of less conservative alignments with $E() < 1$ may minimize false negative results (²).

The objective of this study was to compare the amino acid sequences of the AAD-12 protein expressed in DAS-68416-4 and DAS-44406-6 with known protein toxins in the public protein sequence database.

METHODS

Query Sequence Preparation

The AAD-12 protein sequence was prepared in FASTA format for use with BLASTp search programs (Appendix 1).

Toxicity Assessment

To assess potential toxicity of the AAD-12 protein expressed in soybean events DAS-68416-4 and DAS-44406-6, a search for similarity of protein sequences was conducted using the BLASTp program (³). The amino acid sequence of the AAD-12 was queried using the BLASTp (Version 2.2.22+) against a non-redundant protein dataset (update to February 18, 2011), which incorporates non-redundant entries from all GenBank and RefSeq nucleotide translations (Genpept “nr”) along with protein sequences from SWISS-PROT (<http://www.expasy.org/sprot/>), PIR (<http://pir.georgetown.edu/>), PRF (<http://www.prf.or.jp/aboutdb-e.html>), and PDB (<http://www.wwpdb.org/>). The search was done through the BLAST program installed in an internal UNIX computer with default settings (Matrix = BLOSUM62, Gap Costs = Existence: 11, Extension: 1) except that a cutoff expectation E-value of 1.0 was used to generate biologically meaningful similarity between the query sequences and proteins in the database, the low complexity filtering was turned off, and the sequence description and alignment display were set to 2000 alignments. Although a statistically significant sequence similarity generally requires a match with an expectation value less than 0.01, a cutoff of $E < 1.0$ ensures that proteins with even limited similarity will not be overlooked in the search (²).

RESULTS AND CONCLUSIONS

The BLASTp search of AAD-12 protein returned a total of 1322 alignments ($E() < 1$). Of those alignments, 1267 show E-value below 0.01. By their annotations, the proteins associated with those alignments can be grouped into the following 11 categories (Table 1): 2,4-D/alpha-ketoglutarate dioxygenase, alkylsulfatase AtsK, alpha-ketoglutarate (dependent) dioxygenase, alpha-ketoglutarate-dependent sulfonate dioxygenase, ketoglutarate dehydratase, taurine catabolism dioxygenase, taurine dioxygenase, dioxygenase, oxidoreductase, pyoverdine biosynthesis protein, and hypothetical (putative) or unnamed proteins. AAD-12 (aryloxyalkanoate dioxygenase-12) itself is an alpha-ketoglutarate dependent dioxygenase. Hypothetical and unnamed proteins are derived from conceptual translation of DNA sequences generated from massive genome sequencing projects of various fungi and bacteria. Those proteins have functional annotations such as “probable taurine catabolism dioxygenase”, “clavaminic acid synthetase (CAS) –like”, and “putative alpha-ketoglutarate dependent dioxygenase”. None of these proteins returned by the BLASTp search is associated with toxicity. In conclusion, AAD-12 protein expressed in soybean events DAS-68416-4 and DAS-44406-6, contains no significant sequence similarity with any known toxic protein that is harmful to humans or animals.

REFERENCES

1. Codex Alimentarius, C. GUIDELINE FOR THE CONDUCT OF FOOD SAFETY ASSESSMENT OF FOODS DERIVED FROM RECOMBINANT-DNA PLANTS; 2009; pp 20-22.
2. Pearson, W. R., Flexible sequence similarity searching with the FASTA3 program package. *Methods Mol Biol* **2000**, *132*, 185-219.
3. Altschul, S. F., W. Gish, W. Miller, E. W. Myers, and D. J. Lipman, Basic local alignment search tool. *J. Mol. Biol.*, 1990. **215**: p. 403-10.

Table 1. BLASTp Search Summary of Proteins in the Alignments (E)<0.01) with AAD-12

Description	Number of alignments	E-value range
2,4-D/alpha-ketoglutarate dioxygenase	70	$7.00 \times 10^{-169} - 3 \times 10^{-4}$
Alkylsulfatase AtsK	7	$5.00 \times 10^{-21} - 2.00 \times 10^{-11}$
Alpha-ketoglutarate dioxygenase	30	$2.00 \times 10^{-33} - 0.006$
Alpha-ketoglutarate-dependent sulfonate dioxygenase	23	$3.00 \times 10^{-13} - 0.008$
Ketoglutarate dehydronase	220	$9.00 \times 10^{-14} - 0.001$
Taurine catabolism dioxygenase	170	$1.00 \times 10^{-79} - 0.006$
Taurine dioxygenase	382	$2.00 \times 10^{-30} - 0.005$
Dioxygenase	166	$8.00 \times 10^{-36} - 0.006$
Oxidoreductase	4	$4.00 \times 10^{-18} - 0.001$
Pyoverdine biosynthesis protein	25	$1.00 \times 10^{-06} - 0.006$
Hypothetical or unnamed proteins	170	$4.00 \times 10^{-32} - 0.006$

APPENDIX

1. Amino Acid Sequence of AAD-12

```
1 MAQTTLQITP TGATLGATVT GVHLATLDDA GFAALHAAWL QHALLIFPGQ
51 HLSNDQQITF AKRFGAIERI GGGDIVAISN VKADGTVRQH SPAEWDDMMK
101 VIVGNMAWHA DSTYMPVMAQ GAVFSAEVVP AVGGRTCFAD MRAAYDALDE
151 ATRALVHQRS ARHSLVYSQS KLGHVQQAGS AYIGYGMDTT ATPLRPLVKV
201 HPETGRPSLL IGRHAHAIPG MDAAESERFL EGLVDWACQA PRVHAHQWAA
251 GDVVVWDNRC LLHRAEPWDF KLPRVMWHSR LAGRPETEGA ALV
```

2. Archive of BLASTp Search Output of AAD-12 Protein Sequence

BLASTp search of AAD-12 protein generated an output file with more than 400 pages. The file is electronically stored in a secured computer in Dow AgroSciences and available for viewing in PDF format.

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Blastp search outputs of AAD-12 Protein

BLASTP 2.2.21 [Jun-14-2009]

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= AAD-12 vl
(293 letters)

Database: /usr/local/blast/db/blastlibs/nr
13,473,798 sequences; 4,621,495,809 total letters

Searching.....done

Sequences producing significant alignments:		Score (bits)	E Value
gb AAP88277.1	S-2,4-dichlorophenoxypropionate/alpha-ketoglutarate...	596	e-168
emb CAF32813.1	(S)-2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	369	e-100
ref ZP_01615308.1	Taurine catabolism dioxygenase TauD/TfdA [mar...	310	1e-82
gb ABL97633.1	24-dichlorophenoxyacetate alpha-ketoglutarate dio...	271	6e-71
gb ADC34025.1	TfdA-like protein [uncultured bacterium]	266	2e-69
emb CBJ20087.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	196	2e-48
emb CBJ20295.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	196	4e-48
emb CBJ20274.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	196	4e-48
emb CBJ20081.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	195	5e-48
emb CBJ20244.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	195	7e-48
emb CBJ20155.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	195	8e-48
emb CBJ20145.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	8e-48
emb CBJ20533.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	9e-48
emb CBJ20525.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	9e-48
emb CBJ20227.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	1e-47
emb CBJ20345.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	1e-47
emb CBJ20085.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	1e-47
emb CBJ20394.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	1e-47
emb CBJ20102.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	1e-47
emb CBJ20083.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	1e-47
emb CBJ20134.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	1e-47
emb CBJ20495.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	1e-47
emb CBJ20327.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	1e-47
emb CBJ20079.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	1e-47
emb CBJ20082.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	1e-47
emb CBJ20524.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	2e-47
emb CBJ20387.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	2e-47
emb CBJ20125.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	194	2e-47
emb CBJ20496.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	193	2e-47
emb CBJ20146.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	193	2e-47
emb CBJ20356.1	2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	193	2e-47

dbj BAB92966.1	alpha KG dependent 2,4-D dioxygenase [alpha prot...	162	6e-38
dbj BAB92964.1	alpha KG dependent 2,4-D dioxygenase [alpha prot...	162	7e-38
ref ZP_07575535.1	Taurine catabolism dioxygenase TauD/TfdA [Sph...	160	2e-37
dbj BAB92965.1	alpha KG dependent 2,4-D dioxygenase [alpha prot...	160	2e-37
ref YP_001203232.1	alpha-ketoglutarate-dependent 2, 4-dichlorop...	158	8e-37
ref YP_001242758.1	Alpha-ketoglutarate-dependent 2,4-dichloroph...	157	1e-36
ref ZP_02186322.1	alpha-ketoglutarate-dependent 2,4-dichlorophe...	156	4e-36
ref YP_002944024.1	Taurine catabolism dioxygenase TauD/TfdA [Va...	152	4e-35
ref NP_768133.1	alpha-ketoglutarate-dependent 2,4-dichloropheno...	151	9e-35
ref YP_001206007.1	TauD/TfdA family dioxygenase [Bradyrhizobium...	151	1e-34
gb ADC33952.1	TfdA-like protein [uncultured bacterium]	150	2e-34
emb CBJ20067.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	149	4e-34
ref YP_001240346.1	TauD/TfdA family dioxygenase [Bradyrhizobium...	149	4e-34
ref ZP_02187434.1	Taurine catabolism dioxygenase TauD/TfdA [alp...	148	8e-34
ref NP_990895.1	TfdA [Achromobacter denitrificans] >gi 44937736...	148	9e-34
gb ACF35465.1	TfdA [Burkholderia sp. TFD36] >gi 194245695 gb AC...	148	1e-33
sp Q45423.1	TFDA_BURSR RecName: Full=Alpha-ketoglutarate-depende...	147	1e-33
ref YP_025400.1	2,4-D / a-ketoglutarate dioxygenase [Ralstonia ...	147	2e-33
gb ACF35485.1	TfdA [Achromobacter xylosoxidans] >gi 194245735 g...	146	3e-33
gb AAM76772.1	2,4-D/alpha-ketoglutarate dioxygenase [Delftia ac...	146	3e-33
gb ADI17634.1	probable taurine catabolism dioxygenase [uncultur...	146	4e-33
gb AAK81681.1	2,4-D/alpha-ketoglutarate dioxygenase [Burkholder...	145	7e-33
gb ACF98189.1	putative TauD/TfdA family dioxygenase [uncultured...	144	2e-32
ref YP_611286.1	taurine catabolism dioxygenase TauD/TfdA [Ruege...	142	8e-32
ref YP_725771.1	taurine catabolism dioxygenase [Ralstonia eutro...	141	1e-31
ref ZP_02187618.1	Taurine catabolism dioxygenase TauD/TfdA [alp...	140	2e-31
ref ZP_01894281.1	alpha-ketoglutarate-dependent 2,4-dichlorophe...	140	3e-31
ref ZP_02186680.1	hypothetical protein BAL199_17688 [alpha prot...	139	3e-31
ref YP_001354176.1	taurine dioxygenase [Janthinobacterium sp. M...	139	7e-31
emb CBJ20072.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	138	9e-31
emb CBJ20071.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	138	1e-30
ref ZP_04945417.1	Probable taurine catabolism dioxygenase [Burk...	137	1e-30
ref NP_881979.1	putative taurine dioxygenase [Bordetella pertus...	136	3e-30
ref YP_001262583.1	taurine dioxygenase [Sphingomonas wittichii ...	135	6e-30
gb ADC34040.1	TfdA-like protein [uncultured bacterium]	135	8e-30
emb CBJ20063.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	135	8e-30
ref YP_293521.1	taurine dioxygenase [Ralstonia eutropha JMP134]...	135	8e-30
gb ADC34036.1	TfdA-like protein [uncultured bacterium]	135	9e-30
ref YP_003982528.1	alpha-ketoglutarate-dependent taurine dioxyg...	134	2e-29
ref YP_001413770.1	taurine dioxygenase [Parvibaculum lavamentiv...	134	2e-29
ref YP_586272.1	taurine dioxygenase (TauD/TfdA family) [Cupriav...	133	2e-29
ref NP_641182.1	taurine dioxygenase [Xanthomonas axonopodis pv....	133	3e-29
ref YP_001773839.1	taurine catabolism dioxygenase TauD/TfdA [Bu...	133	3e-29
ref YP_004115686.1	Taurine dioxygenase [Pantoea sp. At-9b] >gi ...	133	4e-29
ref YP_002800232.1	taurine catabolic dioxygenase protein [Azoto...	132	4e-29
ref NP_882351.1	putative taurine catabolism dioxygenase [Bordet...	132	4e-29
ref YP_626229.1	taurine catabolism dioxygenase TauD/TfdA [Burkh...	132	4e-29
gb ADC34003.1	TfdA-like protein [uncultured bacterium] >gi 2850...	132	5e-29
ref YP_001633627.1	taurine dioxygenase [Bordetella petrii DSM 1...	132	5e-29
ref NP_886536.1	putative taurine catabolism dioxygenase [Bordet...	132	6e-29
ref YP_299483.1	taurine dioxygenase [Ralstonia eutropha JMP134]...	132	8e-29
ref YP_553184.1	putative alpha KG dependent 2,4-D dioxygenase [...	131	9e-29
ref ZP_04943904.1	hypothetical protein BCPG_05482 [Burkholderia...	131	1e-28
ref ZP_03265714.1	Taurine dioxygenase [Burkholderia sp. H160] >...	131	1e-28
ref YP_002008624.1	taurine dioxygenase, 2-oxoglutarate-dependen...	131	1e-28
ref YP_345870.1	taurine catabolism dioxygenase TauD/TfdA [Pseud...	130	2e-28
ref YP_257284.1	taurine catabolism dioxygenase TauD [Pseudomona...	130	2e-28
ref YP_001666439.1	taurine dioxygenase [Pseudomonas putida GB-1...	130	2e-28
gb ADO34964.1	putative (S)-2,4-dichlorophenoxypropionate dioxyg...	130	2e-28
ref YP_002942895.1	Taurine dioxygenase [Variovorax paradoxus S1...	130	2e-28
ref YP_244520.1	taurine dioxygenase [Xanthomonas campestris pv....	130	3e-28
ref YP_003977545.1	taurine catabolism dioxygenase TauD, TfdA fa...	129	4e-28
ref ZP_06704693.1	Taurine dioxygenase [Xanthomonas fuscans subs...	129	4e-28

ref ZP_04586493.1	TauD/TfdA family dioxygenase [Pseudomonas syr...	129	4e-28
ref YP_001904982.1	Taurine dioxygenase [Xanthomonas campestris ...	129	5e-28
ref YP_003606832.1	Taurine dioxygenase [Burkholderia sp. CCGE10...	129	6e-28
ref YP_003910369.1	Taurine dioxygenase [Burkholderia sp. CCGE10...	129	6e-28
ref YP_605938.1	taurine catabolic dioxygenase [Pseudomonas ento...	128	8e-28
ref YP_001751903.1	taurine dioxygenase [Pseudomonas putida W619...	128	1e-27
ref NP_794929.1	dioxygenase, TauD/TfdA family [Pseudomonas syri...	128	1e-27
ref YP_002869819.1	putative taurine catabolism dioxygenase [Pse...	127	1e-27
ref YP_998536.1	taurine dioxygenase [Verminephrobacter eiseniae...	127	1e-27
ref YP_003210470.1	hypothetical protein CTU_21070 [Cronobacter ...	127	1e-27
gb AAB47567.1	2,4-D dioxygenase [Burkholderia cepacia]	127	2e-27
ref NP_959172.1	hypothetical protein MAP0238c [Mycobacterium av...	127	2e-27
ref ZP_03397512.1	dioxygenase, TauD/TfdA family [Pseudomonas sy...	127	2e-27
ref NP_636166.1	taurine dioxygenase [Xanthomonas campestris pv...	127	2e-27
ref YP_001586000.1	taurine dioxygenase [Burkholderia multivoran...	127	2e-27
ref ZP_06878755.1	putative taurine catabolism dioxygenase [Pseu...	127	2e-27
ref ZP_06485157.1	taurine dioxygenase [Xanthomonas campestris p...	127	2e-27
ref ZP_06842038.1	Taurine dioxygenase [Burkholderia sp. Chl-1] ...	127	3e-27
ref ZP_07254236.1	dioxygenase, TauD/TfdA family protein [Pseudo...	127	3e-27
ref YP_555428.1	taurine dioxygenase [Burkholderia xenovorans LB...	126	3e-27
ref YP_001941299.1	taurine dioxygenase [Burkholderia multivoran...	126	3e-27
ref ZP_06492039.1	taurine dioxygenase [Xanthomonas campestris p...	126	3e-27
ref YP_879528.1	taurine catabolism dioxygenase TauD/TfdA [Mycob...	126	4e-27
ref ZP_04948709.1	Probable taurine catabolism dioxygenase [Burk...	126	4e-27
ref ZP_05214809.1	taurine catabolism dioxygenase TauD/TfdA [Myc...	126	4e-27
ref ZP_07796648.1	putative taurine catabolism dioxygenase [Pseu...	126	4e-27
ref YP_790929.1	putative taurine catabolism dioxygenase [Pseudo...	126	4e-27
ref YP_001265549.1	taurine dioxygenase [Pseudomonas putida Fl] ...	126	4e-27
ref ZP_08185828.1	putative taurine catabolism dioxygenase [Xant...	125	5e-27
ref NP_251000.1	hypothetical protein PA2310 [Pseudomonas aerugi...	125	5e-27
ref ZP_08187882.1	putative taurine catabolism dioxygenase [Xant...	125	5e-27
ref YP_841732.1	taurine catabolism dioxygenase [Ralstonia eutro...	125	5e-27
gb AAT51290.1	PA2310 [synthetic construct]	125	5e-27
ref ZP_05635920.1	TauD/TfdA family dioxygenase [Pseudomonas syr...	125	6e-27
ref YP_002908767.1	Taurine dioxygenase [Burkholderia glumae BGR...	125	6e-27
ref YP_001117391.1	taurine dioxygenase [Burkholderia vietnamien...	125	6e-27
ref ZP_08183773.1	putative taurine catabolism dioxygenase [Xant...	125	7e-27
ref YP_362614.1	taurine dioxygenase [Xanthomonas campestris pv...	125	7e-27
ref YP_002153811.1	putative taurine dioxygenase [Burkholderia c...	125	7e-27
ref ZP_04934071.1	hypothetical protein PA2G_01415 [Pseudomonas ...	125	7e-27
ref ZP_02468555.1	Taurine dioxygenase [Burkholderia thailandens...	125	8e-27
ref ZP_02189759.1	Alpha-ketoglutarate-dependent taurine dioxyge...	125	8e-27
ref YP_001437971.1	hypothetical protein ESA_01880 [Cronobacter ...	125	9e-27
ref NP_742338.1	TauD/TfdA family dioxygenase [Pseudomonas putid...	125	9e-27
ref YP_954965.1	taurine catabolism dioxygenase TauD/TfdA [Mycob...	125	9e-27
ref ZP_06840724.1	Taurine catabolism dioxygenase TauD/TfdA [Bur...	125	9e-27
gb ADC34043.1	TfdA-like protein [uncultured bacterium]	124	1e-26
ref ZP_02884179.1	Taurine dioxygenase [Burkholderia graminis C4...	124	1e-26
ref ZP_06495450.1	taurine dioxygenase [Pseudomonas syringae pv...	124	1e-26
ref ZP_08177331.1	putative taurine catabolism dioxygenase [Xant...	124	1e-26
ref YP_002551991.1	taurine dioxygenase [Acidovorax ebreus TPSY]...	124	1e-26
ref ZP_01365674.1	hypothetical protein PaerPA_01002800 [Pseudom...	124	1e-26
ref ZP_07265737.1	taurine dioxygenase [Pseudomonas syringae pv...	124	2e-26
ref ZP_03572034.1	alpha-ketoglutarate-dependent taurine dioxyge...	124	2e-26
ref ZP_03578265.1	alpha-ketoglutarate-dependent taurine dioxyge...	124	2e-26
ref ZP_07772746.1	alpha-ketoglutarate-dependent taurine dioxyge...	124	2e-26
ref ZP_01894021.1	Taurine catabolism dioxygenase TauD/TfdA [Mar...	124	2e-26
ref ZP_06685128.1	taurine dioxygenase [Achromobacter piechaudii...	124	2e-26
gb ABD16716.1	alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	123	2e-26
ref ZP_06458047.1	TauD/TfdA family dioxygenase [Pseudomonas syr...	123	2e-26
ref ZP_08138932.1	taurine dioxygenase [Pseudomonas sp. TJI-51] ...	123	2e-26
gb ABD16700.1	alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	123	3e-26
gb ABD16703.1	alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	123	3e-26

ref YP_003753223.1	alpha-ketoglutarate-dependent 2, 4-dichlorop...	123	3e-26
gb ABD16698.1	alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	123	3e-26
gb ABD16699.1	alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	123	3e-26
ref YP_558852.1	taurine dioxygenase [Burkholderia xenovorans LB...	123	3e-26
ref YP_272623.1	TauD/TfdA family dioxygenase [Pseudomonas syrin...	123	4e-26
ref YP_003450157.1	taurine dioxygenase [Azospirillum sp. B510] ...	123	4e-26
ref YP_616210.1	taurine catabolism dioxygenase TauD/TfdA [Sphin...	123	4e-26
gb ABD16701.1	alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	122	4e-26
gb EFV82234.1	taurine dioxygenase [Achromobacter xylosoxidans C54]	122	4e-26
ref YP_233447.1	taurine dioxygenase [Pseudomonas syringae pv. s...	122	5e-26
ref YP_004017351.1	taurine dioxygenase [Frankia sp. Eu1lc] >gi ...	122	5e-26
ref ZP_04943924.1	Taurine dioxygenase [Burkholderia cenocepacia...	122	6e-26
ref YP_202406.1	taurine dioxygenase [Xanthomonas oryzae pv. ory...	122	6e-26
ref YP_001507295.1	taurine catabolism dioxygenase TauD/TfdA [Fr...	122	6e-26
ref YP_001859789.1	taurine dioxygenase [Burkholderia phymatum S...	122	7e-26
gb ABD16697.1	alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	122	7e-26
ref YP_001912283.1	taurine dioxygenase [Xanthomonas oryzae pv. ...	122	8e-26
ref ZP_05636704.1	TauD/TfdA family dioxygenase [Pseudomonas syr...	122	8e-26
gb ABD16715.1	alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	122	9e-26
gb ABD16714.1	alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	121	9e-26
ref ZP_07003248.1	Alpha-ketoglutarate-dependent taurine dioxyge...	121	1e-25
ref YP_001071988.1	taurine catabolism dioxygenase TauD/TfdA [My...	121	1e-25
ref YP_640870.1	taurine catabolism dioxygenase TauD/TfdA [Mycob...	121	1e-25
ref ZP_03585090.1	alpha-ketoglutarate-dependent taurine dioxyge...	121	1e-25
emb CBJ20513.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	121	1e-25
ref YP_002980735.1	taurine dioxygenase [Ralstonia pickettii 12D...	121	1e-25
gb ABD16710.1	alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	121	1e-25
gb ACX54976.1	putative (S)-2,4-dichlorophenoxypropionate dioxyg...	121	1e-25
ref ZP_08206675.1	taurine dioxygenase [Gordonia neofelifaecis N...	120	2e-25
ref YP_001773806.1	taurine dioxygenase [Burkholderia cenocepaci...	120	2e-25
gb ABD16713.1	alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	120	2e-25
ref XP_002482822.1	alpha-ketoglutarate-dependent taurine dioxyg...	120	2e-25
gb ACX54984.1	putative (S)-2,4-dichlorophenoxypropionate dioxyg...	120	2e-25
ref ZP_01627763.1	putative alpha-ketoglutarate-dependent taurin...	120	2e-25
gb ABD16705.1	alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	120	2e-25
ref YP_452585.1	taurine dioxygenase [Xanthomonas oryzae pv. ory...	120	2e-25
ref ZP_06411142.1	Taurine catabolism dioxygenase TauD/TfdA [Fra...	120	3e-25
ref YP_778414.1	taurine dioxygenase [Burkholderia ambifaria AMM...	120	3e-25
ref ZP_04590344.1	TauD/TfdA family dioxygenase [Pseudomonas syr...	120	3e-25
ref ZP_02891645.1	Taurine dioxygenase [Burkholderia ambifaria I...	120	3e-25
ref YP_001816237.1	taurine dioxygenase [Burkholderia ambifaria ...	120	3e-25
ref ZP_07675624.1	taurine dioxygenase, TauD/TfdA family [Ralsto...	120	3e-25
gb ACX54994.1	putative (S)-2,4-dichlorophenoxypropionate dioxyg...	120	3e-25
ref YP_621125.1	taurine dioxygenase [Burkholderia cenocepacia A...	120	3e-25
ref ZP_02466092.1	dioxygenase TauD/TfdA family protein [Burkhol...	120	3e-25
gb ADC33992.1	TfdA-like protein [uncultured bacterium]	120	3e-25
ref YP_004153368.1	taurine dioxygenase [Variovorax paradoxus EP...	120	3e-25
ref ZP_04941965.1	Taurine dioxygenase [Burkholderia cenocepacia...	120	3e-25
gb ABD16709.1	alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	119	4e-25
gb ABD16702.1	alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	119	4e-25
ref ZP_02909532.1	Taurine dioxygenase [Burkholderia ambifaria M...	119	4e-25
ref YP_002799399.1	taurine dioxygenase protein [Azotobacter vin...	119	5e-25
ref YP_001898279.1	Taurine dioxygenase [Ralstonia pickettii 12J...	119	6e-25
ref ZP_02241915.1	taurine dioxygenase [Xanthomonas oryzae pv. o...	118	8e-25
gb ABG66523.1	alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	118	8e-25
gb ADO85592.1	PenD [Streptomyces exfoliatus]	118	8e-25
ref YP_724558.1	Alpha-ketoglutarate-dependent taurine dioxygena...	118	8e-25
emb CBJ20078.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	118	1e-24
ref YP_837647.1	taurine dioxygenase [Burkholderia cenocepacia H...	118	1e-24
ref ZP_01616423.1	alpha-ketoglutarate-dependent taurine dioxyge...	118	1e-24
ref YP_624207.1	taurine dioxygenase [Burkholderia cenocepacia A...	118	1e-24
ref YP_001777149.1	taurine dioxygenase [Burkholderia cenocepaci...	117	1e-24
ref ZP_01224852.1	alpha-ketoglutarate-dependent taurine dioxyge...	117	1e-24

gb ADO34974.1 putative (S)-2,4-dichlorophenoxypropionate dioxyg...	117	2e-24
gb ABD16694.1 alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	117	2e-24
ref YP_004190416.1 putative dioxygenase [Vibrio vulnificus MO6-...	117	2e-24
gb ABD16695.1 alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	117	2e-24
ref ZP_02382540.1 Taurine dioxygenase [Burkholderia ubonensis Bu]	117	2e-24
ref ZP_06410725.1 Taurine dioxygenase [Frankia sp. EUN1f] >gi 2...	116	3e-24
gb ACX54968.1 putative (S)-2,4-dichlorophenoxypropionate dioxyg...	116	3e-24
ref ZP_06840718.1 Taurine catabolism dioxygenase TauD/TfdA [Bur...	116	4e-24
ref YP_003778031.1 alpha-ketoglutarate-dependent taurine dioxyg...	116	4e-24
ref YP_004236557.1 taurine dioxygenase [Acidovorax avenae subsp...	116	5e-24
gb ABD16690.1 alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	115	5e-24
ref NP_518867.1 putative alpha-ketoglutarate-dependent taurine ...	115	5e-24
ref YP_553178.1 putative alpha KG dependent 2,4-D dioxygenase [...]	115	6e-24
ref YP_553195.1 putative alpha KG dependent 2,4-D dioxygenase [...]	115	7e-24
gb ABD16692.1 alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	115	7e-24
emb CBJ38903.1 Alpha-ketoglutarate-dependent 2, 4-dichloropheno...	115	7e-24
ref NP_883162.1 putative taurine dioxygenase [Bordetella parapne...	115	7e-24
ref ZP_03585567.1 taurine dioxygenase [Burkholderia multivorans...	115	8e-24
gb ADC34031.1 TfdA-like protein [uncultured bacterium]	115	8e-24
gb ABD16689.1 alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	115	8e-24
ref ZP_01893643.1 Taurine catabolism dioxygenase TauD/TfdA [Mar...	115	9e-24
ref NP_936287.1 taurine catabolism dioxygenase [Vibrio vulnific...	115	9e-24
ref YP_002256592.1 alpha-ketoglutarate-dependent taurine dioxyg...	114	1e-23
ref ZP_05126397.1 taurine catabolism dioxygenase TauD/TfdA [gam...	114	1e-23
ref XP_002482838.1 alpha-ketoglutarate-dependent taurine dioxyg...	114	1e-23
ref YP_110835.1 dioxygenase [Burkholderia pseudomallei K96243] ...	114	1e-23
gb ACX54990.1 putative (S)-2,4-dichlorophenoxypropionate dioxyg...	114	1e-23
ref ZP_02894178.1 Taurine dioxygenase [Burkholderia ambifaria I...	114	1e-23
ref ZP_00951769.1 alpha-ketoglutarate-dependent taurine dioxyge...	114	1e-23
ref YP_004015268.1 taurine dioxygenase [Frankia sp. Eu11c] >gi ...	114	1e-23
ref ZP_02406371.1 dioxygenase TauD/TfdA family protein [Burkhol...	114	2e-23
ref ZP_04881190.1 dioxygenase, TauD/TfdA family [Burkholderia m...	114	2e-23
gb ADI12795.1 dioxygenase [Streptomyces bingchenggensis BCW-1]	114	2e-23
gb ABD16693.1 alpha-ketoglutarate-dependent 2,4-dichlorophenoxy...	114	2e-23
ref YP_105432.1 TauD/TfdA family dioxygenase [Burkholderia mall...	114	2e-23
ref ZP_02906934.1 Taurine dioxygenase [Burkholderia ambifaria M...	114	2e-23
ref YP_324822.1 taurine catabolism dioxygenase TauD/TfdA [Anaba...	114	2e-23
ref YP_724557.1 Alpha-ketoglutarate-dependent taurine dioxygena...	114	2e-23
ref ZP_02269820.2 dioxygenase, TauD/TfdA family [Burkholderia m...	114	2e-23
ref YP_775305.1 taurine dioxygenase [Burkholderia ambifaria AMM...	114	2e-23
ref YP_003115013.1 Taurine dioxygenase [Catenulispora acidiphil...	114	2e-23
gb ACG80560.1 TfdA [uncultured bacterium]	114	2e-23
ref ZP_06840735.1 Taurine catabolism dioxygenase TauD/TfdA [Bur...	114	2e-23
ref YP_884706.1 dioxygenase, TauD/TfdA family protein [Mycobact...	114	2e-23
ref YP_001584537.1 taurine dioxygenase [Burkholderia multivoran...	114	2e-23
ref ZP_03569865.1 taurine dioxygenase [Burkholderia multivorans...	113	3e-23
ref ZP_06688428.1 TauD/TfdA family dioxygenase [Achromobacter p...	113	3e-23
ref ZP_06305801.1 Taurine catabolism dioxygenase TauD/TfdA [Rap...	113	3e-23
ref YP_001564064.1 taurine dioxygenase [Delftia acidovorans SPH...	113	3e-23
ref YP_003749822.1 taurine dioxygenase [Ralstonia solanacearum ...]	113	3e-23
ref YP_001062210.1 TauD/TfdA family dioxygenase [Burkholderia p...	113	3e-23
ref YP_003796616.1 taurine dioxygenase, 2-oxoglutarate-dependen...	113	3e-23
gb ADC33990.1 TfdA-like protein [uncultured bacterium]	113	4e-23
ref YP_372822.1 taurine dioxygenase [Burkholderia sp. 383] >gi ...	113	4e-23
emb CAY27313.1 alpha-KG-dehydrogenase [uncultured bacterium]	112	4e-23
ref ZP_02459133.1 dioxygenase TauD/TfdA family protein [Burkhol...	112	5e-23
ref YP_001345669.1 hypothetical protein PSPA7_0273 [Pseudomonas...	112	5e-23
ref ZP_06876180.1 hypothetical protein PaerPab_01055 [Pseudomon...	112	5e-23
ref NP_248884.1 hypothetical protein PA0194 [Pseudomonas aerugi...	112	5e-23
ref YP_002260459.1 alpha-ketoglutarate-dependent taurine dioxyg...	112	6e-23
gb EGD03386.1 taurine dioxygenase [Burkholderia sp. TJI49]	112	6e-23
emb CAY27207.1 alpha-KG-dehydrogenase [uncultured bacterium]	112	6e-23
ref ZP_00945987.1 TauD / TfdA family dioxygenase [Ralstonia sol...	112	6e-23

ref ZP_01039757.1	alpha-ketoglutarate-dependent taurine dioxyge...	112	6e-23
ref ZP_05002612.1	taurine dioxygenase [Streptomyces sp. Mg1] >g...	112	7e-23
ref YP_002765055.1	dioxygenase [Rhodococcus erythropolis PR4] >...	112	7e-23
ref ZP_06411827.1	Taurine dioxygenase [Frankia sp. EUN1f] >gi 2...	112	7e-23
gb ACX54980.1	putative (S)-2,4-dichlorophenoxypropionate dioxyg...	112	8e-23
gb ACG80550.1	TfdA [uncultured bacterium]	112	8e-23
ref ZP_01986043.1	alpha-ketoglutarate-dependent taurine dioxyge...	112	8e-23
ref YP_001508977.1	taurine dioxygenase [Frankia sp. EAN1pec] >g...	112	8e-23
ref ZP_02190257.1	Alpha-ketoglutarate-dependent taurine dioxyge...	111	9e-23
gb ACX54973.1	putative (S)-2,4-dichlorophenoxypropionate dioxyg...	111	1e-22
ref YP_788350.1	hypothetical protein PA14_02435 [Pseudomonas ae...	111	1e-22
emb CAY27218.1	alpha-KG-dehydrogenase [uncultured bacterium]	111	1e-22
ref ZP_01101038.1	alpha-ketoglutarate-dependent taurine dioxyge...	111	1e-22
ref YP_001859330.1	taurine dioxygenase [Burkholderia phymatum S...	111	1e-22
ref YP_001505084.1	taurine dioxygenase [Frankia sp. EAN1pec] >g...	111	1e-22
ref ZP_06054723.1	taurine dioxygenase [alpha proteobacterium HI...	111	1e-22
ref ZP_02196896.1	Probable taurine catabolism dioxygenase [Vibr...	111	1e-22
ref YP_002233739.1	putative taurine dioxygenase [Burkholderia c...	111	1e-22
ref ZP_08205418.1	Taurine dioxygenase [Gordonia neofelifaecis N...	111	1e-22
ref YP_001810606.1	taurine dioxygenase [Burkholderia ambifaria ...	111	1e-22
ref ZP_05069657.1	alpha-ketoglutarate-dependent taurine dioxyge...	111	1e-22
ref NP_885378.1	alpha-ketoglutarate-dependent taurine dioxygena...	111	1e-22
ref ZP_01894276.1	alpha-ketoglutarate-dependent 2,4-dichlorophe...	110	2e-22
ref YP_001133737.1	taurine catabolism dioxygenase TauD/TfdA [My...	110	2e-22
emb CAY27226.1	alpha-KG-dehydrogenase [uncultured bacterium]	110	2e-22
ref YP_002911540.1	Dioxygenase, TauD/TfdA family protein [Burkh...	110	3e-22
ref ZP_02909524.1	Taurine catabolism dioxygenase TauD/TfdA [Bur...	110	3e-22
ref YP_002799309.1	TauD/TfdA family taurine catabolism dioxygen...	110	3e-22
ref YP_004076394.1	taurine catabolism dioxygenase [Mycobacteriu...	110	3e-22
ref ZP_07387052.1	Taurine dioxygenase [Paenibacillus curdlanoly...	110	3e-22
ref ZP_02450971.1	dioxygenase [Burkholderia pseudomallei 91] >g...	110	3e-22
emb CAY27315.1	alpha-KG-dehydrogenase [uncultured bacterium]	110	3e-22
gb AAT51196.1	PA0194 [synthetic construct]	109	3e-22
gb ADI19985.1	probable taurine catabolism dioxygenase [uncultur...	109	4e-22
ref YP_004015333.1	taurine catabolism dioxygenase TauD/TfdA [Fr...	109	4e-22
ref ZP_02493282.1	dioxygenase [Burkholderia pseudomallei NCTC 1...	109	4e-22
ref ZP_06850473.1	taurine dioxygenase [Mycobacterium parascrofu...	109	4e-22
ref YP_001613684.1	hypothetical protein sce3045 [Sorangium cell...	109	4e-22
ref NP_880388.1	alpha-ketoglutarate-dependent 2,4-dichloropheno...	109	4e-22
gb ADC34004.1	TfdA-like protein [uncultured bacterium]	109	4e-22
gb ADC34044.1	TfdA-like protein [uncultured bacterium]	109	5e-22
ref NP_763286.1	putative dioxygenase [Vibrio vulnificus CMCP6] ...	109	5e-22
ref ZP_07902029.1	hypothetical protein PVOR_27050 [Paenibacillu...	109	5e-22
ref ZP_02501489.1	dioxygenase TauD/TfdA family protein [Burkhol...	109	5e-22
ref ZP_01040254.1	alpha-ketoglutarate-dependent taurine dioxyge...	109	6e-22
ref YP_001508017.1	taurine catabolism dioxygenase TauD/TfdA [Fr...	108	7e-22
ref YP_001831695.1	taurine dioxygenase [Beijerinckia indica sub...	108	8e-22
gb ADC33995.1	TfdA-like protein [uncultured bacterium]	108	8e-22
gb ADC34035.1	TfdA-like protein [uncultured bacterium]	108	9e-22
gb ADC33991.1	TfdA-like protein [uncultured bacterium]	108	9e-22
gb ABB69741.1	PlaO1 [Streptomyces sp. Tu6071]	108	9e-22
ref YP_001633079.1	alpha-ketoglutarate-dependent taurine dioxyg...	108	9e-22
ref YP_001445968.1	hypothetical protein VIBHAR_02787 [Vibrio ha...	108	1e-21
gb ADC34011.1	TfdA-like protein [uncultured bacterium]	108	1e-21
ref YP_046272.1	putative alkylsulfatase (AtsK) [Acinetobacter s...	108	1e-21
gb ADZ91865.1	Taurine dioxygenase [Marinomonas mediterranea MMB-1]	108	1e-21
ref ZP_08119928.1	dioxygenase [Pseudonocardia sp. P1]	108	1e-21
ref YP_001508606.1	taurine catabolism dioxygenase TauD/TfdA [Fr...	108	1e-21
ref YP_003272551.1	Taurine dioxygenase [Gordonia bronchialis DS...	108	1e-21
ref XP_001394361.1	2,4-dichlorophenoxyacetate alpha-ketoglutara...	107	1e-21
emb CAY27310.1	alpha-KG-dehydrogenase [uncultured bacterium]	107	1e-21
ref ZP_07387050.1	Taurine dioxygenase [Paenibacillus curdlanoly...	107	1e-21
gb AAM90964.2	AF516751_1 R-2,4-dichlorophenoxypropionate dioxyge...	107	1e-21

ref ZP_07301372.1	dioxygenase [Streptomyces viridochromogenes D...	107	2e-21
ref YP_001134372.1	taurine dioxygenase [Mycobacterium gilvum PY...	107	2e-21
ref YP_004016966.1	taurine dioxygenase [Frankia sp. EuIlc] >gi ...	107	2e-21
gb ACX54967.1	putative (S)-2,4-dichlorophenoxypropionate dioxyg...	107	2e-21
gb ADY81784.1	putative alkylsulfatase [Acinetobacter calcoaceti...	107	2e-21
gb ADC33998.1	TfdA-like protein [uncultured bacterium]	107	2e-21
ref YP_001413275.1	taurine dioxygenase [Parvibaculum lavamentiv...	107	2e-21
ref ZP_07980743.1	alpha-ketoglutarate-dependent taurine dioxyge...	107	2e-21
gb ACX54972.1	putative (S)-2,4-dichlorophenoxypropionate dioxyg...	107	2e-21
ref ZP_04384517.1	alpha-ketoglutarate-dependent taurine dioxyge...	107	2e-21
ref YP_003551220.1	putative dioxygenase [Candidatus Puniceispir...	107	2e-21
gb ADC34041.1	TfdA-like protein [uncultured bacterium]	107	2e-21
ref YP_274684.1	TauD/TfdA family dioxygenase [Pseudomonas syrin...	107	2e-21
gb AAT51068.1	PA3935 [synthetic construct]	107	3e-21
gb EFW80548.1	TauD/TfdA family dioxygenase [Pseudomonas syringa...	107	3e-21
ref ZP_06413630.1	Taurine dioxygenase [Frankia sp. EUNlf] >gi 2...	107	3e-21
ref ZP_07262985.1	taurine catabolism dioxygenase TauD/TfdA [Pse...	107	3e-21
ref YP_789182.1	taurine dioxygenase [Pseudomonas aeruginosa UCB...	107	3e-21
gb AB010421.1	(R)-2,4-dichlorophenoxypropionate dioxygenase [Bu...	106	3e-21
ref YP_002869936.1	taurine dioxygenase [Pseudomonas fluorescens...	106	4e-21
ref YP_001511337.1	taurine catabolism dioxygenase TauD/TfdA [Fr...	106	4e-21
gb ADC34015.1	TfdA-like protein [uncultured bacterium]	106	4e-21
gb ADC33988.1	TfdA-like protein [uncultured bacterium]	106	4e-21
gb ADC34006.1	TfdA-like protein [uncultured bacterium]	106	4e-21
ref YP_003563864.1	taurine catabolism dioxygenase TauD [Bacillu...	106	4e-21
ref YP_002978871.1	Taurine catabolism dioxygenase TauD/TfdA [Rh...	106	4e-21
ref XP_002149830.1	alpha-ketoglutarate-dependent 2,4-dichloroph...	106	4e-21
ref YP_001505765.1	taurine catabolism dioxygenase TauD/TfdA [Fr...	106	4e-21
gb ADC33994.1	TfdA-like protein [uncultured bacterium]	105	5e-21
ref YP_004017313.1	taurine catabolism dioxygenase TauD/TfdA [Fr...	105	5e-21
ref YP_002798036.1	Taurine dioxygenase [Azotobacter vinelandii ...	105	6e-21
gb ADI22956.1	probable taurine catabolism dioxygenase [uncultur...	105	6e-21
ref YP_003342517.1	taurine dioxygenase [Streptosporangium roseu...	105	6e-21
gb ADC33996.1	TfdA-like protein [uncultured bacterium]	105	6e-21
ref ZP_07706655.1	putative taurine dioxygenase [Dermacoccus sp....	105	6e-21
ref ZP_07603054.1	Taurine dioxygenase [Streptomyces violaceusni...	105	6e-21
ref YP_702048.1	taurine dioxygenase [Rhodococcus jostii RHA1] >...	105	6e-21
ref YP_479369.1	taurine dioxygenase [Frankia sp. CcI3] >gi 8656...	105	7e-21
ref ZP_05226146.1	taurine catabolism dioxygenase TauD/TfdA [Myc...	105	7e-21
ref ZP_08197519.1	taurine dioxygenase, TauD/TfdA family [Nocard...	105	7e-21
ref NP_252624.1	taurine dioxygenase [Pseudomonas aeruginosa PAO...	105	8e-21
ref ZP_01367370.1	hypothetical protein PaerPA_01004522 [Pseudom...	105	8e-21
ref YP_003732168.1	putative alkylsulfatase (AtsK) [Acinetobacte...	105	8e-21
gb ADC34001.1	TfdA-like protein [uncultured bacterium] >gi 2850...	105	8e-21
gb ACX54981.1	putative (S)-2,4-dichlorophenoxypropionate dioxyg...	105	9e-21
ref NP_824171.1	dioxygenase [Streptomyces avermitilis MA-4680] ...	105	9e-21
ref ZP_05217892.1	taurine catabolism dioxygenase TauD, TfdA fam...	105	1e-20
ref YP_119465.1	putative dioxygenase [Nocardia farcinica IFM 10...	105	1e-20
ref ZP_07603129.1	Taurine dioxygenase [Streptomyces violaceusni...	105	1e-20
gb EGB10818.1	hypothetical protein AURANDRAFT_5093 [Aureococcus...	104	1e-20
ref ZP_06414085.1	Taurine catabolism dioxygenase TauD/TfdA [Fra...	104	1e-20
ref ZP_06494532.1	taurine catabolism dioxygenase TauD/TfdA [Pse...	104	1e-20
gb ADC34008.1	TfdA-like protein [uncultured bacterium]	104	1e-20
ref ZP_06308911.1	Taurine catabolism dioxygenase TauD/TfdA [Cyl...	104	1e-20
ref YP_002778947.1	dioxygenase [Rhodococcus opacus B4] >gi 2262...	104	1e-20
ref ZP_05884985.1	alpha-ketoglutarate-dependent taurine dioxyge...	104	1e-20
gb ACX54974.1	putative (S)-2,4-dichlorophenoxypropionate dioxyg...	104	1e-20
gb ACX54986.1	putative (S)-2,4-dichlorophenoxypropionate dioxyg...	104	1e-20
ref NP_962069.1	hypothetical protein MAP3135c [Mycobacterium av...	104	1e-20
ref ZP_07795333.1	taurine dioxygenase [Pseudomonas aeruginosa 3...	104	1e-20
ref YP_003490344.1	dioxygenase [Streptomyces scabiei 87.22] >gi...	104	2e-20
gb ADO85576.1	PntD [Streptomyces arenae]	104	2e-20
gb ADC33997.1	TfdA-like protein [uncultured bacterium]	104	2e-20

gb ACX54971.1 putative (S)-2,4-dichlorophenoxypropionate dioxyg...	104	2e-20
emb CBX81704.1 K03119 taurine dioxygenase [Erwinia amylovora AT...	104	2e-20
ref YP_702440.1 alpha-ketoglutarate-dependent taurine dioxygena...	103	2e-20
ref YP_003592886.1 taurine dioxygenase [Caulobacter segnis ATCC...	103	2e-20
ref YP_003906658.1 Taurine dioxygenase [Burkholderia sp. CCGE10...	103	2e-20
ref YP_004227685.1 Taurine dioxygenase [Burkholderia sp. CCGE10...	103	2e-20
ref YP_553181.1 putative alpha KG dependent 2,4-D dioxygenase [...	103	2e-20
ref YP_639655.1 taurine dioxygenase [Mycobacterium sp. MCS] >gi...	103	2e-20
ref ZP_05521627.1 dioxygenase [Streptomyces lividans TK24] >gi ...	103	2e-20
ref YP_001757617.1 taurine dioxygenase [Methylobacterium radiot...	103	2e-20
gb ADC33999.1 TfdA-like protein [uncultured bacterium]	103	2e-20
ref NP_631553.1 dioxygenase [Streptomyces coelicolor A3(2)] >gi...	103	3e-20
ref ZP_07005112.1 Dioxygenase, TauD/TfdA family [Pseudomonas sa...	103	3e-20
ref ZP_02186917.1 taurine dioxygenase, TauD/TfdA family protein...	103	3e-20
ref YP_001105490.1 taurine catabolism dioxygenase TauD [Sacchar...	103	3e-20
ref YP_110629.1 TauD/TfdA family dioxygenase [Burkholderia pseu...	103	3e-20
ref ZP_02371424.1 dioxygenase, TauD/TfdA family protein [Burkho...	103	3e-20
ref NP_792423.1 dioxygenase, TauD/TfdA family [Pseudomonas syri...	103	3e-20
ref ZP_02358219.1 TauD/TfdA family dioxygenase [Burkholderia ok...	103	3e-20
ref ZP_04700699.1 putative taurine catabolism dioxygenase [Stre...	103	3e-20
ref YP_002779396.1 dioxygenase [Rhodococcus opacus B4] >gi 2262...	103	3e-20
ref ZP_05127143.1 taurine dioxygenase [gamma proteobacterium NO...	103	3e-20
ref ZP_04953283.1 dioxygenase, TauD/TfdA family [Burkholderia p...	103	3e-20
ref YP_001061907.1 TauD/TfdA family dioxygenase [Burkholderia p...	103	3e-20
ref YP_004008831.1 taurine dioxygenase [Rhodococcus equi 103S] ...	103	3e-20
ref ZP_01616095.1 alpha-ketoglutarate-dependent taurine dioxyge...	103	3e-20
ref ZP_07772879.1 alpha-ketoglutarate-dependent taurine dioxyge...	103	3e-20
ref ZP_07260263.1 dioxygenase, TauD/TfdA family protein [Pseudo...	103	4e-20
ref YP_001507682.1 taurine catabolism dioxygenase TauD/TfdA [Fr...	103	4e-20
ref ZP_07230626.1 dioxygenase, TauD/TfdA family protein [Pseudo...	103	4e-20
ref YP_458158.1 alpha-ketoglutarate-dependent taurine dioxygena...	103	4e-20
ref ZP_05642075.1 TauD/TfdA family dioxygenase [Pseudomonas syr...	103	4e-20
ref ZP_06914719.1 dioxygenase [Streptomyces sviveus ATCC 29083]...	103	4e-20
ref YP_340645.1 taurine dioxygenase [Pseudoalteromonas haloplan...	102	4e-20
ref YP_883118.1 taurine catabolism dioxygenase TauD, TfdA famil...	102	4e-20
ref YP_001412118.1 taurine dioxygenase [Parvibaculum lavamentiv...	102	5e-20
ref ZP_06846090.1 Taurine dioxygenase [Burkholderia sp. Chl-1] ...	102	5e-20
ref ZP_05226007.1 alpha-ketoglutarate-dependent taurine dioxyge...	102	5e-20
ref YP_001074852.1 TauD/TfdA family dioxygenase [Burkholderia p...	102	5e-20
ref XP_001216119.1 conserved hypothetical protein [Aspergillus ...	102	5e-20
ref YP_003339338.1 taurine dioxygenase [Streptosporangium roseu...	102	5e-20
ref ZP_02450610.1 TauD/TfdA family dioxygenase [Burkholderia ps...	102	6e-20
emb CAJ89608.1 putative dioxygenase [Streptomyces ambofaciens A...	102	6e-20
ref YP_001869285.1 taurine catabolism dioxygenase TauD/TfdA [No...	102	6e-20
ref YP_001346557.1 taurine dioxygenase [Pseudomonas aeruginosa ...	102	6e-20
gb ADC34019.1 TfdA-like protein [uncultured bacterium]	102	6e-20
ref ZP_06415360.1 Taurine catabolism dioxygenase TauD/TfdA [Fra...	102	6e-20
ref YP_235431.1 taurine catabolism dioxygenase TauD/TfdA [Pseud...	102	7e-20
ref ZP_06840721.1 Taurine catabolism dioxygenase TauD/TfdA [Bur...	102	7e-20
ref ZP_06851972.1 TauD/TfdA family dioxygenase [Mycobacterium p...	102	7e-20
ref ZP_06410990.1 Taurine catabolism dioxygenase TauD/TfdA [Fra...	102	8e-20
gb ACX54970.1 putative (S)-2,4-dichlorophenoxypropionate dioxyg...	102	8e-20
gb ADC33993.1 TfdA-like protein [uncultured bacterium]	102	9e-20
ref ZP_07309248.1 taurine dioxygenase [Streptomyces griseoflavu...	102	9e-20
gb ADC34018.1 TfdA-like protein [uncultured bacterium]	102	9e-20
gb ACX54979.1 putative (S)-2,4-dichlorophenoxypropionate dioxyg...	102	9e-20
ref YP_001824503.1 putative taurine catabolism dioxygenase [Str...	101	9e-20
ref ZP_01078548.1 Probable taurine catabolism dioxygenase [Mari...	101	9e-20
ref ZP_05218298.1 alpha-ketoglutarate-dependent taurine dioxyge...	101	1e-19
ref ZP_01765753.1 dioxygenase, TauD/TfdA family [Burkholderia p...	101	1e-19
gb ADC34000.1 TfdA-like protein [uncultured bacterium] >gi 2850...	101	1e-19
gb ACX54982.1 putative (S)-2,4-dichlorophenoxypropionate dioxyg...	101	1e-19
ref YP_001508006.1 taurine catabolism dioxygenase TauD/TfdA [Fr...	101	1e-19

ref ZP_01627520.1	alpha-ketoglutarate-dependent taurine dioxyge...	101	1e-19
gb ADC34017.1	TfdA-like protein [uncultured bacterium]	101	1e-19
ref YP_003116441.1	Taurine dioxygenase [Catenulispora acidiphil...	101	1e-19
ref YP_003411151.1	Taurine dioxygenase [Geodermatophilus obscur...	101	1e-19
ref YP_004084309.1	taurine dioxygenase [Micromonospora sp. L5] ...	101	1e-19
ref YP_001412109.1	taurine dioxygenase [Parvibaculum lavamentiv...	101	1e-19
ref YP_002278025.1	taurine dioxygenase [Rhizobium leguminosarum...	101	1e-19
ref YP_761331.1	TauD/TfdA family dioxygenase [Hyphomonas neptun...	101	1e-19
ref YP_001240347.1	putative dioxygenase [Bradyrhizobium sp. BTA...	101	1e-19
ref YP_001895833.1	Taurine dioxygenase [Burkholderia phytofirma...	101	1e-19
ref YP_002978144.1	Taurine dioxygenase [Rhizobium leguminosarum...	101	1e-19
ref ZP_08156958.1	taurine dioxygenase [Rhodococcus equi ATCC 33...	101	2e-19
ref YP_883488.1	alpha-ketoglutarate-dependent taurine dioxygena...	101	2e-19
ref YP_003836819.1	taurine dioxygenase [Micromonospora aurantia...	100	2e-19
gb ADC34012.1	TfdA-like protein [uncultured bacterium]	100	2e-19
ref NP_902525.1	taurine dioxygenase [Chromobacterium violaceum ...	100	2e-19
ref YP_345986.1	taurine dioxygenase [Pseudomonas fluorescens Pf...	100	2e-19
ref YP_001504833.1	taurine catabolism dioxygenase TauD/TfdA [Fr...	100	2e-19
ref YP_003009527.1	Taurine dioxygenase [Paenibacillus sp. JDR-2...	100	2e-19
ref XP_572683.1	2,4-dichlorophenoxyacetate alpha-ketoglutarate ...	100	2e-19
ref ZP_03498565.1	Taurine dioxygenase [Rhizobium etli Kim 5]	100	2e-19
ref NP_217923.1	dioxygenase [Mycobacterium tuberculosis H37Rv] ...	100	2e-19
gb ACX54969.1	putative (S)-2,4-dichlorophenoxypropionate dioxyg...	100	2e-19
ref YP_001869111.1	taurine catabolism dioxygenase TauD/TfdA [No...	100	2e-19
ref ZP_03421998.1	dioxygenase [Mycobacterium tuberculosis 94_M4...	100	3e-19
ref ZP_02414516.1	dioxygenase, TauD/TfdA family protein [Burkho...	100	3e-19
gb ADC34033.1	TfdA-like protein [uncultured bacterium]	100	3e-19
ref YP_002947816.1	Taurine dioxygenase [Variovorax paradoxus S1...	100	3e-19
ref YP_001985889.1	taurine dioxygenase protein [Rhizobium etli ...	100	3e-19
ref YP_496820.1	taurine dioxygenase [Novosphingobium aromaticiv...	100	3e-19
ref YP_001684358.1	taurine dioxygenase [Caulobacter sp. K31] >g...	100	3e-19
ref YP_004019382.1	taurine catabolism dioxygenase TauD/TfdA [Fr...	100	3e-19
gb ADO34971.1	putative (S)-2,4-dichlorophenoxypropionate dioxyg...	100	4e-19
ref ZP_06474456.1	Taurine dioxygenase [Frankia symbiont of Dati...	100	4e-19
ref YP_001683423.1	taurine dioxygenase [Caulobacter sp. K31] >g...	100	4e-19
ref YP_439438.1	TauD/TfdA family dioxygenase [Burkholderia thai...	100	4e-19
ref ZP_02370755.1	dioxygenase, TauD/TfdA family protein [Burkho...	100	5e-19
ref ZP_06062866.1	taurine catabolism dioxygenase TauD/TfdA [Aci...	99	5e-19
ref ZP_06192658.1	hypothetical protein SOD_h00590 [Serratia odo...	99	5e-19
ref ZP_06271905.1	Taurine dioxygenase [Streptomyces sp. ACTE] >...	99	5e-19
ref ZP_06711045.1	taurine dioxygenase [Streptomyces sp. e14] >g...	99	6e-19
ref ZP_08224952.1	putative taurine catabolism dioxygenase [Stre...	99	6e-19
ref ZP_06412415.1	Taurine dioxygenase [Frankia sp. EUN1f] >gi 2...	99	6e-19
ref NP_631410.1	dioxygenase [Streptomyces coelicolor A3(2)] >gi...	99	6e-19
ref ZP_01896407.1	Probable taurine catabolism dioxygenase [Mori...	99	6e-19
ref ZP_07300902.1	taurine dioxygenase [Streptomyces hygrosopic...	99	6e-19
ref YP_001106845.1	taurine dioxygenase, 2-oxoglutarate-dependen...	99	6e-19
ref YP_002129572.1	alpha-ketoglutarate-dependent taurine dioxyg...	99	7e-19
ref YP_003102078.1	taurine dioxygenase [Actinosynnema mirum DSM...	99	7e-19
ref YP_003133666.1	Probable taurine catabolism dioxygenase [Sac...	99	7e-19
gb ADC34047.1	TfdA-like protein [uncultured bacterium]	99	8e-19
ref YP_710871.1	putative taurine dioxygenase [Frankia alni ACN1...	99	8e-19
ref YP_001563031.1	taurine dioxygenase [Delftia acidovorans SPH...	99	8e-19
ref YP_003329314.1	TauD [Sinorhizobium meliloti] >gi 76880817 g...	99	8e-19
ref YP_002129780.1	alpha-ketoglutarate-dependent taurine dioxyg...	99	9e-19
ref ZP_01616036.1	putative dioxygenase [marine gamma proteobact...	99	9e-19
ref YP_001700840.1	putative taurine dioxygenase [Mycobacterium ...	98	1e-18
ref ZP_01065145.1	Probable taurine catabolism dioxygenase [Vibr...	98	1e-18
ref ZP_01812660.1	Probable taurine catabolism dioxygenase [Vibr...	98	1e-18
ref ZP_05521780.1	dioxygenase [Streptomyces lividans TK24] >gi ...	98	1e-18
ref YP_442487.1	dioxygenase, TauD/TfdA [Burkholderia thailanden...	98	1e-18
ref YP_472514.1	putative taurine dioxygenase protein [Rhizobium...	98	1e-18
gb ACF98187.1	putative alpha-ketoglutarate-dependent taurine di...	98	1e-18

emb CAK48578.1	unnamed protein product [Aspergillus niger]	98	1e-18
ref YP_004018287.1	taurine catabolism dioxygenase TauD/TfdA [Fr...	98	1e-18
ref ZP_05225744.1	taurine catabolism dioxygenase TauD, TfdA fam...	98	1e-18
ref ZP_02374281.1	dioxygenase, TauD/TfdA [Burkholderia thailand...	98	2e-18
ref XP_002152412.1	alpha-ketoglutarate-dependent 2,4-dichloroph...	98	2e-18
ref ZP_02363324.1	dioxygenase, TauD/TfdA [Burkholderia oklahome...	98	2e-18
ref YP_001511156.1	taurine catabolism dioxygenase TauD/TfdA [Fr...	98	2e-18
ref YP_003594362.1	taurine dioxygenase [Caulobacter segnis ATCC...	97	2e-18
ref YP_857443.1	taurine dioxygenase [Aeromonas hydrophila subsp...	97	2e-18
gb ADY81776.1	putative alkylsulfatase [Acinetobacter calcoaceti...	97	2e-18
ref YP_001260806.1	taurine catabolism dioxygenase TauD/TfdA [Sp...	97	2e-18
dbj BAJ32846.1	putative alkylsulfatase [Kitasatospora setae KM-...	97	3e-18
ref NP_822287.1	taurine catabolism dioxygenase [Streptomyces av...	97	3e-18
ref ZP_07989330.1	taurine dioxygenase [Corynebacterium variabil...	97	3e-18
ref ZP_05096186.1	Taurine catabolism dioxygenase TauD, TfdA fam...	97	3e-18
ref YP_002417336.1	putative taurine catabolism dioxygenase [Vib...	97	3e-18
emb CAY27324.1	alpha-KG-dehydrogenase [uncultured bacterium]	97	3e-18
ref YP_605995.1	taurine dioxygenase [Pseudomonas entomophila L4...	97	3e-18
ref YP_905004.1	taurine catabolism dioxygenase, TauD [Mycobacte...	97	3e-18
ref YP_003771048.1	taurine dioxygenase [Amycolatopsis mediterranea...	97	3e-18
ref YP_257415.1	taurine dioxygenase [Pseudomonas fluorescens Pf...	97	3e-18
ref ZP_06917085.1	taurine catabolism dioxygenase [Streptomyces ...	97	3e-18
ref XP_003195730.1	2,4-dichlorophenoxyacetate alpha-ketoglutarate...	97	4e-18
ref ZP_08138776.1	taurine dioxygenase [Pseudomonas sp. TJI-51] ...	97	4e-18
ref YP_003732176.1	putative alkylsulfatase [Acinetobacter sp. D...	97	4e-18
ref ZP_03270351.1	Taurine dioxygenase [Burkholderia sp. H160] >...	96	4e-18
gb EGD02376.1	Taurine catabolism dioxygenase TauD/TfdA [Burkhol...	96	4e-18
pdb 1OIJ C Chain C, Crystal Structure Of The Alkylsulfatase Atsk...		96	4e-18
pdb 1OIH A Chain A, Crystal Structure Of The Alkylsulfatase Atsk...		96	4e-18
ref YP_619823.1	putative alpha-ketoglutarate-dependent taurine ...	96	4e-18
ref ZP_06834222.1	taurine dioxygenase [Gluconacetobacter hansen...	96	4e-18
pdb 1OIJ A Chain A, Crystal Structure Of The Alkylsulfatase Atsk...		96	5e-18
ref ZP_07283312.1	dioxygenase [Streptomyces sp. AA4] >gi 302439...	96	5e-18
ref YP_001505977.1	taurine catabolism dioxygenase TauD/TfdA [Fr...	96	5e-18
ref YP_003114519.1	Taurine dioxygenase [Catenulispora acidiphil...	96	5e-18
ref YP_046264.1	putative alkylsulfatase [Acinetobacter sp. ADP1...	96	5e-18
ref ZP_02468961.1	dioxygenase TauD/TfdA family protein [Burkhol...	96	5e-18
ref YP_759632.1	TauD/TfdA family dioxygenase [Hyphomonas neptun...	96	5e-18
ref YP_458641.1	alpha-ketoglutarate-dependent taurine dioxygena...	96	6e-18
ref YP_001666503.1	taurine dioxygenase [Pseudomonas putida GB-1...	96	6e-18
ref ZP_01770198.1	dioxygenase TauD/TfdA family [Burkholderia ps...	96	6e-18
ref ZP_06414132.1	Taurine catabolism dioxygenase TauD/TfdA [Fra...	96	6e-18
dbj BAC00965.1	alpha-ketoglutarate-dependent dioxygenase [Pseud...	96	7e-18
gb ADI06110.1	Taurine dioxygenase [Streptomyces bingchenggensis...	96	7e-18
ref ZP_04522662.1	taurine dioxygenase [Burkholderia pseudomalle...	96	7e-18
ref YP_001062636.1	TauD/TfdA family dioxygenase [Burkholderia p...	96	7e-18
gb ADW07602.1	Taurine dioxygenase [Streptomyces flavogriseus AT...	96	7e-18
ref ZP_02406873.1	dioxygenase TauD/TfdA family protein [Burkhol...	96	7e-18
ref ZP_02356184.1	dioxygenase, TauD/TfdA [Burkholderia oklahome...	96	7e-18
ref YP_003942972.1	Taurine dioxygenase [Enterobacter cloacae SC...	96	7e-18
ref ZP_03546154.1	Taurine dioxygenase [Comamonas testosteroni K...	96	7e-18
ref YP_111178.1	alpha-ketoglutarate-dependent taurine dioxygena...	96	7e-18
ref ZP_02403488.1	dioxygenase, TauD/TfdA [Burkholderia pseudoma...	96	8e-18
ref ZP_02451448.1	dioxygenase TauD/TfdA family protein [Burkhol...	96	8e-18
ref YP_001618162.1	taurine dioxygenase [Sorangium cellulosum 'S...	96	8e-18
ref YP_003563776.1	alpha-ketoglutarate-dependent taurine dioxyg...	95	9e-18
ref XP_001801431.1	hypothetical protein SNOG_11187 [Phaeosphaer...	95	9e-18
ref ZP_04690003.1	dioxygenase [Streptomyces ghanaensis ATCC 146...	95	9e-18
ref YP_108822.1	putative sulfur metabolism-related protein [Bur...	95	1e-17
ref ZP_02485616.1	dioxygenase TauD/TfdA family protein [Burkhol...	95	1e-17
ref YP_001666482.1	taurine dioxygenase [Pseudomonas putida GB-1...	95	1e-17
ref YP_002799405.1	Taurine dioxygenase protein [Azotobacter vin...	95	1e-17
ref YP_335290.1	TauD/TfdA family dioxygenase [Burkholderia pseu...	95	1e-17

ref ZP_04954431.1	dioxygenase, TauD/TfdA family [Burkholderia p...	95	1e-17
emb CAY27239.1	alpha-KG-dehydrogenase [uncultured bacterium]	95	1e-17
ref ZP_07674287.1	taurine dioxygenase, TauD/TfdA family [Ralsto...	95	1e-17
ref YP_003532176.1	taurine dioxygenase [Erwinia amylovora CFBP1...	95	1e-17
emb CAY27508.1	alpha-KG-dehydrogenase [uncultured bacterium]	95	1e-17
emb CAY27432.1	alpha-KG-dehydrogenase [uncultured bacterium]	95	1e-17
ref YP_004005470.1	taurine dioxygenase [Rhodococcus equi 103S] ...	95	1e-17
ref YP_004236558.1	taurine dioxygenase [Acidovorax avenae subsp...	94	2e-17
ref ZP_08207133.1	taurine dioxygenase [Novosphingobium nitrogen...	94	2e-17
ref YP_001480784.1	taurine dioxygenase [Serratia proteamaculans...	94	2e-17
ref YP_003280552.1	Taurine catabolism dioxygenase TauD/TfdA [Co...	94	2e-17
ref ZP_07046181.1	Taurine catabolism dioxygenase TauD/TfdA [Com...	94	2e-17
emb CAY27303.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	94	2e-17
ref YP_118167.1	putative taurine dioxygenase [Nocardia farcinic...	94	2e-17
emb CAY27532.1	alpha-KG-dehydrogenase [uncultured bacterium]	94	2e-17
emb CAY27285.1	alpha-KG-dehydrogenase [uncultured bacterium]	94	2e-17
ref ZP_07965125.1	TfdA family Taurine catabolism dioxygenase Ta...	94	2e-17
ref YP_001863223.1	taurine dioxygenase [Burkholderia phymatum S...	94	2e-17
ref YP_003989699.1	Taurine dioxygenase [Geobacillus sp. Y4.1MC1...	94	3e-17
ref NP_887599.1	putative dioxygenase [Bordetella bronchiseptica...	94	3e-17
ref YP_001751827.1	taurine dioxygenase [Pseudomonas putida W619...	94	3e-17
ref YP_884597.1	alpha-ketoglutarate-dependent taurine dioxyg...	94	3e-17
emb CAY27276.1	alpha-KG-dehydrogenase [uncultured bacterium]	94	3e-17
emb CAY27521.1	alpha-KG-dehydrogenase [uncultured bacterium]	94	3e-17
emb CAY27476.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	94	3e-17
ref NP_742398.1	taurine dioxygenase [Pseudomonas putida KT2440]...	94	3e-17
ref YP_103265.1	dioxygenase, TauD/TfdA [Burkholderia mallei ATC...	94	3e-17
ref YP_003187897.1	alpha-ketoglutarate-dependent taurine dioxyg...	94	3e-17
ref YP_001059547.1	dioxygenase, TauD/TfdA [Burkholderia pseudom...	94	3e-17
gb ADR57960.1	TauD [Pseudomonas putida BIRD-1]	94	3e-17
ref YP_002799353.1	TauD/TfdA family taurine catabolism dioxygen...	93	4e-17
ref YP_002396447.1	taurine dioxygenase [Escherichia coli ED1a] ...	93	4e-17
ref YP_001412266.1	taurine dioxygenase [Parvibaculum lavamentiv...	93	4e-17
emb CAY27235.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	93	4e-17
emb CAY27510.1	alpha-KG-dehydrogenase [uncultured bacterium]	93	4e-17
ref YP_701701.1	taurine dioxygenase [Rhodococcus jostii RHA1] >...	93	4e-17
ref ZP_03426827.1	dioxygenase [Mycobacterium tuberculosis T92]	93	4e-17
emb CAY27216.1	alpha-KG-dehydrogenase [uncultured bacterium]	93	4e-17
gb ACX54985.1	putative (S)-2,4-dichlorophenoxypropionate dioxyg...	93	4e-17
emb CAY27268.1	alpha-KG-dehydrogenase [uncultured bacterium]	93	4e-17
emb CAY27440.1	alpha-KG-dehydrogenase [uncultured bacterium]	93	5e-17
ref YP_002768378.1	dioxygenase [Rhodococcus erythropolis PR4] >...	93	5e-17
emb CAY27211.1	alpha-KG-dehydrogenase [uncultured bacterium]	93	5e-17
emb CAY27305.1	alpha-KG-dehydrogenase [uncultured bacterium]	93	5e-17
emb CAJ89754.1	putative dioxygenase [Streptomyces ambofaciens A...	93	5e-17
emb CAY27393.1	alpha-KG-dehydrogenase [uncultured bacterium]	93	5e-17
ref YP_608305.1	dioxygenase, TauD [Pseudomonas entomophila L48]...	93	5e-17
ref YP_296355.1	taurine dioxygenase [Ralstonia eutropha JMP134]...	92	6e-17
gb ACX54996.1	putative (S)-2,4-dichlorophenoxypropionate dioxyg...	92	6e-17
ref YP_257356.1	taurine catabolism dioxygenase TauD [Pseudomona...	92	6e-17
emb CAY27418.1	alpha-KG-dehydrogenase [uncultured bacterium]	92	6e-17
ref YP_001563037.1	taurine dioxygenase [Delftia acidovorans SPH...	92	6e-17
emb CAY27497.1	alpha-KG-dehydrogenase [uncultured bacterium]	92	7e-17
emb CAY27456.1	alpha-KG-dehydrogenase [uncultured bacterium]	92	7e-17
gb EGB71242.1	TfdA family protein Taurine catabolism dioxygenas...	92	7e-17
gb ACX54987.1	putative (S)-2,4-dichlorophenoxypropionate dioxyg...	92	7e-17
gb ACG80557.1	TfdA [uncultured bacterium]	92	7e-17
emb CAY27485.1	alpha-KG-dehydrogenase [uncultured bacterium]	92	7e-17
emb CAY27277.1	alpha-KG-dehydrogenase [uncultured bacterium]	92	7e-17
gb ABR27343.1	TfdA [uncultured bacterium]	92	7e-17
emb CAY27526.1	alpha-KG-dehydrogenase [uncultured bacterium]	92	8e-17
gb ADC34016.1	TfdA-like protein [uncultured bacterium]	92	8e-17
ref YP_003598515.1	alpha-ketoglutarate-dependent taurine dioxyg...	92	9e-17

ref ZP_02144821.1	dioxygenase, TauD/TfdA family protein [Phaeob...	92	9e-17
gb AAS64583.1	alpha-KG-dependent dioxygenase [uncultured soil b...	92	9e-17
ref YP_729160.1	Alpha-ketoglutarate-dependent taurine dioxygena...	92	9e-17
ref YP_004016993.1	taurine dioxygenase [Frankia sp. Eu11c] >gi ...	92	1e-16
ref ZP_05001574.1	taurine dioxygenase [Streptomyces sp. Mg1] >g...	92	1e-16
ref ZP_07742091.1	putative taurine catabolism dioxygenase [Vibr...	92	1e-16
ref ZP_01039422.1	Taurine dioxygenase [Erythrobacter sp. NAP1] ...	92	1e-16
gb ACG80551.1	TfdA [uncultured bacterium] >gi 196482324 gb ACG8...	92	1e-16
ref ZP_07576719.1	Taurine catabolism dioxygenase TauD/TfdA [Sph...	92	1e-16
gb ACG80584.1	TfdA [uncultured bacterium]	92	1e-16
emb CAY27274.1	alpha-KG-dehydrogenase [uncultured bacterium]	92	1e-16
ref YP_322991.1	taurine catabolism dioxygenase TauD/TfdA [Anaba...	92	1e-16
emb CAY27255.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	92	1e-16
ref YP_668361.1	taurine dioxygenase [Escherichia coli 536] >gi ...	92	1e-16
ref ZP_02884967.1	Taurine dioxygenase [Burkholderia graminis C4...	92	1e-16
ref YP_002327887.1	taurine dioxygenase [Escherichia coli O127:H...	92	1e-16
ref ZP_06069264.1	taurine catabolism dioxygenase TauD/TfdA [Aci...	91	1e-16
emb CAY27260.1	alpha-KG-dehydrogenase [uncultured bacterium]	91	1e-16
emb CAY27350.1	alpha-KG-dehydrogenase [uncultured bacterium]	91	1e-16
ref YP_003298992.1	Taurine dioxygenase [Thermomonospora curvata...	91	1e-16
ref YP_004154990.1	taurine dioxygenase [Variovorax paradoxus EP...	91	1e-16
ref YP_457842.1	taurine dioxygenase [Erythrobacter litoralis HT...	91	1e-16
ref YP_345946.1	taurine dioxygenase [Pseudomonas fluorescens Pf...	91	1e-16
ref ZP_06413046.1	Taurine catabolism dioxygenase TauD/TfdA [Fra...	91	1e-16
ref ZP_07289824.1	taurine dioxygenase [Streptomyces sp. C] >gi ...	91	2e-16
ref YP_841739.1	taurine catabolism dioxygenase [Ralstonia eutro...	91	2e-16
ref ZP_07042961.1	taurine dioxygenase [Comamonas testosteroni S...	91	2e-16
emb CAY27406.1	alpha-KG-dehydrogenase [uncultured bacterium]	91	2e-16
ref YP_003980365.1	alpha-ketoglutarate-dependent taurine dioxyg...	91	2e-16
ref ZP_06707925.1	taurine dioxygenase [Streptomyces sp. e14] >g...	91	2e-16
emb CAY27542.1	alpha-KG-dehydrogenase [uncultured bacterium]	91	2e-16
ref ZP_08120023.1	taurine dioxygenase [Pseudonocardia sp. P1]	91	2e-16
ref YP_001265603.1	taurine dioxygenase [Pseudomonas putida F1] ...	91	2e-16
emb CAY27281.1	alpha-KG-dehydrogenase [uncultured bacterium]	91	2e-16
ref YP_539419.1	taurine dioxygenase [Escherichia coli UTI89] >g...	91	2e-16
gb ACG80564.1	TfdA [uncultured bacterium]	91	2e-16
ref YP_888161.1	alpha-ketoglutarate-dependent taurine dioxygena...	91	2e-16
emb CAY27454.1	alpha-KG-dehydrogenase [uncultured bacterium]	91	2e-16
emb CAY27352.1	alpha-KG-dehydrogenase [uncultured bacterium]	91	2e-16
emb CAY27428.1	alpha-KG-dehydrogenase [uncultured bacterium]	91	2e-16
emb CAP74907.1	alpha-ketoglutarate-dependent taurine dioxygenas...	91	2e-16
emb CAY27538.1	alpha-KG-dehydrogenase [uncultured bacterium]	91	2e-16
ref ZP_06728473.1	taurine dioxygenase [Acinetobacter haemolytic...	91	2e-16
emb CAY27270.1	alpha-KG-dehydrogenase [uncultured bacterium]	91	2e-16
ref YP_001262589.1	taurine catabolism dioxygenase TauD/TfdA [Sp...	91	2e-16
ref XP_002342012.1	alpha-ketoglutarate-dependent 2,4-dichloroph...	91	2e-16
emb CAY27395.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	91	2e-16
ref YP_003339620.1	taurine dioxygenase [Streptosporangium roseu...	91	2e-16
gb ACG80562.1	TfdA [uncultured bacterium]	91	2e-16
gb ABL97729.1	taurine dioxygenase [uncultured marine bacterium ...	91	2e-16
ref YP_001267994.1	taurine dioxygenase [Pseudomonas putida F1] ...	91	2e-16
ref YP_002008631.1	taurine dioxygenase, 2-oxoglutarate-dependen...	91	3e-16
ref YP_701700.1	taurine dioxygenase [Rhodococcus jostii RHA1] >...	90	3e-16
ref ZP_02509143.1	putative alpha-ketoglutarate-dependent taurin...	90	3e-16
ref ZP_07576777.1	Taurine catabolism dioxygenase TauD/TfdA [Sph...	90	3e-16
emb CAY27536.1	alpha-KG-dehydrogenase [uncultured bacterium]	90	3e-16
ref ZP_04899281.1	dioxygenase TauD/TfdA family [Burkholderia ps...	90	3e-16
ref ZP_01626396.1	taurine dioxygenase [marine gamma proteobacte...	90	3e-16
ref YP_001751848.1	taurine dioxygenase [Pseudomonas putida W619...	90	3e-16
emb CAY27306.1	alpha-KG-dehydrogenase [uncultured bacterium]	90	3e-16
ref ZP_08196821.1	taurine dioxygenase, TauD/TfdA family [Nocard...	90	3e-16
emb CAY27531.1	alpha-KG-dehydrogenase [uncultured bacterium]	90	3e-16
ref ZP_02406094.1	putative alpha-ketoglutarate-dependent taurin...	90	4e-16

ref ZP_03450440.1	dioxygenase, TauD/TfdA family [Burkholderia p...	90	4e-16
gb ACG80549.1	TfdA [uncultured bacterium]	90	4e-16
ref NP_900474.1	taurine dioxygenase [Chromobacterium violaceum ...	90	4e-16
ref YP_002383757.1	taurine dioxygenase [Escherichia fergusonii ...	90	4e-16
emb CAY27272.1	alpha-KG-dehydrogenase [uncultured bacterium]	90	4e-16
gb ADW06790.1	Taurine dioxygenase [Streptomyces flavogriseus AT...	90	4e-16
emb CAY27459.1	alpha-KG-dehydrogenase [uncultured bacterium]	90	4e-16
emb CAY27444.1	alpha-KG-dehydrogenase [uncultured bacterium]	90	4e-16
ref ZP_06656271.1	taurine dioxygenase [Escherichia coli B185] >...	90	4e-16
gb ACG80558.1	TfdA [uncultured bacterium]	90	4e-16
emb CAY27353.1	alpha-KG-dehydrogenase [uncultured bacterium]	90	4e-16
gb ACG80569.1	TfdA [uncultured bacterium]	90	4e-16
ref ZP_07447356.1	taurine dioxygenase [Escherichia coli NC101] ...	90	4e-16
ref ZP_03504692.1	Taurine dioxygenase [Rhizobium etli Brasil 5]	90	4e-16
gb ACG80568.1	TfdA [uncultured bacterium] >gi 196482352 gb ACG8...	90	4e-16
ref YP_001240769.1	putative dioxygenase [Bradyrhizobium sp. BTA...	90	4e-16
ref YP_605974.1	alkylsulfatase AtsK [Pseudomonas entomophila L4...	90	5e-16
ref YP_001895727.1	Taurine dioxygenase [Burkholderia phytofirma...	90	5e-16
emb CAY27222.1	alpha-KG-dehydrogenase [uncultured bacterium]	90	5e-16
ref YP_001629701.1	taurine dioxygenase [Bordetella petrii DSM 1...	90	5e-16
emb CAY27374.1	alpha-KG-dehydrogenase [uncultured bacterium]	89	5e-16
emb CAY27503.1	alpha-KG-dehydrogenase [uncultured bacterium]	89	5e-16
gb AAP21654.1	Shy7 [Streptomyces hygroscopicus subsp. yingcheng...	89	5e-16
emb CAY27355.1	alpha-KG-dehydrogenase [uncultured bacterium]	89	5e-16
ref YP_295812.1	taurine dioxygenase [Ralstonia eutropha JMP134]...	89	5e-16
ref ZP_07500810.1	taurine dioxygenase [Escherichia coli M605]	89	5e-16
ref ZP_06354055.1	taurine dioxygenase [Citrobacter youngae ATCC...	89	5e-16
emb CAY27334.1	alpha-KG-dehydrogenase [uncultured bacterium]	89	5e-16
emb CAY27463.1	alpha-KG-dehydrogenase [uncultured bacterium]	89	5e-16
ref YP_714407.1	putative taurine dioxygenase [Frankia alni ACN1...	89	5e-16
ref YP_110680.1	alpha-ketoglutarate-dependent taurine dioxygena...	89	5e-16
gb AAM87510.1	AE014000_14 taurine dioxygenase [Yersinia pestis K...	89	5e-16
ref ZP_04896195.1	dioxygenase TauD/TfdA family [Burkholderia ps...	89	5e-16
ref YP_001412108.1	taurine dioxygenase [Parvibaculum lavamentiv...	89	5e-16
ref ZP_06066452.1	taurine dioxygenase [Acinetobacter junii SH20...	89	6e-16
ref YP_072200.1	taurine dioxygenase [Yersinia pseudotuberculosi...	89	6e-16
emb CAY27414.1	alpha-KG-dehydrogenase [uncultured bacterium]	89	6e-16
gb ACG80555.1	TfdA [uncultured bacterium] >gi 196482302 gb ACG8...	89	6e-16
ref ZP_04889621.1	dioxygenase TauD/TfdA family [Burkholderia ps...	89	6e-16
gb EGC08562.1	TfdA family protein Taurine catabolism dioxygenas...	89	6e-16
ref ZP_01908082.1	taurine dioxygenase [Plesiocystis pacifica SI...	89	6e-16
ref ZP_04746502.1	putative dioxygenase [Mycobacterium kansasii ...	89	6e-16
emb CAY27209.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	89	7e-16
gb EGB79347.1	taurine dioxygenase [Escherichia coli MS 57-2]	89	7e-16
ref YP_001669049.1	taurine dioxygenase [Pseudomonas putida GB-1...	89	7e-16
ref YP_337380.1	putative alpha-ketoglutarate-dependent taurine ...	89	7e-16
emb CAY27340.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	89	7e-16
ref YP_402198.1	taurine dioxygenase [Shigella dysenteriae Sd197...	89	8e-16
ref ZP_04382578.1	alpha-ketoglutarate-dependent taurine dioxyge...	89	8e-16
ref YP_002869897.1	putative taurine dioxygenase [Pseudomonas fl...	89	8e-16
gb ACG80565.1	TfdA [uncultured bacterium]	89	8e-16
ref YP_002401497.1	taurine dioxygenase [Escherichia coli 55989]...	89	8e-16
ref YP_001454351.1	taurine dioxygenase [Citrobacter koseri ATCC...	89	8e-16
ref YP_003451475.1	taurine dioxygenase [Azospirillum sp. B510] ...	89	9e-16
emb CAY27424.1	alpha-KG-dehydrogenase [uncultured bacterium]	89	9e-16
ref ZP_06907775.1	taurine dioxygenase [Streptomyces pristinaesp...	89	9e-16
ref YP_002411171.1	taurine dioxygenase [Escherichia coli UMN026...	89	9e-16
gb ACG80581.1	TfdA [uncultured bacterium] >gi 196482344 gb ACG8...	89	9e-16
ref YP_001610738.1	putative taurine dioxygenase [Sorangium cell...	89	9e-16
emb CAY27514.1	alpha-KG-dehydrogenase [uncultured bacterium]	89	1e-15
ref XP_002151041.1	alpha-ketoglutarate-dependent 2,4-dichloroph...	89	1e-15
gb EGC96200.1	taurine dioxygenase [Escherichia fergusonii ECD227]	88	1e-15
ref ZP_07966578.1	TfdA family Taurine catabolism dioxygenase Ta...	88	1e-15

emb CAY27257.1	alpha-KG-dehydrogenase [uncultured bacterium]	88	1e-15
emb CAY27430.1	alpha-KG-dehydrogenase [uncultured bacterium]	88	1e-15
ref ZP_06860409.1	alpha-ketoglutarate-dependent taurine dioxyge...	88	1e-15
emb CAY27220.1	alpha-KG-dehydrogenase [uncultured bacterium]	88	1e-15
ref YP_001262249.1	taurine catabolism dioxygenase TauD/TfdA [Sp...	88	1e-15
emb CAY27328.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	88	1e-15
ref ZP_05434206.1	taurine dioxygenase [Shigella sp. D9]	88	1e-15
emb CAY27323.1	alpha-KG-dehydrogenase [uncultured bacterium]	88	1e-15
emb CAY27290.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	88	1e-15
emb CAY27363.1	alpha-KG-dehydrogenase [uncultured bacterium]	88	1e-15
emb CAY27228.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	88	1e-15
ref YP_001846143.1	taurine catabolism dioxygenase [Acinetobacte...	88	1e-15
gb AAS64597.1	alpha-KG-dependent dioxygenase [uncultured soil b...	88	1e-15
ref ZP_02149378.1	alpha-ketoglutarate-dependent taurine dioxyge...	88	1e-15
gb AAS64589.1	alpha-KG-dependent dioxygenase [uncultured soil b...	88	1e-15
gb EFZ56791.1	alpha-ketoglutarate-dependent taurine dioxygenase...	88	1e-15
ref YP_587247.1	taurine catabolism dioxygenase TauD/TfdA (2-oxo...	88	1e-15
ref ZP_07516225.1	taurine dioxygenase [Escherichia coli TA143]	88	1e-15
gb AAS64590.1	alpha-KG-dependent dioxygenase [uncultured soil b...	88	1e-15
ref YP_294247.1	taurine dioxygenase [Ralstonia eutropha JMP134]...	88	1e-15
emb CAY27551.1	alpha-KG-dehydrogenase [uncultured bacterium]	88	1e-15
ref ZP_02380861.1	Taurine dioxygenase [Burkholderia ubonensis Bu]	88	1e-15
ref ZP_03049591.1	taurine dioxygenase [Escherichia coli E110019...	88	1e-15
ref YP_001457202.1	taurine dioxygenase [Escherichia coli HS] >g...	88	1e-15
ref ZP_06877015.1	taurine dioxygenase [Pseudomonas aeruginosa P...	88	1e-15
ref YP_586764.1	taurine dioxygenase 2-oxoglutarate-dependent [C...	88	1e-15
gb EFX23899.1	taurine dioxygenase [Escherichia coli O55:H7 str....	88	1e-15
ref ZP_06840794.1	Taurine dioxygenase [Burkholderia sp. Ch1-1] ...	88	1e-15
ref ZP_01765614.1	taurine dioxygenase [Burkholderia pseudomalle...	88	1e-15
ref ZP_06473474.1	Taurine dioxygenase [Frankia symbiont of Dati...	88	1e-15
ref YP_003682823.1	Taurine dioxygenase [Nocardiopsis dassonvill...	88	2e-15
ref NP_752410.1	taurine dioxygenase [Escherichia coli CFT073] >...	88	2e-15
ref YP_003592890.1	taurine dioxygenase [Caulobacter segnis ATCC...	88	2e-15
gb ADC34024.1	TfdA-like protein [uncultured bacterium]	88	2e-15
ref NP_821782.1	taurine catabolism dioxygenase [Streptomyces av...	88	2e-15
ref NP_286110.1	taurine dioxygenase [Escherichia coli O157:H7 E...	88	2e-15
ref YP_004017356.1	taurine catabolism dioxygenase TauD/TfdA [Fr...	88	2e-15
ref NP_414902.1	taurine dioxygenase, 2-oxoglutarate-dependent [...	88	2e-15
ref ZP_04627176.1	Alpha-ketoglutarate-dependent taurine dioxyge...	88	2e-15
ref ZP_02493042.1	putative alpha-ketoglutarate-dependent taurin...	88	2e-15
ref YP_555387.1	taurine dioxygenase [Burkholderia xenovorans LB...	88	2e-15
ref YP_587420.1	taurine dioxygenase [Cupriavidus metallidurans ...	88	2e-15
ref ZP_07506274.1	taurine dioxygenase [Escherichia coli M718]	88	2e-15
ref YP_003227485.1	taurine dioxygenase, 2-oxoglutarate-dependen...	88	2e-15
ref ZP_07965013.1	TfdA family Taurine catabolism dioxygenase Ta...	88	2e-15
emb CAY27347.1	alpha-KG-dehydrogenase [uncultured bacterium]	87	2e-15
ref ZP_04002432.1	taurine dioxygenase [Escherichia coli 83972] ...	87	2e-15
emb CAY27376.1	alpha-KG-dehydrogenase [uncultured bacterium]	87	2e-15
gb EFW49871.1	Alpha-ketoglutarate-dependent taurine dioxygenase...	87	2e-15
emb CAY27457.1	alpha-KG-dehydrogenase [uncultured bacterium]	87	2e-15
gb ACG80563.1	TfdA [uncultured bacterium]	87	2e-15
ref ZP_03541010.1	Taurine dioxygenase [Comamonas testosteroni K...	87	2e-15
emb CAY27469.1	alpha-KG-dehydrogenase [uncultured bacterium]	87	2e-15
ref ZP_07300800.1	TauD/TfdA family taurine dioxygenase [Strepto...	87	2e-15
ref NP_706204.1	taurine dioxygenase [Shigella flexneri 2a str. ...	87	2e-15
emb CAY27528.1	alpha-KG-dehydrogenase [uncultured bacterium]	87	2e-15
emb CAY27367.1	alpha-KG-dehydrogenase [uncultured bacterium]	87	2e-15
gb AAS64588.1	alpha-KG-dependent dioxygenase [uncultured soil b...	87	2e-15
ref ZP_06787243.1	taurine dioxygenase [Acinetobacter sp. 601405...	87	2e-15
gb ACI70549.1	taurine dioxygenase [Escherichia coli] >gi 320643...	87	2e-15
emb CAY27525.1	alpha-KG-dehydrogenase [uncultured bacterium]	87	2e-15
ref ZP_02486273.1	taurine dioxygenase [Burkholderia pseudomalle...	87	2e-15
emb CAY27478.1	alpha-KG-dehydrogenase [uncultured bacterium]	87	2e-15

ref YP_001412268.1	taurine catabolism dioxygenase TauD/TfdA [Pa...	87	2e-15
ref ZP_04900578.1	putative alpha-ketoglutarate-dependent taurin...	87	3e-15
ref YP_001008090.1	taurine dioxygenase [Yersinia enterocolitica...	87	3e-15
gb AAT41922.1	putative dioxygenase [Fremyella diplosiphon Fd33]	87	3e-15
gb EGB60776.1	TfdA family protein Taurine catabolism dioxygenas...	87	3e-15
ref YP_003270569.1	taurine dioxygenase [Haliangium ochraceum DS...	87	3e-15
ref ZP_02902232.1	taurine dioxygenase [Escherichia albertii TW0...	87	3e-15
emb CBY29263.1	alpha-ketoglutarate-dependent taurine dioxygenas...	87	3e-15
ref ZP_05827549.1	alpha-ketoglutarate-dependent taurine dioxyge...	87	3e-15
ref ZP_05824825.1	alpha-ketoglutarate-dependent taurine dioxyge...	87	3e-15
ref YP_003606990.1	Taurine dioxygenase [Burkholderia sp. CCGE10...	87	3e-15
emb CAY27436.1	alpha-KG-dehydrogenase [uncultured bacterium]	87	3e-15
gb ABO11873.2	taurine dioxygenase [Acinetobacter baumannii ATCC...	87	3e-15
ref ZP_08155918.1	taurine dioxygenase [Rhodococcus equi ATCC 33...	87	3e-15
ref ZP_02501235.1	putative alpha-ketoglutarate-dependent taurin...	87	3e-15
ref ZP_02510493.1	taurine dioxygenase [Burkholderia pseudomalle...	87	3e-15
ref ZP_04560819.1	taurine dioxygenase [Citrobacter sp. 30_2] >g...	87	3e-15
emb CAY27287.1	alpha-KG-dehydrogenase [uncultured bacterium]	87	3e-15
gb AAS64596.1	alpha-KG-dependent dioxygenase [uncultured soil b...	87	3e-15
ref YP_001461543.1	taurine dioxygenase [Escherichia coli E24377...	87	3e-15
ref ZP_04698014.1	putative taurine catabolism dioxygenase [Stre...	87	3e-15
emb CAY27330.1	alpha-KG-dehydrogenase [uncultured bacterium]	87	3e-15
ref ZP_02450703.1	putative alpha-ketoglutarate-dependent taurin...	87	3e-15
ref YP_001603688.1	alpha-ketoglutarate-dependent taurine dioxyg...	87	3e-15
ref YP_842033.1	Alpha-ketoglutarate-dependent taurine dioxygena...	87	3e-15
emb CAY27499.1	alpha-KG-dehydrogenase [uncultured bacterium]	87	3e-15
ref YP_004005855.1	taurine dioxygenase [Rhodococcus equi 103S] ...	87	4e-15
ref ZP_06414550.1	Taurine catabolism dioxygenase TauD/TfdA [Fra...	87	4e-15
gb ACG80570.1	TfdA [uncultured bacterium]	87	4e-15
ref ZP_06056572.1	alpha-ketoglutarate-dependent taurine dioxyge...	87	4e-15
emb CAY27249.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	87	4e-15
ref ZP_04640756.1	Alpha-ketoglutarate-dependent taurine dioxyge...	87	4e-15
gb ACG80580.1	TfdA [uncultured bacterium]	87	4e-15
ref YP_003611636.1	taurine dioxygenase [Enterobacter cloacae su...	87	4e-15
gb ADY81414.1	taurine dioxygenase [Acinetobacter calcoaceticus ...	87	4e-15
ref YP_111581.1	taurine dioxygenase [Burkholderia pseudomallei ...	87	4e-15
emb CAY27279.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	87	4e-15
ref ZP_05968819.1	taurine dioxygenase [Enterobacter cancerogenu...	87	4e-15
emb CAY27540.1	alpha-KG-dehydrogenase [uncultured bacterium]	87	4e-15
emb CAY27507.1	alpha-KG-dehydrogenase [uncultured bacterium]	87	4e-15
ref YP_001683427.1	taurine catabolism dioxygenase TauD/TfdA [Ca...	86	4e-15
ref YP_003280390.1	Taurine catabolism dioxygenase TauD/TfdA [Co...	86	4e-15
emb CAY27543.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	4e-15
emb CAY27472.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	4e-15
ref YP_295875.1	taurine dioxygenase [Ralstonia eutropha JMP134]...	86	4e-15
ref XP_381837.1	hypothetical protein FG01661.1 [Gibberella zeae...	86	4e-15
emb CAY27483.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	4e-15
ref ZP_07617352.1	taurine dioxygenase [Escherichia coli TA280]	86	4e-15
emb CAY27448.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	4e-15
ref YP_001704936.1	putative dioxygenase [Mycobacterium abscessu...	86	4e-15
ref NP_106571.1	hypothetical protein mll5998 [Mesorhizobium lot...	86	4e-15
ref ZP_07303772.1	taurine catabolism dioxygenase [Streptomyces ...	86	4e-15
ref YP_001345668.1	hypothetical protein PSPA7_0272 [Pseudomonas...	86	4e-15
ref XP_001383599.2	hypothetical protein PICST_43041 [Schefferso...	86	5e-15
emb CAY27338.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	5e-15
ref YP_001063217.1	taurine dioxygenase [Burkholderia pseudomall...	86	5e-15
emb CAY27534.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	5e-15
gb ADZ44154.1	taurine dioxygenase [Yersinia enterocolitica subs...	86	5e-15
ref ZP_06690679.1	conserved hypothetical protein [Acinetobacter...	86	5e-15
ref ZP_07046346.1	Taurine catabolism dioxygenase TauD/TfdA [Com...	86	5e-15
ref ZP_04624706.1	Alpha-ketoglutarate-dependent taurine dioxyge...	86	5e-15
ref YP_001504880.1	taurine catabolism dioxygenase TauD/TfdA [Fr...	86	5e-15
gb EFW59470.1	Alpha-ketoglutarate-dependent taurine dioxygenase...	86	5e-15

emb CAY27434.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	5e-15
emb CAY27283.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	5e-15
gb AAT51233.1	PA0193 [synthetic construct]	86	5e-15
ref ZP_06842052.1	Taurine dioxygenase [Burkholderia sp. Chl-1] ...	86	5e-15
ref ZP_01617748.1	Taurine dioxygenase [marine gamma proteobacte...	86	5e-15
emb CAY27438.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	5e-15
ref NP_248883.1	hypothetical protein PA0193 [Pseudomonas aerugi...	86	6e-15
ref YP_001909093.1	taurine dioxygenase [Erwinia tasmaniensis Et...	86	6e-15
ref YP_002319044.1	taurine dioxygenase [Acinetobacter baumannii...	86	6e-15
emb CAY27317.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	6e-15
gb ADC34007.1	TfdA-like protein [uncultured bacterium]	86	6e-15
emb CAY27442.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	6e-15
gb ADC34045.1	TfdA-like protein [uncultured bacterium]	86	7e-15
ref YP_309357.1	taurine dioxygenase [Shigella sonnei Ss046] >gi...	86	7e-15
emb CAN89617.1	putative taurine dioxygenase [Streptomyces colli...	86	7e-15
ref ZP_07952776.1	TfdA family Taurine catabolism dioxygenase Ta...	86	7e-15
emb CAY27492.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	7e-15
emb CAY27309.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	7e-15
gb EFW79602.1	TauD/TfdA family dioxygenase [Pseudomonas syringa...	86	7e-15
emb CAY27416.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	7e-15
ref YP_273987.1	TauD/TfdA family dioxygenase [Pseudomonas syrin...	86	7e-15
gb ADC34020.1	TfdA-like protein [uncultured bacterium]	86	7e-15
ref ZP_05639075.1	TauD/TfdA family dioxygenase [Pseudomonas syr...	86	7e-15
emb CBJ20068.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	86	8e-15
gb ACG80553.1	TfdA [uncultured bacterium] >gi 196482332 gb ACG8...	86	8e-15
ref ZP_02474390.1	putative alpha-ketoglutarate-dependent taurin...	86	8e-15
emb CAY27213.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	8e-15
emb CAY27410.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	8e-15
ref YP_001714059.1	taurine dioxygenase [Acinetobacter baumannii...	86	8e-15
emb CAY27480.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	8e-15
ref YP_004006885.1	taurine dioxygenase [Rhodococcus equi 103S] ...	86	8e-15
emb CAY27505.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	8e-15
ref YP_001084475.1	taurine dioxygenase [Acinetobacter baumannii...	86	8e-15
emb CAY27266.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	8e-15
ref YP_348002.1	taurine dioxygenase [Pseudomonas fluorescens Pf...	86	9e-15
ref ZP_08152263.1	TauD/TfdA family dioxygenase [Rhodococcus equ...	86	9e-15
emb CAY27467.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	9e-15
emb CAY27381.1	alpha-KG-dehydrogenase [uncultured bacterium]	86	9e-15
ref ZP_08152264.1	taurine dioxygenase [Rhodococcus equi ATCC 33...	85	9e-15
ref ZP_01363100.1	hypothetical protein PaerPA_01000192 [Pseudom...	85	9e-15
ref YP_722716.1	taurine dioxygenase [Trichodesmium erythraeum I...	85	1e-14
ref YP_558866.1	putative alpha-ketoglutarate-dependent taurine ...	85	1e-14
ref YP_002008878.1	taurine dioxygenase [Cupriavidus taiwanensis...	85	1e-14
ref ZP_06415883.1	Taurine dioxygenase [Frankia sp. EUN1f] >gi 2...	85	1e-14
ref ZP_04662843.1	taurine dioxygenase [Acinetobacter baumannii ...	85	1e-14
ref ZP_04382852.1	alpha-ketoglutarate-dependent taurine dioxyge...	85	1e-14
ref YP_002767959.1	dioxygenase [Rhodococcus erythropolis PR4] >...	85	1e-14
emb CAY27496.1	alpha-KG-dehydrogenase [uncultured bacterium]	85	1e-14
ref ZP_04891715.1	putative alpha-ketoglutarate-dependent taurin...	85	1e-14
ref ZP_04520779.1	alpha-ketoglutarate-dependent taurine dioxyge...	85	1e-14
gb ADC34028.1	TfdA-like protein [uncultured bacterium]	85	1e-14
ref ZP_06637645.1	taurine dioxygenase [Serratia odorifera DSM 4...	85	1e-14
emb CAY27398.1	alpha-KG-dehydrogenase [uncultured bacterium]	85	1e-14
emb CAY27297.1	alpha-KG-dehydrogenase [uncultured bacterium]	85	1e-14
ref YP_003491531.1	dioxygenase [Streptomyces scabiei 87.22] >gi...	85	1e-14
emb CAY27379.1	alpha-KG-dehydrogenase [uncultured bacterium]	85	1e-14
ref YP_112297.1	taurine catabolism dioxygenase TauD, TfdA famil...	85	1e-14
ref YP_002780830.1	dioxygenase [Rhodococcus opacus B4] >gi 2262...	85	1e-14
ref ZP_07004378.1	Alpha-ketoglutarate-dependent taurine dioxyge...	85	1e-14
ref ZP_08155875.1	taurine dioxygenase [Rhodococcus equi ATCC 33...	85	1e-14
ref YP_299246.1	taurine dioxygenase [Ralstonia eutropha JMP134]...	85	1e-14
ref YP_001206008.1	putative dioxygenase; putative taurine dioxy...	85	1e-14
ref YP_583867.1	taurine catabolism dioxygenase TauD/TfdA [Cupri...	85	2e-14

ref YP_788349.1	hypothetical protein PA14_02420 [Pseudomonas ae...	85	2e-14
ref YP_003278927.1	Taurine catabolism dioxygenase TauD/TfdA [Co...	84	2e-14
ref ZP_05127632.1	alpha-ketoglutarate-dependent taurine dioxyge...	84	2e-14
ref ZP_06462103.1	taurine dioxygenase [Pseudomonas syringae pv....	84	2e-14
emb CAY27372.1	alpha-KG-dehydrogenase [uncultured bacterium]	84	2e-14
ref YP_001439004.1	taurine dioxygenase [Cronobacter sakazakii A...	84	2e-14
ref ZP_04636549.1	Alpha-ketoglutarate-dependent taurine dioxyge...	84	2e-14
ref ZP_04632718.1	Alpha-ketoglutarate-dependent taurine dioxyge...	84	2e-14
emb CAY27365.1	alpha-KG-dehydrogenase [uncultured bacterium]	84	2e-14
emb CAY27555.1	alpha-KG-dehydrogenase [uncultured bacterium]	84	2e-14
ref ZP_02409593.1	taurine dioxygenase [Burkholderia pseudomalle...	84	2e-14
emb CAY27346.1	alpha-KG-dehydrogenase [uncultured bacterium]	84	2e-14
emb CAY27342.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	84	2e-14
gb ACG80554.1	TfdA [uncultured bacterium]	84	2e-14
ref ZP_06055483.1	taurine dioxygenase [alpha proteobacterium HI...	84	2e-14
ref ZP_08206063.1	putative dioxygenase [Gordonia neofelifaecis ...	84	2e-14
ref YP_298049.1	taurine dioxygenase [Ralstonia eutropha JMP134]...	84	2e-14
emb CAY27231.1	alpha-KG-dehydrogenase [uncultured bacterium]	84	2e-14
ref ZP_02503717.1	dioxygenase TauD/TfdA family protein [Burkhol...	84	2e-14
ref YP_004117507.1	Taurine dioxygenase [Pantoea sp. At-9b] >gi ...	84	2e-14
ref YP_002240174.1	taurine dioxygenase [Klebsiella pneumoniae 3...	84	2e-14
emb CAY27523.1	alpha-KG-dehydrogenase [uncultured bacterium]	84	2e-14
ref YP_335782.1	taurine dioxygenase [Burkholderia pseudomallei ...	84	2e-14
ref ZP_03269249.1	Taurine dioxygenase [Burkholderia sp. H160] >...	84	2e-14
ref NP_768765.1	dioxygenase [Bradyrhizobium japonicum USDA 110]...	84	2e-14
emb CAY27396.1	alpha-KG-dehydrogenase [uncultured bacterium]	84	2e-14
ref ZP_02466907.1	taurine dioxygenase [Burkholderia thailandens...	84	2e-14
emb CAY27299.1	alpha-KG-dehydrogenase [uncultured bacterium]	84	2e-14
ref YP_001175576.1	taurine dioxygenase [Enterobacter sp. 638] >...	84	2e-14
ref YP_714255.1	putative taurine catabolism dioxygenase [Franki...	84	3e-14
ref ZP_04383171.1	alpha-ketoglutarate-dependent taurine dioxyge...	84	3e-14
ref ZP_03542510.1	Taurine dioxygenase [Comamonas testosteroni K...	84	3e-14
ref ZP_06511502.1	dioxygenase [Mycobacterium tuberculosis T92] ...	84	3e-14
ref YP_703743.1	taurine dioxygenase [Rhodococcus jostii RHA1] >...	84	3e-14
ref ZP_01615851.1	taurine dioxygenase [marine gamma proteobacte...	84	3e-14
ref ZP_06660873.1	tauD [Escherichia coli B088] >gi 291324966 gb...	84	3e-14
emb CAY27288.1	alpha-KG-dehydrogenase [uncultured bacterium]	84	3e-14
ref ZP_05068539.1	alpha-ketoglutarate-dependent 2,4-dichlorophe...	83	3e-14
emb CAY27404.1	alpha-KG-dehydrogenase [uncultured bacterium]	83	4e-14
ref XP_003042406.1	hypothetical protein NECHADRAFT_97202 [Nectr...	83	4e-14
ref YP_003209304.1	taurine dioxygenase [Cronobacter turicensis ...	83	4e-14
ref ZP_02487377.1	dioxygenase TauD/TfdA family protein [Burkhol...	83	4e-14
ref YP_003645662.1	Taurine dioxygenase [Tsukamurella paurometab...	83	4e-14
gb ABL97678.1	taurine dioxygenase [uncultured marine bacterium ...	83	4e-14
ref YP_003732553.1	taurine dioxygenase [Acinetobacter sp. DR1] ...	83	4e-14
ref YP_004006884.1	taurine dioxygenase [Rhodococcus equi 103S] ...	83	4e-14
ref ZP_07043442.1	Taurine catabolism dioxygenase TauD/TfdA [Com...	83	4e-14
emb CAY27518.1	alpha-KG-dehydrogenase [uncultured bacterium]	83	4e-14
ref ZP_08124447.1	Dioxygenase, TauD/TfdA family protein [Pseudo...	83	5e-14
ref NP_746577.1	TauD/TfdA family dioxygenase [Pseudomonas putid...	83	5e-14
emb CAY27560.1	alpha-KG-dehydrogenase [uncultured bacterium]	83	5e-14
emb CAY27412.1	alpha-KG-dehydrogenase [uncultured bacterium]	83	5e-14
ref YP_001333996.1	taurine dioxygenase [Klebsiella pneumoniae s...	83	5e-14
ref YP_106556.1	alpha-ketoglutarate-dependent taurine dioxygena...	83	5e-14
ref ZP_08022192.1	taurine dioxygenase [Dietzia cinnamea P4] >gi...	83	5e-14
ref YP_003364051.1	alpha-ketoglutarate-dependent taurine dioxyg...	83	5e-14
ref YP_003766141.1	taurine dioxygenase [Amycolatopsis mediterranea...	82	7e-14
emb CAY27446.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	82	7e-14
gb ADC34039.1	TfdA-like protein [uncultured bacterium]	82	7e-14
ref YP_406805.1	taurine dioxygenase [Shigella boydii Sb227] >gi...	82	8e-14
ref ZP_07576923.1	Taurine dioxygenase [Sphingobium chlorophenol...	82	8e-14
ref NP_767577.1	dioxygenase [Bradyrhizobium japonicum USDA 110]...	82	8e-14
emb CAY27465.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	82	8e-14

ref YP_001260879.1	taurine catabolism dioxygenase TauD/TfdA [Sp...	82	8e-14
emb CAY27359.1	alpha-KG-dehydrogenase [uncultured bacterium]	82	1e-13
ref YP_002781052.1	dioxygenase [Rhodococcus opacus B4] >gi 2262...	82	1e-13
ref ZP_04386335.1	alpha-ketoglutarate-dependent taurine dioxyge...	82	1e-13
ref YP_004017667.1	taurine dioxygenase [Frankia sp. EuIlc] >gi ...	82	1e-13
gb ADC33965.1	TfdA-like protein [uncultured bacterium]	82	1e-13
emb CAY27470.1	alpha-KG-dehydrogenase [uncultured bacterium]	82	1e-13
ref YP_729190.1	Alpha-ketoglutarate-dependent taurine dioxygena...	82	1e-13
emb CBK85931.1	Probable taurine catabolism dioxygenase [Enterob...	82	1e-13
ref YP_990665.1	alpha-ketoglutarate-dependent taurine dioxygena...	82	1e-13
ref ZP_02407529.1	taurine dioxygenase [Burkholderia pseudomalle...	82	1e-13
emb CAY27203.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	81	1e-13
ref YP_002230865.1	alpha-ketoglutarate-dependent taurine dioxyg...	81	1e-13
gb ADC33936.1	TfdA-like protein [uncultured bacterium]	81	2e-13
ref YP_003647917.1	Taurine dioxygenase [Tsukamurella paurometab...	81	2e-13
ref YP_002767506.1	dioxygenase [Rhodococcus erythropolis PR4] >...	81	2e-13
ref YP_002650372.1	taurine dioxygenase [Erwinia pyrifoliae Epl/...	81	2e-13
gb ADC33939.1	TfdA-like protein [uncultured bacterium]	81	2e-13
emb CAY27402.1	alpha-KG-dehydrogenase [uncultured bacterium]	81	2e-13
gb ACF09927.1	probable taurine catabolism dioxygenase [uncultur...	81	2e-13
ref ZP_04382576.1	alpha-ketoglutarate-dependent taurine dioxyge...	81	2e-13
emb CAY27383.1	alpha-KG-dehydrogenase [uncultured bacterium]	81	2e-13
gb EFQ95338.1	hypothetical protein PTT_06701 [Pyrenophora teres...	81	2e-13
gb ADC33935.1	TfdA-like protein [uncultured bacterium] >gi 2850...	81	2e-13
ref NP_928338.1	hypothetical protein plu1004 [Photorhabdus lumi...	81	2e-13
ref ZP_06057387.1	taurine dioxygenase [Acinetobacter calcoaceti...	81	2e-13
ref ZP_06410835.1	Taurine dioxygenase [Frankia sp. EUN1f] >gi 2...	81	2e-13
emb CAY27389.1	alpha-KG-dehydrogenase [uncultured bacterium]	81	2e-13
ref YP_004017671.1	taurine dioxygenase [Frankia sp. EuIlc] >gi ...	81	2e-13
ref ZP_06500435.1	taurine dioxygenase [Pseudomonas syringae pv....	81	2e-13
ref YP_586543.1	taurine dioxygenase 2-oxoglutarate-dependent [C...	81	2e-13
gb ADC34027.1	TfdA-like protein [uncultured bacterium]	80	2e-13
ref ZP_01103984.1	Alpha-ketoglutarate-dependent taurine dioxyge...	80	2e-13
ref YP_001808308.1	taurine dioxygenase [Burkholderia ambifaria ...	80	2e-13
ref XP_388431.1	hypothetical protein FG08255.1 [Gibberella zeae...	80	2e-13
ref YP_001704349.1	taurine dioxygenase [Mycobacterium abscessus...	80	2e-13
ref YP_004018099.1	taurine dioxygenase [Frankia sp. EuIlc] >gi ...	80	2e-13
emb CAY27517.1	alpha-KG-dehydrogenase [uncultured bacterium]	80	3e-13
ref XP_002148602.1	alpha-ketoglutarate-dependent taurine dioxyg...	80	3e-13
ref XP_003042850.1	hypothetical protein NECHADRAFT_86763 [Nectr...	80	3e-13
emb CAY27494.1	alpha-KG-dehydrogenase [uncultured bacterium]	80	3e-13
gb ADI03640.1	taurine catabolism dioxygenase [Streptomyces bing...	80	3e-13
gb ACG80552.1	TfdA [uncultured bacterium]	80	3e-13
gb ADC33937.1	TfdA-like protein [uncultured bacterium]	80	3e-13
emb CAY27245.1	alpha-KG-dehydrogenase [uncultured bacterium]	80	3e-13
ref ZP_02894534.1	Taurine dioxygenase [Burkholderia ambifaria I...	80	3e-13
ref XP_001387107.2	alpha-ketoglutarate catabolism dioxygenase [...	80	3e-13
gb ADZ69844.1	Putative taurine dioxygenase protein [Polymorphum...	80	3e-13
emb CAY27344.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	80	3e-13
emb CAY27311.1	alpha-KG-dehydrogenase [uncultured bacterium]	80	3e-13
ref YP_002768589.1	dioxygenase [Rhodococcus erythropolis PR4] >...	80	3e-13
ref ZP_07264205.1	taurine dioxygenase [Pseudomonas syringae pv....	80	3e-13
gb ACG80577.1	TfdA [uncultured bacterium]	80	4e-13
ref YP_001506858.1	taurine dioxygenase [Frankia sp. EANlpec] >g...	80	4e-13
gb ADC33975.1	TfdA-like protein [uncultured bacterium]	80	4e-13
emb CAY27422.1	alpha-KG-dehydrogenase [uncultured bacterium]	80	4e-13
emb CAY27501.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	80	4e-13
ref ZP_06411856.1	Taurine dioxygenase [Frankia sp. EUN1f] >gi 2...	80	4e-13
gb ABR27342.1	TfdA [uncultured bacterium]	80	4e-13
ref YP_298356.1	taurine dioxygenase [Ralstonia eutropha JMP134]...	80	4e-13
ref YP_003731487.1	taurine dioxygenase [Acinetobacter sp. DR1] ...	80	4e-13
ref ZP_07308884.1	taurine catabolism dioxygenase [Streptomyces ...	80	4e-13
ref YP_001791206.1	taurine dioxygenase [Leptothrix cholodnii SP...	80	4e-13

ref XP_001482071.1	hypothetical protein PGUG_05834 [Meyerozyma ...	80	4e-13
emb CAY27408.1	alpha-KG-dehydrogenase [uncultured bacterium]	80	4e-13
emb CAY27224.1	alpha-KG-dehydrogenase [uncultured bacterium]	80	4e-13
ref ZP_08208480.1	taurine dioxygenase [Novosphingobium nitrogen...	80	4e-13
ref YP_003609092.1	Taurine dioxygenase [Burkholderia sp. CCGE10...	80	5e-13
gb ADC34038.1	TfdA-like protein [uncultured bacterium]	80	5e-13
ref ZP_03267080.1	Taurine catabolism dioxygenase TauD/TfdA [Bur...	79	5e-13
ref XP_002179018.1	predicted protein [Phaeodactylum tricornutum...	79	5e-13
ref YP_004016948.1	taurine dioxygenase [Frankia sp. EuIlc] >gi ...	79	5e-13
gb EDK37093.2	hypothetical protein PGUG_01191 [Meyerozyma guill...	79	5e-13
ref ZP_07572418.1	Taurine catabolism dioxygenase TauD/TfdA [Sph...	79	5e-13
ref YP_001386601.1	hypothetical protein PICST_33987 [Schefferso...	79	6e-13
ref YP_369080.1	taurine dioxygenase [Burkholderia sp. 383] >gi ...	79	6e-13
gb EFV82889.1	hypothetical protein HMPREF0005_00146 [Achromobac...	79	7e-13
gb ACG80566.1	TfdA [uncultured bacterium]	79	7e-13
ref ZP_03822519.1	alpha-ketoglutarate-dependent taurine dioxyge...	79	7e-13
gb ADC33972.1	TfdA-like protein [uncultured bacterium]	79	7e-13
ref XP_001728977.1	hypothetical protein MGL_3971 [Malassezia gl...	79	7e-13
ref YP_003932509.1	taurine dioxygenase, 2-oxoglutarate-dependen...	79	7e-13
gb ADC33957.1	TfdA-like protein [uncultured bacterium]	79	7e-13
ref YP_773478.1	taurine dioxygenase [Burkholderia ambifaria AMM...	79	7e-13
gb ADY82284.1	taurine dioxygenase [Acinetobacter calcoaceticus ...	79	7e-13
ref YP_003521938.1	TauD [Pantoea ananatis LMG 20103] >gi 291154...	79	8e-13
ref ZP_06411796.1	Taurine dioxygenase [Frankia sp. EUN1f] >gi 2...	79	8e-13
ref XP_001883209.1	predicted protein [Laccaria bicolor S238N-H8...	79	8e-13
ref YP_234880.1	taurine dioxygenase [Pseudomonas syringae pv. s...	79	8e-13
emb CAY27545.1	alpha-KG-dehydrogenase [uncultured bacterium]	79	8e-13
gb ADC34034.1	TfdA-like protein [uncultured bacterium]	79	9e-13
gb ADC33941.1	TfdA-like protein [uncultured bacterium]	79	9e-13
ref YP_001166963.1	taurine dioxygenase [Rhodobacter sphaeroides...	79	1e-12
ref XP_001834704.1	alpha-ketoglutarate catabolism dioxygenase [...	79	1e-12
gb ACG80559.1	TfdA [uncultured bacterium] >gi 196482328 gb ACG8...	79	1e-12
gb ADC33942.1	TfdA-like protein [uncultured bacterium]	78	1e-12
ref YP_002763816.1	dioxygenase [Rhodococcus erythropolis PR4] >...	78	1e-12
gb ADP10566.1	taurine dioxygenase [Erwinia sp. Ejp617]	78	1e-12
ref YP_003658919.1	taurine dioxygenase [Segniliparus rotundus D...	78	1e-12
gb ADC33945.1	TfdA-like protein [uncultured bacterium]	78	1e-12
gb ACG80571.1	TfdA [uncultured bacterium]	78	1e-12
emb CAY27370.1	alpha-KG-dehydrogenase [uncultured bacterium]	78	1e-12
ref YP_498356.1	taurine catabolism dioxygenase TauD/TfdA [Novos...	78	1e-12
ref ZP_08156118.1	taurine dioxygenase [Rhodococcus equi ATCC 33...	78	1e-12
gb ADC33940.1	TfdA-like protein [uncultured bacterium]	78	2e-12
ref YP_003532757.1	taurine dioxygenase, 2-oxoglutarate-dependen...	78	2e-12
gb ADC33967.1	TfdA-like protein [uncultured bacterium]	78	2e-12
gb ADC33973.1	TfdA-like protein [uncultured bacterium]	78	2e-12
ref YP_948716.1	taurine dioxygenase [Arthrobacter aurescens TC1...	78	2e-12
ref YP_004006193.1	taurine dioxygenase [Rhodococcus equi 103S] ...	78	2e-12
gb ADC33983.1	TfdA-like protein [uncultured bacterium]	78	2e-12
gb ADC33986.1	TfdA-like protein [uncultured bacterium]	77	2e-12
ref ZP_08206375.1	taurine dioxygenase [Gordonia neofelifaecis N...	77	2e-12
emb CAY27400.1	alpha-KG-dehydrogenase [uncultured bacterium]	77	2e-12
ref ZP_07300240.1	taurine dioxygenase [Streptomyces hygroscopic...	77	2e-12
ref ZP_07379660.1	Taurine dioxygenase [Pantoea sp. aB] >gi 3043...	77	2e-12
ref YP_003101613.1	taurine dioxygenase [Actinosynnema mirum DSM...	77	2e-12
ref XP_001270812.1	alpha-ketoglutarate-dependent taurine dioxyg...	77	2e-12
ref XP_001382805.1	hypothetical protein PICST_29419 [Schefferso...	77	3e-12
ref ZP_05095314.1	Taurine catabolism dioxygenase TauD, TfdA fam...	77	3e-12
ref YP_001206266.1	putative alpha-ketoglutarate-dependent tauri...	77	3e-12
gb ADD83004.1	PtnO6 [Streptomyces platensis]	77	3e-12
gb EFW99864.1	alpha-ketoglutarate-dependent taurine dioxygenase...	77	3e-12
ref ZP_02186847.1	Alpha-ketoglutarate-dependent taurine dioxyge...	77	3e-12
emb CAY27332.1	alpha-KG-dehydrogenase [uncultured bacterium]	77	3e-12
emb CAY27426.1	alpha-KG-dehydrogenase [uncultured bacterium]	77	3e-12

emb CAY27215.1	alpha-KG-dehydrogenase [uncultured bacterium]	77	3e-12
gb EFW71811.1	Alpha-ketoglutarate-dependent taurine dioxygenase...	77	3e-12
emb CAY27369.1	alpha-KG-dehydrogenase [uncultured bacterium]	77	3e-12
gb ACB30160.1	2,4-D/alpha-ketoglutarate dioxygenase [Paenibacil...	77	3e-12
gb AAD50457.1	AF170704_7 similar to dioxygenase [Streptomyces sp...	77	4e-12
emb CAY27229.1	alpha-KG-dehydrogenase [uncultured bacterium]	77	4e-12
gb ADC33984.1	TfdA-like protein [uncultured bacterium]	77	4e-12
ref YP_003072835.1	taurine dioxygenase [Teredinibacter turnerae...	77	4e-12
ref XP_001487814.1	hypothetical protein PGUG_01191 [Meyerozyma ...	77	4e-12
ref ZP_02906590.1	Taurine dioxygenase [Burkholderia ambifaria M...	76	4e-12
ref XP_002485629.1	alpha-ketoglutarate-dependent taurine dioxyg...	76	4e-12
ref YP_002007367.1	taurine dioxygenase; taud/tfdA taurine catab...	76	4e-12
ref XP_001557971.1	hypothetical protein BC1G_03553 [Botryotinia...	76	4e-12
ref XP_001937023.1	alpha-ketoglutarate-dependent taurine dioxyg...	76	5e-12
ref XP_760142.1	hypothetical protein UM03995.1 [Ustilago maydis...	76	6e-12
ref XP_001396406.1	alpha-ketoglutarate-dependent taurine dioxyg...	76	6e-12
ref XP_001935765.1	alpha-ketoglutarate-dependent taurine dioxyg...	76	6e-12
ref ZP_05006078.1	taurine dioxygenase [Streptomyces clavuligeru...	76	6e-12
gb ADC34002.1	TfdA-like protein [uncultured bacterium]	76	7e-12
ref YP_372823.1	taurine dioxygenase [Burkholderia sp. 383] >gi ...	76	7e-12
emb CBJ20070.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	76	7e-12
ref ZP_02359146.1	taurine dioxygenase [Burkholderia oklahomensis...	76	7e-12
gb ADC33938.1	TfdA-like protein [uncultured bacterium]	75	7e-12
gb ADC33946.1	TfdA-like protein [uncultured bacterium]	75	7e-12
ref ZP_00990204.1	Probable taurine catabolism dioxygenase [Vibr...	75	8e-12
ref YP_001625716.1	alkylsulfate dioxygenase (2-oxoglutarate-dep...	75	8e-12
emb CAY27319.1	alpha-KG-dehydrogenase [uncultured bacterium]	75	8e-12
ref YP_438996.2	taurine dioxygenase [Burkholderia thailandensis...	75	9e-12
gb EFQ87300.1	hypothetical protein PTT_17264 [Pyrenophora teres...	75	9e-12
gb ACO31277.1	PtmO3 [Streptomyces platensis]	75	9e-12
ref ZP_02384176.1	taurine dioxygenase [Burkholderia thailandens...	75	9e-12
ref YP_003940920.1	Taurine dioxygenase [Enterobacter cloacae SC...	75	1e-11
gb ACO31282.1	PtmO6 [Streptomyces platensis]	75	1e-11
ref XP_001560734.1	hypothetical protein BC1G_00762 [Botryotinia...	75	1e-11
ref YP_001584538.1	taurine dioxygenase [Burkholderia multivoran...	75	1e-11
ref XP_001209049.1	conserved hypothetical protein [Aspergillus ...	75	1e-11
gb ABC34147.1	alpha-ketoglutarate-dependent taurine dioxygenase...	75	1e-11
ref ZP_03585565.1	taurine dioxygenase [Burkholderia multivorans...	75	1e-11
ref YP_001239290.1	putative alpha-ketoglutarate-dependent tauri...	75	1e-11
ref ZP_07045848.1	Taurine catabolism dioxygenase TauD/TfdA fami...	75	1e-11
gb ADC33980.1	TfdA-like protein [uncultured bacterium]	75	1e-11
ref ZP_02366215.1	taurine dioxygenase [Burkholderia oklahomensis...	75	1e-11
ref XP_001598281.1	hypothetical protein SS1G_00367 [Sclerotinia...	75	2e-11
ref NP_826592.1	taurine catabolism dioxygenase [Streptomyces av...	75	2e-11
ref XP_001836817.2	alpha-ketoglutarate-dependent taurine dioxyg...	75	2e-11
gb ADC33989.1	TfdA-like protein [uncultured bacterium]	75	2e-11
gb ADC33944.1	TfdA-like protein [uncultured bacterium]	74	2e-11
ref XP_001799620.1	hypothetical protein SNOG_09325 [Phaeosphaer...	74	2e-11
ref YP_001777150.1	taurine dioxygenase [Burkholderia cenocepaci...	74	2e-11
ref ZP_07576730.1	Taurine catabolism dioxygenase TauD/TfdA [Sph...	74	2e-11
ref YP_001834136.1	taurine dioxygenase [Beijerinckia indica sub...	74	2e-11
ref YP_002406356.1	taurine dioxygenase, 2-oxoglutarate-dependen...	74	2e-11
ref ZP_01742153.1	taurine dioxygenase, 2-oxoglutarate-dependent...	74	2e-11
ref NP_962663.1	hypothetical protein MAP3729 [Mycobacterium avi...	74	2e-11
gb ADC33963.1	TfdA-like protein [uncultured bacterium]	74	2e-11
ref ZP_02370264.1	taurine dioxygenase [Burkholderia thailandens...	74	2e-11
ref XP_001397270.2	2,4-dichlorophenoxyacetate alpha-ketoglutara...	74	2e-11
ref ZP_03569866.1	taurine dioxygenase [Burkholderia multivorans...	74	2e-11
ref ZP_01864402.1	alpha-ketoglutarate-dependent taurine dioxyge...	74	2e-11
gb AAS64591.1	alpha-KG-dependent dioxygenase [uncultured soil b...	74	2e-11
gb EDZ70798.1	YLL057Cp-like protein [Saccharomyces cerevisiae A...	74	3e-11
ref YP_002233738.1	putative taurine dioxygenase [Burkholderia c...	74	3e-11
ref YP_837646.1	taurine dioxygenase [Burkholderia cenocepacia H...	74	3e-11

ref XP_003049797.1 predicted protein [Nectria haematococca mpVI...	74	3e-11
ref NP_013043.1 Jlp1p [Saccharomyces cerevisiae S288c] >gi 2497...	74	3e-11
ref ZP_06274956.1 Taurine catabolism dioxygenase TauD/TfdA [Str...	74	3e-11
gb AAS64584.1 alpha-KG-dependent dioxygenase [uncultured soil b...	74	3e-11
ref ZP_04941966.1 Taurine dioxygenase [Burkholderia cenocepacia...	74	3e-11
gb EGA57698.1 Jlp1p [Saccharomyces cerevisiae FostersB]	74	3e-11
ref XP_681848.1 hypothetical protein AN8579.2 [Aspergillus nidu...	74	3e-11
gb EGA77784.1 Jlp1p [Saccharomyces cerevisiae Vin13]	74	3e-11
gb EDV09264.1 alpha-ketoglutarate-dependent sulfonate dioxygena...	74	3e-11
gb ADI34062.1 2,4-D/alpha-ketoglutarate dioxygenase [Burkholder...	74	3e-11
ref XP_457814.2 DEHA2C03036p [Debaryomyces hansenii CBS767] >gi...	74	3e-11
gb EGA61415.1 Jlp1p [Saccharomyces cerevisiae FostersO]	74	3e-11
ref XP_001834709.1 alpha-ketoglutarate catabolism dioxygenase [...]	74	4e-11
ref ZP_00515418.1 similar to Probable taurine catabolism dioxyg...	74	4e-11
ref ZP_06922104.1 taurine catabolism dioxygenase [Streptomyces ...]	73	4e-11
gb ABR27328.1 TfdA [uncultured bacterium] >gi 149394950 gb ABR2...	73	4e-11
gb ADC33962.1 TfdA-like protein [uncultured bacterium]	73	4e-11
gb ACB30159.1 2,4-D/alpha-ketoglutarate dioxygenase [Rhodococcu...	73	4e-11
ref XP_660564.1 hypothetical protein AN2960.2 [Aspergillus nidu...	73	4e-11
ref YP_832515.1 taurine dioxygenase [Arthrobacter sp. FB24] >gi...	73	5e-11
ref XP_001834272.1 alpha-ketoglutarate-dependent taurine dioxyg...	73	5e-11
gb ADC33953.1 TfdA-like protein [uncultured bacterium]	73	5e-11
ref YP_556155.1 putative taurine catabolism dioxygenase TauD/Tf...	73	5e-11
ref YP_298736.1 taurine dioxygenase [Ralstonia eutropha JMP134]...	73	5e-11
ref XP_002563150.1 Pc20g06210 [Penicillium chrysogenum Wisconsi...	73	5e-11
gb EGD74176.1 hypothetical protein PTSG_06184 [Salpingoeca sp. ...]	73	6e-11
ref ZP_03541596.1 Taurine dioxygenase [Comamonas testosteroni K...	73	6e-11
gb EFW97628.1 alpha-ketoglutarate catabolism dioxygenase [Pichi...	72	7e-11
ref YP_001237505.1 putative taurine dioxygenase, 2-oxoglutarate...	72	7e-11
gb EGD03387.1 taurine dioxygenase [Burkholderia sp. TJI49]	72	7e-11
ref ZP_06844898.1 Taurine dioxygenase [Burkholderia sp. Chl-1] ...	72	7e-11
gb ADC33960.1 TfdA-like protein [uncultured bacterium]	72	9e-11
ref YP_002486908.1 Taurine dioxygenase [Arthrobacter chlorophen...	72	9e-11
ref XP_001525134.1 conserved hypothetical protein [Lodderomyces...	72	9e-11
ref XP_003052895.1 predicted protein [Nectria haematococca mpVI...	72	1e-10
gb ADC33951.1 TfdA-like protein [uncultured bacterium]	72	1e-10
dbj BAG68904.1 hypothetical protein [Schizosaccharomyces pombe]	72	1e-10
ref YP_298943.1 taurine dioxygenase [Ralstonia eutropha JMP134]...	72	1e-10
gb ADC33949.1 TfdA-like protein [uncultured bacterium]	72	1e-10
gb ACG80548.1 TfdA [uncultured bacterium]	72	1e-10
gb ADI21798.1 probable taurine catabolism dioxygenase [uncultur...	71	1e-10
ref YP_004019220.1 taurine catabolism dioxygenase TauD/TfdA [Fr...	71	1e-10
ref YP_552626.1 taurine dioxygenase [Burkholderia xenovorans LB...	71	1e-10
ref XP_001903417.1 hypothetical protein [Podospira anserina S m...	71	1e-10
emb CBJ18784.1 alpha-ketoglutarate dioxygenase-like protein [un...	71	1e-10
ref XP_001387108.1 Fe(II)-dependent sulfonate/alpha-ketoglutara...	71	1e-10
gb ADC33987.1 TfdA-like protein [uncultured bacterium]	71	1e-10
gb EFQ31073.1 TfdA family Taurine catabolism dioxygenase TauD [...]	71	1e-10
gb ADC34042.1 TfdA-like protein [uncultured bacterium]	71	2e-10
ref XP_003004622.1 alpha-ketoglutarate-dependent sulfonate diox...	71	2e-10
ref YP_587951.1 taurine dioxygenase 2-oxoglutarate-dependent [C...	71	2e-10
ref XP_502948.1 YALI0D17622p [Yarrowia lipolytica] >gi 49648816...	71	2e-10
ref YP_003279809.1 Taurine catabolism dioxygenase TauD/TfdA [Co...	71	2e-10
gb ABR27308.1 TfdA [uncultured bacterium] >gi 149394910 gb ABR2...	71	2e-10
emb CBJ18839.1 alpha-ketoglutarate dioxygenase-like protein [un...	71	2e-10
gb AAS64592.1 alpha-KG-dependent dioxygenase [uncultured soil b...	71	2e-10
gb ADC33954.1 TfdA-like protein [uncultured bacterium]	71	2e-10
gb ACG80567.1 TfdA [uncultured bacterium]	71	2e-10
gb ADC33955.1 TfdA-like protein [uncultured bacterium]	71	2e-10
ref XP_001263646.1 alpha-ketoglutarate-dependent taurine dioxyg...	71	2e-10
ref XP_001816593.2 alpha-ketoglutarate-dependent taurine dioxyg...	71	2e-10
ref XP_001397508.2 alpha-ketoglutarate-dependent taurine dioxyg...	71	2e-10
ref XP_716238.1 potential taurine catabolic dioxygenase [Candid...	71	2e-10

ref XP_716155.1 potential taurine catabolic dioxygenase [Candid...	71	2e-10
emb CAY81185.1 Jlp1p [Saccharomyces cerevisiae EC1118]	70	2e-10
ref XP_775060.1 hypothetical protein CNBE5360 [Cryptococcus neo...	70	3e-10
ref YP_002007493.1 alpha-ketoglutarate-dependent taurine dioxyg...	70	3e-10
gb ADC33948.1 TfdA-like protein [uncultured bacterium]	70	3e-10
emb CBJ18844.1 alpha-ketoglutarate dioxygenase-like protein [un...	70	3e-10
gb ADC34021.1 TfdA-like protein [uncultured bacterium]	70	3e-10
emb CBJ18740.1 alpha-ketoglutarate dioxygenase-like protein [un...	70	3e-10
gb ABR27316.1 TfdA [uncultured bacterium] >gi 149394926 gb ABR2...	70	3e-10
ref ZP_07280249.1 taurine catabolism dioxygenase [Streptomyces ...	70	3e-10
ref ZP_01461615.1 putative dioxygenase [Stigmatella aurantiaca ...	70	3e-10
gb ABR27323.1 TfdA [uncultured bacterium] >gi 149394940 gb ABR2...	70	4e-10
emb CBJ18751.1 alpha-ketoglutarate dioxygenase-like protein [un...	70	4e-10
gb ADC34029.1 TfdA-like protein [uncultured bacterium]	70	4e-10
gb ADC33947.1 TfdA-like protein [uncultured bacterium]	70	4e-10
ref XP_003000766.1 alpha-ketoglutarate-dependent sulfonate diox...	70	4e-10
ref XP_003192522.1 taurine dioxygenase [Cryptococcus gattii WM2...	70	4e-10
ref XP_002422326.1 alpha-ketoglutarate-dependent sulfonate diox...	70	4e-10
ref XP_571061.1 hypothetical protein [Cryptococcus neoformans v...	70	4e-10
ref XP_002372616.1 alpha-ketoglutarate-dependent taurine dioxyg...	70	4e-10
emb CBJ18803.1 alpha-ketoglutarate dioxygenase-like protein [un...	70	4e-10
ref YP_004243121.1 taurine catabolism dioxygenase [Arthrobacter...	70	4e-10
gb ADC34046.1 TfdA-like protein [uncultured bacterium]	70	4e-10
gb EFQ34669.1 TfdA family Taurine catabolism dioxygenase TauD [...	70	4e-10
emb CBJ18756.1 alpha-ketoglutarate dioxygenase-like protein [un...	70	4e-10
emb CBJ18795.1 alpha-ketoglutarate dioxygenase-like protein [un...	70	5e-10
ref XP_002614428.1 hypothetical protein CLUG_05914 [Clavispora ...	70	5e-10
ref XP_001215509.1 conserved hypothetical protein [Aspergillus ...	70	5e-10
gb ADC33974.1 TfdA-like protein [uncultured bacterium]	70	5e-10
ref XP_505767.1 YALIOF22825p [Yarrowia lipolytica] >gi 49651637...	69	5e-10
ref XP_002502918.1 predicted protein [Micromonas sp. RCC299] >g...	69	5e-10
gb EDP53557.1 alpha-ketoglutarate-dependent taurine dioxygenase...	69	5e-10
gb ADC33959.1 TfdA-like protein [uncultured bacterium]	69	6e-10
emb CAY27490.1 alpha-KG-dehydrogenase [uncultured bacterium]	69	6e-10
gb ADC34032.1 TfdA-like protein [uncultured bacterium]	69	6e-10
ref XP_002487959.1 alpha-ketoglutarate-dependent taurine dioxyg...	69	6e-10
ref ZP_04967409.1 dioxygenase TauD/TfdA family [Burkholderia ps...	69	6e-10
emb CBJ18907.1 alpha-ketoglutarate dioxygenase-like protein [un...	69	6e-10
gb EFY95010.1 alpha-ketoglutarate-dependent taurine dioxygenase...	69	6e-10
emb CAY27357.1 alpha-KG-dehydrogenase [uncultured bacterium]	69	6e-10
emb CBJ18759.1 alpha-ketoglutarate dioxygenase-like protein [un...	69	7e-10
ref XP_001820787.2 alpha-ketoglutarate-dependent taurine dioxyg...	69	7e-10
emb CAY27420.1 alpha-KG-dehydrogenase [uncultured bacterium]	69	7e-10
emb CBJ18754.1 alpha-ketoglutarate dioxygenase-like protein [un...	69	7e-10
ref XP_002836505.1 hypothetical protein [Tuber melanosporum Mel...	69	7e-10
ref YP_003951319.1 Taurine catabolism dioxygenase TauD/TfdA [St...	69	8e-10
ref ZP_08227343.1 putative taurine catabolism dioxygenase [Stre...	69	8e-10
emb CAY27452.1 alpha-KG-dehydrogenase [uncultured bacterium]	69	8e-10
ref XP_002376513.1 alpha-ketoglutarate-dependent sulfonate diox...	69	8e-10
ref YP_001826806.1 putative taurine catabolism dioxygenase [Str...	69	8e-10
emb CAY27378.1 alpha-KG-dehydrogenase [uncultured bacterium]	69	8e-10
emb CBJ18720.1 alpha-ketoglutarate dioxygenase-like protein [un...	69	9e-10
emb CBJ18782.1 alpha-ketoglutarate dioxygenase-like protein [un...	69	9e-10
gb AAR38315.1 alpha-ketoglutarate-dependent taurine dioxygenase...	69	9e-10
gb ADC33982.1 TfdA-like protein [uncultured bacterium]	69	9e-10
gb AAS64586.1 alpha-KG-dependent dioxygenase [uncultured soil b...	69	9e-10
emb CBJ18765.1 alpha-ketoglutarate dioxygenase-like protein [un...	69	9e-10
ref XP_001794409.1 hypothetical protein SNOG_03864 [Phaeosphaer...	69	9e-10
ref XP_001258733.1 alpha-ketoglutarate-dependent taurine dioxyg...	69	9e-10
emb CBJ19170.1 alpha-ketoglutarate dioxygenase-like protein [un...	69	1e-09
gb ADC34014.1 TfdA-like protein [uncultured bacterium]	69	1e-09
ref XP_001387045.1 predicted protein [Scheffersomyces stipitis ...	69	1e-09
ref XP_569951.1 taurine dioxygenase [Cryptococcus neoformans va...	69	1e-09

gb EFW99341.1	alpha-ketoglutarate-dependent taurine dioxygenase...	69	1e-09
ref XP_001801455.1	hypothetical protein SNOG_11212 [Phaeosphaer...	69	1e-09
emb CBJ18969.1	alpha-ketoglutarate dioxygenase-like protein [un...	68	1e-09
ref XP_754818.2	alpha-ketoglutarate-dependent taurine dioxygena...	68	1e-09
gb AAS64598.1	alpha-KG-dependent dioxygenase [uncultured soil b...	68	1e-09
ref XP_001031479.1	hypothetical protein TTHERM_00823770 [Tetrah...	68	1e-09
emb CBJ18774.1	alpha-ketoglutarate dioxygenase-like protein [un...	68	1e-09
ref XP_569491.1	sulfonate dioxygenase [Cryptococcus neoformans ...	68	1e-09
emb CBJ18760.1	alpha-ketoglutarate dioxygenase-like protein [un...	68	1e-09
gb ADC33966.1	TfdA-like protein [uncultured bacterium]	68	1e-09
ref XP_003042297.1	predicted protein [Nectria haematococca mpVI...	68	1e-09
gb AAS64593.1	alpha-KG-dependent dioxygenase [uncultured soil b...	68	1e-09
ref YP_002799362.1	TauD/TfdA family taurine catabolism dioxygen...	68	1e-09
gb ADC34026.1	TfdA-like protein [uncultured bacterium]	68	1e-09
ref XP_002152850.1	alpha-ketoglutarate-dependent taurine dioxyg...	68	1e-09
emb CBJ18836.1	alpha-ketoglutarate dioxygenase-like protein [un...	68	1e-09
emb CBJ18778.1	alpha-ketoglutarate dioxygenase-like protein [un...	68	1e-09
ref XP_748422.1	alpha-ketoglutarate-dependent taurine dioxygena...	68	2e-09
emb CBJ18775.1	alpha-ketoglutarate dioxygenase-like protein [un...	68	2e-09
ref XP_659804.1	hypothetical protein AN2200.2 [Aspergillus nidu...	68	2e-09
gb ACG80578.1	TfdA [uncultured bacterium]	68	2e-09
ref XP_001273439.1	alpha-ketoglutarate-dependent taurine dioxyg...	68	2e-09
emb CBJ19198.1	alpha-ketoglutarate dioxygenase-like protein [un...	68	2e-09
ref XP_001483210.1	hypothetical protein PGUG_05165 [Meyerozyma ...	68	2e-09
emb CBJ18750.1	alpha-ketoglutarate dioxygenase-like protein [un...	68	2e-09
ref ZP_01692308.1	putative dioxygenase [Microscilla marina ATCC...	68	2e-09
ref XP_001261550.1	alpha-ketoglutarate-dependent taurine dioxyg...	68	2e-09
ref ZP_02414615.1	putative alpha-ketoglutarate-dependent taurin...	67	2e-09
ref ZP_03545787.1	Taurine dioxygenase [Comamonas testosteroni K...	67	2e-09
ref ZP_02484885.1	putative alpha-ketoglutarate-dependent taurin...	67	2e-09
emb CBJ18745.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	2e-09
gb ADI34074.1	2,4-D/alpha-ketoglutarate dioxygenase [Burkholder...	67	2e-09
ref XP_001389970.1	alpha-ketoglutarate-dependent taurine dioxyg...	67	2e-09
gb ADI34073.1	2,4-D/alpha-ketoglutarate dioxygenase [Burkholder...	67	2e-09
emb CAY25791.1	alpha-KG-dehydrogenase [uncultured bacterium]	67	2e-09
ref YP_713492.1	putative taurine dioxygenase [Frankia alni ACN1...	67	2e-09
emb CBJ18744.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	3e-09
ref XP_001816815.2	alpha-ketoglutarate-dependent sulfonate diox...	67	3e-09
ref YP_728585.1	taurine catabolism dioxygenase [Ralstonia eutro...	67	3e-09
emb CAY27450.1	alpha-KG-dehydrogenase [uncultured bacterium]	67	3e-09
ref ZP_08209666.1	taurine dioxygenase [Novosphingobium nitrogen...	67	3e-09
gb EFY87660.1	alpha-ketoglutarate-dependent taurine dioxygenase...	67	3e-09
gb ADC34009.1	TfdA-like protein [uncultured bacterium]	67	3e-09
emb CBJ18952.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	3e-09
ref XP_001483830.1	hypothetical protein PGUG_04559 [Meyerozyma ...	67	3e-09
emb CBJ18724.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	3e-09
gb EDK40461.2	hypothetical protein PGUG_04559 [Meyerozyma guill...	67	3e-09
ref YP_001701411.1	putative dioxygenase [Mycobacterium abscessu...	67	3e-09
emb CBJ18733.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	3e-09
ref YP_841050.1	taurine catabolism dioxygenase [Ralstonia eutro...	67	3e-09
ref XP_384843.1	hypothetical protein FG04667.1 [Gibberella zeae...	67	3e-09
emb CBJ18723.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	3e-09
emb CBJ18732.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	3e-09
gb EFX01178.1	alpha-ketoglutarate-dependent sulfonate dioxygena...	67	3e-09
emb CBJ19174.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	3e-09
ref XP_388516.1	hypothetical protein FG08340.1 [Gibberella zeae...	67	3e-09
emb CBJ18743.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	4e-09
emb CBJ18849.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	4e-09
emb CBJ19206.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	4e-09
ref YP_003060914.1	Taurine dioxygenase [Hirschia baltica ATCC 4...	67	4e-09
gb AAS64595.1	alpha-KG-dependent dioxygenase [uncultured soil b...	67	4e-09
emb CBJ19175.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	4e-09
emb CBJ18828.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	4e-09

emb CBJ18763.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	4e-09
emb CBJ19203.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	4e-09
emb CBJ18796.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	4e-09
ref XP_003006979.1	alpha-ketoglutarate-dependent sulfonate diox...	67	4e-09
emb CBJ19055.1	alpha-ketoglutarate dioxygenase-like protein [un...	67	4e-09
ref XP_002153466.1	alpha-ketoglutarate-dependent taurine dioxyg...	67	4e-09
gb ADC33969.1	TfdA-like protein [uncultured bacterium]	67	4e-09
gb EDP48989.1	alpha-ketoglutarate-dependent taurine dioxygenase...	67	4e-09
emb CBJ18779.1	alpha-ketoglutarate dioxygenase-like protein [un...	66	4e-09
emb CBJ18729.1	alpha-ketoglutarate dioxygenase-like protein [un...	66	4e-09
emb CBJ18870.1	alpha-ketoglutarate dioxygenase-like protein [un...	66	5e-09
gb ADC33976.1	TfdA-like protein [uncultured bacterium]	66	5e-09
emb CBJ18739.1	alpha-ketoglutarate dioxygenase-like protein [un...	66	5e-09
ref XP_459245.1	DEHA2D17446p [Debaryomyces hansenii CBS767] >gi...	66	5e-09
gb EFW97202.1	taurine catabolism dioxygenase [Pichia angusta DL-1]	66	5e-09
ref YP_003344598.1	taurine dioxygenase [Streptosporangium roseu...	66	5e-09
emb CBJ18776.1	alpha-ketoglutarate dioxygenase-like protein [un...	66	5e-09
gb EFQ86963.1	hypothetical protein PTT_17760 [Pyrenophora teres...	66	6e-09
emb CBJ18738.1	alpha-ketoglutarate dioxygenase-like protein [un...	66	6e-09
emb CBJ18721.1	alpha-ketoglutarate dioxygenase-like protein [un...	66	6e-09
ref XP_002486586.1	alpha-ketoglutarate-dependent taurine dioxyg...	66	6e-09
emb CBJ18837.1	alpha-ketoglutarate dioxygenase-like protein [un...	66	6e-09
emb CBJ19213.1	alpha-ketoglutarate dioxygenase-like protein [un...	66	6e-09
emb CBJ18853.1	alpha-ketoglutarate dioxygenase-like protein [un...	66	6e-09
ref XP_748907.1	alpha-ketoglutarate-dependent taurine dioxygena...	66	6e-09
ref XP_001804284.1	hypothetical protein SNOG_14085 [Phaeosphaer...	66	6e-09
emb CBJ18741.1	alpha-ketoglutarate dioxygenase-like protein [un...	66	7e-09
emb CBJ18749.1	alpha-ketoglutarate dioxygenase-like protein [un...	66	7e-09
gb ACR50790.1	putative oxidoreductase [Streptomyces longisporof...	66	7e-09
ref XP_003052483.1	hypothetical protein NECHADRAFT_77499 [Nectr...	66	7e-09
emb CBJ18777.1	alpha-ketoglutarate dioxygenase-like protein [un...	66	7e-09
emb CBJ18914.1	alpha-ketoglutarate dioxygenase-like protein [un...	66	7e-09
ref XP_001031478.1	Taurine catabolism dioxygenase TauD, TfdA fa...	65	8e-09
dbj BAE58785.1	unnamed protein product [Aspergillus oryzae]	65	8e-09
emb CBJ18975.1	alpha-ketoglutarate dioxygenase-like protein [un...	65	8e-09
gb EDP48444.1	alpha-ketoglutarate-dependent taurine dioxygenase...	65	8e-09
gb ADC33977.1	TfdA-like protein [uncultured bacterium] >gi 2850...	65	8e-09
gb ABD39118.1	alpha-ketoglutarate dioxygenase [uncultured bacte...	65	8e-09
gb AAS64585.1	alpha-KG-dependent dioxygenase [uncultured soil b...	65	8e-09
emb CBJ19168.1	alpha-ketoglutarate dioxygenase-like protein [un...	65	8e-09
emb CBJ19044.1	alpha-ketoglutarate dioxygenase-like protein [un...	65	8e-09
ref XP_001227262.1	hypothetical protein CHGG_09335 [Chaetomium ...	65	9e-09
ref XP_457378.2	DEHA2B09768p [Debaryomyces hansenii CBS767] >gi...	65	9e-09
emb CBJ18974.1	alpha-ketoglutarate dioxygenase-like protein [un...	65	9e-09
emb CBJ18813.1	alpha-ketoglutarate dioxygenase-like protein [un...	65	9e-09
emb CBJ18737.1	alpha-ketoglutarate dioxygenase-like protein [un...	65	1e-08
emb CBJ18753.1	alpha-ketoglutarate dioxygenase-like protein [un...	65	1e-08
ref XP_001482070.1	hypothetical protein PGUG_05833 [Meyerozyma ...	65	1e-08
gb ADC33950.1	TfdA-like protein [uncultured bacterium]	65	1e-08
ref XP_001273815.1	alpha-ketoglutarate-dependent taurine dioxyg...	65	1e-08
emb CBJ18829.1	alpha-ketoglutarate dioxygenase-like protein [un...	65	1e-08
emb CBJ18819.1	alpha-ketoglutarate dioxygenase-like protein [un...	65	1e-08
gb ACG80583.1	TfdA [uncultured bacterium]	65	1e-08
ref XP_002548797.1	alpha-ketoglutarate-dependent sulfonate diox...	65	1e-08
emb CBJ18973.1	alpha-ketoglutarate dioxygenase-like protein [un...	65	1e-08
ref XP_001939295.1	alpha-ketoglutarate-dependent taurine dioxyg...	65	1e-08
dbj BAB92967.1	alpha KG dependent 2,4-D dioxygenase [alpha prot...	65	1e-08
ref XP_001193736.1	PREDICTED: hypothetical protein [Strongyloce...	65	1e-08
ref XP_002497214.1	ZYRO0F00286p [Zygosaccharomyces rouxii] >gi ...	65	1e-08
gb EFQ87965.1	hypothetical protein PTT_16348 [Pyrenophora teres...	65	1e-08
ref XP_002562688.1	Pc20g01290 [Penicillium chrysogenum Wisconsi...	65	1e-08
emb CBJ18735.1	alpha-ketoglutarate dioxygenase-like protein [un...	65	1e-08
gb EFW97392.1	taurine catabolism dioxygenase [Pichia angusta DL-1]	65	1e-08

emb CBJ19204.1	alpha-ketoglutarate dioxygenase-like protein [un...	65	1e-08
ref XP_001391238.1	alpha-ketoglutarate-dependent taurine dioxyg...	65	1e-08
emb CAY25793.1	alpha-KG-dehydrogenase [uncultured bacterium]	65	1e-08
ref YP_003743531.1	Taurine dioxygenase, N-terminal fragment [Er...	65	1e-08
ref XP_003040888.1	hypothetical protein NECHADRAFT_97607 [Nectr...	65	2e-08
emb CBJ19210.1	alpha-ketoglutarate dioxygenase-like protein [un...	65	2e-08
emb CBJ18821.1	alpha-ketoglutarate dioxygenase-like protein [un...	64	2e-08
emb CBJ18746.1	alpha-ketoglutarate dioxygenase-like protein [un...	64	2e-08
emb CBJ18722.1	alpha-ketoglutarate dioxygenase-like protein [un...	64	2e-08
ref XP_746985.1	alpha-ketoglutarate-dependent taurine dioxygena...	64	2e-08
ref XP_001818415.2	alpha-ketoglutarate-dependent taurine dioxyg...	64	2e-08
emb CAY67032.1	Alpha-ketoglutarate-dependent sulfonate dioxygen...	64	2e-08
emb CBJ18770.1	alpha-ketoglutarate dioxygenase-like protein [un...	64	2e-08
ref XP_003043934.1	hypothetical protein NECHADRAFT_76975 [Nectr...	64	2e-08
gb ADC33971.1	TfdA-like protein [uncultured bacterium]	64	2e-08
ref XP_002617710.1	hypothetical protein CLUG_03154 [Clavispora ...	64	2e-08
ref XP_001906307.1	hypothetical protein [Podospira anserina S m...	64	2e-08
ref XP_002567705.1	Pc21g06600 [Penicillium chrysogenum Wisconsi...	64	2e-08
dbj BAE54591.1	unnamed protein product [Aspergillus oryzae]	64	3e-08
emb CBJ19018.1	alpha-ketoglutarate dioxygenase-like protein [un...	64	3e-08
ref XP_002383506.1	alpha-ketoglutarate-dependent taurine dioxyg...	64	3e-08
ref YP_001263745.1	taurine dioxygenase [Sphingomonas wittichii ...	64	3e-08
ref XP_002150987.1	TfdA family taurine dioxygenase, putative [P...	64	3e-08
emb CBJ18752.1	alpha-ketoglutarate dioxygenase-like protein [un...	64	3e-08
ref XP_001593138.1	hypothetical protein SS1G_06060 [Sclerotinia...	64	3e-08
emb CBJ19021.1	alpha-ketoglutarate dioxygenase-like protein [un...	64	3e-08
ref XP_001593310.1	hypothetical protein SS1G_06232 [Sclerotinia...	64	3e-08
gb ABD39120.1	alpha-ketoglutarate dioxygenase [uncultured bacte...	64	3e-08
emb CBJ18950.1	alpha-ketoglutarate dioxygenase-like protein [un...	64	3e-08
gb ADC33981.1	TfdA-like protein [uncultured bacterium]	64	3e-08
emb CBI54184.1	unnamed protein product [Sordaria macrospora]	64	3e-08
emb CBJ18767.1	alpha-ketoglutarate dioxygenase-like protein [un...	64	4e-08
emb CBJ19209.1	alpha-ketoglutarate dioxygenase-like protein [un...	64	4e-08
emb CBJ18768.1	alpha-ketoglutarate dioxygenase-like protein [un...	64	4e-08
emb CBJ18728.1	alpha-ketoglutarate dioxygenase-like protein [un...	64	4e-08
ref XP_001803696.1	hypothetical protein SNOG_13485 [Phaeosphaer...	63	4e-08
ref YP_003276123.1	Taurine catabolism dioxygenase TauD/TfdA [Co...	63	4e-08
emb CBJ18725.1	alpha-ketoglutarate dioxygenase-like protein [un...	63	4e-08
emb CBJ18956.1	alpha-ketoglutarate dioxygenase-like protein [un...	63	4e-08
ref XP_001828620.2	alpha-ketoglutarate-dependent sulfonate diox...	63	4e-08
gb EGB09898.1	hypothetical protein AURANDRAFT_62958 [Aureococcu...	63	4e-08
emb CBJ18808.1	alpha-ketoglutarate dioxygenase-like protein [un...	63	4e-08
emb CBJ18987.1	alpha-ketoglutarate dioxygenase-like protein [un...	63	4e-08
emb CBJ18742.1	alpha-ketoglutarate dioxygenase-like protein [un...	63	5e-08
emb CBJ18726.1	alpha-ketoglutarate dioxygenase-like protein [un...	63	5e-08
emb CBJ18868.1	alpha-ketoglutarate dioxygenase-like protein [un...	63	5e-08
ref XP_001525561.1	alpha-ketoglutarate-dependent sulfonate diox...	63	5e-08
ref ZP_07044532.1	Taurine catabolism dioxygenase TauD/TfdA [Com...	63	5e-08
emb CBJ18971.1	alpha-ketoglutarate dioxygenase-like protein [un...	63	5e-08
emb CBJ18789.1	alpha-ketoglutarate dioxygenase-like protein [un...	63	5e-08
emb CAY27234.1	alpha-KG-dehydrogenase [uncultured bacterium]	63	5e-08
ref XP_001836179.1	alpha-ketoglutarate-dependent sulfonate diox...	63	5e-08
emb CBJ18785.1	alpha-ketoglutarate dioxygenase-like protein [un...	63	6e-08
emb CBJ18727.1	alpha-ketoglutarate dioxygenase-like protein [un...	62	7e-08
ref ZP_02189793.1	putative alpha-ketoglutarate-dependent taurin...	62	7e-08
emb CBI56031.1	unnamed protein product [Sordaria macrospora]	62	7e-08
emb CBJ18736.1	alpha-ketoglutarate dioxygenase-like protein [un...	62	7e-08
ref XP_456245.1	hypothetical protein [Kluyveromyces lactis NRRL...	62	7e-08
gb ABD39112.1	alpha-ketoglutarate dioxygenase [uncultured bacte...	62	7e-08
ref ZP_06496700.1	taurine catabolism dioxygenase [Pseudomonas s...	62	8e-08
gb ABD39116.1	alpha-ketoglutarate dioxygenase [uncultured bacte...	62	8e-08
ref XP_001830736.2	alpha-ketoglutarate-dependent taurine dioxyg...	62	8e-08
emb CBJ19178.1	alpha-ketoglutarate dioxygenase-like protein [un...	62	8e-08

ref YP_237385.1	taurine catabolism dioxygenase [Pseudomonas syr...	62	9e-08
ref XP_001409620.1	hypothetical protein MGG_12505 [Magnaporthe ...	62	9e-08
ref XP_661715.1	hypothetical protein AN4111.2 [Aspergillus nidu...	62	9e-08
gb ABD39117.2	alpha-ketoglutarate dioxygenase [uncultured bacte...	62	9e-08
emb CBJ18855.1	alpha-ketoglutarate dioxygenase-like protein [un...	62	9e-08
emb CBJ18897.1	alpha-ketoglutarate dioxygenase-like protein [un...	62	9e-08
ref XP_002615194.1	hypothetical protein CLUG_05209 [Clavispora ...	62	1e-07
gb ABD39115.1	alpha-ketoglutarate dioxygenase [uncultured bacte...	62	1e-07
emb CAK42812.1	unnamed protein product [Aspergillus niger]	62	1e-07
gb ABD39111.1	alpha-ketoglutarate dioxygenase [uncultured bacte...	62	1e-07
emb CBJ18747.1	alpha-ketoglutarate dioxygenase-like protein [un...	62	1e-07
ref XP_454600.1	hypothetical protein [Kluyveromyces lactis NRRL...	62	1e-07
emb CBJ18874.1	alpha-ketoglutarate dioxygenase-like protein [un...	62	1e-07
gb EFW97400.1	TfdA family taurine dioxygenase, putative [Pichia...	62	1e-07
emb CBJ18941.1	alpha-ketoglutarate dioxygenase-like protein [un...	62	1e-07
ref XP_001584962.1	hypothetical protein SS1G_14059 [Sclerotinia...	62	1e-07
emb CBJ18783.1	alpha-ketoglutarate dioxygenase-like protein [un...	62	1e-07
emb CBJ18748.1	alpha-ketoglutarate dioxygenase-like protein [un...	61	1e-07
ref XP_002740180.1	PREDICTED: hypothetical protein [Saccoglossu...	61	1e-07
emb CBJ18867.1	alpha-ketoglutarate dioxygenase-like protein [un...	61	2e-07
dbj BAD15042.1	hypothetical protein [Bradyrhizobium sp. BDV5419]	61	2e-07
emb CBJ19194.1	alpha-ketoglutarate dioxygenase-like protein [un...	61	2e-07
ref NP_302343.1	putative oxidoreductase [Mycobacterium leprae T...	61	2e-07
emb CBJ18811.1	alpha-ketoglutarate dioxygenase-like protein [un...	61	2e-07
ref ZP_06477056.1	Taurine catabolism dioxygenase TauD/TfdA [Fra...	61	2e-07
ref XP_001394064.1	alpha-ketoglutarate-dependent taurine dioxyg...	61	2e-07
emb CBJ19211.1	alpha-ketoglutarate dioxygenase-like protein [un...	61	2e-07
emb CBJ18766.1	alpha-ketoglutarate dioxygenase-like protein [un...	61	2e-07
emb CBJ19184.1	alpha-ketoglutarate dioxygenase-like protein [un...	61	2e-07
ref ZP_04588005.1	TauD/TfdA family dioxygenase [Pseudomonas syr...	61	2e-07
ref ZP_07308634.1	alpha-ketoglutarate-dependent taurine dioxyge...	61	2e-07
emb CBJ19014.1	alpha-ketoglutarate dioxygenase-like protein [un...	61	2e-07
ref XP_002147238.1	alpha-ketoglutarate-dependent sulfonate diox...	61	2e-07
ref YP_003766480.1	taurine dioxygenase [Amycolatopsis mediterranea...	61	2e-07
emb CBJ19208.1	alpha-ketoglutarate dioxygenase-like protein [un...	61	2e-07
gb ABN51234.1	2,4-dichlorophenoxyacetate alpha-ketoglutarate di...	60	2e-07
ref XP_459311.1	DEHA2D18986p [Debaryomyces hansenii CBS767] >gi...	60	2e-07
ref XP_001268478.1	TfdA family taurine dioxygenase, putative [A...	60	3e-07
ref NP_983695.2	ACR293Cp [Ashbya gossypii ATCC 10895] >gi 29978...	60	3e-07
ref XP_001830759.2	alpha-ketoglutarate-dependent taurine dioxyg...	60	3e-07
ref XP_001526244.1	hypothetical protein LELG_02802 [Lodderomyce...	60	3e-07
ref XP_360574.1	hypothetical protein MGG_03117 [Magnaporthe ory...	60	3e-07
ref XP_001821088.1	alpha-ketoglutarate-dependent sulfonate diox...	60	3e-07
ref YP_003899861.1	Taurine catabolism dioxygenase TauD/TfdA [Cy...	60	3e-07
ref XP_001221616.1	conserved hypothetical protein [Chaetomium g...	60	3e-07
emb CAY25737.1	alpha-KG-dehydrogenase [uncultured bacterium]	60	3e-07
gb ADI34063.1	2,4-D/alpha-ketoglutarate dioxygenase [Burkholder...	60	3e-07
emb CAY25758.1	alpha-KG-dehydrogenase [uncultured bacterium]	60	3e-07
ref NP_001191877.1	hypothetical protein LOC100163446 [Acyrtosia...	60	3e-07
ref ZP_06861621.1	Taurine dioxygenase [Citromicrobium bathyomar...	60	4e-07
emb CBJ19164.1	alpha-ketoglutarate dioxygenase-like protein [un...	60	4e-07
ref XP_002376836.1	alpha-ketoglutarate-dependent sulfonate diox...	60	4e-07
dbj BAD15034.1	hypothetical protein [Bradyrhizobium elkanii USD...	60	4e-07
ref ZP_07964195.1	TfdA family Taurine catabolism dioxygenase Ta...	60	4e-07
ref XP_003009781.1	alpha-ketoglutarate-dependent taurine dioxyg...	60	4e-07
ref XP_001387469.1	taurine catabolism dioxygenase [Scheffersomy...	60	4e-07
emb CBJ18771.1	alpha-ketoglutarate dioxygenase-like protein [un...	60	4e-07
emb CBJ19181.1	alpha-ketoglutarate dioxygenase-like protein [un...	60	4e-07
emb CBJ19183.1	alpha-ketoglutarate dioxygenase-like protein [un...	60	4e-07
ref NP_214611.1	oxidoreductase [Mycobacterium tuberculosis H37R...	60	5e-07
emb CBJ18780.1	alpha-ketoglutarate dioxygenase-like protein [un...	60	5e-07
ref YP_001417667.1	taurine dioxygenase [Xanthobacter autotrophica...	60	5e-07
ref XP_001558157.1	hypothetical protein BC1G_03189 [Botryotinia...	60	5e-07

ref XP_002376025.1	alpha-ketoglutarate-dependent sulfonate diox...	60	5e-07
ref XP_003030923.1	hypothetical protein SCHCODRAFT_56708 [Schiz...	59	5e-07
emb CBJ18858.1	alpha-ketoglutarate dioxygenase-like protein [un...	59	5e-07
ref XP_002836921.1	hypothetical protein [Tuber melanosporum Mel...	59	5e-07
ref XP_664343.1	hypothetical protein AN6739.2 [Aspergillus nidu...	59	6e-07
emb CBJ18772.1	alpha-ketoglutarate dioxygenase-like protein [un...	59	6e-07
ref XP_002376500.1	alpha-ketoglutarate-dependent taurine dioxyg...	59	6e-07
ref ZP_07421035.1	oxidoreductase [Mycobacterium tuberculosis SU...	59	6e-07
ref YP_003039151.1	taurine dioxygenase, 2-oxoglutarate-dependen...	59	6e-07
emb CBJ19201.1	alpha-ketoglutarate dioxygenase-like protein [un...	59	6e-07
ref XP_001820775.1	alpha-ketoglutarate-dependent taurine dioxyg...	59	6e-07
ref XP_962940.1	hypothetical protein NCU07319 [Neurospora crass...	59	6e-07
emb CBJ18919.1	alpha-ketoglutarate dioxygenase-like protein [un...	59	6e-07
emb CAY27326.1	alpha-KG-dehydrogenase [uncultured bacterium]	59	6e-07
ref XP_001805839.1	hypothetical protein SNOG_15699 [Phaeosphaer...	59	6e-07
ref XP_001727715.2	tfdA family taurine dioxygenase [Aspergillus...	59	7e-07
emb CAY25785.1	alpha-KG-dehydrogenase [uncultured bacterium]	59	7e-07
emb CBJ19188.1	alpha-ketoglutarate dioxygenase-like protein [un...	59	7e-07
ref XP_962844.2	hypothetical protein NCU07610 [Neurospora crass...	59	7e-07
ref XP_500006.1	YALI0A12177p [Yarrowia lipolytica] >gi 49645871...	59	8e-07
gb EFQ34526.1	TfdA family Taurine catabolism dioxygenase TauD [...]	59	8e-07
ref XP_001383149.1	taurine catabolism dioxygenase [Scheffersomy...	59	8e-07
ref XP_001905437.1	hypothetical protein [Podospira anserina S m...	59	8e-07
emb CAY25764.1	alpha-KG-dehydrogenase [uncultured bacterium]	59	8e-07
ref XP_001014128.1	hypothetical protein TTHERM_00405520 [Tetrah...	59	8e-07
gb ADI34064.1	2,4-D/alpha-ketoglutarate dioxygenase [Burkholder...	59	9e-07
ref XP_001941451.1	taurine dioxygenase [Pyrenophora tritici-rep...	59	9e-07
ref XP_001258197.1	alpha-ketoglutarate-dependent taurine dioxyg...	59	9e-07
tpe CBF78371.1	TPA: TfdA family taurine dioxygenase, putative (...]	59	1e-06
emb CAY25795.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	59	1e-06
ref XP_002490893.1	Fe(II)-dependent sulfonate/alpha-ketoglutara...	59	1e-06
emb CBJ20076.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	59	1e-06
emb CBJ18797.1	alpha-ketoglutarate dioxygenase-like protein [un...	59	1e-06
emb CAY27301.1	alpha-KG-dehydrogenase [uncultured bacterium]	59	1e-06
dbj BAF81037.1	2,4-D dioxygenase [Bradyrhizobium sp. M75-VN10-2W]	59	1e-06
ref ZP_04982597.1	hypothetical oxidoreductase [Mycobacterium tu...	59	1e-06
ref XP_681863.1	hypothetical protein AN8594.2 [Aspergillus nidu...	59	1e-06
emb CAY25719.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	58	1e-06
ref XP_002486237.1	alpha-ketoglutarate-dependent sulfonate diox...	58	1e-06
gb AAO39411.1	TfdA alpha-like protein [uncultured bacterium]	58	1e-06
gb ABR27336.1	TfdA [uncultured bacterium]	58	1e-06
gb ADC33958.1	TfdA-like protein [uncultured bacterium] >gi 2850...	58	1e-06
ref XP_001880709.1	predicted protein [Laccaria bicolor S238N-H8...	58	1e-06
emb CBJ19162.1	alpha-ketoglutarate dioxygenase-like protein [un...	58	1e-06
emb CAY25745.1	alpha-KG-dehydrogenase [uncultured bacterium]	58	1e-06
emb CAY25747.1	alpha-KG-dehydrogenase [uncultured bacterium]	58	1e-06
ref XP_001909009.1	hypothetical protein [Podospira anserina S m...	58	1e-06
emb CAY25751.1	alpha-KG-dehydrogenase [uncultured bacterium]	58	1e-06
ref YP_003467274.1	Pyoverdine biosynthesis protein [Xenorhabdus...	58	2e-06
gb AAO39410.1	TfdA alpha-like protein [uncultured bacterium]	58	2e-06
emb CBJ18761.1	alpha-ketoglutarate dioxygenase-like protein [un...	58	2e-06
emb CBJ19182.1	alpha-ketoglutarate dioxygenase-like protein [un...	58	2e-06
ref ZP_03790613.1	dioxygenase TauD/TfdA family [Burkholderia ps...	58	2e-06
gb ADC33943.1	TfdA-like protein [uncultured bacterium]	58	2e-06
ref XP_001522837.1	hypothetical protein MGCH7_ch7g935 [Magnapor...	58	2e-06
emb CAY25729.1	alpha-KG-dehydrogenase [uncultured bacterium]	58	2e-06
gb AAO39412.1	TfdA alpha-like protein [uncultured bacterium] >g...	58	2e-06
gb EFQ35578.1	TfdA family Taurine catabolism dioxygenase TauD [...]	58	2e-06
ref XP_956199.1	hypothetical protein NCU01562 [Neurospora crass...	58	2e-06
gb AAO39408.1	TfdA alpha-like protein [uncultured bacterium]	58	2e-06
ref YP_001265314.1	taurine catabolism dioxygenase TauD/TfdA [Sp...	58	2e-06
emb CAY25765.1	alpha-KG-dehydrogenase [uncultured bacterium]	58	2e-06
ref XP_001555605.1	hypothetical protein BC1G_05880 [Botryotinia...	58	2e-06

gb ADI34068.1	2,4-D/alpha-ketoglutarate dioxygenase [Burkholder...	58	2e-06
gb ADI34071.1	2,4-D/alpha-ketoglutarate dioxygenase [Burkholder...	58	2e-06
gb AAO39409.1	TfdA alpha-like protein [uncultured bacterium]	58	2e-06
gb ADC34030.1	TfdA-like protein [uncultured bacterium]	57	2e-06
gb ADC34022.1	TfdA-like protein [uncultured bacterium]	57	2e-06
ref XP_001908518.1	hypothetical protein [Podospira anserina S m...	57	2e-06
gb EFQ35233.1	TfdA family Taurine catabolism dioxygenase TauD [...	57	2e-06
ref XP_002483625.1	alpha-ketoglutarate-dependent sulfonate diox...	57	2e-06
ref XP_002339994.1	TfdA family taurine dioxygenase, putative [T...	57	2e-06
dbj BAD15040.1	hypothetical protein [Bradyrhizobium sp. BDV5111]	57	2e-06
emb CBJ18731.1	alpha-ketoglutarate dioxygenase-like protein [un...	57	2e-06
ref XP_960110.1	hypothetical protein NCU09800 [Neurospora crass...	57	2e-06
emb CAY25732.1	alpha-KG-dehydrogenase [uncultured bacterium]	57	3e-06
ref YP_001869152.1	taurine catabolism dioxygenase TauD/TfdA [No...	57	3e-06
emb CAY25797.1	alpha-KG-dehydrogenase [uncultured bacterium]	57	3e-06
emb CBJ19195.1	alpha-ketoglutarate dioxygenase-like protein [un...	57	3e-06
dbj BAD15036.1	hypothetical protein [Bradyrhizobium sp. th-b2] ...	57	3e-06
ref XP_002502407.1	predicted protein [Micromonas sp. RCC299] >g...	57	3e-06
emb CAY25723.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	57	3e-06
dbj BAD15035.1	hypothetical protein [Bradyrhizobium sp. jwc91-2]	57	3e-06
gb EGD92386.1	taurine dioxygenase [Trichophyton rubrum CBS 118892]	57	3e-06
dbj BAD15037.1	hypothetical protein [Bradyrhizobium sp. DesT1]	57	3e-06
emb CBJ18790.1	alpha-ketoglutarate dioxygenase-like protein [un...	57	3e-06
emb CBJ18862.1	alpha-ketoglutarate dioxygenase-like protein [un...	57	3e-06
ref XP_003015010.1	alpha-ketoglutarate-dependent taurine dioxyg...	57	3e-06
emb CAY25752.1	alpha-KG-dehydrogenase [uncultured bacterium]	57	3e-06
ref XP_003025681.1	alpha-ketoglutarate-dependent taurine dioxyg...	57	3e-06
ref XP_001264040.1	TfdA family taurine dioxygenase, putative [N...	57	3e-06
emb CAY25784.1	alpha-KG-dehydrogenase [uncultured bacterium]	57	3e-06
emb CAY25778.1	alpha-KG-dehydrogenase [uncultured bacterium]	57	3e-06
emb CAY25736.1	alpha-KG-dehydrogenase [uncultured bacterium]	57	3e-06
ref XP_753085.1	TfdA family taurine dioxygenase [Aspergillus fu...	57	3e-06
ref YP_857772.1	pyoverdine chromophore biosynthetic protein Pvc...	57	4e-06
ref XP_661174.1	hypothetical protein AN3570.2 [Aspergillus nidu...	57	4e-06
ref XP_003195287.1	hypothetical protein CGB_G4140W [Cryptococcu...	57	4e-06
ref XP_001217728.1	hypothetical protein ATEG_09106 [Aspergillus...	57	4e-06
emb CAY25776.1	alpha-KG-dehydrogenase [uncultured bacterium]	57	4e-06
emb CAY25720.1	alpha-KG-dehydrogenase [uncultured bacterium]	57	4e-06
gb ADC33956.1	TfdA-like protein [uncultured bacterium]	57	4e-06
emb CAY25799.1	alpha-KG-dehydrogenase [uncultured bacterium]	57	4e-06
emb CBJ18922.1	alpha-ketoglutarate dioxygenase-like protein [un...	57	4e-06
emb CBJ18981.1	alpha-ketoglutarate dioxygenase-like protein [un...	57	4e-06
emb CBJ18872.1	alpha-ketoglutarate dioxygenase-like protein [un...	57	4e-06
emb CAY25786.1	alpha-KG-dehydrogenase [uncultured bacterium]	57	4e-06
emb CBJ19197.1	alpha-ketoglutarate dioxygenase-like protein [un...	57	4e-06
emb CBJ18902.1	alpha-ketoglutarate dioxygenase-like protein [un...	57	4e-06
gb AAQ21538.1	2,4-D/alpha-ketoglutarate dioxygenase [Burkholder...	57	4e-06
emb CBJ18832.1	alpha-ketoglutarate dioxygenase-like protein [un...	57	4e-06
emb CAY25771.1	alpha-KG-dehydrogenase [uncultured bacterium]	57	4e-06
emb CAY25740.1	alpha-KG-dehydrogenase [uncultured bacterium]	56	5e-06
ref ZP_07778867.1	alpha-ketoglutarate-dependent taurine dioxyge...	56	5e-06
emb CAY25757.1	alpha-KG-dehydrogenase [uncultured bacterium]	56	5e-06
ref XP_001526245.1	hypothetical protein LELG_02803 [Lodderomyce...	56	5e-06
gb AAQ21542.1	2,4-D/alpha-ketoglutarate dioxygenase [Burkholder...	56	5e-06
ref XP_001821071.1	tfdA family taurine dioxygenase [Aspergillus...	56	5e-06
ref XP_002376815.1	TfdA family taurine dioxygenase, putative [A...	56	5e-06
emb CBJ18896.1	alpha-ketoglutarate dioxygenase-like protein [un...	56	5e-06
ref XP_002736248.1	PREDICTED: hypothetical protein [Saccoglossu...	56	5e-06
ref XP_002373641.1	alpha-ketoglutarate-dependent taurine dioxyg...	56	5e-06
emb CBJ19033.1	alpha-ketoglutarate dioxygenase-like protein [un...	56	6e-06
ref XP_500332.2	YALI0A21439p [Yarrowia lipolytica] >gi 19942491...	56	6e-06
emb CAY25796.1	alpha-KG-dehydrogenase [uncultured bacterium]	56	6e-06
ref YP_001870085.1	taurine catabolism dioxygenase TauD/TfdA [No...	56	6e-06

ref YP_001508997.1	taurine dioxygenase [Frankia sp. EANlpec] >g...	56	6e-06
emb CAY25759.1	alpha-KG-dehydrogenase [uncultured bacterium]	56	6e-06
ref XP_002384446.1	alpha-ketoglutarate-dependent sulfonate diox...	56	6e-06
ref XP_001827203.1	alpha-ketoglutarate-dependent sulfonate diox...	56	6e-06
ref ZP_05095406.1	hypothetical protein GPB2148_781 [marine gamm...	56	6e-06
ref XP_002392556.1	hypothetical protein MPER_07845 [Moniliophth...	56	6e-06
ref ZP_04996765.1	taurine catabolism dioxygenase TauD/TfdA [Str...	56	6e-06
ref YP_001565905.1	taurine dioxygenase [Delftia acidovorans SPH...	56	6e-06
emb CBJ18869.1	alpha-ketoglutarate dioxygenase-like protein [un...	56	6e-06
emb CBJ18815.1	alpha-ketoglutarate dioxygenase-like protein [un...	56	6e-06
emb CAY25753.1	alpha-KG-dehydrogenase [uncultured bacterium]	56	6e-06
ref YP_002007989.1	taurine dioxygenase, 2-oxoglutarate-dependen...	56	7e-06
ref XP_002484418.1	alpha-ketoglutarate-dependent taurine dioxyg...	56	7e-06
ref YP_003468246.1	hypothetical protein XBJ1_2349 [Xenorhabdus ...	56	7e-06
emb CBJ18835.1	alpha-ketoglutarate dioxygenase-like protein [un...	56	7e-06
ref ZP_03525650.1	putative taurine dioxygenase protein [Rhizobi...	56	7e-06
emb CAY25768.1	alpha-KG-dehydrogenase [uncultured bacterium]	56	7e-06
emb CAY25746.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	56	7e-06
emb CAY25725.1	alpha-KG-dehydrogenase [uncultured bacterium]	56	8e-06
ref XP_001267511.1	taurine dioxygenase family protein [Neosarto...	56	8e-06
ref XP_001389376.2	tfdA family taurine dioxygenase [Aspergillus...	55	8e-06
emb CBJ19084.1	alpha-ketoglutarate dioxygenase-like protein [un...	55	8e-06
ref YP_003270385.1	taurine catabolism dioxygenase TauD/TfdA [Ha...	55	8e-06
emb CAK44006.1	unnamed protein product [Aspergillus niger]	55	8e-06
ref XP_001031480.1	hypothetical protein THERM_00823780 [Tetra...	55	8e-06
emb CAY25783.1	alpha-KG-dehydrogenase [uncultured bacterium]	55	8e-06
emb CBI55832.1	unnamed protein product [Sordaria macrospora]	55	8e-06
emb CAY25781.1	alpha-KG-dehydrogenase [uncultured bacterium]	55	8e-06
emb CAY25749.1	alpha-KG-dehydrogenase [uncultured bacterium]	55	8e-06
ref XP_750960.1	alpha-ketoglutarate-dependent taurine dioxygena...	55	8e-06
gb ACB30158.1	2,4-D/alpha-ketoglutarate dioxygenase [Terrabacte...	55	9e-06
ref XP_001265562.1	taurine catabolism dioxygenase TauD, TfdA fa...	55	9e-06
ref XP_501183.1	YALI0B21472p [Yarrowia lipolytica] >gi 49647049...	55	9e-06
emb CBJ18986.1	alpha-ketoglutarate dioxygenase-like protein [un...	55	9e-06
emb CAY25726.1	alpha-KG-dehydrogenase [uncultured bacterium]	55	9e-06
emb CBJ19176.1	alpha-ketoglutarate dioxygenase-like protein [un...	55	1e-05
emb CAY25722.1	alpha-KG-dehydrogenase [uncultured bacterium]	55	1e-05
emb CAY25787.1	alpha-KG-dehydrogenase [uncultured bacterium]	55	1e-05
dbj BAE92218.1	2,4-D/alpha-ketoglutarate dioxygenase [Ralstonia...	55	1e-05
ref XP_001387032.1	predicted protein [Scheffersomyces stipitis ...	55	1e-05
ref ZP_06475349.1	dioxygenase, TauD/TfdA [Frankia symbiont of D...	55	1e-05
ref XP_002165715.1	PREDICTED: similar to Taurine catabolism dio...	55	1e-05
ref YP_003040556.1	pyoverdine biosynthesis protein PvcB-like pr...	55	1e-05
ref XP_001903801.1	hypothetical protein [Podospira anserina S m...	55	1e-05
ref ZP_07151278.1	taurine dioxygenase domain protein [Escherich...	55	1e-05
ref XP_002900145.1	alpha-ketoglutarate-dependent sulfonate diox...	55	1e-05
ref XP_571891.1	hypothetical protein [Cryptococcus neoformans v...	55	1e-05
dbj BAD15043.1	hypothetical protein [Bradyrhizobium sp. BDV5680]	55	1e-05
ref XP_002149540.1	alpha-ketoglutarate-dependent sulfonate diox...	55	1e-05
emb CAY25721.1	alpha-KG-dehydrogenase [uncultured bacterium]	55	1e-05
ref XP_002549195.1	alpha-ketoglutarate-dependent sulfonate diox...	55	1e-05
ref XP_003028210.1	hypothetical protein SCHCODRAFT_70480 [Schiz...	55	1e-05
emb CAY25754.1	alpha-KG-dehydrogenase [uncultured bacterium]	55	1e-05
ref XP_459377.1	DEHA2E01188p [Debaryomyces hansenii CBS767] >gi...	55	1e-05
ref NP_930051.1	hypothetical protein plu2817 [Photorhabdus lumi...	55	1e-05
emb CAY25738.1	alpha-KG-dehydrogenase [uncultured bacterium]	55	1e-05
ref XP_001268176.1	alpha-ketoglutarate-dependent taurine dioxyg...	55	1e-05
ref XP_003051284.1	hypothetical protein NECHADRAFT_41873 [Nectr...	55	1e-05
emb CAY25743.1	alpha-KG-dehydrogenase [uncultured bacterium]	55	2e-05
emb CAY25730.1	alpha-KG-dehydrogenase [uncultured bacterium]	55	2e-05
ref XP_746445.1	TfdA family taurine dioxygenase [Aspergillus fu...	54	2e-05
gb EFY94168.1	hypothetical protein MAA_10359 [Metarhizium aniso...	54	2e-05
emb CBJ18856.1	alpha-ketoglutarate dioxygenase-like protein [un...	54	2e-05

emb CAY25761.1	alpha-KG-dehydrogenase [uncultured bacterium]	54	2e-05
emb CAY25748.1	alpha-KG-dehydrogenase [uncultured bacterium]	54	2e-05
gb EFX06123.1	taurine catabolism dioxygenase [Grosmannia clavig...	54	2e-05
emb CAY25755.1	alpha-KG-dehydrogenase [uncultured bacterium]	54	2e-05
gb AAL65149.1	2,4-dichlorophenoxyacetate monooxygenase [Burkhol...	54	2e-05
ref XP_002896478.1	poly [ADP-ribose] polymerase, putative [Phyt...	54	2e-05
ref XP_002587293.1	hypothetical protein BRAFLDRAFT_129135 [Bran...	54	2e-05
ref ZP_06458186.1	taurine catabolism dioxygenase TauD/TfdA [Pse...	54	2e-05
emb CBJ18885.1	alpha-ketoglutarate dioxygenase-like protein [un...	54	2e-05
emb CBJ19165.1	alpha-ketoglutarate dioxygenase-like protein [un...	54	2e-05
emb CBJ18957.1	alpha-ketoglutarate dioxygenase-like protein [un...	54	2e-05
ref ZP_07276031.1	hypothetical protein SSMG_00071 [Streptomyces...	54	2e-05
emb CAY25741.1	alpha-KG-dehydrogenase [uncultured bacterium]	54	3e-05
ref ZP_06478274.1	taurine catabolism dioxygenase TauD/TfdA [Pse...	54	3e-05
gb ABD39119.1	alpha-ketoglutarate dioxygenase [uncultured bacte...	54	3e-05
gb EFY85365.1	hypothetical protein MAC_08614 [Metarhizium acrid...	54	3e-05
ref NP_968348.1	pyoverdine biosynthesis protein PvcB [Bdellovib...	54	3e-05
emb CBJ18895.1	alpha-ketoglutarate dioxygenase-like protein [un...	54	3e-05
emb CBJ18888.1	alpha-ketoglutarate dioxygenase-like protein [un...	54	3e-05
ref XP_661712.1	hypothetical protein AN4108.2 [Aspergillus nidu...	54	3e-05
ref ZP_03831920.1	pyoverdine biosynthesis protein PvcB [Pectoba...	54	3e-05
ref XP_001595570.1	hypothetical protein SS1G_03659 [Sclerotinia...	54	3e-05
dbj BAE92213.1	2,4-D/alpha-ketoglutarate dioxygenase [Ralstonia...	54	3e-05
emb CAY25735.1	alpha-KG-dehydrogenase [uncultured bacterium]	54	3e-05
emb CAY25779.1	alpha-KG-dehydrogenase [uncultured bacterium]	54	3e-05
emb CAY25789.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	54	3e-05
ref YP_908226.1	oxidoreductase [Mycobacterium ulcerans Agy99] >...	54	3e-05
ref XP_002472070.1	predicted protein [Postia placenta Mad-698-R...	54	3e-05
emb CAY25769.1	alpha-KG-dehydrogenase [uncultured bacterium]	54	3e-05
ref XP_003048696.1	hypothetical protein NECHADRAFT_46558 [Nectr...	54	3e-05
emb CAY25766.1	alpha-KG-dehydrogenase [uncultured bacterium]	54	4e-05
gb EFX01815.1	alpha-ketoglutarate-dependent sulfonate dioxygena...	54	4e-05
ref XP_001547565.1	hypothetical protein BC1G_13809 [Botryotinia...	54	4e-05
emb CAY25750.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	54	4e-05
ref XP_659802.1	hypothetical protein AN2198.2 [Aspergillus nidu...	54	4e-05
ref NP_925626.1	taurine dioxygenase [Gloeobacter violaceus PCC ...	54	4e-05
gb AAD55077.1	AF176240_1 2,4-D-alpha ketoglutarate dioxygenase [...	53	4e-05
ref YP_001140900.1	pyoverdine biosynthesis protein [Aeromonas s...	53	4e-05
emb CBJ18887.1	alpha-ketoglutarate dioxygenase-like protein [un...	53	4e-05
emb CAY25727.1	alpha-KG-dehydrogenase [uncultured bacterium]	53	4e-05
emb CBJ18788.1	alpha-ketoglutarate dioxygenase-like protein [un...	53	4e-05
ref XP_002419144.1	alpha-ketoglutarate-dependent sulfonate diox...	53	4e-05
ref XP_503099.1	YALI0D21098p [Yarrowia lipolytica] >gi 49648967...	53	4e-05
emb CBJ18962.1	alpha-ketoglutarate dioxygenase-like protein [un...	53	4e-05
gb ACG80575.1	TfdA [uncultured bacterium]	53	4e-05
ref XP_003174143.1	alpha-ketoglutarate-dependent sulfonate diox...	53	5e-05
emb CAY25718.1	alpha-KG-dehydrogenase [uncultured bacterium]	53	5e-05
gb ADI34070.1	2,4-D/alpha-ketoglutarate dioxygenase [Burkholder...	53	5e-05
ref XP_001826717.1	alpha-ketoglutarate-dependent sulfonate diox...	53	5e-05
emb CBX93828.1	hypothetical protein [Leptosphaeria maculans]	53	5e-05
ref XP_002841597.1	hypothetical protein [Tuber melanosporum Mel...	53	5e-05
ref YP_004015360.1	taurine catabolism dioxygenase TauD/TfdA [Fr...	53	5e-05
gb EGA73988.1	Jlplp [Saccharomyces cerevisiae AWRI796]	53	5e-05
ref XP_721596.1	potential taurine catabolic dioxygenase Tcd3 [C...	53	6e-05
ref ZP_03517935.1	putative taurine dioxygenase protein [Rhizobi...	53	6e-05
ref XP_002385365.1	alpha-ketoglutarate-dependent sulfonate diox...	53	6e-05
emb CAY25760.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	53	6e-05
ref XP_002419281.1	alpha-ketoglutarate-dependent sulfonate diox...	53	6e-05
ref XP_002569045.1	Pc21g20580 [Penicillium chrysogenum Wisconsi...	52	7e-05
gb EFQ27447.1	TfdA family Taurine catabolism dioxygenase TauD [...	52	7e-05
dbj BAF81030.1	2,4-D dioxygenase [Burkholderia sp. M3-VN6-5W] >...	52	7e-05
dbj BAF81045.1	2,4-D dioxygenase [Burkholderia sp. 51-VN3-2W]	52	8e-05
emb CBJ18798.1	alpha-ketoglutarate dioxygenase-like protein [un...	52	8e-05

dbj BAF81035.1	2,4-D dioxygenase [Nocardioide sp. 116-VN10-1W]	52	8e-05
dbj BAF81044.1	2,4-D dioxygenase [Burkholderia sp. M38-VN3-2W] ...	52	8e-05
dbj BAD15039.1	hypothetical protein [Bradyrhizobium sp. ApB16]	52	9e-05
ref XP_001526184.1	hypothetical protein LELG_02742 [Lodderomyce...	52	9e-05
ref XP_001201468.1	PREDICTED: hypothetical protein, partial [St...	52	9e-05
ref XP_001211559.1	conserved hypothetical protein [Aspergillus ...	52	9e-05
ref XP_002472100.1	predicted protein [Postia placenta Mad-698-R...	52	9e-05
gb EGD74167.1	taurine catabolism dioxygenase TauD [Salpingoeca ...	52	1e-04
ref XP_001391155.2	tfdA family taurine dioxygenase [Aspergillus...	52	1e-04
ref ZP_06192176.1	hypothetical protein SOD_f01220 [Serratia odo...	52	1e-04
dbj BAD15041.1	hypothetical protein [Bradyrhizobium sp. BDV5329]	52	1e-04
ref YP_003711498.1	Pyoverdine biosynthesis protein [Xenorhabdus...	52	1e-04
emb CBJ18982.1	alpha-ketoglutarate dioxygenase-like protein [un...	52	1e-04
ref XP_382474.1	hypothetical protein FG02298.1 [Gibberella zeae...	52	1e-04
emb CBJ18755.1	alpha-ketoglutarate dioxygenase-like protein [un...	52	1e-04
ref YP_003531145.1	pyoverdine biosynthesis protein PvcB [Erwini...	52	1e-04
emb CBJ19101.1	alpha-ketoglutarate dioxygenase-like protein [un...	52	1e-04
gb ABI95434.1	2,4-D/alpha-ketoglutarate dioxygenase [uncultured...	52	1e-04
ref XP_001598964.1	hypothetical protein SS1G_01054 [Sclerotinia...	52	1e-04
ref XP_001216869.1	hypothetical protein ATEG_08248 [Aspergillus...	52	1e-04
ref ZP_03827804.1	pyoverdine biosynthesis protein PvcB [Pectoba...	51	1e-04
ref ZP_02383058.1	pyoverdine biosynthesis protein PvcB [Burkhol...	51	2e-04
emb CBJ19133.1	alpha-ketoglutarate dioxygenase-like protein [un...	51	2e-04
emb CAY25731.1	alpha-KG-dehydrogenase [uncultured bacterium]	51	2e-04
gb EEQ91806.1	alpha-ketoglutarate-dependent taurine dioxygenase...	51	2e-04
emb CBJ19006.1	alpha-ketoglutarate dioxygenase-like protein [un...	51	2e-04
ref XP_001217671.1	hypothetical protein ATEG_09049 [Aspergillus...	51	2e-04
gb ABD39113.1	alpha-ketoglutarate dioxygenase [uncultured bacte...	51	2e-04
ref YP_001848583.1	oxidoreductase [Mycobacterium marinum M] >gi...	51	2e-04
emb CBJ18942.1	alpha-ketoglutarate dioxygenase-like protein [un...	51	2e-04
gb ABD39121.1	alpha-ketoglutarate dioxygenase [uncultured bacte...	51	2e-04
emb CBJ19136.1	alpha-ketoglutarate dioxygenase-like protein [un...	51	2e-04
emb CBJ18830.1	alpha-ketoglutarate dioxygenase-like protein [un...	51	2e-04
dbj BAF81036.1	2,4-D dioxygenase [Burkholderia sp. M36-VN10-2W]	50	3e-04
ref ZP_06474867.1	Taurine catabolism dioxygenase TauD/TfdA [Fra...	50	3e-04
ref YP_001476938.1	taurine catabolism dioxygenase TauD/TfdA [Se...	50	3e-04
emb CBJ18781.1	alpha-ketoglutarate dioxygenase-like protein [un...	50	3e-04
ref XP_001224283.1	hypothetical protein CHGG_05069 [Chaetomium ...	50	3e-04
emb CBJ19135.1	alpha-ketoglutarate dioxygenase-like protein [un...	50	3e-04
ref XP_003057027.1	predicted protein [Micromonas pusilla CCMP15...	50	3e-04
gb ACB21020.1	TfdA [uncultured bacterium]	50	4e-04
emb CBJ19127.1	alpha-ketoglutarate dioxygenase-like protein [un...	50	4e-04
emb CBJ19060.1	alpha-ketoglutarate dioxygenase-like protein [un...	50	4e-04
gb EGD93099.1	hypothetical protein TSEG_00655 [Trichophyton ton...	50	4e-04
emb CBJ18908.1	alpha-ketoglutarate dioxygenase-like protein [un...	50	4e-04
gb EGE04589.1	taurine dioxygenase [Trichophyton equinum CBS 127...	50	4e-04
gb EFW98179.1	alpha-ketoglutarate-dependent sulfonate dioxygena...	50	5e-04
ref XP_002476351.1	predicted protein [Postia placenta Mad-698-R...	50	5e-04
ref XP_001947612.1	PREDICTED: hypothetical protein, partial [Ac...	50	5e-04
emb CBX80659.1	pyoverdine biosynthesis protein PvcB [Erwinia am...	50	5e-04
emb CBJ18943.1	alpha-ketoglutarate dioxygenase-like protein [un...	50	5e-04
emb CAY25780.1	alpha-KG-dehydrogenase [uncultured bacterium]	50	5e-04
ref XP_001594485.1	hypothetical protein SS1G_04292 [Sclerotinia...	50	5e-04
emb CBJ19142.1	alpha-ketoglutarate dioxygenase-like protein [un...	50	5e-04
emb CBJ18944.1	alpha-ketoglutarate dioxygenase-like protein [un...	50	5e-04
ref YP_003262840.1	Taurine catabolism dioxygenase TauD/TfdA [Ha...	49	6e-04
emb CBJ18984.1	alpha-ketoglutarate dioxygenase-like protein [un...	49	6e-04
emb CBJ18927.1	alpha-ketoglutarate dioxygenase-like protein [un...	49	6e-04
ref XP_001548982.1	hypothetical protein BC1G_12213 [Botryotinia...	49	6e-04
emb CBJ19138.1	alpha-ketoglutarate dioxygenase-like protein [un...	49	6e-04
ref XP_001552854.1	hypothetical protein BC1G_09036 [Botryotinia...	49	6e-04
emb CBJ20077.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	49	6e-04
ref XP_002621709.1	alpha-ketoglutarate-dependent taurine dioxyg...	49	6e-04

ref XP_003038633.1	hypothetical protein SCHCODRAFT_28913 [Schiz...	49	7e-04
emb CBJ18894.1	alpha-ketoglutarate dioxygenase-like protein [un...	49	7e-04
emb CBJ18939.1	alpha-ketoglutarate dioxygenase-like protein [un...	49	7e-04
dbj BAE60876.1	unnamed protein product [Aspergillus oryzae]	49	7e-04
emb CBJ18892.1	alpha-ketoglutarate dioxygenase-like protein [un...	49	8e-04
ref XP_002904406.1	taurine dioxygenase, putative [Phytophthora ...	49	8e-04
emb CBJ18980.1	alpha-ketoglutarate dioxygenase-like protein [un...	49	8e-04
gb EFY94724.1	alpha-ketoglutarate-dependent sulfonate dioxygena...	49	8e-04
emb CAY25739.1	alpha-KG-dehydrogenase [uncultured bacterium]	49	9e-04
emb CBJ18993.1	alpha-ketoglutarate dioxygenase-like protein [un...	49	9e-04
emb CBJ18823.1	alpha-ketoglutarate dioxygenase-like protein [un...	49	9e-04
gb EFQ93253.1	hypothetical protein PTT_09428 [Pyrenophora teres...	49	0.001
gb AAB08969.1	alpha ketoglutarate dioxygenase [Variovorax parad...	49	0.001
emb CBJ19160.1	alpha-ketoglutarate dioxygenase-like protein [un...	49	0.001
emb CBJ19070.1	alpha-ketoglutarate dioxygenase-like protein [un...	49	0.001
emb CBJ19042.1	alpha-ketoglutarate dioxygenase-like protein [un...	49	0.001
gb AAX51275.1	TdfA [uncultured bacterium]	49	0.001
gb ACB21019.1	TfdA [uncultured bacterium]	49	0.001
emb CBJ18792.1	alpha-ketoglutarate dioxygenase-like protein [un...	49	0.001
emb CBJ18773.1	alpha-ketoglutarate dioxygenase-like protein [un...	49	0.001
emb CBJ19037.1	alpha-ketoglutarate dioxygenase-like protein [un...	49	0.001
gb ACB21025.1	TfdA [uncultured bacterium]	48	0.001
sp P83309.1	SDPA_DELAC RecName: Full=(S)-2-(2,4-dichlorophenoxy)...	48	0.001
emb CBJ19008.1	alpha-ketoglutarate dioxygenase-like protein [un...	48	0.001
ref ZP_01630848.1	taurine dioxygenase [Nodularia spumigena CCY9...	48	0.001
gb ACB21023.1	TfdA [uncultured bacterium]	48	0.001
ref ZP_04588004.1	taurine dioxygenase [Pseudomonas syringae pv....	48	0.001
emb CBJ19082.1	alpha-ketoglutarate dioxygenase-like protein [un...	48	0.002
gb ACB21028.1	TfdA [uncultured bacterium]	48	0.002
emb CBJ18890.1	alpha-ketoglutarate dioxygenase-like protein [un...	48	0.002
gb AAB18140.1	2,4-dichlorophenoxyacetate dioxygenase [Halomonad...	48	0.002
gb EFQ92006.1	hypothetical protein PTT_10996 [Pyrenophora teres...	48	0.002
gb AAX51279.1	TdfA [uncultured bacterium]	48	0.002
gb ABE68889.1	TfdA [Burkholderia glathei]	48	0.002
emb CBJ19079.1	alpha-ketoglutarate dioxygenase-like protein [un...	48	0.002
gb ACB21024.1	TfdA [uncultured bacterium]	48	0.002
emb CBJ18764.1	alpha-ketoglutarate dioxygenase-like protein [un...	48	0.002
ref ZP_05883092.1	PvcB protein [Vibrio metschnikovii CIP 69.14]...	48	0.002
emb CBJ19143.1	alpha-ketoglutarate dioxygenase-like protein [un...	48	0.002
ref ZP_06188335.1	PvcB [Legionella longbeachae D-4968] >gi 2891...	48	0.002
gb AAX51272.1	TfdA [uncultured bacterium] >gi 61661373 gb AAX51...	48	0.002
emb CBJ19153.1	alpha-ketoglutarate dioxygenase-like protein [un...	48	0.002
ref XP_001559770.1	hypothetical protein BC1G_01926 [Botryotinia...	48	0.002
emb CBJ18734.1	alpha-ketoglutarate dioxygenase-like protein [un...	47	0.002
gb ADP12603.1	putative siderophore biosynthesis protein [Erwini...	47	0.002
gb AAF02720.2	alpha ketoglutarate dependent dioxygenase [Ralsto...	47	0.002
gb EFY88508.1	alpha-ketoglutarate-dependent sulfonate dioxygena...	47	0.002
emb CBJ19158.1	alpha-ketoglutarate dioxygenase-like protein [un...	47	0.002
emb CBJ18931.1	alpha-ketoglutarate dioxygenase-like protein [un...	47	0.002
emb CBJ18906.1	alpha-ketoglutarate dioxygenase-like protein [un...	47	0.002
ref XP_002736252.1	PREDICTED: hypothetical protein [Saccoglossu...	47	0.003
emb CAK48940.1	unnamed protein product [Aspergillus niger]	47	0.003
emb CBJ19057.1	alpha-ketoglutarate dioxygenase-like protein [un...	47	0.003
ref YP_125606.1	hypothetical protein lp10237 [Legionella pneumo...	47	0.003
emb CBJ19054.1	alpha-ketoglutarate dioxygenase-like protein [un...	47	0.003
emb CBJ19163.1	alpha-ketoglutarate dioxygenase-like protein [un...	47	0.003
gb ABI94568.1	TfdA [Burkholderia hospita]	47	0.003
emb CBJ19169.1	alpha-ketoglutarate dioxygenase-like protein [un...	47	0.003
gb ADO34958.1	putative (R)-2,4-dichlorophenoxypropionate dioxyg...	47	0.003
gb AAX51288.1	TdfA [uncultured bacterium]	47	0.003
gb AAX51276.1	TdfA [uncultured bacterium]	47	0.003
gb EEQ42086.1	alpha-ketoglutarate-dependent sulfonate dioxygena...	47	0.003
ref XP_002419465.1	alpha-ketoglutarate-dependent sulfonate diox...	47	0.003

ref XP_657819.1	hypothetical protein AN0215.2 [Aspergillus nidu...	47	0.003
ref XP_713065.1	potential taurine catabolic dioxygenase [Candid...	47	0.003
emb CBJ19159.1	alpha-ketoglutarate dioxygenase-like protein [un...	47	0.004
gb AAX51287.1	TdfA [uncultured bacterium]	47	0.004
gb EEQ44600.1	hypothetical protein CAWG_02874 [Candida albicans...	47	0.004
ref XP_001937063.1	taurine dioxygenase family protein [Pyrenoph...	47	0.004
gb ADO34952.1	putative (R)-2,4-dichlorophenoxypropionate dioxyg...	47	0.004
ref ZP_02357712.1	pyoverdine biosynthesis protein PvcB [Burkhol...	47	0.004
emb CBW98417.1	hypothetical protein LPW_02691 [Legionella pneum...	47	0.004
ref ZP_02364837.1	pyoverdine biosynthesis protein PvcB [Burkhol...	47	0.004
emb CBJ18810.1	alpha-ketoglutarate dioxygenase-like protein [un...	47	0.005
emb CBJ19063.1	alpha-ketoglutarate dioxygenase-like protein [un...	47	0.005
ref XP_002383259.1	alpha-ketoglutarate-dependent sulfonate diox...	47	0.005
gb EFN53016.1	hypothetical protein CHLNCDRAFT_137505 [Chlorella...	46	0.005
emb CBJ19019.1	alpha-ketoglutarate dioxygenase-like protein [un...	46	0.005
emb CBJ19189.1	alpha-ketoglutarate dioxygenase-like protein [un...	46	0.005
ref YP_001629703.1	Alpha-ketoglutarate-dependent taurine dioxyg...	46	0.005
gb EEQ44372.1	hypothetical protein CAWG_02639 [Candida albicans...	46	0.005
emb CBJ18912.1	alpha-ketoglutarate dioxygenase-like protein [un...	46	0.006
emb CBJ19023.1	alpha-ketoglutarate dioxygenase-like protein [un...	46	0.006
ref YP_003018467.1	Taurine catabolism dioxygenase TauD/TfdA [Pe...	46	0.006
ref XP_720183.1	potential taurine catabolic dioxygenase [Candid...	46	0.006
emb CBJ18997.1	alpha-ketoglutarate dioxygenase-like protein [un...	46	0.006
ref YP_094229.1	pyoverdine biosynthesis protein PvcB [Legionell...	46	0.006
emb CBJ19026.1	alpha-ketoglutarate dioxygenase-like protein [un...	46	0.006
ref XP_714705.1	potential taurine catabolic dioxygenase [Candid...	46	0.007
gb ACG80556.1	TfdA [uncultured bacterium]	46	0.007
ref XP_003002132.1	alpha-ketoglutarate-dependent sulfonate diox...	45	0.008
ref YP_122580.1	hypothetical protein lpp0237 [Legionella pneumo...	45	0.009
gb ADC33970.1	TfdA-like protein [uncultured bacterium]	45	0.009
ref XP_387766.1	hypothetical protein FG07590.1 [Gibberella zeae...	45	0.010
ref ZP_02484143.1	pyoverdine biosynthesis protein PvcB [Burkhol...	45	0.010
gb AAX51278.1	TdfA [uncultured bacterium]	45	0.010
gb AAX51283.1	TdfA [uncultured bacterium] >gi 61661369 gb AAX51...	45	0.010
emb CBJ18883.1	alpha-ketoglutarate dioxygenase-like protein [un...	45	0.010
gb ADC33968.1	TfdA-like protein [uncultured bacterium]	45	0.011
emb CBJ18865.1	alpha-ketoglutarate dioxygenase-like protein [un...	45	0.011
ref ZP_04522600.1	PvcB [Burkholderia pseudomallei MSHR346] >gi ...	45	0.012
emb CBJ18758.1	alpha-ketoglutarate dioxygenase-like protein [un...	45	0.013
emb CBJ20073.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	45	0.013
ref XP_003039403.1	hypothetical protein NECHADRAFT_98371 [Nectr...	45	0.013
gb AAZ39276.1	oxygenase [uncultured organism]	45	0.014
ref ZP_04896071.1	pyoverdine biosynthesis protein PvcB [Burkhol...	45	0.014
ref ZP_03454489.1	pyoverdine biosynthesis protein PvcB [Burkhol...	45	0.015
gb EFQ32023.1	TfdA family Taurine catabolism dioxygenase TauD [...	45	0.016
emb CBJ18960.1	alpha-ketoglutarate dioxygenase-like protein [un...	45	0.016
ref ZP_02405336.1	pyoverdine biosynthesis protein PvcB [Burkhol...	45	0.016
ref ZP_02449958.1	pyoverdine biosynthesis protein PvcB [Burkhol...	45	0.017
ref YP_106451.1	pyoverdine chromophore biosynthetic protein Pvc...	45	0.018
ref ZP_02495768.1	pyoverdine chromophore biosynthetic protein P...	44	0.018
ref XP_001903241.1	hypothetical protein [Podospira anserina S m...	44	0.019
gb AAX51281.1	TdfA [uncultured bacterium]	44	0.019
gb EFX05042.1	taurine catabolism dioxygenase [Grosmannia clavig...	44	0.020
gb ABD39114.1	alpha-ketoglutarate dioxygenase [uncultured bacte...	44	0.020
ref XP_002484628.1	conserved hypothetical protein [Talaromyces ...	44	0.021
gb AAX51277.1	TdfA [uncultured bacterium]	44	0.022
gb ACB21022.1	TfdA [uncultured bacterium]	44	0.022
ref ZP_06035601.1	PvcB protein [Vibrio cholerae RC27] >gi 26202...	44	0.023
emb CBJ18923.1	alpha-ketoglutarate dioxygenase-like protein [un...	44	0.024
ref XP_003041645.1	hypothetical protein NECHADRAFT_49706 [Nectr...	44	0.024
ref ZP_01680907.1	PvcB protein [Vibrio cholerae V52] >gi 147673...	44	0.025
dbj BAD15044.1	hypothetical protein [Sphingomonas sp. B6-5]	44	0.025
emb CBJ20460.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	44	0.028

ref	XP_002395867.1	hypothetical protein MPER_04001 [Moniliophth...	44	0.030
ref	ZP_01767510.1	pyoverdine biosynthesis protein PvcB [Burkhol...	44	0.030
ref	XP_001214255.1	hypothetical protein ATEG_05077 [Aspergillus...	44	0.032
emb	CBJ20476.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	44	0.034
ref	YP_001249599.1	pyoverdine biosynthesis protein PvcB [Legion...	44	0.036
ref	YP_001061325.1	pyoverdine biosynthesis protein PvcB [Burkho...	43	0.040
emb	CBJ20449.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	43	0.041
emb	CAY25794.1	alpha-KG-dehydrogenase [uncultured bacterium] >g...	43	0.042
ref	ZP_04967066.1	pyoverdine biosynthesis protein PvcB [Burkhol...	43	0.043
emb	CBJ20434.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	43	0.047
ref	ZP_01981895.1	PvcB protein [Vibrio cholerae 623-39] >gi 148...	43	0.048
ref	ZP_06050330.1	PvcB protein [Vibrio cholerae CT 5369-93] >gi...	43	0.049
emb	CBJ18838.1	alpha-ketoglutarate dioxygenase-like protein [un...	43	0.050
emb	CBJ20482.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	43	0.050
emb	CBJ20170.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	43	0.052
ref	ZP_07276033.1	hypothetical protein SSMG_00073 [Streptomyces...	43	0.052
emb	CBJ20074.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	43	0.054
emb	CBJ18991.1	alpha-ketoglutarate dioxygenase-like protein [un...	43	0.055
ref	ZP_05419250.1	PvcB protein [Vibrio cholera CIRS 101] >gi 26...	43	0.055
ref	ZP_04418422.1	PvcB protein [Vibrio cholerae 12129(1)] >gi 2...	43	0.056
emb	CAY67029.1	Alpha-ketoglutarate-dependent sulfonate dioxygen...	43	0.056
ref	XP_001224155.1	hypothetical protein CHGG_04941 [Chaetomium ...	43	0.060
ref	NP_231578.1	PvcB protein [Vibrio cholerae O1 biovar El Tor ...	43	0.062
ref	ZP_04961829.1	PvcB protein [Vibrio cholerae AM-19226] >gi 1...	43	0.064
ref	ZP_01677582.1	PvcB protein [Vibrio cholerae 2740-80] >gi 15...	42	0.070
ref	ZP_02458135.1	pyoverdine chromophore biosynthetic protein P...	42	0.073
emb	CBJ18859.1	alpha-ketoglutarate dioxygenase-like protein [un...	42	0.074
ref	YP_001074272.1	pyoverdine biosynthesis protein PvcB [Burkho...	42	0.076
emb	CBJ20175.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	42	0.077
ref	YP_003018783.1	Taurine catabolism dioxygenase TauD/TfdA [Pe...	42	0.077
gb	ABR27314.1	TfdA [uncultured bacterium]	42	0.079
emb	CBJ18850.1	alpha-ketoglutarate dioxygenase-like protein [un...	42	0.091
ref	YP_106166.1	taurine dioxygenase-related protein [Burkholder...	42	0.092
emb	CBJ20438.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	42	0.096
ref	YP_004022174.1	hypothetical protein RBRH_04238 [Burkholderi...	42	0.100
gb	EFZ38396.1	alpha-ketoglutarate-dependent taurine dioxygenase...	42	0.10
emb	CAK44165.1	unnamed protein product [Aspergillus niger]	42	0.10
emb	CBJ20437.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	42	0.11
emb	CBJ20463.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	42	0.11
ref	ZP_01909755.1	pyoverdine biosynthesis protein [Plesiocystis...	42	0.11
ref	YP_438432.1	pyoverdine biosynthesis protein PvcB [Burkholde...	42	0.12
ref	XP_001936735.1	taurine catabolism dioxygenase TauD [Pyrenop...	42	0.12
ref	YP_051469.1	pyoverdine biosynthesis protein [Pectobacterium...	42	0.12
ref	XP_003188569.1	hypothetical protein ANI_1_3376014 [Aspergil...	42	0.13
emb	CBJ20176.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	42	0.13
emb	CBJ20300.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	42	0.14
emb	CBJ20465.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.15
emb	CBJ20432.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.16
emb	CBJ20446.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.16
emb	CBJ20166.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.16
emb	CBJ20456.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.17
ref	YP_336837.1	pyoverdine chromophore biosynthetic protein Pvc...	41	0.17
emb	CBJ20468.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.18
emb	CBJ20110.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.18
emb	CBJ20112.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.18
emb	CBJ20454.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.20
emb	CBJ20455.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.20
emb	CBJ20282.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.21
emb	CBJ20447.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.21
emb	CBJ20177.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.21
emb	CBJ20204.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.21
emb	CBJ20485.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.21
ref	YP_110182.1	siderophore biosynthesis-related protein [Burkh...	41	0.21

ref	YP_003258525.1	taurine catabolism dioxygenase TauD/TfdA [Pe...	41	0.22
emb	CBJ20223.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.22
ref	ZP_02369596.1	pyoverdine biosynthesis protein PvcB [Burkhol...	41	0.23
emb	CBJ20471.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.24
emb	CBJ20162.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	41	0.25
emb	CBJ20459.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.26
emb	CBJ20443.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.26
emb	CBJ20436.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.27
emb	CAY25744.1	alpha-KG-dehydrogenase [uncultured bacterium]	40	0.27
gb	AAX51280.1	TdFA [uncultured bacterium]	40	0.28
emb	CBJ20479.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.28
emb	CBJ20252.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.29
emb	CBJ20427.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.29
emb	CBJ20231.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.34
emb	CAY25788.1	alpha-KG-dehydrogenase [uncultured bacterium]	40	0.34
gb	ACF09926.1	alpha-ketoglutarate-dependent taurine dioxygenase...	40	0.38
ref	XP_772077.1	hypothetical protein CNBM2340 [Cryptococcus neo...	40	0.39
emb	CBJ20265.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.40
ref	ZP_05225172.1	putative taurine dioxygenase [Mycobacterium i...	40	0.41
emb	CBJ20466.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.41
ref	ZP_05073584.1	taurine catabolism dioxygenase TauD/TfdA [Rho...	40	0.42
emb	CBJ20277.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.42
emb	CBJ20409.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.43
emb	CBJ20286.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.45
emb	CBJ20478.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.47
emb	CBJ20349.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.47
emb	CBJ20420.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.47
emb	CBJ20276.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.47
emb	CBJ20328.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.48
emb	CBJ20375.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.50
emb	CBJ20186.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.50
emb	CBJ20188.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.54
ref	YP_003743530.1	Taurine dioxygenase, C-terminal fragment [Er...	40	0.55
emb	CBJ20255.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.55
ref	ZP_01038110.1	hypothetical protein ROS217_03160 [Roseovariu...	40	0.55
emb	CBJ20206.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.56
emb	CBJ20444.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	40	0.57
emb	CBJ20163.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	39	0.62
ref	ZP_01881466.1	hypothetical conserved membrane protein [Rose...	39	0.63
emb	CBJ20273.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	39	0.64
emb	CBJ20337.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	39	0.66
emb	CAI47587.1	alpha-ketoglutarate dependent xanthine dioxygena...	39	0.66
emb	CBJ20281.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	39	0.67
emb	CBJ20279.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	39	0.68
emb	CBJ20296.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	39	0.69
emb	CBJ20470.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	39	0.71
emb	CBJ20336.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	39	0.71
emb	CBJ20292.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	39	0.71
gb	EFZ46473.1	alpha-ketoglutarate-dependent taurine dioxygenase...	39	0.72
emb	CBJ20397.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	39	0.72
tpe	CBF89386.1	TPA: Alpha-ketoglutarate dependent xanthine diox...	39	0.72
emb	CBJ20344.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	39	0.74
emb	CBJ20239.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	39	0.75
emb	CBJ20241.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	39	0.77
ref	XP_658092.1	hypothetical protein AN0488.2 [Aspergillus nidu...	39	0.77
emb	CBJ20509.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	39	0.81
emb	CBJ20111.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	39	0.86
emb	CBJ20205.1	2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate...	39	0.87
emb	CBJ18807.1	alpha-ketoglutarate dioxygenase-like protein [un...	39	0.89

>gb|AAP88277.1| S-2,4-dichlorophenoxypropionate/alpha-ketoglutarate dioxygenase
[Delftia acidovorans]
Length = 292

Score = 596 bits (1537), Expect = e-168, Method: Compositional matrix adjust.
Identities = 291/291 (100%), Positives = 291/291 (100%)

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Query: 3  QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
          QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK
Sbjct: 2  QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 61

Query: 63  RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
          RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
Sbjct: 62  RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 121

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
          VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY
Sbjct: 122 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 181

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPR 242
          IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPR
Sbjct: 182 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPR 241

Query: 243 VHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAALV 293
          VHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAALV
Sbjct: 242 VHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAALV 292
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>emb|CAF32813.1| (S)-2-(2,4-dichlorophenoxy)propionate, 2- oxoglutarate dioxygenase
[Sphingobium herbicidovorans]
gb|ABD67501.1| (S)-2-(2,4-dichlorophenoxy)propionate/alpha-ketoglutarate
dioxygenase [Rhodoferax sp. P230]
Length = 287

Score = 369 bits (947), Expect = e-100, Method: Compositional matrix adjust.
Identities = 182/286 (63%), Positives = 217/286 (75%), Gaps = 7/286 (2%)

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Query: 6  LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
          I P AT GA VTGV LA LDDAG+ L AAWL++ALL+FP QHL+ +QQI FA+RFG
Sbjct: 5  FDIAPLDATFGAVVTGVKLADLDDAGWLDLQAAWLEYALLVFPDQHLTREQQIAFARRFG 64

Query: 66  AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
          +E ++ AISNV+ DG++R S + DMMK++ GNM WHADSTYMPV A+GAVFS
Sbjct: 65  PLEF---EMAAISNVRPDGSLRVES--DNDDMMKILKGNMGWHADSTYMPVQAKGAVFS 118

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA-YIG 184
          AEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH +A Y G
Sbjct: 119 AEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGHQTKAADGEYSG 178

Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH 244
          YG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L+D+ACQ PR++
Sbjct: 179 YGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQLIDFACQPPRIY 238

Query: 245 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGA 290
          H WA GD V+WDNRCLLH+A PWD R+MWHSR+AG P +E A
Sbjct: 239 HHDWAPGDAVLWDNRCLLHQATPWDMTQKRIMWHSRIAGDPASETA 284
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>ref|ZP_01615308.1| Taurine catabolism dioxygenase TauD/TfdA [marine gamma
proteobacterium HTCC2143]
gb|EAW32391.1| Taurine catabolism dioxygenase TauD/TfdA [marine gamma
proteobacterium HTCC2143]
Length = 289

Score = 310 bits (795), Expect = 1e-82, Method: Compositional matrix adjust.
Identities = 161/279 (57%), Positives = 194/279 (69%), Gaps = 7/279 (2%)

Query: 14 TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG 73
T GA VT + L LD+ F+AL+ AWL++ LLIFPGQ+LS+ +Q TFA RFG + I G
Sbjct: 16 TFGAIVTDIRLNELDNRFQSFALYQAWLEYGLLIFPGQYLSDAEQQTFAARFGDL--IKGV 73

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVG 133
+ V +SNV +G++R A DDMMK+I GNM WH D+TYMPV A+GAVFSA+VVP
Sbjct: 74 EAVELSNVLPNGSLRD---APDDDDMMKIIIRGNMHHWQDNTYMPVQAKGAVFSAKVVPQAQ 130

Query: 134 GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG-HVQQAGSAYIGYGMDDTTAT 192
G T FADMRAA+DALD R V SA HSLV+SQ +G + S YIGYG+D T
Sbjct: 131 GDTGFADMRAAWDALDGGRRNQVAGLSAYHSLVHSQKLVGEETKSVDSEYIGYGLDIDDT 190

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAP-RVHAHQWAAG 251
PLRPL+K+HPETGR SL IGRHA IP M ES +FL L+D+A P R + +QW G
Sbjct: 191 PLRPLLLKIHPETGRKSLAIGRHAFIGPEMSEGESESKFLADLMDFATGDPQRTYQYQWTKG 250

Query: 252 DVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGA 290
D VVWDNRCLLHRA WD+ PRVM HSR+AG PETE A
Sbjct: 251 DAVVWDNRCLLHRACSWDYSEPRVMLHSRIAGDPETESA 289

>gb|ABL97633.1| 24-dichlorophenoxyacetate alpha-ketoglutarate dioxxygenase
[uncultured marine bacterium EB0_39H12]
Length = 284

Score = 271 bits (694), Expect = 6e-71, Method: Compositional matrix adjust.
Identities = 135/288 (46%), Positives = 184/288 (63%), Gaps = 9/288 (3%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
+++ P + GA V + L L+ ++ WL++ALLIFPGQHLSNDQQI FAK FG
Sbjct: 1 MRVEPLKRSFQAKVYDLSLPDLNTEQAQDVYDLWLKYALLIFPGQHLSNDQQIKFAKNFG 60

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
A+E D+ ISNV+ DG++R A DD++K + GNM WH DSTYMP+ A+GAVF+
Sbjct: 61 ALE----FDLSPISNVRNDGSIIRD---ANDDDIVKSLRGNMEWHHDSTYMPIQAKGAVFT 113

Query: 126 AEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ-SKLGHVQQAGSAYIG 184
A VP+ GG T +ADMRAAY+ALD++ + +++ SA HS +SQ + GH S +
Sbjct: 114 AHKVP SHGGETGWADMRAAYEALDQSMKDKINELSAHSYSEWSQKERFGHKDPKVSEFNS 173

Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPR-V 243
YG D PLRPLVK H ETG+ L IGRH + IPG+ E++ + L ++AC V
Sbjct: 174 YGFDIDPKPLRPLVKTHNETGQKCLTIGRHINKIPGLSDQEAQNLAKELEEYACSNKEWV 233

Query: 244 HAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAA 291
+ H W GD V+WDNRCL+H+A WD R+M+HSR+ G P E A+
Sbjct: 234 YHHAWEVGDAVIWDNRCLMHQASMWDLSEGRIMYHSRIEGDPIAEAAAS 281

>gb|ADC34025.1| TfdA-like protein [uncultured bacterium]
Length = 201

Score = 266 bits (681), Expect = 2e-69, Method: Compositional matrix adjust.
Identities = 135/207 (65%), Positives = 155/207 (74%), Gaps = 7/207 (3%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
QQI FAK+FG +E ++ AISNV+ DGTVR AE DD++KV+ GNM WH DSTYM
Sbjct: 1 QQIAFAKKFGPLEF---EMAAISNVRKDGTVRIE--AENDDVVKVLKGNMGWHCDSTYM 54

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
PV A+GAVFSAEVVPAVGGRTCFADMRAAYDALD+A R+ V +A HSL YSQSKLGH
Sbjct: 55 PVQAKGAVFSAEVVPSVGGRTGWADMRAAYDALDDALRSKVETLTAYHSLYYSQSKLGHQ 114

Query: 176 QQA-GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
+ GS Y GYG PLRPLVK HPETGR SLLIGRHAH IP MD ESER L+ LV
Sbjct: 115 PKTQGS DYSGYGFHDGPVPLRPLVKSHPETGRKSLIGRHAHNIPNMDKDESERLLQALV 174

Query: 235 DWACQAPRVHAHQWAAGDVVWDNRCL 261
D+ACQ PR++ H W GD VVWDNRC+
Sbjct: 175 DFACQPPRIYHHTWTPGDAVVWDNRCV 201

>emb|CBJ20087.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 196 bits (499), Expect = 2e-48, Method: Compositional matrix adjust.
Identities = 98/142 (69%), Positives = 112/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG+ AESERFL+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLAPAESERFLQEL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WAAGD V+
Sbjct: 121 IDFACQRPRIYHHDWAAGDAVL 142

>emb|CBJ20295.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20360.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 196 bits (497), Expect = 4e-48, Method: Compositional matrix adjust.
Identities = 97/142 (68%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGGRT FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGRTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20274.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 196 bits (497), Expect = 4e-48, Method: Compositional matrix adjust.
Identities = 98/142 (69%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 +A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG+ AESERFL L
 Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLAPAESERFLREL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
 +D+ACQ PR++ H WAAGD V+
 Sbjct: 121 IDFACQRPRIYHHDWAAGDAVL 142

>emb|CBJ20081.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
 [uncultured bacterium]
 Length = 142

Score = 195 bits (496), Expect = 5e-48, Method: Compositional matrix adjust.
 Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
 MPV A+GAVFSAEVVP VGG+T FADMRAAYDALD+A + V Q A HSL YSQSKLGH
 Sbjct: 1 MPVQAKGAVFSAEVVPTVGGQTGFADMRAAYDALDDARKERVEQLQAHHSLHYSQSKLGH 60

Query: 175 -VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 Q+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
 Sbjct: 61 QTQKADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
 +D+ACQ PR++ H WA GD V+
 Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20244.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
 [uncultured bacterium]
 Length = 142

Score = 195 bits (495), Expect = 7e-48, Method: Compositional matrix adjust.
 Identities = 95/142 (66%), Positives = 112/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
 MPV A+GAVFSAEVVP +GG+T FADMRAAYDALD+A + V Q A HSL YSQSKLGH
 Sbjct: 1 MPVQAKGAVFSAEVVPTIGGQTGFADMRAAYDALDDARKERVEQLQAHHSLHYSQSKLGH 60

Query: 175 -VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 ++A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPGM AES+RFL+ L
 Sbjct: 61 QTKKADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGMAPAESDRFLQEL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
 +D+ACQ PR++ H W+AGD V+
 Sbjct: 121 IDFACQRPRIYHHDWSAGDAVL 142

>emb|CBJ20155.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
 [uncultured bacterium]
 Length = 142

Score = 195 bits (495), Expect = 8e-48, Method: Compositional matrix adjust.
 Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
 MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
 Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEGLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 +A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
 Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
 +D+ACQ PR++ H WA GD V+
 Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20145.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 142

Score = 194 bits (494), Expect = 8e-48, Method: Compositional matrix adjust.
 Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
 MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
 Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 +A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
 Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
 +D+ACQ PR++ H WA GD V+
 Sbjct: 121 IDFACQPPRIYLHDWAPGDAVL 142

>emb|CBJ20533.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 142

Score = 194 bits (494), Expect = 9e-48, Method: Compositional matrix adjust.
 Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
 MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
 Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 +A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
 Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
 +D+ACQ PR++ H WA GD V+
 Sbjct: 121 IDFACQPPRIYHHNWAPGDAVL 142

>emb|CBJ20525.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 emb|CBJ20526.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 142

Score = 194 bits (494), Expect = 9e-48, Method: Compositional matrix adjust.
 Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
 MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
 Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKACVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 +A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
 Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20227.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 194 bits (494), Expect = 1e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDYACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20345.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 194 bits (494), Expect = 1e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVESLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20085.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 194 bits (494), Expect = 1e-47, Method: Compositional matrix adjust.
Identities = 97/142 (68%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
VD+ACQ PR++ H WA GD V+
Sbjct: 121 VDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20394.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
Length = 142

Score = 194 bits (493), Expect = 1e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDMKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20102.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
Length = 142

Score = 194 bits (493), Expect = 1e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 113/142 (79%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALD+A + V Q A HSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDDARKERVEQLQAHSLHYSQSKLGH 60

Query: 175 -VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
++A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPGM A+S+RFL+ L
Sbjct: 61 QTKKADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGMALADSDRFLQEL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H W+AGD V+
Sbjct: 121 IDFACQRPRIYHHDWSAGDAVL 142

>emb|CBJ20083.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
emb|CBJ20084.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
emb|CBJ20086.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
emb|CBJ20088.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
emb|CBJ20089.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
emb|CBJ20090.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
emb|CBJ20091.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
emb|CBJ20093.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
emb|CBJ20098.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
emb|CBJ20100.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
emb|CBJ20101.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase

emb|CBJ20532.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20534.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20536.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20538.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20539.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20540.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20541.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20542.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20544.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20545.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20547.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20548.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20550.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20551.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20552.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20553.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20554.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 194 bits (493), Expect = 1e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20134.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 194 bits (493), Expect = 1e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 -VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 + A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
 Sbjct: 61 QTKAADGVYSGYGLHDGPVPLRPLVKIHPETGRKSLLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
 +D+ACQ PR++ H WA GD V+
 Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20495.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 142

Score = 194 bits (493), Expect = 1e-47, Method: Compositional matrix adjust.
 Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
 MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
 Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVKTQLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 +A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
 Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
 +D+ACQ PR++ H WA GD V+
 Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20327.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 142

Score = 194 bits (492), Expect = 1e-47, Method: Compositional matrix adjust.
 Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
 MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
 Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 +A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
 Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRESLLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
 +D+ACQ PR++ H WA GD V+
 Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20079.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 142

Score = 194 bits (492), Expect = 1e-47, Method: Compositional matrix adjust.
 Identities = 95/142 (66%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
 MPV A+GAVFSAEVVP++GG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
 Sbjct: 1 MPVQAKGAVFSAEVVPSIGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 +A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
 Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20082.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 194 bits (492), Expect = 1e-47, Method: Compositional matrix adjust.
Identities = 94/142 (66%), Positives = 113/142 (79%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP++GG+T FADMRAAYDALD+A + V Q A HSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSIGGQTGFADMRAAYDALDDARKERVEQLQAHHSLHYSQSKLGH 60

Query: 175 -VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
++A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPGM A+S+RFL+ L
Sbjct: 61 QTKKADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGMALADSDRFLQEL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H W+AGD V+
Sbjct: 121 IDFACQRPRIYHHDWSAGDAVL 142

>emb|CBJ20524.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 194 bits (492), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKAHVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20387.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20506.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 194 bits (492), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20125.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 194 bits (492), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAG-SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAAVGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20496.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 193 bits (491), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVRAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20146.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 193 bits (491), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQA-GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAVDGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20356.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
Length = 142

Score = 193 bits (491), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGVHDGPVPLRPLVKIHPETGRKSLLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20535.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
Length = 142

Score = 193 bits (491), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRRSLLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20543.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
Length = 142

Score = 193 bits (491), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHVGPVPLRPLVKIHPETGRKSLLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR + H WA GD V+
Sbjct: 121 IDFACQPPRTYHHDWAPGDAVL 142

>emb|CBJ20107.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase

[uncultured bacterium]
Length = 142

Score = 193 bits (491), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHA PG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDEPVPLRPLVKIHPETGRKSLIGRHAHAATPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20493.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20519.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 193 bits (491), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D ACQ PR++ H WA GD V+
Sbjct: 121 IDLACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20410.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20504.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 193 bits (490), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVGTLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20216.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20546.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 193 bits (490), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLRQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20330.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 193 bits (490), Expect = 3e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR+ H WA GD V+
Sbjct: 121 IDFACQPPRIDHHDWAPGDAVL 142

>emb|CBJ20092.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 193 bits (490), Expect = 3e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERSLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20492.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase

[uncultured bacterium]
Length = 142

Score = 192 bits (489), Expect = 3e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG+ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLGPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20405.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 192 bits (489), Expect = 3e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMR AYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMR TAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20228.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 192 bits (489), Expect = 3e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T F DMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGF TDMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20099.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20124.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]

Length = 142

Score = 192 bits (489), Expect = 3e-47, Method: Compositional matrix adjust.
 Identities = 95/142 (66%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
 MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
 Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 +A Y GYG+ PLRPLV++HPETGR SLLIGRHAHAIPG++ AESER L+ L
 Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVRIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
 +D+ACQ PR++ H WA GD V+
 Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20488.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 142

Score = 192 bits (489), Expect = 3e-47, Method: Compositional matrix adjust.
 Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
 MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
 Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 +A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ ESER L+ L
 Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPVEESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
 +D+ACQ PR++ H WA GD V+
 Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20290.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 emb|CBJ20528.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 142

Score = 192 bits (489), Expect = 3e-47, Method: Compositional matrix adjust.
 Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
 MPV A+GAVFSAEVVP+VGG+T FADMR AYDALDE +A V ARHSL YSQSKLGH
 Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRVAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 +A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
 Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
 +D+ACQ PR++ H WA GD V+
 Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20139.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 142

Score = 192 bits (489), Expect = 3e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYD LDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDVLDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20123.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 192 bits (489), Expect = 3e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ CQ PR++ H WA GD V+
Sbjct: 121 IDFCVCQPPRIYHHDWAPGDAVL 142

>emb|CBJ20080.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 192 bits (489), Expect = 3e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAH IPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHVIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20160.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 192 bits (489), Expect = 4e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSA+VVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAKVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20369.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 192 bits (489), Expect = 4e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVPAVGG+T F DMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFDPMDRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20365.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 192 bits (489), Expect = 4e-47, Method: Compositional matrix adjust.
Identities = 96/142 (67%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVPAVGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGPDPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20416.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20421.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 192 bits (488), Expect = 4e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MP A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YS QSKLGH
Sbjct: 1 MPAQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20413.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 192 bits (488), Expect = 5e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YS Q KLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQPKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20117.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 192 bits (488), Expect = 5e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVF AEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YS QSKLGH
Sbjct: 1 MPVQAKGAVFGAEVVPVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20516.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 192 bits (488), Expect = 5e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 111/142 (78%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YS QSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+ A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ + WA GD V+
Sbjct: 121 IDFACQPPRIYHNDWAPGDAVL 142

>emb|CBJ20515.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 192 bits (487), Expect = 5e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+ A Y GYG+ PLRPLVK+HPETGR SLLI RHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLISRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20233.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 192 bits (487), Expect = 5e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+ A Y GYG+ PLRPLVK+HPETGR SLLI RHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETSRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20097.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 192 bits (487), Expect = 5e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+V G+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+ A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L

Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
 +D+ACQ PR++ H WA GD V+

Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20203.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
 [uncultured bacterium]
 Length = 142

Score = 192 bits (487), Expect = 6e-47, Method: Compositional matrix adjust.
 Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
 MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YS QSKLGH

Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 +A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIP ++ AESER L+ L

Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPDLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
 +D+ACQ PR++ H WA GD V+

Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20095.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
 [uncultured bacterium]
 Length = 142

Score = 192 bits (487), Expect = 6e-47, Method: Compositional matrix adjust.
 Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
 MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YS QSKLGH

Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 +A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AE ER L+ L

Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAEFERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
 +D+ACQ PR++ H WA GD V+

Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20096.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
 [uncultured bacterium]
 Length = 142

Score = 192 bits (487), Expect = 7e-47, Method: Compositional matrix adjust.
 Identities = 95/142 (66%), Positives = 109/142 (76%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
 MPV A GAVFSAEVVP+VGG+T FADMRAAYD LDE +A V ARHSL YS QSKLGH

Sbjct: 1 MPVQAMGAVFSAEVVPSVGGQTGFADMRAAYDTLDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
 +A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L

Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255

+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20530.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 191 bits (486), Expect = 8e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSK GH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKPGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20323.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 191 bits (486), Expect = 8e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRP VK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPPVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20108.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 191 bits (486), Expect = 8e-47, Method: Compositional matrix adjust.
Identities = 95/141 (67%), Positives = 109/141 (77%), Gaps = 1/141 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARAETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHGGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVV 254
+D+ACQ PR++ H WA GD V
Sbjct: 121 IDFACQPPRIYHHDWAPGDAV 141

>emb|CBJ20529.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
Length = 142

Score = 191 bits (486), Expect = 9e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG- 173
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLG
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGP 60

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+ A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20189.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
Length = 142

Score = 191 bits (485), Expect = 9e-47, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIP ++ AESER L+ L
Sbjct: 61 QTKAADGEYGGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPSLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20507.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
emb|CBJ20537.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
Length = 142

Score = 191 bits (485), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+ +ACQ PR++ H WA GD V+
Sbjct: 121 IGFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20399.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 191 bits (485), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAY ALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYGALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20549.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 191 bits (485), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HP TGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPGTGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20406.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 191 bits (485), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALD +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDGDLDKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20490.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 191 bits (485), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V AR SL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARRSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20153.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 191 bits (485), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGR AHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRRAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20137.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 191 bits (485), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 94/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAE+VP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEMVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLI RHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLISRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20200.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20505.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 191 bits (485), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
M V A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MSVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20520.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 191 bits (484), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T ADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVSSAEVVPVSGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20224.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 191 bits (484), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T ADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGSADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20157.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 191 bits (484), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADM AAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMCAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20143.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 190 bits (483), Expect = 2e-46, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAA DALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAACDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20522.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 190 bits (483), Expect = 2e-46, Method: Compositional matrix adjust.
Identities = 96/141 (68%), Positives = 109/141 (77%), Gaps = 1/141 (0%)

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
PV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 2 PVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGHQ 61

Query: 176 QQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ LV
Sbjct: 62 TKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQLV 121

Query: 235 DWACQAPRVHAHQWAAGDVVV 255
D+ACQ PR + H WA GD V+
Sbjct: 122 DFACQPPRNYHHDWAPGDAVL 142

>emb|CBJ20122.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 189 bits (481), Expect = 3e-46, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
M V A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MLVRAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20254.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 189 bits (481), Expect = 3e-46, Method: Compositional matrix adjust.
Identities = 95/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V A HSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQAWHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20109.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 189 bits (480), Expect = 4e-46, Method: Compositional matrix adjust.
Identities = 94/142 (66%), Positives = 109/142 (76%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE RA V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLRARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PL PLVK+HPETGR S+LIGRH HAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLPLVKIHPETGRKSVLIGRHPHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20418.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 189 bits (480), Expect = 4e-46, Method: Compositional matrix adjust.
Identities = 94/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
+PV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V AR SL YSQSKLGH
Sbjct: 1 VPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARRSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L

Sbjct: 61 QTKAADGEYSGYGLHDGPAPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+

Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20354.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
Length = 142

Score = 189 bits (479), Expect = 5e-46, Method: Compositional matrix adjust.
Identities = 94/142 (66%), Positives = 109/142 (76%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH

Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR S LI RHAHAIPG++ AESER L+ L

Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSPLIDRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+

Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20417.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
Length = 142

Score = 189 bits (479), Expect = 5e-46, Method: Compositional matrix adjust.
Identities = 94/142 (66%), Positives = 110/142 (77%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH

Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AESER L+ L

Sbjct: 61 QTKAADGEYSGYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+AC+ PR++ H A GD V+

Sbjct: 121 IDFACRPPRIYHHDRA PGDAVL 142

>emb|CBJ20512.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
Length = 142

Score = 189 bits (479), Expect = 5e-46, Method: Compositional matrix adjust.
Identities = 92/142 (64%), Positives = 109/142 (76%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP+VGG+T FADMRAAYD LD+ + V + A HSL YSQSKLGH

Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDVLDDGRKERVEKLQAHHSLHYSQSKLGH 60

Query: 175 -VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
++A Y GYG+ PLRPLVK HPETGR SLLIGRHAHAIPG++ AESER L+ L

Sbjct: 61 QAKKADGEYSGYGLHDGPVPLRPLVKTHPETGRKSLIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255

+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20412.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 189 bits (479), Expect = 5e-46, Method: Compositional matrix adjust.
Identities = 93/142 (65%), Positives = 109/142 (76%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV ++G VFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQSKGTVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SLLIGRHAHAIPG++ AES R L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGLEPAESGRLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20388.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 188 bits (477), Expect = 9e-46, Method: Compositional matrix adjust.
Identities = 93/142 (65%), Positives = 108/142 (76%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVPAVGG+T FADMR AYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRTAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPE GR S LIGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSPILIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20309.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 187 bits (476), Expect = 1e-45, Method: Compositional matrix adjust.
Identities = 94/142 (66%), Positives = 109/142 (76%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVPAVGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y G G+ PLRPLVK+HPETGR SLLIGR AHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLIGRRAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H WA GD V+
Sbjct: 121 IDFACQPPRIYHHDWAPGDAVL 142

>emb|CBJ20500.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 139

Score = 187 bits (474), Expect = 2e-45, Method: Compositional matrix adjust.
Identities = 93/139 (66%), Positives = 107/139 (76%), Gaps = 1/139 (0%)

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH +
Sbjct: 1 QAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGHQTK 60

Query: 178 AGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW 236
A Y GYG+ PLRPLVK HPETGR SLLIGRHAHAIPG++ AESER L+ L+D+
Sbjct: 61 AADGEYSYGLHDGPVPLRPLVKTHPETGRKSLIGRHAHAIPGLEPAESERLLQLIDF 120

Query: 237 ACQAPRVHAHQWAAGDVVV 255
ACQ PR++ H WA GD V+
Sbjct: 121 ACQPPRIYHHDWAPGDAVL 139

>emb|CBJ20094.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 184 bits (468), Expect = 1e-44, Method: Compositional matrix adjust.
Identities = 93/142 (65%), Positives = 108/142 (76%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
M V A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH
Sbjct: 1 MLVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ PLRPLVK+HPETGR SL IGRHAHAIPG++ AESER L+ L
Sbjct: 61 QTKAADGEYSYGLHDGPVPLRPLVKIHPETGRKSLXIGRHAHAIPGLEPAESERLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H A GD V+
Sbjct: 121 IDFACQPPRIYHHDRA PGDAVL 142

>emb|CBJ20064.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 177 bits (449), Expect = 2e-42, Method: Compositional matrix adjust.
Identities = 86/142 (60%), Positives = 103/142 (72%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAE+VP +GGRT FADMRAAYDALD A +A + +A HSL YSQ ++GH
Sbjct: 1 MPVQAKGAVFSAEIVPTIGGRTGFADMRAAYDALDPAMKARIEGLNAYHSLHYSQGRVGH 60

Query: 175 -VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
++A Y GYG+ PLRPLVK HPETGR SLL GRHAH IPG+ ES+R L L
Sbjct: 61 QTKKADGEYSYGLHDGPVPLRPLVKTHPETGRKSLLAGRHAHNIPGLAQEESDRLLREL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+D+ACQ PR++ H W GD VV
Sbjct: 121 IDFACQPPRIYHHDWTPGDAVV 142

>emb|CBJ20065.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]

Length = 142

Score = 176 bits (445), Expect = 4e-42, Method: Compositional matrix adjust.
Identities = 87/142 (61%), Positives = 102/142 (71%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAE VP +GGRT FADMRAAYDALD A +A + +A HSL YSQ ++GH
Sbjct: 1 MPVQAKGAVFSAEEVPTIGGRTGFADMRAAYDALDPAMKARIEGLNAHHSLHYSQGRVGH 60

Query: 175 -VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
++A Y GYG+ PLRPLVK HPETGR SLL GRHAH IPG+ ES+R L L
Sbjct: 61 QTKKADGEYSYGLHDGVPPLRPLVKTHPETGRKSLLAGRHAHNIPGLGQDESDRLREL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
VD+ACQ PR++ H W GD VV
Sbjct: 121 VDFACQPPRIYHHDWTPGDAVV 142

>emb|CBJ20514.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 174 bits (440), Expect = 2e-41, Method: Compositional matrix adjust.
Identities = 88/142 (61%), Positives = 105/142 (73%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV A+GAVFSAEVVP VGG+T FADMRAA+DAL E +A V ARHSL YSQSKLGH
Sbjct: 1 MPVQAKGAVFSAEVVPRVGGQTGFADMRAAFDALAEDLKARVETLQARHSLHYSQSKLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ P RPLVK+HPETGR SLLIGRHAHAIPG++ AESER ++ L
Sbjct: 61 QTKAADGEYSYGLHDGVPVPRPLVKIHPETGRKSLIGRHAHAIPGLEPAESERLVQQ 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
++ + Q PR++ WA GD V+
Sbjct: 121 IELSYQLPRIYHQDWAPGDVAVL 142

>dbj|BAB92966.1| alpha KG dependent 2,4-D dioxygenase [alpha proteobacterium HW13]
Length = 295

Score = 162 bits (410), Expect = 6e-38, Method: Compositional matrix adjust.
Identities = 96/262 (36%), Positives = 136/262 (51%), Gaps = 23/262 (8%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F GQ +S+DQQ+ FA FG E GG + +SN+
Sbjct: 33 IEAGMDKYAVLVFHGQDISDDQQMAFALNFGKRENARGGTVTKKEDYRLSSGLNDVSNLG 92

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM 141
DG P D + +GN WH+DS++ P+ A+ ++ SA VV GG T FADM
Sbjct: 93 KDG-----KPLPKDHRTHLFLNGLNCLWHSDSSFRPIPAKFSLLSARVVPKGGNTEFADM 147

Query: 142 RAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVH 201
RAAYDALD+ T+ + HSL+YS+ LG + Y + L+ LV+ H
Sbjct: 148 RAAYDALDDETKTEIDDMICEHSLMYSRGSLGFLD-----YTDEEKEMFKPVLQRLVRTH 202

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVVDNRCL 261
P GR SL + HA AI GM E+ L L + A Q V+ H+W D+V+WDNR
Sbjct: 203 PAHGRKSLYLSSHAGAIRGMSMPEARLLLRDLTEHATQPEFVYVHKWTVHDLVMWDNRQT 262

Query: 262 LHRAEPWDFKLPRVMWHSRLAG 283
+HR +D PR M + +AG
Sbjct: 263 VHRVRRYDQSQPRDMRRATVAG 284

>dbj|BAB92964.1| alpha KG dependent 2,4-D dioxygenase [alpha proteobacterium RD5-C2]
Length = 295

Score = 162 bits (409), Expect = 7e-38, Method: Compositional matrix adjust.
Identities = 96/262 (36%), Positives = 136/262 (51%), Gaps = 23/262 (8%)

```
Query: 35  LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
          + A  ++A+L+F GQ +S+DQQ+ FA FG E GG + +SN+
Sbjct: 33  IEAGMDKYAVLVFHGQDISDDQQMAFALNFGERENARGGTVTKKEDYRLSSGLNDVSNLG 92

Query: 83  ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADM 141
          DG P D + +GN WH+DS++ P+ A+ ++ SA VV GG T FADM
Sbjct: 93  KDG-----KPLPKDHRTHLFLNGLNCLWHS DSSFRPIPAKFSLLSARVVNPKGGNTEFADM 147

Query: 142 RAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVH 201
          RAAYDALD+ T+ + HSL+YS+ LG + Y + L+ LV+ H
Sbjct: 148 RAAYDALDDETKTEIDDMICEHSLMYSRGSLGFLD-----YTDEEKEMFKPVLQRLVVRTH 202

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
          P GR SL + HA AI GM E+ L L + A Q V+ H+W D+V+WDNR
Sbjct: 203 PAHGRKSLYLSSHAGAIRGMSMPEARLLLLRDLTEHATQPEFVYVHKWTVHDLVMWDNRQT 262

Query: 262 LHRAEPWDFKLPRVMWHSRLAG 283
          +HR +D PR M + +AG
Sbjct: 263 VHRVRRYDQSQPRDMRRATVAG 284
```

>ref|ZP_07575535.1| Taurine catabolism dioxygenase TauD/TfdA [Sphingobium
chlorophenolicum L-1]
gb|EFN09579.1| Taurine catabolism dioxygenase TauD/TfdA [Sphingobium
chlorophenolicum L-1]
Length = 304

Score = 160 bits (405), Expect = 2e-37, Method: Compositional matrix adjust.
Identities = 103/288 (35%), Positives = 154/288 (53%), Gaps = 30/288 (10%)

```
Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L+ TP A G+ L L AA+ A ++ +++FP Q +S+D+Q FA++F
Sbjct: 14 LRCTPAHPHFAARAEGIDLRQPLTAEQKAAVKGAMDRYGVVFPNQMMSDDEQAFAEQF 73

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EW--DDMMKVI-VGNMAWHA 110
          GAIE RI I ISN+ DG + W DD ++ +GN+ WH+
Sbjct: 74 GAIEETPTLVDQERRRIANMKINDISNLGPDGQI-----WGADDRRRMYNLGNLLWHS 126

Query: 111 DSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS 170
          DS++ P A ++ A V+P VGG T + D R A+D L + +A+ A HSL+YS+
Sbjct: 127 DSSFKPTPAYWSMLQARVIPPVGGATEYIDTRVAWDHLPDELKAIARDLVAYHSLIYSRE 186

Query: 171 KLGHVQQAGSAYIGYGM-DTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF 229
          ++G A+ ++ T P R LV++H E+GR +L + H AI G E+
Sbjct: 187 QMGF-----DAFSPEEVERCTPVPQR-LVRLHKESGRLALYLSAHIGAIEGWPRPEAMAL 240

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPW-DFKLPRVM 276
          + L ++A Q P V+AHQWA GD+V+WDNRC +HR + D K PR M
Sbjct: 241 IRELTEFATQRPFVYAHQWAVGDLVIWDNRCTMHRGTRFDDKKYPRDM 288
```

>dbj|BAB92965.1| alpha KG dependent 2,4-D dioxygenase [alpha proteobacterium HWK12]
Length = 295

Score = 160 bits (405), Expect = 2e-37, Method: Compositional matrix adjust.

Identities = 97/262 (37%), Positives = 135/262 (51%), Gaps = 23/262 (8%)

```
Query: 35  LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
          + A  ++A+L+F GQ +S+DQQ+ FA FG E GG + +SN+
Sbjct: 33  IEAGMDKYAVLVFHGQDISDDQQMAFALNFGKRENARGGTVTKKEDYRLSSGLNDVSNLG 92

Query: 83  ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM 141
          DG P D + +GN WH+DS++ P+ A+ ++ SA VV GG T FADM
Sbjct: 93  KDG-----KPLPKDHRTHLFLNLGNCLWHSDDSSFRPIPAKFSLLSARVVNPKGGNTEFADM 147

Query: 142 RAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVH 201
          RAAYDALD+ TRA + HSL+YS+ LG + Y L+ LV+ H
Sbjct: 148 RAAYDALDDETRAIEIDDMICEHSLMYSRGSLGFLD-----YTDEEKQMFKPVLQRLVRTH 202

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
          P GR SL + HA AI GM E+ L L + A V+ H+W D+V+WDNR
Sbjct: 203 PGHGRSLYLSSHAGAIRGMSVPEARVLLRDLNEHATSPEFVYVHKWTVHDLVMWDNRQT 262

Query: 262 LHRAEPWDFKLPRVMWHSRLAG 283
          +HR +D PR M + +AG
Sbjct: 263 MHRVRRYDQSQPRDMRRATVAG 284
```

>ref|YP_001203232.1| alpha-ketoglutarate-dependent 2, 4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium sp. ORS278]
emb|CAL74995.1| Alpha-ketoglutarate-dependent 2, 4-dichlorophenoxyacetate
dioxxygenase (EC 1.14.11.-) (2,4-D dioxxygenase)
[Bradyrhizobium sp. ORS278]
Length = 295

Score = 158 bits (400), Expect = 8e-37, Method: Compositional matrix adjust.
Identities = 103/285 (36%), Positives = 146/285 (51%), Gaps = 36/285 (12%)

```
Query: 19  VTGV---HLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDI 75
          V+GV H T D+ A L AA +A+L+F Q + ++QQ+ FA FG E+ GG +
Sbjct: 16  VSGVDLRHPLTRDEV--AELQAAIDHYAVLVFHDQDIGDEQQLAFALNFGDREKARGGTV 73

Query: 76  VA-----ISNVKADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGA 122
          +SN+ DG P D + +GN WH+DS++ P+ A+ +
Sbjct: 74  TKKEDYRLTTGLNDVSNLGKDG-----KPLPPDHRTHLFLNLGNCLWHSDDSSFRPIPAKYS 128

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
          + SA +V GG T FADMRAAYDALDE T+A + + HSL+YS+ LG +
Sbjct: 129 ILSARIVNPKGGNTEFADMRAAYDALDEQTKAEIDDLVSEHSLMYSRGSLG-----F 180

Query: 183 IGYGMDTTATPLRP----LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC 238
          + Y D +P LV+ HP GR SL + HA A+ GM E L L + A
Sbjct: 181 LDY-TDEEKKMFKPVRQRLVRTHPAHGRKSLYLSSHAGAVVGMSMEGRLLLRDLTEHAT 239

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          Q V+ H+W D+V+WDNR +HR +D PR M + +AG
Sbjct: 240 QPEFVYVHKWRLHDLVMWDNRQTVHRVRRYDQSQPRDMRRATVAG 284
```

>ref|YP_001242758.1| Alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium sp. BTAi1]
gb|ABQ38852.1| 2,4-dichlorophenoxyacetate monooxygenase [Bradyrhizobium sp. BTAi1]
Length = 295

Score = 157 bits (398), Expect = 1e-36, Method: Compositional matrix adjust.
Identities = 95/265 (35%), Positives = 137/265 (51%), Gaps = 25/265 (9%)

```
Query: 33  AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISN 80
```

```

      A L A  +A+L+F  Q  +++++QQ+ FA  FG  E+  GG  +          +SN
Sbjct: 31  AELQTAIDHYAVLVFHDQDITDEQQALAFALSFGEREQARGGTVTKKEDYRLTTGLNDVSN 90

Query: 81  VKADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCF 139
      +  DG      P  D      +  +GN  WH+DS++ P+ A+ ++ SA +V  GG T FA
Sbjct: 91  LGKDG-----RPLPRDHRTHLFNLGNCLWHSDDSSFRPIPAKYSILSARIVNPKGGNTEFA 145

Query: 140  DMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRP-LV 198
      DMRAAYDALD  T+A +      HSL+YS+  LG  +  +      +      P+R  LV
Sbjct: 146  DMRAAYDALDPETKAEIEDLVCEHSLMYSRGALGFLDYSDEEKEMF-----KPVRQRLV 199

Query: 199  KVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDN 258
      + HP  GR SL +  HA A+ GM  E      L  L + A Q  VH H+WA  D+++WDN
Sbjct: 200  RTHPAHGRKSLYLSSHAGAVVGMSLPEGRLLLRDLTEHATQREFVHVHKWALHDLIMWDN 259

Query: 259  RCLLHRAEPWDFKLPRVMWHSRLAG 283
      R  +HR  +D  PR M  + +AG
Sbjct: 260  RQTMHRVRRYDQSQPRDMRRATVAG 284

```

>ref|ZP_02186322.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [alpha proteobacterium BAL199]
gb|EDP66559.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [alpha proteobacterium BAL199]
Length = 295

Score = 156 bits (394), Expect = 4e-36, Method: Compositional matrix adjust.
Identities = 102/295 (34%), Positives = 150/295 (50%), Gaps = 23/295 (7%)

```

Query: 1  MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
      MA +  I P      A VTG+ +A  + A  + A  ++A+L+FP Q +++DQQ
Sbjct: 1  MALSIROPINPKRDDFVAEVTGLDIAAGVSKAVAEIEIDAINRYAVLVFPEQRVNDQQYV 60

Query: 60  FAKRFGAIERIGGG-----DIVAISNVKADGTVRQHSPAEWDDMMKVI-VGNMA 107
      F+  FG +E  G      DI  ISN+  +G V Q      DD  ++  +GNM
Sbjct: 61  FSTHFGPMETATGDIAAQGDRRLSMDINDISNLDKNGQVLQR-----DDRRRLFGLGNML 115

Query: 108  WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
      WH DS++  A+ ++ SA  +P  GG T  FADMRAA+D LD  T+A +  A HS +Y
Sbjct: 116  WHTDSSFKAATPAKFSLLSARTIPGEGGNTEFADMRAAWDDLDPKTQADLMPLVAEHSQLY 175

Query: 168  SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
      S+  LG  Q      +      P R +V+ HP +GR S+ +  HA  I G  E+
Sbjct: 176  SRGLLGFDQFTDEERAKWA----PVPQR-MVRRHPGSGRLSVFLASHAGTIQGWPIPEAR 230

Query: 228  RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLA 282
      F+  L  + A Q      +AH+W  D+V+WDNR ++HRA  +D  PR M  + +A
Sbjct: 231  MFIRDLTEHATQREYTYAHRWRQYDLVMWDNRVAMHRARRYDHTQPRDMHRTTVA 285

```

>ref|YP_002944024.1| Taurine catabolism dioxygenase TauD/TfdA [Variovorax paradoxus
S110]
gb|ACS18758.1| Taurine catabolism dioxygenase TauD/TfdA [Variovorax paradoxus
S110]
Length = 293

Score = 152 bits (385), Expect = 4e-35, Method: Compositional matrix adjust.
Identities = 98/296 (33%), Positives = 150/296 (50%), Gaps = 23/296 (7%)

```

Query: 4  TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
      ++L++TP      A  G+ +  L  +  ++AA  ++A+L++ GQ L+  QQI FAK
Sbjct: 2  SSLELTPLHPLFAAEARGIDIRQPLSPSEVKQINAAMNRYAVLVWRGQPLTGQQQIDFAK 61

```

Query: 63 RFGAI-----ERIGGGDIVAISNVKADGTV-RQHSPA EWDDMMKVIVGNMAWHA 110
FG + ER+ ++ ISNV A+G V R+ SP + N WH+
Sbjct: 62 AFGPLDLGLKKVFKRPERLEDERLIDISNVDAEGKVARRDSPKNLSNF-----ANQLWHS 116

Query: 111 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS 170
DS++ A ++ A V+P+ GG T FA++RAAYDAL E TR+ + A H ++++
Sbjct: 117 DSSFQNPRAAYSMLHALVLPWGGNTEFAELRAAYDALPERTRSEIEGLRAEHYALHTRI 176

Query: 171 KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFL 230
LG AY + PL + HP +GR L +G HA I G AE FL
Sbjct: 177 LLG-----DEAYTDDQKKAIPPAVWPLAQTHPGSGRKL LFGVGHAREIIGWPVAEGRMFL 231

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPE 286
L++ A + V+ H+W GD+V+WDNR LHR +D R + + + PE
Sbjct: 232 SDLLEHATRREFVYTHEWQVGD LVMWDNRSTLHRGRRYDIGERRELRRTTIEDVPE 287

>ref|NP_768133.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium japonicum USDA 110]
dbj|BAC46758.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium japonicum USDA 110]
Length = 295

Score = 151 bits (382), Expect = 9e-35, Method: Compositional matrix adjust.
Identities = 91/262 (34%), Positives = 132/262 (50%), Gaps = 23/262 (8%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ +A ++A+L+F Q ++++QQ+ FA FG E GG + +SN+
Sbjct: 33 VESAMDKYAVLVFHDQDITDEQQMAFALNFGQREDARGGTVTKEKDYRLQSG LNDVSNLG 92

Query: 83 ADGTVRQHSPA EWDDMMKVI-VGNMAWHDSTYMPVMAQGAVFSAEVVPAVGGRTCFADM 141
DG P D + +GN WH+DS++ P+ A+ ++ SA VV GG T FADM
Sbjct: 93 KDG-----KPLAKDSRTHLFNLGNCLWHS DSSFRPIPAKFSLLSARVVNPTGGNTEFADM 147

Query: 142 RAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVH 201
RAAYDALD+ T+A + HSL+YS+ LG + Y L+ LV+ H
Sbjct: 148 RAAYDALDDETKAEIEDLVCEHSLMYSRGSLGFTE-----YTDEEKQMFKPVLQRLVRTH 202

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
P R SL + HA I M E L L + A Q V+ H+W D+V+WDNR
Sbjct: 203 PVHRRKSLYLSSHAGKIASMSVPEGRLLLRDLNEHATQPEFVYVHKWKLHDLVMWDNRQT 262

Query: 262 LHRAEPWDFKLPRVMWHSRLAG 283
+HR +D PR M + +AG
Sbjct: 263 MHRVRRYDQSQPRDMRRATVAG 284

>ref|YP_001206007.1| TauD/TfdA family dioxxygenase [Bradyrhizobium sp. ORS278]
emb|CAL77782.1| putative TauD/TfdA family dioxxygenase [Bradyrhizobium sp. ORS278]
Length = 308

Score = 151 bits (382), Expect = 1e-34, Method: Compositional matrix adjust.
Identities = 96/295 (32%), Positives = 149/295 (50%), Gaps = 30/295 (10%)

Query: 3 QTTLQITPTGATLGATVTVGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
+++++I PTGA LGA V V L LDD FA+L A+ H++L+ GQ+L++ I F++
Sbjct: 25 RSSIEIVPTGAALGA EVNRNVDLRHLDDQAFASLLQAFHDH SVLLVRGQNLT DQDLIAFSR 84

Query: 63 RFGAIE-----RIGGG--DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHD 111
RFG ++ R G +I +SNVK +G + + G WH D
Sbjct: 85 RFGDLDFAPIQENGRRFVDGLPEIYIVSNVKVNGEA-----IGSLGAGEAVWHTD 134

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171

```

      +Y+      +   A  +P VGG T F   M A YDAL      +A +      +H   Y+
Sbjct: 135 MSYLDTPPIASALYALEIPVGGNTSFCSMYAVYDALPADLKARIADLKIKHDGTNSG- 193

Query: 172 LGHVQQAGSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESER 228
      G V+Q      +   D   +P  + PLV  HP++GR  L +GR  +A + G++ AESE
Sbjct: 194 -GFVRQG-----VTPTDDPRTSPGAVHPLVCTHPDSCRQMLYLGRRRNAYLTGLELAESEA 248

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
      L+ +      +   H W  GD+V+WDNRC +HR +P+D      R+M  +++ G
Sbjct: 249 LLDEIWITHVARPAFAWEHAWKVGDLVIWDNRCTMHRDPFDDHSRRIMHRTQIKG 303

```

>gb|ADC33952.1| TfdA-like protein [uncultured bacterium]
Length = 123

Score = 150 bits (380), Expect = 2e-34, Method: Compositional matrix adjust.
Identities = 71/126 (56%), Positives = 89/126 (70%), Gaps = 3/126 (2%)

```

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
      T F DMRAA+DALD A R  +   +A HS+ YSQS+LG+      + Y   G      PLR
Sbjct: 1   TEFCDMRAAWDALDPAMRKKLEGLNAYHSIYYSQSRLYGTHGTDNLY---GFHDKGEPLR 57

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
      P+VK HPETGR S+  GRHAH IPGMD AESERFL+ L+++AC+APR + H+W  GD+VV
Sbjct: 58  PVVKTHPETGRKSIYTGRAHGIPGMDPAESERFLDDLLEFACRAPRTYLHRWTLGDLVV 117

Query: 256 WDNRCV 123
      WDNRC+
Sbjct: 118 WDNRCV 123

```

>emb|CBJ20067.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 138

Score = 149 bits (377), Expect = 4e-34, Method: Compositional matrix adjust.
Identities = 78/141 (55%), Positives = 96/141 (68%), Gaps = 3/141 (2%)

```

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
      M V A  ++ SA V P+ GG+T +ADMRAAYDALD+A R  +   SA HSL YSQS++GH
Sbjct: 1   MRVSALASILSAHVTPSHGGQTEWADMRAAYDALDDAVRTRIEGLSAFHSRLYSQSQIGH 60

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
      +AGS+Y   G+      PLRPLVK HP  TGR SL IGRHA+ IPG+  ES+  L  LV
Sbjct: 61  DAKAGSSY---GLSEDIPPLRPLVKTHPVTGRKSLFIGRHAYGIPGLAEDESKALLSELV 117

Query: 235 DWACQAPRVHAHQWAAGDVVV 255
      D+AC+ PR +AH W  GDV V
Sbjct: 118 DFACRPRTYAHAWTPGDVAV 138

```

>ref|YP_001240346.1| TauD/TfdA family dioxygenase [Bradyrhizobium sp. BTAi1]
gb|ABQ36440.1| putative TauD/TfdA family dioxygenase [Bradyrhizobium sp. BTAi1]
Length = 296

Score = 149 bits (377), Expect = 4e-34, Method: Compositional matrix adjust.
Identities = 97/298 (32%), Positives = 150/298 (50%), Gaps = 32/298 (10%)

```

Query: 5   TLQITPTGATLGATVTGVHLATLDDAGFAALHAALQHALLIFFGQHLSNDQQITFAKRF 64
      ++I PT  +LGA +   V L  LDDA FAA+  A+  H++L+  GQHLS+   I F++RF
Sbjct: 15  NIEIVPTDRSLGAEIRNVDLRQLDDAAFAAVLRAFHTHSVLLVRGQHLSQDLIAFSRRF 74

Query: 65  GAIE-----RIGGG--DIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADST 113

```

G ++ R G +I +SNVK +G + + G WH D +
Sbjct: 75 GDLDWAPVQENGRRFVEGLPEIYIVSNVKVNGEA-----IGSLGAGEAVWHTDMS 124

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
Y+ + A +P VGG T F M A YDAL + + +H Y+ G
Sbjct: 125 YLETPPIASALYALEIPPVGNTSFCSMYAVYDALPTLKHRIADLKIKHDTYNSG--G 182

Query: 174 HVQQAGSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFL 230
V+Q + D ++P + PLV HP++GR L +GR +A + G++ AESE L
Sbjct: 183 FVRQG----VTPTDDPRSSPGAVHPLVCTHPDSEGRQMLYLGRRRNAYLVGLELAESEALL 238

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG--RPE 286
+ L + + H W GD+V+WDNR +HR +P+D + R+M +++ G RP+
Sbjct: 239 DELWTTYVARPEFAWEHVWQVGDVLIWDNRSTMHRRDPFDDQARRIMHRTQIKGTERPQ 296

>ref|ZP_02187434.1| Taurine catabolism dioxygenase TauD/TfdA [alpha proteobacterium
BAL199]
gb|EDP65776.1| Taurine catabolism dioxygenase TauD/TfdA [alpha proteobacterium
BAL199]
Length = 295

Score = 148 bits (374), Expect = 8e-34, Method: Compositional matrix adjust.
Identities = 92/287 (32%), Positives = 140/287 (48%), Gaps = 25/287 (8%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L IT +G V G+ L LD G L++ W++H +L+FP Q ++++QQI FA+ F
Sbjct: 8 LAITRRHPLIGTEVRGIDLTPLDRDGLDRLNSIWMHPLVFPNQKITDEQQIVFARNF 67

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMP 116
G +E ++ +SNV G + EW + + WH DS++
Sbjct: 68 GELEVHPSVAHRSSKNPEVYRVSNVDEQGNILPSESKEW----QYLELTWLWHTDSSFRE 123

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS---LVYSQSKLG 173
+ + G++ VP GG T FA+M AAY+AL + T+A + + RHS ++ +KL
Sbjct: 124 IPSMGSILHGIEVPKDGGDTLFANMYAAYEALSDBGTKAEIEGLTVRHSDDAVIARSALKS 183

Query: 174 HVQQAGSAYIGYGMDDTTATPL-RPLVKVHPETGRPSLLIGRHA-HAIPGMDAAESERFLE 231
Q G+ T P+ +PLV+ HP TGR SL + H I GM + L+
Sbjct: 184 ARQDKGTY-----TELPPEQPLVRRHPVTGRRSLFLSPHTMDGIVGMPNDKGFALLD 236

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWH 278
L A V+ H W DV++WDNRC +H P+D R + H
Sbjct: 237 DLTKHATHERFVYRHSWHQDDVIMWDNRCTMHAVMPYDSANQRRIMH 283

>ref|NP_990895.1| TfdA [Achromobacter denitrificans]
gb|AAS49436.1| TfdA [Achromobacter denitrificans]
Length = 287

Score = 148 bits (374), Expect = 9e-34, Method: Compositional matrix adjust.
Identities = 94/251 (37%), Positives = 125/251 (49%), Gaps = 28/251 (11%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQ 89
Q A+L+F GQ L DQOI FA+ FG +E R ++ ISNV DG VR+
Sbjct: 39 QKAVLVFRGQPLDQDQQIAFARNFGQLEGGFIVKVNQRPSRFKYAELADISNVSVDGKVVRE 98

Query: 90 HSPAEDDMMKVIVGNMA---WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYD 146
E +VGN A WH+DS++ A+ ++ SA V+P GG T F DMRAAYD
Sbjct: 99 RDARE-----VVGNFANQLWHSDDSSFQQAARYSMLSAILVPPSGGDTEFCDMRAAYD 151

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVHPETG 205
L E + + A H + S+ LG + S P+ PLV+ H +G

Sbjct: 152 DLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWPLVRTHAGSG 205

Query: 206 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
 R L IG HA I G AE L L++ A Q V+ H W GD+V+WDNRC+LHR

Sbjct: 206 RKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQPKFVYRHSWKVGDLVMWDNRCVLHRG 265

Query: 266 EPWDFKLPRVM 276
 +D R +

Sbjct: 266 RRYDITARREL 276

>gb|ACF35465.1| TfdA [Burkholderia sp. TFD36]
 gb|ACF35466.1| TfdA [Burkholderia sp. TFD6]
 gb|ACF35467.1| TfdA [Burkholderia sp. TFD2]
 gb|ACF35468.1| TfdA [Burkholderia tropica]
 gb|ACF35469.1| TfdA [Burkholderia sp. TFD4]
 gb|ACF35470.1| TfdA [Burkholderia sp. TFD17]
 gb|ACF35471.1| TfdA [Burkholderia sp. TFD20]
 gb|ACF35472.1| TfdA [Burkholderia sp. TFD21]
 gb|ACF35473.1| TfdA [Burkholderia sp. TFD23]
 gb|ACF35474.1| TfdA [Burkholderia sp. TFD28]
 gb|ACF35475.1| TfdA [Burkholderia sp. TFD31]
 gb|ACF35476.1| TfdA [Burkholderia sp. TFD32]
 gb|ACF35477.1| TfdA [Burkholderia sp. TFD34]
 gb|ACF35478.1| TfdA [Burkholderia sp. TFD52]
 Length = 297

Score = 148 bits (373), Expect = 1e-33, Method: Compositional matrix adjust.
 Identities = 94/259 (36%), Positives = 129/259 (49%), Gaps = 28/259 (10%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQ 89
 Q A+L+F GQ L DQOI FA+ FG +E R ++ ISNV DG V +
 Sbjct: 39 QKAVLVFRGQPLDQDQQIAFARNFGQLEGGFIVNQRPSRFKYAELADISNVSVGKVAE 98

Query: 90 HSPAEDDDMMKVIVGNMA---WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYD 146
 E +VGN A WH+DS++ A+ ++ SA V+P GG T F DMRAAYD
 Sbjct: 99 RDARE-----VVGNFANQLWHSDDSSFQQAARYSMLSAIVLPPSGGDTEFCDMRAAYD 151

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVHPETG 205
 L E + + A H ++S+ LG + + S P+ PL++ H +G
 Sbjct: 152 DLPEDFKKELQGLRAEHYALHSRFILGDTYESES-----QRNAMPPVSWPLIRTHAGSG 205

Query: 206 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
 R L IG HA I G AE L L++ A Q V+ H W GD+V+WDNRC+LHR
 Sbjct: 206 RKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQPKFVYRHSWKVGDLVMWDNRCVLHRG 265

Query: 266 EPWDFKLPRVMWHSRLAGR 284
 +D R + + GR

Sbjct: 266 RRYDVTARRELRRATTGLGR 284

>sp|Q45423.1|TFDA_BURSR RecName: Full=Alpha-ketoglutarate-dependent
 2,4-dichlorophenoxyacetate dioxygenase; Short=2,4-D
 dioxygenase
 gb|AAB17363.1| 2,4-dichlorophenoxyacetate alpha-ketoglutarate dioxygenase
 [Burkholderia sp. RASC]
 Length = 297

Score = 147 bits (372), Expect = 1e-33, Method: Compositional matrix adjust.
 Identities = 96/259 (37%), Positives = 131/259 (50%), Gaps = 28/259 (10%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQ 89
 Q A+L+F GQ L DQOI FA+ FG +E R ++ ISNV DG V

Sbjct: 39 QKAVLVFRGQPLDQDQQIAFARNFGQLEGGFIKVNQRPSRFKYAELADISNVSDGKV-- 96

Query: 90 HSPAEDDDMMKVIVGNMA---WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYD 146
AE D + +VGN A WH+DS++ A+ ++ SA V+P GG T F DMRAAYD

Sbjct: 97 ---AEAD--AREVVGNFANQLWHSDDSSFQQAARYSMLSAIVLPPSGGDTEFCDMRAAYD 151

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR-PLVKVHPETG 205
L E + + A H ++S+ LG + + S P+ PL++ H +G

Sbjct: 152 DLPEDFKKELQGLRAEHYALHSRFLGDTEYSES-----QRNAMPVSWPLIRTHAGSG 205

Query: 206 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
R L IG HA I G AE L L++ A Q V+ H W GD+V+WDNRC+LHR

Sbjct: 206 RKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQPKFVYRHSWKVGDLVMWDNRCVLHRG 265

Query: 266 EPWDFKLPRVMWHSRLAGR 284
+D R + + GR

Sbjct: 266 RRYDVTARRELRRATTGLR 284

>ref|YP_025400.1| 2,4-D / a-ketoglutarate dioxygenase [Ralstonia eutropha JMP134]
ref|YP_293634.1| taurine catabolism dioxygenase TauD/TfdA [Ralstonia eutropha JMP134]
sp|P10088.1|TFDA_RALEJ RecName: Full=Alpha-ketoglutarate-dependent
2,4-dichlorophenoxyacetate dioxygenase; Short=2,4-D
dioxygenase
gb|AAA21983.1| 2,4-dichlorophenoxyacetate monooxygenase (gtg start codon)
[Cupriavidus necator]
gb|AAR31052.1| 2,4-D / a-ketoglutarate dioxygenase [Ralstonia eutropha JMP134]
gb|AAZ65777.1| Taurine catabolism dioxygenase TauD/TfdA [Ralstonia eutropha JMP134]
gb|ACF35489.1| TfdA [Burkholderia sp. TFD19]
gb|ACF35490.1| TfdA [Cupriavidus sp. TFD33]
gb|ACF35491.1| TfdA [Cupriavidus sp. TFD38]
gb|ACF35492.1| TfdA [Pseudomonas sp. TFD39]
gb|ACF35493.1| TfdA [Cupriavidus sp. TFD51]
gb|ACF35494.1| TfdA [Ralstonia eutropha JMP134]
Length = 287

Score = 147 bits (371), Expect = 2e-33, Method: Compositional matrix adjust.
Identities = 92/251 (36%), Positives = 128/251 (50%), Gaps = 28/251 (11%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQ 89
+ ++L+F GQ LS DQOI FA+ FG +E R ++ ISNV DG V Q

Sbjct: 39 EKSVLVFRGQPLSQDQQIAFARNFGPLEGGFIKVNQRPSRFKYAELADISNVSLDGKVAQ 98

Query: 90 HSPAEDDDMMKVIVGNMA---WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYD 146
E +VGN A WH+DS++ A+ ++ SA VVP GG T F DMRAAYD

Sbjct: 99 RDARE-----VVGNFANQLWHSDDSSFQQAARYSMLSAVVVPPSGGDTEFCDMRAAYD 151

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR-PLVKVHPETG 205
AL ++ + A H + S+ LG + + P+ PLV+ H +G

Sbjct: 152 ALPRDLQSELEGLRAEHYALNSRFLLGDTDYSEA-----QRNAMPVNWPLVRTHAGSG 205

Query: 206 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
R L IG HA + G+ AE L L++ A Q V+ H+W GD+V+WDNRC+LHR

Sbjct: 206 RKFLFIGAHASHVEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGDLVMWDNRCVLHRG 265

Query: 266 EPWDFKLPRVM 276
+D R +

Sbjct: 266 RRYDISARREL 276

>gb|ACF35485.1| TfdA [Achromobacter xylosoxidans]

gb|ACF35486.1| TfdA [Achromobacter xylosoxidans]
gb|ACF35487.1| TfdA [Cupriavidus sp. TFD42]
gb|ACF35488.1| TfdA [Burkholderia sp. TFD29]
Length = 287

Score = 146 bits (369), Expect = 3e-33, Method: Compositional matrix adjust.
Identities = 92/251 (36%), Positives = 128/251 (50%), Gaps = 28/251 (11%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQ 89
+ ++L+F GQ LS DQOI FA+ FG +E R ++ ISNV DG V Q
Sbjct: 39 EKSVLVFRGQPLSQDQQIAFARNFGPLEGGFIKVNQRPSRFKYAELADISNVSLDGKVAQ 98

Query: 90 HSPAEDDDMMKVIVGNMA---WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYD 146
E +VGN A WH+DS++ A+ ++ SA VVP GG T F DMRAAYD
Sbjct: 99 RDARE-----VVGNFANQLWHSDDSSFQQPAARYSMLSAVVPPSGGDTEFCDMRAAYD 151

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR-PLVKVHPETG 205
AL ++ + A H + S+ LG + + P+ PLV+ H +G
Sbjct: 152 ALPRDLQSELEGLRAEHYALNSRFLLGDTDYSEA-----QRNAMPPVNWPLVRTHAGSG 205

Query: 206 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
R L IG HA + G+ AE L L++ A Q V+ H+W GD+V+WDNRC+LHR
Sbjct: 206 RKFLFIGAHAGHVEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGDLMWDNRCLVLRH 265

Query: 266 EPWDFKLPRVM 276
+D R +
Sbjct: 266 RRYDISARREL 276

>gb|AAM76772.1| 2,4-D/alpha-ketoglutarate dioxygenase [Delftia acidovorans]
Length = 287

Score = 146 bits (368), Expect = 3e-33, Method: Compositional matrix adjust.
Identities = 93/251 (37%), Positives = 125/251 (49%), Gaps = 28/251 (11%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQ 89
Q A+L+F GQ L DQOI FA+ FG +E R ++ ISNV DG V +
Sbjct: 39 QKAVLVFRGQPLDQDQQIAFARNFGQLEGGFIKVNQRPSRFKYAELADISNVSDGKVAE 98

Query: 90 HSPAEDDDMMKVIVGNMA---WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYD 146
E +VGN A WH+DS++ A+ ++ SA V+P GG T F DMRAAYD
Sbjct: 99 RDARE-----VVGNYANQLWHSDDSSFQQPAARYSMLSAIVLPPSGGDTEFCDMRAAYD 151

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR-PLVKVHPETG 205
L E + + A H ++S+ LG + S P+ PLV+ H +G
Sbjct: 152 DLPEDFKKELQGLRAEHYALHSRFLGDTDYSES-----QRNAMPPVSWPLVRTHAGSG 205

Query: 206 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
R L IG HA I G AE L L++ A Q V+ H W GD+V+WDNRC+LHR
Sbjct: 206 RKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQRFVYRHSWKVGDLMWDNRCLVLRH 265

Query: 266 EPWDFKLPRVM 276
+D R +
Sbjct: 266 RRYDITARREL 276

>gb|ADI17634.1| probable taurine catabolism dioxygenase [uncultured alpha
proteobacterium HF0130_20P23]
Length = 290

Score = 146 bits (368), Expect = 4e-33, Method: Compositional matrix adjust.
Identities = 84/287 (29%), Positives = 144/287 (50%), Gaps = 14/287 (4%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++I G VTG+ L A+H ++A+L F Q L+ ++Q+ F+K+
Sbjct: 3 VEIRQVGECEFAEVTGIDFTEPLSTENVNAIHEGMDKYAVLFRKQPLTAEQLAFSKQL 62

Query: 65 GAIERIGGGDIVAISNVKADGTV-----RQHSPAEWDDMMKVI-VGNMAWHADSTYMP 116
G IE G + + + T ++ P + +D ++ +GN WH+DS++
Sbjct: 63 GDIEHAIGTSLREDKDARLPSTFADVSNLDKEDRPFIDINDRRRLFAIGNRLWHS DSSFKV 122

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
V A+ ++ A +P+ GG T FA M +AYDALD+ + + HS ++S+ ++G
Sbjct: 123 VPAKYSILHAISIPSKGGNTEFAHMPSAYDALDDEIKEELDGLICEHSQIFSRQQVGF-- 180

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW 236
+ + +D + L++ HP TGR SL + HA I G+ +++ L LV+
Sbjct: 181 ---TDFTEEIDRFKPVRLIRKHPATGRKSLYLSSHAGRIDGLSVPDAKLLLLLDLVNH 237

Query: 237 ACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
A Q V+ H+W GD+V+WDNR +HR P+ PR M + + G
Sbjct: 238 ATQQKFVYVHEWQKGDLMWDNRQTMHRVRPFPVDEPRDMRRTTIVG 284

>gb|AAK81681.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia cepacia]
gb|ACF35479.1| TfdA [Variovorax soli]
gb|ACF35480.1| TfdA [Cupriavidus sp. TFD45]
gb|ACF35481.1| TfdA [Cupriavidus sp. TFD40]
gb|ACF35482.1| TfdA [Cupriavidus respiraculi]
gb|ACF35483.1| TfdA [Pseudomonas putida]
gb|ACF35484.1| TfdA [Pseudomonas sp. TFD50]
Length = 287

Score = 145 bits (366), Expect = 7e-33, Method: Compositional matrix adjust.
Identities = 93/251 (37%), Positives = 124/251 (49%), Gaps = 28/251 (11%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQ 89
Q A+L+F GQ L DQQI FA+ FG +E R ++ ISNV DG V +
Sbjct: 39 QKAVLVFRGQPLDQDQQIAFARNFGQLEGGFIVNQRPSRFKYAELADISNVSVDGKVAE 98

Query: 90 HSPAEWDDMMKVIVGNMA---WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYD 146
E +VGN A WH+DS++ A+ ++ SA V+P GG T F DMRAAYD
Sbjct: 99 RDARE-----VVGNFANQLWHS DSSFQQAARYSMLSAIVLPPSGGDTEFCDMRAAYD 151

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVHPETG 205
L E + + A H + S+ LG + S P+ PLV+ H +G
Sbjct: 152 DLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVSWPLVRTHAGSG 205

Query: 206 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
R L IG HA I G AE L L++ A Q V+ H W GD+V+WDNRC+LHR
Sbjct: 206 RKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDLMWDNRCVLHRG 265

Query: 266 EPWDFKLPRVM 276
+D R +
Sbjct: 266 RRYDITARREL 276

>gb|ACF98189.1| putative TauD/TfdA family dioxygenase [uncultured bacterium 1114]
Length = 287

Score = 144 bits (362), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 89/272 (32%), Positives = 139/272 (51%), Gaps = 22/272 (8%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
++TT + P AT+GA + + ++ D + AA+ QH LL F GQ L+++Q FA
Sbjct: 7 SRTTARFQPLSATMGADTSDIDVSHADAVPMDDVLAARFQHLLSFRGQTLTDEQIYNFA 66

Query: 62 KRFGAIE----RIGGGDIVA----ISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST 113
+FG +E R G ++A I+N+ ADG P+ D+ + N WH+D +
Sbjct: 67 AKFGPVEQNKRRYADGTVMASVHGITNL DADG-----KPSSRPDVRE----NYYWHS DKS 117

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
+ V A + +P GG T FADM AY AL T+ + HS Y + +
Sbjct: 118 HQEVPALT TMLYGVEIPPAGGETEFADMTRAYAALPPETKRRIDDLKVEHSWGYMRET V- 176

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
AG A + + PLV++HP+TG SL +G + + GMD +E L+ +
Sbjct: 177 ----AGLAPTEEEKLKSPPIVHPLVRIHPDTGAKSLYVGM YCSR VIGMDVSEGREL LKEM 232

Query: 234 VD WACQAPRVHAHQWAAGDVVW DNRCL LHRA 265
+D A + + ++W GD+V+W DNRCL+HRA
Sbjct: 233 IDHATRPEFLFRYKWRQGD LVMW DNRCLVHRA 264

>ref|YP_611286.1| taurine catabolism dioxygenase TauD/TfdA [Ruegeria sp. TM1040]
gb|ABF62024.1| Taurine catabolism dioxygenase TauD/TfdA [Ruegeria sp. TM1040]
Length = 294

Score = 142 bits (357), Expect = 8e-32, Method: Compositional matrix adjust.
Identities = 89/282 (31%), Positives = 138/282 (48%), Gaps = 18/282 (6%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDA-GFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
TT++ P G V+G+ L+ + FA L + +H+ L+F Q +SN++ + A+
Sbjct: 2 TTIETKPLTPCFGVEVSGMTLSEVSKGHDFARLRDLFEEHSALLFRAQEISNEEHMALAQ 61

Query: 63 RFGAIE-----RIGGG--DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTY 114
FG IE R G ++ +SNV+ DGT + E D + N WH+DST+
Sbjct: 62 LFGPIEDRKADERKPGAEFEVPEVSNVQKDGT----TSGEMDLHTLNLKSNFLWHS DSTF 117

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
+P A + VV GG T A RAA+ A+ E ++ + R H +S+ K+
Sbjct: 118 LPTPALTNILIGRVVTTTEGGATELASTRAAWAAMPEELKSRI RGRGIWHRYSHSRRKIS- 176

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
+ A D + + P +P GR L I HA + G D AES+ L+ L+
Sbjct: 177 PELAKLPMFNKWP DQHS AVWP---NPVNGREGLYIASHAFKVDGYDEAESQELLDEL M 232

Query: 235 DWACQAPRVHAHQWAAGDVVW DNRCL LHRAEPWDFKLPRVM 276
+ Q +AHQW GDV++WD R +LHR PW ++ PR +
Sbjct: 233 AFCTQPEFTYAHQWNVGDVLIWDQRAVLHRGTPWPYEQPRTL 274

>ref|YP_725771.1| taurine catabolism dioxygenase [Ralstonia eutropha H16]
emb|CAJ92403.1| probable taurine catabolism dioxygenase [Ralstonia eutropha H16]
Length = 265

Score = 141 bits (355), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 91/264 (34%), Positives = 134/264 (50%), Gaps = 26/264 (9%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T+QI P ++ A VTGV L LDDA F LH A+L+H +L+F GQ L Q+ FA+R
Sbjct: 3 TIQIKPLTGSVAAAVTGVDLNLQPLDDASFEILHRAFLEHGVLVFRGQQQLQPAAQVAFARR 62

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
+G + + G ++ G A+ + K AWH+DS Y V + ++
Sbjct: 63 WG--KP VQGNPLLK-----GLTEFP ELAQVTRIPKETASTEAWHS DSIYTEVPPKISI 113

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
SA +P +GG T + + +YD L A + ++ AR +S ++L +

Sbjct: 114 LSAVTIP-IGGDTMWCNQYVSYDRLSPAMQRMIDGLRAR----FSGARLARMT----- 161

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGR--HAHAIPGMDAAESERFLEGLVDWACQAP 241
G D T + P+V+ HPETGR +L +G A I GM AES L+ L + +

Sbjct: 162 --GSDKVPTAVHPIVRTHPETGRKALYVGHPDTAQCIEGMTEAESRPLLDFLYEHSVTPD 219

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRA 265
V+ H W GDVV+WDNRC +H A

Sbjct: 220 NVYRHMWQEGDVVMWDNRCTMHYA 243

>ref|ZP_02187618.1| Taurine catabolism dioxygenase TauD/TfdA [alpha proteobacterium
BAL199]
gb|EDP65960.1| Taurine catabolism dioxygenase TauD/TfdA [alpha proteobacterium
BAL199]
Length = 296

Score = 140 bits (353), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 88/279 (31%), Positives = 137/279 (49%), Gaps = 25/279 (8%)

Query: 2 AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
++ ++ P LGA + G+ L + +A FA ++ +L+ L++F L Q+ F

Sbjct: 13 SRRPFEVRPLHPALGAEIAGITLEEAVGEAVFAEIIYDVFLERGLILFHDVDLPPATQVAF 72

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHAD 111
A+RFG ++ +I ++N+ ADG P DM G M WH D

Sbjct: 73 ARRFGEVQVHVMNQYHGYADHPYIYRLANLDADGNPNGKHP---DM----GTMYWHTD 123

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
++ P + +E+VP+ GG T FADM AY++L + + A H+L +S+++

Sbjct: 124 GSWRPTTGATMMYSEMVPSEGGETHFADMYGAYESLSPQWKERLGLSLKAFHNLDFSRTR 183

Query: 172 LGHVQQAGSAYIGYGMDTTATPL-RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFL 230
+ G + P+ P+V+ HPETGR SL +G HA I GMD AE +

Sbjct: 184 -----RHGHDPMTTEEKAKVPPVAHPVVRTHPETGRKSLFLGDHAEWIDGMDYAEGRALI 238

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD 269
E + A V+ H W+ +VWDNRCLLHRA +D

Sbjct: 239 EEINAMATPDHLVYRHHWSRQCIVWDNRCLLHRATGYD 277

>ref|ZP_01894281.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Marinobacter algicola DG893]
gb|EDM47650.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Marinobacter algicola DG893]
Length = 301

Score = 140 bits (352), Expect = 3e-31, Method: Compositional matrix adjust.
Identities = 95/285 (33%), Positives = 144/285 (50%), Gaps = 34/285 (11%)

Query: 6 LQITPTGATLGATVTGVHLA---TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
+ I P A V V L+ + DD+ A+ A+ ++A+L+FPQG L+ +Q I FAK

Sbjct: 3 ISIYPITQNFAAEVDVLSKPLSADDS--EAIKEAFWRYAVLVFPGQSLTPEQHIAFAK 60

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVI-----VGNM 106
FG +E G + S D T + HS +E D+ + +GN

Sbjct: 61 EFGPLE---GENPTIASYRNRDVTTKSHS-SELADVSNLSPKNEVWTSGSRARMFHLGNQ 116

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
WH DS++ V A+ ++ A + +GG T FAD RAAYDAL EA + + A HS+

Sbjct: 117 LWHTDSSFHHVPARASLLYAREIAPIGGHTFADERAAAYDALPEAMKRRIEGLIAEHSIF 176

Query: 167 YSQSKLGHVQQAGSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGRHAHAIPGMDAA 224

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 + + + V+ H+W D++ WDNR L+H A
 Sbjct: 245 EHSVKEPHVYRHRWOPHDLIFWDNRSLMHLA 275

>emb|CBJ20072.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 138

Score = 138 bits (348), Expect = 9e-31, Method: Compositional matrix adjust.
Identities = 69/141 (48%), Positives = 91/141 (64%), Gaps = 3/141 (2%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MP+ ++ A+ +A VVP GG T FADMRAA+DALDE T+A + A HS+ YSQ++ G
Sbjct: 1 MPIASKAAMLAALVVPPEGGETEFADMRAAWDALDEDTQARLEGLCAYHSIYYSQARAGF 60

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
+ + Y G PLRP+VK HPETGR S+ GRHA+ IPG+ ESE L L+
Sbjct: 61 IHKTDHLY---GFHDKGAPLRPIVKTHPETGRKSIYTGRHAYGIPGLSETESETLLNKL 117

Query: 235 DWACQAPRVHAHQWAAGDVVV 255
D AC+ PR++ H W GD+VV
Sbjct: 118 DDACRPPRLYRHIWQPGDLVV 138

>emb|CBJ20071.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 138

Score = 138 bits (347), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 65/141 (46%), Positives = 92/141 (65%), Gaps = 3/141 (2%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MP+ ++ A+ A VVP GG T F+DMRAA+DALD+ +A + + SA HS+ YSQ ++G
Sbjct: 1 MPLASKAAMLYAVVVPPDGGETEFSDMRAAWDALDKTMQARLEKLSAYHSIYYSQEIQIF 60

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
V + Y G PLRP+++ HPETGR S+ GRHAH IPGM +S+ L+ L+
Sbjct: 61 VHKTQVY---GFHDKGAPLRPIIRTHPETGRKSIYTGRHAHDIPGMSKEDSKALLDKLI 117

Query: 235 DWACQAPRVHAHQWAAGDVVV 255
+ AC+ PR++ H W GD+VV
Sbjct: 118 EDACRPPRLYKHAWTTGDLVV 138

>ref|ZP_04945417.1| Probable taurine catabolism dioxygenase [Burkholderia dolosa
AU0158]
gb|EAY68588.1| Probable taurine catabolism dioxygenase [Burkholderia dolosa
AU0158]
Length = 317

Score = 137 bits (346), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 97/291 (33%), Positives = 146/291 (50%), Gaps = 32/291 (10%)

Query: 5 TLQITPTGATLGATV---TGVHLATLDDAGFA-ALHAAWLQHALLIFPGQHLNSNDQQQITF 60
+L++ P A V +G+ L + A A+ AA ++A+L+F GQ L+ DQQ+ F
Sbjct: 14 SLEVVPIDAARADVFGLASGIDLTSPVSERLACAIDAAMNRYAVLVFRGQPLTQDQQLAF 73

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMA-- 107
A+ G ++ R+ ++ ISNV G + + + + IVGN+A
Sbjct: 74 ARALGPLDLGFKRVARPHARLAYQELADISNVDESGQIAERT-----HRRIVGNLANQ 126

Query: 108 -WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
WH+DS++ A+ ++ A VVP GG T FADMRAA+DALD + + A H +
Sbjct: 127 LWHSDSSFQQPAARYSMLHAVVVPESGGGETEFADMRAAWDALDPREQRELEGLEAEHYAL 186

Query: 167 YSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAE 225

+S+ LG + P+R PLV+ H +GR L IG HA I G AE
Sbjct: 187 HSRFLLGDTDYSDE-----QRNALPPVRWPLVREHAGSGRRHLFIGAHATHIVGRTLAE 240

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276

L L++ A V++H+W GD+V+WDNRC LHR D + R +
Sbjct: 241 GRVLLMDLLEHATARRFVYSHRWLPGLDVIWDNRCTLHRGRRHDLNVRREL 291

>ref|NP_881979.1| putative taurine dioxygenase [Bordetella pertussis Tohama I]
ref|NP_887474.1| putative taurine dioxygenase [Bordetella bronchiseptica RB50]
emb|CAE43718.1| putative taurine dioxygenase [Bordetella pertussis Tohama I]
emb|CAE31424.1| putative taurine dioxygenase [Bordetella bronchiseptica RB50]
Length = 302

Score = 136 bits (343), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 93/296 (31%), Positives = 138/296 (46%), Gaps = 32/296 (10%)

Query: 4 TTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
+ + + P G GA V+G+ L L A L AAW +H +L+FPGQ L+ Q I F +
Sbjct: 2 SDITVRPLGYAAGAAVSGIDLRLQALQPEQLARLRAAWHEHLVLFVPGQDLNAPQLIDFTR 61

Query: 63 RFGAIERIGG-----GDIVASNVKADGTVRQHSPAEDDMMKVIVGNMAWHADST 113
FG +ER +++ ++N DG P++ + + WH+D +
Sbjct: 62 HFGDVERNDSVPYRDPDYEVLLVTNKPRDG----KPSQTRNTGR-----NWHSDLS 110

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH--SLVYSQSK 171
Y A+G+V + P VGG T FA+M AY++L + V A H SL+ +
Sbjct: 111 YTDPAKGSVLMCKEKPVGDDTMFANMYQAYESLSAPFKRFVDGLHAVHDISLIKGFDR 170

Query: 172 LGHVQQAGSAYIGYGMDTTATPL-RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFL 230
Q A + P+ P+V++HPETGR L + GM ES L
Sbjct: 171 RDPEQTAA-----LKRRNPPIAHPVVRHPETGRKCLFVSDRVRTFVGMTEESRPIL 223

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEP-WDFKLPRVMWHSRLAGRP 285
+ L A V+ H+W+ D+V+WDNRC LH A P +D PR M + G P
Sbjct: 224 DFLNRHATSPEFVYRHRWSVNDIVMWDNRCTLHIALPDFDQSKPRHMMRCSMLGEP 279

>ref|YP_001262583.1| taurine dioxygenase [Sphingomonas wittichii RW1]
gb|ABQ68445.1| Taurine dioxygenase [Sphingomonas wittichii RW1]
Length = 293

Score = 135 bits (340), Expect = 6e-30, Method: Compositional matrix adjust.
Identities = 103/301 (34%), Positives = 146/301 (48%), Gaps = 38/301 (12%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
+ I A +GA V GV L+ LD A L AA L+H +L F GQ LS ++ + F +
Sbjct: 1 MDIRKVTANIGADVHGVDLSQPLDKGVVAELRAALLEHLVLFVRGQRKLSVEEHVRFGRY 60

Query: 64 FGAIE----RIGGG---DIVASNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMP 116
FG I+ R +++ + G G +WHAD+TYMP
Sbjct: 61 FGDIDPPLFRTASSPAPEVIVLDQKNPKGE-----GADSWHADNTYMP 103

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
G++ A+++P++GG TCFA+M AAYDAL RA++ A HSL + HV
Sbjct: 104 APPMGSILQAQILPSIGGDTCFANMYAAYDALSPGLRAMLDGLHAIHSLEQMAERTKHVM 163

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
A + +D L P+V VHPETGR L + + AI GM AES+ L L D
Sbjct: 164 ---GASLRDKVDQWPPVLHPVAVHPETGRRLNANVTVAIDGMSRAESDALLRLLYD 220

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWH-----SRLAGRPETEG 289
++P +W GDV WDNR + H A D++ R+M +R+ G P+ E

Sbjct: 221 -HVRSPFEQVRLRWNTGDVAFWDNRSVQHYAVA-DYRERRMMQRVTIAGTRIQQIPDAER 278

Query: 290 A 290

A

Sbjct: 279 A 279

>gb|ADC34040.1| TfdA-like protein [uncultured bacterium]
Length = 209

Score = 135 bits (340), Expect = 8e-30, Method: Compositional matrix adjust.
Identities = 83/219 (37%), Positives = 111/219 (50%), Gaps = 23/219 (10%)

Query: 56 QQITFAKRFGAIERIGGGDIVA-----ISNVKADGTVRQHSPAEWDDMMKVI- 102
QQI FA FG E GG+I +SN+ DG P D +
Sbjct: 1 QQIAFALNFGERENARGGNITKKEDYRLTTGLNDVSNLKGKG-----KPLPRDSRAHLFN 55

Query: 103 VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR 162
+GN WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A +
Sbjct: 56 LGNCLWHSDSSFRPIPAKFSLLSARVVPKGGNTEFADMRAAYDALDDDTKAEIDDLICE 115

Query: 163 HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMD 222
HSL+YS+ LG + Y L+ LV+ HP R SL + HA AI GM
Sbjct: 116 HSLMYSRGLGFLD-----YTDEEKAMFKPVLQRLVRTHPVHRRKSLYLSSHAGAIQGMT 170

Query: 223 AAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCL 261
E+ L L + A Q V+ H+W D+V+WDNRC+
Sbjct: 171 MPEARLLLLRDLTEHATQPEFVYVHKWTLHDLVMWDNRCV 209

>emb|CBJ20063.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20066.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20069.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 138

Score = 135 bits (339), Expect = 8e-30, Method: Compositional matrix adjust.
Identities = 66/141 (46%), Positives = 91/141 (64%), Gaps = 3/141 (2%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MP+ ++ A+ A V P GG T FADMRAA++AL++AT+A + + SA HSL YSQ + G
Sbjct: 1 MPLASKAAMLYALVTPPEGGETEFADMRAAWEALNKATQAQLEKLSAYHSLYYSQEQAGF 60

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
+ + Y G LRP++K HPETGR S+ GRHAH IPGM ES+ L+ L+
Sbjct: 61 IHKTDQVY---GFHDKGATLRPIIKTHPETGRKSIYTGRHAHDIPGMSKEESKALLDKLM 117

Query: 235 DWACQAPRVHAHQWAAGDVVV 255
+ AC+ PR++ H W GD+VV
Sbjct: 118 EDACRPRLYKHAWTPGDLVV 138

>ref|YP_293521.1| taurine dioxygenase [Ralstonia eutropha JMP134]
gb|AAZ65664.1| Taurine dioxygenase [Ralstonia eutropha JMP134]
Length = 264

Score = 135 bits (339), Expect = 8e-30, Method: Compositional matrix adjust.
Identities = 87/270 (32%), Positives = 133/270 (49%), Gaps = 38/270 (14%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T++I P ++GA+VTGV+L ++DA F LH A+L+H +L+F GQ L Q+ FA+

Query:	2	AQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF	60
		A I P A GA + G+ L+ L A FA +H A L H LL+F Q ++ Q I F	
Sbjct:	17	ATQAFSIRPLAAVTGAEIVGIDLSRELAPADFAQVHRAHLDDHLLVFRDQRITPKQHIDF	76
Query:	61	AKRFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS	112
		++RFG + G +I+ +SN+ DG P D K WH+D	
Sbjct:	77	SRRFRGLMIHVLHQFHLPGHPEILIVSNIVEDG-----QPIGLGDAGKY-----WHSDI	125
Query:	113	TYMPVMAQGAVFSAEVPVAVGGRTCFADMR AAYDALDEATRALVHQRSARHSLVYSQSKL	172
		+Y + + G++ A+ +PA GG T FADM AYD L R + + A HS + +K	
Sbjct:	126	SYKELPSLGSLLHAQELPAQGGDTL FADMHVAYDTLPVLRDAIEGKRAVHSYL---AKY	182

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVM 276
L L++ A V++H+W GD+V+WDNRC LHR D + R +
Sbjct: 229 GRVLLMDLLEHATARRFVYSHRWQPGDLVIWDNRCTLHRGRRHDLVSRRRL 279

>ref|YP_004115686.1| Taurine dioxygenase [Pantoea sp. At-9b]
gb|ADU69130.1| Taurine dioxygenase [Pantoea sp. At-9b]
Length = 284

Score = 133 bits (334), Expect = 4e-29, Method: Compositional matrix adjust.
Identities = 98/296 (33%), Positives = 142/296 (47%), Gaps = 31/296 (10%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L++ P +G V V +D A F AL A H++L+ Q ++ Q + FA+ F
Sbjct: 2 LELRPLTDHIGMEVLNVDATQPIDPATFTALRDALNTHSVLLLRNQPVTEAQHVAFAREF 61

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
G ++ ++ +SNVK DG + W+ WH+D +Y
Sbjct: 62 GELQVHVLSQYLTPPELYVLSNVKQDGKPIGNHKEGWN-----WHSWDSYYE 110

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
V G+V A VP VG T F+ M AAYDALD+ T+ L+ SA HS +K +
Sbjct: 111 VPCFGSVLHAVEVPPVGADTLFSSMFAAYDALDDDTKRLIQPLSAVHSYSTYYAKAFADR 170

Query: 177 QAGSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGL 233
+ SA ATP + PLV+ H ETGRPSL +G+ I G+ ES L L
Sbjct: 171 EPLSA-----EQKAATPDVVHPLVRRHQETGRPSLVFGQDIVKEIVGLTPEESTALLARL 225

Query: 234 VDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPW-DFKLPRVMWHSRLAG--RPE 286
A + H+W A D+++WDNRC +H+A P+ D RVM + + G RP+
Sbjct: 226 NAHAISSETFYRHKWQAHDLLIWDNRCTMHQATPYDDVAYRRVMHRATVKGSRPQ 281

>ref|YP_002800232.1| taurine catabolic dioxygenase protein [Azotobacter vinelandii DJ]
gb|AC079257.1| taurine catabolic dioxygenase protein [Azotobacter vinelandii DJ]
Length = 273

Score = 132 bits (333), Expect = 4e-29, Method: Compositional matrix adjust.
Identities = 87/281 (30%), Positives = 137/281 (48%), Gaps = 25/281 (8%)

Query: 15 LGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
LGA + G+ L+ ++ A FA +H A+L H +L+F Q ++ +QQI F++RFG ++
Sbjct: 2 LGAEILGLDLSLPVNSADFARIHQAFLDHRVLVLFREQRITPEQQIAFSRRFGELQIHVLK 61

Query: 69 ---RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
G +I ISN+ +G P D K+ WH+D +Y + + GA+
Sbjct: 62 QFLLAGHPEIFIISNIVENG-----RPIGLGDAGKL-----WHSLSYKEIPSMGAMLY 110

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQAGSAYI 183
A ++P GG T FAD + AY++L EA R V R A HS Y +++
Sbjct: 111 ARILPEEGDTLFADQQLAYESLPEALRKAVEGRRVHSHYTAHYEDEVFKGIRR--PTLT 168

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAPR 242
++ + P+V+ HPETGR L + + I + ES R L L + +
Sbjct: 169 TAQLEEVKEVVHPVVRTHPETGRKGLFVNENFTTRILDPEDESRRLLAELYAHSIRPEF 228

Query: 243 VHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ H+W D++ WDNR L+H A LPR M + + G
Sbjct: 229 TYRHRWQENDLLFWDNRALIHLATGCPNHLPRRMRHTTIQG 269

>ref|NP_882351.1| putative taurine catabolism dioxygenase [Bordetella pertussis
Tohama I]
ref|NP_891532.1| putative taurine catabolism dioxygenase [Bordetella bronchiseptica
RB50]
emb|CAE44111.1| putative taurine catabolism dioxygenase [Bordetella pertussis

Tohama I]
emb|CAE35362.1| putative taurine catabolism dioxygenase [Bordetella bronchiseptica
RB50]
Length = 307

Score = 132 bits (333), Expect = 4e-29, Method: Compositional matrix adjust.
Identities = 90/289 (31%), Positives = 143/289 (49%), Gaps = 27/289 (9%)

Query: 8 ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
+ P LGA + G+ LA L A FA + A L H L++F Q ++ Q I F++RFG
Sbjct: 29 VRPLNDALGAEIVGIDLARALSAADFARVRRALDHHLVFRDQRITPRQHIDFSRRFGR 88

Query: 67 I-----ERIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVM 118
+ +I+ +SN+ +G +P D K WH+D +Y P+
Sbjct: 89 LMIHVLHQFHLAHNPEILVVSNIENG-----APVGLGDAGKY-----WHSIDISYKPLP 137

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
+ G++ A+ +PA+GG T FA+M AY+ L A R V R A HS + +K G +Q+
Sbjct: 138 SLGSLHLHAQELPAIGGDTLAFANMHRAYETLPRALREAVDGRRAVHSYL---AKYGLQKE 194

Query: 179 GS---AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
G+ + P+V+ HPETGR +L + I G+ A ES + L+ L
Sbjct: 195 GNWRPTLSAAQLAQVQEVAPVVRTHPETGRRALFVSEGFTRIIEGVAADESRQILDEL 254

Query: 235 DWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ ++ ++ HQW D+V WDNR L+H A +L R ++ + + G
Sbjct: 255 AHSTRSEHIYRHQWRDHDLVFWDNRSLIHLAAGCPPELRRKLYRTTIEG 303

>ref|YP_626229.1| taurine catabolism dioxygenase TauD/TfdA [Burkholderia cenocepacia
AU 1054]
ref|YP_840249.1| taurine catabolism dioxygenase TauD/TfdA [Burkholderia cenocepacia
HI2424]
gb|ABF81256.1| 2,4-dichlorophenoxyacetate monooxygenase [Burkholderia cenocepacia
AU 1054]
gb|ABK13356.1| 2,4-dichlorophenoxyacetate monooxygenase [Burkholderia cenocepacia
HI2424]
Length = 305

Score = 132 bits (333), Expect = 4e-29, Method: Compositional matrix adjust.
Identities = 96/291 (32%), Positives = 146/291 (50%), Gaps = 32/291 (10%)

Query: 5 TLQITPTGATLGATV---TGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
+L++ P A V +GV L A + + A+ AA ++A+L+F Q L+ DQQ+ F
Sbjct: 2 SLEVVPIIDAARPDFVGLASGVDLTAPVSEPLACAIDAAMNRYAVLVFRAQPLTQDQQLAF 61

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMA-- 107
A+ G ++ R+ ++ ISNV G + D + IVGN+A
Sbjct: 62 ARALGPLDVGFKRVARPHARLAHQELADISNVDESGQIA-----DRAHRRIVGNLANQ 114

Query: 108 -WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
WH+DS++ A+ ++ A VVP GG T +ADMRAA+DALD + + A H +
Sbjct: 115 LWHSDSSFQQPAARYSMLHAVVVPWEGGETEYADMRAAWDALDPREQRELDGLEAEHYAL 174

Query: 167 YSQSKLGHVQQAQSAYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAE 225
+S+ LG + + P+R PLV+ H +GR L IG HA + G AE
Sbjct: 175 HSRFLLGDTDYSDA-----QRNALPPVRWPLVREHAGSGRRHLFIGAHATHVVGRTLAE 228

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVM 276
L L++ A V++H+W GD+V+WDNRC LHR D + R +
Sbjct: 229 GRVLLMDLLEHATARRFVYSHRWPRGDLVIWDNRCTLHRGRRHDLVSRREL 279

>gb|ADC34003.1| TfdA-like protein [uncultured bacterium]
gb|ADC34010.1| TfdA-like protein [uncultured bacterium]
gb|ADC34037.1| TfdA-like protein [uncultured bacterium]
Length = 208

Score = 132 bits (333), Expect = 5e-29, Method: Compositional matrix adjust.
Identities = 82/221 (37%), Positives = 120/221 (54%), Gaps = 28/221 (12%)

Query: 56 QQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEW--DDMMKVI 102
QQI FA +FG IE RI I ISN+ DG + W DD ++
Sbjct: 1 QQIAFALQFGEIEDTPTLVDQERRRIANMKINDISNLGPDGKI-----WAADDRRRMY 53

Query: 103 -VGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSA 161
+GN+ WH+DS++ P A ++ A V+P VGG T F D R A+D L + T+A + A
Sbjct: 54 NLGNLLWHSDDSFKPTPAYWSMLQARVIPPVGGNTEFLDTRVAWDHLPQETKAEIKDLIA 113

Query: 162 RHSLVYSQSKLGHVQQAGSAYIGYGMD-TTATPLRPLVKVHPETGRPSLLIGRHAHAIPG 220
HSL+YS+++LG A+ + T P R LV++H E+GR ++ + H AI G
Sbjct: 114 YHSLIYSRAQLGF-----EAFSPEEQERCPTVPQR-LVRLHQESGRLAVYLSAHIGAIEG 167

Query: 221 MDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
E+ + L ++A Q V+AHQW+ GD+V+WDNRC+
Sbjct: 168 WQRPEALALINHLTEFATQREFVYAHQWSVGD LVIWDNRCV 208

>ref|YP_001633627.1| taurine dioxygenase [Bordetella petrii DSM 12804]
emb|CAP45360.1| taurine dioxygenase [Bordetella petrii]
Length = 304

Score = 132 bits (332), Expect = 5e-29, Method: Compositional matrix adjust.
Identities = 90/295 (30%), Positives = 140/295 (47%), Gaps = 27/295 (9%)

Query: 2 AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A + P +GA + G+ L L D FA + A L+H +++F Q ++ Q I F
Sbjct: 20 ADQDFDVRPLPGGIGAEIVGIDLGRPLGDFARVRRAHLEHHVVVFRDQRITPQQHIDF 79

Query: 61 AKRFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
++RFG + G +I+ +SN+ DG P D K WH+D
Sbjct: 80 SRRFGKLMVHVLHQFHLPGHPEILIVSNIIEDG-----KPVGLGDAGKY-----WHSDI 128

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+Y P+ + G++ A+ +PA GG T FADM AYD L R + R A HS + +K
Sbjct: 129 SYKPLPSLGSLLHAQELPAEGGDTLFDAMHKAYDTLPAHLRQAIAGRRVHVSYL---AKY 185

Query: 173 GHVQQAGSAYIGYGMDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESER 228
G +Q+ G+ D A + P+V+ HPETGR +L + I G+ ES +
Sbjct: 186 GQMKEGNWRPNLSADQLAQVQEVVHPVVRTHPETGRKALFVSEGFTTTRIEGLPEDESQ 245

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L+ L + + ++ H W D+V WDNR L+H A L R ++ + + G
Sbjct: 246 VLDELFAHSIRPEHIYRHAWRERDLVFDNRALIHLAGCPPHLRRKLYRTTIEG 300

>ref|NP_886536.1| putative taurine catabolism dioxygenase [Bordetella parapertussis
12822]
emb|CAE39689.1| putative taurine catabolism dioxygenase [Bordetella parapertussis]
Length = 307

Score = 132 bits (332), Expect = 6e-29, Method: Compositional matrix adjust.
Identities = 90/289 (31%), Positives = 143/289 (49%), Gaps = 27/289 (9%)

Query: 8 ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
+ P LGA + G+ LA L A FA + A L H L++F Q ++ Q I F++RFG

Sbjct: 29 VRPLNDALGAEIVGIDLARALSVADFARVRRALHDHHLVVFRDQRITPRQHIDFSRRFRGR 88

Query: 67 I-----ERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVM 118
+ +I+ +SN+ +G +P D K WH+D +Y P+

Sbjct: 89 LMIHVLHQFHLAHNPEILVVSNIENG-----APVGLGDAGKY-----WHSIDISYKPLP 137

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
+ G++ A+ +PA+GG T FA+M AY+ L A R V R A HS + +K G +Q+

Sbjct: 138 SLGSLHLHAQELPAIGGDTLAFANMHRAYETLPRALREAVDGRRAVHSYL---AKYQQLQKE 194

Query: 179 GS---AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR--HAHAIPGMDAAESERFLEGLV 234
G+ + P+V+ HPETGR +L + I G+ A ES + L+ L

Sbjct: 195 GNWRPTLSAAQLAQVQVEAHPVVRTHPETGRRALFVSEGFTRIEGVAADESRQILDEL 254

Query: 235 DWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ ++ ++ HQW D+V WDNR L+H A +L R ++ + + G

Sbjct: 255 AHSTRSEHIYRHQWRDHDLVFWDNRSLIHLAAGCPPELRRKLYRTTIEG 303

>ref|YP_299483.1| taurine dioxygenase [Ralstonia eutropha JMP134]
gb|AAZ64639.1| Taurine dioxygenase [Ralstonia eutropha JMP134]
Length = 264

Score = 132 bits (331), Expect = 8e-29, Method: Compositional matrix adjust.
Identities = 85/270 (31%), Positives = 132/270 (48%), Gaps = 38/270 (14%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T++I P ++GA+VTGV+L ++DA F LH A+L+H +L+F GQ L Q+ FA+

Sbjct: 2 TIEIKPLTGSVGVASVTGVNLNDPINDATFKVLHQAFLEHGMLVFRGQFLQPAAQVAFARL 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVI-----VGNMAWHADSTYMPV 117
+G G AE+ ++ +V AWH+DS Y V

Sbjct: 62 WGT-----PVQGNPLKGLAEFPELFQVTKIPKETASTEAWHSDSIYTAV 106

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 177
+ ++ S +P +GG T + + +Y+ L + L+ AR +S ++L +

Sbjct: 107 PPKISILSGVTIP-IGGDTMWCNQYLSYERLSPVMQRLIEGLRAR---FSGARLAKMT- 160

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR--HAHAIPGMDAAESERFLEGLVD 235
G D + + P+V+ HPETGR +L +G A I GM AES L+ L +

Sbjct: 161 -----GSDKVPSAVHPIVRTHPETGRKALYVGHDPDTEACIEGMTEAESRPLLDFLYE 212

Query: 236 WACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
+ V+ H W GDVV+WDNRC +H A

Sbjct: 213 HSVTPDNVYRHMWQEGDVVMWDNRCTMHYA 242

>ref|YP_553184.1| putative alpha KG dependent 2,4-D dioxygenase [Burkholderia
xenovorans LB400]
gb|ABE33834.1| Putative alpha KG dependent 2,4-D dioxygenase [Burkholderia
xenovorans LB400]
Length = 301

Score = 131 bits (330), Expect = 9e-29, Method: Compositional matrix adjust.
Identities = 84/276 (30%), Positives = 138/276 (50%), Gaps = 23/276 (8%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+L + + A + G+ L+ L D + A Q+ +LIFP Q++ +DQ + FA

Sbjct: 2 SLNVEAAHPFIAARIHGLDLKPLSDERIVEIEQASGQYPVLIFPRQYIDDDQLLAFAAG 61

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHAD 111
FG ++ R+ I ISN+ + + P + M + + WH+D

Sbjct: 62 FGPLQVAVSYSTRPEDHRLAPM-INDISNLSKENQT--YRPGDRRRMNNLT--SRRWHS 116

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
++Y+P+ A+ + + +VPAVGG+T FADMRAAYD L + R +V S + ++ S++
Sbjct: 117 ASYLPLPARYSFLLSYIVPAVGGQTQFADMRAAYDKLPDHLRKVVEGLSCHYDIMASRAA 176

Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE 231
G + A + LV+ HP +GR SL + HA + G E L
Sbjct: 177 AGFYDASDEE-----RKALAPCIHELVRTHPISGRKSLYLSSHATHVVGWPEPEGRDLLR 231

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEP 267
L ++A Q V++H+W+ D+V+WDNR L+HR P
Sbjct: 232 ELTEFATQPQFVYSHEWSVRDLVMWDNRALMHRGRP 267

>ref|ZP_04943904.1| hypothetical protein BCPG_05482 [Burkholderia cenocepacia PC184]
gb|EAY67075.1| hypothetical protein BCPG_05482 [Burkholderia cenocepacia PC184]
Length = 317

Score = 131 bits (330), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 95/291 (32%), Positives = 145/291 (49%), Gaps = 32/291 (10%)

Query: 5 TLQITPTGATLGATV---TGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
+L++ P A V +G+ L A + + A+ AA ++A+L+F Q L+ DQQ+ F
Sbjct: 14 SLEVVPIDAARPDFVGLASGIDLTAPVSEPLACAIDAAMNRYAVLVFRAQPLTQDQQLAF 73

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMA-- 107
A+ G ++ R+ ++ ISNV G + D + IVGN+A
Sbjct: 74 ARALGPLDVGFKRVARPHARLAYQELADISNVDESGQI-----ADRAHRRIVGNLANQ 126

Query: 108 -WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
WH+DS++ A+ ++ A VVP GG T +ADMRAA+DALD + + A H +
Sbjct: 127 LWHSDSSFQQAARYSMLHAVVVPEWGGTEYADMRAAWDALDPREQLDGLAEHYAL 186

Query: 167 YSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAE 225
+S+ LG + P+R PLV+ H +GR L IG HA + G AE
Sbjct: 187 HSRFLLGDDTDYTD-----QRNALPPVRWPLVREHAGSGRRHLFIGAHATHVVGRTLAE 240

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
L L++ A V++H+W GD+V+WDNRC LHR D + R +
Sbjct: 241 GRVLLMDLLEHATARRFVYSHRWRPGDLVIWDNRCTLHRGRRHDLVRREL 291

>ref|ZP_03265714.1| Taurine dioxygenase [Burkholderia sp. H160]
gb|EEA02686.1| Taurine dioxygenase [Burkholderia sp. H160]
Length = 295

Score = 131 bits (330), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 88/289 (30%), Positives = 140/289 (48%), Gaps = 21/289 (7%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+ +I A LGA V G+ L L D FA +H A L H +L+F Q ++ DQOI F++R
Sbjct: 14 SFEIRAFDAPLGAEVLGLDLGQPLGDDDFARIHRAHLDDHHVLVVFREQRITPDQQIAFSRR 73

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYM 115
FG ++ G +++ +SN+ +G P D WH+D +Y
Sbjct: 74 FGPLQIHVLHQFGLSGYSEVLVVSNIENG-----KPIGLGD-----AGHYWHSDSL SYK 122

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
+ G++ A+ +PA GG T FA+M A+D L R+ V RSA H+ + ++L
Sbjct: 123 DKPSLGSLLHAQELPAEGGDTLAFANMHLAWDTLP SHLRS AVEGRSAEHTYLAKYAELQKR 182

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLV 234
+ + P+V+ HPETGR +L + H + G+ ES L+ L

Sbjct: 183 SPWRPNLSAEQIAQVRPVVHPIVRTHPETGRKALFVSEHFTTRVIGLPEDESRALLDEL 242

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ + ++ H+WAA D+V WDNR L+H A L R ++ + + G

Sbjct: 243 AHSVRPEHLRHRWAAHDMVFWDNRSMLHLAAGTPDHLRRKLYRTTIEG 291

>ref|YP_002008624.1| taurine dioxygenase, 2-oxoglutarate-dependent [Cupriavidus taiwanensis LMG 19424]

emb|CAQ72572.1| taurine dioxygenase, 2-oxoglutarate-dependent [Cupriavidus taiwanensis LMG 19424]

Length = 309

Score = 131 bits (329), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 90/289 (31%), Positives = 139/289 (48%), Gaps = 21/289 (7%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63

+I P A LGA V G+ L+ L DA FA +H A L + +++F Q ++ QQI F++R

Sbjct: 28 NFEIRPLDAPLGAEVIGLDLSQPLSDADFARIHRAHLDYHVVFVRDQQITPAQQIGFSRR 87

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYM 115

FG ++ G +++ +SNV +G P D WH+D +Y

Sbjct: 88 FGPLQIHVLHQFQLPGHPEVLVVSNNVENG-----KPIGLGD-----AGHFWHSDLSYK 136

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175

+ G++ A +PA GG T FA+M A+D L A + V A H+ + ++L

Sbjct: 137 EKPSLGSLLHARELPAEGGDTLFANMHLAWDTLPAALQRAVDGLQAEHTYLARYAELQQR 196

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLV 234

+ L+P+V+ HPETGR +L + H I G+ ES L+ L

Sbjct: 197 SPWRPNLTPEQVAQVRPVLQPVVVRTHPETGRKALFVSEHFTTRIVIGLPEDESRDLLDQLF 256

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ + ++ HQW D+V WDNR LLH A +L RVM+ + + G

Sbjct: 257 AHSVKAHIYRHQWQPHDLVFWDNRSLLHLAAGCPPELRRVMYRTTIEG 305

>ref|YP_345870.1| taurine catabolism dioxygenase TauD/TfdA [Pseudomonas fluorescens Pf0-1]

gb|ABA71881.1| putative taurine catabolism dioxygenase [Pseudomonas fluorescens Pf0-1]

Length = 298

Score = 130 bits (328), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 84/291 (28%), Positives = 140/291 (48%), Gaps = 25/291 (8%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63

T +I P +GA + G+ L ++D FA++H A L H +++F Q ++ QQI F++R

Sbjct: 17 TFEIRPFSGAVGAIEIIGLDLTRPVNDEDFASIHRAHLDHHVVVFVRDQRITPQQQIDFSRR 76

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMA--WHADST 113

FG ++ +I+ +SN+ +G + +G+ WH+D +

Sbjct: 77 FGVQLQIHVLKQFLLANHPEILIVSNIVENG-----QNIIGLDAGKFWHSDLS 123

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173

Y + + G++ A+ +P GG T FADM A+D+L +A R V RSA HS S+

Sbjct: 124 YKELPSLGSMLHAQELPPEGGDTLFADMHKAWDSLDPALRKAVEGRSAAHSYTARYSETK 183

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232

+ A + P+V+ HPE GR +L + I G+ ES++ L+

Sbjct: 184 FEGNWRPTLTPEQLAQVAEVVHPVVRTHPENGRKALFVSEGFTTRIVIGLPEDESKQLLDE 243

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

```
>gb|AD034964.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
      [uncultured bacterium]
```

gb|ADO34965.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ADO34966.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ADO34967.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ADO34968.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ADO34969.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ADO34970.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ADO34975.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ADO34976.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ADO34977.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ADO34978.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 96

Score = 130 bits (327), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 67/96 (69%), Positives = 74/96 (77%), Gaps = 1/96 (1%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYMPV A+GAVFSAEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQ
Sbjct: 1 ADSTYMPVQAKGAVFSAEVVPSVGGQTGFADMRAAYDALDEDLKARVETLQARHSLHYSQ 60

Query: 170 SKLGHVQQAGSA-YIGYGMDTTATPLRPLVKVHPET 204
SKLGH +A Y GYG+ PLRPLVK+HPET
Sbjct: 61 SKLGHQTKAADGEYSGYGLHDPVPLRPLVKIHPET 96

>ref|YP_002942895.1| Taurine dioxygenase [Variovorax paradoxus S110]
gb|ACS17629.1| Taurine dioxygenase [Variovorax paradoxus S110]
Length = 287

Score = 130 bits (327), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 80/270 (29%), Positives = 131/270 (48%), Gaps = 21/270 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ P A +GA + G+ ++ ++D FA +H A L H +L+F Q ++ + I F++RF
Sbjct: 7 FEVRPFNAPVGAEIVGLDISKPINDEDFARIHRAHLDDHVLVFRNQITPAEHIEFSRRF 66

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
G +E +I+ +SN+K +G P D + WH+D +Y P
Sbjct: 67 GPLEIHVLHQFHLKNHPEILIVSNIKENG-----EPIGLGD-----AGVYWHSDISYKP 115

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ G++ A+ +P+ GG T FAD A++ L + + A HS + L
Sbjct: 116 QPSLGSLLHAQELPSEGGDTLFADQHLAWETLSPELQQRILPLKAEHSYLAKYEALRAKN 175

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
+D A ++P+V+ HPETGR +L + H I G+ ES+ L L
Sbjct: 176 PWRPKLSQEIDQVAPAVQPVVRTHPETGRKALFVSEHFTTRIVGLSPQESDALLAELFA 235

Query: 236 WACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
+ + V+ HQWA D+V WDNR L+H A
Sbjct: 236 HSVKPPQFVYRHQWAPHDLVFWDNRSMLHLA 265

>ref|YP_244520.1| taurine dioxygenase [Xanthomonas campestris pv. campestris str.

Query:	6	LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG	65
		+ P +GA V V L TLDDA F ++A +L+H LL+F Q LS + Q+ F++R G	
Sbjct:	2	MNAIPLSPLIGAAVHDVDLETLDDAAFEDVNALFLRHQLLVFKNQRLSPGQLRFSRRLG	61
Query:	66	AIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV	117
		++ +I +SN +G PA D G WH+D +	
Sbjct:	62	ELDIHVLAQYNHAEYPEIFVLSNEVKNGV-----PAGIAD-----GGSYWHSDFAFREC	110
Query:	118	MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRA-----LVHQRSARHSLVY--SQ	169
		A+ + +A+++P GG T F +M AY+ LD A ++ VH+ +++ +Q	
Sbjct:	111	PAKATILNAQLIPPEGGNTLFINMYRAYEELDGAVQSQLAGLQAVHRYRPKNTRAEEGTQ	170
Query:	170	SKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDA-----	223
		K+ Q AG+ + + P+V+ HPETGR +L + PGM A	
Sbjct:	171	VKMDASQLAGTPDVEH-----PIVIRTHPETGRKALYVH-----PGMTAEVSGWG	214
Query:	224	-AESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDF--KLPRVMWHSR	280
		A+S+ LE L Q +A QW GDVV+WDNRC++H+A + + R ++ +	
Sbjct:	215	EADSQELLERLFAHCTQEKYQYALQWEPGDVVMWDNRCVMHKATTRELPASMRRTIYRTT	274
Query:	281	LAG-RP 285	
		+ G RP	
Sbjct:	275	VMGERP 280	

```
>ref|ZP_06704693.1| Taurine dioxygenase [Xanthomonas fuscans subsp. aurantifolii str.
ICPB 11122]
ref|ZP_06730962.1| taurine dioxygenase [Xanthomonas fuscans subsp. aurantifolii str.
ICPB 10535]
gb|EFF43750.1| Taurine dioxygenase [Xanthomonas fuscans subsp. aurantifolii str.
ICPB 11122]
gb|EFF47905.1| taurine dioxygenase [Xanthomonas fuscans subsp. aurantifolii str.
ICPB 10535]
Length = 305
```

Score = 129 bits (325), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 84/272 (30%), Positives = 133/272 (48%), Gaps = 21/272 (7%)

```
Query: 4   TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
++++I P  A LGA V G+ LA  LD A FA +H A L H +L+F  Q ++  QQ+ F++
Sbjct: 23  SSVRIVPFDAPLGAEVIGLDLAQPLDAATFARIHRAHLDDHVLVFRDQRITPAQQVEFSR 82

Query: 63  RFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY 114
RFG ++          G  +++ +SN+K +G      P      D          WH+D +Y
Sbjct: 83  RFGPLQIHVLRNFQLRGQPEVLVVSNIKENG-----EPIGLGD-----AGHYWHSLSY 131

Query: 115  MPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
+ G++  A+ +P+ GG T FA+  A+  L E+ +  V    A HS +    +L
Sbjct: 132  KQTPSLGSLHAQELPSEGGDTLFANQHLAWQTLPESLKRTVQDLRAEHSYLAKYEELRA 191

Query: 175  VQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGL 233
      A      +          P+V+ HPETGR +L +  H      I G+   ES   L+ L
Sbjct: 192  RNPWRPALTPAQIAEVTVPVQHVPVVRTHPETGRKALFVSEHFTTRIVGLPEDESALLQTL 251

Query: 234  VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      + +  A  V+ H+W  D+V WDNR ++H A
Sbjct: 252  FEHSTHAALVYRHRWQPHDMVFWDNRSVMHLA 283
```

```
>ref|ZP_04586493.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. oryzae str.
1_6]
Length = 298
```

Score = 129 bits (324), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 83/270 (30%), Positives = 131/270 (48%), Gaps = 21/270 (7%)

```
Query: 6   LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ P      +GA V G+ L+  L DA FA +H A L H +++F  QH++  QQI F++RF
Sbjct: 18  FDVRPFDTKVGAEVVGDLDSRPLKDADFARVHQAHNLHHVVVFRDQHITPQQQIDFSRRF 77

Query: 65  GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
G ++          +I+ +SN+ +G      P      D K          WH+D +Y
Sbjct: 78  GVLQIHVLKQFLLPDHPEILIVSNIVENG-----QPVGLGDAGKY-----WHSLSYKE 126

Query: 117  VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ + G++  A+ +P+ GG T FADM  A+D L +  R  V  RSA HS    ++  +
Sbjct: 127  LPSLGSMLYAQELPSEGGDTLFADMHQAWDTLPQHLLRDAVEGRSAVHSYTARYAEGHNAA 186

Query: 177  QAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
      +          P+V+ HPE GR +L +          I G+   AES + L+ +
Sbjct: 187  SWRPTLTAEQLAQVVEVSHPIVRTHPENGRKALFVSEGFTRILGLPEAESRQILDEIYA 246

Query: 236  WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      + +  ++ HQW  GD+V WDNR L+H A
Sbjct: 247  HSVKPEHIYRHQWQPGDMVFWDNRSIHLA 276
```

```
>ref|YP_001904982.1| Taurine dioxygenase [Xanthomonas campestris pv. campestris str.
```

B100]
emb|CAP52942.1| Taurine dioxygenase [Xanthomonas campestris pv. campestris]
Length = 300

Score = 129 bits (324), Expect = 5e-28, Method: Compositional matrix adjust.
Identities = 85/270 (31%), Positives = 131/270 (48%), Gaps = 21/270 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+QI P A LGA V G+ L+ LD FA +H A L H +L+F Q ++ QQ+ F++RF
Sbjct: 20 VQIVPFDAPLGAIEVIGLALSQPLDADTFARIHRAHLDDHVLVFRDQRITPAQQVEFSRRF 79

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMP 116
G ++ G +++ +SN+K +G P D WH+D +Y
Sbjct: 80 GPLQIHVLRNFQLRGHPVLVVSNIKENG-----QPIGLGD-----AGHYWHSLSYKE 128

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ G++ A+ +PA GG T FA+ A+ L +A + V R A HS + +L
Sbjct: 129 TPSLGSLHAQELPAEGGDTLAFANQHLAWQTLPDALKRAVEGRQAHSYLAKEYEELRARN 188

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
A + P+V+ HPETGR +L + H I G+ ES L+ L D
Sbjct: 189 PWRPALTAEQIAEVPVQHPPIVTRHPETGRKALFVSEHFTTRIVGLPDDESHALLQALFD 248

Query: 236 WACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
+ + V+ H+W D+V WDNR ++H A
Sbjct: 249 HSTRDALVYRHRWQPHDMVFWDNRSVMHLA 278

>ref|YP_003606832.1| Taurine dioxygenase [Burkholderia sp. CCGE1002]
gb|ADG17321.1| Taurine dioxygenase [Burkholderia sp. CCGE1002]
Length = 298

Score = 129 bits (323), Expect = 6e-28, Method: Compositional matrix adjust.
Identities = 87/289 (30%), Positives = 139/289 (48%), Gaps = 21/289 (7%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+ +I A LGA V G+ L L D FA +H A L H +L+F Q ++ +QI F++R
Sbjct: 17 SFEIRAFDAPLGAIEVLGLDLGQPLGDDFARIHRAHLDDHVLVFRDQRITPEQQIAFSRR 76

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYM 115
FG ++ G +++ +SNV +G P D WH+D +Y
Sbjct: 77 FGPLQIHVLHQFGLAGYPEVLVVSNIENG-----KPVGLGD-----AGHYWHSLSYK 125

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
+ G++ A+ +PA GG T FA+M A+D L R+ V RSA H+ + +L
Sbjct: 126 EKPSLGSLHAQELPAEGGDTLAFANMHLAWDTLPARLSAVEGRSAEHTYLAKYAELQKR 185

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLV 234
+ + P+V+ HPETGR +L + H + G+ ES L+ L
Sbjct: 186 SPWRPNLSAEQIAQVKPVVHPPIVTRHPETGRKALFVSEHFTTRVIGLPEDESRALLDEL 245

Query: 235 DWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ + ++ H+WA D+V WDNR L+H A L R ++ + + G
Sbjct: 246 AHSVRPEHLYRHRWAEDMVFWDNRSMLHLAAGTPDHLRRKLYRTTIEG 294

>ref|YP_003910369.1| Taurine dioxygenase [Burkholderia sp. CCGE1003]
gb|ADN61078.1| Taurine dioxygenase [Burkholderia sp. CCGE1003]
Length = 305

Score = 129 bits (323), Expect = 6e-28, Method: Compositional matrix adjust.
Identities = 87/296 (29%), Positives = 149/296 (50%), Gaps = 27/296 (9%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
+A ++I P +GA V + L+ L+ FA +H A L H +L+F Q ++ D+QI
Sbjct: 20 IASQPIEIRPFDGPVGAIEVLRDLDSKPLNQDFARIHRAHLDDHVLVFRDQRITPDEQIA 79

Query: 60 FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHAD 111
F++RFG ++ G +++ +SN+ +G P D WH+D
Sbjct: 80 FSRRFGPLQIHVLHQFQLPGYPEVLVSNIVENG-----KPIGLGD-----AGHYWHS 128

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
+Y + G++ A+ +PA GG T FA+M A+D L R+ V R+A H+ + +K
Sbjct: 129 LSYKEKPSLGSLLHAQELPAEGGDTLFLANMHLAWDTLPAHLRSVEGRRTAEHTYL---AK 185

Query: 172 LGHVQQAGSAYIGYGMDDTTA--TPLR-PLVKVHPETGRPSLLIGRH-AHAIPGMDAAESE 227
+Q+ + A P++ P+V+ HPETGR +L + H + G+ ES+
Sbjct: 186 YAEQLQRSPWRPNLSPEQIAQVKPVQHPIVRTHPETGRKALFVSEHFTTRVIGLPEDESK 245

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ L+ + + +A V+ H+WA D+V WDN R L+H A L R ++ + + G
Sbjct: 246 QLLDEIFAHSVRAEHVYRHRWAEDHMFVWDNRSLMHLAAGTPDHLRRKLYRTTIEG 301

>ref|YP_605938.1| taurine catabolic dioxygenase [Pseudomonas entomophila L48]
emb|CAK13121.1| putative taurine catabolic dioxygenase [Pseudomonas entomophila L48]
Length = 299

Score = 128 bits (322), Expect = 8e-28, Method: Compositional matrix adjust.
Identities = 89/294 (30%), Positives = 145/294 (49%), Gaps = 31/294 (10%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T I P +GA + G+ LA ++ F +H A L H +L+F Q +S +QQI F++R
Sbjct: 18 TFDIRPFPFAGVGAIEIVGLDLARPVNVEDFTRIHRALDDHVLVFRDQRISPEQQIAFSRR 77

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMA--WHADST 113
FG ++ G +I+ +SN+ DG V +G+ WH+D +
Sbjct: 78 FGELQIHVLKQFLLAGHPEILIVSNIVEDGR-----NVGLGDAGKFWHSDLS 124

Query: 114 YMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSK 171
Y + + G++ A+ +P+ GG T FADM A+DA+ +A R +V R A HS Y+++K
Sbjct: 125 YKELPSLGSMLHAQELPSEGGDTLFLADMHKAWDAVPDALRKVVEGRDAHSTARYAETK 184

Query: 172 L-GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERF 229
G+ + +A + + P+V+ HPE GR +L + I G+ ES
Sbjct: 185 FEGNWRPTLTA--EQLAQVQEVHPVVRTHPENGRKALFVSEGFTTRIVGLPDDES RDV 241

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L+ L + ++ HQW D+V WDN R L+H A L R ++ + + G
Sbjct: 242 LQQLYALSVLEQHIYRHQWQPNLDLVFWDNRSLIHLAAGCPAHLRRKLYRTTIQ 295

>ref|YP_001751903.1| taurine dioxygenase [Pseudomonas putida W619]
gb|ACA75534.1| Taurine dioxygenase [Pseudomonas putida W619]
Length = 299

Score = 128 bits (321), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 89/292 (30%), Positives = 146/292 (50%), Gaps = 27/292 (9%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T +I P +GA + G+ LA ++ F+ +H A L+H +L+ Q +S +QQI F++R
Sbjct: 18 TFEIRPFSAGVGAIEIIGLDLAKPVNAEDFSLIHRALHHLVLRDQRISPEQQIAFSRR 77

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYM 115
FG ++ G +I+ +SN+ +G H+ D WH+D +Y

Sbjct: 78 FGQLQIHVLKQFLLKGHP EILIVSNIIENG---HNIGLGD-----AGKFWHSDLSYK 126

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKL- 172
+ + G++ A+ +P+ GG T FADM A+DA+ +A R V RSA HS Y+++K

Sbjct: 127 ELPSLGSM LHAQELPSEGGDTL FADMHKAWDAVPQALRKQVEGRSAAHSYTARYAETKFE 186

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLE 231
G+ + SA + + P+V+ HPE GR +L + I G+ ES L+

Sbjct: 187 GNWRPTLSA---EQLAQVQEVVHPVVRTHPENGRKALFVSEGFTTRIVGLPDDES RDVLQ 243

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + ++ HQW D+V WDNR L+H A L R ++ + + G

Sbjct: 244 QLYALSVLEQNIYRHQWQPHDLVFWDNRSLIHLATGCPAHLRRKLFRTTIQG 295

>ref|NP_794929.1| dioxygenase, TauD/TfdA family [Pseudomonas syringae pv. tomato str. DC3000]
gb|AA058624.1| dioxygenase, TauD/TfdA family [Pseudomonas syringae pv. tomato str. DC3000]
Length = 298

Score = 128 bits (321), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 89/282 (31%), Positives = 135/282 (47%), Gaps = 37/282 (13%)

Query: 2 AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A + + P +GA + G+ L+ L+DA FA +H A L H +++F Q ++ QQI F

Sbjct: 14 ASQSFDVRPFAGKMGAEIVGLDL SRPLNDADFARVHRAHLDDHHVVVFRDQQITPQQQIDF 73

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS 112
++RFG ++ +I+ +SN+ V P D K WH+D

Sbjct: 74 SRRFGVLQIHVLKQFLLANHPEILIVSNI-----VENEKPVGLGDAGKY-----WHSDL 122

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+Y + + G++ A+ +P+ GG T FADM A+D L + R V RSA HS S+

Sbjct: 123 SYKELPSLGSM LYAQELPSEGGDTL FADMHQAWDTLPQH LRDAVEGRSAVHSYTARYSE- 181

Query: 173 GHVQQAGSAYIGYGMDTTATPL-----RPLVKVHPETGRPSLLI--GRHAHAIPGMDA 223
G + + TA L P+V+ HPE GR +L + G H I G+

Sbjct: 182 -----GHNAVNRPTLTAEQLAQVVEVSHPIVRTHPENGRKALFVSEGFTTH-ILGLPE 234

Query: 224 AESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
ES L L + + ++ HQW A D+V WDNR L+H A

Sbjct: 235 DESREILGELYAHSVRPEHIYRHQWQANDMV FWDNRSLIHLA 276

>ref|YP_002869819.1| putative taurine catabolism dioxygenase [Pseudomonas fluorescens SBW25]
emb|CAY46407.1| putative taurine catabolism dioxygenase [Pseudomonas fluorescens SBW25]
Length = 297

Score = 127 bits (320), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 84/291 (28%), Positives = 137/291 (47%), Gaps = 25/291 (8%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T +I P ++GA + G+ L ++D FA +H A L H +++F Q ++ +QQI F++R

Sbjct: 16 TFEIRPLPGSVGA EIIIGLDLTRAINDKDFARIHRAHLDDHHVVVFRDQRITPEQQIAFSRR 75

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA--WHADST 113
FG ++ +I+ +SN+ +G + +G+ WH+D +

Sbjct: 76 FGV LQIHVLKQFLLANHPEILIVSNIENG-----QSIGLGDAGKFWHSDLS 122

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173

Y + + G++ A+ +P+ GG T FADM A+D L E R V RSA HS S+
Sbjct: 123 YKELPSLGSM LHAQELPSEGGDTL FADM HKAWDQLPEHL RNAVEGRSAAHSYTARYSETK 182
Query: 174 HVQQAGSAYIGYGM DTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
+ A + P+V+ HPE GR +L + I G+ ES L
Sbjct: 183 FEGNWRPTLTPEQLAQVAEVVHPIVRTHPENGRKALFVSEGFTTRIVGLPEDESRLLAQ 242
Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + ++ HQW D+V WDNR L+H A L R ++ + + G
Sbjct: 243 LYAHSVLPQNIYRHQWQPHDLVFWDNRS LIHLAAGCPSHLRRKLFRTTIQ 293

>ref|YP_998536.1| taurine dioxygenase [Verminephrobacter eiseniae EF01-2]
gb|ABM59518.1| Taurine dioxygenase [Verminephrobacter eiseniae EF01-2]
Length = 267

Score = 127 bits (320), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 85/265 (32%), Positives = 132/265 (49%), Gaps = 24/265 (9%)

Query: 4 TTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T ++TP ++GA+V G+ L +DDA FAALH A+L H +L++ GQ L Q+ FA+
Sbjct: 2 TKPKVPTPLTGSIGASVEGIDL NKPVDATFAALHDAFLTHCVLVYRQQQLQPAQVEFAR 61
Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
+G I ++++ + Q + + K AWH DS Y+PV + +
Sbjct: 62 CWGTPLN TNP----LIKHIESHPEIVQVT-----KIPKATASTEAWHYDSPYIPVPPKIS 112
Query: 123 VFSAEVVP AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ SA VP GG T + + +YD L + + + + +LG + A +A
Sbjct: 113 ILSAVTVPH-GGDTMWCNQCLSYDRLSPTMKGALEGLRVK----FVGLRLGRMMGADAAS 167
Query: 183 IGYGM DTTATPLRPLVKVHPETGRPSLLIGRH--AHAIPGMDAAESERFLEGLVDWACQA 240
+ + + PLV+ HPETGR +L +G A I GM A ES L+ L +
Sbjct: 168 L-----PSAVHPLVRTHPETGRKALYVGHRETAQLIDGMTAEESRPLLDFLYQHSTSP 220
Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRA 265
++ H W GDVV+WDNRC +H A
Sbjct: 221 DNIYRHMWQPGDVVMWDNRCTMHYA 245

>ref|YP_003210470.1| hypothetical protein CTU_21070 [Cronobacter turicensis z3032]
emb|CBA30822.1| hypothetical protein CTU_21070 [Cronobacter turicensis z3032]
Length = 316

Score = 127 bits (320), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 93/296 (31%), Positives = 142/296 (47%), Gaps = 28/296 (9%)

Query: 1 MAQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
+A + ITP A LGA +TG+ L +++A FA +H A L H +++F Q L+ QQI
Sbjct: 32 VAAQSFTITPF-ARLGAEITGLDLRLPVNNADFARIHQAHLDHHVVVFRDQKLTPRQQID 90
Query: 60 FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHAD 111
F++RFG ++ +I+ +SN+ +G P D K WH+D
Sbjct: 91 FSRRFGPLQIHVLKQFLLPDHPEILIVSNIIENG-----QPTGLGDAGKF-----WHSD 139
Query: 112 STYMPVMAQGAVFSAEVVP AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQ 169
+Y + + G++ A+ +P GG T FADM AY+ L R + + A HS YS+
Sbjct: 140 LSYKTLPSLGSM LYAQELPEEGGDTL FADMELAYETLP AELRRAIEGKKAHVHSYTATYSR 199
Query: 170 SKLGHVQQAGSAYIGYGM DTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESE 227
K G + P+V+ HPET R +L + G H I G+ ES
Sbjct: 200 PKFG--SHWRPQLTEQQLAEVQAVSHPVVRTHPETRRKALFVSEGFTTH-IEGLPETESR 256

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
LE L + + ++ HQW GD+V WDNR L+H A L R ++ + + G
Sbjct: 257 EILEALWAHSVRPEHIYRHQWQPGDMVFWDNRSLIHLATGCPAHLRRKLYRTTIEG 312

>gb|AAB47567.1| 2,4-D dioxygenase [Burkholderia cepacia]
Length = 288

Score = 127 bits (319), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 86/249 (34%), Positives = 122/249 (48%), Gaps = 23/249 (9%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQ 89
+ A+L+F GQ L DQOI FA+ FG +E R ++ ISNV DG V
Sbjct: 39 KKAVLVFRGQPLDQDQQIAFARNFGQLEGGFIKVNQRPSRFKYAELADISNVSVDGKV-- 96

Query: 90 HSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-YDAL 148
+ E + + N WH+DS++ A+ ++ SA V+P +GG T F D+ A
Sbjct: 97 -ADREARESVMNFANNQLWHSDDSSFQAAAARYSMLSASVLPPLGGDTEFWDIHATNLGGR 155

Query: 149 DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVHPETGRP 207
D+ R L R+ R+ L S+ LG + S P+ PLV+ H +GR
Sbjct: 156 DDLPRELQGLRAERY-LQNSRFILGDDTDSYES-----QRNAMPVSWPLVRTHAGSGRK 208

Query: 208 SLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEP 267
L IG HA I G AE L L++ A Q V+ H+W GD+V+WDNRC+LHR
Sbjct: 209 FLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHRWKVGDLMWDNRCVLHRGRG 268

Query: 268 WDFKLPRVM 276
+D R +
Sbjct: 269 YDITARREL 277

>ref|NP_959172.1| hypothetical protein MAP0238c [Mycobacterium avium subsp.
paratuberculosis K-10]
gb|AAS02555.1| hypothetical protein MAP_0238c [Mycobacterium avium subsp.
paratuberculosis K-10]
Length = 295

Score = 127 bits (319), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 91/287 (31%), Positives = 144/287 (50%), Gaps = 21/287 (7%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAG--FAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++I +G A + GV +A + + +A + AA+ +H++LIF QH+S++ Q+ F++R
Sbjct: 1 MEIVASGPGFAAELRGVTIADVAASPDVYAQVRAAFEEHSLIFRDQHVSDEAQLAFSRR 60

Query: 64 FGAIE--RIG---GGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPV 117
FG +E ++G G +V + + DG V P + ++ N WH DS++ V
Sbjct: 61 FGPLEVTKVGAVGRGSHLVVLKTLDDDDGNV---VPTDHRLELEN-KANQLWHTDSSFKRV 116

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
A +V S+ +VP GG T + R A++ LD R V A H YS+ K+
Sbjct: 117 PALASVLSRIVPGRGGETEYVSTRIAIFERLDPGLRERVENSAWHEYAYSRGKI----- 171

Query: 178 AGSAYIGYGMDDTTATPLR--PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD 235
+ + + A P + LV +P GR +L + HA+ I GM+ A + L L +
Sbjct: 172 --APDLARPEERAALPPQCWRLVWRNPVNGRKALYLASHAYGIEGMEPAAARELLAALTE 229

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLA 282
A + H W AGDVV+WDNR +HR PW PR M S +A
Sbjct: 230 AATAPGASYLHWRAGDVVMWDNRATMHRGRPWPAHQPRYMVRSTIA 276

>ref|ZP_03397512.1| dioxygenase, TauD/TfdA family [Pseudomonas syringae pv. tomato T1]

ref|ZP_07235053.1| dioxygenase, TauD/TfdA family protein [Pseudomonas syringae pv. tomato Max13]
ref|ZP_07259849.1| dioxygenase, TauD/TfdA family protein [Pseudomonas syringae pv. tomato NCPPB 1108]
gb|EEB59304.1| dioxygenase, TauD/TfdA family [Pseudomonas syringae pv. tomato T1]
Length = 298

Score = 127 bits (319), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 89/282 (31%), Positives = 136/282 (48%), Gaps = 37/282 (13%)

Query: 2 AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A + + P +GA + G+ L+ L+DA FA +H A L H +++F Q ++ QQI F
Sbjct: 14 ASQSFDVRPFTGKVGAEIVGLDLRPLNDADFARVHRAHLDDHVVVFRDQQITPQQQIDF 73

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
++RFG ++ +I+ +SN+ V P D K WH+D
Sbjct: 74 SRRFGVLQIHVLKQFLLANHPEILIVSNI-----VENEKPVGLGDAGKY-----WHS DL 122

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+Y + + G++ A+ +P+ GG T FADM A+D L + R V RSA HS S+
Sbjct: 123 SYKELPSLGSMLYAQELPSEGGDTLFDAMHQAWDTLPQHRLDAVEGRSAVHSYTARYSE- 181

Query: 173 GHVQQAGSAYIGYGMDDTTATPL-----RPLVKVHPETGRPSLLI--GRHAHAIPGMDA 223
G + + TA L P+V+ HPE GR +L + G H I G+
Sbjct: 182 -----GHNAVNWRPTLTAEQLAQVVEVSHPIVRTHPENGRKALFVSEGFTH-ILGLPE 234

Query: 224 AESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
ES + L L + + ++ HQW A D+V WDNR L+H A
Sbjct: 235 DESRQILGELYAHSVRPEHIYRQWQANDMVFWDNRS LIHLA 276

>ref|NP_636166.1| taurine dioxygenase [Xanthomonas campestris pv. campestris str. ATCC 33913]
gb|AAM40090.1| taurine dioxygenase [Xanthomonas campestris pv. campestris str. ATCC 33913]
Length = 300

Score = 127 bits (319), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 85/270 (31%), Positives = 130/270 (48%), Gaps = 21/270 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+QI P A LGA V G+ L+ LD FA LH A L H +L+F Q ++ QQ+ F++RF
Sbjct: 20 VQIVPFDAPLGAIEVIGLALSQPLDADTFARLHRAHLDDHVLVFRDQRITPAQQVEFSRRF 79

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
G ++ G +++ +SN+K +G P D WH+D +Y
Sbjct: 80 GPLQIHVLRNFQLRGHPVLVVSNIKENG-----QPIGLGD-----AGHYWHS DLSYKE 128

Query: 117 VMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ G++ A+ +PA GG T FA+ A+ L +A + V R A HS + +L
Sbjct: 129 TPSLGSLHLAQELPAEGGDTLFANQH LAWQTL PDALKRAVEGRQAHSYLAKEYEELRARN 188

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
A + P+V+ HP TGR +L + H I G+ ES L+ L D
Sbjct: 189 PWRPALTAEQIAEVTVPQHPIVRTHPATGRKALFVSEHFTTRIVGLPDDESHALLQALFD 248

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
+ + V+ H+W D+V WDNR ++H A
Sbjct: 249 HSTRDALVYRHRWQPHDMVFWDNRSVMHLA 278

>ref|YP_001586000.1| taurine dioxygenase [Burkholderia multivorans ATCC 17616]
gb|ABX19708.1| Taurine dioxygenase [Burkholderia multivorans ATCC 17616]

Length = 291

Score = 127 bits (318), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 88/292 (30%), Positives = 138/292 (47%), Gaps = 21/292 (7%)

```
Query: 2  AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
          A   +I P  A LGA V G+ L+ LD   FA +  A L H +L+F  Q ++ D+ + F
Sbjct: 7  APQRFEIVPFDAPLGAEEVVGIDLSQPLDADAFARIRRAHLDDHVLVFRDQRITPDEHVAF 66

Query: 61 AKRFGAIER-----IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
          ++RFG ++          G +++ +SN+ +G          P   D          WH+D
Sbjct: 67 SRRFGPLQTHVLHQFALPGHPEVLIVSNIVENG-----KPIGLGD-----AGYFWHSDL 115

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
          +Y   + G++  A+ +PA GG T FA+M  A+D L EA R  V  R A H+ +  ++L
Sbjct: 116 SYKRRPSLGSLLHAQELPAEGGDTLFANMHLAWDTLPEALRRAVEGRRRAEHTYLARYAEL 175

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE 231
          +          + P+V+ HPETGR +L +  H   I G+  ES   L+
Sbjct: 176 QARSPWRPNLSAEQIAQVEPVVHPVVRTHPETGRRALFVSEHFTTRIVGLPDDESRLLD 235

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          L   + +A   + H+W   D+V WDNR LLH A          L R ++ + + G
Sbjct: 236 ELFAHSVRAEHQYRHRWRDHDLVFWDNRSLHLAAGTPDHLRRKLYRTTIEG 287
```

>ref|ZP_06878755.1| putative taurine catabolism dioxygenase [Pseudomonas aeruginosa
Pab1]
Length = 295

Score = 127 bits (318), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 94/295 (31%), Positives = 145/295 (49%), Gaps = 27/295 (9%)

```
Query: 2  AQTTLQITPTGATLGATVTGVHLATLDDAG-FAALHAAWLQHALLIFPGQHLSNDQQITF 60
          A   LQI   A  GA V G+ L   AG F  +H A L H +L+F  Q ++  QQI F
Sbjct: 11 ADVPLQIRALDAAFGAEVLGLDLGLPLAAGDFRRIHRAHLDDHVLVFRDQRITPAQQIAF 70

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
          ++RFG ++          G +I+ +SN+ +G          P   D K          WH+D
Sbjct: 71 SRRFGELQIHVLKQFLLPGHPEILIVSNIVENG-----QPVGLGDAGKF-----WHSDDL 119

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQS 170
          +Y   + + G++  A+ +P  GG T FADM  A+D+L EA R  +  R+A HS   YS+
Sbjct: 120 SYKELPSLGSMLHAQELPEEGGDTLFADMHKAWDSLPEALRKAIEGRRTAAHSYTARYSEP 179

Query: 171 KL-GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESER 228
          +  G+ +   SA   +          + P+V+ HPE+GR +L +          I G+ A ES +
Sbjct: 180 RFEGNWRPTLSA---AQLAEVREVVHPIVRTHPESGRKALFVSEGFTTRIVGLPADESAQ 236

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          L  L   + +   ++ H+W A D+V WDNR L+H A          L R ++ + + G
Sbjct: 237 LLAELYAHSVRPEHIYRHRWQAHDLVFWDNRSLIHLAGGCPAHLRRKLYRTTIQ 291
```

>ref|ZP_06485157.1| taurine dioxygenase [Xanthomonas campestris pv. vasculorum
NCPPB702]
Length = 305

Score = 127 bits (318), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 81/275 (29%), Positives = 134/275 (48%), Gaps = 21/275 (7%)

```
Query: 1  MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
          +  ++++I P   LGA V G+ L+ LD   FA +H A L H +L+F  Q ++  QQ+
```

Sbjct: 20 LQSSSVRIVPFDGPLGAEVIGLDLSQPLDADTFARIHRAHLDDHVLVFRDQRITPAQQVE 79

Query: 60 FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHAD 111
F++RFG ++ G +++ +SN+K +G P D WH+D

Sbjct: 80 FSRRFGPLQIHVLRNFQLRGHPEVLVVSNIKENG-----EPIGLGD-----AGHYWHS 128

Query: 112 STYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
+Y + G++ A+ +P+ GG T FA+ A+ L E+ + V A HS + +

Sbjct: 129 LSYKETPSLGSLLHAQELPSEGDDTLFANQHLAWQTLPESLKRTVQDLRAEHSYLAKYEE 188

Query: 172 LGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL 230
L A + + P+V+ HPETGR +L + H I G+ ES L

Sbjct: 189 LRARNPWRPALMPEQIAEVTVPVQHPVVRTHPETGRKALFVSEHFTTRIVGLPKDESRALL 248

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ L + + +A V+ H+W D+V WDNR ++H A

Sbjct: 249 QTLFEHSTRAALVYRHRWQPHDMVFWDNRSVMHLA 283

>ref|ZP_06842038.1| Taurine dioxygenase [Burkholderia sp. Chl-1]
gb|EFG70263.1| Taurine dioxygenase [Burkholderia sp. Chl-1]
Length = 302

Score = 127 bits (318), Expect = 3e-27, Method: Compositional matrix adjust.
Identities = 88/283 (31%), Positives = 139/283 (49%), Gaps = 29/283 (10%)

Query: 15 LGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
+GA V G+ L L F +H A L H +L+F Q ++ DQOI F++RFG ++

Sbjct: 31 VGAEVLGLDLGRPLSQDDFERIHRAHLDDHVLVFRDQRITPDQQIAFSRRFGPLQIHVLH 90

Query: 69 ---RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
G +++ +SN+ +G P D WH+D +Y + G++

Sbjct: 91 QFQLPGHPEVLVVSNIKENG-----QPIGLGD-----AGHFWSLSYKETPSLGSLLH 139

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY--- 182
A+ +PA GG T FA+M A+D L RA V RSA H+ + ++L Q S +

Sbjct: 140 AQELPAEGGDTLAFANMHLAWDTLPAHLRAAVEGRSAEHTYLAKYAEL----QKRSPWRPD 195

Query: 183 IGYMDTTATPL-RPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQA 240
+ G P+ P+V+ HPETGR +L + H + G+ ES+ LE + + +

Sbjct: 196 LTAGQIAQVKPVTHPIVRTHPETGRKALFVSEHFTTRIVIGLPEDESQSLEEIFAHSVRP 255

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
++ HQWA D+V WDNR L+H A L R ++ + + G

Sbjct: 256 EHLYRHQWAEHDMVFWDNRLMHLAAGTPDHLRRLYRTTIEG 298

>ref|ZP_07254236.1| dioxygenase, TauD/TfdA family protein [Pseudomonas syringae pv.
tomato K40]
Length = 298

Score = 127 bits (318), Expect = 3e-27, Method: Compositional matrix adjust.
Identities = 89/282 (31%), Positives = 136/282 (48%), Gaps = 37/282 (13%)

Query: 2 AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A + + P +GA + G+ L+ L+DA FA +H A L H +++F Q ++ QQI F

Sbjct: 14 ASQSFDVRPFTGKVGAEIVGLDLSRPLNDADFARVHRAHLDDHVVVFRDQQITPQQQIDF 73

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADS 112
++RFG ++ +I+ +SN+ V P D K WH+D

Sbjct: 74 SRRFGVLQIHVLKQFLLANHPEILIVSNI-----VENEKPVGLGDAGKY-----WHS 122

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172

Query:	2	AQTTLQIITPGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF	60
		A +I P A LGA V G+ L+ LD FA + A L H +L+F Q ++ D+ + F	
Sbjct:	25	APQRFEIVPFDAPLGAEEVVGIDLSQPLDADAFARIRRAHLDDHVLVFRDQRITPDEHVAF	84
Query:	61	AKRFGAIER-----IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS	112
		++RFG ++ G +++ +SN+ +G P D WH+D	
Sbjct:	85	SRRFGPLQTHVLHQFALPGHPEVLIVSNIVENG-----KPIGLGD-----AGYFWHSDL	133
Query:	113	TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL	172
		+Y + G++ A+ +PA GG T FA+M A+D L EA R V R A H+ + ++L	
Sbjct:	134	SYKRPSLGSLLHAQELPAEGGDTLFLANMHLAWDTLPEALRRAVEGRRAEHTYLARYAEL	193
Query:	173	GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE	231
		+ + P+V+ HPETGR +L+ H I G+ ES L+	
Sbjct:	194	OARSPWRPNLSAEQIAOEVVHPVVRTHPETGRRALFVSEHFTTRIVGLPDDESRALLD	253

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + +A + H+W D+V WDNR LLH A L R ++ + + G
Sbjct: 254 ELFAHSVRAEHQYRHRWRDHDLVFWDNRSLHLAAGTPDHLRRLKLYRTTIEG 305

>ref|ZP_06492039.1| taurine dioxygenase [Xanthomonas campestris pv. musacearum
NCPPB4381]
Length = 305

Score = 126 bits (317), Expect = 3e-27, Method: Compositional matrix adjust.
Identities = 81/275 (29%), Positives = 134/275 (48%), Gaps = 21/275 (7%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
+ ++++I P LGA V G+ L+ LD FA +H A L H +L+F Q ++ QQ+
Sbjct: 20 LQSSSVRIVPFDGPLGAEVIGLDLSQPLDADTFARIHRAHLDDHVLVFRDQRITPAQQME 79

Query: 60 FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHAD 111
F++RFG ++ G +++ +SN+K +G P D WH+D
Sbjct: 80 FSRRFGPLQIHVLRNFQLRGHPEVLVVSNIKENG-----EPIGLGD-----AGHYWHS 128

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
+Y + G++ A+ +P+ GG T FA+ A+ L E+ + V A HS + +
Sbjct: 129 LSYKETPSLGSLLHAQELPSEGGDTLFANQHLAWQTLPELSKRTVQDLRAEHSYLAKYEE 188

Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL 230
L A + + P+V+ HPETGR +L + H I G+ ES L
Sbjct: 189 LRARNPWRPALMPEQIAEVTPVQHPVVRTHPETGRKALFVSEHFTTRIVGLPKDESALL 248

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ L + + +A V+ H+W D+V WDNR ++H A
Sbjct: 249 QTLFEHSTRAALVYRHRWQPHDMVFWDNRSVMHLA 283

>ref|YP_879528.1| taurine catabolism dioxygenase TauD/TfdA [Mycobacterium avium 104]
gb|ABK68373.1| taurine catabolism dioxygenase TauD/TfdA [Mycobacterium avium 104]
Length = 295

Score = 126 bits (316), Expect = 4e-27, Method: Compositional matrix adjust.
Identities = 90/287 (31%), Positives = 144/287 (50%), Gaps = 21/287 (7%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAG--FAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++I +G A + GV +A + + +A + AA+ +H++L+F QH+S++ Q+ F++R
Sbjct: 1 MEIVASGPGFAAELRGVTIADVAASPDVYAQVRAAFEEHSLVLFVRDQHVSDAQALAFSRR 60

Query: 64 FG--AIERIG---GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV 117
FG + ++G G +V + + DG V PA+ ++ N WH DS++ V
Sbjct: 61 FGPLGVTKVGAVGHGSHLVVLKTLDDDGNV--VPADHRLALEN-KANQLWHTDSSFKRV 116

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
A +V S+ +VP GG T + R A++ LD R V A H YS+ K+
Sbjct: 117 PALASVLSSRIVPGRGGETEYVSTRIAIFERLDPGLRERVENSFAWHEYAYSRGKI----- 171

Query: 178 AGSAYIGYGMDDTTATPLR--PLVKVHPETGRPSLLIGRHHAHAIPGMDAAESERFLEGLVD 235
+ + + A P + LV +P GR +L + HA+ I GM+ A + L L +
Sbjct: 172 --APDLARPEERAALPPQCWRLVWRNPVNGRKALYLASHAYGIEGMEPAAARELLAALTE 229

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLA 282
A + H W AGDVV+WDNR +HR PW PR M S +A
Sbjct: 230 AATAPGASYLHWSRAGDVVMWDNRATMHRGRPWPAHQPRCMVRSTIA 276

>ref|ZP_04948709.1| Probable taurine catabolism dioxygenase [Burkholderia dolosa
AU0158]

gb|EAY71880.1| Probable taurine catabolism dioxygenase [Burkholderia dolosa AU0158]
Length = 310

Score = 126 bits (316), Expect = 4e-27, Method: Compositional matrix adjust.
Identities = 86/292 (29%), Positives = 139/292 (47%), Gaps = 21/292 (7%)

Query: 2 AQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A + I P A LGA V G+ L+ L DA FA +H A L H +L+F Q ++ D+ + F
Sbjct: 26 AAQSFDIVPFDAPLGAEEVVGIDLSRPLADADFACIHRALDHHVLFVFRDQRITPDEHVAF 85

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
++RFG ++ G +++ +SN+ +G P D WH+D
Sbjct: 86 SRRFGPLQIHVLHQFALAGHPEVLIVSNIVENG-----KPIGLGD-----AGHFWHSDL 134

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+Y + G++ A+ +PA GG T FA+M A+D L R V R A H+ + ++L
Sbjct: 135 SYKEKPSLGSLLHAQELPAEGGDTLFANMHLAWDTLPAHLRRAVEGRRAEHTYLARYAEL 194

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE 231
+ + P+V+ HPETGR +L + H I + ES L+
Sbjct: 195 QARSPWRPNLSPEQIAQVKPVVHPVVRTHPETGRKALFVSEHFTTRIVDLPDDESRLALD 254

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + +A ++ H+W D+V WDNR L+H A +L R ++ + + G
Sbjct: 255 ELFAHSVRAEHLRHRWRDHDLVFWDNRSLMHLAAGTPDRLRRKLYRTTIEG 306

>ref|ZP_05214809.1| taurine catabolism dioxygenase TauD/TfdA [Mycobacterium avium subsp. avium ATCC 25291]
Length = 295

Score = 126 bits (316), Expect = 4e-27, Method: Compositional matrix adjust.
Identities = 90/287 (31%), Positives = 144/287 (50%), Gaps = 21/287 (7%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAG--FAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++I +G A + GV +A + + +A + AA+ +H++L+F QH+S++ Q+ F++R
Sbjct: 1 MEIVASGPGFAAELRGVTIADVAASPDVYAQVRAAFEEHSLVLFVFRDQHVSDAQALAFSRR 60

Query: 64 FGAIE--RIG---GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV 117
FG + ++G G +V + + DG V PA+ ++ N WH DS++ V
Sbjct: 61 FGPLRVTKVGAVGHGSHLVVLKTLDDDGNV---VPADHRLALEN-KANQLWHTDSSFKRV 116

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
A +V S+ +VP GG T + R A++ LD R V A H YS+ K+
Sbjct: 117 PALASVLSSRIVPGRGGETEYVSTRIAFERLDPGLRERVENSFAWHEYAYSRGKI----- 171

Query: 178 AGSAYIGYGMDTTATPLR--PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD 235
+ + + A P + LV +P GR +L + HA+ I GM+ A + L L +
Sbjct: 172 --APDLARPEERAALPPQCWRLVWRNPVNGRKALYLASHAYGIEGMEPAAARELLAALTE 229

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLA 282
A + H W AGDVV+WDNR +HR PW PR M S +A
Sbjct: 230 AATAPGASYLHWRAGDVVMWDNRATMHRGRPWPAHQPRCMVRSTIA 276

>ref|ZP_07796648.1| putative taurine catabolism dioxygenase [Pseudomonas aeruginosa 39016]
gb|EFQ41744.1| putative taurine catabolism dioxygenase [Pseudomonas aeruginosa 39016]
Length = 295

Score = 126 bits (316), Expect = 4e-27, Method: Compositional matrix adjust.

Identities = 93/295 (31%), Positives = 144/295 (48%), Gaps = 27/295 (9%)

```
Query: 2  AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
          A  LQI   A  GA V G+ L  L  F  +H A L H +L+F  Q ++  QQI F
Sbjct: 11 ADVPLQIRALDAAFGAEVLGLDLGLPLAAEDFRRIHRAHLDDHVLVLFREQRITPAQQIAF 70

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
          ++RFG ++          G  +I+ +SN+  +G          P    D K          WH+D
Sbjct: 71 SRRFGELQIHVLKQFLLPGHPEILIVSNIVENG-----QPVGLGDAGKF-----WHSDL 119

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMR AAYDALDEATRALVHQRSARHSLV--YSQS 170
          +Y  + + G++  A+ +P  GG T FADM  A+D+L EA R  +  R+A HS    YS+
Sbjct: 120 SYKELPSLGSMLHAQELPKEGGDTL FADM HKAWDSLPEALRKAIEGRTAAHSYTARYSEP 179

Query: 171 KL-GHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESER 228
          +  G+ +  SA      +          + P+V+ HPE+GR +L +          I G+ A ES +
Sbjct: 180 RFEGNWRPTLSA--AQLAEVREV VHP IVRTHPESGRKALFVSEGFTTRIVGLPADESAQ 236

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          L  L  + +  ++ H+W A D+V WDNR L+H A          L R ++ + + G
Sbjct: 237 LLAELYAHSVRPEHIYRHRWQAHDLVFWDNRSLIHLAGGCPAHLRRKLYRTTIQG 291
```

>ref|YP_790929.1| putative taurine catabolism dioxygenase [Pseudomonas aeruginosa
UCBPP-PA14]
gb|ABJ11490.1| putative taurine catabolism dioxygenase [Pseudomonas aeruginosa
UCBPP-PA14]
Length = 295

Score = 126 bits (316), Expect = 4e-27, Method: Compositional matrix adjust.
Identities = 93/295 (31%), Positives = 144/295 (48%), Gaps = 27/295 (9%)

```
Query: 2  AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
          A  LQI   A  GA V G+ L  L  F  +H A L H +L+F  Q ++  QQI F
Sbjct: 11 ADVPLQIRALDAAFGAEVLGLDLGLPLAAEDFRRIHRAHLDDHVLVLFREQRITPAQQIAF 70

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
          ++RFG ++          G  +I+ +SN+  +G          P    D K          WH+D
Sbjct: 71 SRRFGELQIHVLKQFLLPGHPEILIVSNIVENG-----QPVGLGDAGKF-----WHSDL 119

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMR AAYDALDEATRALVHQRSARHSLV--YSQS 170
          +Y  + + G++  A+ +P  GG T FADM  A+D+L EA R  +  R+A HS    YS+
Sbjct: 120 SYKELPSLGSMLHAQELPEEGGDTL FADM HKAWDSLPEALRKAIEGRTAAHSYTARYSEP 179

Query: 171 KL-GHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESER 228
          +  G+ +  SA      +          + P+V+ HPE+GR +L +          I G+ A ES +
Sbjct: 180 RFEGNWRPTLSA--AQLAEVREV VHP IVRTHPESGRKALFVSEGFTTRILGLPADESAQ 236

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          L  L  + +  ++ H+W A D+V WDNR L+H A          L R ++ + + G
Sbjct: 237 LLAELYAHSVRPEHIYRHRWQAHDLVFWDNRSLIHLAGGCPAHLRRKLYRTTIQG 291
```

>ref|YP_001265549.1| taurine dioxygenase [Pseudomonas putida F1]
gb|ABQ76365.1| Taurine dioxygenase [Pseudomonas putida F1]
Length = 299

Score = 126 bits (316), Expect = 4e-27, Method: Compositional matrix adjust.
Identities = 85/294 (28%), Positives = 144/294 (48%), Gaps = 31/294 (10%)

```
Query: 5  TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
          ++ P    +GA + G+ LA  +  F  +H A L H +L+F  Q +S +QQI F++R
Sbjct: 18 VFEVRPFSGAVGAEEIIGLDLAKPVSAEDFTRI HRAHLDDHVLVFRDQRISPEQQIAFSRR 77
```

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDWDDMMKVIVGNMA--WHADST 113
FG ++ G +I+ +SN+ +G + +G+ WH+D +
Sbjct: 78 FGELQIHVLKQFLLTGHPEILIVSNIIENG-----QNIGLGDAKGFVHSDLS 124

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSK 171
Y + + G++ A+ +P+ GG T FADM A+DA+ + R +V RSA HS Y+++K
Sbjct: 125 YKELPSLGSMLHAQELPSEGGDTLFDAMHKAWDAVPDTRLKVVVEGRSAAHSYTARYAETK 184

Query: 172 L-GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERF 229
G+ + +A + + P+V+ HPE GR +L + I G+ ES
Sbjct: 185 FEGNWRPTLTA---EQLAQVKEVIHPVVRTHPENGRKALFVSEGFTTRIVGLPDDES RDV 241

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L+ L + ++ HQW D+V WDNR L+H A L R ++ + + G
Sbjct: 242 LQQLYALSVLEQNIYRHQWQPHDLVFWDNRS LIHLATGCPAHLRRKLYRTTIQG 295

>ref|ZP_08185828.1| putative taurine catabolism dioxygenase [Xanthomonas gardneri ATCC

19865]

gb|EGD16544.1| putative taurine catabolism dioxygenase [Xanthomonas gardneri ATCC 19865]

Length = 305

Score = 125 bits (315), Expect = 5e-27, Method: Compositional matrix adjust.
Identities = 82/270 (30%), Positives = 131/270 (48%), Gaps = 21/270 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+QI P A LGA V G+ L+ LD FA +H A L H +L+F Q +S QQ+ F++RF
Sbjct: 25 VQIVPFDAPLGAEVIGLDLSQPLDADTFARIHQAHLDHHVLVFRDQRISPAQQVDFSRRF 84

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDWDDMMKVIVGNMAWHADSTYMP 116
G ++ G +++ +SN+K +G P D WH+D +Y
Sbjct: 85 GPLQIHVLRNRFQLRGHPVLVVSNIKENG-----EPIGLGD-----AGHYWHS DLSYKE 133

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ G++ A+ +P+ GG T FA+ A+ L +A + V A HS + +L
Sbjct: 134 TPSLGSLLHAQELPSEGGDTLFANQHLAWQTLDPALKRTVQDLRAEHSYLAKYEELRARN 193

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
A + P+V+ HPETG+ +L + H I G+ ES+ L+ L +
Sbjct: 194 PWRPALTAEQIAEVTVPVQHPIVRTHPETGQKALFVSEHFTTRIVGLPDDES DALLQALFE 253

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ + V+ H+W D+V WDNR ++H A
Sbjct: 254 HSTREALVYRHRWQPHDMVFWDNRSVMHLA 283

>ref|NP_251000.1| hypothetical protein PA2310 [Pseudomonas aeruginosa PA01]
ref|YP_002440583.1| putative taurine catabolism dioxygenase [Pseudomonas aeruginosa LESB58]
ref|ZP_04928643.1| hypothetical protein PACG_01220 [Pseudomonas aeruginosa C3719]
gb|AAG05698.1|AE004657_5 hypothetical protein PA2310 [Pseudomonas aeruginosa PA01]
gb|EAZ52762.1| hypothetical protein PACG_01220 [Pseudomonas aeruginosa C3719]
emb|CAW27721.1| putative taurine catabolism dioxygenase [Pseudomonas aeruginosa LESB58]
Length = 295

Score = 125 bits (315), Expect = 5e-27, Method: Compositional matrix adjust.
Identities = 93/295 (31%), Positives = 144/295 (48%), Gaps = 27/295 (9%)

Query: 2 AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60

```

      A  LQI      A  GA V G+ L  L      F  +H A L H +L+F  Q ++  QQI F
Sbjct: 11  ADVPLQIRALDAAFGAEVLGLDLGLPLAAEDFRRIHRAHLDDHVLVLFREQRITPAQQIAF 70

Query: 61  AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADS 112
      ++RFG ++          G  +I+ +SN+  +G      P      D  K      WH+D
Sbjct: 71  SRRFGELQIHVLKQFLLPGHPEILIVSNIVENG-----QPIGLGDAGKF-----WHS DL 119

Query: 113  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQS 170
      +Y  + + G++  A+ +P  GG T FADM  A+D+L EA R  +  R+A HS      YS+
Sbjct: 120  SYKELPSLGSMLHAQELPEEGGDTLFDAMHKAWDSLPEALRKAIEGRTAAHSYTARYSEP 179

Query: 171  KL-GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESER 228
      +  G+ +  SA      +          + P+V+ HPE+GR +L +          I G+ A ES +
Sbjct: 180  RFEGNWRPTLSA--AQLAEVREVVHPIVIRTHPESGRKALFVSEGFTTRIVGLPADESAQ 236

Query: 229  FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
      L  L  + +  ++ H+W A D+V WDNR L+H A      L R ++ + + G
Sbjct: 237  LLAELYAHSVRPEHIYRHRWQAHDLVFWDNRSLIHLAGGCPAHLRRKLYRTTIQ 291

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>ref|ZP_08187882.1| putative taurine catabolism dioxygenase [Xanthomonas perforans 91-118]
 gb|EGD14521.1| putative taurine catabolism dioxygenase [Xanthomonas perforans 91-118]
 Length = 305

Score = 125 bits (315), Expect = 5e-27, Method: Compositional matrix adjust.
 Identities = 83/272 (30%), Positives = 132/272 (48%), Gaps = 21/272 (7%)

```

Query: 4    TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
      ++++I P  A LGA V G+ LA  LD A FA +H A L + +L+F  Q ++  QQ+ F++
Sbjct: 23  SSVRIVPFDAPLGAEVIGLDLAQPLDAATFARIHRAHLDYHVLVFRDQRITPAQQVEFSR 82

Query: 63  RFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTY 114
      RFG ++          G  +++ +SN+K +G      P      D      WH+D +Y
Sbjct: 83  RFGPLQIHVLRFQLRGHPEVLVVSNIKENG-----EPIGLGD-----AGHYWHS DLSY 131

Query: 115  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
      + G++  A+ +P  GG T FA+  A+  L E+ +  V      A HS +      +L
Sbjct: 132  KQTPSLGSLHAQELPGEAGDTLAFANQHLAWQTLPESLKRAVQDLRAEHSYLAKYEELRA 191

Query: 175  VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGL 233
      A      +          P+V+ HPETGR +L +  H      I G+  ES  L+ L
Sbjct: 192  RNPWRPALTPEQIAEVTVPQHPVVRTHPETHGRKALFVSEHFTTRIVGLPEDES RALLQRL 251

Query: 234  VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      + +  A  V+ H+W  D+V WDNR ++H A
Sbjct: 252  FEHSTHAALVYRHRWQPHDMVFWDNRSMHLA 283

```

>ref|YP_841732.1| taurine catabolism dioxygenase [Ralstonia eutropha H16]
 emb|CAJ97002.1| taurine catabolism dioxygenase [Ralstonia eutropha H16]
 Length = 309

Score = 125 bits (315), Expect = 5e-27, Method: Compositional matrix adjust.
 Identities = 87/289 (30%), Positives = 136/289 (47%), Gaps = 21/289 (7%)

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Query: 5    TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
      +I P  A LGA V G+ L+  L DA      +H A L + +++F  Q ++  QQI F++R
Sbjct: 28  NFEIRPLDAPLGAEVIGLDLSQPLSDADVRIHRAHLDYHVVVFRDQQITPAQQIDFSRR 87

Query: 64  FGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYM 115
      FG ++          G  +++ +SNV  +G      P      D      WH+D +Y

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Sbjct: 88 FGPLQIHVLHQFQLPGHAEVLVVSNNVENG-----KPIGLGD-----AGHFWHSDLSYK 136

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
+ G++ A +PA GG T FA+M A+D L A + V A H+ + ++L

Sbjct: 137 EKPSLGSLLHARELPAEGGDTLGFANMHLAWDTLPSALQRAVDGLHAEHTYLARYAELQQR 196

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLV 234
+ L+P+V+ HPETGR +L + H I G+ ES L+ L

Sbjct: 197 SPWRPDLTPEQIAQVRPVLQPVVRTHPETGRKALFVSEHFTTRIVGLPEQESRDLLDQLF 256

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ + ++ HQW D+V WDNR LLH A + RVM+ + + G

Sbjct: 257 AHSVKAHIYRHWQPHDLVFWDNRSLLHLAAGCPPEQRRVMYRTTIEG 305

>gb|AAT51290.1| PA2310 [synthetic construct]
Length = 296

Score = 125 bits (315), Expect = 5e-27, Method: Compositional matrix adjust.
Identities = 93/295 (31%), Positives = 144/295 (48%), Gaps = 27/295 (9%)

Query: 2 AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A LQI A GA V G+ L L F +H A L H +L+F Q ++ QQI F

Sbjct: 11 ADVPLQIRALDAAFGAEVLGLDLGLPLAAEDFRRIHRAHLDHHVLFVREQRITPAQQIAF 70

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
++RFG ++ G +I+ +SN+ +G P D K WH+D

Sbjct: 71 SRRFGELQIHVLKQFLLPGHPEILIVSNIVENG-----QPIGLGDAGKF-----WHSDL 119

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQS 170
+Y + + G++ A+ +P GG T FADM A+D+L EA R + R+A HS YS+

Sbjct: 120 SYKELPSLGSMLHAQELPEEGGDTLGFADMHKAWDSLPEALRKAIEGRTAAHSYTARYSEP 179

Query: 171 KL-GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESER 228
+ G+ + SA + + P+V+ HPE+GR +L + I G+ A ES +

Sbjct: 180 RFEGNWRPTLSA---AQLAEVREVHPHIVRTHPESGRKALFVSEGFTTRIVGLPADESAQ 236

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L L + + ++ H+W A D+V WDNR L+H A L R ++ + + G

Sbjct: 237 LLAELYAHSVRPEHIYRHRWQAHDLVFWDNRSLIHLAGGCPAHLRRKLYRTTIQG 291

>ref|ZP_05635920.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. tabaci
ATCC
11528]
Length = 298

Score = 125 bits (315), Expect = 6e-27, Method: Compositional matrix adjust.
Identities = 82/288 (28%), Positives = 135/288 (46%), Gaps = 21/288 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ P +GA + G+ L+ L+DA FA +H A L H +++F Q ++ QQ+ F++RF

Sbjct: 18 FDVRPFTGKVGAEIVGLDLSMPLNDADFARVHQAHLDHHVVVFRDQQITPQQQVDFSRRF 77

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
G ++ +I+ +SN+ V P D K WH+D +Y

Sbjct: 78 GVLQIHVLKQFLLANHPILIVSNI-----VENEKPVGLGDAGKY-----WHSDLSYKE 126

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ + G++ A+ +P+ GG T FADM A+D L + R V RSA HS ++ +

Sbjct: 127 LPSLGSMLYAQELPSEGGDTLGFADMHQAWDTLPQHRLDAVEGRSAVHSYTARYAEGHNAA 186

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235

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+          P+V+ HPETGR +L +          I +          ES + L +
Sbjct: 187 NWRPTLTAEQLAQVVEVSHPIVRTHPETGRKALFVSEGFTTRILDLPEDES RQILNEIYA 246

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ + ++ HQW A D+V WDNR L+H A          L R ++ + + G
Sbjct: 247 HSVKPEHIYRHQWQANDMVFDNRSLIHLAAGCPAHLRRKLYRTTIQG 294

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>ref|YP_002908767.1| Taurine dioxygenase [Burkholderia glumae BGR1]
gb|ACR31532.1| Taurine dioxygenase [Burkholderia glumae BGR1]
Length = 305

Score = 125 bits (314), Expect = 6e-27, Method: Compositional matrix adjust.
Identities = 85/288 (29%), Positives = 137/288 (47%), Gaps = 21/288 (7%)

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Query: 6  LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
I P  LGA V G+ L+ L +A FA +H A L H LL+F Q ++ +QQ+ F++RF
Sbjct: 25  FDIVPFDGPLGAEVVGLDLSQPLGEAAFARIHRAHLDHHLVLFREQRITPEQQVAFSRRF 84

Query: 65  GAIER-----IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
G ++          G +++ +SN+ +G          P          D          WH+D +Y
Sbjct: 85  GPLQTHVLHQFALPGHPEVLIVSNIVENG-----KPIGLGD-----AGHFWHSDLSYKE 133

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ G++ A+ +P GG T FA+M A++ L EA + V R A H+ + ++L
Sbjct: 134 KPSLGSLHLHAQELPTEGGDTL FANMHLAWETLPEALKQAVRGRRAEHTYLARYAELQARS 193

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
+          +P+V+ HPETGR +L + H          I G+          ES          L+ L
Sbjct: 194 PWRPNLSAEQLAQVKAVQQPIVRTHPETGRRALFVSEHFTTRIVGLPEDES RALLDELFA 253

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ + V+ H+W D+V WDNR L+H A          L R ++ + + G
Sbjct: 254 HSVRDEFVYRHRWREHDLVFDNRSLMHLAAGTPDHLRRKLYRTTIEG 301

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>ref|YP_001117391.1| taurine dioxygenase [Burkholderia vietnamiensis G4]
gb|AB057926.1| Taurine dioxygenase [Burkholderia vietnamiensis G4]
Length = 309

Score = 125 bits (314), Expect = 6e-27, Method: Compositional matrix adjust.
Identities = 86/292 (29%), Positives = 138/292 (47%), Gaps = 21/292 (7%)

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Query: 2  AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A          I P  A +GA V G+ L+ LD A FA +H A L H +L+F Q ++ +Q I F
Sbjct: 25  AAQRFDIIPLDAPVGAEVVGIDLSQPLDAAAFARIHRAHLDHHLVLFVRDQRITPEQHIAF 84

Query: 61  AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
++RFG ++          G +++ +SN+ +G          P          D          WH+D
Sbjct: 85  SRRFGPLQIHVLHQFALAGHPEVLIVSNIVENG-----KPIGLGD-----AGHFWHSDL 133

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+Y          + G++ A+ +PA GG T FA+M A+D L          R V R A H+ + ++L
Sbjct: 134 SYKEKPSLGSLHLHAQELPADGGDTL FANMHLAWDTLPAHLRRAVEGRRAEHTYLARYAEL 193

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE 231
+          +          + P+V+ HPETGR +L + H          I + A ES          L+
Sbjct: 194 QARNRWRPVL SAEQLAQVEAVVHPIVRTHPETGRKALFVSEHFTTRIVDLPADES RALLD 253

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L          + + ++ H+W D+V WDNR L+H A          L R ++ + + G
Sbjct: 254 ELFAHSVRDEHLYRHRWRDHDLVFDNRSLMHLAAGTPDHLRRKLYRTTIEG 305

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>ref|ZP_08183773.1| putative taurine catabolism dioxygenase [Xanthomonas gardneri ATCC

19865]
gb|EGD18602.1| putative taurine catabolism dioxygenase [Xanthomonas gardneri ATCC
19865]
Length = 309

Score = 125 bits (314), Expect = 7e-27, Method: Compositional matrix adjust.
Identities = 81/272 (29%), Positives = 133/272 (48%), Gaps = 21/272 (7%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
++++I P A LGA V G+ L+ LD FA +H A L H +L+F Q +S QQ+ F++
Sbjct: 27 SSVRIVPFDAPLGAIEVIGLDLSQPLDADTFARIHQAHLDHHVLVFRDQRISPAQVDFSR 86

Query: 63 RFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTY 114
RFG ++ G +++ +SN+K +G P D WH+D +Y
Sbjct: 87 RFGPLQIHVLRNFQLRGHPEVLVVSNIKENG-----EPIGLGD-----AGHYWHSLSY 135

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
+ G++ A+ +P+ GG T FA+ A+ L +A + V A HS + +L
Sbjct: 136 KETPSLGSLLHAQELPSEGGDTLAFANQHLAWQTLPDALKRTVQDLRAEHSYLAKYEELRA 195

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGL 233
A + P+V+ HPETG+ +L + H I G+ ES+ L+ L
Sbjct: 196 RNPWRPALTAEQIAEVTVPVQHPIVTRHPETGQKALFVSEHFTTRIVGLPDDESALLQAL 255

Query: 234 VDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
+ + + V+ H+W D+V WDNR ++H A
Sbjct: 256 FEHSTREALVYRHRWQPHDMVFWDNRSMHLA 287

>ref|YP_362614.1| taurine dioxygenase [Xanthomonas campestris pv. vesicatoria str.
85-10]
emb|CAJ22514.1| Taurine dioxygenase [Xanthomonas campestris pv. vesicatoria str.
85-10]
Length = 305

Score = 125 bits (314), Expect = 7e-27, Method: Compositional matrix adjust.
Identities = 83/272 (30%), Positives = 132/272 (48%), Gaps = 21/272 (7%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
++++I P A LGA V G+ LA LD A FA +H A L + +L+F Q ++ QQ+ F++
Sbjct: 23 SSVRIVPFDAPLGAIEVIGLDLAQPLDAATFARIHRAHLDYHVLVFRDQRITPAQVDFSR 82

Query: 63 RFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTY 114
RFG ++ G +++ +SN+K +G P D WH+D +Y
Sbjct: 83 RFGPLQIHVLRNFQLRGHPEVLVVSNIKENG-----EPIGLGD-----AGHYWHSLSY 131

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
+ G++ A+ +P+ GG T FA+ A+ L E+ + V A HS + +L
Sbjct: 132 KQTPSLGSLLHAQELPGEGGDTLAFANQHLAWQTLPESLKRAVQDLRAEHSYLAKYEELRA 191

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGL 233
A + P+V+ HPETGR +L + H I G+ ES L+ L
Sbjct: 192 RNPWRPALTPEQIAEVTVPVQHPVVRTHPETGRKALFVSEHFTTRIVGLPEDESALLQRL 251

Query: 234 VDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
+ + A V+ H+W D+V WDNR ++H A
Sbjct: 252 FEHSTHAGLVYRHRWQPHDMVFWDNRSMHLA 283

>ref|YP_002153811.1| putative taurine dioxygenase [Burkholderia cenocepacia J2315]

emb|CAR57354.1| putative taurine dioxygenase [Burkholderia cenocepacia J2315]
Length = 290

Score = 125 bits (314), Expect = 7e-27, Method: Compositional matrix adjust.
Identities = 87/288 (30%), Positives = 136/288 (47%), Gaps = 21/288 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
I P A LGA V G+ L+ LD FA +H A L H +L+F Q ++ D+ I F++RF
Sbjct: 10 FDIVPFDAPLGAEVIGLDLSQPLDADDFARIHRAHLDDHVLVFRDQRITPDEHIAFSRRF 69

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
G ++ G +++ +SN+ +G P D WH+D +Y
Sbjct: 70 GPLQIHVLHQFALAGHPEVLIVSNIVENG-----KPVGLGD-----AGHFWHSDLSYKE 118

Query: 117 VMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ G++ A+ +PA GG T FA+M A+D L R V R A H+ + ++L
Sbjct: 119 KPSLGSLHLHAQELPAEGGDTLAFANMHLAWDTLPAHLRRAVEGRRAEHTYLARYAELQARS 178

Query: 177 QAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
+ A + P+V+ HPETGR +L + H I G+ ES L+ L
Sbjct: 179 PWRPNLSPEQIAQVAHVHPVVRTHPETGRKALFVSEHFTTRIVGLPEDESRRALLDELFT 238

Query: 236 WACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +A ++ H W D+V WDNR L+H A L R ++ + + G
Sbjct: 239 HSVRAEHLRHAWRDHDLVFWDNRSLMHLAAGTPDHLRRKLYRTTIEG 286

>ref|ZP_04934071.1| hypothetical protein PA2G_01415 [Pseudomonas aeruginosa 2192]
gb|EAZ58190.1| hypothetical protein PA2G_01415 [Pseudomonas aeruginosa 2192]
Length = 295

Score = 125 bits (314), Expect = 7e-27, Method: Compositional matrix adjust.
Identities = 93/295 (31%), Positives = 144/295 (48%), Gaps = 27/295 (9%)

Query: 2 AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A LQI A GA V G+ L L F +H A L H +L+F Q ++ QQI F
Sbjct: 11 ADFPLQIRALDAAFGAEVLGLDLGLPLAEDFRRIHRAHLDDHVLVFRDQRITPAQQIAF 70

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
++RFG ++ G +I+ +SN+ +G P D K WH+D
Sbjct: 71 SRRFGELQIHVLKQFLLPGHPEILIVSNIVENG-----QPIGLGDAGKF-----WHSDL 119

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQS 170
+Y + + G++ A+ +P GG T FADM A+D+L EA R + R+A HS YS+
Sbjct: 120 SYKELPSLGSMHLHAQELPEEGGDTLAFADMHKAWDSLPEALRKAIEGRRTAAHSYTARYSEP 179

Query: 171 KL-GHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESER 228
+ G+ + SA + + P+V+ HPE+GR +L + I G+ A ES +
Sbjct: 180 RFEGNWRPTLSA---AQLAEVREVHPHIVRTHPESGRKALFVSEGFTTRIVGLPADESAQ 236

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L L + + ++ H+W A D+V WDNR L+H A L R ++ + + G
Sbjct: 237 LLAELYAHSVRPEHIYRHRWQAHDLVFWDNRSLIHLAGGCPAHLRRKLYRTTIQG 291

>ref|ZP_02468555.1| Taurine dioxygenase [Burkholderia thailandensis MSMB43]
Length = 309

Score = 125 bits (314), Expect = 8e-27, Method: Compositional matrix adjust.
Identities = 87/288 (30%), Positives = 134/288 (46%), Gaps = 21/288 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
I P A LGA V G+ L+ LD A FA +H A L H +L+F Q ++ D+ I F++RF

Sbjct: 29 FDIVPFDAPLGAEEVVGIDLSQPLDAADFARIHRAHLDDHVLVFRDQRITPDKHIAFSRRF 88

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMP 116
G ++ +++ +SN+ DG P D WH+D +Y

Sbjct: 89 GPLQIHVLHQFALAAHPEVLIVSNIVEDG-----KPIGLGD-----AGHFVHSDLSYKE 137

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ G++ A+ +PA GG T FA+M A+D L R V R A H+ + ++L

Sbjct: 138 KPSLGSLHLHAQELPAEGGDTLAFANMHLAWDTLPAHLRRAVEGRRAEHTYLARYAELQARS 197

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
+ + P+V+ HPETGR +L + H I + ES L+ L

Sbjct: 198 PWRPNLSAEQIAQVEAVVHPVVRTHPETGRRALFVSEHFTTRIVDVPEDSRALLDELFA 257

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +A +H H W D+V WDNR L+H A L R ++ + + G

Sbjct: 258 HSVRAEHLRHHWRDHDLVFVDNRSLMHLAAGTPDHLRRKLYRTTIEG 305

>ref|ZP_02189759.1| Alpha-ketoglutarate-dependent taurine dioxygenase [alpha
proteobacterium BAL199]
gb|EDP63364.1| Alpha-ketoglutarate-dependent taurine dioxygenase [alpha
proteobacterium BAL199]
Length = 291

Score = 125 bits (313), Expect = 8e-27, Method: Compositional matrix adjust.
Identities = 96/273 (35%), Positives = 136/273 (49%), Gaps = 24/273 (8%)

Query: 5 TLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T+QI P G ++GA + GV L A L + +H A+L+H+++ F Q L + ++ A R

Sbjct: 9 TIQIEPIGGSIGAVIHGVDLGAFLSNRQAKEVHDAFLEHSVVFVRDQKLDPPERQKRAAR 68

Query: 64 FGAIERIGGGDIVAISNVKA-DGTVRQHSP-----AEWDDMMKVIVGNMAWHADSTYMPV 117
G+ VAI VK+ DG H E +D K G +WH D+T++

Sbjct: 69 LF-----GEPVAIPFVKSLDG----HPEIIDIVKEAEDAGKYNFGG-SWHTDTTFLET 116

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHS---LVYSQSKL-G 173
A G++ A VP+ GG T FAD AAY+ L + R L+ +A HS SQSK G

Sbjct: 117 PALGSLLYALQVPSRGGDTLFAAQYAAAYETLSGMRRLLDGLTAVHSGSRYSQSQSKFQG 176

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEG 232
Q+ S I D P+V+ HPETGR L + + + M AES+ L+

Sbjct: 177 GKNQSVSMTIDANADGDLVEHPVVRTHPETGRKCLFVNPNTLRLKDMTEAESKPLDDF 236

Query: 233 LVDWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
L A + + +W AG V VVDNRC +HRA

Sbjct: 237 LYAHAIIRDEFICRFRWQAGSVAVVDNRCTMHRA 269

>ref|YP_001437971.1| hypothetical protein ESA_01880 [Cronobacter sakazakii ATCC BAA-
894]
gb|ABU77134.1| hypothetical protein ESA_01880 [Cronobacter sakazakii ATCC BAA-894]
Length = 294

Score = 125 bits (313), Expect = 9e-27, Method: Compositional matrix adjust.
Identities = 93/302 (30%), Positives = 143/302 (47%), Gaps = 36/302 (11%)

Query: 4 TTLQITPTGAT-----LGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLS 53
TTL TP A LGA +TG+ L +++A FA +H A L H +++F Q ++

Sbjct: 3 TTLNATPVAAQPFTITPFAFLGAEITGLDLRLPVNNADFARIHQHLDHVVVFRDQKIT 62

Query: 54 NDQQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGN 105
QQI F++RFG ++ +I+ +SN+ +G P D K

Sbjct: 63 PRQQIDFSRRFGPLQIHVLKQFLLPDHPEILIVSNIIENG-----QPIGLGDAGKF----- 113

Query: 106 MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL 165
WH+D +Y + + G++ A+ +P GG T FADM AY+ L + + + A HS

Sbjct: 114 --WHSDSLKYKTLPSLGSMLEYAQELPEEGGDTLFDADMELAYETLPADLKRAIEGKKAVHSY 171

Query: 166 V--YSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGM 221
YS+ K G + P+++ HPETGR +L + G H I G+

Sbjct: 172 TATYSRPFKG--SHWRPQLTEQQLAEVQAVSHPMRTHPETGRKALFVSEGFTH-IEGL 228

Query: 222 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRL 281
AES LE L + + ++ HQW GD+V WDNR L+H A L R ++ + +

Sbjct: 229 PEAESRDILEALWAHSVRPEHLYRHQWQPGDMVFWDNRSLIHLATGCPAHLRRKLYRTTI 288

Query: 282 AG 283
G

Sbjct: 289 EG 290

>ref|NP_742338.1| TauD/TfdA family dioxygenase [Pseudomonas putida KT2440]
gb|AAN65802.1|AE016209_1 dioxygenase, TauD/TfdA family [Pseudomonas putida KT2440]
Length = 299

Score = 125 bits (313), Expect = 9e-27, Method: Compositional matrix adjust.
Identities = 84/293 (28%), Positives = 144/293 (49%), Gaps = 31/293 (10%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ P +GA + G+ LA + F +H A L H +L+F Q ++ +QOI F++RF

Sbjct: 19 FEVRPFSGAVGAIEILGLDLAKPVSAEDFTRIHAHLDDHVLVFRDQRITPEQQIAFSRRF 78

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMA--WHADSTY 114
G ++ G +I+ +SN+ +G + +G+ WH+D +Y

Sbjct: 79 GELQIHVLKQFLLTGHPEILIVSNIIENG-----QNIGLGDAGKFWHSDLSY 125

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKL 172
+ + G++ A+ +P+ GG T FADM A+DA+ + R +V RSA HS Y+++K

Sbjct: 126 KELPSLGSMLEHAQELPSEGGDTLFDAMHKAWDVDPDLRKVVEGRSAHSTARYAETKF 185

Query: 173 -GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL 230
G+ + +A + + P+V+ HPE GR +L + I G+ ES L

Sbjct: 186 EGNWRPTLTA---EQLAQVKEVIHPVVRTHPENGRKALFVSEGFTRIVGLPDDESRLV 242

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ L + ++ HQW D+V WDNR L+H A L R ++ + + G

Sbjct: 243 QQLYALSVLEQNIYRHQWQPYDLVFWDNRSLIHLATGCPAHLRRKLYRTTIQ 295

>ref|YP_954965.1| taurine catabolism dioxygenase TauD/TfdA [Mycobacterium vanbaalenii
PYR-1]
gb|ABM14959.1| Taurine catabolism dioxygenase TauD/TfdA [Mycobacterium vanbaalenii
PYR-1]
Length = 281

Score = 125 bits (313), Expect = 9e-27, Method: Compositional matrix adjust.
Identities = 102/289 (35%), Positives = 135/289 (46%), Gaps = 23/289 (7%)

Query: 4 TTLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
T L I +++GA VTG+ L DDA A+ A + +L+FPG HL + Q+ F

Sbjct: 2 TLLTINKLTSSVGA EVTGLDPGRLAGDDALGTAVLDALEDNGVLVFPGLHLEPEVQVEFC 61

Query: 62 KRFGAIERIGGG--DIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTY----- 114
+R G I+ G + I V D + ++S A + + WH D

Sbjct: 62 RRLGEIDFSSDGHHRVAGIYPVTLDKS--KNSSAAY-----LRATFDWHIDGCTPTGDD 113

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
P MA V SA+ V GG T FA AAYDAL +A + HSL SQ +
Sbjct: 114 YPQMA--TVLSAKQVAESGGGETEFASSYAAAYDALTDAEKQRFASLRVVSLEASQRR--- 168

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
V S T PLV H TGR SL++G A I GMD E L L+
Sbjct: 169 VNPDPSPHEELARWRARPTHEHPLVWTH-RTGRKSLVLGASADYIVGMDPEEGRALLSELL 227

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
D A A +V++H WA GD V+WDNR +LHRA +D PR M + + G
Sbjct: 228 DRATTADKVYSHHWAVGDTVWIDNRGVLHRAARYDENSPREMLRTTVLG 276

>ref|ZP_06840724.1| Taurine catabolism dioxygenase TauD/TfdA [Burkholderia sp. Ch1-1]
gb|EFG71444.1| Taurine catabolism dioxygenase TauD/TfdA [Burkholderia sp. Ch1-1]
Length = 301

Score = 125 bits (313), Expect = 9e-27, Method: Compositional matrix adjust.
Identities = 82/276 (29%), Positives = 136/276 (49%), Gaps = 23/276 (8%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+L + + A + G+ L+ L D + A Q+ +LIFP Q++ +DQ + FA
Sbjct: 2 SLNVEAVHPFIAARIHGLDLSKPLSDERIVEIEQASGQYPVLIFPRQYIDDDQLLAFAG 61

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHAD 111
FG ++ R+ I ISN+ + + P + M + + WH+D
Sbjct: 62 FGPLQIAVSYSRTPEDHRLAPM-INDISNLSKENQT--YRPGDRRRMNNLT--SRRWHS 116

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
++Y+P+ A+ + + +VPAVGG+T FADMRAAYD L + R +V S + ++ S++
Sbjct: 117 ASYLPLPARYSFLLSYIVPAVGGQTQFADMRAAYDNLPDHLRKVVEGLSCHYDIMASRAA 176

Query: 172 LGHVQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE 231
G + A + LV+ H + R SL + HA + G E L
Sbjct: 177 AGFYDASDEE----RKALAPCIHELVRTHAISRRKSLYLSSHATHVVGWPEPEGRDLLR 231

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEP 267
L ++A Q V++H+W+ D+V+WDNR L+HR P
Sbjct: 232 ELTEFATQPQFVYSHEWSVRDLVMWDNRALMHRGRP 267

>gb|ADC34043.1| TfdA-like protein [uncultured bacterium]
Length = 207

Score = 124 bits (312), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 76/221 (34%), Positives = 116/221 (52%), Gaps = 29/221 (13%)

Query: 56 QQITFAKRFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVG 104
QQI FA+ +G + ER +I+ ISNV +G V + S +
Sbjct: 1 QQIAFARHYGPLNVGLKKAGKRRERYANREIIDISNVDPGRVYERS-----HTATIS 53

Query: 105 NMA---WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA 161
N+A WH+DS++ + ++ SA VVP GG+T FAD+RAA+D+L + + + ++A
Sbjct: 54 NLANQLWHSDDSSSQKPKAMKYSMLSAVVVPENGGQTEFADLRAAFDLSLPDEMRELKGA 113

Query: 162 RHSLVYSQSKLGHVQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPG 220
H +S+ LG A T P++ PLV+ HP +GR L +G H +PG
Sbjct: 114 EHYAHSREWLGDTITPEQA-----ETFPVQWPLVRKHPGSGRDVLFVGIHCTKVP 166

Query: 221 MDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
M AE + GL++ A Q V+ H+W GD+V+WDNR+
Sbjct: 167 MTLAEGRMILIAGLLEHATQRELVRHEWRPGDLVMWDNRV 207

>ref|ZP_02884179.1| Taurine dioxygenase [Burkholderia graminis C4D1M]
gb|EDT10183.1| Taurine dioxygenase [Burkholderia graminis C4D1M]
Length = 308

Score = 124 bits (312), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 83/275 (30%), Positives = 135/275 (49%), Gaps = 21/275 (7%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
+A ++I LGA V G+ L+ L A FA +H A L + +L+F Q ++ D+QI
Sbjct: 23 IAGQPIEIRAFDGPLGAEVLGLDLKPLAQADFARIHRAHLDYHVLVFRDQRITPDEQIA 82

Query: 60 FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHAD 111
F++RFG ++ +++ +SN+ +G P D WH+D
Sbjct: 83 FSRRFGPLQIHVLHQFQLPDYPEVLVVSNIENG-----KPIGLGD-----AGHYWHSD 131

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
+Y + G++ A+ +PA GG T FA+M A+D L R+ V R+A H+ + ++
Sbjct: 132 LSYKEKPSLGSLLHAQELPAEGGDTLAFANMHLAWDTLPAHLRSVEGRTAEHTYLAKYAE 191

Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL 230
L + + P+V+ HPETGR +L + H + G+ ES + L
Sbjct: 192 LQKRSPWRPNLSPEQIAQVKPVVHPIVRTHPETGRKALFVSEHFTTRVIGLPEDESRLQL 251

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
E L + +A V+ H+WA D+V WDNR L+H A
Sbjct: 252 EELFAHSVRAEHVYRHRWAEHDMVFWDNRSLMHLA 286

>ref|ZP_06495450.1| taurine dioxygenase [Pseudomonas syringae pv. syringae FF5]
Length = 298

Score = 124 bits (312), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 80/274 (29%), Positives = 131/274 (47%), Gaps = 21/274 (7%)

Query: 2 AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A + ++ P +GA + G+ L+ L+DA FA +H A L H +++F Q ++ QQI F
Sbjct: 14 ASQSFEVRPFTEKVGAEIVGLDLRPLNDADFARVHQAHLDDHVVVFRDQQITPQQQIDF 73

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
++RFG ++ +I+ +SN+ V P D K WH+D
Sbjct: 74 SRRFGVLQIHVLKQFLLANHPEILIVSNI-----VENDKPVGLGDAGKY-----WHS DL 122

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+Y + + G++ A+ +P+ GG T FADM A++ L + R V RSA HS ++
Sbjct: 123 SYKELPSLGSMLYAQELPSEGGDTLAFADMLAWETLPQHRLDAVEGRSAVHSYTARYAEG 182

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLE 231
+ + P+V+ HPE GR +L + I G+ ES + L
Sbjct: 183 HNAANWRPPLTAEQLAQVVEVSHPIVRTHPENRRALFVSEGFTTRILGLPEDESRLILN 242

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ + + ++ HQW A D+V WDNR L+H A
Sbjct: 243 EIIAHSVKEPHIYRHQWQANDMVFWDNRLIHLA 276

>ref|ZP_08177331.1| putative taurine catabolism dioxygenase [Xanthomonas vesicatoria
ATCC 35937]
gb|EGD10453.1| putative taurine catabolism dioxygenase [Xanthomonas vesicatoria
ATCC 35937]
Length = 305

Score = 124 bits (312), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 82/270 (30%), Positives = 129/270 (47%), Gaps = 21/270 (7%)

```
Query: 6  LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      ++I P  A LGA V G+ L+ LD  FA +H A L H +L+F Q ++ QQ+ F++RF
Sbjct: 25 VRIVPFDAPLGAQVLGLDLSQPLDATTFARIHQAHLDHHVLVFRDQRITPAQQVDFSRRF 84

Query: 65  GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
      G ++          G  +++ +SN+K +G      P      D      WH+D +Y
Sbjct: 85  GPLQIHVLRNFQLPGHPEVLVVSNIKENG-----EPIGLGD-----AGHYWHSLSYKE 133

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
      + G++  A+ +P+ GG T FA+  A+  L E  +  V  A HS +  +L
Sbjct: 134 TPSLGSLLLHAQELPSEGGDTLFANQHLAWHTLPEPLKRRVQDLRAEHSYLAKYEELRARN 193

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
      A      +      P+V+ HPETG+ +L +  H      I G+  ESE L+ L +
Sbjct: 194 PWRPALTPAQIAEVKPVQHPIVRTHPETGQKALFVSEHFTTRIVGLPEDESEALLQTLFE 253

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      +      V+ HQW  D+V WDNR ++H A
Sbjct: 254 HSTDALVYRHQWQPYDMVFDNRSMHLA 283
```

>ref|YP_002551991.1| taurine dioxygenase [Acidovorax ebreus TPSY]
gb|ACM31991.1| Taurine dioxygenase [Acidovorax ebreus TPSY]
Length = 299

Score = 124 bits (311), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 86/274 (31%), Positives = 132/274 (48%), Gaps = 20/274 (7%)

```
Query: 2  AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
      A      +I  A LGA V G+ LA  L DA F  +  A  +H +L+F Q ++ QQ+ F
Sbjct: 14 ASQEFEIIRRLPAPLGAEVLGLDLAQPLSDADFDRLRAHWEHVVLVFRNQRITPAQQVAF 73

Query: 61  AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
      ++RFG ++          G  +++ +SN++ +      P      D      G++ WH+D
Sbjct: 74 SRRFGPLQIHVQRKFALQGHPEVLVVSNIIRDENG-----EPTGLGD-----AGSL-WHSDL 123

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
      +Y      + G++  A+ +P VGG T FAD AAYDAL EAT+  +  A HS +  +L
Sbjct: 124 SYKDKPSLGSLLLHAQELPNVGGDTLFADQYAAYDALPEATQQRI AHLRAEHSYLARYEEL 183

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE 231
      +      A  + P+V+ HP TGR +L +  H      I  +  ES  L+
Sbjct: 184 RQRNPWRPRLTPAQIAEVAPAVHPVVRTHPATGRKALFVSEHFTTRILDLP EEESRALLQ 243

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      L  + +      V+ HQW  D+V WDNR +LH A
Sbjct: 244 ELFAASVRPEFVYRHQWQPHDLVFWDNR AVLHLA 277
```

>ref|ZP_01365674.1| hypothetical protein PaerPA_01002800 [Pseudomonas aeruginosa PACS2]
Length = 281

Score = 124 bits (311), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 91/291 (31%), Positives = 143/291 (49%), Gaps = 27/291 (9%)

```
Query: 6  LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      +QI  A  GA V G+ L  L      F +H A L H +L+F Q ++ QQI F++RF
Sbjct: 1  MQIRALDAAFGAEVLGLDLGLPLAEDFRRIHRAHLDDHHVLVVFREQRITPAQQIAFSRRF 60
```

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
G ++ G +I+ +SN+ +G P D K WH+D +Y
Sbjct: 61 GELQIHVLKQFLLPGHPEILIVSNIVENG-----QPVGLGDAGKF-----WHS DLSYKE 109

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKL-G 173
+ + G++ A+ +P GG T FADM A+D+L EA R + R+A HS YS+ + G
Sbjct: 110 LPSLGSM LHAQELPEEGDTL FADM HKAWDSLPEALRKAIEGR TAAHSYTARYSEPRFEG 169

Query: 174 HVQQAGSAYIGYGM DTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
+ + SA + + P+V+ HPE+GR +L + I G+ A ES + L
Sbjct: 170 NWRPTLSA---AQLAEVREV VHPIVRTHPESGRKALFVSEGFTTRIVGLPADESAQLLAE 226

Query: 233 LVDWACQAPRVHAHQWAAGDVVVW DNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + + ++ H+W A D+V W DNR L+H A L R ++ + + G
Sbjct: 227 LYAHSVRPEHIYRHRWQA HDLVFWDNRSLIHLAGGCPAHLRRKLYRTTIQG 277

>ref|ZP_07265737.1| taurine dioxygenase [Pseudomonas syringae pv. syringae 642]
Length = 298

Score = 124 bits (311), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 79/270 (29%), Positives = 129/270 (47%), Gaps = 21/270 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ P +GA + G+ L+ L+DA FA +H A L H +++F Q ++ QQI F++RF
Sbjct: 18 FEVRPFTEKVGAEIVGLDL SRPLNDADFARVHQAHLNHHVVVFRDQQITPQQQIDFSRRF 77

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
G ++ +I+ +SN+ V P D K WH+D +Y
Sbjct: 78 GVLQIHVLKQFLLANHPEILIVSNI-----VENDKPVGLGDAGKY-----WHS DLSYKE 126

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ + G++ A+ +P+ GG T FADM A++ L + R V RSA HS ++ +
Sbjct: 127 LPSLGSM LYAQELPSEGGDTL FADMHLAWETLPQH LRD AVQGRSAVHSYTARYAEGHNAA 186

Query: 177 QAGSAYIGYGM DTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ P+V+ HPE GR +L + I G+ ES + L +
Sbjct: 187 NWRPTLTAEQLAQVVEVSHPIVRTHPENGRKALFVSEGFTTRILGLPEDES RQILNEIYA 246

Query: 236 WACQAPRVHAHQWAAGDVVVW DNRCLLHRA 265
+ + ++ HQW A D+V W DNR L+H A
Sbjct: 247 HSVKPEHIYRHQWRANDMV FWDNRSLIHLA 276

>ref|ZP_03572034.1| alpha-ketoglutarate-dependent taurine dioxygenase
(2-aminoethanesulfonate dioxygenase) (Sulfate
starvation-induced protein3) (SSI3) [Burkholderia
multivorans CGD2M]
gb|EEE13842.1| alpha-ketoglutarate-dependent taurine dioxygenase
(2-aminoethanesulfonate dioxygenase) (Sulfate
starvation-induced protein3) (SSI3) [Burkholderia
multivorans CGD2M]
Length = 295

Score = 124 bits (311), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 87/292 (29%), Positives = 137/292 (46%), Gaps = 21/292 (7%)

Query: 2 AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A +I P A LGA V G+ L+ LD FA + A L H +L+F Q ++ D+ + F
Sbjct: 11 APQRF EIVPFDAPLGA EVVGIDLSQPLDADAFARIRRAHL DHHV L VFRDQRITPDEHVAF 70

Query: 61 AKRFGAIER-----IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS 112
++RFG ++ G +++ +SN+ +G P D WH+D

Sbjct: 71 SRRFGPLQTHVLHQFALPGHPEVLIVSNIVENG-----RPIGLGD-----AGYFWHSDL 119

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+Y + G++ A+ +PA GG T FA+M A+D L A R V R A H+ + ++L

Sbjct: 120 SYKRRPSLGSLLHAQELPAEGGDTLAFNMHLAWDTLPAALRRAVEGRRAEHTYLARYAEL 179

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE 231
+ + P+V+ HPETGR +L + H I G+ ES L+

Sbjct: 180 QARSPWRPNLSAEQIAQVEPVVHPVVRTHPETGRRALFVSEHFTTRIVGLPDDESRLALD 239

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + +A + H+W D+V WDNR LLH A L R ++ + + G

Sbjct: 240 ELFAHSVRAEHQYRHRWRDHDLVFWDNRSLHLAAGTPDHLRRKLYRTTIEG 291

>ref|ZP_03578265.1| alpha-ketoglutarate-dependent taurine dioxygenase
(2-aminoethanesulfonate dioxygenase) (Sulfate
starvation-induced protein3) (SSI3) [Burkholderia
multivorans CGD2]
gb|EEE07471.1| alpha-ketoglutarate-dependent taurine dioxygenase
(2-aminoethanesulfonate dioxygenase) (Sulfate
starvation-induced protein3) (SSI3) [Burkholderia
multivorans CGD2]
Length = 309

Score = 124 bits (310), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 87/292 (29%), Positives = 137/292 (46%), Gaps = 21/292 (7%)

Query: 2 AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A +I P A LGA V G+ L+ LD FA + A L H +L+F Q ++ D+ + F

Sbjct: 25 APQRFEIVPFDAPLGAEVVGIDLSQPLDADAFARIRRAHLDDHVLVFRDQRITPDEHVAE 84

Query: 61 AKRFGAIER-----IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
++RFG ++ G +++ +SN+ +G P D WH+D

Sbjct: 85 SRRFGPLQTHVLHQFALPGHPEVLIVSNIVENG-----RPIGLGD-----AGYFWHSDL 133

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+Y + G++ A+ +PA GG T FA+M A+D L A R V R A H+ + ++L

Sbjct: 134 SYKRRPSLGSLLHAQELPAEGGDTLAFNMHLAWDTLPAALRRAVEGRRAEHTYLARYAEL 193

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE 231
+ + P+V+ HPETGR +L + H I G+ ES L+

Sbjct: 194 QARSPWRPNLSAEQIAQVEPVVHPVVRTHPETGRRALFVSEHFTTRIVGLPDDESRLALD 253

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + +A + H+W D+V WDNR LLH A L R ++ + + G

Sbjct: 254 ELFAHSVRAEHQYRHRWRDHDLVFWDNRSLHLAAGTPDHLRRKLYRTTIEG 305

>ref|ZP_07772746.1| alpha-ketoglutarate-dependent taurine dioxygenase [Pseudomonas
fluorescens WH6]
gb|EFQ66049.1| alpha-ketoglutarate-dependent taurine dioxygenase [Pseudomonas
fluorescens WH6]
Length = 297

Score = 124 bits (310), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 80/272 (29%), Positives = 130/272 (47%), Gaps = 25/272 (9%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ P ++GA + G+ L+ ++D FA +H A L H +++F Q +S +QQI F++RF

Sbjct: 17 FEVRPLPGSVGAIEIIGLDSRPVNDQDFARIHRAHLDDHVVVFRDQRISPEQQIAFSRRF 76

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA--WHADSTY 114

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Query: 5      TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
              +   I P      +GA + G+ L+   L  A F+ +H A L H LL+F  Q ++   Q I F++R
Sbjct: 21     SFDINPLPGPVGAIEIIGLDSRELTAADF SRVHQAHLDDHLLVFRDQRITPRQHIDFSRR 80

Query: 64     FGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
              FG +                G +I+ +SN+  DG          P    D  K          WH+D +Y
Sbjct: 81     FGPLMIHVLHQFHLEGHPEILTVSNIVEDG-----KPIGLGDAGKY-----WHSDISYK 129

Query: 116     PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
              + + G++  A+ +P+ GG T FA+M  AYD L  A R  V  + A HS +   ++ G +

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Sbjct: 130 ELPSLGSLHHAQELPSEGGDTLAFANMHLAYDTLPAALRNAVVGKRAVHSYL---AQYGQL 186

Query: 176 QQAGSAYIGYGMDDTTA---TPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFL 230
Q+ G+ A + P+V+ HPE GR +L + G H + G+ ES L

Sbjct: 187 QKEGNWRPNLSAQQIAQVREVVHPVVRTHPENGRRALFVSEGFTTHIV-GLPEDESRLAL 245

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + +A ++ H+W D+V WDNR L+H A L R ++ + + G

Sbjct: 246 TELFAHSVRAEHIYRHRWQPHDLVFWDNRLIHLAGGTPDHLRRKLYRTTIEG 298

>gb|ABD16716.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium sp. Cf1]
Length = 153

Score = 123 bits (309), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 65/157 (41%), Positives = 90/157 (57%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA +V GG T FADMRAAYDALD+ T+A + HSL+Y

Sbjct: 2 WHSDSSFRPIPAKFSLLSARIVNPKGGNTEFADMRAAYDALDDETKAEIEDMVCEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+

Sbjct: 62 SRGSLGFLD-----YTDEEKEMFKPVLQRLVVRTHPVHGRKSLYLSSHAGAIRGMSMPEAR 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
L L + A Q V+ H+W D+V+WDNR +HR

Sbjct: 117 LLLRDLTEHATQPEFVYVHKWTVHDLVMWDNRQTVHR 153

>ref|ZP_06458047.1| TauD/TfdA family dioxxygenase [Pseudomonas syringae pv. aesculi
str.
NCPBP3681]
ref|ZP_06481584.1| TauD/TfdA family dioxxygenase [Pseudomonas syringae pv. aesculi
str.
2250]
Length = 298

Score = 123 bits (309), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 79/270 (29%), Positives = 128/270 (47%), Gaps = 21/270 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64

+ P +GA + G+ L+ L+DA FA +H A L H +++F Q ++ QQ+ F++RF
Sbjct: 18 FDVRPFTGKVGAEIVGLDLRPLNDADFARVHQAHLDDHVVVFRDQQITPQQQVDFSRRF 77

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMP 116
G ++ +I+ +SN+ V P D K WH+D +Y

Sbjct: 78 GVLQIHVLKQFLLANHPEILIVSNI-----VENEKPVGLGDAGKY-----WHSLSYKE 126

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ + G++ A+ +P+ GG T FADM A+D L + R V RSA HS ++ +

Sbjct: 127 LPSLGSMLYAQELPSEGGDTLAFADMHQAWDTLPQHRLDAVEGRSAVHSYTARYAEGHNAA 186

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ P+V+ HPETGR +L + I + ES + L +

Sbjct: 187 NWRPTLTAEQLAQVVEVSHPIVRTHPETGRKALFVSEGFTTRILDLPEDSRQILNEIYA 246

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ + ++ HQW A D+V WDNR L+H A

Sbjct: 247 HSVKPEHIYRHQWQANDMVFWDNRLIHLA 276

>ref|ZP_08138932.1| taurine dioxygenase [Pseudomonas sp. TJI-51]
gb|EGB99777.1| taurine dioxygenase [Pseudomonas sp. TJI-51]
Length = 299

Score = 123 bits (309), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 88/293 (30%), Positives = 147/293 (50%), Gaps = 31/293 (10%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+I P GA + G+ LA ++ F+ + A L H +L+F Q +S +QQI F++RF
Sbjct: 19 FEIRPFAGASGAEEIIGLDLARPVNAEDFSRIRRAHLDDHVLVFRDQRI SPEQQAIFSRRF 78

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA--WHADSTY 114
G ++ G +I+ +SN+ +G QH + +G+ WH+D +Y
Sbjct: 79 GELQIHVLKQFLLAGHPEILIVSNIIENG---QH-----IGLDAGKFWHSDLSY 125

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKL 172
+ + G++ A+ +P+ GG T FADM A+DA+ +A R +V RSA HS Y+++K
Sbjct: 126 KELPSLGSM LHAQELPSEGGDTL FADMHKAWDAVPDALRKVVEGRSAAHSYTARYAETKF 185

Query: 173 -GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL 230
G+ + +A + + P+V+ HPE GR +L + I G+ ES L
Sbjct: 186 EGNWRPTLTA---EQLAQVKEVIHPVVRTHPENRRALFVSEGFTTRIVGLPDDES RDVL 242

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ L + ++ HQW D+V WDNR L+H A L R++ + + G
Sbjct: 243 QQLYALSLEQNL YRHQWQPHDLVFWDNRS LIHLATGCPSHLRKLYRTTIQG 295

>gb|ABD16700.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. Ppar1-31]
Length = 153

Score = 123 bits (309), Expect = 3e-26, Method: Compositional matrix adjust.
Identities = 65/157 (41%), Positives = 90/157 (57%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA +V GG T FADMRAAYDALD+ T+A + HSL+Y
Sbjct: 2 WHSDSSFRPIPAKFSLLSARIVNPKGGNTEFADMRAAYDALDDETKAEIDDMICEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+
Sbjct: 62 SRGSLGFLD-----YTDEEKEMFKPVLQRLVRTHPVHGRKSLYLSSHAGAIRGMSMPPEAR 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
L L + A Q V+ H+W D+V+WDNR +HR
Sbjct: 117 LLLRDLTEHATQGEFVYVHKWTVHDLVMWDNRQTVHR 153

>gb|ABD16703.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. LcCT6]
gb|ABD16704.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. ApE4.8]
gb|ABD16708.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. onl92.10]
Length = 153

Score = 123 bits (309), Expect = 3e-26, Method: Compositional matrix adjust.
Identities = 66/157 (42%), Positives = 89/157 (56%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A + HSL+Y
Sbjct: 2 WHSDSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAYDALDDETKAEIEDMICEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
S+ LG + Y L+ LV+ HP GR SL + HA AI GM E+
Sbjct: 62 SRGSLGFLD-----YTDEEKQMFKPVLRVTHPVHGRKSLYLSSHAGAIRGMSMPPEAR 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
L L + A Q V+ H+W D+V+WDNR +HR
Sbjct: 117 LLLRDLTEHATQGEFVYVHKWTVHDLVMWDNRQTVHR 153

>ref|YP_003753223.1| alpha-ketoglutarate-dependent 2, 4-dichlorophenoxyacetate
dioxxygenase (2,4-D dioxxygenase) [Ralstonia solanacearum
PSI07]
emb|CBJ51960.1| Alpha-ketoglutarate-dependent 2, 4-dichlorophenoxyacetate
dioxxygenase (2,4-D dioxxygenase) [Ralstonia solanacearum
PSI07]
Length = 301

Score = 123 bits (309), Expect = 3e-26, Method: Compositional matrix adjust.
Identities = 86/266 (32%), Positives = 129/266 (48%), Gaps = 24/266 (9%)

Query: 12 GATLGATVTGVH-LATLDDAGFAALHAAWLQH-ALLIFPGQHLSDNDQQITFAKRFGAIE- 68
GA LGA + G++ A L DA AA+ AWL H LL+F L+ Q+ F++RFG ++
Sbjct: 26 GAPLGAELLGLNDAAGLSDADIAAIRQAWLAHDGLLVFRDVLAPRAQVDFSRFRGPLQV 85

Query: 69 -----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
+I+ +SNV +G P D + WH+D +Y P + G
Sbjct: 86 HVLNQFHLPDHPEILVVSNNVENG-----KPIGLGDAGR-----DWHSDSLKYKPQPSLG 134

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
++ A +P GG T FA+M AY+ L + ++ R A HS VY +L +
Sbjct: 135 SLLLARELPQAGGDTLFANMVRAYETLPaelKRIIEGRRVHSYVRYERLRALSTWRPP 194

Query: 182 YIGYGMDDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVDWACQ 239
D P+V+ HPETG+ +L + G +H IPG+ ES LE L + Q
Sbjct: 195 LTQAQRDAVPPVDHPVVRTHPETGKRALFVNAGFTSH-IPGLPEDESTAVLEQLFAHSIQ 253

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
++ H+W GD++ WDNR +H A
Sbjct: 254 PDNIYTHRWQPGDMLFWDNRSTIHFA 279

>gb|ABD16698.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium sp. Vgn-2]
Length = 153

Score = 123 bits (309), Expect = 3e-26, Method: Compositional matrix adjust.
Identities = 66/157 (42%), Positives = 90/157 (57%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A + HSL+Y
Sbjct: 2 WHSDSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAYDALDDETKAEIDDMICEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+
Sbjct: 62 SRGSLGFLD-----YTDEEKEMFKPVLRVTHPVHGRKSLYLSSHAGAIRGMSMPPEAR 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
L L + A Q V+ H+W D+V+WDNR +HR
Sbjct: 117 LLLRDLTEHATQPEFVYVHKWTVHDLVMWDNRQTVHR 153

>gb|ABD16699.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium sp. Leb-12]

gb|ABD16711.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. BtLT4]
gb|ABD16712.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. DrLT5]
Length = 153

Score = 123 bits (308), Expect = 3e-26, Method: Compositional matrix adjust.
Identities = 65/157 (41%), Positives = 90/157 (57%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA +V GG T FADMRAAYDALD+ T+A + HSL+Y
Sbjct: 2 WHSDSSFRPIPAKFSLLSARIVNPKGGNTEFADMRAAYDALDDETKAEIDDMICEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+
Sbjct: 62 SRGSLGFLD-----YTDEEKEMFKPVLQRLVRTHPVHGRKSLYLSSHAGAIRGMSMPEAR 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
L L + A Q V+ H+W D+V+WDNR +HR
Sbjct: 117 LLLRDLTEHATQPEFVYVHKWTVHDLVMWDNRQTVHR 153

>ref|YP_558852.1| taurine dioxygenase [Burkholderia xenovorans LB400]
gb|ABE30800.1| Taurine dioxygenase [Burkholderia xenovorans LB400]
Length = 302

Score = 123 bits (308), Expect = 3e-26, Method: Compositional matrix adjust.
Identities = 82/288 (28%), Positives = 135/288 (46%), Gaps = 21/288 (7%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++I +GA V G+ L L F +H A L H +L+F Q ++ DQOI F++RF
Sbjct: 22 IEIRAFDGPVGAEVLGLDLGRPLSQHDFERIHRAHLDDHHVLVFRDQRITPDQQIAFSRRF 81

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
G ++ G +++ +SN+ +G P D WH+D +Y
Sbjct: 82 GPLQIHVLHQFQLPGHPEVLVVSNIENG-----QPIGLGD-----AGHFWHSDLSYKE 130

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ G++ A+ +PA GG T FA+M A+D RA V RSA H+ + ++L
Sbjct: 131 TPSLGSLLLHAQELPAQGGDTLAFANMHLAWDTFPAHLRAAVEGRSAEHTYLAKYAEQLKRS 190

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
+ + P+V+ HPETGR +L + H + G+ ES LE +
Sbjct: 191 PWRPDLAEQIAQVKPVVHPIVRTHPETGRKALFVSEHFTTRVIGLPEDESRSLLLEEIFA 250

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ + ++ H+W+ D+V WDNR L+H A L R ++ + + G
Sbjct: 251 HSVRPEHLRHEWSEHDMVFWDNRLMHLAAGTPDHLRRKLYRTTIEG 298

>ref|YP_272623.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. phaseolicola
1448A]
gb|AAZ37170.1| dioxygenase, TauD/TfdA family [Pseudomonas syringae pv.
phaseolicola 1448A]
gb|EFW78230.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. glycinea
str. B076]
gb|EFW86740.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. glycinea
str. race 4]
Length = 298

Score = 123 bits (308), Expect = 4e-26, Method: Compositional matrix adjust.
Identities = 79/270 (29%), Positives = 128/270 (47%), Gaps = 21/270 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ P +GA + G+ L+ L+DA FA +H A L H +++F Q ++ QQ+ F++RF
Sbjct: 18 FDVRPFTGKVGAEIVGLDLRPLNDADFARVHQAHLDHHVVVFRDQQITPQQQVDFSRRF 77

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
G ++ +I+ +SN+ V P D K WH+D +Y
Sbjct: 78 GVLQIHVLKQFLLANHP EILIVSNI-----VENEKPVGLGDAGKY-----WHS DLSYKE 126

Query: 117 VMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ + G++ A+ +P+ GG T FADM A+D L + R V RSA HS ++ +
Sbjct: 127 LPSLGSMLYAQELPSEGDTL FADMHQAWDTLPQH LRDAVEGRSAVHSYTARYAEGHNAA 186

Query: 177 QAGSAYIGYGM DTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ P+V+ HPETGR +L + I + ES + L +
Sbjct: 187 NWRPTLTAEQLAQVVEVSHPIVRSHPETGRKALFVSEGFTTRILDLPEDESRQILNEIYA 246

Query: 236 WACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
+ + ++ HQW A D+V WDNR L+H A
Sbjct: 247 HSVKPEHIYRHQWQANDMVFWDNRS LIHLA 276

>ref|YP_003450157.1| taurine dioxygenase [Azospirillum sp. B510]
dbj|BAI73613.1| taurine dioxygenase [Azospirillum sp. B510]
Length = 300

Score = 123 bits (308), Expect = 4e-26, Method: Compositional matrix adjust.
Identities = 93/295 (31%), Positives = 137/295 (46%), Gaps = 27/295 (9%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
M T I P TLGA V G+ L+ L A + L A +H +L+F Q LS+ +
Sbjct: 1 MTDTGFTIDPVSP TLGA EVRGLDLSQPLSPATTSVLADALDRHLVLVFRDQTLSADLVR 60

Query: 60 FAKRFGAIERI-----GGGDIV AISNVKADGTVRQHSPA EWDDMMKVIVGNMAW 108
+ FG +++ G ++ ISN+ A+G + + G W
Sbjct: 61 VSGHFGPLDKAPITENGR LHAPGYEEVYVISNITANGR-----PIGALGAGESVW 110

Query: 109 HADSTYMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
HAD TY+ + A VP GG T F M AAYDAL E + V S +H +
Sbjct: 111 HADMTYLETPPYASSLYALEVPVEGGDTGFLSMFAAYDALPEPLKRRVEGLSIKHDSTTN 170

Query: 169 QSKLGHVQQAGSAYIGYGM DTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESE 227
G+++Q + T+ + PLV HP TG +LL+GR HA IPG+ ESE
Sbjct: 171 SG--GYLRQGFAPPANVA--TSPGTVHPLVITHPVTGARALLLGRRPHAHIPGLSVPESE 226

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLA 282
L+ + A + H+W GD+V+WDNR +HR +P+ R M +++A
Sbjct: 227 ALLDEIWATAVRPELAWHHRWRVGDLMWDNRWTMHRDPFPDSQRRRMHRTQIA 281

>ref|YP_616210.1| taurine catabolism dioxygenase TauD/TfdA [Sphingopyxis alaskensis
RB2256]
gb|ABF52877.1| Taurine catabolism dioxygenase TauD/TfdA [Sphingopyxis alaskensis
RB2256]
Length = 281

Score = 123 bits (308), Expect = 4e-26, Method: Compositional matrix adjust.
Identities = 95/272 (34%), Positives = 125/272 (45%), Gaps = 25/272 (9%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
TL I P+G GA VTGV LA LD AA+ AAWL H +L FP Q +S+D F
Sbjct: 2 TLAIIPSGQACGAHVTVGDLAHLPLDPGTIAAIRAAWLDHHVLAFPDQKMSDDDLERFTAY 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA---EWDDMMKVIVGNMAWHADSTYMPVMAQ 120

FG G GD I + R+H A D+ + N WH+D ++
Sbjct: 62 FG-----GFGDDPFIRPIPG-----RKHIIAVKRRADETAPLFAEN--WHSDFSQARPPA 110

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
G +P VGG T FA+ AA DA+ RA + A HS + G G+
Sbjct: 111 GTCLFGITIPPVGGNTEFANQHAALDAMPAGLRARIEGLRAIHSARAGYAPSG---MYGA 167

Query: 181 AYIGYGMDDTTA-----TPLRPLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGL 233
G MD + T L P V+ HPETGR L + GMD AE+ L L
Sbjct: 168 NDRGRSMDIRSDDALETLQHPFVRAHPETGRLGLFGCAGYIIGFEGMDDAEARPLLHEL 227

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ W + ++H+W +V+WDNR +LHRA
Sbjct: 228 IQWQGREEFYRSHRWEPMMLVMWDNRSLVHRA 259

>gb|ABD16701.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium sp. aeky3]
Length = 153

Score = 122 bits (307), Expect = 4e-26, Method: Compositional matrix adjust.
Identities = 66/157 (42%), Positives = 89/157 (56%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A + HSL+Y
Sbjct: 2 WHSDSSFRPIPAKFSLLSARVVNPPGGNTEFADMRAAYDALDDETKAEIEDMICEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
S+ LG + Y L+ LV+ HP GR SL + HA AI GM E+
Sbjct: 62 SRGSLGFLD-----YTDEEKQMFKPVLRVTHPVHGRKSLYLSSHAGAIRGMSMPPEAR 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
L L + A Q V+ H+W D+V+WDNR +HR
Sbjct: 117 LLLRDLTEHATQGEFVYVHKWTVHDLVMWDNRQTVHR 153

>gb|EFV82234.1| taurine dioxxygenase [Achromobacter xylosoxidans C54]
Length = 304

Score = 122 bits (307), Expect = 4e-26, Method: Compositional matrix adjust.
Identities = 89/292 (30%), Positives = 138/292 (47%), Gaps = 29/292 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ P +GA + G+ L L A F +H A L H LL+F Q ++ Q I F++RF
Sbjct: 24 FELRPLPGPVGAELIGLDLQELSPADFKRVHQAHLDHLLLVFRDQRITPQQHIDFSRRF 83

Query: 65 GAI-----ERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMP 116
G + +I+ +SN+ +G P D K WH+D +Y
Sbjct: 84 GPLMIHVLHQFHLANHPEILIVSNIVENG-----KPVGLGDAGKY-----WHSDISYKE 132

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ + G++ A+ +PA GG T FA+M AYD L A R V R A HS + +K G +Q
Sbjct: 133 LPSLGSLLHAQELPAQGGDTLFANMHLAYDTLPAALRNAVQGRRVHVSYL---AKYGQLQ 189

Query: 177 QAGSAYIGYGMDDTTATPL---RPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLE 231
+ G+ A P+V+ HPE GR +L + G H I G+ ES + L+
Sbjct: 190 KEGNWRPNLSAQQVAQVQAVSHPVVRTHPENRRALFVSEGFTTH-IEGLPEDESRLQLD 248

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + + ++ H+W D+V WDNR L+H A L R ++ + + G
Sbjct: 249 ELFAHSVRPEHIYRHRWQPHDLVFWDNRSLLIHLAGGTPDHLRRKLYRTTIEG 300

>ref|YP_233447.1| taurine dioxygenase [Pseudomonas syringae pv. syringae B728a]
gb|AA35409.1| Taurine dioxygenase [Pseudomonas syringae pv. syringae B728a]
Length = 298

Score = 122 bits (306), Expect = 5e-26, Method: Compositional matrix adjust.
Identities = 79/270 (29%), Positives = 128/270 (47%), Gaps = 21/270 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ P +GA + G+ L+ L+DA FA +H A L H +++F Q ++ QQI F++RF
Sbjct: 18 FEVRPFTEKVGAEIVGLDLRPLNDADFARVHQAHLDHHVVVFRDQQITPQQQIDFSRRF 77

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMP 116
G ++ +I+ +SN+ V P D K WH+D +Y
Sbjct: 78 GVLQIHVLKQFLLANHPILIVSNI-----VENDKPVGLGDAGKY-----WHSLSYKE 126

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ + G++ A+ +P+ GG T FADM A++ L + R V RSA HS ++ +
Sbjct: 127 LPSLGSMLYAQELPSEGGDTLFAFMHLAWETLPQHRLDAVEGRSAVHSYTARYAEGHNAA 186

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ P+V+ HPE GR +L + I G+ ES + L +
Sbjct: 187 NWRPTLTAEQLAQVVEVSHPIVTRHPENGRKALFVSEGFTTRILGLPEDESRLNEIYA 246

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
+ + ++ HQW A D+V WDNR L H A
Sbjct: 247 HSKVPEHIYRHQWRANDMVFDNRSLTHLA 276

>ref|YP_004017351.1| taurine dioxygenase [Frankia sp. Eu1lc]
gb|ADP81481.1| Taurine dioxygenase [Frankia sp. Eu1lc]
Length = 303

Score = 122 bits (306), Expect = 5e-26, Method: Compositional matrix adjust.
Identities = 98/292 (33%), Positives = 133/292 (45%), Gaps = 20/292 (6%)

Query: 5 TLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
LQI P A GA +TGV L LD AAL AWL + ++ FP QHL+ DQQ+ F +
Sbjct: 8 NLQIRPLNAAFGEITGVDLRGLDAETVAALRQAWLDYQVVFPEQHLTIDQQVAFTRN 67

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG E I+A + V S ++ +KV + WH D T+ G+V
Sbjct: 68 FG--ELTAPSAILAPVDADHREVVAFDSREFREEYVKV--GRHHGWHVDITFQATPPAGSV 124

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
F+ +P VGG T FA +AAY+ L L+ A HS G +AG
Sbjct: 125 FNIVKLPPVGGATLFASAQAAYETLSPPIHDLGLVAIHS-----FGRPSRAGGGIS 177

Query: 184 GYGMDDTTATPL-----RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
G+ P+ P+V VHPETGR L + AI G+ ES LE L D
Sbjct: 178 ATGV-WEDEPVDGGFVEHPVAVHPETGRKGLFVNPGFTRAIKGLSPRESAALLELLYDH 236

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLH-RAEPWDFKLPRVMWHSRLAGRPET 287
+ ++W G V WDNR + H RA+ +D R++ +L G T
Sbjct: 237 TLDIDNIIQYRWNNGGVGFWDNRRAIWHRRADDFDPDAVRIVHRVQLRGSAPT 288

>ref|ZP_04943924.1| Taurine dioxygenase [Burkholderia cenocepacia PC184]
gb|EAY67095.1| Taurine dioxygenase [Burkholderia cenocepacia PC184]
Length = 308

Score = 122 bits (306), Expect = 6e-26, Method: Compositional matrix adjust.
Identities = 86/288 (29%), Positives = 136/288 (47%), Gaps = 21/288 (7%)

Query: 4	TTLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA	61
	TT+ P AT+GA V+GV L DD A+ A Q+ +L+F G HL+ + Q+ F	
Sbjct: 3	TTISCEPLAATVGAEVSGVDAGQLAHDDTVATAVLEALEQYGVLVFRGLHLAPETQVAFG	62
Query: 62	KRFGAIERIGGGDIVA-ISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQ	120
	+R G I+ G V+ I V D + +++ A++ + WH D P+ +	
Sbjct: 63	RRLGEIDYEQGHHVPVSGIYRVTLDS--KNTSADY-----LRATFEWHMDGC-TPLHGE	113

Query: 121 ----GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ SA+ V GG T FA+ AAY+AL + + H++ SQ + V
Sbjct: 114 PPQKATILSAKAVATSGGETEFANTYAAEYALSDGEKEEFGLRVVHTMEASQRR---VT 170

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW 236
+ T PLV H TGR SL+IG +A + GM E L+ L+D
Sbjct: 171 PDPTPEQLQRWRNRPTSTHPLVWTH-RTGRRSLVIGANASHVVGMGLNEGPSLLQELDDR 229

Query: 237 ACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
A RV+ HQW+ GD V+WDN ++HRA P+D PR M + + G
Sbjct: 230 ATAPDRVYRHQWSVGDTVIWDNTGVVHRAAPYDSHSPREMLRTTVFG 276

>ref|YP_001859789.1| taurine dioxygenase [Burkholderia phymatum STM815]
gb|ACC72743.1| Taurine dioxygenase [Burkholderia phymatum STM815]
Length = 304

Score = 122 bits (305), Expect = 7e-26, Method: Compositional matrix adjust.
Identities = 84/292 (28%), Positives = 137/292 (46%), Gaps = 21/292 (7%)

Query: 2 AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A T I A +GA V G+ L L FA +H A L + +L+F Q ++ +Q + F
Sbjct: 20 ALQTFDIVAFDAPVGAEVLGLDLNEPLSADDFARIHRAHLDYHVLVFREQRITPEQHVAF 79

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
++RFG ++ G +++ +SN++ +G P D WH+D
Sbjct: 80 SRRFGPLQIHVLRQFQLPGHPEVLIVSNIRENG-----QPIGLGD-----AGHFWHSDL 128

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+Y + G++ A+ +P+ GG T FA+M A+D L E R V R+A H+ + ++L
Sbjct: 129 SYKEKPSLGSLLHAQELPSEGGDTLFA NMHLAWDTLPEHLRKAVEGR TAEHTYLAKYAEL 188

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLE 231
+ + P+V+ HPETGR +L + H I G+ ES L
Sbjct: 189 QKRSPWRPNLSAEQVAEVKPVVHPVVRTHPETGRKALFVSEHFTTHIVGLPEDES RDLLG 248

Query: 232 GLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + + ++ HQWA D+V WDNR L+H A L R ++ + + G
Sbjct: 249 ALFVHSVRDEHIYRHQWAEHDLVFWDNRSIMHLAAGTPDHLRRKLYRTTIEG 300

>gb|ABD16697.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium elkanii]
Length = 153

Score = 122 bits (305), Expect = 7e-26, Method: Compositional matrix adjust.
Identities = 68/161 (42%), Positives = 91/161 (56%), Gaps = 13/161 (8%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A + HSL+Y
Sbjct: 2 WHSDSSFRPIP AKFSLLSARVVNPKGGNTEFADMRAAYDALDDETKAEIEDMICEHS LMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDTTATPLRP----LVKVHPETGRPSLLIGRHAHAIPGMDA 223
S+ LG ++ Y D RP LV+ HP GR SL + HA AI GM
Sbjct: 62 SRGSLG-----FLDYT-DEEKQMFVRPVLQRLVRTHPVHGRRSLYLSSHAGAIRGMSM 112

Query: 224 AESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHR 264
E+ L L + A Q V+ H+W D+V+WDNR +HR
Sbjct: 113 PEARLLLRDLTEHATQPEFVYVHKWTVHDLVMWDNRQTVHR 153

>ref|YP_001912283.1| taurine dioxygenase [Xanthomonas oryzae pv. oryzae PX099A]

gb|ACD57751.1| taurine dioxygenase [Xanthomonas oryzae pv. oryzae PX099A]
Length = 305

Score = 122 bits (305), Expect = 8e-26, Method: Compositional matrix adjust.
Identities = 83/275 (30%), Positives = 131/275 (47%), Gaps = 21/275 (7%)

```
Query: 1  MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
      + ++ ++I P    LGA V G++L+ LD  FA LH A L H +L+F Q +S QQ+
Sbjct: 20 VQRSGVRIAPFDGPLGAEVIGLNLSQPLDADAFARLHRAHLDDHVLVFRDQRISPAQQVE 79

Query: 60 FAKRFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHAD 111
      F++RFGA+          + G +++ +SN+K +G      P    D          WH+D
Sbjct: 80  FSRRFGALQIHVLRNFQLRGHPEVLVVSNIKENG-----EPIGLGD-----AGHDWHS 128

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
      +Y    + G++ A+ +P+ GG T FA+   A+  L E+   V    A HS +
Sbjct: 129 LSYKETPSLGSLLHAQQLPSEGGDTLFANQHLAWQTLPESLTRTVQDLRAEHSYLARYEA 188

Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL 230
      L      A      +          P+V+ HPETGR +L +  H    I G+   ES   L
Sbjct: 189 LRARNPWCALPTEQIAEVTPVHHVVRTHPETGRKALFVSEHFTTRILGLPEDESRL 248

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      + L  + +  V+ H+W  D+V WDNR ++H A
Sbjct: 249 QTLFAHSTRPALVYRHRWQPYDMVFWDNRSVMHLA 283
```

>ref|ZP_05636704.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. tabaci
ATCC

11528]
gb|AA063153.1| TblC [Pseudomonas syringae]
Length = 287

Score = 122 bits (305), Expect = 8e-26, Method: Compositional matrix adjust.
Identities = 81/290 (27%), Positives = 139/290 (47%), Gaps = 26/290 (8%)

```
Query: 6  LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      L++ P    +G V G+ + + L D    AL+ AW+   +L+F GQ ++ DQQ+ F++ F
Sbjct: 2  LELVPITNLIGTEVRGIDVNSKLSDDVIEALYEAWISSTILLFRGQSMTPDQQLKFSRNF 61

Query: 65 GAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
      G +          +I+ +SN+ DG          ++  V    WH D Y+
Sbjct: 62 GELVSYTRSQFSEKTQPEILILSNITKDGK-----LIGSPVSGRVWHTDGHYLE 110

Query: 117 VMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
      V    G++ A  +P  GG T FA+M AAY+AL E+ +  +          S    S+    +
Sbjct: 111 VPPAGSMLHALEIPPEGGDTWFANMFAAYEALPESVKQRIEDLKVIISRTQSRPYNYPDR 170

Query: 177 QAGSAY-IGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAAH-AIPGMDAAESERFLEGLV 234
      A SA +   +D    +PLV+ H  +GR +L G +   I G+   ES   +  L
Sbjct: 171 PAPSQELAEWVDVA----QPLVRRHEVSGRKALYAGGNVPWRIEGLPLEESAPLITFLQ 226

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR 284
      +++ Q    ++ H+W  GD+++WDNR  +H+A  +D K  R++  + +  R
Sbjct: 227 EFSVQPQFIYRHRWVPGDIILWDNRSAMHKATVYDDKYRLLHRTTIGAR 276
```

>gb|ABD16715.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. LcRI3]
Length = 153

Score = 122 bits (305), Expect = 9e-26, Method: Compositional matrix adjust.
Identities = 64/157 (40%), Positives = 89/157 (56%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA +V GG T FADMRAAYDALD+ T+ + HSL+Y
Sbjct: 2 WHSDSSFRPIPAPKFSLLSARIVNPKGGNTEFADMRAAYDALDDETKTEIDDMICEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+
Sbjct: 62 SRGSLGFLD-----YTDEEKEMFKPVLQRLVRTHPVHGRKSLYLSSHAGAIRGMSMPPEAR 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
L L + A Q V+ H+W D+V+WDNR +HR
Sbjct: 117 LLLRDLTEHATQPEFVYVHKWTVHDLVMWDNRQTVHR 153

>gb|ABD16714.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium sp. Lh10]
Length = 153

Score = 121 bits (304), Expect = 9e-26, Method: Compositional matrix adjust.
Identities = 64/157 (40%), Positives = 89/157 (56%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA +V GG T FADMRAAYDALD+ T+ + HSL+Y
Sbjct: 2 WHSDSSFRPIPAPKFSLLSARIVNPKGGNTEFADMRAAYDALDDETKTEIDDMICEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+
Sbjct: 62 SRGSLGFLD-----YTDEEKEMFKPVLQRLVRTHPVHGRKSLYLSSHAGAIRGMSMPPEAR 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
L L + A Q V+ H+W D+V+WDNR +HR
Sbjct: 117 LLLRDLTEHATQPEFVYMHKWTVHDLVMWDNRQTVHR 153

>ref|ZP_07003248.1| Alpha-ketoglutarate-dependent taurine dioxxygenase [Pseudomonas
savastanoi pv. savastanoi NCPPB 3335]
gb|EFI01344.1| Alpha-ketoglutarate-dependent taurine dioxxygenase [Pseudomonas
savastanoi pv. savastanoi NCPPB 3335]
Length = 298

Score = 121 bits (304), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 78/270 (28%), Positives = 127/270 (47%), Gaps = 21/270 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ P +GA + G+ L+ L+DA FA +H A L H +++F Q ++ QQ+ F++RF
Sbjct: 18 FDVRPFTGKVGAEIVGLDLRPLNDADFARVHQAHLDHHVVVFRDQQITPQQQVDFSRRF 77

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
G ++ +I+ +SN+ V P D K WH+D +Y
Sbjct: 78 GVLQIHVLKQFLLANHPFILIVSNI-----VENEKPVGLGDAGKY-----WHSLSYKE 126

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ + G++ A+ +P+ GG T FADM A+D L + R V RSA HS ++ +
Sbjct: 127 LPSLGSMLYAQELPSEGGDTLFADMHQAWDTLPQHRLDAVEGRSAVHSYTARYAEGHNAA 186

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ P+V+ HPE GR +L + I + ES + L +
Sbjct: 187 NWRPTLTAEQLAQVVEVSHPIVRTHPEAGRKALFVSEGFTTRILDLPEDSRQILNEIYA 246

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ + ++ HQW A D+V WDNR L+H A
Sbjct: 247 HSVKPEHIYRHQWQANDMVFDNRSLIHLA 276

>ref|YP_001071988.1| taurine catabolism dioxygenase TauD/TfdA [Mycobacterium sp. JLS]
gb|ABN99497.1| Taurine catabolism dioxygenase TauD/TfdA [Mycobacterium sp. JLS]
Length = 281

Score = 121 bits (304), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 98/289 (33%), Positives = 134/289 (46%), Gaps = 23/289 (7%)

```
Query: 4   TTLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
          T L I   A++GA VTG+   L D+A AA+ A   + +L+FPG HL   Q+ F
Sbjct: 2   TVLTINKLTASVGA EVTGLDPDALAGDEALGA AVLEALEDN GVLVFPGLHLD PQAQVEFC 61

Query: 62  KRFGAIERIGGG--DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTY----- 114
          +R G ++   G   + I V D + ++S A +   +   WH D
Sbjct: 62  RRLGEVDHSSDGHHPVAGIYPVTLDKS--KNSSAAY-----LRATFDWHIDGCTPTGDE 113

Query: 115  MPVMAQGA VFSAE VVPVAVGGRTCFADMR AAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
          P MA   V SA V   GG T FA   AYD LD+ + +   HSL SQ +
Sbjct: 114  YPQMA--TVLSARQVAESGGETEFASSYGAYDHLDDDEKQRLASLRVVHSLEASQRR--- 168

Query: 175  VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
          V   S +   + T   PLV H +GR SL++G A I GMD E   L L+
Sbjct: 169  VTPDPSPPELLARWRSRP THEHPLVWTH-RSGR KSLVLGASADYIVGMDLDEGRALLADLL 227

Query: 235  DWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          D A Q   V++H W+ GD V+WDNR +LHRA P+   PR M + + G
Sbjct: 228  DRATQPELVYSHTWSVGDTVIWDNRGVLHRAAPYPENSPREMLRTTVLG 276
```

>ref|YP_640870.1| taurine catabolism dioxygenase TauD/TfdA [Mycobacterium sp. MCS]
ref|YP_939764.1| taurine catabolism dioxygenase TauD/TfdA [Mycobacterium sp. KMS]
gb|ABG09814.1| Taurine catabolism dioxygenase TauD/TfdA [Mycobacterium sp. MCS]
gb|ABL92974.1| Taurine catabolism dioxygenase TauD/TfdA [Mycobacterium sp. KMS]
Length = 281

Score = 121 bits (304), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 98/289 (33%), Positives = 134/289 (46%), Gaps = 23/289 (7%)

```
Query: 4   TTLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
          T L I   A++GA VTG+   L D+A AA+ A   + +L+FPG HL   Q+ F
Sbjct: 2   TVLTINKLTASVGA EVTGLDPDALAGDEALGA AVLEALEDN GVLVFPGLHLD PQAQVEFC 61

Query: 62  KRFGAIERIGGG--DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTY----- 114
          +R G ++   G   + I V D + ++S A +   +   WH D
Sbjct: 62  RRLGEVDHSSDGHHPVAGIYPVTLDKS--KNSSAAY-----LRATFDWHIDGCTPTGDE 113

Query: 115  MPVMAQGA VFSAE VVPVAVGGRTCFADMR AAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
          P MA   V SA V   GG T FA   AYD LD+ + +   HSL SQ +
Sbjct: 114  YPQMA--TVLSARRVAESGGETEFASSYGAYDHLDDDEKQRLASLRVVHSLEASQRR--- 168

Query: 175  VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
          V   S +   + T   PLV H +GR SL++G A I GMD E   L L+
Sbjct: 169  VTPDPSPPELLARWRSRP THEHPLVWTH-RSGR KSLVLGASADYIVGMDLDEGRALLADLL 227

Query: 235  DWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          D A Q   V++H W+ GD V+WDNR +LHRA P+   PR M + + G
Sbjct: 228  DRATQPELVYSHTWSVGDTVIWDNRGVLHRAAPYPENSPREMLRTTVLG 276
```

>ref|ZP_03585090.1| alpha-ketoglutarate-dependent taurine dioxygenase
(2-aminoethanesulfonate dioxygenase) (Sulfate
starvation-induced protein3) (SSI3) [Burkholderia
multivorans CGD1]

gb|EEE00666.1| alpha-ketoglutarate-dependent taurine dioxygenase
(2-aminoethanesulfonate dioxygenase) (Sulfate
starvation-induced protein3) (SSI3) [Burkholderia
multivorans CGD1]
Length = 309

Score = 121 bits (304), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 86/292 (29%), Positives = 137/292 (46%), Gaps = 21/292 (7%)

Query: 2 AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A +I P A LGA V G+ L+ LD FA + A L +L+F Q ++ D+ + F
Sbjct: 25 APQRFEIVPFDAPLGAEVVGIDLSQPLDADAFARIRRAHLDLHVLVFRDQRITPDEHVAF 84

Query: 61 AKRFGAIER-----IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
++RFG ++ G +++ +SN+ +G P D WH+D
Sbjct: 85 SRRFGPLQTHVLHQFALPGHPEVLIVSNIVENG-----KPIGLGD-----AGYFWHSDL 133

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+Y + G++ A+ +PA GG T FA+M A+D L +A R V R A H+ + ++L
Sbjct: 134 SYKRRPSLGSLLHAQELPAEGGDTLFAFMHLAWDTLPDALRRAVEGRRAEHTYLARYAEL 193

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE 231
+ + P+V+ HPETGR +L + H I G+ ES L+
Sbjct: 194 QARSPWRPNLSAEQIAQVEPVVHPVVRTHPETGRRALFVSEHFTTRIVGLPDDESRLLD 253

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + +A + H+W D+V WDNR LLH A L R ++ + + G
Sbjct: 254 ELFAHSVRAEHQYRHRWRDHDLVFWDNRSLHLAAGTPDHLRRKLYRTTIEG 305

>emb|CBJ20513.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 142

Score = 121 bits (303), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 65/142 (45%), Positives = 84/142 (59%), Gaps = 1/142 (0%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
MPV+A+G V AEVVP VGG F MRA YD L E +A V R SL Y LGH
Sbjct: 1 MPVLARGPVLIAEVVPMVGGHNGFLHMRAGYDWLHEDLKARVETHQDRSLRYGLDNLGH 60

Query: 175 VQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+A Y GYG+ P+ L +HPETGR SLLIGRH HA G++A +S+R L+ L
Sbjct: 61 PTKAADGEYSYGLFDGPVPLALENIHPETGRVSLIGRHPHAFHGLEARQSQRLLQQL 120

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255
+ + C +P ++ + A GD +V
Sbjct: 121 IYFPCHSPPYHQLAPGDALV 142

>ref|YP_002980735.1| taurine dioxygenase [Ralstonia pickettii 12D]
gb|ACS62063.1| Taurine dioxygenase [Ralstonia pickettii 12D]
Length = 300

Score = 121 bits (303), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 89/283 (31%), Positives = 132/283 (46%), Gaps = 24/283 (8%)

Query: 13 ATLGATVTGVHLAT-LDDAGFAALHAAWLQH-ALLIFPGQHLSNDQQITFAKRFGA---- 66
A LGA V G+ A+ L DA AA+ AWL H LL+F + Q+ F++RFG
Sbjct: 26 APLGAEVLGLGDASDLSADIAAIRQAWLAHDGLLVFRDVEFTPQAQVAFSRRFGPQQVH 85

Query: 67 ----IERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
G +I+ +SNV +G P D + WH+D +Y P+ + G+

Sbjct: 86 VLNQFHLSGYPEILVVSNNVENG-----KPIGLGDAGR-----DWHS DLSYKPLPSLGS 134

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ +P GG T FA+M AY+ L + ++ R A HS VY +L +

Sbjct: 135 MLLTRELPEEGD TLFANMVRAYETLPANLKRVI EGRRVHSYVYRYDRLRALSTWRPPL 194

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVDWACQA 240
D P+V+ HPETG+ +L + G +H I G+ ES LE L + +A

Sbjct: 195 TQAQRDAVPPVDHPVVRTHPETGKRALFVNEGFTSHII-GLPEDESTSVLEQLFAHSVRA 253

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
V+ HQW GD++ WDNR +H A K R + + + G

Sbjct: 254 DNVYTHQWRPGDMLFWDNRSTIHFAPGCPDKYRRTLHRTTIEG 296

>gb|ABD16710.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. BtRI3]
Length = 153

Score = 121 bits (303), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 64/157 (40%), Positives = 89/157 (56%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA +V GG T FADMRAAYDALD+ T+ + HSL+Y

Sbjct: 2 WHSDSSFRPIPAKFSLLSARIVNPKGGNTEFADMRAAYDALDDETKTEIDDMICEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+

Sbjct: 62 SRGSLGFLD-----YTDEEKEMFKPVLQRLVRTHPVHGRKSLYLSSHAGAIRGMSMPPEAR 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
L L + A Q V+ H+W D+V+WDNR +HR

Sbjct: 117 LLLRDLTEHATQPGFVYVHKWTVHDLVMWDNRQTVHR 153

>gb|ACX54976.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ACX54983.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ACX54997.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 96

Score = 121 bits (303), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 61/96 (63%), Positives = 72/96 (75%), Gaps = 1/96 (1%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYMPV A+GAVFSAE VP+VGGRT FADMRAAYDALD A +A + +A HSL YSQ

Sbjct: 1 ADSTYMPVQAKGAVFSAEEVPSVGGRTGFADMRAAYDALDPAIKARIEGLNAYHSLHYSQ 60

Query: 170 SKLGH-VQQAGSAYIGYGMDTTATPLRPLVKVHPET 204
++GH ++ Y GYG+ PLRPLVK+HPET

Sbjct: 61 GRVGHQTKKLDGEYSGYGLHDGPVPLRPLVKIHPET 96

>ref|ZP_08206675.1| taurine dioxygenase [Gordonia neofelifaecis NRRL B-59395]
gb|EGD53494.1| taurine dioxygenase [Gordonia neofelifaecis NRRL B-59395]
Length = 312

Score = 120 bits (302), Expect = 2e-25, Method: Compositional matrix adjust.
Identities = 86/282 (30%), Positives = 131/282 (46%), Gaps = 19/282 (6%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63

T ++TP G T+GA + GV LA +DD A LH A L+ +L F Q L+ Q I+ A+R
Sbjct: 44 TRFEVTPAGPTIGAYIEGVDLADIDDELHAEHLRALLEFKVLFFRDQSLTGPQHISLAR 103

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
+G++E +++ +G ++ S DM + WH+D+++ + ++
Sbjct: 104 WGSVE-----VNDFFPNGEAQEISRLAKGDMS--VGTEENVHSDTSFRKDPSMASI 152

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
A VP VGG T +ADM AAYD L E + + A H+ S +Q +
Sbjct: 153 LRAVEVPPVGGNTVWADMAAAYDNLPEPVKEKIEGLRAIHTFTKSWGLAMSAEQVEA--- 209

Query: 184 GYGMDTTATPL-RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAP 241
M P+ P+V+ HPETGR L + I G+ + ++ L+ L+ A
Sbjct: 210 ---MSKIHPPIAHPIVRTHPETGRLLYVNEPFTSEIVGLPKGDGQQLLDYLMFQARTPE 266

Query: 242 RVHAHQWAAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
QW V +WDNR H A F RVM +AG
Sbjct: 267 YQIRFQWEPNSVAIWDNRSTQHYAVNDYFPHRRVMERVTVAG 308

>ref|YP_001773806.1| taurine dioxygenase [Burkholderia cenocepacia MC0-3]
gb|ACA95311.1| Taurine dioxygenase [Burkholderia cenocepacia MC0-3]
Length = 308

Score = 120 bits (302), Expect = 2e-25, Method: Compositional matrix adjust.
Identities = 85/288 (29%), Positives = 135/288 (46%), Gaps = 21/288 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
I P A LG V G++L+ L FA +H A L H +L+F Q ++ D+ I F++RF
Sbjct: 28 FDIVPFDAPLGVEVIGLNLSQLGADDFARIHRAHLDDHVLVFRDQRITPDEHIAFSRRF 87

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMP 116
G ++ G +++ +SN+ +G P D WH+D +Y
Sbjct: 88 GPLQIHVLHQFALAGHPEVLIVSNIVENG-----KPVGLGD-----AGHFWSHSDLSYKE 136

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ G++ A+ +PA GG T FA+M A+D L R V R A H+ + ++L
Sbjct: 137 KPSLGSLHLAQELPAEGGDTLFANMHLAWDTLPAPHLRRAVEGRRAEHTYLARYAELQARS 196

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
+ A + P+V+ HPETGR +L + H I G+ ES L+ L
Sbjct: 197 PWRPNLSPEQIAQVAHVHPIVRTHPETGRKALFVSEHFTTRIVGLPDDESRAALLDEL FV 256

Query: 236 WACQAPRVHAHQWAAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +A ++ H W D+V WDNR L+H A L R ++ + + G
Sbjct: 257 HSVRAEHLRHAWRDHDLVFWDNRSLMHLAAGTPDHLRRKLYRTTIEG 304

>gb|ABD16713.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. Tep5]
Length = 153

Score = 120 bits (302), Expect = 2e-25, Method: Compositional matrix adjust.
Identities = 64/157 (40%), Positives = 89/157 (56%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA +V GG T FADMRAAYDALD+ T+ + HSL+Y
Sbjct: 2 WHSDSSFRPIPAKFSLLSARIVNPKGGNTEFADMRAAYDALDDETKTEIDDMICEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+
Sbjct: 62 SRGSLGFLD-----YTDEEKEMFKPVLQRLVRTHPVHGRKSLYLSSHAGAIRGMSMPEAL 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
 L L + A Q V+ H+W D+V+WDNR +HR
 Sbjct: 117 LLLRDLTEHATQPEFVYVHKWTVHDLVMWDNRQTVHR 153

>ref|XP_002482822.1| alpha-ketoglutarate-dependent taurine dioxygenase, putative
 [Talaromyces stipitatus ATCC 10500]
 gb|EED18830.1| alpha-ketoglutarate-dependent taurine dioxygenase, putative
 [Talaromyces stipitatus ATCC 10500]
 Length = 290

Score = 120 bits (302), Expect = 2e-25, Method: Compositional matrix adjust.
 Identities = 85/284 (29%), Positives = 126/284 (44%), Gaps = 33/284 (11%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
 L I GA V G T+ AL +AWL++ +L F G L+++ Q+ F KR
 Sbjct: 10 LTIVANKVGAGADVLGDFDTMPSHQVGALRSALWKYILRFRGYDLTDEHQLNFKR-- 67

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVG-----NMAWHADSTYMP 116
 E G A + K D V M +I G + WH DS +
 Sbjct: 68 --EEDG-----APTTYKDDEKVTV-----MTNLINGVPSGAGSNVELEWHTDSWFWE 112

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
 G + A +P GG T +ADM A YDAL E R+ + R + VY+ G+++
 Sbjct: 113 YPPVGEILRAMELPQTGGDTYWADMYAVYDALPEDLRSTIEGRLIQFDTVYNGH--GNLR 170

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA---IPGMDAAESERFLEGL 233
 + A P+++ HPE+GR ++ +G+ H I G+ ES+ L +
 Sbjct: 171 KGKEAPKTDFFRLWEHIRHPIIRTHPESGRKAVFVGQSKHEKNWIVGLPLEESKEILAKI 230

Query: 234 VDWACQAPRVHAHQ-WAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
 + + + P HQ W GD V+WDNRC +HR E W R+M
 Sbjct: 231 LSY-VEKPEFQLHQWQPGDVTIWDNRCTMHRRETWPDDQTRIM 273

>gb|ACX54984.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
 [uncultured bacterium]
 Length = 97

Score = 120 bits (301), Expect = 2e-25, Method: Compositional matrix adjust.
 Identities = 63/97 (64%), Positives = 70/97 (72%), Gaps = 2/97 (2%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
 ADSTYMPV A+GAVFSAE VP +GG T FADMRAAYDALDE TRA + SA HSL YSQ
 Sbjct: 1 ADSTYMPVQAKGAVFSAEEVPTIGGHTGFADMRAAYDALDEPTRARLEGLSAFHSLYYSQ 60

Query: 170 SKLGH--VQQAGSAYIGYGMDTTATPLRPLVKVHPET 204
 SKLGH +++ Y GYG P R L+KVHPET
 Sbjct: 61 SKLGHQPKKKSDGEYSYGFHDGPVPRRALIKVHPET 97

>ref|ZP_01627763.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
 oxidoreductase protein [marine gamma proteobacterium
 HTCC2080]
 gb|EAW39610.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
 oxidoreductase protein [marine gamma proteobacterium
 HTCC2080]
 Length = 295

Score = 120 bits (301), Expect = 2e-25, Method: Compositional matrix adjust.
 Identities = 84/288 (29%), Positives = 130/288 (45%), Gaps = 37/288 (12%)

Query: 3 QTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61

Q T + PT GA V+ ++ T + A+ A W +H LL+F Q+L + ++F+
Sbjct: 16 QNTRSLAPT---FGAEVSDYTISSTTSNEENTAIAKALWAKHKLLLFNRQNLDEETLVSF 72

Query: 62 KRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADST 113
+ FG +E +++ +SN+K +G M + + WH D

Sbjct: 73 RVFGDLEIHVRTEYLSSAFPEVLYVSNMKNNG-----KKMGILADTEVGVWHYDQI 122

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
Y+P A G++ A +P GG T FADM AY L E + + A S S

Sbjct: 123 YLPRPAVGSLLMAHTLPPTGGNTEFADMTTAYSELPEEVKQQLLEGARAVQSYEAFNSAYS 182

Query: 174 ----HVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSL-LIGRHAHAIPGMDAAESER 228
Q+ S I + P+V+ HP TG +L L I G +AA+S

Sbjct: 183 VPTSKEQKQRPDIH-----PIVRTHPVTGEKALYLCPGMTTEIVGWEAADSRA 232

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
L+ L +W Q V++H W GD ++WDN C +HR +P+D R+M

Sbjct: 233 MLDYLFWEVTVQPRYVYSHSWQPGDALLWDNACTMHRDPFDQNHDRML 280

>gb|ABD16705.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium sp. onl92.6]
gb|ABD16706.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium sp. ApT2]
gb|ABD16707.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium sp. DesT1]
Length = 153

Score = 120 bits (301), Expect = 2e-25, Method: Compositional matrix adjust.
Identities = 66/160 (41%), Positives = 91/160 (56%), Gaps = 11/160 (6%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A + HSL+Y

Sbjct: 2 WHSDSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAYDALDDETKAEIEDMICHESLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMTTAT---PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAA 224
S+ LG ++ Y + A L+ LV+ HP GR SL + HA AI M

Sbjct: 62 SRGSLG-----FLDYTDEEKAMFKPVLQRLVRTHPVHGRKSLYLSSHAGAIRDMSMP 113

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
E+ L L + A Q V+ H+W D+V+WDNR +HR

Sbjct: 114 EARLLLRDLTEHATQGEFVYVHKWTVHDLVMWDNRQTVHR 153

>ref|YP_452585.1| taurine dioxxygenase [Xanthomonas oryzae pv. oryzae MAFF 311018]
dbj|BAE70311.1| taurine dioxxygenase [Xanthomonas oryzae pv. oryzae MAFF 311018]
Length = 305

Score = 120 bits (301), Expect = 2e-25, Method: Compositional matrix adjust.
Identities = 83/275 (30%), Positives = 129/275 (46%), Gaps = 21/275 (7%)

Query: 1 MAQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
+ ++ ++I P LGA V G+ L LD FA LH A L H +L+F Q +S QQ+

Sbjct: 20 VQRSGVRIAPFDGPLGAEVIGLDLLQPLDADAFARLHRAHLDHHLVLFVRDQRISPAQQVE 79

Query: 60 FAKRFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHAD 111
F++RFGA+ + G +++ +SN+K +G P D WH+D

Sbjct: 80 FSRRFGALQIHVLRNFQLRGHPEVLYVSNIKENG-----EPIGLGD-----AGHDWHSD 128

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
+Y + G++ A+ +P+ GG T FA+ A+ L E+ V A HS +

Sbjct: 129 LSYRETPSLGSLHAQQLPSEGGYTLFANQHLAWQTLPELSTRVQDLRAEHSYLARYEA 188

Query: 236 WACQAPRVHAHQWAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +A ++ H W A D+V WDNR L+H A L R ++ + + G
Sbjct: 257 HSVRAEHLRHHWRAHDLVFWDNRLMHLAAGTPDHLRRKLYRTTIEG 304

>ref|ZP_04590344.1| TauD/TfdA family dioxygenase [*Pseudomonas syringae* pv. *oryzae* str. 1_6]
Length = 287

Score = 120 bits (300), Expect = 3e-25, Method: Compositional matrix adjust.
Identities = 81/290 (27%), Positives = 138/290 (47%), Gaps = 26/290 (8%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L++ P +G V G+ + + L D AL+ AW+ +L+F GQ ++ DQQ+ F++ F
Sbjct: 2 LELVPITNLIGTEVRGIDVNSKLSDDVIEALYEAWISSSTILLFRGQSMTPDQQLKFSRNF 61

Query: 65 GAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
G + +I+ +SN+ DG ++ V WH D Y+
Sbjct: 62 GELVSYTRSQFSEKTQPEILILSNITKDGK-----LIGSPVSGRVWHTDGHYLE 110

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
V G++ A +P GG T FA+M AAY+AL E+ + + S S+ +
Sbjct: 111 VPPAGSMLHALEIPPEGGDTWFANMFAAYEALPESVKQRIDDLKVIISRTQSRPYNYPDR 170

Query: 177 QAGSAY-IGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLV 234
A SA + +D +PLV+ H +GR +L G + I G+ ES + L
Sbjct: 171 PAPSAQELAEWVDVA----QPLVRRHEVSGRKALYAGGNVPWRIEGLPLEESAPLITFLQ 226

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGR 284
+++ Q + H+W GD+++WDNR +H+A +D K R++ + + R
Sbjct: 227 EFSVQPQFTYRHRWVPGDIILWDNRSAMHKATVYDDKYRRLHRTTIGAR 276

>ref|ZP_02891645.1| Taurine dioxygenase [*Burkholderia ambifaria* IOP40-10]
gb|EDT02751.1| Taurine dioxygenase [*Burkholderia ambifaria* IOP40-10]
Length = 308

Score = 120 bits (300), Expect = 3e-25, Method: Compositional matrix adjust.
Identities = 84/288 (29%), Positives = 134/288 (46%), Gaps = 21/288 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
I P A LGA V G+ L+ L A FA +H A L H +L+F Q ++ D+ + F++RF
Sbjct: 28 FDIVPFDAPLGAEEVVGIDLSQPLGAADFARVHRAHLDDHVLVFRDQRITPDEHVAFSRRF 87

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
G ++ +++ +SN+ +G P D WH+D +Y
Sbjct: 88 GPLQIHVLHQFALAAHPEVLIVSNIVENG-----RPIGLGD-----AGHFWHSDLSYKE 136

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ G++ A+ +PA GG T FA+M A+D L R V R A H+ + ++L
Sbjct: 137 KPSLGSLLHAQELPAEGGDTLFANMHLAWDTLPAHLRRAVEGRRAEHTYLARYAELQARS 196

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
+ + P+V+ HPETGR +L + H I + ES L+ L
Sbjct: 197 PWRPNLSAEQIAQVEAVVHPVVRTHPETGRKALFVSEHFTTRIVDLPEDESRAALLDELFA 256

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +A ++ H W A D+V WDNR L+H A L R ++ + + G
Sbjct: 257 HSVRAEHLRYHHWRAHDLVFWDNRSMLMHLAAGTPDHLRRKLYRTTIEG 304

>ref|YP_001816237.1| taurine dioxygenase [*Burkholderia ambifaria* MC40-6]
gb|ACB68684.1| Taurine dioxygenase [*Burkholderia ambifaria* MC40-6]
Length = 308

Score = 120 bits (300), Expect = 3e-25, Method: Compositional matrix adjust.

SKLGH ++A Y GYG P R L+KVHPET
Sbjct: 61 SKLGHQPKKKADGEYSYSGYGFHDGPVPRRALIKVHPET 97

>ref|YP_621125.1| taurine dioxygenase [Burkholderia cenocepacia AU 1054]
ref|YP_840210.1| taurine dioxygenase [Burkholderia cenocepacia HI2424]
gb|ABF76152.1| Taurine dioxygenase [Burkholderia cenocepacia AU 1054]
gb|ABK13317.1| Taurine dioxygenase [Burkholderia cenocepacia HI2424]
Length = 308

Score = 120 bits (300), Expect = 3e-25, Method: Compositional matrix adjust.
Identities = 85/288 (29%), Positives = 135/288 (46%), Gaps = 21/288 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
I P A LGA V G++L+ L FA +H A L H +L+F Q ++ D+ I F++RF
Sbjct: 28 FDIVPFDAPLGAIEVIGLNLSQLGADDFARIHRAHLDDHVLVFRDQRITPDEHIAFSRRF 87

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
G ++ G +++ +SN+ +G P D WH+D +Y
Sbjct: 88 GPLQIHVLHQFALAGHPEVLTVSNIVENG----KPVGLGD-----AGHFVHSDLSYKE 136

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ G++ A+ +PA GG T FA+M A+D L R V A H+ + ++L
Sbjct: 137 KPSLGSLLHAQELPAEGGDTLFANMHLAWDTLPAHLRRAVEGLRAEHTYLARYAELQARS 196

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
+ A + P+V+ HPETGR +L + H I G+ ES L+ L
Sbjct: 197 PWRPNLSPEQIAQVAHVHPIVRTHPETGRKALFVSEHFTTRIVGLPDDESRLLDLDELFA 256

Query: 236 WACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +A ++ H W D+V WDNR L+H A L R ++ + + G
Sbjct: 257 HSVRAEHLRYHAWRDHDLVFWDNRSLMHLAAGTPDHLRRKLYRTTIEG 304

>ref|ZP_02466092.1| dioxygenase TauD/TfdA family protein [Burkholderia thailandensis
MSMB43]
Length = 297

Score = 120 bits (300), Expect = 3e-25, Method: Compositional matrix adjust.
Identities = 98/295 (33%), Positives = 138/295 (46%), Gaps = 27/295 (9%)

Query: 4 TTLQITPTGATLGATVTGVH-LATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
+TL I P A LGA + GV A LD A+ AAWL+ LL+F GQ L + + F +
Sbjct: 5 STLCIRPLSALGAQIDGVDARADLDADTVRAIRAARLRFGLLVFRGQALDPAFLVAFTR 64

Query: 63 RFGA-----IERIGGG--DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY 114
RFG E G D++ +SN+ DG + + WH D +
Sbjct: 65 RFGEPPVYTRAENACDGPDLVLSNIVKDGP-----IGAAISGRYWHTDGHF 113

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
+ G + + PA GG TCF +M AAY AL RA + R+ V Q+ H
Sbjct: 114 LACPPAGTLLFGDETPEAGGDTCFVNMATAAYRALPAWLRARIDGRFTVMDRV--QTLPHF 171

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGL 233
+ A L+P+V+ HPETG+ +L IG I GM+ E + L
Sbjct: 172 YPRR-PAPPPDQKRVWPDMLQPVVVTHPETGQNALYIGGVVPWRIVGMERRYGEALMAHL 230

Query: 234 VDWACQAPRV-HAHQWAAGDVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RP 285
A R + H+W AGD+++WDNRCL HRA +D + R M+ + +AG RP
Sbjct: 231 HAIAFDEARFGYRHRWRAGDLLMWDNRCLAHRAATDYDMARYRRTMYRTTIIAGDRP 285

>gb|ADC33992.1| TfdA-like protein [uncultured bacterium]

Length = 208

Score = 120 bits (300), Expect = 3e-25, Method: Compositional matrix adjust.
Identities = 71/221 (32%), Positives = 113/221 (51%), Gaps = 28/221 (12%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVR-----QHSPA EWDDM---MKV 101
QQI FA+ FG +E I ++ D +R H W + +
Sbjct: 1 QQIAFARNFGPLE-----TTIKAIRKDAKLRLPAE IADVSNLDHEAKRWTEQSRHRRF 53

Query: 102 IVGNMAWHADSTYMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSA 161
N WH DS++ V A+ ++ + VGG T FADMRAAYDALD+AT+ + A
Sbjct: 54 EAANKLWHTDSSFKRVPAKASLLYQRSIAPVGGHTEFADMRAAYDALDDATKQRLRGLVA 113

Query: 162 RHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPL-RPLVKVHPETGRPSLLIGRHAHAIPG 220
HS+ YS+++LG + + D P+ + +V+ HP++GR +L + HA I G
Sbjct: 114 NHSIKYSRAQLGFDEYSEDE-----DIALQPVPMVRRHPDSGRMTLYLASHAGHIYG 167

Query: 221 MDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
M E++ + L++ A Q +++H+W D+V+WDNRC+
Sbjct: 168 MPDDEAKPLIRRLIEHATQRQFIYSHRWRLHDLVMWDNRCV 208

>ref|YP_004153368.1| taurine dioxygenase [Variovorax paradoxus EPS]
gb|ADU35257.1| Taurine dioxygenase [Variovorax paradoxus EPS]
Length = 296

Score = 120 bits (300), Expect = 3e-25, Method: Compositional matrix adjust.
Identities = 75/270 (27%), Positives = 129/270 (47%), Gaps = 21/270 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ P A +GA + G+ ++ ++ F +H A L H +L+F Q ++ + + F+ RF
Sbjct: 16 FEVRPFADAPVGA EIIGLDISKPINAE DFQRIHKAHLDDHVLVFRNQQITPQEHVDFSHRF 75

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
G +E +I+ +SN+K +G P D + WH+D +Y P
Sbjct: 76 GPLEIHVLHQFQLKDHPEILIVSNIKENG-----EPIGLGD-----AGVYWHSDISYKP 124

Query: 117 VMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ G++ A+ +P+ GG T FAD A+++L + + A HS + +L
Sbjct: 125 KPSLGSLLLHAQELPSEGGDTL FADQHLAWESLSPELQQRILPLKAEHSYLAKYEELRAKN 184

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
+D A ++P+V+ HPETGR +L + H I G+ ES+ L L
Sbjct: 185 PWRPKLSQAQIDQVAPAVQPVVTRHPETGRKALFVSEHFTTRIVGLPQDES DALLAELFA 244

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ + V+ H WA D++ WDNR L+H A
Sbjct: 245 HSVKPEFVYRHTWAPHDLMFWDNRSLMHLA 274

>ref|ZP_04941965.1| Taurine dioxygenase [Burkholderia cenocepacia PC184]
gb|EAY65136.1| Taurine dioxygenase [Burkholderia cenocepacia PC184]
Length = 317

Score = 120 bits (300), Expect = 3e-25, Method: Compositional matrix adjust.
Identities = 92/270 (34%), Positives = 130/270 (48%), Gaps = 20/270 (7%)

Query: 2 AQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQH-LSDNDQQIT 59
A LQ+ +GA ++GV L ATLDDA F A+HAA L+H +L F GQH L + Q
Sbjct: 22 ATVPLQLRQVAGRIGAEISGVRLSATLDDATF DAVHAALLRHKVLFFRGGQHLLDDTAQEA 81

Query: 60 FAKRFGAIERIGGGDIVAISNVKA-DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM 118
FA+RFG D VA V + DG+ + E D +WH D T++

Sbjct: 82 FARRFG-----DTVAHPTVPSVDGSA---ALLELDSAHGARAN--SWHTDVTFVDAY 128

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
+ ++ A V+P GG T +A+ AAY L + RAL A H+ Y + HV

Sbjct: 129 PKISILRAVVIPFPGDITVWANTAAAYANLPDPLRALADTLWALHTNAYDYAST-HVHAD 187

Query: 179 GSAYIGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD 235
+ Y T+T P+V+VHPETG +L++G I G+ + +S L+ L +

Sbjct: 188 DTQLKRYREVFTSTVYETEHPVVRVHPETGERTLVLGHFVQKIKGLSSQSAHLLQVLHE 247

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ W GDV +WDNR H A

Sbjct: 248 HVTRLENTVRWNWQEGDVAIWDNRATQHYA 277

>gb|ABD16709.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. ApCV2]
Length = 153

Score = 119 bits (299), Expect = 4e-25, Method: Compositional matrix adjust.
Identities = 65/157 (41%), Positives = 89/157 (56%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A + HSL+Y

Sbjct: 2 WHSDSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAYDALDDETKAEIDDMICEHSLMY 61

Query: 168 SQSKLGHVQQAQSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+

Sbjct: 62 SRGSLGFLD-----YTDEEKEMFKPVLQRLVRTHPVHGRKSLYLSSHAGAIRGMSMPPEAR 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
L L + A Q V+ H+W D+V+WDN +HR

Sbjct: 117 LLLRDLTEHATQPEFVYVHKWTVHDLVMWDNCQTVHR 153

>gb|ABD16702.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. th.b2]
Length = 153

Score = 119 bits (299), Expect = 4e-25, Method: Compositional matrix adjust.
Identities = 65/157 (41%), Positives = 88/157 (56%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A + HSL+Y

Sbjct: 2 WHSDSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAYDALDDETKAEIADMICEHSLMY 61

Query: 168 SQSKLGHVQQAQSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
S+ LG + Y L+ LV+ HP GR SL + HA AI GM E+

Sbjct: 62 SRGSLGFLD-----YTDEEKQMFVKPVLQRLVRTHPVHGRKSLYLSSHAGAIRGMSMPPEAR 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
L L + A V+ H+W D+V+WDNR +HR

Sbjct: 117 LLLRDLTEHATSPEFVYVHKWTVHDLVMWDNRQTVHR 153

>ref|ZP_02909532.1| Taurine dioxygenase [Burkholderia ambifaria MEX-5]
gb|EDT39344.1| Taurine dioxygenase [Burkholderia ambifaria MEX-5]
Length = 308

Score = 119 bits (299), Expect = 4e-25, Method: Compositional matrix adjust.
Identities = 84/288 (29%), Positives = 134/288 (46%), Gaps = 21/288 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64

```

      I P A LGA V G+ L+ L A FA +H A L H +L+F Q ++ D+ + F++RF
Sbjct: 28 FDIVPFDAPLGAEVVGIDLSQPLGAADFARVHRAHLDDHHVLVFRDQRITPDEHVAFSRRF 87

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
      G ++          +++ +SN+ +G      P      D      WH+D +Y
Sbjct: 88 GPLQIHVLHQFALAAHPEVLIVSNIVENG-----RPIGLGD-----AGHFWHSDLSYKE 136

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
      + G++ A+ +PA GG T FA+M A+D L      R V R A H+ + ++L
Sbjct: 137 KPSLGSLHLHAQELPAEGGDTLAFANMHLAWDTLPAHLRRAVEGRRAEHTYLARYAELQARS 196

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
      +          + P+V+ HPETGR +L + H      I +      ES L+ L
Sbjct: 197 PWRPNLSAEQIAQVDAVVHPVVRTHPETGRKALFVSEHFTTRIVDLPEDESRRALLDELFA 256

Query: 236 WACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
      + +A ++ H W A D+V WDNR L+H A      L R ++ + + G
Sbjct: 257 HSVRAEHLRYHHWRAHDLVFWDNRSLMHLAAGTPDHLRRKLYRTTIEG 304

```

>ref|YP_002799399.1| taurine dioxygenase protein [Azotobacter vinelandii DJ]
gb|AC078424.1| taurine dioxygenase protein [Azotobacter vinelandii DJ]
Length = 304

Score = 119 bits (298), Expect = 5e-25, Method: Compositional matrix adjust.
Identities = 78/265 (29%), Positives = 120/265 (45%), Gaps = 24/265 (9%)

```

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      +L I P +GA V+GV L LD+A FA L A L++ L QHL++ +Q F++RF
Sbjct: 2 SLDIRPVTGRIGAIVSGVRLTDLDEAQFAELQQAVLKYKALFLRDQHLTDAEQEAFSRRF 61

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGN-----MAWHADSTYMPVMA 119
      G      D V +P E + + V + +WH D +++
Sbjct: 62 G-----DLVVHPTTPTTEQNTAGILEVDSERSRANSWHTDISFVVDYP 103

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ-A 178
      + + EV+P GG T FA+ AY L E + L RH+ Y + ++ A
Sbjct: 104 KITILRGEVIPEAGGDTVFAANTVTAYQELPEPLQRLADSLWVRHTNDYDYAAPKQIEVVA 163

Query: 179 GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAAHAIPGMDAAESERFLEGLVDWAC 238
      + T PLV+VHPETG +LL+G A I G+++ +S L+
Sbjct: 164 NKRFFREQFTSTIYESEHPLVRVHPETGEKALLLGHFAERIVGLNSRDSRALLDLFQSHIV 223

Query: 239 QAPRVHAHQWAAGDVVWDNRCLLH 263
      + + +W+ GDV +WDNR H
Sbjct: 224 KLENIVRWRWSEGDVALWDNRATQH 248

```

>ref|YP_001898279.1| Taurine dioxygenase [Ralstonia pickettii 12J]
gb|ACD25847.1| Taurine dioxygenase [Ralstonia pickettii 12J]
Length = 300

Score = 119 bits (297), Expect = 6e-25, Method: Compositional matrix adjust.
Identities = 86/283 (30%), Positives = 130/283 (45%), Gaps = 24/283 (8%)

```

Query: 13 ATLGATVTGV-HLATLDDAGFAALHAAWLQH-ALLIFPGQHLSNDQQITFAKRFGA---- 66
      A LGA + G+ A L DA A + AWL H LL+F + Q+ F++RFG
Sbjct: 26 APLGAIEILGLGDGADLSADATIIRQAWLAHDGLLVFRDVEFTPQAQVAFSRRFGPQQVH 85

Query: 67 ----IERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
      G +I+ +SNV +G      P      D +      WH+D +Y P+ + G+
Sbjct: 86 VLNQFHLSGHSEILVVSNNVENG-----KPIGLGDAGR-----DWHSLSYKPLPSLGS 134

```


Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ +P GG T FA+M AY+ L + ++ R A HS VY +L +
Sbjct: 135 MLLTRELPEEGDTLAFANMVRAYETLPANLKRIIEGRRVHSYVYRYERLRALSTWRPPL 194

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVDWACQA 240
D P+V+ HPETG+ +L + G +H I G+ ES LE L + +A
Sbjct: 195 TQAQRDAVPPVDHPVVRTHPETGKRALFVNEGFTSHII--GLPEDESTSVLEQLFAHSIRA 253

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
V+ H+W GD++ WDNR +H A K R + + + G
Sbjct: 254 DNVYTHRWCPCGDMFLWDNRSTIHFAPGCPDKYRRTLHRTTIEG 296

>ref|ZP_02241915.1| taurine dioxygenase [Xanthomonas oryzae pv. oryzicola BLS256]
Length = 305

Score = 118 bits (296), Expect = 8e-25, Method: Compositional matrix adjust.
Identities = 82/275 (29%), Positives = 130/275 (47%), Gaps = 21/275 (7%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
+ ++ ++I P LGA V G+ L+ L FA LH A L H +L+F Q +S QQ+
Sbjct: 20 VQRSGVRIAPFDGPLGAEVIGLDLSQPLHADAFARLHRAHLDDHVLVFRDQRISPAQQVE 79

Query: 60 FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHAD 111
F++RFGA++ G +++ +SN+K +G P D WH+D
Sbjct: 80 FSRRFGALQIHVLRNFQLRGHPEVLVVSNIKENG-----EPIGLGD-----AGHDWHSD 128

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
+Y + G++ A+ +P+ GG T FA+ A+ L E+ + V A HS +
Sbjct: 129 LSYKETPSLGSLLHAQQLPSEGGDTLAFANQHLAWQTLPESLKRTVQDLRAEHSYLARYEA 188

Query: 172 LGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL 230
L A + P+V+ HPETGR +L + H I G+ ES L
Sbjct: 189 LRARNPWCALPTEQIAEVTPEVHPVRRHPETGRKALFVSEHFTTRILGLPEDESRALL 248

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ L + + V+ H+W D+V WDNR ++H A
Sbjct: 249 QTLFAHSTRPALVYRHRWQPYDMVFWDNRSVMHLA 283

>gb|ABG66523.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium canariense]
Length = 153

Score = 118 bits (296), Expect = 8e-25, Method: Compositional matrix adjust.
Identities = 64/157 (40%), Positives = 87/157 (55%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A + HSL+Y
Sbjct: 2 WHSDSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAYDALDDETKAEIEDLVCEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
S+ LG + Y L+ LV+ HP R SL + HA I GM E
Sbjct: 62 SRGSLGFTE-----YTDDEKQMFKPVQLRVRTHPVHRRKSLYLSSHAGKIVGMSVPEGR 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
L L + A Q+ V+ H+W D+V+WDNR +HR
Sbjct: 117 LLLRDLNEHATQSEFVYVHKWKLHDLVMWDNRQTMHR 153

>gb|AD085592.1| PenD [Streptomyces exfoliatus]
Length = 298

Score = 118 bits (296), Expect = 8e-25, Method: Compositional matrix adjust.
Identities = 88/289 (30%), Positives = 136/289 (47%), Gaps = 29/289 (10%)

```
Query: 6   LQITPT-GATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHL-SNDQQITFAK 62
          + +TP  GA LGA V G H+   +D   F   + AA   H +L+F G   S ++ + F +
Sbjct: 1   MDVTPIPGAALGAVVHGAHVTGDMDKTQFEEIWAALDAHLVLVFRGHRTPSYEEFLAFGR 60

Query: 63  RFGAIERIG-----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY 114
          RFG I + G               +I+ +SN+  DG           AEW           M WH D ++
Sbjct: 61  RFGYIPKTGLTSGAHPDHNEILIVSNLVEDGRKIGVGDAEW-----MGWHTDYSF 110

Query: 115 MPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKL 172
          P ++Q       A VP+ GG T F DM A Y++L   R   +H   RH++   Y ++
Sbjct: 111 RPRVSQVGFLAEVEVPSCGGETLFTDMYALYESLSPEERKRMHSYRVRHAMRTGYEETIE 170

Query: 173 GHVQQ----AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESE 227
          +Q+       GS           D T+T + PL+   +P TGR S+ I   +   I   +   +S
Sbjct: 171 EKLQREVS LGSGEQILPEDGTST-IHPLIARNPRTGRQSVYISTLNTERIVDLAPDDSR 229

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
          + L+ L+  A +       +AH W   GD+V+WD   +H   + +D   RVM
Sbjct: 230 KLLDELLSHAGKPEHTYAHTWQPGDIVMWDQLGTVHAKQAFDPAELRVM 278
```

>ref|YP_724558.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Ralstonia
eutropha H16]
emb|CAJ91190.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Ralstonia
eutropha H16]
Length = 283

Score = 118 bits (296), Expect = 8e-25, Method: Compositional matrix adjust.
Identities = 89/267 (33%), Positives = 124/267 (46%), Gaps = 17/267 (6%)

```
Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          +Q+ P   A   GA V G+ L   L DA  A +   WL+H +L F  Q L+ +   FA
Sbjct: 3   MQVLPQDAPCGALVLGLDLKQALTDQAQVAEIRRHVLEHKVLAFTDQDLAIEDIERFASTI 62

Query: 65  GAIERIGGGD--IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
          G +       G D   AI           VR+       D   +   +   +WH+D +++
Sbjct: 63  GPL----GSDPYFTAIPGHPHVAQVRR-----DANERTPIFAESWHSWSDWSFLAQPPAAT 112

Query: 123 VFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YS-QSKLGHVQQAG 179
          V       V+P VGG T FAD  AA+DAL   ++LV R   HS   YS Q   G   +
Sbjct: 113 VLYGNVIPPVGGDTLFDADQYAAWDALPAELKSLVDGRQGVHSARRGYSRQAYGEKDKGR 172

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWAC 238
          S   I Y       AT L P+ + HPETGR +L +   +   I GM   E+   L L +
Sbjct: 173 SMAIRYSDSAMATQLHPIARKHPETGR TALFVSVGYTIGIDGMSDEEAAPILRALFEHQA 232

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          +   V+ H+W+ G +VVWDNRC+ H A
Sbjct: 233 RPEFVYRHRWSQGMLVVWDNRCVNHAA 259
```

>emb|CBJ20078.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 87

Score = 118 bits (295), Expect = 1e-24, Method: Compositional matrix adjust.
Identities = 55/87 (63%), Positives = 68/87 (78%), Gaps = 1/87 (1%)

```
Query: 170 SKLGH-VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER 228
          SKLGH ++A   Y GYG+       PLRPLVK+HPETGR SLLIGRHAHAIPGM A+S+R
```

Sbjct: 1 SKLGHQTKKADGEYSGLHDGPVPLRPLVKIHPETGRKSLIGRHAHAIPGMALADSDR 60

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVV 255

FL+ L+D+ACQ PR++ H W+AGD V+

Sbjct: 61 FLQELIDFACQRPRIYHHDWSAGDAVL 87

>ref|YP_837647.1| taurine dioxygenase [Burkholderia cenocepacia HI2424]

gb|ABK10754.1| Taurine dioxygenase [Burkholderia cenocepacia HI2424]

Length = 317

Score = 118 bits (295), Expect = 1e-24, Method: Compositional matrix adjust.

Identities = 91/270 (33%), Positives = 129/270 (47%), Gaps = 20/270 (7%)

Query: 2 AQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQIT 59

A LQ+ +GA ++GV L ATLDDA F A+HAA L+H +L F GQH L + Q

Sbjct: 22 AAVPLQLRQVAGRIGAEISGVRLSATLDDATFDAVHAALLRHKVLFFRGQHHLDDTAQEA 81

Query: 60 FAKRFGAIERIGGGDIVAISNVKA-DGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118

FA+RFG D VA V + DG+ + E D +WH D T++

Sbjct: 82 FARRFG-----DTVAHPTVPSVDGSA---ALLELSAHGARAN--SWHTDVTFVDAY 128

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178

+ ++ A V+P GG T +A+ AY L + RAL A H+ Y + HV

Sbjct: 129 PKISILRAVVIPIPPGGDTVWANTATAYANLPDPLRALADTLWALHTNAYDYAST-HVHAD 187

Query: 179 GSAYIGYGMDDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD 235

+ Y T+T P+V+VHPETG +L++G I G+ + +S L+ L +

Sbjct: 188 DTQLKRYREVF+TSTVYETEHPVVRVHPETGERTLVLGHFVQKIKGLSSQDSAHLLQVLHE 247

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ W GDV +WDNR H A

Sbjct: 248 HVTRLENTVRWNWQEGDVAIWDNRATQHHA 277

>ref|ZP_01616423.1| alpha-ketoglutarate-dependent taurine dioxygenase [marine gamma
proteobacterium HTCC2143]

gb|EAW31932.1| alpha-ketoglutarate-dependent taurine dioxygenase [marine gamma
proteobacterium HTCC2143]

Length = 280

Score = 118 bits (295), Expect = 1e-24, Method: Compositional matrix adjust.

Identities = 83/272 (30%), Positives = 127/272 (46%), Gaps = 26/272 (9%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64

L++T +G GAT+TGV L+ LD AA+ AAWL+H ++ FP Q +S++ F F

Sbjct: 3 LKVTASGEACGATITGVDLSDQLDDETIAAIRAAWLEHHVVAFPDQSMSDEDLERFTLCF 62

Query: 65 GAIERIGGGDIVAISNVKADGTV-----RQHSPAEDDMMKVIVGNMAWHADSTYMPVMA 119

G GD +++ + R H A + G WH D ++M V

Sbjct: 63 GEF-----GDDPYFESIEGHTNIAAIERRAHETA-----PLFAG--GWHTDWSFMAVPP 109

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG----HV 175

+P +GG T FA+ AYD + ++ R+ V +A HS Y+ + G

Sbjct: 110 IATCLYGITIPPIGGDTLFANQHKAYDQMPDSLRSRVEGLTAIHSAYAYAPRGVFDTEK 169

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL--IGRHAHAIPGMDAAESERFLEGL 233

+ S I D A P ++ H ETGRP L +G + ++ A+S+ L+ L

Sbjct: 170 EADRSKIVLSEDAKQEHFPIRNHSETGRPLFSTLG-YIQGFVELEKADSDALLQEL 228

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

D+ P V H+W +V+WDNR +LH A

Sbjct: 229 YDYGSEPFVFRHKWQPNMLVMWDNRSVLHMA 260

>ref|YP_624207.1| taurine dioxygenase [Burkholderia cenocepacia AU 1054]
gb|ABF79234.1| Taurine dioxygenase [Burkholderia cenocepacia AU 1054]
Length = 317

Score = 118 bits (295), Expect = 1e-24, Method: Compositional matrix adjust.
Identities = 90/266 (33%), Positives = 128/266 (48%), Gaps = 20/266 (7%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
LQ+ +GA ++GV L ATLDDA F A+HAA L+H +L F GQH L + Q FA+R
Sbjct: 26 LQLRQVAGRIGAEISGVRLSATLDDATFDAVHAALLRHKVLFFRGQHHLDDTAQEAFAARR 85

Query: 64 FGAIERIGGGDIVAISNVKA-DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG D VA V + DG+ + E D +WH D T++ + +
Sbjct: 86 FG-----DTVAHPTVPSVDGSA---ALLELDSA HGARAN--SWHTDVT FVDAYPKIS 132

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ A V+P GG T +A+ AY L + RAL A H+ Y + HV +
Sbjct: 133 ILRAVVIPPFGGDTVWANTATAYANLPDPLRALADTLWALHTNAYDYAST-HVHADDTQL 191

Query: 183 IGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
Y T+T P+V+VHPETG +L++G I G+ + +S L+ L + +
Sbjct: 192 KRYREVFTSTVYETEHFVVRVHPETGERTLVLGHFVQKIKGLSSQDSAHLQLVLEHVTR 251

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
W GDV +WDNR H A
Sbjct: 252 LENTVRWNWQEGDVAIWDNRATQHYA 277

>ref|YP_001777149.1| taurine dioxygenase [Burkholderia cenocepacia MC0-3]
gb|ACA92659.1| Taurine dioxygenase [Burkholderia cenocepacia MC0-3]
Length = 317

Score = 117 bits (294), Expect = 1e-24, Method: Compositional matrix adjust.
Identities = 91/270 (33%), Positives = 129/270 (47%), Gaps = 20/270 (7%)

Query: 2 AQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQIT 59
A LQ+ +GA ++GV L ATLDDA F A+HAA L+H +L F GQH L + Q
Sbjct: 22 AAVPLQLRQVAGRIGAEISGVRLSATLDDATFDAVHAALLRHKVLFFRGQHHLDDTAQEA 81

Query: 60 FAKRFGAIERIGGGDIVAISNVKA-DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM 118
FA+RFG D VA V + DG+ + E D +WH D T++
Sbjct: 82 FARRFG-----DTVAHPTVPSVDGSA---ALLELDSA HGARAN--SWHTDVT FVDAY 128

Query: 119 AQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
+ ++ A V+P GG T +A+ AAY L + RAL A H+ Y + HV
Sbjct: 129 PKISILRAVVIPPFGGDTVWANTAAAYANLPDPLRALADTLWALHTNAYDYAST-HVHAD 187

Query: 179 GSAYIGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD 235
+ Y T+T P+V+VHPETG +L++G + G+ A +S L+ L + +
Sbjct: 188 DTQLKRYREVFTSTVYETEHFVVRVHPETGERTLVLGHFVQRLKGLSAQDSAHLQLVFHE 247

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ W GDV +WDNR H A
Sbjct: 248 HVTRLENTVRWNWQEGDVAIWDNRATQHYA 277

>ref|ZP_01224852.1| alpha-ketoglutarate-dependent taurine dioxygenase [marine gamma
proteobacterium HTCC2207]
gb|EAS46514.1| alpha-ketoglutarate-dependent taurine dioxygenase [marine gamma
proteobacterium HTCC2207]
Length = 276

Score = 117 bits (294), Expect = 1e-24, Method: Compositional matrix adjust.
Identities = 78/262 (29%), Positives = 119/262 (45%), Gaps = 10/262 (3%)

```
Query: 6  LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
      +++TP      GA V+ + LAT++DA      L A+ +H LL F Q L ++ + FA RFG
Sbjct: 1  MKVTPFSPNCGAVVSDLQLATMNDALQLEQLRDAFTEHGLLFFRDQQLPPEEHLRFANRFG 60

Query: 66  AIERIGGGDIVAISNVKADGTVRQHSPAEDWMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
      I      S + A+ VR+      + + +G WH D +Y + A G++
Sbjct: 61  KIVVNKFFKTTEESPLIAE--VRK-----EKTQQTNIGG-GWHTDHSYDDIPALGSILV 111

Query: 126  AEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 185
      A ++P GG T FA++ AAYDAL      + + A HS + + G +
Sbjct: 112  ARILPETGGNTQFANLAAAYDALPNTLTKRLEGLRAVHSNTHLYGENGLYRFTDLKDQLG 171

Query: 186  GMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVH 244
      GMD      P+V HP++GR L + H      G + +S L+ L Q
Sbjct: 172  GMDRVGDATHPVVITHPQSGRKVLVYNPGHTIQFEGWEFDKSRELLDELYAHVAQPQFTC 231

Query: 245  AHQWAAGDVVVWDNRCLLHRAE 266
      + W G V WDNRC H+A+
Sbjct: 232  SFNWQPGSVTFWDNRCTWHQAD 253
```

>gb|ADO34974.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 97

Score = 117 bits (293), Expect = 2e-24, Method: Compositional matrix adjust.
Identities = 61/97 (62%), Positives = 69/97 (71%), Gaps = 2/97 (2%)

```
Query: 110  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
      ADSTYMPV A+GAVFSAE VP +GG T FADMRAAYDALDE+ RA + A HSL YSQ
Sbjct: 1  ADSTYMPVQAKGAVFSAEEVPTIGGHTGFADMRAAYDALDESMRAKLEGLCAFHSLYYSQ 60

Query: 170  SKLGH--VQQAGSAYIGYGMDTTATPLRPLVKVHPET 204
      SKLGH +++ Y GYG      P R L+KVHPET
Sbjct: 61  SKLGHQPKKSDGEYSYGFHDPVPRRALIKVHPET 97
```

>gb|ABD16694.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. Lpsp.1b]
Length = 153

Score = 117 bits (293), Expect = 2e-24, Method: Compositional matrix adjust.
Identities = 67/160 (41%), Positives = 88/160 (55%), Gaps = 11/160 (6%)

```
Query: 108  WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
      WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A V HSL+Y
Sbjct: 2  WHSDSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAYDALDDETKAEVEDLVCEHSLMY 61

Query: 168  SQSKLGHVQQAGSAYIGYGMDTTAT---PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAA 224
      S+ LG      + Y D A L+ LV+ HP R SL + HA I M
Sbjct: 62  SRGSLG-----FTEYTDDEKAMFKPVLQRLVRTHPVHRRKSLYLSSHAGKIVSMSVP 113

Query: 225  ESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
      E L L + A QA V+ H+W D+V+WDNR +HR
Sbjct: 114  EGRLLLRDLNEHATQAEFVYVHKWKLHDLVMWDNRQTMHR 153
```

>ref|YP_004190416.1| putative dioxygenase [Vibrio vulnificus MO6-24/O]
gb|ADV88213.1| probable dioxygenase [Vibrio vulnificus MO6-24/O]

Length = 288

Score = 117 bits (293), Expect = 2e-24, Method: Compositional matrix adjust.
Identities = 79/275 (28%), Positives = 126/275 (45%), Gaps = 27/275 (9%)

```
Query: 1  MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
      + + T++ITP  + GA V  V L+ +++  F AL+ A+L H +L F  Q L+ +Q +
Sbjct: 4  IERETMKITPLATSFGALVEDVQLSAINERQFEALYHAFHHKVLFFRDQLLTAEQHLAL 63

Query: 61 AKRFGAIERI-----GGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS 112
      +RFG +E I          +V I          R+ P          G  WH D
Sbjct: 64 GQRFGELEPIHPFFPHLADAPQVVVIE-----TREGLPP-----GESYWHTDL 106

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-VYSQSK 171
      T+  ++ A+  A+  P  GG T + DM A + +LD++ + +  A H+L + S+
Sbjct: 107 TWKARPSKCALLHAQHCPPSGGDTIWTDM EAVWRS LDDSLKQQLRPLYATHALHAFENS R 166

Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL 230
      H  + G +Y+          P+V  HPETG+ +L I          I G++ A+S+  L
Sbjct: 167 YDHKDEDES YVVKKSREFFAVHHPVVAQHPETGQETLYINEQFTRCIDGLEKAQSQALL 226

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      E L  A +A          QW A + +WDNR  H A
Sbjct: 227 EMLFAMAREAKFQVR FQWQANSLAIWDNRATQHFA 261
```

>gb|ABD16695.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium sp. DesT10]
Length = 153

Score = 117 bits (293), Expect = 2e-24, Method: Compositional matrix adjust.
Identities = 63/157 (40%), Positives = 86/157 (54%), Gaps = 5/157 (3%)

```
Query: 108 WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
      WH+DS++ P+ A+ ++ SA VV  GG T FADMRAAYDALD+ T+A +  HSL+Y
Sbjct: 2  WHSDSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAYDALDDETKAEIEDLVCEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
      S+  LG          Y  +  L+ LV+ HP+  R SL + HA  I M  E
Sbjct: 62 SRGSLGFTD-----YTDDEKEMFKPVLQRLVRTHPQHRRKSLYLSSHAGKIASMSVPEGR 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
      L  L + A Q  V+ H+W  D+V+WDNR  +HR
Sbjct: 117 LLLRDLNEHATQPEFVYVHKWRLHDLVMWDNRQTMHR 153
```

>ref|ZP_02382540.1| Taurine dioxxygenase [Burkholderia ubonensis Bu]
Length = 300

Score = 117 bits (292), Expect = 2e-24, Method: Compositional matrix adjust.
Identities = 81/288 (28%), Positives = 134/288 (46%), Gaps = 21/288 (7%)

```
Query: 6  LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      +I          LGA V G+ L+  LDDAGF  +H A L H +L+F  Q ++ ++ + F++RF
Sbjct: 20 FEIRAFDGLGAEVIGLDLSKPLDDAGFTRIHRALDHHVLVFRDQRITPERHVAFSRRF 79

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
      G ++          G  +++ +SN+  +G          P  D          WH+D +Y
Sbjct: 80 GPLQIHVLHQFGLAGHPEVLVVSNIENG-----RPIGLGD-----AGHYWHS DLSYKD 128

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
      + G++  A+ +P+ GG T FA+M  A+D L  R          A H+ +  ++L
Sbjct: 129 KPSLGSLLHAQELPSEGGDTLFANMHLAWDTLPAHLRRAADGLRAEHTYLARYAELQARN 188
```

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
+ + P+V+ HPETGR +L + H I G+ ES L+ L
Sbjct: 189 PWRPNLSAEQVAQVKPVVHPVVRTHPETGRKALFVSEHFTTRIVGLPEDESRRALLDELFA 248

Query: 236 WACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +A ++ H W D+V WDNR L+H A L R ++ + + G
Sbjct: 249 HSVRAEHLRYHVWRDHLVFDNRSLMHLAAGTPDHLRRKLYRTTIEG 296

>ref|ZP_06410725.1| Taurine dioxygenase [Frankia sp. EUN1f]
gb|EFC86523.1| Taurine dioxygenase [Frankia sp. EUN1f]
Length = 285

Score = 116 bits (291), Expect = 3e-24, Method: Compositional matrix adjust.
Identities = 89/272 (32%), Positives = 123/272 (45%), Gaps = 29/272 (10%)

Query: 4 TTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T L++ P T+GA V GV + LD A A + A L H + GQHL +QQ FA+
Sbjct: 9 TLLRVEPIHPTIGAVVHGVDASRPLDPATVAFVRQALLDHKAIFLRGQHLDLEQQGRFAE 68

Query: 63 RFG-----AIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPV 117
FG I+ + GG + EW + WH+D ++P
Sbjct: 69 HFGDLTPHPIQELAGG-----YPDFEWMQQSIRTRAEGWHSMDAFLPE 112

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL--GHV 175
+ + V+P VGG T F D+ AAY+ L E R LV + H Q +V
Sbjct: 113 PPFATLLTLPVIPPVGGDTLFLDLEAAYNDLSEPVRTLVDLTVIHYADNFQDWAAGPNV 172

Query: 176 QQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGL 233
+A I + A P+ PLV+VHPETGR L + A I G+ ES+ L L
Sbjct: 173 DEARRNQI---LSWAARPVEHPLVRVHPETGRRMLFAVTGFARRIKGLSEESKGLILALL 229

Query: 234 VDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
+A V +W+ GD+ WDNR +LHRA
Sbjct: 230 AAHVSRAEYVARFKWSPGDIAFDNRNRTLHRA 261

>gb|ACX54968.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 96

Score = 116 bits (291), Expect = 3e-24, Method: Compositional matrix adjust.
Identities = 59/96 (61%), Positives = 70/96 (72%), Gaps = 1/96 (1%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYMPV A+GAVFSAE VP+ GGRT FADMRAAYDALD +A + +A HSL YSQ
Sbjct: 1 ADSTYMPVQAKGAVFSAEEVPSGGGRTGFADMRAAYDALDPDMKARIEGLNAYHSLHYSQ 60

Query: 170 SKLGH-VQQAGSAYIGYGMDTTATPLRPLVKVHPET 204
++GH ++ Y GYG+ PLRPLVK+HPET
Sbjct: 61 GRVGHQTKKLDGEYSGYGLHDGPVPLRPLVKIHPET 96

>ref|ZP_06840718.1| Taurine catabolism dioxygenase TauD/TfdA [Burkholderia sp. Ch1-1]
gb|EFG71438.1| Taurine catabolism dioxygenase TauD/TfdA [Burkholderia sp. Ch1-1]
Length = 299

Score = 116 bits (290), Expect = 4e-24, Method: Compositional matrix adjust.
Identities = 79/276 (28%), Positives = 127/276 (46%), Gaps = 29/276 (10%)

Query: 5 TLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T + + A +TG+ L L A AL A Q+ +L+FP Q + ++Q + F++

Sbjct: 2 TFAVEAIQKPIAARITGLDLRQPLSAADAQALDKAIAQYPVLVFPAQDIDDNQLLAFSEN 61

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS 112
FG + E I ISN+ D + A + M V WH+D

Sbjct: 62 FGPVQVSVQYATRQNEHRLQPRISDISNLGKDNETFK---AGDNRRMNTFVSR-RWHS DQ 117

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+Y P+ A+ + VP GG + FADMR YD+L + R + SA +++++

Sbjct: 118 SYQPIPARYSFLLNYSVPTRGGESQFADMRLVYDSL PQDLRETIENLSAEFDILHTRAMC 177

Query: 173 GHVQQAGSAYIGYGMTTATPLRP----LVKVHPETGRPSLLIGRHAHAIPGMDAAESER 228
G + + + A L+P LVK HP +GR +L + HA + E

Sbjct: 178 G-----FTDFPEERAM-LKPSIHRLVKTHPLSGRKTLYLSVHATHVVDWPIPEGRD 228

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVW DNRCLLHR 264
L L+++A Q ++ H W D+V+WDNR L+HR

Sbjct: 229 LLRELMEFATQPQFIYTHHWTVKDLVMWDNR TLIHR 264

>ref|YP_003778031.1| alpha-ketoglutarate-dependent taurine dioxygenase oxidoreductase
[Herbaspirillum seropedicae SmR1]
gb|ADJ66123.1| alpha-ketoglutarate-dependent taurine dioxygenase oxidoreductase
protein [Herbaspirillum seropedicae SmR1]
Length = 324

Score = 116 bits (290), Expect = 4e-24, Method: Compositional matrix adjust.
Identities = 80/289 (27%), Positives = 138/289 (47%), Gaps = 23/289 (7%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+I A LGA + G+ L + + A + A ++H +++F Q ++ Q + F++RF

Sbjct: 44 FEIHRFDAPLGAIEIVGLDLNKPVSASELARIRKALVEHGVVFRDQRITPQQHVDFSRRF 103

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
G ++ G +I+ +SNV +G + ++ WH+D +YMP

Sbjct: 104 GPLQVHVLNRFHLAGHPEILIVSNVVEN GK-----PIGLVDAGADWHS DLSYMP 152

Query: 117 VMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ GA+ ++ +PA G T +A+ AA+D+L A + L+ + A HS VY +L +

Sbjct: 153 KPSLGALLHSQELPAERGD TLYANTAAWDSLPAALKTLLEGKRAVHSYVRYERLRKLS 212

Query: 177 QAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLV 234
+ +D P+V HPE+GR L + G +H I G+ ES+ L+ L

Sbjct: 213 PWRAPLTQQQIDEVPPVEHPV VITHPESGRKILFVSEGFTSHII-GIPRDESDALLKELH 271

Query: 235 DWACQAPRVHAHQWAAGDVVVW DNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ V+ H+W A D+V W DNR H A L R ++ + + G

Sbjct: 272 THITRPENVYTHRWQA HDLVFWDNRSTQHYAAITPQHLRRTLYRTTVEG 320

>ref|YP_004236557.1| taurine dioxygenase [Acidovorax avenae subsp. avenae ATCC 19860]
gb|ADX47990.1| Taurine dioxygenase [Acidovorax avenae subsp. avenae ATCC 19860]
Length = 306

Score = 116 bits (290), Expect = 5e-24, Method: Compositional matrix adjust.
Identities = 90/274 (32%), Positives = 131/274 (47%), Gaps = 27/274 (9%)

Query: 6 LQITP-TGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+I P GA LGA V G+ L+ L DA FA LH A L H +++F Q ++ Q I F++R

Sbjct: 24 FEIRPLPGAPLGAIEVLGLDL SRPLGDADFARLHQAHLDDHHVVFRDQRITPRQHIDFSRR 83

Query: 64 FGAIE-----RIGGGDIVAISNVK-ADGTVRQHSPA EWDDMMKVIVGNMA--WHADS 112
FG ++ +I+ +SN+K A G + +G+ WH+D

Sbjct: 84 FGPLQIHVLKNFQLADHPEILVVSNIK DASG-----QPIGLGDAGHYWHS DL 130

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+Y + G++ A+ +P GG T FAD AAYDAL A R ++ A HS + +L
Sbjct: 131 SYKERPSLGSLLHAQELPGEGGDTLFDQHAAYDALPAALRRVIGPLRAEHSYLARYEEL 190

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE 231
A + A + P+V+ HPETGR +L + H I G+ ES L
Sbjct: 191 RARSPWRPALTPAQIAEVAPVHPVVRTHPETGRRALFVNEHFTTRIVGLPEDESALLA 250

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L A + V+ H W D+V WDNR + H A
Sbjct: 251 ELFAAAVKPEFVYRHVWQPHDLVFWDNRSVQHLA 284

>gb|ABD16690.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. ApB16]
gb|ABD16691.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. ApT12]
Length = 153

Score = 115 bits (289), Expect = 5e-24, Method: Compositional matrix adjust.
Identities = 63/157 (40%), Positives = 85/157 (54%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A + HSL+Y
Sbjct: 2 WHSDSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAYDALDDETKAEIEDLVCEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
S+ LG + Y L+ LV+ HP R SL + HA I M E
Sbjct: 62 SRGSLGFTE-----YTDDEKQMFKPVLRVLRTHPVHRRKSLYLSSHAGKIVSMSVPEGR 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
L L + A Q V+ H+W D+V+WDNR +HR
Sbjct: 117 LLLRDLNEHATQGEFVYVHKWKLHDLVMWDNRQTMHR 153

>ref|NP_518867.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
oxidoreductase protein [Ralstonia solanacearum GMI1000]
emb|CAD14276.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
oxidoreductase protein [Ralstonia solanacearum GMI1000]
Length = 301

Score = 115 bits (289), Expect = 5e-24, Method: Compositional matrix adjust.
Identities = 83/265 (31%), Positives = 123/265 (46%), Gaps = 22/265 (8%)

Query: 12 GATLGATVTGVH-LATLDDAGFAALHAAWLQH-ALLIFPGQHLSNDQQITFAKRFGAIE- 68
GA LGA + G++ A L DA AA+ AWL H LL+F L+ Q+ F++RFG ++
Sbjct: 26 GAPLGAEILGLNDAAGLSADVAIRQAWLAHDGLLVFRDVR LAPRAQVDFSRRFGPLQV 85

Query: 69 -----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
+I+ +SNV +G P D + WH+D +Y P + G
Sbjct: 86 HVLNQFHLPAHPEILVSVNVVENG-----KPIGLGDAGR-----DWHSDLSYRPRPSLG 134

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
++ A +P GG T FA+M AY+ L + + R A HS VY +L +
Sbjct: 135 SLLLARELPQAGGDTL FANMVRAYETLPAELKHSIEGRRVHSYVYRYERLRALSARPP 194

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQA 240
D P+V+ HPETGR +L + I G+ ES L L + +
Sbjct: 195 LTQAQRDAVPPVDHPVVRTHPETGRRALFVNEGFTSRILGLPEDESTTVLAQLFAHSIRP 254

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRA 265
++ H+W GD++ WDNR LH A

Sbjct: 255 DNIYTHRWQPGDMLFWDNRSTLHFA 279

>ref|YP_553178.1| putative alpha KG dependent 2,4-D dioxygenase [Burkholderia
xenovorans LB400]
gb|ABE33828.1| Putative alpha KG dependent 2,4-D dioxygenase [Burkholderia
xenovorans LB400]
Length = 299

Score = 115 bits (289), Expect = 6e-24, Method: Compositional matrix adjust.
Identities = 79/276 (28%), Positives = 127/276 (46%), Gaps = 29/276 (10%)

Query: 5 TLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T + + A +TG+ L L A A+ Q+ +L+FP Q + ++Q + F++
Sbjct: 2 TFAVEAIQEPIAARITGLDLRQPLSAADAQAIDNVIAQYPVLVFPAQDIDNQLLAFSEN 61

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
FG + E I ISNV D + A + M V WH+D
Sbjct: 62 FGPVQVSVQYATRQNEHRLQPRISDISNVGKDNFTK---AGDNRRMNTFVSR-RWHSQ 117

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+Y P+ A+ + VPA GG + FADMR YD+L + R + SA +++++
Sbjct: 118 SYQPIPARYSFLLNYSVPARGGESQFADMRVLVYDQLRETIENTLSAEFDILHTRAMC 177

Query: 173 GHVQQAGSAYIGYGMTTATPLRP---LVKVHPETGRPSLLIGRHAHAIPGMDAAESER 228
G + + + A L+P LVK HP +GR +L + HA + E
Sbjct: 178 G-----FTDFPEERAM-LKPSIHLRVKTHPLSGRKTLYLSVHATHVVDWPIPEGRD 228

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
L L+++A Q ++ H W D+V+WDNR L+HR
Sbjct: 229 LLRELMEFATQPQFIYTHHWTVKDLVMWDNRSLIHR 264

>ref|YP_553195.1| putative alpha KG dependent 2,4-D dioxygenase [Burkholderia
xenovorans LB400]
gb|ABE33845.1| Putative alpha KG dependent 2,4-D dioxygenase [Burkholderia
xenovorans LB400]
Length = 298

Score = 115 bits (288), Expect = 7e-24, Method: Compositional matrix adjust.
Identities = 82/273 (30%), Positives = 129/273 (47%), Gaps = 21/273 (7%)

Query: 5 TLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+L I P T+ A + G+ L L D + A + +LIFP Q + + Q + F++
Sbjct: 2 SLDIEPAHPTIAARIRGLDLRQPLSDEQVDEIGQASAIYPVLIFPNQLIDDAQLMAFSQN 61

Query: 64 FGAIERI-----GGGD-----IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
FG ++ + D + ISNV + PA D + + WH D
Sbjct: 62 FGPLQPVVSFHTAKADHRLSPMVSDISNLDKNNRT---FPAG-DRRRMNFLLSSRRWHTDG 117

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+Y+P + ++ A V VGG+T FADMRRAAYDAL LV + H++++S++
Sbjct: 118 SYLPTPNRYSMLLAYTVARVGGQTQFADMRRAAYDALPAEWLELVEDLTLEHNMHSRAVA 177

Query: 173 GHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG 232
G + + LV+ HP +GR SL + HA + G E L
Sbjct: 178 GFTDFDEEERRR-----PATHKKLVRRHPVSGRLSLYLSGHASHVVGWPVPEGLDLLRE 232

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L ++A Q V+ H+W+ D+V+WDNR L+HRA
Sbjct: 233 LTEFATQPQFVYTHEWSVRDLVMWDNRSLMHRA 265

>gb|ABD16692.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium sp. DcE2.8]
gb|ABD16696.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium sp. Dp6.5]
Length = 153

Score = 115 bits (288), Expect = 7e-24, Method: Compositional matrix adjust.
Identities = 63/157 (40%), Positives = 85/157 (54%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A + HSL+Y
Sbjct: 2 WHSDSSFRPIPAKFSLLSARVNVNPKGGNTEFADMRAAYDALDDDTKAEIEDLVCEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
S+ LG + Y L+ LV+ HP R SL + HA I M E
Sbjct: 62 SRGSLGFTE-----YTDDEKQMFKPVLRVLRTHPVHRRKSLYLSSHAGKIVSMSVPEGR 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
L L + A Q V+ H+W D+V+WDNR +HR
Sbjct: 117 LLLRDLNEHATQGEFVYVHKWKLHDLVMWDNRQTMHR 153

>emb|CBJ38903.1| Alpha-ketoglutarate-dependent 2, 4-dichlorophenoxyacetate
dioxxygenase (2,4-D dioxxygenase) [Ralstonia solanacearum
CMR15]
Length = 301

Score = 115 bits (288), Expect = 7e-24, Method: Compositional matrix adjust.
Identities = 82/265 (30%), Positives = 123/265 (46%), Gaps = 22/265 (8%)

Query: 12 GATLGATVTGVH-LATLDDAGFAALHAAWLQH-ALLIFPGQHLSDNDQQITFAKRFGAIE- 68
GA LGA + G++ A L DA AA+ AWL H LL+F L+ Q+ F++RFG ++
Sbjct: 26 GAPLGAIEILGLNDAAGLSDADVAAIRQAWLAHDGLLVFRDRLAPRAQVDFSRFGPLQV 85

Query: 69 -----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQG 121
+I+ +SNV +G P D + WH+D +Y P + G
Sbjct: 86 HVLNQFHLPAHPEILVSVNVVENG-----KPIGLGDAGR-----DWHSDDLSTYTPRPSLG 134

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
++ A +P GG T FA+M AY+ L + + R A HS VY +L +
Sbjct: 135 SLLLARELPQAGGDTLAFNMVRAYETLPAELKRSIEGRRAEHSYVYRYERLRALSTWRPP 194

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQA 240
D P+V+ HPETGR +L + I G+ ES L L + +
Sbjct: 195 LTQAQRDAVPPVDHPVVRTHPETGRRALFVNEGFTSRILGLPEDESVAVLAQLFAHSIRP 254

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRA 265
++ H+W GD++ WDNR +H A
Sbjct: 255 DNIYTHRWPQGDMLFWDNRSTVHF 279

>ref|NP_883162.1| putative taurine dioxxygenase [Bordetella parapertussis 12822]
emb|CAE40240.1| putative taurine dioxxygenase [Bordetella parapertussis]
Length = 260

Score = 115 bits (288), Expect = 7e-24, Method: Compositional matrix adjust.
Identities = 78/255 (30%), Positives = 115/255 (45%), Gaps = 31/255 (12%)

Query: 44 LLIFPGQHLSDNDQQITFAKRFGAIERIGG-----GDIVAIISNVKADGTVRQHSPA 94
+L+FPGQ L+ Q I F + FG +ER +++ ++N DG
Sbjct: 1 MLVFPQDLNAPQLIDFTRHFGDVERNDSPYRDPDYPEVLLVTNKPRDGKP----- 53

Query: 95 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA 154

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      ++      WH+D +Y      A+G+V      + P VGG T FA+M AY++L      +
Sbjct: 54 ----LQTRNTGRNWHSDLSYTDRPAKGSVLMCKEKPVPVGGDTMFANMYQAYESLSAPFKR 109

Query: 155 LVHQRSARH--SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL-RPLVKVHPETGRPSLLI 211
      V      A H SL+      + Q A      +      P+ P+V++HPETGR L +
Sbjct: 110 FVDGLHAVHDISLIKGFDRRDPEQTAA-----LKRRNPPIAHPVVRIPHETGRKCLFV 162

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEP-WDF 270
      GM ES L+ L A      V+ H+W+ D+V+WDNRC LH A P +D
Sbjct: 163 SDRVRTFVGMTEEESRPILDFLNRHATSPEFVYRHRWSVNDIVMWDNRCTLHIALPDFDQ 222

Query: 271 KLPRVMWHSRLAGRP 285
      PR M      + G P
Sbjct: 223 SKPRHMMRCSMLGEP 237

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>ref|ZP_03585567.1| taurine dioxygenase [Burkholderia multivorans CGD1]
gb|EEE00159.1| taurine dioxygenase [Burkholderia multivorans CGD1]
Length = 314

Score = 115 bits (288), Expect = 8e-24, Method: Compositional matrix adjust.
Identities = 90/266 (33%), Positives = 126/266 (47%), Gaps = 20/266 (7%)

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Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
      LQ+      +GA ++GV L ATLDDA F A+ AA L+H +L F GQH L + Q FA+R
Sbjct: 23 LQLRQVAGRIGAEISGVRLSATLDDATFDAIQAALLRHKVLFRGQHHLDDAAQEAFARR 82

Query: 64 FGAIERIGGGDIVAISNVKA-DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
      FG      D VA V + DG+      E D      + WH D T++      + +
Sbjct: 83 FG-----DTVAHPTVPSVDGSAHL---LELDSAHGARAN--WHTDVTFVDAYPKIS 129

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
      + A V+P VGG T +A+ AAY L +A R L A H+ Y + HV +
Sbjct: 130 ILRAVVIPPVGGDTVWANTAAAYAHLPDALRTLADTLWAVHTNAYDYAST-HVHADETQL 188

Query: 183 IGYGMDDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
      Y T+T      P+V+VHPETG +L++G I G+ +S L+ + +
Sbjct: 189 KRYREVFTSTVYETEHFVVRVHPETGERTLVLGHFVQRIKGLSTQDSAHLQLQVFHEHVTR 248

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
      W GDV +WDNR H A
Sbjct: 249 LENTVRWSWQEGDVAIWDNRATQHYA 274

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>gb|ADC34031.1| TfdA-like protein [uncultured bacterium]
Length = 210

Score = 115 bits (288), Expect = 8e-24, Method: Compositional matrix adjust.
Identities = 75/219 (34%), Positives = 107/219 (48%), Gaps = 22/219 (10%)

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Query: 56 QQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVI 102
      QQI FA+ FG I      R+ +I ISN+ D V + D +
Sbjct: 1 QQIAFARHFGPIHSSAQRARHKS IKHRLASDEIADISNLDGDNKVM DQTARRRLDGL--- 57

Query: 103 VGNMAWHADSTYMPVMAQGA VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSAR 162
      N WH D+++ V      ++ A VVP GG T FAD+RAAYDAL +A +A + A
Sbjct: 58 -ANRLWHTDASFRVPGALSMLYAHVVPEEGDTEFADLRAAYDALPDARKAEIDGLIAE 116

Query: 163 HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMD 222
      HS+ +S+ +L + +      P R +V+ HP + R +L I HA I GM
Sbjct: 117 HSIWHSRGQLDVTKYSP EELASL----PPVPQR-VVRTHPGSRRKTLTYIASHASHIVGMP 171

Query: 223 AAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

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+ L L++ A Q VHAH+W GD+V+WDNRC+
Sbjct: 172 VPDGRLLLLDLIEHATQPRFVHAHRWRRGDLVIWDNRCV 210

>gb|ABD16689.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium sp. Ppau3-41]
Length = 153

Score = 115 bits (287), Expect = 8e-24, Method: Compositional matrix adjust.
Identities = 65/160 (40%), Positives = 87/160 (54%), Gaps = 11/160 (6%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A + HSL+Y
Sbjct: 2 WHSDSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAYDALDDETKAEIEDLVCEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMTTAT---PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAA 224
S+ LG + Y D A L+ LV+ HP R SL + HA I M
Sbjct: 62 SRGSLG-----FTEYTDDEKAMFKPVLQRLVRTHPVHRRKSLYLSSHAGKIVSMSVP 113

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
E L L + A A V+ H+W D+V+WDNR +HR
Sbjct: 114 EGRLLLRDLNEHATNAEFVYVHKWKLHDLVMWDNRQTMHR 153

>ref|ZP_01893643.1| Taurine catabolism dioxxygenase TauD/TfdA [Marinobacter algicola
DG893]
gb|EDM48213.1| Taurine catabolism dioxxygenase TauD/TfdA [Marinobacter algicola
DG893]
Length = 290

Score = 115 bits (287), Expect = 9e-24, Method: Compositional matrix adjust.
Identities = 78/275 (28%), Positives = 128/275 (46%), Gaps = 26/275 (9%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
++I P GA +T V L ++ A+L H +L+ Q L+ +Q+ F +R+G
Sbjct: 1 MKINPFANDFGAEITDVLKDPSSSEITERIYQAFLDHQMLVIRDQDLNPLEQVAFTERY 60

Query: 66 AIE-----RIGGGD---IVAISN-VKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMP 116
+E + D ++ +SN ++ DGT + V+ WH+DS++
Sbjct: 61 TLEWQENVKYAHPDHDKVLILSNEIRPDGTA-----VGVDAGDFWHSDSSHHE 109

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH---SLVYSQSKLG 173
+ V + P+ GG T F DM A Y+AL EAT+ + R H + + K+
Sbjct: 110 EPVKVTVLMSVRTPSKGGATDFCDMYAVYNALPEATKQKISGRYGIHHASKALNPRVKIS 169

Query: 174 HVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEG 232
+ + T +PLV+ H ETGR +L + R I MD AE++ L+
Sbjct: 170 ENRPGAKEFYAKQAQERPTVRQPLVRTHDETGRQALYVSPRFTLGIEDMDDAEAQPLLDE 229

Query: 233 LVDWACQAPRV--HAHQWAAGDVVVWDNRCLLHRA 265
L + R + H + GD+V+WDNRC++HRA
Sbjct: 230 LFSYITDEARKYHYRHYRTGDLVLWDNRCIVHRA 264

>ref|NP_936287.1| taurine catabolism dioxxygenase [Vibrio vulnificus YJ016]
dbj|BAC96257.1| probable taurine catabolism dioxxygenase [Vibrio vulnificus YJ016]
Length = 288

Score = 115 bits (287), Expect = 9e-24, Method: Compositional matrix adjust.
Identities = 78/275 (28%), Positives = 126/275 (45%), Gaps = 27/275 (9%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
+ + T++ITP + GA V V L+ +++ F AL+ A+L + +L F Q L+ +Q +

Sbjct: 4 IERETMKITPLATSFGALVEDVQLSAINERQFEALYHAF LHYKVLFFRDQLLTAEQHLAL 63

Query: 61 AKRFGAIERI-----GGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS 112
+RFG +E I +V I R+ P G WH D

Sbjct: 64 GQRFGELEPIHPFFPHLADAPQVVVIE-----TREGLPP-----GESYWHTDL 106

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-VYSQSK 171
T+ ++ A+ A+ P GG T + DM A + +LD++ + + A H+L + S+

Sbjct: 107 TWKARPSKCALLHAQHCPPSGGDTIWTDM EAVWRSLLDDSLKQQLRPLYATHALHAFENS R 166

Query: 172 LGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL 230
H + G +Y+ P+V HPETG+ +L I I G++ A+S+ L

Sbjct: 167 YDHKDEDEGESYVVKKSREFPAVHHVPVVAQHPETGQETLYINEQFTRCIDGLEKAQSQALL 226

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
E L A +A QW A + +WDNR H A

Sbjct: 227 EMLFAMAREAKFQVRFQWQANSLAIWDNRATQHFA 261

>ref|YP_002256592.1| alpha-ketoglutarate-dependent taurine dioxygenase protein
[Ralstonia solanacearum MolK2]
emb|CAQ57055.1| alpha-ketoglutarate-dependent taurine dioxygenase protein
[Ralstonia solanacearum MolK2]
Length = 281

Score = 114 bits (286), Expect = 1e-23, Method: Compositional matrix adjust.
Identities = 83/266 (31%), Positives = 125/266 (46%), Gaps = 24/266 (9%)

Query: 12 GATLGATVTGVH-LATLDDAGFAALHAAWLQH-ALLIFPGQHLSNDQQITFAKRFGAIE- 68
GA LGA + G+ A L DA A + AWL H LL+F L+ Q+ F++RFG ++

Sbjct: 6 GAPLGAIEILGLSDAAGLSADAVIRRAWLAHDGLLVFRDVMLAPRAQVDFSRFRGPLQV 65

Query: 69 -----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQG 121
+I+ +SNV +G P D + WH+D +Y P + G

Sbjct: 66 HVLNQFHLPDHPEILVSVNVVENG-----KPIGLGDAGR-----DWHS DLSYKPQPSLG 114

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
++ A +P GG T FA+M AY+ L + ++ R A HS VY +L +

Sbjct: 115 SLLLARELPQAGGDTL FANMVRAYETLPAGLKRIIEGRRVHSYVRYERLRALS AWRPP 174

Query: 182 YIGYMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVDWACQ 239
D P+V+ HPETG+ +L + G +H + G+ ES LE L + Q

Sbjct: 175 LTQAQRDAVPPVDHPVVRTHPETGKRALFVNEGFTSHIL-GLPEDESTAVLEQLFAHSIQ 233

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
+ H+W GD++ WDN R +H A

Sbjct: 234 PDNRYTHRWQPGDMLFWDNRSTIHFA 259

>ref|ZP_05126397.1| taurine catabolism dioxygenase TauD/TfdA [gamma proteobacterium
NOR5-3]
gb|EED32944.1| taurine catabolism dioxygenase TauD/TfdA [gamma proteobacterium
NOR5-3]
Length = 282

Score = 114 bits (286), Expect = 1e-23, Method: Compositional matrix adjust.
Identities = 88/271 (32%), Positives = 123/271 (45%), Gaps = 21/271 (7%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++ + P+G GATV G+ LA L A+ AAWL+H +L FP Q L++D F

Sbjct: 2 SIHVEPSGQACGATVRGLDLAQPLSSDTVQAIRAAWLEHHVLA FPEQTLNDDDLERFTGY 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA-EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122

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          FG          G+   I+ V          R+H A E          + +   AWH+D ++          G
Sbjct: 62  FGPFG-----GEDPFIAPVPG----REHVI AVERRAQEQA PLFAEAWHSDWSFQATPPIGT 112

Query: 123 VFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
          +P   GG T FA+   A D L A R +   A HS          + G + A A
Sbjct: 113 CLHGITIPPTGGDTL FANQHKALDTLPSALRGRIEGLMAMHSAKVGYPADG-LYGAADAA 171

Query: 183 IGYGMDTTATP-----LRPLVKVHPETGRPSL--LIGRHAHAIPGMDAAESERFLEGLV 234
          MD   +P          PL++ H ETGR SL   +G +   I GM   E+   L L
Sbjct: 172 SDRSMDIRPSPEAQAVQSHPLIRRHSETGRASLYSCLG-YIVGIEGMPDEEAEVLLMELY 230

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          W   +   ++ HQW   G +++WDNRCLLHRA
Sbjct: 231 AWQTREENIYTHQWETGMLIMWDNRCLLHRA 261

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>ref|XP_002482838.1| alpha-ketoglutarate-dependent taurine dioxygenase, putative
[Talaromyces stipitatus ATCC 10500]
gb|EED18846.1| alpha-ketoglutarate-dependent taurine dioxygenase, putative
[Talaromyces stipitatus ATCC 10500]
Length = 284

Score = 114 bits (286), Expect = 1e-23, Method: Compositional matrix adjust.
Identities = 79/284 (27%), Positives = 123/284 (43%), Gaps = 27/284 (9%)

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Query: 6   LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
          + + P A+ GA + G   L   A+ AAW + +L F G ++ Q   F+ FG
Sbjct: 1   MNVIPIQASCGADIIGFDFEHLYPDQVDAVRAAWRDYGVLRFRGYDITTQQHAKFSNLF 60

Query: 66  AIERIGG-----GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGN--MAWHADSTYM 115
          + G          +I   ISN K DG   P          +GN + WH DS Y
Sbjct: 61  HYVPVKGTSIAHHDQKEITVISNAKVDG-----KPVG-----TLGNVDLEWHTDSWYF 108

Query: 116 PVMAQGA VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
          G + A +P   GG T + +M A YDAL E TR ++ R + ++VY   +G V
Sbjct: 109 DKPPCGQILRALELPRTGGDTYVWNMYAVYDALPEFTRKIIIEGRLIQFNIVY--DAVGRV 166

Query: 176 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH---AHAIPGMDAAESERFLEG 232
          +          P+V+ +PE+GR ++ IG   + I G+   +S+ LE
Sbjct: 167 RPGQEKPETDDFRLWKHVRHPIVRTNPESGRKAVYIGYFDSTKNWIVGLPLEQSKAILEE 226

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
          +          V   +W   D+++WDNRC +HR + W+   R+M
Sbjct: 227 IYSLIDSGKFVFQQKWQPNDIIMWDNRCTMHRRDGWNETDMRIM 270

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>ref|YP_110835.1| dioxygenase [Burkholderia pseudomallei K96243]
ref|ZP_02509390.1| dioxygenase [Burkholderia pseudomallei BCC215]
ref|ZP_04896401.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pasteur
52237]
emb|CAH38286.1| putative dioxygenase [Burkholderia pseudomallei K96243]
gb|EDO93239.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pasteur
52237]
Length = 297

Score = 114 bits (286), Expect = 1e-23, Method: Compositional matrix adjust.
Identities = 99/300 (33%), Positives = 138/300 (46%), Gaps = 28/300 (9%)

```

Query: 6   LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L I P A LGA + G+   A LD   A+ AAWL+ LL+F GQ L   + + F +RF
Sbjct: 7   LGIRPLSAAALGARIDGIDARAELDADTVRAIRA AAWLRFGLLVFRGQALDPPRLVAFTRRF 66

Query: 65  G---AIERI-----GGGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116

```

```

      G      R      G  +++ +SNV  DG              +  +      WH D  Y+
Sbjct: 67  GEPVYTRACNACDGQPEVLVLNSNVKDGKP-----IGAALSGRYWHTDGHYLA 115

Query: 117  VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
      G  +      +PAVGG T F +M AAY AL      R  +  R+      V  Q+  H
Sbjct: 116  CPPAGTLLFGAEIPAVGGDTHFVNMTAAYRALPAWVRTQIDGRTFVMDRV--QTLPFHYP 173

Query: 177  QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLVD 235
      Q  +      P +P+V+ HPETG +L IG      I GM+  S+  +  L
Sbjct: 174  QRPAPPPDQKQAWPDMP-QPVVRTHPETGENALYIGGVVPWRIVGMEQGLSDALMAHLHA 232

Query: 236  WACQAPRV-HAHQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RPE-TEGAA 291
      A      R  + H+W AGD+++WDNRCL HRA  +D  +  R M+  + +AG RP      GAA
Sbjct: 233  IAFDEARFGYRHRWRAGDLLMWDNRCLAHRATDYDMVRHRRTMYRTTIAGDRPRYVRGAA 292

```

>gb|ACX54990.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 98

Score = 114 bits (286), Expect = 1e-23, Method: Compositional matrix adjust.
Identities = 61/98 (62%), Positives = 69/98 (70%), Gaps = 3/98 (3%)

```

Query: 110  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
      ADSTYMPV A+GAVFSAE+VPA G  T +ADMRAAYDALDEATR L+  + A HSL YSQ
Sbjct: 1    ADSTYMPVQAKGAVFSAEIVPASGAPTGWADMRAAYDALDEATRELIADKLAYHSLYYSQ 60

Query: 170  SKLGHV---QQAGSAYIGYGMDTTATPLRPLVKVHPET 204
      + G++  Q  G  Y  YG      LRPLVKVHPET
Sbjct: 61  GRAGYLPQNDGGGYDQYGYHDLPSLRPLVKVHPET 98

```

>ref|ZP_02894178.1| Taurine dioxygenase [Burkholderia ambifaria IOP40-10]
gb|EDT00241.1| Taurine dioxygenase [Burkholderia ambifaria IOP40-10]
Length = 318

Score = 114 bits (286), Expect = 1e-23, Method: Compositional matrix adjust.
Identities = 89/266 (33%), Positives = 127/266 (47%), Gaps = 20/266 (7%)

```

Query: 6    LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
      L++      +GA + GV L+ TLDDA F A+ AA L+H +L F  Q HL +  Q  FA+R
Sbjct: 27  LELRQVAGRIGAEIAGVRLSSTLDDATFDAIQAALLRHKVLFFRNQEHLDDAAQEAFAARR 86

Query: 64  FGAIERIGGGDIVAISNVK-ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
      FG      D VA      V  ADG+      E D      +WH D T++      +  +
Sbjct: 87  FG-----DTVAHPTVPPADGSAHL---LELDSAHGARAN--SWHTDVTTFVDAYPKVS 133

Query: 123  VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
      +  A V+P  GG T +A+  AAY  L E+ RAL      A H+  Y  +  HV      +
Sbjct: 134  ILRAVVIPPFGGDTVWANTAAAYAHLPESLRALADTLWALHTNAYDYAST-HVHADDTQL 192

Query: 183  IGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
      Y      T+T      P+V+VHPETG  +L++G      I G+  + +S  L+ L  +  +
Sbjct: 193  KRYREVFTSTVYETEHFVVRVHPETGERTLVLGHFVQRIKGLSSQDSAHLQLVLEHVTR 252

Query: 240  APRVHAHQWAAGDVVVWDNRCLLHRA 265
      +W  GDV +WNR      H A
Sbjct: 253  LENTVRWRWQQGDVAIWDNRATQHYA 278

```

>ref|ZP_00951769.1| alpha-ketoglutarate-dependent taurine dioxygenase [Oceanicaulis
alexandrii HTCC2633]
gb|EAP90922.1| alpha-ketoglutarate-dependent taurine dioxygenase [Oceanicaulis

Score = 114 bits (285), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 99/300 (33%), Positives = 138/300 (46%), Gaps = 28/300 (9%)

```
Query: 6  LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L I P A LGA + G+ A LD A+ AAWL+ LL+F GQ L + + F +RF
Sbjct: 7  LGIRPLSAALGARIDGIDARAELDADTVRAIRAALWRFGLLVFRGQALDPPRLVAFTRRF 66

Query: 65 G---AIERI-----GGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
          G R G +++ +SNV DG + + WH D Y+
Sbjct: 67 GEPVVYTRACNACDGQPEVLVLSNVVKDGKP-----IGAALSGRYWHTDGHYLA 115

Query: 117 VMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
          G + +PAVGG T F +M AAY AL R + R+ V Q+ H
Sbjct: 116 CPPAGTLLFGAEIPAVGGDTHFVNMTAAYRALPAWVRTQIDGRTFVMDRV--QTLPFHY 173

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLVD 235
          Q + P +P+V+ HPETG +L IG I GM+ S+ + L
Sbjct: 174 QRPAPPPDQKQAWPDMP-QPVVTRHPETGENALYIGGVVPWRIVGMEQRLSDALMAHLHA 232

Query: 236 WACQAPRV-HAQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RPE-TEGAA 291
          A R + H+W AGD+++WDNRCL HRA +D + R M+ + +AG RP GAA
Sbjct: 233 IAFDEARFGYRHRWRAGDLLMWDNRCLAHRATDYDMVRHRRTMYRTTIAGDRPRYVRGAA 292
```

>ref|ZP_04881190.1| dioxygenase, TauD/TfdA family [Burkholderia mallei ATCC 10399]
ref|ZP_04910487.1| dioxygenase, TauD/TfdA family [Burkholderia mallei FMH]
gb|EDK52093.1| dioxygenase, TauD/TfdA family [Burkholderia mallei FMH]
gb|EDP85544.1| dioxygenase, TauD/TfdA family [Burkholderia mallei ATCC 10399]
Length = 307

Score = 114 bits (285), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 99/300 (33%), Positives = 138/300 (46%), Gaps = 28/300 (9%)

```
Query: 6  LQITPTGATLGATVTGVH-LATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L I P A LGA + G+ A LD A+ AAWL+ LL+F GQ L + + F +RF
Sbjct: 17 LGIRPLSAALGARIDGIDARAELDADTVRAIRAALWRFGLLVFRGQALDPPRLVAFTRRF 76

Query: 65 G---AIERI-----GGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
          G R G +++ +SNV DG + + WH D Y+
Sbjct: 77 GEPVVYTRACNACDGQPEVLVLSNVVKDGKP-----IGAALSGRYWHTDGHYLA 125

Query: 117 VMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
          G + +PAVGG T F +M AAY AL R + R+ V Q+ H
Sbjct: 126 CPPAGTLLFGAEIPAVGGDTHFVNMTAAYRALPAWVRTQIDGRTFVMDRV--QTLPFHY 183

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLVD 235
          Q + P +P+V+ HPETG +L IG I GM+ S+ + L
Sbjct: 184 QRPAPPPDQKQAWPDMP-QPVVTRHPETGENALYIGGVVPWRIVGMEQRLSDALMAHLHA 242

Query: 236 WACQAPRV-HAQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RPE-TEGAA 291
          A R + H+W AGD+++WDNRCL HRA +D + R M+ + +AG RP GAA
Sbjct: 243 IAFDEARFGYRHRWRAGDLLMWDNRCLAHRATDYDMVRHRRTMYRTTIAGDRPRYVRGAA 302
```

>gb|ADI12795.1| dioxygenase [Streptomyces bingchengensis BCW-1]
Length = 299

Score = 114 bits (285), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 87/290 (30%), Positives = 133/290 (45%), Gaps = 30/290 (10%)

```
Query: 6  LQITPT-GATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHL-SNDQQITFAK 62
          + +TP GA LGA V G H+ +D + AA H +L+F G S ++ + F +
Sbjct: 1  MDVTPIPGAALGAVVHGAHVTDMDKTQLEEIWAALDAHLVLVFRGHETPSFEEFLAFGR 60
```

Query: 63 RFGAIERIG-----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY 114
RFG I + G +I+ +SN+ DG AEW M WH D ++
Sbjct: 61 RFGYIPKTLTSGAHPDHNEILIVSNLVEDGRKIGVGDAEW-----MGWHTDYSF 110

Query: 115 MPVMAQGAVFSAEVVPAVGG-RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
P ++Q A VP+ GG T F DM A Y++L R +H ARH+L +
Sbjct: 111 RPRVSQVGFLAEVVPSSGGGETLFTDMYALYESLSPEERRRLHSYRARHALRTGYEETI 170

Query: 174 HVQQAGSAYIGYGM-----DTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAES 226
+ G +G D T+T + PL+ +P TGR S+ I + I + +S
Sbjct: 171 EEELQGEVSLGESTEQIQPEDGTST-IHPLIARNPRTGRQSVYISTLNTKRIVDLAPDDS 229

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
+ L+ L+ A + +AH W GD+VVWD +H + +D R+M
Sbjct: 230 RKLLELLSHAGKPQHTYAHTWQPGDIVVWDQLGTVHAKQAFDPAERRIM 279

>gb|ABD16693.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bradyrhizobium sp. Lppb2]
Length = 153

Score = 114 bits (285), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 62/157 (39%), Positives = 85/157 (54%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+DS++ P+ A+ ++ SA VV GG T FADMRAA+DALD+ T+A + HSL+Y
Sbjct: 2 WHSDSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAFDALDDDTKAEIEDLVCEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
S+ LG + Y L+ LV+ HP R SL + HA I M E
Sbjct: 62 SRGSLGFTE-----YTDDEKQMFKPVQLRVLVTRHPVHRRKSLYLSSHAGKIVSMSVPEGR 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
L L + A Q V+ H+W D+V+WDNR +HR
Sbjct: 117 LLLRDLNEHATQGEFVYVHKWKLHDLVMWMDNRQTMHR 153

>ref|YP_105432.1| TauD/TfdA family dioxxygenase [Burkholderia mallei ATCC 23344]
ref|YP_337565.1| TauD/TfdA family dioxxygenase [Burkholderia pseudomallei 1710b]
ref|YP_001024592.1| TauD/TfdA family dioxxygenase [Burkholderia mallei NCTC 10229]
ref|YP_001078924.1| TauD/TfdA family dioxxygenase [Burkholderia mallei NCTC 10247]
ref|YP_001075173.1| TauD/TfdA family dioxxygenase [Burkholderia pseudomallei 1106a]
ref|ZP_01765536.1| dioxxygenase TauD/TfdA family [Burkholderia pseudomallei 305]
ref|ZP_02414882.1| dioxxygenase TauD/TfdA family protein [Burkholderia pseudomallei 14]
ref|ZP_03450025.1| dioxxygenase, TauD/TfdA family [Burkholderia pseudomallei 576]
ref|ZP_04521659.1| dioxxygenase, TauD/TfdA family [Burkholderia pseudomallei MSHR346]
ref|ZP_00442490.2| dioxxygenase, TauD/TfdA family [Burkholderia mallei GB8 horse 4]
ref|ZP_04812458.1| dioxxygenase, TauD/TfdA family [Burkholderia pseudomallei 1106b]
ref|ZP_04889852.1| dioxxygenase TauD/TfdA family [Burkholderia pseudomallei 1655]
ref|ZP_04899361.1| dioxxygenase TauD/TfdA family [Burkholderia pseudomallei S13]
ref|ZP_04953910.1| dioxxygenase, TauD/TfdA family [Burkholderia pseudomallei 1710a]
ref|ZP_04967610.1| dioxxygenase TauD/TfdA family [Burkholderia pseudomallei 406e]
ref|ZP_04971897.1| dioxxygenase, TauD/TfdA family [Burkholderia mallei 2002721280]
gb|AAU47037.1| dioxxygenase, TauD/TfdA family [Burkholderia mallei ATCC 23344]
gb|ABA51696.1| dioxxygenase, TauD/TfdA family [Burkholderia pseudomallei 1710b]
gb|ABN00471.1| dioxxygenase, TauD/TfdA family [Burkholderia mallei NCTC 10229]
gb|ABN95133.1| dioxxygenase TauD/TfdA family [Burkholderia pseudomallei 1106a]
gb|ABO02276.1| dioxxygenase, TauD/TfdA family [Burkholderia mallei NCTC 10247]
gb|EBA49323.1| dioxxygenase TauD/TfdA family [Burkholderia pseudomallei 305]
gb|EDK82772.1| dioxxygenase, TauD/TfdA family [Burkholderia mallei 2002721280]
gb|EDO87497.1| dioxxygenase TauD/TfdA family [Burkholderia pseudomallei 406e]

gb|EDS82373.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei S13]
 gb|EDU10836.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 1655]
 gb|EEC37837.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 576]
 gb|EEP50573.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei MSHR346]
 gb|EEP88579.1| dioxygenase, TauD/TfdA family [Burkholderia mallei GB8 horse 4]
 gb|EES23083.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1106b]
 gb|EET03432.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1710a]
 Length = 297

Score = 114 bits (285), Expect = 2e-23, Method: Compositional matrix adjust.
 Identities = 99/300 (33%), Positives = 138/300 (46%), Gaps = 28/300 (9%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 L I P A LGA + G+ A LD A+ AAWL+ LL+F GQ L + + F +RF
 Sbjct: 7 LGIRPLSAAALGARIDGIDARAELDADTVRAIRAARLRFGLLVFRGQALDPPRLVAFTRRF 66

Query: 65 G---AIERI-----GGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
 G R G +++ +SNV DG + + WH D Y+
 Sbjct: 67 GEPVYTRACNACDGQPEVLVLSNVKDGKPE-----IGAALSGRYWHTDGHYLA 115

Query: 117 VMAQGA VFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
 G + +PAVGG T F +M AAY AL R + R+ V Q+ H
 Sbjct: 116 CPPAGTLLFGAEIPAVGGDTHFVNMTAAYRALPAWVRTQIDGRTFVMDRV--QTLPFHYP 173

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLVD 235
 Q + P +P+V+ HPETG +L IG I GM+ S+ + L
 Sbjct: 174 QRPAPPPDQKQAWPDMP-QPVVRTHPETGENALYIGGVVPWRIVGMEQRLSDALMAHLHA 232

Query: 236 WACQAPRV-HAHQWAAGDVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RPE-TEGAA 291
 A R + H+W AGD+++WDNRCL HRA +D + R M+ + +AG RP GAA
 Sbjct: 233 IAFDEARFGYRHRWRAGDLLMWDNRLAHRATDYDMVRHRRTMYRTTIAGDRPRYVRGAA 292

>ref|ZP_02906934.1| Taurine dioxygenase [Burkholderia ambifaria MEX-5]
 gb|EDT41955.1| Taurine dioxygenase [Burkholderia ambifaria MEX-5]
 Length = 318

Score = 114 bits (285), Expect = 2e-23, Method: Compositional matrix adjust.
 Identities = 87/266 (32%), Positives = 126/266 (47%), Gaps = 20/266 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
 LQ+ +GA + GV L++ LDD F A+HAA L+H +L F Q HL + Q FA+R
 Sbjct: 27 LQLRQVAGRIGAEIAGVRLSSALDDGTFDAIHAALLRHKVLFFRNQEHLDDTAQEAFARR 86

Query: 64 FGAIERIGGDIVAISNVK-ADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
 FG D VA V DG+ E D +WH D T++ + +
 Sbjct: 87 FG-----DTVAHPTVPPVDGSAHL---LELDSAHGARAN--SWHTDVTFTVDAYPKVS 133

Query: 123 VFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
 + A V+P GG T +A+ AAY L E+ RAL A H+ Y + HV +
 Sbjct: 134 ILRAVVIPPFGGDTVWANTAAAYAHLPESLRALADTLWALHTNAYDYAST-HVHADDTQL 192

Query: 183 IGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
 Y T+T P+V+VHPETG +L++G I G+ + +S ++ L + +
 Sbjct: 193 KRYREVFTSTVYETEHFVVRVHPETGERTLVLGHFVQKIKGLSSQDSAHLMQVLHEHVTR 252

Query: 240 APRVHAHQWAAGDVVWDNRCLLHRA 265
 +W GDV +WDNR H A
 Sbjct: 253 LENTVRWRWQQGDVAIWDNRATQHYA 278

>ref|YP_324822.1| taurine catabolism dioxygenase TauD/TfdA [Anabaena variabilis ATCC 29413]

gb|ABA23927.1| Taurine catabolism dioxygenase TauD/TfdA [Anabaena variabilis ATCC 29413]
Length = 305

Score = 114 bits (285), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 81/270 (30%), Positives = 119/270 (44%), Gaps = 18/270 (6%)

```
Query: 1  MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
          M      I P      +GA + GV L+T L D      + +  A ++H ++ F GQ++  +QQ+
Sbjct: 1  MGSQYFDIKPIAGRIGAKIIGVDLSTNLSDEIISDIRKALVKHKVIFFRGQNIDANQQVA 60

Query: 60  FAKRFGAIERIGGGDIVAISNVKADGTVRQ--HSPAEDDMMKVIVGNMAWHADSTYMP 116
          FA+RFG +              A TV      +P   D +  K +      WH D T++
Sbjct: 61  FARRFGEV-----TTAHTVPSLDPDNPEVLNLNYGKTVARANNWHTDVTFLVD 107

Query: 117  VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG-HV 175
          G+V  A V+P  GG T +A+  AY+ L   R L  Q  A HS  Y  +      +
Sbjct: 108  SPPLGSLRALVIPPSGGDTIWANSVTAYEDLPHTLRNLADQLWAVHSNAYDYAAATVDL 167

Query: 176  QQAGSAYIGYGMTDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD 235
          +  AY      T      L P+V+VHPE+G  L IG      I G+  ES+  ++ L
Sbjct: 168  PEEVRAYRAVFTSTVYETLHPVVRVHPESGERGLFIGGFVRRIRGLSQNESDEIVKLLQA 227

Query: 236  WACQAPRVHAHQWAAGDVVWVDNRCLLHRA 265
          +  +              +W  GDV  WDNR   H A
Sbjct: 228  YVTRPENTVRWRWQVGDAFWDNRATQHHA 257
```

>ref|YP_724557.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Ralstonia eutropha H16]
emb|CAJ91189.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Ralstonia eutropha H16]
Length = 291

Score = 114 bits (285), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 83/275 (30%), Positives = 122/275 (44%), Gaps = 31/275 (11%)

```
Query: 6  LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          + + P      LGA ++GV L+  + D  FA + +A   H ++ F  Q L+ DQ   F+ RF
Sbjct: 7  IDVQPIAGALGAEISGVDLSPVPDETFAEIRSALHNHQVIFFRDQQLTPDQHKAFSARF 66

Query: 65  GAIERI-----GGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPV 117
          G +  +      G +I+ +  KA+ T R              AWH D +Y  +
Sbjct: 67  GDLLEVPFVRALEGHAEILPVMKGKAEQTKRNF-----GAWHTDMSYAEI 112

Query: 118  MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
          G+   A V+P  GG T +A M  AYDAL +  + ++ +  A HS V S      G V
Sbjct: 113  PPLGSALYARVIPPYGGDTMWASMYHAYDALSDGLKLVLDKLRVHSPVRSYGARGAVVN 172

Query: 178  AGSAYIGYGMT-----TATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL 230
          G      + MD      +  L P+V+VHP TGR +L +  +      GM  ES  L
Sbjct: 173  NGDP--AHKMDVRTDDRANSEVLHPVVRVHPATGRKALYVNSTYTMRFEGMTEESAPLL 230

Query: 231  EGLVDWACQAPRVHAHQWAAGDVVWVDNRCLLHRA 265
          + L   A +      +W  G +  VWDNRC  H A
Sbjct: 231  QYLYAHAARPEFTCRFRWTRGALAVWDNRCTQHHA 265
```

>ref|ZP_02269820.2| dioxygenase, TauD/TfdA family [Burkholderia mallei PRL-20]
ref|ZP_04915452.1| dioxygenase, TauD/TfdA family [Burkholderia mallei JHU]
gb|EDK57398.1| dioxygenase, TauD/TfdA family [Burkholderia mallei JHU]
gb|EES42725.1| dioxygenase, TauD/TfdA family [Burkholderia mallei PRL-20]
Length = 331

Score = 114 bits (284), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 99/300 (33%), Positives = 138/300 (46%), Gaps = 28/300 (9%)

```

Query: 6   LQITPTGATLGATVTGVH-LATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L I P A LGA + G+ A LD A+ AAWL+ LL+F GQ L + + F +RF
Sbjct: 41  LGIRPLSAAALGARIDGIDARAELDADTVRAIRAARLRFGLLVFRGQALDPPRLVAFTTRRF 100

Query: 65  G-----AIERIGG-GDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
          G A G +++ +SNV DG + + WH D Y+
Sbjct: 101 GEPVVYTRACNACDGQPEVLVLSNVVKDGKP-----IGAALSGRYWHTDGHYLA 149

Query: 117 VMAQGA VFSAE VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
          G + +PAVGG T F +M AAY AL R + R+ V Q+ H
Sbjct: 150 CPPAGTLLFGAEIPAVGGDTHFVNMTAAYRALPAWVRTQIDGRTFVMDRV--QTLPFHY 207

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLVD 235
          Q + P +P+V+ HPETG +L IG I GM+ S+ + L
Sbjct: 208 QRPAPPPDQKQAWPDMP-QPVVRTHPETGENALYIGGVVPRIVGMEQRLSDALMAHLHA 266

Query: 236 WACQAPRV-HAHQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RPE-TEGAA 291
          A R + H+W AGD+++WDNRCL HRA +D + R M+ + +AG RP GAA
Sbjct: 267 IAFDEARFGYRHRWRAGDLLMWDNRCLAHRAATDYDMVRHRRRTMYRTTIAGDRPRYVRGAA 326

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>ref|YP_775305.1| taurine dioxygenase [Burkholderia ambifaria AMMD]
gb|ABI88971.1| Taurine dioxygenase [Burkholderia ambifaria AMMD]
Length = 318

Score = 114 bits (284), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 89/266 (33%), Positives = 126/266 (47%), Gaps = 20/266 (7%)

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Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
          LQ+ +GA + GV L+ TLDDA F A+ AA L+H +L F Q HL + Q FA+R
Sbjct: 27  LQLRQVAGRIGAEIAGVRLSNTLDDATFDAIQAALLRHKVLFFRNQEHLDDAAQEAFA 86

Query: 64  FGAIERIGGGDIVAISNVK-ADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
          FG D VA V ADG+ + E D +WH D T++ + +
Sbjct: 87  FG-----DTVAHPTVPPADGSAQL---LELDSAHGARAN--SWHTDVTFFVDAYPKVS 133

Query: 123 VFSAEV VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
          + A V+P GG T +A+ AY L E RAL A H+ Y + HV +
Sbjct: 134 ILRAVVIPPFGGDTVWANTATAYAHLPEPLRALADTLWALHTNAYDYAST-HVHADDTQL 192

Query: 183 IGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
          Y T+T P+V+VHPETG +L++G I G+ + +S L+ L + +
Sbjct: 193 KRYREVFTSTVYETEHVVRVHPETGERTLVLGHFVQKIKGLSSQDSAHLQLVLEHVTR 252

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
          +W GDV +WDNR H A
Sbjct: 253 LENTVRWRWQQGDVAIWDNRATQHYA 278

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>ref|YP_003115013.1| Taurine dioxygenase [Catenulispora acidiphila DSM 44928]
gb|ACU73172.1| Taurine dioxygenase [Catenulispora acidiphila DSM 44928]
Length = 303

Score = 114 bits (284), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 87/282 (30%), Positives = 124/282 (43%), Gaps = 15/282 (5%)

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Query: 4   TTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
          T I G +GA +TGV LA LD+ + AA L+H L+F Q+L ++ Q+ FA
Sbjct: 6   TDFDIRRIGGRIGAEITGVDLAGNLDEGILKEVKAALLEHKALVFRNQNLDDDEGQLRFAS 65

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Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
 +FG + A V Q P + + + WH D T++ + +
 Sbjct: 66 QFGPLTS-----AHPTVPGIAEQPQILPVDSEGAANV-----WHTDVTFFVQSPPKAS 113

Query: 123 VFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
 V+P GG T A+ AAY L + R L A H+ Y + + Y
 Sbjct: 114 TLRGIVIPPYGGNTLIANTAAAYRDLPKPLRDLADTLWAVHTNDYDYAGPKGDDEKRQQY 173

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPR 242
 + T P+V+VHPETG L IG A I G+ ES+ L L + +
 Sbjct: 174 RDVVFSTKYRTAHPVVRVHPETGERGLFIGAFAQTIEGLSTTESKDVLRLQLQAYVNRPEN 233

Query: 243 VHAHQWAAGDVVVWDNRCLLHRAEPWDFK-LPRVMWHSRLAG 283
 V QW GDVV++DNR H A P D+ LPR + +AG
 Sbjct: 234 VLRVQWNPQGDVVFIDNRITQHYA-PDDYDTLPRRLNRVTIAG 274

>gb|ACG80560.1| TfdA [uncultured bacterium]
 Length = 121

Score = 114 bits (284), Expect = 2e-23, Method: Compositional matrix adjust.
 Identities = 57/124 (45%), Positives = 73/124 (58%), Gaps = 3/124 (2%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
 T F DMRAAYDALD+ + HS YSQ K+G +++ + M
 Sbjct: 1 TEFCDMRAAYDALDDERKQQFEGLLGTHSYAYSQGVGGLEEVFTPEARARMVDIE---H 57

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
 PLV+ HP TGR SL IGRH + + GM +++ LEGL+ WACQ PRV HQW GD+V+
 Sbjct: 58 PLVRTHPATGRKSLFIGRHVYRVVTGMADDDAQAMLEGLIAWACQPPRVFKHQWTVGDIVM 117

Query: 256 WDNR 259
 WDNR
 Sbjct: 118 WDNR 121

>ref|ZP_06840735.1| Taurine catabolism dioxygenase TauD/TfdA [Burkholderia sp. Ch1-1]
 gb|EFG71455.1| Taurine catabolism dioxygenase TauD/TfdA [Burkholderia sp. Ch1-1]
 Length = 298

Score = 114 bits (284), Expect = 2e-23, Method: Compositional matrix adjust.
 Identities = 81/273 (29%), Positives = 128/273 (46%), Gaps = 21/273 (7%)

Query: 5 TLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
 +L I P T+ A + G+ L D + A + +LIFP Q + + Q + F++
 Sbjct: 2 SLDIEPAHPTIAARIRGLDLRQPFSDQVDEIGQASAIYPVLIFPNQLIDDAQLMAFSQN 61

Query: 64 FGAIERI-----GGGD-----IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS 112
 FG ++ + D + ISN+ + PA D + + WH D
 Sbjct: 62 FGPLQPVVSFHTAKADHRLSPMVSDISNLDKNNRT---FPAG-DRRRMNFLSSRRWHTDG 117

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
 +Y+P + ++ A V VGG+T FADMRAAYDAL LV + H++++S++
 Sbjct: 118 SYLPTPNRYSMLLAYTVARVGGQTQFADMRAAYDALPAEWLELVEDLTLEHNMVMSRAVA 177

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG 232
 G + + LV+ HP +GR SL + HA + G E L
 Sbjct: 178 GFTDFDEEERRRF-----PATHKKLVRRHPVSGRLSLYLSGHASHVVGWPIPEGLDLLRE 232

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 L ++A Q V+ H+W+ D+V+WDNR L+HRA
 Sbjct: 233 LTEFATQPQFVYTHEWSVRDLVMWDNRSLMHRA 265

>ref|YP_884706.1| dioxygenase, TauD/TfdA family protein [Mycobacterium smegmatis str. MC2 155]
gb|ABK75785.1| dioxygenase, TauD/TfdA family protein [Mycobacterium smegmatis str. MC2 155]
Length = 281

Score = 114 bits (284), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 95/292 (32%), Positives = 140/292 (47%), Gaps = 29/292 (9%)

Query: 4 TTLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
+ L I A++GA V G+ L DD AA+ A + +L+F G +L + Q+ F+
Sbjct: 2 SVLTINKLTASVGAEEVVGIDSERLATDDGIAAAVLDALEDNGVLVFRGLYLEPEAQVAFS 61

Query: 62 KRFGAIERIGGG--DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM- 118
+R G ++R G + I + D T ++ AE+ + WH D P+
Sbjct: 62 QRLGEVDRSADGHHPVSGIYPITLDQT--KNKAAEY-----LKATFDWHIDGC-TPLND 112

Query: 119 ---AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR---HSLVYSQSK 171
+ V SA V A GG T FA+ AAY++LD + QR AR HSL SQ +
Sbjct: 113 ECPQKATVLSAIEVAARGGETEFANAYAAYESLDADEK----QRYARLRVVSLEASQRR 168

Query: 172 LGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE 231
V +A T PLV H GR SL++G A I GMD E L+
Sbjct: 169 ---VYPDPTAEQRRRWAARPTHENPLVWTH-RNGRKS LVLGASADHIVGMDRDEGRALLD 224

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
GL+ +V++H+W+ GD V+WDN+ +LHRA P++ PR M + + G
Sbjct: 225 GLLARTTTTPDKVYSHKWSVGDTVIWDNQGV LHRAPYEPD SPRHMLRTTVLG 276

>ref|YP_001584537.1| taurine dioxygenase [Burkholderia multivorans ATCC 17616]
ref|YP_001948339.1| taurine dioxygenase [Burkholderia multivorans ATCC 17616]
gb|ABX18245.1| Taurine dioxygenase [Burkholderia multivorans ATCC 17616]
dbj|BAG45803.1| taurine dioxygenase [Burkholderia multivorans ATCC 17616]
Length = 314

Score = 114 bits (284), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 89/266 (33%), Positives = 125/266 (46%), Gaps = 20/266 (7%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
LQ+ +GA ++GV L ATLDDA F A+ AA L+H +L F GQH L + Q FA+R
Sbjct: 23 LQLRQVAGRIGAEISGVRLSATLDDATFDIAIQAALLRHKVLFFRQGHHLDAAQEAFAARR 82

Query: 64 FGAIERIGGGDIVAISNVKA-DGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG D VA V + DG+ E D + WH D T++ + +
Sbjct: 83 FG-----DTVAHPTVPSVDGSAHL---LELDSAHGARAN--WHTDVTTFVDAYPKIS 129

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ A V+P VGG T +A+ AAY L + R L A H+ Y + HV +
Sbjct: 130 ILRAVVIPPVGGDTVWANTAAAYAHLPDTLRTLADTLWAVHTNAYDYAST-HVHADETQL 188

Query: 183 IGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
Y T+T P+V+VHPETG +L++G I G+ +S L+ + +
Sbjct: 189 KRYREVFTSTVYETEHVPVVRVHPETGERTLVLGHFVQRIKGLSTQDSAHL LQVFHEHVTR 248

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
W GDV +WDNR H A
Sbjct: 249 LENTVRWSWQEGDVAIWIDNRATQHYA 274

>ref|ZP_03569865.1| taurine dioxygenase [Burkholderia multivorans CGD2M]

ref|ZP_03576506.1| taurine dioxygenase [Burkholderia multivorans CGD2]
gb|EEE09849.1| taurine dioxygenase [Burkholderia multivorans CGD2]
gb|EEE15772.1| taurine dioxygenase [Burkholderia multivorans CGD2M]
Length = 314

Score = 113 bits (283), Expect = 3e-23, Method: Compositional matrix adjust.
Identities = 89/266 (33%), Positives = 125/266 (46%), Gaps = 20/266 (7%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
LQ+ +GA ++GV L ATLDDA F A+ AA L+H +L F GQH L + Q FA+R
Sbjct: 23 LQLRQVAGRIGAEISGVRLSATLDDATFDAIQAALLRHKVLFFRGQHHLDDAAQEAFARR 82

Query: 64 FGAIERIGGGDIVAISNVKA-DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG D VA V + DG+ E D + WH D T++ + +
Sbjct: 83 FG-----DTVAHPTVPSVDGSAHL---LELDSAHGARANS--WHTDVTFFVDAYPKIS 129

Query: 123 VFSAE VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ A V+P VGG T +A+ AAY L + R L A H+ Y + HV +
Sbjct: 130 ILRAVVIPPVGGDTVWANTAAAYAHLPDTLRTLADTLWAIHTNAYDYAST-HVHADETQL 188

Query: 183 IGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
Y T-T P+V+VHPETG +L++G I G+ +S L+ + +
Sbjct: 189 KRYREVFTSTVYETEHPPVVRVHPETGERTLVLGHFVQRIKGLSTQDSAHLQVFHEHVTR 248

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
W GDV +WDNR H A
Sbjct: 249 LENTVRWSWQEGDVAIWDNRATQHYA 274

>ref|ZP_06688428.1| TauD/TfdA family dioxygenase [Achromobacter piechaudii ATCC 43553]
gb|EFF74634.1| TauD/TfdA family dioxygenase [Achromobacter piechaudii ATCC 43553]
Length = 307

Score = 113 bits (283), Expect = 3e-23, Method: Compositional matrix adjust.
Identities = 90/291 (30%), Positives = 132/291 (45%), Gaps = 20/291 (6%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ITP GA VT + D L AW H++L F G ++ + I F++R
Sbjct: 1 MKITPNSTGFGEVTDPCAGLKM TDELNELVRAWTDHSILCFRGVDMTPAEHIAFSRRL 60

Query: 65 GAIERI-----GGGDIVAISNV-KADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM 115
G + + G ++ +SN KAD + AE D ++ +H D
Sbjct: 61 GELHIMTPLKFNLDGYPEV FVVSNA SKADPSKPVAGNAEGDAGLRR--AGEGFHTDGEDK 118

Query: 116 PVMAQGA VFSAE VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
+ G+ A VP G T F DM AAY+AL + + L+ R AR YS+ L
Sbjct: 119 AIPNTGSFLYARQVPPERGDTL FVD MYAAYEALPQRIKTLIAGRARR---YSRIDLHAT 174

Query: 176 QQAGSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
A + + A P PL + HP +GR SL IGR A + G+ E + ++ L
Sbjct: 175 HYPLMAPLT-DEEKLARPDVYHPLARKHPVSGRTSLYIGRWACDVEGLPEDEGQALVKFL 233

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPW-DFKLPRVMWHSRLAG 283
D+A Q ++ H+W GD V+WDNRC H A + D K R M + L G
Sbjct: 234 QDFARQPQFIYTHKWNIGDAVLWDNRCTQHCATGFDDTKYVRTMHR TTLEG 284

>ref|ZP_06305801.1| Taurine catabolism dioxygenase TauD/TfdA [Raphidiopsis brookii D9]
gb|EFA72187.1| Taurine catabolism dioxygenase TauD/TfdA [Raphidiopsis brookii D9]
Length = 305

Score = 113 bits (283), Expect = 3e-23, Method: Compositional matrix adjust.
Identities = 81/270 (30%), Positives = 118/270 (43%), Gaps = 18/270 (6%)

Query: 1 MAQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
M L+I P +GA + + L L DA + + A +++ ++ F QHLS + QI
Sbjct: 1 MTYQYLKIKPIAGRIGAKILEIDLQENLSDAIISEIRRALVEYKVIFFRNQHLSAENQID 60

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHS--PAEWD-DMMKVIVGNMAWHADSTYMP 116
FA+RFG I A TV + P D D K WH D T++
Sbjct: 61 FARRFGEI-----TTAHTVPSLTGHPEILDLDYGKTAARANNWHTDVTFDV 107

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG-HV 175
G++ A +PA GG T + + AY L E R L + A HS Y ++ ++
Sbjct: 108 RPPLGSILRALEIPAYGGDTIWGNSVTAYRDLPEHLRQLADELWAVHSNAYDYAEAAVN 167

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD 235
+ AY T L P+V+VHPE+G L IG I G+ ES+ ++ L
Sbjct: 168 SEDLKAYREVFVTSTVYETLHPVVRVHPESGEKGLFIGGFVRQIRGLSTTESDHIIQLLQS 227

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ + +W GDV WDNR H A
Sbjct: 228 YVTRPENTVRWRWKVGDVAFWDNRATQHYA 257

>ref|YP_001564064.1| taurine dioxygenase [Delftia acidovorans SPH-1]
gb|ABX35679.1| Taurine dioxygenase [Delftia acidovorans SPH-1]
Length = 333

Score = 113 bits (283), Expect = 3e-23, Method: Compositional matrix adjust.
Identities = 91/275 (33%), Positives = 118/275 (42%), Gaps = 28/275 (10%)

Query: 3 QTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITF 60
Q LQI P +GA V G L+ L F +HAA L+H +L F GQH L++ F
Sbjct: 35 QQPLQIQPLSGRIGAVVHGARLSGELAAEQFTQIHAALLRHRVLFRRGQHHLTDASHQAF 94

Query: 61 AKRFGAIER---IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV 117
+ FG IE + D A + + R S WH D T+
Sbjct: 95 GRLFGEIESHPTVPAPDGTAFLELNSQHGGGRADS-----WHTDVTFKAA 138

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS-----QSK 171
+ V A +P GG T +A+ AAY+ L E R L Q A H Y Q+
Sbjct: 139 FPKVCVLRVAVTLPGHGGDTVWANTVAAAYEGLPEPLRQLAEQLWAVHGNDYDYAENFRQNA 198

Query: 172 LGHVQQAGSA-YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFL 230
+ AG A Y T +PLV VHPETG +LL+G A I G+ A ES L
Sbjct: 199 ASQTETAGRASYRKVFTRKTIESEQPLVHVPETGEKALLLGHFAKRIKGLRANESTALL 258

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ + + QWA GDV +WDNR H A
Sbjct: 259 QLFNERIIRLENTVRWQWAGDVVAIWDNRATQHYA 293

>ref|YP_003749822.1| taurine dioxygenase [Ralstonia solanacearum PSI07]
emb|CBJ35196.1| Taurine dioxygenase [Ralstonia solanacearum PSI07]
Length = 298

Score = 113 bits (283), Expect = 3e-23, Method: Compositional matrix adjust.
Identities = 88/292 (30%), Positives = 137/292 (46%), Gaps = 26/292 (8%)

Query: 4 TTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
+ L I P A GA + G+ A + A+ AAWL+ +L+F GQ L +Q+ F +
Sbjct: 5 SILHIRPLTAGFGAEIEGIDTGADMTSDTVRAIRAARLRFGLVFGGQTLDPARQVAFTR 64

Query: 63 RFGA-----IERIGGG--DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY 114
RFG E G +++ +SNV DG + + + WH D +

Sbjct: 65 RFGEPLVYTRSENACAGHPEVLVLSNVVDGKP-----IGAAISSRYWHTDGHF 113

Query: 115 MPVMAQGAVFSAEVPVAVGGRTCFADMR AAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
+ G + + VP GG TCF DM AAY AL R ++ R+ V Q+ H

Sbjct: 114 LQCPPAGTLLYGKDVPEGGDTCTCFVDM A AAYRALPVRLRTEINGRTFLMDRV--QTLPFH 171

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGL 233
+ + + P +P+V+ HPETG +L IG I GM+ + S+ + L

Sbjct: 172 YPERPAPPPDQKLRWPDMP-QPVVVRTHPETGANALYIGGGVPWRIVGMEPSRS DALMAQL 230

Query: 234 VDWACQAPRV-HAHQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG 283
A R + H+W AGD+++WDNR + HRA +D + R+M+ + +AG

Sbjct: 231 HAIAFDELRFGYRHRWRAGDLLMWDNRRAHRAATAYDMARYRRLMYRTTIAG 282

>ref|YP_001062210.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei 668]
gb|ABN86056.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 668]
Length = 297

Score = 113 bits (282), Expect = 3e-23, Method: Compositional matrix adjust.
Identities = 98/300 (32%), Positives = 138/300 (46%), Gaps = 28/300 (9%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I P A LGA + G+ A LD A+ AAWL+ LL+F GQ L + + F +RF

Sbjct: 7 LGIRPLS AALGARIDGIDARAELDADTVRAIRA AAWLRFGLLVFRGQALDPPRLVAFTRRF 66

Query: 65 G---AIERI-----GGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
G R G +++ +SNV DG + + WH D Y+

Sbjct: 67 GEPVVYTRACNACDGQPEVLVLSNVVKD GKP-----IGAALSGRYWHTDGHYLA 115

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMR AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
G + +PAVGG T F +M AAY AL R + R+ + Q+ H

Sbjct: 116 CPPAGTLLFGAEIPAVGGDTHFVNMTAAYRALPAWVRTQIDGRT--FVMDRLQTLPFHY 173

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLVD 235
Q + P +P+V+ HPETG +L IG I GM+ S+ + L

Sbjct: 174 QRPAPPPDQKQAWPDMP-QPVVVRTHPETGENALYIGGGVPWRIVGMEQRLSDALMAHLHA 232

Query: 236 WACQAPRV-HAHQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RPE-TEGAA 291
A R + H+W AGD+++WDNRCL HRA +D + R M+ + +AG RP GAA

Sbjct: 233 IAFDEARFGYRHRWRAGDLLMWDNRCLAHRA TDYDMVRHRRTMYRTTIAGDRPRYVRGAA 292

>ref|YP_003796616.1| taurine dioxygenase, 2-oxoglutarate-dependent [Candidatus
Nitrospira defluviil]
emb|CBK40690.1| Taurine dioxygenase, 2-oxoglutarate-dependent [Candidatus
Nitrospira defluviil]
Length = 292

Score = 113 bits (282), Expect = 3e-23, Method: Compositional matrix adjust.
Identities = 80/273 (29%), Positives = 126/273 (46%), Gaps = 19/273 (6%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ G LGA VTG++L T L L W +H +L+F GQ +++++ + FA+RF

Sbjct: 2 MRFRKLGGALGA EVTGLNLQTPLGRCEADQLTKEWFRHGV LVFRGQMITDEEHVRFARF 61

Query: 65 GAIERIGGGD-----IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
G +E + I +N G + P++ D+ +K++ N WH DS+Y

Sbjct: 62 GRLETFTQPNGIASFVPEIFCSANTDES GRL---LPSD-DERIKMLRLNLWHLIDSSYRA 117

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMR AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ +G V A V GG T FAD AA++AL + + A H+ Y V+

Sbjct: 118 MPVKGVVLRALHVAEEGGDTIFADNVAAFEALPGTIKTRIEGLRAIHNFAYL-----VR 171

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW 236
Q G + + PLV+ H + R L + I G A+S L L+ W
Sbjct: 172 QGGDLRPEEVASLPRAEHPLVRRHADGRRSLYLSPPYMEKIVGWSEADSCALLHELMW 231

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD 269
A Q + H+W DV++WDN +H P+D
Sbjct: 232 ATQERFLFRHRWQLHDVIMWDNAWTMHCVTYPYD 264

>gb|ADC33990.1| TfdA-like protein [uncultured bacterium]
Length = 208

Score = 113 bits (282), Expect = 4e-23, Method: Compositional matrix adjust.
Identities = 71/219 (32%), Positives = 106/219 (48%), Gaps = 24/219 (10%)

Query: 56 QQITFAKRFGA-----IERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVI- 102
QQI FA+RF R+G + ISN+ +G + + DD ++
Sbjct: 1 QQIAFAQRFDGQLHTKTGISALRKNRLGNEALGDISNLDENGEL-----LKSDDRRRMYG 55

Query: 103 VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR 162
+GN WH D+++ + ++ +A+V+P VG T FADMRAAYDAL +A +
Sbjct: 56 LGNRLWHTDASFQDPPGRYSLLAQKVLPPVGAETEFADMRAAYDALPPDFQAQLEGLRVH 115

Query: 163 HSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMD 222
HS+ +S+ LG A D + PL++ P + R SL + HA I
Sbjct: 116 HSLAHSRQMLGFEFSEKEA-----DLLKGAHVPLIRTLPHSQRSKSLYVASHASKIIDRP 169

Query: 223 AAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
E L L++ A Q V+ HQW GD+V+WDNRC+
Sbjct: 170 VPEGRLLRLRELIEHATQPEFVYRHQWRMGDLVIWDNRCV 208

>ref|YP_372822.1| taurine dioxygenase [Burkholderia sp. 383]
gb|ABB12178.1| Taurine dioxygenase [Burkholderia sp. 383]
Length = 317

Score = 113 bits (282), Expect = 4e-23, Method: Compositional matrix adjust.
Identities = 88/266 (33%), Positives = 124/266 (46%), Gaps = 20/266 (7%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
LQ+ +GA + GV L+ TLDDA F A+ AA L+H +L F GQH L + Q FA+R
Sbjct: 26 LQLRQVAGRIGAEIAGVRLSGTLDDATFDALQAALLRHKVLFRGQHHLDDTAQEAFAARR 85

Query: 64 FGAIERIGGGDIVAISNVK-ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG DIVA V DG+ E D +WH D T++ + +
Sbjct: 86 FG-----DIVAHTVPPVDGSAHL---LELDSAHGARAN--SWHTDVTFTVDAYPKIS 132

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ A +P GG T +A+ AAY L+ RAL A H+ Y + HV +
Sbjct: 133 ILRAVAIPPFGGDTVWANTAAAYTHLPDPLRALADTLWALHTNAYDYAST-HVHADDTQL 191

Query: 183 IGYGMDTTATPLR--PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
Y T+T P+V+VHPETG +L++G + G+ A +S L+ + +
Sbjct: 192 KRYREVFTSTVYETEHFVVRVHPETGERTLVLGHFVQRLKGLSAQDSAHLQLQVFHEHVTR 251

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
W GDV +WDNR H A
Sbjct: 252 LENTVRWNWQEGDVAIWDNRATQHYA 277

>emb|CAY27313.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 121

Score = 112 bits (281), Expect = 4e-23, Method: Compositional matrix adjust.
Identities = 57/124 (45%), Positives = 75/124 (60%), Gaps = 3/124 (2%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALD+ +A + HS YSQ K+G +++ + M
Sbjct: 1 TEFADMRAAYDALDDQRKAQLEGLLGTHSYAYSQGVGGLEEVFTPEARARMVDVE---H 57

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ HP TGR SL IGRH + + GM +++ LE L+ WACQ PRV H+W GD+V+
Sbjct: 58 PLVRTHPATGRKSLFIGRHVYRVGTMTDDDAQAMLEELLAWACQPPRVFKHRWTVGDIVM 117

Query: 256 WDNR 259
WDNR
Sbjct: 118 WDNR 121

>ref|ZP_02459133.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei 9]
ref|ZP_03793250.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pakistan 9]
gb|EEH26296.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pakistan 9]
Length = 297

Score = 112 bits (281), Expect = 5e-23, Method: Compositional matrix adjust.
Identities = 98/300 (32%), Positives = 138/300 (46%), Gaps = 28/300 (9%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I P A LGA + G+ A LD A+ AAWL+ LL+F GQ L + + F +RF
Sbjct: 7 LGIGPLSAAALGARIDGIDARAELDADTVRAIRAAWLRFGLLVFRGQALDPPRLVAFTRRF 66

Query: 65 G---AIERI-----GGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMP 116
G R G +++ +SNV DG + + WH D Y+
Sbjct: 67 GEPVVYTRACNACDGQPEVLVLSNVKDGKP-----IGAALSGRYWHTDGHYLA 115

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
G + +PAVGG T F +M +AY AL R + R+ V Q+ H
Sbjct: 116 CPPAGTLLFGAEIPAVGGDTHFVNMTSAYRALPAWVRTQIDGRTFVMDRV--QTLPFHYP 173

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLVD 235
Q + P +P+V+ HPETG +L IG I GM+ S+ + L
Sbjct: 174 QRPAPPPDQKQAWPDMP-QPVVRTHPETGENALYIGGVVPWRIVGMEQRLSDALMAHLHA 232

Query: 236 WACQAPRV-HAQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RPE-TEGAA 291
A R + H+W AGD+++WDNRCL HRA +D + R M+ + +AG RP GAA
Sbjct: 233 IAFDEARFGYRHRWRAGDLLMWDNRCLAHRAATDYDMVRHRRRTMYRTTIAGDRPRYVRGAA 292

>ref|YP_001345669.1| hypothetical protein PSPA7_0273 [Pseudomonas aeruginosa PA7]
gb|ABR84406.1| hypothetical protein PSPA7_0273 [Pseudomonas aeruginosa PA7]
Length = 299

Score = 112 bits (281), Expect = 5e-23, Method: Compositional matrix adjust.
Identities = 85/272 (31%), Positives = 130/272 (47%), Gaps = 20/272 (7%)

Query: 2 AQTTLQITPTGATLGATVTGVH-LATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A +ITP A LGA V G+ L AL A +H +L+F QHL ++Q + F
Sbjct: 14 AAFAFRITPLQAPLGAEVRLDARRPLAPEQVLALKQALREHHILVFRQQHLDDEQYLR 73

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVI-----VGNMAW--HADS 112
A FG++ + DI +S+ DG V D++KV +GN A H D
Sbjct: 74 ATLFGSVFQ-PPADIPVLSS-GDGKV-----PDIVKVANTGDGELGNFALPAHIDH 123

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172

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      + PV + G+   A  VP+ GG T F ++  AY++LDEATR  +      +  +  +
Sbjct: 124 QWTPVPSSGSFLYALEVPSSGGETRFTNLARAYESLDEATRREIDGLRLINYNPFIRLRE 183

Query: 173 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLE 231
      G      + Y      ++      PLV+ HPE+GR  L + H      IPG D A  +  +
Sbjct: 184 GGYGGGFATYRTPDIEPIQGSEHPLVRTHPESGRRVLFSLAHEVEIPGYDPARGQALIG 243

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH 263
      L +  +      ++H W+ GD+V WDN+ +LH
Sbjct: 244 RLREHLARPELSYSHAWSVGDIVVWDNQAVLH 275

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>ref|ZP_06876180.1| hypothetical protein PaerPab_01055 [Pseudomonas aeruginosa PAb1]
Length = 299

Score = 112 bits (281), Expect = 5e-23, Method: Compositional matrix adjust.
Identities = 84/268 (31%), Positives = 129/268 (48%), Gaps = 20/268 (7%)

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Query: 6   LQITPTGATLGATVTGVH-LATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      +ITP  A LGA V G+   L      AL  A  +H +L+F  QHL ++Q + FA  F
Sbjct: 18  FRITPLEAPLGAEVRLDARRPLAPEQVLALKQALREHHILVFRQQHLDDEQYLRFATLF 77

Query: 65  GAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVI-----VGNMAW--HADSTYMP 116
      G++ +   DI  +S+   DG V      D++KV      +GN A   H D  + P
Sbjct: 78  GSVFQ-PPADIPVLSS-GGDGKV-----PDIVKVANTGDGELGNFALPAHIDHQWTP 127

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
      V + G++  A  VP+ GG T F ++  AY++LDEATR  +      +  +  +  G
Sbjct: 128 VPSSGSLLYALEVPSSGGETRFTNLARAYESLDEATRREIDGLRLINYNPFIRLREGGYG 187

Query: 177 QAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVD 235
      + Y      ++      PLV+ HPE+GR  L + H      IPG D A  +  +  L +
Sbjct: 188 GGFATYRTPDIEPIQGSEHPLVRTHPESGRRVLFSLAHEVEIPGYDPARGQALIGRLRE 247

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLH 263
      ++H W+ GD+V WDN+ +LH
Sbjct: 248 HLAHPELSYSHAWSVGDIVVWDNQAVLH 275

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>ref|NP_248884.1| hypothetical protein PA0194 [Pseudomonas aeruginosa PA01]
ref|ZP_01363101.1| hypothetical protein PaerPA_01000193 [Pseudomonas aeruginosa PACS2]
ref|YP_002437803.1| hypothetical protein PLES_01951 [Pseudomonas aeruginosa LESB58]
ref|ZP_04930891.1| hypothetical protein PACG_03649 [Pseudomonas aeruginosa C3719]
ref|ZP_04936625.1| hypothetical protein PA2G_04111 [Pseudomonas aeruginosa 2192]
gb|AAG03584.1|AE004457_5 hypothetical protein PA0194 [Pseudomonas aeruginosa PA01]
gb|EAZ55010.1| hypothetical protein PACG_03649 [Pseudomonas aeruginosa C3719]
gb|EAZ60744.1| hypothetical protein PA2G_04111 [Pseudomonas aeruginosa 2192]
emb|CAW24922.1| hypothetical protein PLES_01951 [Pseudomonas aeruginosa LESB58]
Length = 299

Score = 112 bits (281), Expect = 5e-23, Method: Compositional matrix adjust.
Identities = 84/268 (31%), Positives = 129/268 (48%), Gaps = 20/268 (7%)

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Query: 6   LQITPTGATLGATVTGVH-LATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      +ITP  A LGA V G+   L      AL  A  +H +L+F  QHL ++Q + FA  F
Sbjct: 18  FRITPLEAPLGAEVRLDARRPLAPEQVLALKQALREHHILVFRQQHLDDEQYLRFATLF 77

Query: 65  GAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVI-----VGNMAW--HADSTYMP 116
      G++ +   DI  +S+   DG V      D++KV      +GN A   H D  + P
Sbjct: 78  GSVFQ-PPADIPVLSS-GGDGKV-----PDIVKVANTGDGELGNFALPAHIDHQWTP 127

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176

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V + G+ A VP+ GG T F ++ AY++LDEATR + + + + G
Sbjct: 128 VPSSGSFLYALEVPSSGGETRFTNLARAYESLDEATRREIDGLRLINYNPFIRLREGGYG 187

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVD 235
+ Y ++ PLV+ HPE+GR L + H IPG D A + + L +
Sbjct: 188 GGFATYRTPDIEPIQGSEHPLVRTHPESGRRVFLFLSAHTEVEIPGYDPARGQALIGRLRE 247

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLH 263
+ ++H W+ GD+V WDN+ +LH
Sbjct: 248 HLARPELSYSHAWSVGDIVWWDNQAVLH 275

>ref|YP_002260459.1| alpha-ketoglutarate-dependent taurine dioxygenase protein
[Ralstonia solanacearum IPO1609]
emb|CAQ62397.1| alpha-ketoglutarate-dependent taurine dioxygenase protein
[Ralstonia solanacearum IPO1609]
Length = 281

Score = 112 bits (280), Expect = 6e-23, Method: Compositional matrix adjust.
Identities = 82/266 (30%), Positives = 124/266 (46%), Gaps = 24/266 (9%)

Query: 12 GATLGATVTGVH-LATLDDAGFAALHAAWLQH-ALLIFPGQHLSNDQQITFAKRFGAIE- 68
GA LGA + G+ A L DA A + AWL H LL+F L+ Q+ F++RFG ++
Sbjct: 6 GAPLGAIEILGLSDAAGLSADADVAVIRRAWLAHDGLLVFRDVMLAPRAQVDFSRFRGPLQV 65

Query: 69 -----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
+I+ +SNV +G P D + WH+D +Y P + G
Sbjct: 66 HVLNQFHLPDHPEILVSVNVVENG-----KPIGLGDAGR-----DWHSDDL SYKPQPSLG 114

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
++ A +P GG T FA+M AY+ L + ++ R A HS VY +L +
Sbjct: 115 SLLLARELPQAGGDTLFANMVRAYETLPAGLKRIIEGRRVHVS YVRYERLRALSARPP 174

Query: 182 YIGYGMDDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVDWACQ 239
D P+V+ HPETG+ +L + G +H + G+ ES LE L + Q
Sbjct: 175 LTQAQRDAVPPVDHPVVRTHPETGKRALFVNEGFTSHIL-GLPEDESTAVLEQLFAHSIQ 233

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
+ H+W D++ WDNR +H A
Sbjct: 234 PDNRYTHRWQPSDMLFWDNRSTIHFA 259

>gb|EGD03386.1| taurine dioxygenase [Burkholderia sp. TJI49]
Length = 314

Score = 112 bits (280), Expect = 6e-23, Method: Compositional matrix adjust.
Identities = 88/266 (33%), Positives = 124/266 (46%), Gaps = 20/266 (7%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
LQ+ +GA ++GV L ATLDDA F A+ AA L+H +L F GQ HL + Q FA+R
Sbjct: 23 LQLRQVAGRIGAEISGVRLSATLDDATFDAIQAALLRHKVLFFRGQRHLDDAAQEAFAARR 82

Query: 64 FGAIERIGGGDIVAISNVKA-DGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG D VA V + DG+ E D + WH D T++ + +
Sbjct: 83 FG-----DTVAHPTVPSVDGSAHL---LELDSAHGARAN--WHTDVTFFVDAYPKIS 129

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ V+P VGG T +A+ AAY L + R L A H+ Y + HV +
Sbjct: 130 ILRGVVIPPVGGDTVWANTAAAYAHLPDTLRTLADTLWAVHTNAYDYAST-HVHADETQL 188

Query: 183 IGYGMDDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
Y T+T P+V+VHPETG +L++G I G+ +S L+ + +
Sbjct: 189 KRYREVFTSTVYETEHPVVRVHPETGERTLVLGHFVQRIKGLSTQDSAHLQVFHEHVTR 248

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
W GDV +WDNR H A
Sbjct: 249 LENTVRWSWQEGDVAIWDNRATQHYA 274

>emb|CAY27207.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 121

Score = 112 bits (280), Expect = 6e-23, Method: Compositional matrix adjust.
Identities = 55/124 (44%), Positives = 76/124 (61%), Gaps = 3/124 (2%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T FADMRAAYDALD+ +A + + HS YSQ K+G +++ + M
Sbjct: 1 TEFADMRAAYDALDDERKAQLERLLGTHSYAYSQGVGGLEEVFTPEARARMIDVE---H 57

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
P+V++HP TGR SL IGRH + + GM +++ LE L+ WACQ PR+ H W GD+V+
Sbjct: 58 PIVRIHPATGRKSLFIGRHVYRVVTGMTDDAQAMLEELLAWACQPPRLFKHIWTVGDIVM 117

Query: 256 WDNR 259
WDNR
Sbjct: 118 WDNR 121

>ref|ZP_00945987.1| TauD / TfdA family dioxygenase [Ralstonia solanacearum UW551]
gb|EAP71487.1| TauD / TfdA family dioxygenase [Ralstonia solanacearum UW551]
Length = 301

Score = 112 bits (280), Expect = 6e-23, Method: Compositional matrix adjust.
Identities = 82/266 (30%), Positives = 124/266 (46%), Gaps = 24/266 (9%)

Query: 12 GATLGATVTGVH-LATLDDAGFAALHAAWLQH-ALLIFPGQHLSNDQQITFAKRFGAIE- 68
GA LGA + G+ A L DA A + AWL H LL+F L+ Q+ F++RFG ++
Sbjct: 26 GAPLGAELGLSDAAGLSADVAVIRRAWLAHDGLLVFRDVMLAPRAQVDFSRFRGPLQV 85

Query: 69 -----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
+I+ +SNV +G P D + WH+D +Y P + G
Sbjct: 86 HVLNQFHLDPHPEILVVSNNVENG-----KPIGLGDAGR-----DWHSLSYKPKPSLG 134

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
++ A +P GG T FA+M AY+ L + ++ R A HS VY +L +
Sbjct: 135 SLLLARELPQAGGDTLFANMVRAYETLPAGLKRIIEGRRVHSYVRYERLRALSARPP 194

Query: 182 YIGYMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVDWACQ 239
D P+V+ HPETG+ +L + G +H + G+ ES LE L + Q
Sbjct: 195 LTQAQRDAVPPVDHPVVRTHPETGKRALFVNEGFTSHIL-GLPEDESTAVLEQLFAHSIQ 253

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
+ H+W D++ WDNR +H A
Sbjct: 254 PDNRYTHRWQPSDMLFWDNRSTIHFA 279

>ref|ZP_01039757.1| alpha-ketoglutarate-dependent taurine dioxygenase [Erythrobacter
sp. NAP1]
gb|EAQ30228.1| alpha-ketoglutarate-dependent taurine dioxygenase [Erythrobacter
sp. NAP1]
Length = 276

Score = 112 bits (280), Expect = 6e-23, Method: Compositional matrix adjust.
Identities = 83/271 (30%), Positives = 128/271 (47%), Gaps = 25/271 (9%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64


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Query: 8      ITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRF 65
              +TP GA +GA + G+ L   LD A  + +  A L+H ++ F GQ HL ND Q  FA+  G
Sbjct: 28     VTPLGAHIGARIDGITLGEHLDPATISLIRQALLEHKVIFFRGQNHLNDNSQYEFAQLLG 87

Query: 66     AIERIGGGDIVAISNVKADGTVRQHS----PAEWDMMKVIVGNMAWHADSTYMPVMAQG 121
              +   A  TV+ H      P +  D+ K          +WH D T++  + +
Sbjct: 88     -----TPTTAHPTVKSHGAKVLPID-SDLGKA----NSWHTDVTVDRIKPA 129

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Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY---SQSKLGHVQQA 178
++ A +P GG T +A AAY+ L + +AL ARH+ VY + S +
Sbjct: 130 SILRAVQLPEYGGSTTWASGVAAAYNGLPDPLKALAENLWARHTNVYDYAATSAERLTEDR 189

Query: 179 GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC 238
+AY T P+V+VHPETG +L++G G+ +S + L D A
Sbjct: 190 TAAYREEFQSTYFETEHPVVRVHPETGERTLVLGHFVKNFVGLSTEQSNQGVFKLLQDHAI 249

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ W AGDV +WDNR H A
Sbjct: 250 KLEYTTRWNWEAGDVAIWDNRATQHYA 276

>ref|ZP_06411827.1| Taurine dioxygenase [Frankia sp. EUN1f]
gb|EFC85375.1| Taurine dioxygenase [Frankia sp. EUN1f]
Length = 315

Score = 112 bits (279), Expect = 7e-23, Method: Compositional matrix adjust.
Identities = 84/271 (30%), Positives = 128/271 (47%), Gaps = 24/271 (8%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
+I P +GA + G+ + TLDD AA+ AAWL + ++ FPGQHL+ + + FA+RFG
Sbjct: 32 FEIVPLSGNIGAEIRGLDVRTLDDREVAARAAWLHYKVVFPGQHLTPAEHLAFARRFG 91

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA---WHADSTYMPVMAQG 121
E G ++ + + + +S A VG ++ WH D T++ G
Sbjct: 92 --EPTGHPVIPGLDGQPEVFEIDYSKARELAAAYGRVGTVSRGLDWHTDVTFFVKRPPLG 149

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
++ A VVP GG T F++ AA+ AL A + + +A H G Q G
Sbjct: 150 SILRAVVPPAGGDTLFSNQEAFAALSPALQEFGLTLTAVHD-----GEAQFKGIL 201

Query: 182 -YIGYGMDDTTATPLR-----PLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEG 232
+G G T +R P+V+ HPETG+ SL + G +H I +D AES+ L
Sbjct: 202 DLVGEGRWEGETFVRLEPAAHPPVVRTHPETGKKSFLVNPFGFTSH-IAELDRAESDALLAF 260

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLH 263
L + + + W G + WDNR H
Sbjct: 261 LYQHSVRPEFTVRYHWQEGTIGFWDNRATQH 291

>gb|ACX54980.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 97

Score = 112 bits (279), Expect = 8e-23, Method: Compositional matrix adjust.
Identities = 59/97 (60%), Positives = 71/97 (73%), Gaps = 2/97 (2%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYMP+ A+GAVF+AE+VPAVG T +ADMRAAY+ALDE TR LV SA HSL YSQ
Sbjct: 1 ADSTYMP LQAKGAVFTA EIVPAVGAATGWADMRAAYEALDEDTRTLVQGLSAYHSLYYSQ 60

Query: 170 SKLGHV--QQAGSAYIGYGMDDTTATPLRPLVKVHPET 204
++ G++ + +Y GYG LRPLVKVHPET
Sbjct: 61 ARAGYMP SKNEKGSYGGYGYHDEPSLRPLVKVHPET 97

>gb|ACG80550.1| TfdA [uncultured bacterium]
Length = 121

Score = 112 bits (279), Expect = 8e-23, Method: Compositional matrix adjust.
Identities = 54/124 (43%), Positives = 76/124 (61%), Gaps = 3/124 (2%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRAAYDALD+ + + HS YSQ K+G +++ + M
Sbjct: 1 TEFGBMRAAYDALDDERKQQLLEGLLGTHSYAYSQKVGGLLEEVFTPEARARMVDVE---H 57

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
P+V+ HP+TGR SL IGRH + + GMD +++ LE L+ WAC+ PR+ H+WA GD+V+
Sbjct: 58 PIVRTHPQTGRKSLFIGRHVYRVGTGMDDDDAQAMLEELLAWACRPPRLFKHKWAVGDIVM 117

Query: 256 WDNR 259
WDNR
Sbjct: 118 WDNR 121

>ref|ZP_01986043.1| alpha-ketoglutarate-dependent taurine dioxygenase [Vibrio harveyi
HY01]
gb|EDL69311.1| alpha-ketoglutarate-dependent taurine dioxygenase [Vibrio harveyi
HY01]
Length = 271

Score = 112 bits (279), Expect = 8e-23, Method: Compositional matrix adjust.
Identities = 74/264 (28%), Positives = 122/264 (46%), Gaps = 15/264 (5%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
++I P +GA + G+ LA + A++ A +++ ++ F GQ +S +QQ+ A+ FG
Sbjct: 2 IEIEPITPHIGARIHGIGLANCNAENLEAIYQALIEYQVIFFDGQTMSPQQLELAQYFG 61

Query: 66 AIE--RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
+E ++V+ V T + ++P E WH D T+ ++GA+
Sbjct: 62 ELEPAHPFFPNVVSPPQVSIETTKGNAPLE-----SYWHTDLTWREQPSKGAI 110

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
A+ VP GG T + M A +DALD + + Q SA HSL + + +
Sbjct: 111 LHAQHVPNTGGDTIWVSMTAVFDALDNTMKTCLRQLSATHSLTAFEVEAEEDIELDWHHR 170

Query: 184 GYGMDTTATP-LRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAP 241
+ P + P++K+HPETG+ +L I I + E ++ L L A Q
Sbjct: 171 LLEVSHQHPVVPVHPVIKHPETGKETLFINEQFTRHINEVGHTGKQLLNELFTIARQPE 230

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRA 265
+W G V +WDNRC H A
Sbjct: 231 YQVRFKWQPGSVAIWDNRCTQHYA 254

>ref|YP_001508977.1| taurine dioxygenase [Frankia sp. EAN1pec]
gb|ABW14071.1| Taurine dioxygenase [Frankia sp. EAN1pec]
Length = 282

Score = 112 bits (279), Expect = 8e-23, Method: Compositional matrix adjust.
Identities = 86/292 (29%), Positives = 127/292 (43%), Gaps = 26/292 (8%)

Query: 1 MAQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
M TTL + P +GAT +GV L LD A+ A L H ++ F Q L+ DQ
Sbjct: 1 MPTTTLDVQPVTPVVGATTSGVDLREPLDLDTVQAIRQALLDHGVIFFDHDELTRDQMRA 60

Query: 60 FAKRFGAI--ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV 117
FG E G+ + P D WH D+TY+
Sbjct: 61 LVAHFGTPIPEPFSAGN-----EPDPLTEGDFQTAKRATSVWHTDTTYVTE 106

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
A +P VGG TC+++M AAY+ L R ++ +A HS+ ++G +
Sbjct: 107 PPSLTALRAISLPPVGGDTCWSNMYAAYNTLSAPLRGMLDGLTAVHSVPVPIQRMGTAGK 166

Query: 178 AGSAY--IGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLV 234

A + + +G + + P+++VHPET R +L + I + AES L L
Sbjct: 167 AHADHSAPAHGFEN---VHPVIRVHPETERKALFVNEAWTTRIVELQPAESAHLALLF 222

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
+ ++WA D+ +WDNR + H A P D+ PRVM LAG RP
Sbjct: 223 EHVKSPDFTMYRWRAPNDLAIWDRNAVQHYAVP-DYDTPRVMQRVVLAGDRP 273

>ref|ZP_02190257.1| Alpha-ketoglutarate-dependent taurine dioxygenase [alpha
proteobacterium BAL199]
gb|EDP62980.1| Alpha-ketoglutarate-dependent taurine dioxygenase [alpha
proteobacterium BAL199]
Length = 279

Score = 111 bits (278), Expect = 9e-23, Method: Compositional matrix adjust.
Identities = 88/285 (30%), Positives = 120/285 (42%), Gaps = 12/285 (4%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
MA TTL + P +GA V GV L+ L DA A+ A L H ++ F Q L+ +Q +
Sbjct: 1 MAATTLTVKPVAGAIGAEVGGVDLSQKLSAMVGAIRKALLDHLVIFFRDQELTPEQLMA 60

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
F+ RFG VA VK + +P + + G + WH+D+ Y V
Sbjct: 61 FSLRFG-----QPVAYPFVKGLDGFPEITPILKREEDRSNFGGL-WHSDTVYQQVPP 111

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
G + A VP GG T FA+ AY+ L E R + +A H ++
Sbjct: 112 MGTILYALEVPPYGGDTEFANQYIAYETLSEPLRNFLGGLTAVHISGKGTAQKTRTDMMK 171

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWAC 238
+ +G D + P V+ HPETGR L + H GM ES LE L
Sbjct: 172 HSSVGLKGDELVS-RHPAVRTHPETGRKVLVNVVAHTTHFEGMTEDESAPILEFLFRHQI 230

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
++ QW G V WDNRC H R+M LAG
Sbjct: 231 KSELTCRFQWTKGAVAFWDRNCTQHNPINDYHGFRMMHRVTLAG 275

>gb|ACX54973.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ACX54975.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ACX54977.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ACX54978.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ACX54991.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ACX54992.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ACX55000.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 98

Score = 111 bits (278), Expect = 1e-22, Method: Compositional matrix adjust.
Identities = 59/98 (60%), Positives = 69/98 (70%), Gaps = 3/98 (3%)

Query: 110 ADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYMP+ A+GAVFSAE+VPA G T +ADMRAAYD LDEATR L+ + A HSL YSQ
Sbjct: 1 ADSTYMPMQAKGAVFSAEIVPAEGAATGWADMRAAYDDLDEATRELLADKVAYHSLYYSQ 60

Query: 170 SKLGHV---QQAGSAYIGYGMDTTATPLRPLVKVHPET 204
+ G++ Q+ G Y YG LRPLVKVHPET

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+ + P+G GA VTG+ L+ LD AL AWL+H +L FP Q +S+D F +
Sbjct: 2 SFNVEPSGOACGARVGTGLDLKLNLDADTVRALRGAWLEHHVLAFPDQISIDDDLERFTQY 61

```

Query: 3      QTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
             QT + + P          GA + GV L    LDDA  A + +A L    ++ F  Q+L + QQ+ F
Sbjct: 8      QTLIDVRPLSGYTGAEIHGVDLREELDDATIAEIRSALLTWKVVFVRDQNLDDHAQQVAFG 67

Query: 62     KRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
             +RFG +          +          +      +E      KV   N   WH D T +      G
Sbjct: 68     RRFGLKLTPAHPHETAPPEGFPEILPIDSRRYSEIIGKRKVTYDN-GWHTDVTALVNPPAG 126

Query: 122    AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
             ++  A++VP  GG T + ++ AAY AL E  R L      ARHS          G
Sbjct: 127    SILRADIVPPYGGDTAWTNLVAAYQALPEPLRTLADSLRARHSFNLQIFDGGE----- 179

```

Query: 182 YIGYGMDDTTATPL---RPLVKVHPETGRPSLLIGRHAHA----IPGMDAAESERFLEGLV 234
 YG + PL P+V+VHPETG +L + A I G+ A +S R LE
 Sbjct: 180 ---YGKRIASNPLVAIHPVVRVHPETGERALFVSPSFTARDNEIIGLSARQSHRVLELFY 236

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283
 + + +W GD+ WDNR H P D RV++ L G
 Sbjct: 237 EQIARPEFTVRFKWNP GDIAFWDNRATAHLG-PSDLGHLD FDRVLYRVLTLEG 287

>ref|ZP_06054723.1| taurine dioxygenase [alpha proteobacterium HIMB114]
 gb|EEY74492.1| taurine dioxygenase [alpha proteobacterium HIMB114]
 Length = 283

Score = 111 bits (277), Expect = 1e-22, Method: Compositional matrix adjust.
 Identities = 81/298 (27%), Positives = 139/298 (46%), Gaps = 39/298 (13%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 ++I +G LGA V G+ L+ L ++ AW ++ +L+F Q+L++ I F+K F
 Sbjct: 1 MEIIKSGLALGAEVKGMDLSKDLSSNEVDQINKAWDENLVLVFKNQNLTDPLIKFSKNF 60

Query: 65 GAIERIGGG-----DIVAISNVKADGTVRQHSPA EWDDMMKVIVGN--MAWHAD 111
 G ++ +I ISNVK +G I+G+ WH+D
 Sbjct: 61 GNL DHPAPNPFGINFSPEYPEINVISNVKKEGKPTG-----ILGDGEATWHSD 108

Query: 112 STYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
 +Y V + + + VP G T FA+M AAY+ + + + + H ++
 Sbjct: 109 MSYQDVPPKAGILYSLEVPKDQGDTHFANMIAAYEDMPDDLKNRIEGKILIHDSAHS-- 166

Query: 172 LGHVQQAGSAYIGYG--MDTTATP--LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAES 226
 AG GY D + TP P+V P TG+ +L IGR HA + G++ +ES
 Sbjct: 167 -----AGQLRKG YEEVSDPSKTPGAKHP IVFKDPNTGKKALFIGRRPHAYVIGLELSES 220

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR 284
 E+ L+ + A Q +W A +++W N +LH+ + +D RVM +++ G
 Sbjct: 221 EKLLDDIWAHATQKKYTWTRQWQANELLMWKNL FVLHKRDAFDPNTRRVMHRTQVTGE 278

>ref|ZP_02196896.1| Probable taurine catabolism dioxygenase [Vibrio sp. AND4]
 gb|EDP58013.1| Probable taurine catabolism dioxygenase [Vibrio sp. AND4]
 Length = 271

Score = 111 bits (277), Expect = 1e-22, Method: Compositional matrix adjust.
 Identities = 79/269 (29%), Positives = 120/269 (44%), Gaps = 25/269 (9%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
 ++I +GA + GV L+T ++ A + H ++ F Q +S DQQ+ AK FG
 Sbjct: 2 IEIEKITPNIGACIHGVDLSTCKTEDLKKVYQALIDHQVVFVDNQRISPDQQLNLAKFFG 61

Query: 66 AIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM 118
 +E R+ V+I T + ++P E WH D T+
 Sbjct: 62 ELEPAHPFFPRVESTPQVSIIE-----TTKGNAPLE-----SYWHTDLTWREN P 105

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
 ++GA+ A+ VP GG T + M + +DALD+A + + SA HSL + V +
 Sbjct: 106 SKGAILHAKHVPDAGGDTIWSMTSVFDALDDAIKMKLRNLSATHSLTAFEDVDEEVIEL 165

Query: 179 GSAYIGYGMDDTTATP-LRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDW 236
 + + P + P+VKVHPETG+ +L I I M AE R L+ L
 Sbjct: 166 DWHHRLREVSHQORPVIHPVVKVHPETGKETLFINEQFTRCINEMRHAEGSRLKELFAV 225

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 A Q +W G + +WDNR H A

Sbjct: 226 ARQPEHQVRFKWQKGLAIWDNRRTTQHYA 254

>ref|YP_002233739.1| putative taurine dioxygenase [Burkholderia cenocepacia J2315]
emb|CAR54979.1| putative taurine dioxygenase [Burkholderia cenocepacia J2315]
Length = 317

Score = 111 bits (277), Expect = 1e-22, Method: Compositional matrix adjust.
Identities = 89/270 (32%), Positives = 126/270 (46%), Gaps = 20/270 (7%)

Query: 2 AQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQIT 59
A LQ+ +GA + V L ATLDDA F A+ AA L+H +L F GQH L + Q
Sbjct: 22 AAVPLQLRQVAGRIGAEIADVRLSATLDDATFDIAQAALLRHKVLFFRGGHLLDDTAQEA 81

Query: 60 FAKRFGAIERIGGGDIVAISNVKA-DGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
FA+RFG D VA V + DG+ + E D + WH D T++
Sbjct: 82 FARRFG-----DTVAHPTVPSVDGSA---ALLELDSAHGARANS--WHTDVTTFVDAY 128

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 178
+ ++ A V+P GG T +A+ AAY L + RAL A H+ Y + HV
Sbjct: 129 PKISILRAVVIPFPGGDTVWANTAAAYAHLPDPLRALADTLWALHTNAYDYAST-HVHAD 187

Query: 179 GSAYIGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD 235
+ Y T+T P+V+VHPETG +L++G + G+ A +S L+ +
Sbjct: 188 DAQLKRYREVFTSTVYETEHPVVRVHPETGERTLVLGHFVQRLKGLSAQDSAHLQLQVFHE 247

Query: 236 WACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
+ W GDV +WDNR H A
Sbjct: 248 HVTRLENTVRWNWREGDVAIWDNRATQHYA 277

>ref|ZP_08205418.1| Taurine dioxygenase [Gordonia neofelifaecis NRRL B-59395]
gb|EGD54686.1| Taurine dioxygenase [Gordonia neofelifaecis NRRL B-59395]
Length = 289

Score = 111 bits (277), Expect = 1e-22, Method: Compositional matrix adjust.
Identities = 90/290 (31%), Positives = 134/290 (46%), Gaps = 25/290 (8%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
+QT L + G +GA V+GV +A+ DDA A + +A + H +LI QHL + + I FA
Sbjct: 10 SQTGLTVELLGPFIGAEVSGVDIASADDARIADIRSALVDHKVLILRNQHLDDAEHIRFA 69

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNM-AWHADSTYMPVMAQ 120
+R GD+ V G V P E + G WH D T+M
Sbjct: 70 RRL-----GDVTFGHPVWDSGDV----PDEVYSLDSTADGFADTWHTDVTFMARPPA 117

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ--- 177
++ ++P+VGG T +AD AAY +L + L + A H + G+ +
Sbjct: 118 ASILRPVILPSVGGDTNWADGEAAYASLSAPLQRLADELVAVHD--GNREFGYLHRHR 174

Query: 178 --AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGL 233
G+ + G + A P+V+VHPE+GR +L + G +H I G+ AES L+
Sbjct: 175 GGEGRWDGERVTELAPVRHPVVRVHPESGRRTLFVNPFGFTSH-IEGVSDAESRGLLDAF 233

Query: 234 VDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPVMMWHSRLAG 283
+ + H+W GDVV+WDNR H A D+ R M L G
Sbjct: 234 YAHLTKPEHIVRHRWRLGDVVLWDNRSTAHYANR-DYTERRRMHRVTLRG 282

>ref|YP_001810606.1| taurine dioxygenase [Burkholderia ambifaria MC40-6]
gb|ACB66390.1| Taurine dioxygenase [Burkholderia ambifaria MC40-6]
Length = 317

Score = 111 bits (277), Expect = 1e-22, Method: Compositional matrix adjust.
Identities = 87/266 (32%), Positives = 125/266 (46%), Gaps = 20/266 (7%)

```
Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
          L++      +GA + GV L+ TLDDA F A+ AA L+H +L F Q HL + Q FA+R
Sbjct: 26  LELRQVAGRIGAEIAGVRLSSTLDDATFDAIQAALLRHKVLFFRNQEHLDDAAQEAFAARR 85

Query: 64  FGAIERIGGGDIVAISNVK-ADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
          FG      D VA V ADG+      E D      +WH D T++ + +
Sbjct: 86  FG-----DTVAHPTVPPADGSAHL---LELDSAHGARAN--SWHTDVTFVDAYPKVS 132

Query: 123  VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
          + A V+P GG T +A+ AY L E RAL A H+ Y + HV +
Sbjct: 133  ILRAVVIPPFGGDTVWANTATAYAHLPEPLRALADTLWALHTNAYDYAST-HVHADDTQL 191

Query: 183  IGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
          Y T++ P+V+VHPETG +L++G I G+ + +S L+ L + +
Sbjct: 192  KRYREVFTSSVYETHPVVRVHPETGERTLVLGHFVQKIKGLSSQDSAHLQLVLEHVTR 251

Query: 240  APRVHAHQWAAGDVVVWDNRCLLHRA 265
          +W GDV +WDNR H A
Sbjct: 252  LENTVRWRWQQGDVAIWDNRATQHYA 277
```

>ref|ZP_05069657.1| alpha-ketoglutarate-dependent taurine dioxygenase [Candidatus
Pelagibacter sp. HTCC7211]
gb|EDZ60656.1| alpha-ketoglutarate-dependent taurine dioxygenase [Candidatus
Pelagibacter sp. HTCC7211]
Length = 277

Score = 111 bits (277), Expect = 1e-22, Method: Compositional matrix adjust.
Identities = 71/293 (24%), Positives = 137/293 (46%), Gaps = 29/293 (9%)

```
Query: 6   LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
          + +      LGA ++G+ L D F ++ L+H ++ F Q ++N+QQI A +FG
Sbjct: 1   MNVKLLSGALGAEISGIDLTDTSQDNFKKINDLLEHKVIFFRDQPITNEQQIALAAKFG 60

Query: 66  AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA-----WHADSTYMPVM 118
          +E      ++ G ++ H +++++I G WH+D +Y
Sbjct: 61  PLE-----THAYVKG-LKDHP-----EIVRIIKGKEKNQWGENWHS DVSYN SKP 104

Query: 119  AQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ-Q 177
          + + + +P VGG TCF++M A++ LD ++ + + A HS + ++ + + +
Sbjct: 105  TKAVILKSVKIPVGGDTCF SNMELAWETLDPKIQSKIINKKAVHSSLGAEFFIDNYKYM 164

Query: 178  AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDW 236
          G+ Y + + P+V+ HPETG+ L + + I G++ ES++ L+ + +
Sbjct: 165  EGNEKRNYD---SYSNEHPIVRTHPETGKKILYVNWYTKQIIGLEKEESDQVLKEIFEH 221

Query: 237  ACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEG 289
          + W V +WDNR ++H A DF R + + R+ R EG
Sbjct: 222  QARLDLTCRFSWETDTVAIWDNRSVIHYAIA-DFPGRGLGYERIMDRIAIEG 273
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>ref|NP_885378.1| alpha-ketoglutarate-dependent taurine dioxygenase [Bordetella
parapertussis 12822]
ref|NP_890196.1| alpha-ketoglutarate-dependent taurine dioxygenase [Bordetella
bronchiseptica RB50]
emb|CAE38494.1| alpha-ketoglutarate-dependent taurine dioxygenase [Bordetella
parapertussis]
emb|CAE35634.1| alpha-ketoglutarate-dependent taurine dioxygenase [Bordetella
bronchiseptica RB50]
Length = 282

Score = 111 bits (277), Expect = 1e-22, Method: Compositional matrix adjust.
Identities = 82/274 (29%), Positives = 119/274 (43%), Gaps = 28/274 (10%)

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Query: 3  QTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
          QT L++ P   + GA + GV L+  L      A+  A L H ++ F  Q L+ +Q   F
Sbjct: 4  QTALEVRPLTGSCGAELFGVDLSQALSADTVKAIQALLDHNVIFFREQTLTPEQHRAFT 63

Query: 62  KRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVI-----VGNMAWHADST 113
          ++FG +      +V      +G      + D+M VI      +G+  WH+D +
Sbjct: 64  RQFGEV-----VVPVYTHVEG-----YPDIMPVIKEPNDRYNIGD-TWHSMS 106

Query: 114  YMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
          YM      G+V      +P  GG T FA+M  AYD L EA R ++  R A HS  Y  S++
Sbjct: 107  YMQEPLPLGSVLYGRDIPEYGGDTLAFANMYLAYDLLPEALRQMIDGRQAYHSDRYLTSRIS 166

Query: 174  HVQQAGSAYIGYGMDDTTAT-PLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLE 231
          S   +   D      L P+V+ H ETGR  L +      I G+  ES   L
Sbjct: 167  ERNAGRSTRLKADADAKENLALHPMVRTHEETGRKCLYVNFPTWQIEGLSREESLPLLH 226

Query: 232  GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          L   A +      +W  G +  WDNRC +H A
Sbjct: 227  QLYAHAARPEFACRFRWRKGSALAFWDNRCTMHYA 260

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>ref|ZP_01894276.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Marinobacter algicola DG893]
gb|EDM47645.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Marinobacter algicola DG893]
Length = 311

Score = 110 bits (275), Expect = 2e-22, Method: Compositional matrix adjust.
Identities = 85/288 (29%), Positives = 136/288 (47%), Gaps = 14/288 (4%)

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Query: 6  LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          +I P   + GA + G+ LA  + DA FAA+  A+ ++ ++ F  Q +      + F  R+
Sbjct: 10  FRINPLTESFGAEILGLDLAKPISDATFAAIQEAQKYHVICFRDQVMDEKAHLDFTLRW 69

Query: 65  GAIERIGGGD--IVAISNVKADGTVRQHSPAEWDDMMKVIVG-NMAWHADSTYMPVMAQG 121
          G +E   D   A +      T R+      DD   +   N  WH DS+Y  V +
Sbjct: 70  GELEVFPEEDKTTTAKTFYNVANTSREGEHLSEDDPRVLFQKVNARWHTDSSYRYVPSFA 129

Query: 122  AV-FSAEVP--AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
          +V +S E++P  A GG T F++M AAYDAL +A +      H   + +      + A
Sbjct: 130  SVMYSTEILPDEARGGETEFSNMLAAYDALSDADKRRFEPLHVMVHYEYFGR---RLYP 185

Query: 179  GSAYIGYGMDDTTATPLRPLVKVHPE-TGRPSLLIGRHA-HAIPGMDAAESERFLEGLVDW 236
          +   D      PLV+VHP+  + SL   +A + I GM  E +      + L ++
Sbjct: 186  LPPITPFERDAVPPVSHPLVRVHPDRDNQRSLSFFTVNAGNEISGMSLEEGQALHKWLDEY 245

Query: 237  ACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG 283
          A +      +++H+W  D+V+WDNR LLHRA  +D  K  R      + +AG
Sbjct: 246  ASKPEFIYSHRCENDLVMWDRVLLHRATHYDMAKYRRAFRRTTVAG 293

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>ref|YP_001133737.1| taurine catabolism dioxxygenase TauD/TfdA [Mycobacterium gilvum
PYR-GCK]
gb|ABP44949.1| Taurine catabolism dioxxygenase TauD/TfdA [Mycobacterium gilvum
PYR-GCK]
Length = 281

Score = 110 bits (275), Expect = 2e-22, Method: Compositional matrix adjust.
Identities = 91/288 (31%), Positives = 135/288 (46%), Gaps = 21/288 (7%)

Query:	6	LQITPTGATLGATVTGVHLA-----TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT	59
		+++ P LGA V G+ L T DD + +H +L+FP +S++QQI	
Sbjct:	1	MKVIPLSPALGAEVRGIDLTRPLSARTRDD-----IVGLLTEHQMLVFPDMSMSSEQQIA	55
Query:	60	FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADS	112
		++ FG +E +I +SNV DG + + WH+D	
Sbjct:	56	MSRNFGELEPHPMTTNTSPYPEITVVSNVTTDGKPLGYTPPFQ-----LWHSDL	105
Query:	113	TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL	172
		Y+ A+ +F AE VP G T FA+M AYD L E+ +A + R+A SL S K	
Sbjct:	106	CYLERPAKMTLFYAESVPEQHGDWTFANMFRAVDTLPEHLKAALDGRNAVFSLDGSLVK-	164
Query:	173	GHVQQAGSAYIGYGMDTTATPLRPLV-----KVHPETGRPSLLIG-RHAHAIPGMDAAES	226
		IG+ ++ A +P V +VHPE+ R S+ + H ++ G +S	
Sbjct:	165	-----RCRKIGFDLNIAADDFKPTVSHPAIRVHPESLRRSIFVNWAHTDSVEGYSPSEQS	218

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEP 267
E LE + ++ H++ AG++V+WDN ++H P
Sbjct: 219 EALLEQVFAHCLNEDFIYRHRYPATAGELVIWDNASVIHTNSP 259

>ref|ZP_02909524.1| Taurine catabolism dioxygenase TauD/TfdA [Burkholderia ambifaria
MEX-5]
gb|EDT39336.1| Taurine catabolism dioxygenase TauD/TfdA [Burkholderia ambifaria
MEX-5]
Length = 281

Score = 110 bits (274), Expect = 3e-22, Method: Compositional matrix adjust.
Identities = 82/277 (29%), Positives = 125/277 (45%), Gaps = 33/277 (11%)

Query: 6 LQITPTGATLGATVTGVHLA-----TLDD-AGFAALHAAWLQHALLIFPGQHLSNDQQI 58
+++ LGA +TG+ + T DD G A +H LL+FPGQ LS +QQ+
Sbjct: 1 MKLRKLSPALGAEITGIDFSQPQSPQTRDDIVGLLA-----EHQLLVFPGQRLSCEQQV 54

Query: 59 TFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHAD 111
+ FGA+E +I +SNV DG + ++ WH+D
Sbjct: 55 AACRDFGALPHPMPTTNTSAFPEITVVSNTVVDGKPVGYPTPPFE-----LWHS 104

Query: 112 STYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
Y+ A+ F AE VP G T FA+M AY+AL + + R+A SL S
Sbjct: 105 LCYLEHPAKMTFFYAESVPEAHGDTWFANMFDAEALPDDLKTAIEGRNAIFSL--DGSL 162

Query: 172 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFL 230
+ ++ G D T P V+ HPET + S+ + H I G ES+ L
Sbjct: 163 VKRCRKKGFDLNI AEEDFKPTVSHPAVRAHPETRKRSIFVNWAHTDRIEGYSPEESDDIL 222

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEP 267
+ + ++ H++AA D+V+WDN L+H P
Sbjct: 223 DRIFAHCTNEAFIYRHYAAADLVIWDNASLIHTNSP 259

>ref|YP_002799309.1| TauD/TfdA family taurine catabolism dioxygenase [Azotobacter
vinelandii DJ]
gb|ACO78334.1| Taurine catabolism dioxygenase, TauD/TfdA family [Azotobacter
vinelandii DJ]
Length = 338

Score = 110 bits (274), Expect = 3e-22, Method: Compositional matrix adjust.
Identities = 95/305 (31%), Positives = 138/305 (45%), Gaps = 32/305 (10%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFA-ALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L +TPTG LGA VTGV LA A A AL AW +H +L+FPGQ L + + A F
Sbjct: 27 LSVTPTGKALGAVVTGVDLAQPLSADIADALRRRAWREHLVLLFPGQFLEPETLLRAASTF 86

Query: 65 GAIE-----RIGG-----GDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWH 109
G + R G ++ I+N+ DGT P +D + + + WH
Sbjct: 87 GQPQEGANRLYIRAAGIAQEERFPALLPITNLGPDGT-----PVRENDGLGSL--EVVWH 139

Query: 110 ADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
+D++Y+ G + A PA G T FA+ AY+ L E + + R A+H S+
Sbjct: 140 SDNSYIEAPPICGLLYALEAPADSGFTSFANQFLAYERLSETLKRDI EGRWAKHD--ASR 197

Query: 170 SKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGHR----AHAIPGMDAAE 225
+ G ++ + P PLV P + R +L +GR + I G+ E
Sbjct: 198 NSAGMLRPG--LRTPSRPEEVPGPFPFHLVIRQPGSARRALFLGRRRIFPSQYIEGLPGVE 255

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR- 284
SE L+ L A H+W GDV++WDN LH P D RVM ++ G+

Sbjct: 256 SEALLDALWAAATHPDITWTHRWTGPDVLLWDNCHTLHHRTPV DATRRRV MVRTQFQGQT 315

Query: 285 PETEG 289

P +G

Sbjct: 316 PRADG 320

>ref|YP_004076394.1| taurine catabolism dioxygenase [Mycobacterium sp. Spyr1]
gb|ADT98559.1| Probable taurine catabolism dioxygenase [Mycobacterium sp. Spyr1]
Length = 281

Score = 110 bits (274), Expect = 3e-22, Method: Compositional matrix adjust.
Identities = 91/287 (31%), Positives = 133/287 (46%), Gaps = 19/287 (6%)

Query: 4 TTLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
+ L I ++GA V GV L D++ AA+ A + +L+FP HL + Q+ F+
Sbjct: 2 SLLTINKLTPSVGAEVLGVDPERLASDESLGAAVLDALESNGVLVFPDLHLDPEAQVAFS 61

Query: 62 KRFGAIERIGGG--DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS---TYMP 116
+R GA++ G + I V D + +++ A + + WH D T
Sbjct: 62 RRLGAVDHSADGHHPVAGIYPVTLDKS--KNASAA Y-----LRATFDWHIDGCTPTGDE 113

Query: 117 VMAQGAVFSAE VVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ V SA V GG T FA+ AAY+A + + HSL SQS+ V
Sbjct: 114 CPQRATVLSAVQVADRGGETEFANSYAA YEAFSDEEKERYAALRVVHSL EASQSR---VN 170

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW 236
S + T PLV H +GR SL++G AH + GMD E L L+D
Sbjct: 171 PDPSPEELARWRSRP THEHPLVWTH-RSGR KSLVLGASAHYVVGMDYDEGRALLAELLDR 229

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
A Q V++H W+ GD V+WDN +LHRA P+D R M + + G
Sbjct: 230 ATQPDLVYSHSWSVGDTVIWDNNGVLHRAAPYDPDSQREMLRTTVLG 276

>ref|ZP_07387052.1| Taurine dioxygenase [Paenibacillus curdlanolyticus YK9]
gb|EFM11267.1| Taurine dioxygenase [Paenibacillus curdlanolyticus YK9]
Length = 315

Score = 110 bits (274), Expect = 3e-22, Method: Compositional matrix adjust.
Identities = 78/267 (29%), Positives = 117/267 (43%), Gaps = 24/267 (8%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFA-ALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T + P G +GA + GV L+ A LH A+L++ +L F Q ++++QQ+ FAK
Sbjct: 46 TLFTVKPLGPIIGAIEGV DLSQPVGAELKQELHRAFLEYKVLFFRNQDITSEQQLAF AK 105

Query: 63 RFGAIER---IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMA 119
+G +E+ + G ++ D KV WH D T+ A
Sbjct: 106 LWGELEKHPFLPQGSAAEVTRFAKDE-----KVTGMENIWHTDVTVRLNPA 151

Query: 120 QGAVFSAE VVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
G+V VP GG T ++DM AAYD L EA + + +A H S + +Q
Sbjct: 152 LGSVLRLTEVPFPGGDTLWSDMAAAYDNLPEAVKERIDGLTAIHDFTPSFGRALSPEQLA 211

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVDWAC 238
+ + P+V++HPETGR +L + G I G++ ESE L+ L D A
Sbjct: 212 VKQVEFPAAE----HPIVRIHPETGRKTLFVNGAFTIRIVGLEPQESEELLOQLFDQAK 266

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
W + WDN H A
Sbjct: 267 TPEYQVRFHWEKNSIAFWDN RATQHYA 293

>ref|ZP_02450971.1| dioxygenase [Burkholderia pseudomallei 91]
ref|ZP_02474645.1| dioxygenase [Burkholderia pseudomallei B7210]
ref|ZP_02485135.1| dioxygenase [Burkholderia pseudomallei 7894]
Length = 286

Score = 110 bits (274), Expect = 3e-22, Method: Compositional matrix adjust.
Identities = 96/293 (32%), Positives = 135/293 (46%), Gaps = 28/293 (9%)

Query: 13 ATL GATV TGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG---AIE 68
A LGA + G+ A LD A+ AAWL+ LL+F GQ L + + F +RFG
Sbjct: 3 AALGARIDGIDARAELDADTVRAIRAAWLRFGLLVFRGQALDPPRLVAFTRRFGEPPVYT 62

Query: 69 RI-----GGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
R G +++ +SNV DG + + WH D Y+ G +
Sbjct: 63 RACNACDGQPEVLVLSNVVKDGKP-----IGAALSGRYWHTDGHYLACPPAGTL 111

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
+PAVGG T F +M AAY AL R + R+ V Q+ H Q +
Sbjct: 112 LFGAEIPAVGGDTHFVNMTAAYRALPAWVRTQIDGRTFVMDRV--QTLPHYPQRPAPPP 169

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLVDWACQAPR 242
P +P+V+ HPETG +L IG I GM+ S+ + L A R
Sbjct: 170 DQKQAWPDMP-QPVVRTHPETGENALYIGGVVPWRIVGMEQGLSDALMAHLHAIAFDEAR 228

Query: 243 V-HAHQWAAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RPE-TEGAA 291
+ H+W AGD+++WDNRCL HRA +D + R M+ + +AG RP GAA
Sbjct: 229 FG YRHRWRAGDLLMWDNRCLAHRATDYDMVRHRRTMYRTTIAGDRPRYVRGAA 281

>emb|CAY27315.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 121

Score = 110 bits (274), Expect = 3e-22, Method: Compositional matrix adjust.
Identities = 55/124 (44%), Positives = 73/124 (58%), Gaps = 3/124 (2%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DMR AYDALD+ +A + HS YSQ K+G +++ + M
Sbjct: 1 TEFPPDMRVAYDALDDQRKAQLEGLLGTHSYAYSQGVGGLEEVFTPEARARMVDVE---H 57

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDVVV 255
PLV+ HP TGR SL IGRH + + GM +++ LE L+ WACQ PRV H+W GD+V+
Sbjct: 58 PLVRTHPATGRKSLFGRHVYRVVTGMTDDAQAMLEELLAWACQPPRVFKHRWTVGDIVM 117

Query: 256 WDNR 259
WDNR
Sbjct: 118 WDNR 121

>gb|AAT51196.1| PA0194 [synthetic construct]
Length = 300

Score = 109 bits (273), Expect = 3e-22, Method: Compositional matrix adjust.
Identities = 88/276 (31%), Positives = 131/276 (47%), Gaps = 36/276 (13%)

Query: 6 LQITPTGATLGATV TGVH-LATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ITP A LGA V G+ L AL A +H +L+F QHL ++Q + FA F
Sbjct: 18 FRITPLEAPLGA EVRGLDARRPLAPEQVLALKQALREHHILVFRQQHLDDEQYLR FATLF 77

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVI-----VGNMAW--HADSTYMP 116
G++ + DI +S+ DG V D++KV +GN A H D + P
Sbjct: 78 GSVFQ-PPADIPVLSS-GGDGV-----PDIVKVANTGDGELGNFALPAHIDHQWTP 127

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176

V + G+ A VP+ G T F ++ AY++LDEATR R + + + ++
Sbjct: 128 VPSSGSFLYALEVPSSGSETRFTNLARAYESLDEATR-----REIDGLRLINYNPFIRLR 182

Query: 177 QAGSAYIGYGMDDTTATP-----LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESE 227
+ G G G T TP PLV+ HPE+GR L + H IPG D A +
Sbjct: 183 EGG---YGGGFATYRTPDIGPIQGSEHPLVRTHPESGRRVLFLSAHTEVEIPGYDPARGQ 239

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH 263
+ L + + ++H W+ GD+V WDN+ +LH
Sbjct: 240 ALIGRLREHLARPELSYSHAWSVGDIVVWDNQAVLH 275

>gb|ADI19985.1| probable taurine catabolism dioxygenase [uncultured gamma
proteobacterium EB000_65A11]
Length = 277

Score = 109 bits (273), Expect = 4e-22, Method: Compositional matrix adjust.
Identities = 87/284 (30%), Positives = 134/284 (47%), Gaps = 22/284 (7%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGD 74
+GA +TGV + L D + + +A+ ++ L+ F QHL+ + I FAKR+G I +
Sbjct: 9 VGAEITGVDIRHLSNDNEYEGIKSAFTENGLIFFRDQHLTEEDHIAFAKRWGEI-----N 62

Query: 75 IVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG 134
I KA+ + + ++ + +G WH D +Y A G++ A+ +P GG
Sbjct: 63 INRF--FKANDKYPEIAMVTKEEHQEONIGG-GWHTDHSYDQEPALGSILVAKELPESGG 119

Query: 135 RTCFADMRAAYDALDEATRALVHQRSARHSLVYS-QSKLGHVQQAGS-AYIGY--GMDTT 190
T F M AYD+L + + + + A HS Y+ +K G Q G+ IG D
Sbjct: 120 DTWFTSMYEAYDSLSDGLKETLERMRVHSAHYAFGTKSGDKQSGGTGGRIGNADAADAL 179

Query: 191 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER--FLEGLVDWACQAPRVHAHQW 248
P+ P+V HP +GR +L + R A + + +E + LE L D A + V QW
Sbjct: 180 ENPVHPVVITHPMSGRKALYVNR-AFTLHFENWSEEDSVPLLEYLYDIAIRDEFVTKFQW 238

Query: 249 AAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL 292
G V WDNR H A+ D++ R H R EG AL
Sbjct: 239 RPGSVAFWDRATWHYAQN-DYQGQRREMH-----RITLEGCAL 276

>ref|YP_004015333.1| taurine catabolism dioxygenase TauD/TfdA [Frankia sp. Eu11c]
gb|ADP79463.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. Eu11c]
Length = 281

Score = 109 bits (273), Expect = 4e-22, Method: Compositional matrix adjust.
Identities = 91/292 (31%), Positives = 131/292 (44%), Gaps = 32/292 (10%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWL--QHALLIFPGQHLSNDQQITFAK 62
TL P AT+GA V GV L AA + +L+FG L + Q+ F +
Sbjct: 4 TLTCEPLAATVGAEVRGVDADQLAHDDAAAAAVALDALERFGVLVFRGLDLGPENQVAFCR 63

Query: 63 RFGAIE-RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQ- 120
R G I+ G + I V D + +++ A++ + G AWH D MP+ +
Sbjct: 64 RLGEIDFEYGHHPVRGIYRVTLDKS--KNTSADY-----LKGTFAWHMDGC-MPLHGEP 114

Query: 121 ---GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA-----LVHQRSARHSLVYSQSK 171
+ SA+ V A GG T FA A Y+AL +A + +VH A VY
Sbjct: 115 PQKATILSAKQVAATGGETEFASTYAGYEALSDADKERFAALRVVHTFEASQRAVYPDPT 174

Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE 231
+++ T PLV H TGR SL++G HA I GMD ES+ L
Sbjct: 175 PDQLER-----WRRRPTSTHPLVWTH-RTGRRSLVVGASHIVGMDVEESDALLR 224

Query: 232 GLVDWACQAPRVHAHQWAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L+D A + H W+ GD V+WDN ++HRA P+D R + + + G
Sbjct: 225 RLIDHTTAAGLTyrHTWSVGDTVIWDNTGVVHRASPYDPNSSRELLRTTVFG 276

>ref|ZP_02493282.1| dioxygenase [Burkholderia pseudomallei NCTC 13177]
Length = 286

Score = 109 bits (273), Expect = 4e-22, Method: Compositional matrix adjust.
Identities = 96/293 (32%), Positives = 135/293 (46%), Gaps = 28/293 (9%)

Query: 13 ATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG---AIE 68
A LGA + G+ A LD A+ AAWL+ LL+F GQ L + + F +RFG
Sbjct: 3 AALGARIDGIDARAELDADTVRAIRAARLRFGLLVFRGQALDPPRLVAFTRRFGEPPVYT 62

Query: 69 RI-----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
R G +++ +SNV DG + + WH D Y+ G +
Sbjct: 63 RACNACDQGPEVLVLSNVVKDGRP-----IGAALSGRYWHTDGHYLACPPAGTL 111

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
+PAVGG T F +M AAY AL R + R+ V Q+ H Q +
Sbjct: 112 LFGAEIPAVGGDTHFVNMTAAYRALPAWVRTQIDGRTFVMDRV--QTLPHYPQRPAPPP 169

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLVDWACQAPR 242
P +P+V+ HPETG +L IG I GM+ S+ + L A R
Sbjct: 170 DQKQAWPDMP-QPVVRTHPETGENALYIGGVVPWRIVGMEQGLSDALMAHLHAIAFDEAR 228

Query: 243 V-HAHQWAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RPE-TEGAA 291
+ H+W AGD+++WDNRCL HRA +D + R M+ + +AG RP GAA
Sbjct: 229 FGyrHRWRAGDLLMWDNRCLAHRAATDYMVRHRTMYRTTIAGDRPRYVRGAA 281

>ref|ZP_06850473.1| taurine dioxygenase [Mycobacterium parascrofulaceum ATCC BAA-614]
gb|EFG76168.1| taurine dioxygenase [Mycobacterium parascrofulaceum ATCC BAA-614]
Length = 302

Score = 109 bits (273), Expect = 4e-22, Method: Compositional matrix adjust.
Identities = 87/284 (30%), Positives = 126/284 (44%), Gaps = 18/284 (6%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
+ +T G+ +GA V GV L LD A + A L H ++ F QH L + QQ+ FA R
Sbjct: 7 ITVTKLGSIRGARVDGVRLLGGDLPAAVDKIRRALLAHKVIFFRHQHLLDDQQQLAFAGR 66

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
G +++A N + +E+ + WH D T++ ++
Sbjct: 67 LGTPVGHPAAELLAAKNAPVITPIN----SEYGKANR-----WHTDVTFFVANYPAASI 115

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
A +P GG T + + AAY+AL +A + LV A HS Y V+ A
Sbjct: 116 LRAVTLPRYGGTTLWTNTAAAYEALPDALKGLVENLWALHSNRYDYVTEESVRAMSDAQR 175

Query: 184 GYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
+ R P+V+VHPETG +LL+G G+D+ ES LE L
Sbjct: 176 TFRQVFKEKPDFRTEHPVVRVHPETGERALLLGDFVRGVGLDSYESSVLELLQRRITVP 235

Query: 241 PRVHAHQWAGDVVVWDNRCLLHRA-EPWDFKLPRVMWHSRLAG 283
WA GDV +WDNR HRA + +D + PR+M L G
Sbjct: 236 ENTIRWSWAPGDVAIWDNRATQHRAIDYDDQ-PRLMHRVTLMG 278

>ref|YP_001613684.1| hypothetical protein sce3045 [Sorangium cellulosum 'So ce 56']
emb|CAN93204.1| tauD2 [Sorangium cellulosum 'So ce 56']
Length = 319

Score = 109 bits (273), Expect = 4e-22, Method: Compositional matrix adjust.
Identities = 82/276 (29%), Positives = 118/276 (42%), Gaps = 29/276 (10%)

```
Query: 1  MAQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQI 58
      +   L+I P      +GA V GV L A LD A  + +  AWL+H ++ F GQH L +  Q
Sbjct: 7  QSNNVLEIVPVAGRIGAEVRGVRLRADLDAATVSEIRKAWLRHKVIFFRGQHLLDDASQE 66

Query: 59  TFAKRFGA-----IERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHAD 111
      FGA      + + G D +  + +  G      +WH D
Sbjct: 67  ALTTLFGAKPVAHPTVPVVGTDYIHELDSREGGRAN-----SWHTD 108

Query: 112 STYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
      T++   + ++  A V+PA GG T +A+  AAY L A RAL   A HS Y
Sbjct: 109 VTFVDAYPRASILRALVIPAYGGDTVWANTVAAYQDLPPALRALADTLWAVHSNEYDYQA 168

Query: 172 LGHVQQAGSA--YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF 229
      A      Y      T      P+V+VHPETG  SL++G  + G+ + +S
Sbjct: 169 RKPNSADDVRRYQEVFTSTVYETEHPPVVRVHPETGERSLVLGHFVKRLLGVSSHDSAHL 228

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      + L +  +      +WAAGDV +WDNR  H A
Sbjct: 229 FQVLQEHVTRLENTVWRWAAGDVAIWDNRATQHYA 264
```

>ref|NP_880388.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bordetella pertussis Tohama I]
emb|CAE41952.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase [Bordetella pertussis Tohama I]
Length = 289

Score = 109 bits (273), Expect = 4e-22, Method: Compositional matrix adjust.
Identities = 85/301 (28%), Positives = 139/301 (46%), Gaps = 32/301 (10%)

```
Query: 5  TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
      T+ ITP  + A++ G+ +  + D  A+  A  Q+ +++  GQ L +D Q  F +R
Sbjct: 2  TITITPIQGEIAASIGGIDVRRGVTDDQVQAIERALDQYIVVVLRGQPLDDDLQQDFIQR 61

Query: 64  FGAIERIGGGDIVAISNVKADGTVRQHSPA EW-----DMMKV-IVGNMAW 108
      FG      + + +K  + R H P  D      MK+ ++ N  W
Sbjct: 62  FGPA-----IVTNTIKELTSRRSHRPHLLDITTVDEHGEPLKDRSFMKLYMLANQLW 113

Query: 109 HADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
      H+D +++  +  S  ++P+  T  FADMRAA+DAL  + +  A HS+ +S
Sbjct: 114 HSDGSHIQPPTRLTALSTRMLPSPDPDTEFADMRAAWDALPADQQEQQLLDLQAEHSIAHS 173

Query: 169 QSKLG-HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
      ++ LG  V Q  +  ++      LV+ +P TGR SL +  HA  I G  +
Sbjct: 174 RTLLGMEVDQ---FSDDSLNRRPPVQHSLSVRTNPRTGRRSLYLSGHASHIIGWPVEQGR 229

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPET 287
      L+ L + A Q  V+AH W  D+V+W+N  +HRA P+  PR++  R +G  E
Sbjct: 230 ALLQQLTEHATQRQFVYAHAWQMDDLVMWNNAASMRALPYTGTEPRLL---RWSGVTEL 286

Query: 288 E 288
      E
Sbjct: 287 E 287
```

>gb|ADC34004.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 109 bits (273), Expect = 4e-22, Method: Compositional matrix adjust.

Identities = 71/213 (33%), Positives = 105/213 (49%), Gaps = 25/213 (11%)

```
Query: 56 QQITFAKRFGAIER--IGGGDIVA-----ISNVKADGTVRQHSPA EWDDMMKVIVGNMAW 108
          QQI FA++FG +ER + V ++N+ DG V + W
Sbjct: 1 QQIAFAEQFGTTLERHVVSNRGTVNPLVHIVTNLGPDKGKPSGK-----VASTQW 48

Query: 109 HADSTYMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
          H+D ++ P + + A V+P GG TCFADM AAY+AL EA +A + + HS S
Sbjct: 49 HSDKSFRPQPSLATILHALVMPPEGGETCFADMIAAYEALPEAEKAELE RVRVHWSWGLS 108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER 228
          Q+++G + I D + PLV+ PETGR +L +G A + G
Sbjct: 109 QARVG--IKVPPEEIADAPDMS---HPLVRTIPETGRKALFMGERAVYLEGQPPEEVGRA 162

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
          LE L +A Q V+ H+W GD+++WDNRC+
Sbjct: 163 RLEKLTAYAVQERFVYRHKWTLGDLLMWDNRCV 195
```

>gb|ADC34044.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 109 bits (272), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 73/213 (34%), Positives = 104/213 (48%), Gaps = 25/213 (11%)

```
Query: 56 QQITFAKRFGAIER---IGGGDIVA-----ISNVKADGTVRQHSPA EWDDMMKVIVGNMAW 108
          QQI FA++FG +ER + G + +SN+ ADG V + W
Sbjct: 1 QQIAFAEQFGTTLERHMAMNRGTVHPLVHIVSNLADGKPSGQ-----VASTLW 48

Query: 109 HADSTYMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
          H+D ++ P + + A V+P GG TCFADM AAY+AL +A +A + HS S
Sbjct: 49 HSDKSFRPQPSLATILHALVMPDGGGETCFADMIAAYEALPDAEKAELDGV RVVHSWEIS 108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER 228
          +++ AGS + PLV+ PETGR +L +G HA G
Sbjct: 109 RAR-----AGSKATPEEIADAPPMTHTPLVRRIPETGRKALFMGEHAS YFEGQPPEEVGRV 162

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
          LE LV A Q V+ H+W GD+++WDNRC+
Sbjct: 163 RLEKLVAHAVQERFVYRHKWTMGDLLMWDNRCV 195
```

>ref|NP_763286.1| putative dioxygenase [Vibrio vulnificus CMCP6]
gb|AA008276.1| Probable dioxygenase [Vibrio vulnificus CMCP6]
Length = 288

Score = 109 bits (272), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 76/275 (27%), Positives = 125/275 (45%), Gaps = 27/275 (9%)

```
Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
          + + T++ITP + GA V V L+ +++ F AL+ A+L + +L F Q L+ +Q +
Sbjct: 4 IERETMKITPLATSFGALVEDVQLSAINERQFEALYQAF LHYKVLFFRDQLLTAEQHLAL 63

Query: 61 AKRFGAIERI-----GGGDIV AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS 112
          +RFG +E I +V I R+ P G WH D
Sbjct: 64 GQRFGELEPIHPFFPHLADAPQVVVIE-----TREGLPP-----GESYWHTDL 106

Query: 113 TYMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-VYSQSK 171
          T+ ++ A+ A+ P GG T + DM A + +LD++ + + A H+L + S+
Sbjct: 107 TWKARPSKCALLHAQHCPPSGGDTIWTMEAVWRS LDDSLKQQLRPLYATHALHAFENS R 166

Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL 230
          + + G +Y+ P+V H ETG+ +L I I G++ A+S+ L
```

Sbjct: 167 YDNKDEGESYVVKKSREFPAVHHFVVAQHLETGQETLYINEQFTRCIDGLEKAQSQALL 226

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

E L A +A QW A + +WDNR H A

Sbjct: 227 EMLFAMAREAKFQVRFQWQANSLAIWDNRATQHFA 261

>ref|ZP_07902029.1| hypothetical protein PVOR_27050 [Paenibacillus vortex V453]
gb|EFU38970.1| hypothetical protein PVOR_27050 [Paenibacillus vortex V453]
Length = 325

Score = 109 bits (272), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 83/267 (31%), Positives = 121/267 (45%), Gaps = 20/267 (7%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAK 62

TL++ P G +GA V G+ L LD A ++ AA L+H +L F Q HL ++ Q FA

Sbjct: 11 TLEVRPIGGRVGAIEVKGITLGGDLQAAVQSIRAALLKHKVLFRRNQQLDDEGQEVFAD 70

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMA--WHADSTYMPVMAQ 120

G A TV+ + + + G A WH D T++

Sbjct: 71 LLG-----EPFAHPTVKTKESRYILEIDSHHGGGRANAWHTDITFIDAYPS 116

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS--KLGHVQQA 178

+V + VVP+ GG T +++ AAYD+L + + L + A H+ +Y + + + +

Sbjct: 117 ISVLRSVVVPSSGGDTVWSNTAAAYDSLPELKEKELWAVHTNLYDYAARRPEASEDS 176

Query: 179 GSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC 238

Y T P+V+VHPETG SLL+G + G+ AAES R E

Sbjct: 177 VKEYQRTFASTVYETEHPVVRVHPETGEKSLLLGSFVKRLLGVSAAESSRLYELFQGHIT 236

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265

WAAGDV +WDNR H A

Sbjct: 237 SLENTVRWHWAAGDVAIWDNRSTQHIA 263

>ref|ZP_02501489.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei
112]
Length = 286

Score = 109 bits (272), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 96/293 (32%), Positives = 135/293 (46%), Gaps = 28/293 (9%)

Query: 13 ATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG--AIE 68

A LGA + G+ A LD A+ AAWL+ LL+F GQ L + + F +RFG

Sbjct: 3 AALGARIDGIDARAELDADTVRAIRAAWLRFGLLVFRGQALDPPRLVAFTRRFGEPPVYT 62

Query: 69 RI----GGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAV 123

R G +++ +SNV DG + + WH D Y+ G +

Sbjct: 63 RACNACDGQPEVLVLSNVVKDGKP-----IGAALSGRYWHTDGHYLACPPAGTL 111

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183

+PAVGG T F +M AAY AL R + R+ V Q+ H Q +

Sbjct: 112 LFGAEIPAVGGDTHFVNMAAAYRALPAWVRTQIDGRTFVMDRV--QTLFPHYQP RPAPPP 169

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLVDWACQAPR 242

P +P+V+ HPETG +L IG I GM+ S+ + L A R

Sbjct: 170 DQKQAWPDMP-QPVVRTHPETGENALYIGGVVPWRIVGMEQRLSDALMAHLHAIAFDEAR 228

Query: 243 V-HAQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RPE-TEGAA 291

+ H+W AGD+++WDNRCL HRA +D + R M+ + +AG RP GAA

Sbjct: 229 FGYYRHRWRAGDLLMWDNRCLAHRATDYMVRHRRTMYRTTIAGDRPRYVRGAA 281

>ref|ZP_01040254.1| alpha-ketoglutarate-dependent taurine dioxygenase [Erythrobacter sp. NAP1]
gb|EAQ30725.1| alpha-ketoglutarate-dependent taurine dioxygenase [Erythrobacter sp. NAP1]
Length = 275

Score = 109 bits (272), Expect = 6e-22, Method: Compositional matrix adjust.
Identities = 84/264 (31%), Positives = 119/264 (45%), Gaps = 16/264 (6%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
+Q+TP G V+GV LA+ DA + A +H + +F Q S ITF KR+G
Sbjct: 1 MQMTPMAPKCGVEVSGVSLASCSDAEMQDIKNAIYEHGVAVFRDQEFQSKQDHITFGKRWG 60

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
I+ + ++ A+ V + P D I G+ WH D +Y + A G+V
Sbjct: 61 GIDV---NNYFPLTEDYAEIAVVKKDP----DQQTNIIGD--WHTDHSYDQIPAMGSVLV 111

Query: 126 AEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQQAGSAYI 183
A +P GG T +A M AAYDAL + + + A H+ +Y L G +
Sbjct: 112 ARELPPKGGDTMWAHMGAAAYDALSQDLKDEIEGLEAFHTADHIYKADGLYAQTMGRSLR 171

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIP--GMDAAESERFLEGLVDWACQAP 241
G+ + T A + P+V HP TGR L + R A I G ES L+ L D A
Sbjct: 172 GHDCLKTGA--VHPVVIRHPHTGRKLLYVNR-AFTINFVGRTEESMPLLQRLYDAALTDD 228

Query: 242 RVHAHQWAAAGDVVVDNRCLLHRA 265
QW G + +WDNR H A
Sbjct: 229 NQCRLQWKPGTIAIWDNRRTWHNA 252

>ref|YP_001508017.1| taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EAN1pec]
gb|ABW13111.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EAN1pec]
Length = 275

Score = 108 bits (271), Expect = 7e-22, Method: Compositional matrix adjust.
Identities = 87/273 (31%), Positives = 125/273 (45%), Gaps = 19/273 (6%)

Query: 15 LGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGG 72
+GA V G+ + L D AA AA +H +L+F ++S+ Q+ F ++ G + +I G
Sbjct: 13 VGAEEVGLDVRLLNDSVPAACLAALAEHGVLLFRELNISHQDQLAFGRKLGDVVKIPG 72

Query: 73 GDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAV 132
I + + D PA + + N WH D + + A+ A+ SA VV A
Sbjct: 73 YPIPEVMEISFD-----PA--NPNAQYFSPNDHWHFDGSMDDIPAKAALMSASVVAE 123

Query: 133 GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTAT 192
GG T FA AYD L + + H+ Q + D +
Sbjct: 124 GGETEFASTYVAYDTLSDEEKERFDDLVRVHTFESIQR-----SYDPDTPPEQKADWASW 178

Query: 193 PLR--PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA 250
P+R PLV H ++ R SL+ G A I GMD E L L + RV H W+
Sbjct: 179 PVREHPLVWEH-QSRRSLVFGASASHIVGMDVDEGRALLADLERRSTLPDRVLRHSWSV 237

Query: 251 GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
GD+V+WDNR L+HRA P+D PR M + LAG
Sbjct: 238 GDMVIWDNRGLVHRACPFDRTPKPTMHRRTTLAG 270

>ref|YP_001831695.1| taurine dioxygenase [Beijerinckia indica subsp. indica ATCC 9039]
gb|ACB94206.1| Taurine dioxygenase [Beijerinckia indica subsp. indica ATCC 9039]
Length = 312

Score = 108 bits (270), Expect = 8e-22, Method: Compositional matrix adjust.

```

Query: 56  QQITFAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA 107
          QQI FA+ FG +E      D          I  ++NV   G  +          W      + I  +
Sbjct: 1   QQIAFARNFGKLEIHPSKDHRRSSRNPEIYRVANVDEQGGILPPKSEAW----RYINISWL 56

Query: 108 WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
          WH+DS++  V  + G++      V   GG T F  ++  AY AL E+ R  V  R ARHS
Sbjct: 57  WHSDSSFREVP SLG SILHGIEVTDQGGETMFCNL YEAYAALSES LRKEVAGRRARHSHAT 116

Query: 168  SQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHA-HAIPGMDAAES 226
          S+ G   +  + Y      D          PLV+ HPETGR SLLI  H      + G D A S
Sbjct: 117 VLSR-GQTLESAKY-----DPLKPVVHPLVRRHPETGRHSLLISPHTMDLVEGCDEAAS 170

```

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCL 261
L+ L+ +A Q V+ H+WA D+++WDNRC+
Sbjct: 171 RALLDELIAFAQQDRFVYRHKWARDIIMWDNRCV 205

>gb|ADC33991.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 108 bits (270), Expect = 9e-22, Method: Compositional matrix adjust.
Identities = 73/213 (34%), Positives = 105/213 (49%), Gaps = 25/213 (11%)

Query: 56 QQITFAKRFGAIER--IGGGDIVA-----ISNVKADGTVRQHSPAEDDMMKVIVGNMAW 108
QQI FA++FG +ER +G V ++N+ ADG V + W
Sbjct: 1 QQIAFAEQFGTLERHVGNRGTVNPLVHIVTNLGADGKPSGK-----VASTQW 48

Query: 109 HADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
H+D ++ P + + A V+P GG TCFADM AAY+AL EA +A + HS S
Sbjct: 49 HSDKSFRPQPSLATILHALVMPPQGGETCFADMIAAYEALPEAEKAELAGVRVHHSWELS 108

Query: 169 QSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER 228
Q+++G + I D + PLV+ PETGR +L +G A + G
Sbjct: 109 QARVG--IKVPPEEIADAPDMS---HPLVRTIPETGRKALFMGERAVHLEGQPEDVGRA 162

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVDNRCL 261
LE L A Q V+ H+W GD+++WDNRC+
Sbjct: 163 RLEKLTAAVQERFVYRHKWTLGDLLMWDNRCV 195

>gb|ABB69741.1| PlaO1 [Streptomyces sp. Tu6071]
Length = 288

Score = 108 bits (270), Expect = 9e-22, Method: Compositional matrix adjust.
Identities = 79/270 (29%), Positives = 120/270 (44%), Gaps = 45/270 (16%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAK 62
T ++ P + LGA + GV L + DA FA L L+H ++ P Q S + +I F +
Sbjct: 7 TAFEVRPLTSALGAEIHGVRLEDITDADFELRRLLLKHLVIFIPDQEGWSAESRIAFGR 66

Query: 63 RFGAIER-----IGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMP 116
RFG +E + G + I + + +G + WH D TY P
Sbjct: 67 RFGELEEHAAYLPHLDGHPQIQIIDSEQNGKI-----PIWHTDMTYAP 108

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
G+V PA GG T +++ AY+ L R L+ +A HS+ H+
Sbjct: 109 NPPIGSVLQIVDGPAGGDTMWSNQYLAYEGLSAPLRDLDGLTAVHSI-----HIP 160

Query: 177 QAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
G+D+ A P+V+VHPETGR +L + R H I ++ ES+ L+ L
Sbjct: 161 -----GLDSQAE--HPVVRVHPETGRRALFVNRAHTSHIAQLNRNESDALLQYLYR 209

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
++ +QW G V +WDNR H A
Sbjct: 210 FSTSPEFTCRYQWRPGSVAIWDNRVTQHYA 239

>ref|YP_001633079.1| alpha-ketoglutarate-dependent taurine dioxygenase [Bordetella
petrii DSM 12804]
emb|CAP44812.1| alpha-ketoglutarate-dependent taurine dioxygenase [Bordetella
petrii]
Length = 274

Score = 108 bits (270), Expect = 9e-22, Method: Compositional matrix adjust.

Identities = 75/267 (28%), Positives = 121/267 (45%), Gaps = 22/267 (8%)

```

Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      +++      +GA + G+ L+  L DA  AA+  A L H ++ F  Q L+ +Q I FA+RF
Sbjct: 1   MEVRKLTGVIGAELLGIDLSRDLPDADVAAIRQALLDHQVIFFRDQTLTPEQHIAFARRF 60

Query: 65  GAIERIGGGDIVAISNVKADGTVRQHS---PAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
      G I          S          T+ ++  P  +  + I+G+  WH D TY P  G
Sbjct: 61  GVI-----STTPVYRTLDEYPEIMPVVKEPTDQDIIGD-TWHTDETYHPTPLG 108

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVYSQSKLGHVQQAG 179
      ++      VP  GG T +A+M  AYD L +  +A +  A H+  + + SK  +  ++
Sbjct: 109 SILYGRQVPETGGDTLWANMYRAYDTLSGDMKAKLANLRAVHTNDFLSANSKYRNSTRST 168

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
      G  + T + P+V+ H ETGR  L +  ++  M  ES  L+ L  +
Sbjct: 169 KLREDVG---SITSVHPVVRTHEETGRKCLFVNHPFTYSFENMTREESLPLQLQFLYQHSA 225

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      +      +W  G +  WDNRC +H A
Sbjct: 226 KPENTCRFRWRKGSMAFWDNRCTMHYA 252

```

>ref|YP_001445968.1| hypothetical protein VIBHAR_02787 [Vibrio harveyi ATCC BAA-1116]
gb|ABU71741.1| hypothetical protein VIBHAR_02787 [Vibrio harveyi ATCC BAA-1116]
Length = 314

Score = 108 bits (269), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 74/264 (28%), Positives = 119/264 (45%), Gaps = 15/264 (5%)

```

Query: 6   LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
      ++I P      +GA + G+ LA          A++ A ++H ++ F GQ +S +QQ+  A+ FG
Sbjct: 45  IEIEPITPYIGARIHGIDLANCTAEDLEAIYQALIEHQVIFFDGQAMSPEQQLELAQYFG 104

Query: 66  AIE--RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
      +E      ++ +  V  T + ++P E          WH D T+  ++GAV
Sbjct: 105 GLEPAHPFFPNVESSPQVSIETTKGNAPLE-----SYWHTDLTWREQPSKGAV 153

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
      A+ VP  GG T +  M A +DALD  +  + Q SA HSL  +  +  +
Sbjct: 154 LHAQHVPNTGGDTIWVSMTAVFDALDNTMKTCLRQLSATHSLTAFEEVAEEDIELDWHHR 213

Query: 184 GYGMDTTATP-LRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAP 241
      +      P + P++K+HPETG+ +L I          I  +  E ++ L  L  Q
Sbjct: 214 LLEVSHLHPVVPVVIKIHHPETGKETLFINEQFTRHINEVGHTGKQLLNELFAIVRQPE 273

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRA 265
      +W  G V +WDNRC  H A
Sbjct: 274 YQVRFKWQPGSVAIWDNRCTQHYA 297

```

>gb|ADC34011.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 108 bits (269), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 69/214 (32%), Positives = 107/214 (50%), Gaps = 27/214 (12%)

```

Query: 56  QQITFAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW 108
      QQI FA++FG +ER  +  + ++N+ ADG          V  +  W
Sbjct: 1   QQIAFAEQFGLERHMASNRGTVNPLVHIVTNLADGKPSGK-----VASTGW 48

Query: 109 HADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
      H+D ++ P  +  +  A+V+P  GG TCFADM AAY+AL +A +A +  +  HS  S

```

Sbjct: 49 HSDKSFRPQPSLATILHAQVMPDGGETCFADMIAAYEALPDAEKAELDRLRVVHSWEIS 108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTATPL-RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
++++G +A I A P+ PLV+ PETG +L +G HA G

Sbjct: 109 RARMG--SKAPPEEIA-----DAPPMVHPLVRTIPETGSKALFMGEHAVYFQGQPEEVGR 161

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
LE L A + ++ H+W GD+++WDNRC+

Sbjct: 162 ARLEKLTAAHAVEERFIYRHKWTVGDLLMWDNRCV 195

>ref|YP_046272.1| putative alkylsulfatase (AtsK) [Acinetobacter sp. ADP1]
emb|CAG68450.1| putative alkylsulfatase (AtsK) [Acinetobacter sp. ADP1]
Length = 317

Score = 108 bits (269), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 77/268 (28%), Positives = 123/268 (45%), Gaps = 24/268 (8%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
LQ+ +GA ++G+HL++ LD + +H A L+H +L F GQ HL + +Q FA+

Sbjct: 12 LQLRKLTRIGAEISGIHLSSELDSSVTQFIHDALLEHKVLFVRGQHLGDTEQEKFAEL 71

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEDWMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG+ + + ADGT D K N +WH D T++ + ++

Sbjct: 72 FGS-----PVKHPTVPAADGTDFIFEL----DSQKGARAN-SWHTDVTFFVDAYPKISI 119

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS-----QSKLGHVQQ 177
++P GG T +A+ AY+ L E + Q A HS Y + +++

Sbjct: 120 LRGLIIPETGGDTTWANTETAYEDLPELLKQFAEQLVAVHSNEYDYGGPKQNVPEQLER 179

Query: 178 AGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
++ +T P+V VHPETG+ SLL+G + G ++S+ L +

Sbjct: 180 LKKVVFVSTKYETE----HPVVIVHPETGKKSLLLGHHFKRLVGFSQSDSQLLFNILQEKV 235

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ QW GDVV+WDNR H A

Sbjct: 236 TRPENTVRWQWQEGDVVIWDNRSTQHYA 263

>gb|ADZ91865.1| Taurine dioxygenase [Marinomonas mediterranea MMB-1]
Length = 277

Score = 108 bits (269), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 73/264 (27%), Positives = 115/264 (43%), Gaps = 15/264 (5%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
++ITP +GA ++ + L L + F+ L++A+L++ +L F Q L+ DQ +RFG

Sbjct: 1 MKITPLSRHIGAEISELQNLSEHEFSRLYSAFLEYKVLFFRDQELTPDQHFALGQRFG 60

Query: 66 AIE--RIGGGDIVAISNVKADGTVRQHSPAEDWMMKVIVGNMAWHADSTYMPVMAQGAV 123
+E + + + T R + P G WH D T+ + ++

Sbjct: 61 ELEPPHPFFPHVESHPQIVVIETSRGNPP-----GESFWHTDMTFQRFPKCSI 109

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-VYSQSKLGHVQQAGSAY 182
A+ VP GG T + M A + +L E+ R + A H L + S+ + G +

Sbjct: 110 LHAQYVPERGGDTLWCSMAAVWQSLPESRRQTLKGLEACHQLHAFKNSRYDQTNEQGESI 169

Query: 183 IGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAP 241
+ PL+ VHPET +L I I GM +SE L+ L + A Q

Sbjct: 170 VDEKSAQYPPVFHPLMYVHPETQEETLFINEQFTRYIDGMTPLDSEACLQELFEIARQDV 229

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRA 265
W AG V +WDNR H A

Sbjct: 230 FQVRFSWKAGSVAIWDNRVTQHFA 253

>ref|ZP_08119928.1| dioxxygenase [Pseudonocardia sp. P1]
Length = 307

Score = 108 bits (269), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 84/263 (31%), Positives = 119/263 (45%), Gaps = 22/263 (8%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGF-AALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+TP G TLGA +TGV L A LH A L+ +L FPGQ ++ +QQ F +
Sbjct: 42 FTVTPVGRITLGAETITGVDLREAPGPELRAELHRLLEWKVLFPPGQDITGEQQRDFGALW 101

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G++E + +D VR + A+ + + WHAD+T+ A GAV
Sbjct: 102 GSLE-----TNPMLDRGGSDEVVRFGAGAKTYENI-----WHADTTFREEPAMGAVL 148

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
P GG T +ADM AAYD L + +A + A H +V ++ +
Sbjct: 149 RMVQTTPFPGDITMWADMAAAYDNLSDEVKARIEGAEAVHDMVPGFARFLDADKLA----- 203

Query: 185 YGMDTTATPL-RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPR 242
G+ P+ P+V+ HPETGR +L + I G+ ES+ L L A
Sbjct: 204 -GLQDEFPPVTHPVVRTHPETGRRTLFVNASFTTEIVGLPREESDALLRHLFAQAHVPEF 262

Query: 243 VHAHQWAAGDVVVDNRCLLHRA 265
H+WA G V WDNR H A
Sbjct: 263 QVRHRWAEGTVAFWDNRATQHYA 285

>ref|YP_001508606.1| taurine catabolism dioxxygenase TauD/TfdA [Frankia sp. EAN1pec]
gb|ABW13700.1| Taurine catabolism dioxxygenase TauD/TfdA [Frankia sp. EAN1pec]
Length = 268

Score = 108 bits (269), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 85/271 (31%), Positives = 121/271 (44%), Gaps = 20/271 (7%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGD 74
LG V GV LDD + A +L+ G HL ++ Q+ F+ + G + + G +
Sbjct: 11 LGVAVDGVG-DILDDTLISRCVEALKWRGVLLVRGAHLDDAQLAFSHKLGDVISLAGRE 69

Query: 75 IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPVAVGG 134
I IS A +PA + + G WH D T V ++ +A V VGG
Sbjct: 70 IFTISLDPA-----KTPA-----AEYLKGTFFHWHIDGTNDVPSKATTLTARHVAMVGG 118

Query: 135 RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS--KLGHVQQAGSAYIGYGMDDTTAT 192
T FA AAY++L E R + HS +Q K + +A+ T+
Sbjct: 119 GTQFASTYAAYESLPELERKRIDGLRVVHSFEEAQLVKPDPTPEELAAWRALPPHETSL 178

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
R GR SL+IG I GM+A ES L+ L+DW+ Q + H W GD
Sbjct: 179 VWRR-----RDGRRSLVIGATTDHIVGMEAESRALDELLEDWSTQERFSYTHDWEVGD 232

Query: 253 VVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+VVVDN +LHRA P+D R M + + G
Sbjct: 233 LVVVDNTGVLHRAMPYDPTSERTMQRTTIVG 263

>ref|YP_003272551.1| Taurine dioxxygenase [Gordonia bronchialis DSM 43247]
gb|ACY20658.1| Taurine dioxxygenase [Gordonia bronchialis DSM 43247]
Length = 306

Score = 108 bits (269), Expect = 1e-21, Method: Compositional matrix adjust.

Identities = 81/266 (30%), Positives = 119/266 (44%), Gaps = 18/266 (6%)

```
Query: 6   LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
          L +   G + GA + G+ +A+   D   A+   A +++ +++   QHL +   I F +R G
Sbjct: 28  LDVDEFGPSFGAELRGIDVASASDDEVRAIRRALIEYKVIIVLRNQHLDDAAHIEFGRRLG 87

Query: 66  AIERIGGGDIVAISNVKADGTVRQHSPAEDWDDMMKVIVGNM-AWHADSTYMPVMAQGAVF 124
          D+       V   G V   P E   +       G   WH D T+MP   G++
Sbjct: 88  -----DLTVGHPVWDSGDV----PDEVYSLDSADNGFADVWHTDVTFMPPRPPMGSIL 135

Query: 125  SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
          V+P   GG T +AD   AY +L E   R L+   A H               ++ G
Sbjct: 136  RPVVLPRNGGDTNWADAELAYLSLSEPVRTLIEGLRAVHDSREFGYLQRRGGKKGNEW 195

Query: 185  YGMDTTATP--LRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVDWACQA 240
          G + T P   P+V+VHPETGR SL +   G   +H I G+   AES   L+ L   +
Sbjct: 196  DGREVTTELPPVTHPVVRVHPETGRKSLFVNPGFTSH-IEGVSDAESRGILDLLYAHLTKP 254

Query: 241  PRVHAHQWAAGDVVVWDNRCLLHRAE 266
          +   H+W   GD+V+WDNR   LH A
Sbjct: 255  EHIVRHRWRLGDLVLWDNRNTLHYAN 280
```

>ref|XP_001394361.1| 2,4-dichlorophenoxyacetate alpha-ketoglutarate dioxygenase
[Aspergillus niger CBS 513.88]
emb|CAK48351.1| unnamed protein product [Aspergillus niger]
Length = 323

Score = 107 bits (268), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 75/288 (26%), Positives = 136/288 (47%), Gaps = 31/288 (10%)

```
Query: 2   AQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
          +   L++   G   GA +TG+   + D F +   A ++   +   +L ++   +
Sbjct: 14  SNPNLKVIKNG--FGAEITGLDFTHGVTDEAFRFIENAVRKYGFVVRKTNLVDETHLEL 71

Query: 61  AKRFGAIE-----RIGGGDIVAISNVKADGT-VRQHSPAEDWDDMMKVIVGNMA 107
          A++FG ++           R+   ++   + N++ DG+ V   +SP           + GN
Sbjct: 72  ARKFGELDDVTPYNKAGRVHRLKYNELFDVGNIEIDGSIVDLNSPRG-----EANKGNSL 126

Query: 108  WHADSTYMPVMAQGAVFSAEVP--AVGGRTCFADMRAAYDALDEATRALVHQRS--ARH 163
          +H DS++ P   A ++   A +P   GG T FADMR AY   LD+   +   +H R+   ARH
Sbjct: 127  FHTDSSFNPFRAGYSLLLAHELPPPGTGGSTAFADMRGAYRDLDDDFKRFLHDRNFVARH 186

Query: 164  SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDA 223
          S+++S+           A   +           L++ H   TG P++ +   +H H++ G+
Sbjct: 187  SILHKK-----MAAPEHFKDVNPTDHFMSRHLQLKHERTGIPTIYLAKHIHSLEGVSP 241

Query: 224  AESERFLEGLVDWACQAPRVHAHQW-AAGDVVVWDNRCLLHRAEPWDF 270
          ES+   L+ L + + Q   V   +W + GD++VWDN C +HRA   +F
Sbjct: 242  EESQGILDRLFEHSSQDKYVIEVEWISVGDMMIVWDNTCTMHRAISGEF 289
```

>emb|CAY27310.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 121

Score = 107 bits (268), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 55/124 (44%), Positives = 73/124 (58%), Gaps = 3/124 (2%)

```
Query: 136  TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
          T F DMRAAYDALD+   +A +           HS   YSQ K+G +++   +           M
Sbjct: 1   TEFQDMRAAYDALDDQRKAQLEGLLGTHSYAYSQKVGGLLEEVFTPEARARMVDVE---H 57

Query: 196  PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
```

LV+ HP TGR SL IGRH + + GM +++ LE L+ WACQ PRV H+W GD+V+
Sbjct: 58 LLVRTHPATGRKSLFIGRHVYRVVTGMTDDDAQAMLEELLAWACQPPRVFKHRWTVGDIVM 117

Query: 256 WDNR 259

WDNR

Sbjct: 118 WDNR 121

>ref|ZP_07387050.1| Taurine dioxygenase [Paenibacillus curdlanolyticus YK9]
gb|EFM11265.1| Taurine dioxygenase [Paenibacillus curdlanolyticus YK9]
Length = 305

Score = 107 bits (268), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 77/275 (28%), Positives = 119/275 (43%), Gaps = 31/275 (11%)

Query: 3 QTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITF 60
Q L++ P +GA V G+ L+ LD A+ A LQH +L F GQ HL +++Q F
Sbjct: 9 QVQLEVPVAVGRIGAEVKGLRLSGDLREDVEAIQRALLQHKVLFVRGQQHLDDEEQERF 68

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST 113
AK G + + G I+ +++ +WH D T
Sbjct: 69 AKLLGELYAHPTVPVKEGSSSILELNSYHGGRA-----NSWHTDVT 109

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK-- 171
++ + ++ V+PA GG T +A+ AAY+ L + R L A H+ Y +
Sbjct: 110 FVDAYPKASILRGVVIPAAGGDTVWANTAAAYEDLPQELRDLADNLRAVHTNAYDYATAI 169

Query: 172 LGHVQQAGSAYIGYGMTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFL 230
V + + ++T P+V+VHPETG LL+G G + +SER
Sbjct: 170 RKEVSEEDAKKSKAIFESTVYETEHPVVRVHPETGERHLLLGHFVKRFVGFGRSPDSERLF 229

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L + + +WA GDV +WDNR H A
Sbjct: 230 HILQEHVTRLENTVRWRWAEGDVAIWDNRATQHYA 264

>gb|AAM90964.2|AF516751_1 R-2,4-dichlorophenoxypropionate dioxygenase [Rhodoferax sp.
P230]
gb|AAM90965.2|AF516752_1 R-2,4-dichlorophenoxypropionate dioxygenase [Sphingobium
herbicidovorans]
gb|AAP88290.1| R-2,4-dichlorophenoxypropionate/alpha-ketoglutarate dioxygenase
[Delftia acidovorans]
emb|CAF32811.1| (R)-2-(2,4-dichlorophenoxy)propionate,2- oxoglutarate dioxygenase
[Sphingobium herbicidovorans]
Length = 295

Score = 107 bits (268), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 80/268 (29%), Positives = 126/268 (47%), Gaps = 14/268 (5%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ + P LGA +TGV L LDD+ + + A+ + ++ FPGQ ++N+Q I F++RF
Sbjct: 15 IAVQPLTGVLGAEITGVDLREPLDDSTWNEILDAFHTYQVIYFPGQAITNEQHIAFSRRF 74

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G ++ + + +I +R+ E ++ +VI + WH DST++ V
Sbjct: 75 GPVDPVPL--LKSIEGYPEVQMIRR----EANESGRVIGDD--WHTDSTFLDAPPAAVVM 126

Query: 125 SAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 127 RAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSNTS 186

Query: 185 YG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A +

Sbjct: 187 VKVMDVDAGDRETVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYEHA 246

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRAEP 267

+W V+VWDN C +HRA P

Sbjct: 247 FDFTCRVWKKDQVLVWDNLCTMHRAPV 274

>ref|ZP_07301372.1| dioxygenase [Streptomyces viridochromogenes DSM 40736]

gb|EFL29741.1| dioxygenase [Streptomyces viridochromogenes DSM 40736]

Length = 324

Score = 107 bits (268), Expect = 2e-21, Method: Compositional matrix adjust.

Identities = 89/296 (30%), Positives = 131/296 (44%), Gaps = 22/296 (7%)

Query: 3 QTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61

+ +++ P +GA ++GV LA+ LDD AA+ AA L+ ++ F GQ L + +TFA

Sbjct: 14 EAGVEVKPVAGHIGAEISGVDLASHLDDTVVAAIRAAVLRWKVVFRRGQRLDHTGHVTFA 73

Query: 62 KRFG---AIERIGGGDIVAISNVKAD-----GTVRQHSPAEWDDMMKVIVGNMAWHADS 112

+RFG + R G ++ G EW + + WH D

Sbjct: 74 RRFGEVVLPRRGKASPPGFPEIETTADRLELGGFRFGMEHDEWLRRRRHTL-LRGWHCDH 132

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172

+ AE VP GG T +++ AAY L R A H L +

Sbjct: 133 GARVDPPAATILRAETVPPYGGDTTWSNLAAAYAGLSAPLREFADGLRAEHRL-----GV 187

Query: 173 GHVQQAGS-AYIGYGMTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFL 230

G+ + G AY+ + +D L PLV+VHPETG L + G + I G+ ES L

Sbjct: 188 GYQPRPGDDAYVRHLDDRQVATLHPLVRVHPETGERVLYVNGYYVEQIAGLSRPESGAIL 247

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283

+ L++ A + +W G V WDNR +H A P D PR+M LAG

Sbjct: 248 DLLLEQAVRPEYTVRFRWEPGSVAFWDNRATMHLA-PGDTAHLDPHPRIMHRVMLAG 302

>ref|YP_001134372.1| taurine dioxygenase [Mycobacterium gilvum PYR-GCK]

ref|YP_004076900.1| taurine catabolism dioxygenase [Mycobacterium sp. Spyr1]

gb|ABP45584.1| Taurine dioxygenase [Mycobacterium gilvum PYR-GCK]

gb|ADT99065.1| Probable taurine catabolism dioxygenase [Mycobacterium sp. Spyr1]

Length = 309

Score = 107 bits (268), Expect = 2e-21, Method: Compositional matrix adjust.

Identities = 83/266 (31%), Positives = 120/266 (45%), Gaps = 21/266 (7%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAA-LHAAWLQHALLIFPGQH-LSNDQQITFAKRF 64

+ GA +GA + GV LA DAG AA ++AA L+H ++ F GQH L +D Q+ FA+

Sbjct: 5 DVVKLGAAIGARIDGVDLARGIDAGTAAQINAALEHKVIFFRGQHDLDGQLEFARAL 64

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124

G A V + G + +D +WH D T++ + + ++

Sbjct: 65 GT-----PTTAHPTVTSRGAKVLPIDSRYDKAD-----SWHTDVTTFVDRIKASLL 110

Query: 125 SAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY-----SQSKLGHVQQAG 179

A +PA GG T +A AAYD L RAL A H+ Y + ++L +

Sbjct: 111 RAVTLPAYGGTTAWASTEAAAYDRLPAPLRALTENLWAVHTNTYDYAADADARLVPLADTE 170

Query: 180 SAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239

Y + P+V+VHPETGR LL+G G+ AES L+ L + +

Sbjct: 171 RQYREEFVSDYYETHPVVRVHPETGRKVLILLGHFVKHFVGLGQAESTALLQLLQNRVTK 230

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265

W GD+ VWDNR H A

Sbjct: 231 LENTIRSWELGDIWVWDNRATQHYA 256

>ref|YP_004016966.1| taurine dioxygenase [Frankia sp. Eu1lc]
gb|ADP81096.1| Taurine dioxygenase [Frankia sp. Eu1lc]
Length = 302

Score = 107 bits (267), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 80/270 (29%), Positives = 120/270 (44%), Gaps = 22/270 (8%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
++ P LGA + G+ L TLDD AA+ A WL + ++ FPGQ L+ + FA+RFG
Sbjct: 19 FEVIPLSGNLGAEIPGLDLRLTDDDTIAAVRATWLHYKVVFPGQDLTPQDHLAFARRFG 78

Query: 66 AIERIGGGDIVA-----ISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQ 120
E G ++ + D T + A + D+ V G + WH D T++
Sbjct: 79 --EPTGHPVIPGLPDQPEVFQIDYTQARELAAAYGDVSDVSRG-LHWHTDVTFVRRPPL 135

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
G++ A VP GG T F++ AA+D L A + + +A H Q + +
Sbjct: 136 GSILRAVEVPRAAGDTLFSNQEAADFDDSPALQEFLLSTLTAVHD---GQDQFKVILD--- 189

Query: 181 AYIGYGM--DTTATPLR----PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL 233
IG G T T L P+V+ HPETG+ SL + I + ES+ L L
Sbjct: 190 -LIGEGTWEKGTFTKLEPVEHPVVRTHPETGKRSLFVNPGFTSRIKELKRTESDALLAYL 248

Query: 234 VDWACQAPRVHAHQWAAGDVVVDNRCLLH 263
+ + + W G + WDNH H
Sbjct: 249 FQHSVRPEFTVRYHWQPGTIAFWDNRATQH 278

>gb|ACX54967.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 97

Score = 107 bits (267), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 58/97 (59%), Positives = 68/97 (70%), Gaps = 2/97 (2%)

Query: 110 ADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYMPV A+GAVF+AE+VPA GG T FADMRAAY+ALD+ TR V + A HSL YSQ
Sbjct: 1 ADSTYMPVQAKGAVFTAIEIVPASGGATGFADMRAAYEALDDETRDRVGRLCAYHSLYYSQ 60

Query: 170 SKLGHV--QQAGSAYIGYGMDDTTATPLRPLVKVHPET 204
+ G++ + A Y YG LRPLVKVHPET
Sbjct: 61 GRAGYLPRRNAMGGYDQYGYHEGEPSSLRPLVKVHPET 97

>gb|ADY81784.1| putative alkylsulfatase [Acinetobacter calcoaceticus PHEA-2]
Length = 317

Score = 107 bits (267), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 73/274 (26%), Positives = 123/274 (44%), Gaps = 36/274 (13%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L + +GA ++G+HL++ LD + +H A L+H +L F GQ HL + +Q FA+
Sbjct: 12 LHVKKLTGRIGAEISGIHLSSLEDSSTVQFIHDALLEHKVLFRRGQQHLGDTEQEKFAEL 71

Query: 64 FGA-----IERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPV 117
FG+ + + G D I + + R +S WH D T++
Sbjct: 72 FGSPVKHPTVPAVDGTDG--IFELDSQKGARANS-----WHTDVTFVDA 113

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY-----SQSK 171
+ ++ + ++P GG T +A+ AY+ L E + Q A HS Y +
Sbjct: 114 YPKISILRLIIPETGGDTTWANTETAYEDLPELLKQFAEQLVAVHSNEYDYGGPKQNV 173

Query: 172 LGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE 231
+++ ++ +T P+V +HPETG+ SLL+G + G ++S+
Sbjct: 174 PEQLERLKKIFVSTKYETE----HPVVVLHPETGKKSLLLGHHFFKRLVGFSSQSDSQLLFN 229

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L + + QW GDVV+WDNR H A
Sbjct: 230 ILQEKVTRPENTVRWQWQEGDVVIWDNRSTQHYA 263

>gb|ADC33998.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 107 bits (267), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 68/213 (31%), Positives = 103/213 (48%), Gaps = 25/213 (11%)

Query: 56 QQITFAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW 108
QQI FA++FG +ER + + ++N+ ADG V + W
Sbjct: 1 QQIAFAEQFGTLERHMASNRGTVNPLVHIVTNLGADGKPSGK-----VASTGW 48

Query: 109 HADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
H+D ++ P + + A+V+P GG TCFA+M AAY+ L EA +A + HS S
Sbjct: 49 HSDKSFRPRPSLATILHAQVMPDGGETCFANMIAAYETLPEAEKAELDGVVVVHSWEIS 108

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER 228
++++G A M+ PLV+ PETG +L +G HA G
Sbjct: 109 RARMGITAPAEIADAPPME-----HPLVRTIPETGSKALFMGEHAVYFDGQPEEVGRA 162

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
LE L A + V+ H+W AGD+++WDNRC+
Sbjct: 163 RLEKLTAAHAVEERFVYRHKWTAGDLLMWDNRVCV 195

>ref|YP_001413275.1| taurine dioxygenase [Parvibaculum lavamentivorans DS-1]
gb|ABS63618.1| Taurine dioxygenase [Parvibaculum lavamentivorans DS-1]
Length = 278

Score = 107 bits (267), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 81/271 (29%), Positives = 122/271 (45%), Gaps = 26/271 (9%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T+Q+ P LGA + GV L+ L + F +H A+L H ++ F Q LS++Q F +R
Sbjct: 2 TIQVKPISGALGAEIEGVDLSKDLNSETFDDIHQAFLDHVVIFFRDQQLSHEQHKAFFGR 61

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
FG + G +I+ I VK E +D + G WH+D +++
Sbjct: 62 FGTLNIHPYVKMGEGHPEIMQI--VK-----EPEDRLNFGGG---WHSDMSFLE 105

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
A G++ A+ VP GG T +A+ AY+ L + +A + A H+ S+ G
Sbjct: 106 EPALGSILYAKEVPPYGGDTLWANQYLAYETLSDGMMKATLDGLKAVHTAKGEYSERGASA 165

Query: 177 QA-GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLV 234
QA S + D T + P+V+ HPETGR +L + G ES L L
Sbjct: 166 QARKSMDVATAGDDTPSYEHPVVRTHPETGRKALYVNPAPFTEKFVGWTRRESRPLLNFL 225

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ Q P +W A + WDNR H A
Sbjct: 226 EHCTQEPLTCRFRWTANALAFWDNRQAQHFA 256

>ref|ZP_07980743.1| alpha-ketoglutarate-dependent taurine dioxygenase [Streptomyces
sp.

SA3_actG]
ref|ZP_07985093.1| alpha-ketoglutarate-dependent taurine dioxygenase [Streptomyces
sp.
SA3_actF]
Length = 297

Score = 107 bits (267), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 83/275 (30%), Positives = 126/275 (45%), Gaps = 26/275 (9%)

Query: 1 MAQTTLQITPTGATLGATVTVGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSDNDQQITF 60
+++ L++TP G GA V + L LDD AA+ AA ++H +L GQ + + QI F
Sbjct: 14 VSEAGRLRLTPLGPRFGAEVHDIDLGRLLDDGQVAAVRAALVEHKVLFVRGQDIDDAQIAF 73

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPA--EWDDMMKVIVGNMAWHADSTYMPVM 118
+R G++ A V G V + A D+ + WH D T++
Sbjct: 74 GRRL-----GEVTAGHPVHDSGDVPVEEFALDSQDNGFADV----WHTDVTFFVARP 120

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV--- 175
+V A V+P GG T +AD AAY++L RAL+ +A H + G+
Sbjct: 121 PAISVLRAVVLPTTGGDTSWADSEAYESLTPLRLALIDPLTAVHD---GNREFGYLLAQ 177

Query: 176 --QQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLE 231
Q G+ + G + P+V+VHPE+GR L + G +H + G+ ES L+
Sbjct: 178 RRQGRGNVWEGEVFTDLSPVEHPVVRVHPESGRRGLFVNPGFTSH-LTGVSEYESRGILD 236

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE 266
L + H+W GDV +WDNR H A
Sbjct: 237 ILYAHLTKPEHTIRHRWQPGDVALWDNRATSHYAN 271

>gb|ACX54972.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ACX54993.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ACX54995.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ACX54998.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ACX55001.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 93

Score = 107 bits (267), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 59/96 (61%), Positives = 69/96 (71%), Gaps = 4/96 (4%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYMP+ A+GAVFSA+VVP GG T +ADMRAAY+ALDE R+ + A HSL YSQ
Sbjct: 1 ADSTYMPQLAKGAVFSAKVVPTTEGGETGWADMRAAYEALDENLRSKLEGLAYHSLYYSQ 60

Query: 170 SK-LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET 204
K LG+ +AGSA YG+ PLR LVKVHPET
Sbjct: 61 GKVLGYAPKAGSA---YGLHEGPPPLRKLKVHPET 93

>ref|ZP_04384517.1| alpha-ketoglutarate-dependent taurine dioxygenase [Rhodococcus
erythropolis SK121]
gb|EEN88282.1| alpha-ketoglutarate-dependent taurine dioxygenase [Rhodococcus
erythropolis SK121]
Length = 325

Score = 107 bits (267), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 82/267 (30%), Positives = 121/267 (45%), Gaps = 27/267 (10%)

Query: 8 ITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFG 65
+T GA +GA + G+ L LD A + + A L+H ++ F GQ HL ND Q FA G
Sbjct: 28 VTTLGAHIGARIDGITLGGHLDPATISLIRQALLEHKVIFFRGQDHLNDSQYEFALLG 87

Query: 66 AIERIGGGDIVAISNVKADGTVRQHS----PAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
+ A TV+ H P + D+ K +WH D T++ + +
Sbjct: 88 -----TPTTAHPTVKSHGAKVLPID-SDLGKA----NSWHTDVTFVDRIPKA 129

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY---SQSKLGHVQQA 178
++ A +P GG T +A AAY+ L + +AL ARH+ VY + S +
Sbjct: 130 SILRAVQLPEYGGSTTWASGVAAAYNGLPDLKALAENLWARHTNVYDYAATS AERLTEDR 189

Query: 179 GSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC 238
+AY T P+V+VHPETG +L++G G+ +S + L D A
Sbjct: 190 TAAYREEFQSTYFETEHPVVRVHPETGERTLVLGHFVKNFVGLSTEQSNQNGVFKLLQDHAI 249

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ W AGDV +WNR H A
Sbjct: 250 KLEYTTRWNWEAGDVAIWDNRATQHYA 276

>ref|YP_003551220.1| putative dioxygenase [Candidatus Puniceispirillum marinum IMCC1322]
gb|ADE39136.1| putative dioxygenase [Candidatus Puniceispirillum marinum IMCC1322]
Length = 301

Score = 107 bits (266), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 79/268 (29%), Positives = 120/268 (44%), Gaps = 18/268 (6%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
+ +TP LGA + G+ +A ++D FA +H A+L H +L F Q ++ + I F KR
Sbjct: 31 IDVTPFAPNLGAEIRGIQIADGVNDEEFAEIHHAFLAHQVLFFKQDREITPEAHIDFGKR 90

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG + +A + H ++ + WH+D + G +
Sbjct: 91 FGPLHAHPAAPTMA--GYPEIFEIHAHKDSK-----VANGEHWHSDVSCDTEPPLGTL 141

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAAGSAYI 183
++P GG T F+DM AA+D L RA++ +A H + + A I
Sbjct: 142 LQLHILPPCGGDTMFSDMYAAFDDLSPTRLRAML DGLTATHESEHFYRGRYADRGRKDADI 201

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPR 242
Y + T P+V+ HPETGR +L I R I + AAES+ L L
Sbjct: 202 SYPVAT-----HPVVRTHPETGRKALYINRTFTTGINELSAAESDAMLGFLF SHIEHVNY 256

Query: 243 VHAHQWAAGDVVVWDNRCLLHRAEPWDF 270
+WA D+ WDNRC +HRA WD+
Sbjct: 257 QIRFRWALNDMAFWDNRCMHRAI-WDY 283

>gb|ADC34041.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 107 bits (266), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 69/214 (32%), Positives = 104/214 (48%), Gaps = 27/214 (12%)

Query: 56 QQITFAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW 108
QQI FA++FG +ER + ++N+ ADG V + W
Sbjct: 1 QQIAFAEQFGTLERHMASNRGTVNPLVHIVTNLGADGKPSGK-----VASTGW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
H+D ++ P + + A+V+P GG TCFA+M AAY+AL E +A + HS S
Sbjct: 49 HSDKSFRPRPSLATILHAQVMPDGGETCFANMIAAYEALPEVEKAELDGV RVVHSWEIS 108

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
++++G A A P+ PLV+ PETG +L +G HA G
Sbjct: 109 RARMGITAPAEI-----ADAPMEHPLVRTIPETGSKALFMGEHAVYFDGQPEEVGR 161

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
LE L A + V+ H+W AGD+++WDNRC+
Sbjct: 162 ARLEKLTAAVEERFVYRHKWTAGDLLMWDNRV 195

>ref|YP_274684.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. phaseolicola
1448A]
gb|AAZ33872.1| dioxygenase, TauD/TfdA family [Pseudomonas syringae pv.
phaseolicola 1448A]
Length = 279

Score = 107 bits (266), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 80/253 (31%), Positives = 124/253 (49%), Gaps = 22/253 (8%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAI--ERIGGGDIVAIS-NVKADGTVRQHSPA EWDD 97
Q +L+FP S+ +QI F + G E G +I IS +VK +PA
Sbjct: 44 QRGVLVFPQIDFSDAEQIAFTRTLGTFCPEASDQGNITKISLDVK-----ENPAG--- 93

Query: 98 MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH 157
+ + G++ WH D T V ++ S +V ++GG T F + AAY+AL A +
Sbjct: 94 -AEFLKGSLYWHIDGTSSDVPILASLLSCKVPASLGGNTGFCNTYAAYEALSSADK---- 148

Query: 158 QRSARHSLVYS--QSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHA 215
QR R +++ S L + + G A + M PLV H +GR SL++G A
Sbjct: 149 QRYERLRVIHAPWASLLYNEPEGLAMLK-AMQAIGKEKELPLVVRH-RSGRKSILIGCTA 206

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRV 275
+ G+ A+S + L GL +WA ++H W GD+V+WDN +HRAE +D R+
Sbjct: 207 QQVVGVSQAQILVGLREWATAEAFSYSHAWQTGDLVIWDNTGTMHRAEAYDPACGRM 266

Query: 276 MWHSRLAGRPETE 288
M ++L G E
Sbjct: 267 MHRTKLQGEFFFE 279

>gb|AAT51068.1| PA3935 [synthetic construct]
Length = 278

Score = 107 bits (266), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 84/265 (31%), Positives = 118/265 (44%), Gaps = 15/265 (5%)

Query: 5 TLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+L I P LGATV+G+ L A LDD G A+ A L+H +L F Q L Q FA R
Sbjct: 2 SLTIQIPISPALGATVSGIDLGA PLDDTGQRAIEQALLEHQVLFRRDQSLEPRSQARFAAR 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG + I + Q D + + N WH D T++ A GAV
Sbjct: 62 FGD LH-----IHPIYP-SVPEQPEVIVLDTAVTDVRDIAIWHTDVTFLETPALGAV 111

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQQAGSA 181
+A+ +P GG T +A AAY+AL R L+ +A H + + + G V +A A
Sbjct: 112 LAAKQLPPYGGDTLWASSTAAYEALSAPLRLLDGLTATHDIGKSFPRERFG-VTEADLA 170

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQA 240
+ P+V+ HP TGR L + I ++ AES+ L+ L A +
Sbjct: 171 RLEEARKNPPRSHPVVRTHPVTGREGLFVSDGFTTRINELEPAESDALLKFLFAHATRP 230

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRA 265

+W DV WDNR H A
Sbjct: 231 EFTVRWRWQENDVAFWDNRVTQHYA 255

>gb|EFW80548.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. glycinea str. B076]
gb|EFW84411.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. glycinea str. race 4]
Length = 288

Score = 107 bits (266), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 80/253 (31%), Positives = 124/253 (49%), Gaps = 22/253 (8%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAI--ERIGGGDIVAIS-NVKADGTVRQHSPA EWDD 97
Q +L+FP S+ +QI F + G E G +I IS +VK +PA
Sbjct: 53 QRGVLVFPQIDFSDAEQIAFTRTLGTFCPEASDQGNITKISLDVK-----ENPAG--- 102

Query: 98 MMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVPVAVGGRTCFADMRAAYDALDEATRALVH 157
+ + G++ WH D T V ++ S +V ++GG T F + AAY+AL A +
Sbjct: 103 -AEFLKGS L YWHIDGTSSDVPILASLLSCKVPASLGGNTGFCNTYAAYEALSSADK---- 157

Query: 158 QRSARHSLVYS--QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHA 215
QR R ++++ S L + + G A + M PLV H +GR SL++G A
Sbjct: 158 QRYERLRVIHAPWASLLY NPEPGLAMLK-AMQAIGEKELPLVWRH-RSGRKS LILGCTA 215

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRV 275
+ G+ A+S + L GL +WA ++H W GD+V+WDN +HRAE +D R+
Sbjct: 216 QQVVGVS LAQSAQILVGLREWATAEAFSYSHAWQTGDLVIWDNTGTMHRAEAYDPACGRM 275

Query: 276 MWHSRLAGRPETE 288
M ++L G E
Sbjct: 276 MHRTKLQGE E PFE 288

>ref|ZP_06413630.1| Taurine dioxygenase [Frankia sp. EUN1f]
gb|EFC83531.1| Taurine dioxygenase [Frankia sp. EUN1f]
Length = 309

Score = 107 bits (266), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 86/298 (28%), Positives = 126/298 (42%), Gaps = 40/298 (13%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ + P GA + GV L LDDA A + +A L ++ F QHL + QQ+ F +RF
Sbjct: 10 IDVRPLSGYTGA EIHGVLDLREDLDDATIAEIRSALLTWKVVFVRDQHL DHAQQVAFGRRF 69

Query: 65 GAI-----ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM 115
G + G +I+ I + + A +D+ WH D T +
Sbjct: 70 GRLTAAHPHETEPAGHPEILPIDSRRYAKLFGDRRKATYDN-----GWHTDVTAL 120

Query: 116 PVMAQGAVFSAE VVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
G++ A++VP GG T + ++ AAY AL E R L ARHS + G
Sbjct: 121 VNPPAGSILRADIVPPYGGDTAWTNLVAA YQALPEPLRVLADGLRARHSFSLPIFEGGE- 179

Query: 176 QQAGSAYIGYGMDDTTATPL---RPLVKVHPETGRPSLLIGRHAHA----IPGMDAAESER 228
YG + PL P+V+VHPETG +L + A I G+ +S R
Sbjct: 180 -----YGRRIQSNPLVAIHVPVRVHPETGERALFVSPSFTARDNDIIGLSPRQSHR 230

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283
LE + + +W GDV WDNR H P D + RV++ + G
Sbjct: 231 VLELFYEQISRPEFTVRFKWNPGDVAFWDNRATAHLG-PSDLSHLEFDRVLYRVVTIEG 287

>ref|ZP_07262985.1| taurine catabolism dioxygenase TauD/TfdA [Pseudomonas syringae pv.

syringae 642]
Length = 279

Score = 107 bits (266), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 84/249 (33%), Positives = 122/249 (48%), Gaps = 22/249 (8%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAI--ERIGGGDIVAIS-NVKADGTVRQHSPA EWDD 97
Q +L+FP H S+ +QI F + G E G +I IS +VK + PA
Sbjct: 44 QRGVLVFPQIHFSDAEQIAFTRTLGTFCEPFGDQGNITRISLDVKEN-----PAG--- 93

Query: 98 MMKVIVGNMAWHADSTYM--PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL 155
+ + G++ WH D T P++A ++ S +V + GG T F + AAY+ L A R
Sbjct: 94 -AEFLKGSlyWHIDGTSSDSPILA--SLLSCKVPASWGGNTGFCNTYAAYEELSSADRQ- 149

Query: 156 VHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHA 215
H S R S L + + G A + M PLV H TGR SL++G A
Sbjct: 150 -HYDSLRLVIHAPWASLLYNNPEPGLAML-EAMQAIGEKELPLVWKH-RTGRKSLILGCTA 206

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRV 275
+ G+ A+S R L GL +WA ++H W GD+V+WDN LHRAE +D + R+
Sbjct: 207 QQVVGVS LAQSARILVGLREWATSEAFSYSHAWQVGD LVIWDNTGTLHRAEAYDPECGRM 266

Query: 276 MWHSRLAGR 284
M ++L G
Sbjct: 267 MHRTKLQGE 275

>ref|YP_789182.1| taurine dioxygenase [Pseudomonas aeruginosa UCBPP-PA14]
gb|ABJ13211.1| TauD [Pseudomonas aeruginosa UCBPP-PA14]
Length = 277

Score = 107 bits (266), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 84/265 (31%), Positives = 118/265 (44%), Gaps = 15/265 (5%)

Query: 5 TLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+L I P LGA V+G+ L A LDDAG A+ A L+H +L F Q L Q FA R
Sbjct: 2 SLTIQPI SPALGAIVSGIDLGA PLDDAGQRAIEQALLEHQVLFRRDQSLEPRSQARFAAR 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG + I + Q D + + N WH D T++ A GAV
Sbjct: 62 FGD LH-----IHPIYP-SVPEQPEVIVLDTAVTDVRD NAIWHTDVTFL ET PALGAV 111

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQQAGSA 181
+A+ +P GG T +A AAY+AL R L+ +A H + + + + G V +A A
Sbjct: 112 LAAKQLPPYGGDTLWASSTAAYEALSAPLRLLDGLTATHDIGKSFP RERFG-VTEADLA 170

Query: 182 YIGYMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQA 240
+ P+V+ HP TGR L + I ++ AES+ L+ L A +
Sbjct: 171 RLEEARLKNPPRSHPVVRTHPLTGRKGLFVSDGFTTRINELEPAESDALLKFLFAHATRP 230

Query: 241 PRVHAHQWAAGDVVWDNRCLLHRA 265
+W DV WDN R H A
Sbjct: 231 EFTVRWRWQENDVAFWDNRVTQH YA 255

>gb|AB010421.1| (R)-2,4-dichlorophenoxypropionate dioxygenase [Burkholderia sp.
EX1152]
Length = 260

Score = 106 bits (265), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 80/264 (30%), Positives = 124/264 (46%), Gaps = 14/264 (5%)

Query: 10 PTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE 68

Sbjct: 3 P LGA +TGV L LDD+ + + A+ + ++ FPGQ ++N+Q I F++RFG ++
PLTGVLGAEITGVDLREPLDDSTWNEILDAFHTYQVIYFPGQAITNEQHIAFSRRFGPVD 62

Query: 69 RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV 128
+ + +I +R+ E ++ +VI + WH DST++ V A

Sbjct: 63 PVPL--LKSIEGYPEVQMIRR----EANESGRVIGDD--WHTDSTFLDAPPAAVVMRAID 114

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG-M 187
VP GG T F M A++ L +A + + HS L Q + M

Sbjct: 115 VPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSNTSVKVM 174

Query: 188 DTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRV 243
D A + PLV HP +GR L + + + I GM AES+ L+ L + A +

Sbjct: 175 DVDAGDRET VHPVTHPGSGRKGLYNQVYQRIEGMTDAESKPLLQFLYEHATRFDF 234

Query: 244 HAHQWAAGDVVVWDNRCLLHRAEP 267
+W V+VWDN C +HRA P

Sbjct: 235 CRVRWKKDQVLVWDNLCTMHRAPV 258

>ref|YP_002869936.1| taurine dioxygenase [Pseudomonas fluorescens SBW25]
emb|CAY46531.1| alpha-ketoglutarate-dependent taurine dioxygenase [Pseudomonas
fluorescens SBW25]
Length = 278

Score = 106 bits (265), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 85/267 (31%), Positives = 120/267 (44%), Gaps = 17/267 (6%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
++L +TP LGA ++GV + LD A+ A L H++L F GQ ++ QQ FA

Sbjct: 2 SSLTVTPLSTALGAQISGVDITQPLDLQRHAIEQALLTHSVLFFRQGAINPQQQARFAA 61

Query: 63 RFGAIERIGGGDIVAI-SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQG 121
FG + I I NV V D + + N WH D T++P A G

Sbjct: 62 NFGDLH-----IHPIYPNVPEQPEV-----LILDTAVTDVRDNAVWHTDVTFLPTPALG 110

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
AV SA+++PA GG T +A AAY+AL E + L+ +A H S L

Sbjct: 111 AVLSAKLLPAFGGDTLWASGIAAYEALSEPFKRLLDGLTATHDFTKS-FPLERFGNTAED 169

Query: 182 YIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
+ + P P+V+ HP +GR SL + I ++ AESE L+ L A

Sbjct: 170 LVRWEETRKNPNPLSHPVVRTHPVSGRKS L FVSDGFTTKINELEPAESEAILKLLFAHAT 229

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ +W DV WDN R H A

Sbjct: 230 RPEFTIRWRWQENDVAFWDNRVTQHYA 256

>ref|YP_001511337.1| taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EAN1pec]
gb|ABW16431.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EAN1pec]
Length = 278

Score = 106 bits (265), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 83/283 (29%), Positives = 130/283 (45%), Gaps = 15/283 (5%)

Query: 5 TLQITPTGATLGATVTGVHLATL-DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++ +TP G LG +TG+ L A AA +H ++I+ H+S+ ++F++

Sbjct: 2 SVTVTPLGPHLGVEITGMSGGDLPTTAAAAACLET LARHGVVIYREAHISDSDLVSFSRSL 61

Query: 64 FG--AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMK-VIVGNMAWHADSTYMPVMAQ 120
G + G + I+ + D PA+ D + GN WH D + +

Sbjct: 62 LGRVVLNPTGEHERAEIATITLD-----PAKTDATLAWYRKGNFLWHIDGATDQLPQK 114

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
+ +A V GG T FA AAY+AL + + + HS +Q + H
Sbjct: 115 ATLLTAREVDETTGGDTEFASTYAAEALPDTEKVALAEHHVLHSFAAAQRR-AHPDATDE 173

Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
+G T PLV GR SLL+G A + G+ AE E L+ L++W+ Q
Sbjct: 174 QQADWGR--VPTRKHPLVWTR-GNGRRSLLLGATAGEVGLPPAEGEALLQRLLEWSTQP 230

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
V H+W AGD+V+WDN +LHRA P+ R+M + L G
Sbjct: 231 QFVLRHRWRAGDLVIWDNTGMLHRALPFAATSRRLMHRITLVG 273

>gb|ADC34015.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 106 bits (265), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 69/214 (32%), Positives = 106/214 (49%), Gaps = 27/214 (12%)

Query: 56 QQITFAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPAEDDMMKVIVGNMAW 108
QQI FA++FG +ER + + ++N+ ADG V + W
Sbjct: 1 QQIAFAEQFGTLERHMASNRGTVSPLVHIVTNLGADGKPSGK-----VASTGW 48

Query: 109 HADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
H+D ++ P + A+V+P GG TCFADM AAY+AL +A +A + + HS S
Sbjct: 49 HSDKSFRPQPPLATILHAQVMPPDGGETCFADMIAAYEALPDAEKAELDRVRVVSWEIS 108

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATPL-RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
++++G +A I A P+ PLV+ PETG +L +G HA G
Sbjct: 109 RARMG--IKAPPEEIA-----DAPPMVHPLVRTIPETGSKALFMGEHAVYFQGQPEEVGR 161

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
LE L A + ++ H+W GD+++WDNRC+
Sbjct: 162 ARLEKLTAAVEERFIYRHKWTVGDLLMWDNRCV 195

>gb|ADC33988.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 106 bits (265), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 72/213 (33%), Positives = 104/213 (48%), Gaps = 25/213 (11%)

Query: 56 QQITFAKRFGAIER--IGGGDIVA-----ISNVKADGTVRQHSPAEDDMMKVIVGNMAW 108
QQI FA++FG +ER + V ++N+ ADG V + W
Sbjct: 1 QQIAFAEQFGTLERHVVSNRGTVNPLVHIVTNLGADGKPSGK-----VASTQW 48

Query: 109 HADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
H+D ++ P + + A V+P GG TCFADM AAY+AL EA +A + HS S
Sbjct: 49 HSDKSFRPQPPLATILHALVMPPQGGETCFADMIAAYEALPEAEKAELAGVRVVSWEIS 108

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER 228
Q+++G + I D + PLV+ PETGR +L +G A + G
Sbjct: 109 QARVG--IKVPPEEIIADAPDMS---HPLVRTIPETGRKALFMGERAVHLEGQPEDVGRA 162

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
LE L A Q V+ H+W GD+++WDNRC+
Sbjct: 163 RLEKLTAAVQERFVYRHKWTLGDLLMWDNRCV 195

>gb|ADC34006.1| TfdA-like protein [uncultured bacterium]
Length = 213

Score = 106 bits (265), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 74/224 (33%), Positives = 110/224 (49%), Gaps = 29/224 (12%)

```
Query: 56  QQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMM 99
          QQI FA  +G +E                      RI  ++  +SN+  G  +          D
Sbjct: 1   QQIAFAGLYGPLEVAPPVQYKPGTFVETRRIRHREVFVDSNLDEQGRILDGL----DQRR 56

Query: 100 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQR 159
          +GN  WH DS++      A  ++  A ++P  GG T FAD RAAYDAL +AT+  +
Sbjct: 57  AYGLGNQLWHTDSSFRQKSATWSLLHARIIPPDGGDTEFADTRAAYDALPQATKDRLDGL 116

Query: 160 SARHSLVYSQSKLGHVQQAGSAYIGYGMTTATP--LRPLVKVHPETGRPSLLIGRHAHA 217
          A HS+ +S++KLG          Y      +  A P      P+V++ P +GR +L I  HA
Sbjct: 117 IAEHSIWHSRALG-----GYTPTEERQARPPAQHPVVRLRPGSGRKALYIASHASH 169

Query: 218 IPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
          I G      E      L  L+ +A Q      V+ H+W++GD+V+WDNR+
Sbjct: 170 IVGWPIEEGRALLAELLAFATQPQFVYTHRWSSGDLVIWDNRV 213
```

>ref|YP_003563864.1| taurine catabolism dioxygenase TauD [Bacillus megaterium QM B1551]
gb|ADE70430.1| taurine catabolism dioxygenase TauD [Bacillus megaterium QM B1551]
Length = 300

Score = 106 bits (264), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 75/268 (27%), Positives = 118/268 (44%), Gaps = 16/268 (5%)

```
Query: 2   AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQIT 59
          A + L++ P      +GA + GVHL++ L+      A++ A L+H ++ F GQ H+ + +Q
Sbjct: 9   ANSVLEVQPIAGHIGAEIKGVHLSSNLNAETLNAINKALLKHKVVFVRGQGHIDDAEQEA 68

Query: 60  FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMA 119
          FA FG E      I  SN  +      +  A          +WH D T++
Sbjct: 69  FAALFGEPEAHPTVPIKEGSNYLFELDSERGGGRAN-----SWHTDVTFTIDTYP 116

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL--GHVQQ 177
          + ++  A VVP  GG T +A+  AY +L      R L  Q  A H+  Y          Q+
Sbjct: 117 KASILRAVVPEAGGDTVWANTAVAYQSLPSELRLADQLWAVHTNDYDYGGRHPNRSQE 176

Query: 178 AGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
          +      T      P+V++HPETG  +L++G      I G+ +++S      L D
Sbjct: 177 DLDRHRKVFFASTVYETEHPVRIHPETGERTLVLGHFVKKIKGLSSSDSNHLFSILQDHV 236

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          +          W AGD+ +WDNR      H A
Sbjct: 237 TRLENTVRWHWKAGDIAIWDNRATQHYA 264
```

>ref|YP_002978871.1| Taurine catabolism dioxygenase TauD/TfdA [Rhizobium leguminosarum
bv. trifolii WSM1325]
gb|ACS60320.1| Taurine catabolism dioxygenase TauD/TfdA [Rhizobium leguminosarum
bv. trifolii WSM1325]
Length = 288

Score = 106 bits (264), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 83/300 (27%), Positives = 126/300 (42%), Gaps = 29/300 (9%)

```
Query: 1   MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
          + +  L+      + +  + G      D  AA+  WLQ+ ++ F      +++ QQ+ F
Sbjct: 2   LTKIRLRAVQHASNVCGDIEGFDFNDYDADDVAVRKFWLQYGVVRFKKAGITDAQQVQF 61
```

```

Query: 61 AKRFGAI-----ERIGGG-----DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNM--AW 108
      ++ FG      +   GG      +I+ ISN   DG      P+      +GN   W
Sbjct: 62 SRHFGEFVIHPKQLQEGGHPHPHPEILVISNAMKDG-----KPSG-----AMGNSEATW 109

Query: 109 HADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
      H D+ +      GA+ A VP   GG T F      AYD L      + V R      VY
Sbjct: 110 HTDTWFYERPPAGAILRAVAVPPSGGDTYFLSTYIAYDTLPAPLKNAVDGRQIFFQNVYD 169

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA--IPGMDAAES 226
      K G ++   S      + + PLV+ H ETGR +L +G      I GM   ES
Sbjct: 170 --KTGKRLRLGKSTPKSQDFREWSGIVHPLVRTHGETGRKALYLGTTTEGAWIVGMSRDES 227

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAAGDVVVWVWNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
      + L L D      +   QW GD+++WDNRC +HR + +D      R+M + +G RP
Sbjct: 228 DALLAELWDHTTNTKHI FVQQWDEGDIMWVWNRCTMHRDSFDPASIRIMHRTTTSGERP 287

```

>ref|XP_002149830.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase, putative [Penicillium marneffeii ATCC 18224]
gb|EEA21221.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase, putative [Penicillium marneffeii ATCC 18224]
Length = 326

Score = 106 bits (264), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 76/284 (26%), Positives = 128/284 (45%), Gaps = 26/284 (9%)

```

Query: 6 LQITPTGATLGATVTGVHLAT--LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      + P T GA G+ + + +      ++ +L+F G L + + + A++
Sbjct: 9 VTFKPLHPTFGAECNGIDFSQPVSSEETVDIIRNGLAKYGILVFRGAELDDARHVALARQL 68

Query: 65 GAIER-----IGG-----GDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHAD 111
      G ++R      + G      ++ +SN++ DG++ Q + W      ++ GN +H D
Sbjct: 69 GELDRSTVFVMPGQKYRLAPFNELTVDVSNIEQDGSIIQKNSLSW----QIGQGNSLFHVD 124

Query: 112 STYMPVMAQGAVFSAEVP--AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
      +Y P A +V A +P GG T FAD R AYD LD+ R + HSL +S+
Sbjct: 125 CSYNPRRAGFSVLRAHKLPPKGNNGGTAFADSR TAYDDLDEKREEIKDYIVCHSLWHSR 184

Query: 170 SKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAESER 228
      +      ++ Y      + R LV++H + R ++ I HAH G ES+
Sbjct: 185 ----RLASPDCFLKMEPEKNSMARHKLVMHEPSKRMNMYIAAHAHFHDGWT HQESQP 240

Query: 229 FLEGLVDWACQAPRVHAHQWAA-GDVVVWVWNRCLLHRAEPWDFK 271
      ++ L+ Q A W GD V+WDN C+LHRA DF+
Sbjct: 241 VIDDLMRHVTQDKYTFVAVNWENDGDFVIWDNTCVLHRACGGDFE 284

```

>ref|YP_001505765.1| taurine catabolism dioxxygenase TauD/TfdA [Frankia sp. EAN1pec]
gb|ABW10859.1| Taurine catabolism dioxxygenase TauD/TfdA [Frankia sp. EAN1pec]
Length = 276

Score = 106 bits (264), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 81/282 (28%), Positives = 130/282 (46%), Gaps = 18/282 (6%)

```

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
      L +      +GA + G+ L D+ A+ A ++ +L+F HL + Q+ F ++
Sbjct: 4 LTLNKLSTHVGAIEILGLDTRLLSDETLPGAVLDALEENGVLVFRNLHLDDATQVAFCRK 63

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
      GA++ I I+ V D PA+ + + + G WH D T + + V
Sbjct: 64 LGAVQSWASHAIEITVVS LD-----PAK-TAIAEYLKGTDFDWHIDGTVDVIPNKATV 115

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183

```

+A + GG+T FA AY+ L + Q HS Q +++ +
 Sbjct: 116 LTAHTLAEEGGQTEFASTYVAYENLTAEKEQYAQLRVLHSFEALQ-----LRRNPNTPT 170
 Query: 184 GYGMDDTATPLR--PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAP 241
 D + P R PL+ H +GR SL++G A + G D A S++ L+GL+ +
 Sbjct: 171 EVAADMKSRRPQREHPLIWRHG-SGRNSVLGATASHVVGWDDAASQQLLDGLLARSTAPQ 229
 Query: 242 RVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
 V+ H+W+ GD V+WDNR +LHR P+D PR M S L G
 Sbjct: 230 LVYRHEWSLGDTVIWDNRGVLHRVSPYDPTSPREMRSTLLG 271

>gb|ADC33994.1| TfdA-like protein [uncultured bacterium]
 Length = 195

Score = 105 bits (263), Expect = 5e-21, Method: Compositional matrix adjust.
 Identities = 70/214 (32%), Positives = 106/214 (49%), Gaps = 27/214 (12%)

Query: 56 QQITFAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW 108
 QQI FA++FG +ER + + ++N+ ADG V + W
 Sbjct: 1 QQIAFAEQFGTLERHIASNRGTVNPLVHIVTNLDADGKPSGK-----VASTRW 48
 Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
 H+D ++ P + + A+V+P G TCFADM AAY+AL +A + + + HS S
 Sbjct: 49 HSDKSFRPQPSLATILHAQVMPPDRGETCFADMIAAYEALPDAEKTELDRVRVVSWEIS 108
 Query: 169 QSKLGHVQQAGSAYIGYGMDDTATPL-RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
 +++LG +A I A P+ PLV+ PETG +L +G HA G
 Sbjct: 109 RARLG--IKAPPEEIA-----DAPPMVHPLVRTIPETGSKALFMGEHAIYFEGQPEEAGR 161
 Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
 LE L A + V+ H+W AGD+++WDNRC+
 Sbjct: 162 ARLEKLTAHAVEERFVYRHKWTAGDLLMWDNRCV 195

>ref|YP_004017313.1| taurine catabolism dioxygenase TauD/TfdA [Frankia sp. Eu1lc]
 gb|ADP81443.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. Eu1lc]
 Length = 277

Score = 105 bits (263), Expect = 5e-21, Method: Compositional matrix adjust.
 Identities = 84/283 (29%), Positives = 129/283 (45%), Gaps = 16/283 (5%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWL-QHALLIFPGQHLSNDQQITFAKR 63
 ++ ++P A +G VTG+ L D AA +L +H ++I+ H+ + + +++
 Sbjct: 2 SVTVSPISAEVGVQVTGLAGHQLADPAVAADTRKYLDEHGVVIYREAHIGDADLVALSRQ 61
 Query: 64 FG--AIERIGGG-DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ 120
 G + +GG D IS + D PA+ + G WH D V +
 Sbjct: 62 LGDVVVAPMGQQDFPEISAISLD-----PAQ-STLAAYRTGTIFYWHIDGANDLVLPQK 113
 Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
 + +A V GG T FA + AAYD+L + +A HS +Q + S
 Sbjct: 114 ATLLTALEVATEGGDTEFASLYAAYDSLSDDDKAQYAALRVVHSFAATQRL---ISPDAS 170
 Query: 181 AYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
 + + + PLV GR SLL+G A I G+ A ES L+ L+DWA Q
 Sbjct: 171 DKVRASWEKVPSREHPLVWTR-RNGRKSLLVGTADYIVGLPADESRAALLDRLLDWATQP 229
 Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
 H WA GD+V+WDN +LHRA+P+ R+M + L G
 Sbjct: 230 RFALRHWWAPGDLVIWDNTGILHRAQPYTAASRRLMHRRTLLG 272

>ref|YP_002798036.1| Taurine dioxygenase [Azotobacter vinelandii DJ]
gb|AC077061.1| Taurine dioxygenase [Azotobacter vinelandii DJ]
Length = 298

Score = 105 bits (263), Expect = 6e-21, Method: Compositional matrix adjust.
Identities = 83/266 (31%), Positives = 119/266 (44%), Gaps = 22/266 (8%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I P +GA + GV L A LD A+ A L++ +L F Q L + +Q A+ F
Sbjct: 14 LDIQPITGRIGAEIRGVKLSAGLDAVTLGAIQDALLRYKVLFFRDQTLDDAEQEGLAELF 73

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPA--EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
G D A V VR+ S E D + +WH D T++ +
Sbjct: 74 G-----DPAAHPTVP----VREGSRCLLELDSTRRA----NSWHTDVTFFVEDYPKIC 117

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ + V PA GG T +A+ AYD L R L + A HS Y + +
Sbjct: 118 ILRSLVAPAFGGDTVWANTATAYDDLPAELRELADRLWAVHSNEYDYTATQKPDVDPTVL 177

Query: 183 IGYGMDTTATPLR--PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
+ T+T PLV+VHP+ G SLL+G + G+ A+S+R L+ +A +
Sbjct: 178 AEHRRVFTSTLYETEHPLVRVHPQNGERSLLVGNFIKRVKGLSKADSQRLLDIFQGYATR 237

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
+W AGDV +WDNR LHRA
Sbjct: 238 EENTVRWRWRAGDVAIWDNRATLHRA 263

>gb|ADI22956.1| probable taurine catabolism dioxygenase [uncultured nuHF2 cluster
bacterium HF0500_39004]
Length = 325

Score = 105 bits (263), Expect = 6e-21, Method: Compositional matrix adjust.
Identities = 77/273 (28%), Positives = 117/273 (42%), Gaps = 34/273 (12%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ + GA LGA V+G L A +DD F+ +H A++++ +L+F +S D QI F K F
Sbjct: 12 ITLKKIGAYLGAEVSGADLSAEVDDVTFSEIHQAFVKNEVLVFRDLVISTDDQIRFGKMF 71

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIV-----GNMAWHADSTY 114
G + TV SP D + ++I+ G WH+D T+
Sbjct: 72 GEL-----TVHPFSPNS-DKIPELIIFDNKEDNPPFGTDIWHSEDTF 112

Query: 115 MPVMAQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
G A VP VGG T FA M AAY+ L + + + A H +
Sbjct: 113 RQCPPLGTCLRALDVPEVGGDTVFA SMSAAYEGLSDRMKNFISGLEAIHDFKPFKQLFDD 172

Query: 175 VQQAGSAYIGYGMDTTATPL-RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEG 232
+ + + P+ P+V+ HP TG S+ + + + GM+ ES L
Sbjct: 173 DDEGRKELQRFEL--MYPPVTHPIVRTHPVTGNKSIFVNPQFTIRVIGMNEIESRSLTLD 230

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L D A + H W +V+WDNR + H A
Sbjct: 231 LFDLAKIPEYQYRHHWYNNMTMVLWDNRSVQHHA 263

>ref|YP_003342517.1| taurine dioxygenase [Streptosporangium roseum DSM 43021]
gb|ACZ89774.1| Taurine dioxygenase [Streptosporangium roseum DSM 43021]
Length = 282

Score = 105 bits (263), Expect = 6e-21, Method: Compositional matrix adjust.
Identities = 74/269 (27%), Positives = 121/269 (44%), Gaps = 30/269 (11%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ P +GA V+GV L L + L WL+H +L F QH+++++ + FA+ F
Sbjct: 2 IEFKPVTRHIGAEVSGVDLRKPLSEGEVQELRRGWLEHKVLFVRDQHINDEEHVRFANF 61

Query: 65 GAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
G+I ++ GG I + G G WH+D+T+ PV
Sbjct: 62 GSINHPAFKKDGGSPIHVLDQTDPKGE-----GGDEWHSNTFEPVPP 104

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
G++ +P+VGG T +A+ AY+ L + L + +A H + S K G
Sbjct: 105 MGSLLRCVQLPSVGGDTMWANSYLAYETLSPPIQRLCDELTAIHDTASMKK---AISKG 161

Query: 180 SAYIGYGMDDTTATPL-RPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWA 237
+ + P+ RP+V+VH ETGR +L + R + + + E+E L L+D
Sbjct: 162 HDFDLAEIQAKWPPIERPVRVHAETGRKALFVNRASTTRLVQLSDRENEALLPYLID-H 220

Query: 238 CQAPRVHAH-QWAAGDVVWDNRCLLHRA 265
++P W G + WDNR H A
Sbjct: 221 IRSPEYQVRLNWRPGTMAFWDNRSTQHYA 249

>gb|ADC33996.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 105 bits (263), Expect = 6e-21, Method: Compositional matrix adjust.
Identities = 69/214 (32%), Positives = 107/214 (50%), Gaps = 27/214 (12%)

Query: 56 QQITFAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW 108
QQI FA++FG +ER + + ++N+ ADG V + W
Sbjct: 1 QQIAFAEQFGLERHMASNRGTVNPLVHIVTNLADGKPSGK-----VASTGW 48

Query: 109 HADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
H+D ++ P + + A+V+P GG TCFADM AAY+AL +A +A + + HS S
Sbjct: 49 HSDKSFRPQPSLVTLHAQVMPPDGGETCFADMIAAYEALPDAEKAELDRVRVVSWEIS 108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPL-RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
++++G +A I A P+ PLV+ PETG +L +G HA G
Sbjct: 109 RARMG--IKAPPEEIA-----DAPPMVHPLVRTIPETGSKALFMGEHAVYFQGQPEEVGR 161

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCL 261
LE L A + ++ H+W GD+++WDNRC+
Sbjct: 162 ARLEKLTAAHAVEERFIYRHKWTVGDLLMWDNRCV 195

>ref|ZP_07706655.1| putative taurine dioxygenase [Dermacoccus sp. Ellin185]
gb|EFP56903.1| putative taurine dioxygenase [Dermacoccus sp. Ellin185]
Length = 317

Score = 105 bits (263), Expect = 6e-21, Method: Compositional matrix adjust.
Identities = 87/271 (32%), Positives = 118/271 (43%), Gaps = 19/271 (7%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQIT 59
+A L+I G GA V GV LA +DDA L A L H +L F GQ +D Q+
Sbjct: 26 VATPGLRIERLGPFAIVHGVDLAQVDDAIAFDLRRALLAHKVLFVRGQDAFDDDAQVR 85

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
G E G + + K ++ P + WH D T+M
Sbjct: 86 LGNLLG--ELTAGHPVASTHERKEIYSIDSSDPE-----FSFSDEWHTDVTFMKEPP 135

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
++ A +P GG T +AD +AAYD+L + R LV Q A H + G +
Sbjct: 136 AISILRAVTLPDYGGDTSWADAQAAYDSLKPFGRGLVDQLIAAHD---GNREWGAYLRKH 192

Query: 243 VHAHQWAAGDVVVWDNRCLLHRA 265
W +GDV +WDNR H A
Sbjct: 248 TTRWNWOSGDVAIWDRNRATOHYA 270

>ref|YP_479369.1| taurine dioxygenase [Frankia sp. CcI3]
gb|ABD09640.1| Taurine dioxygenase [Frankia sp. CcI3]
Length = 308

Score = 105 bits (262), Expect = 7e-21, Method: Compositional matrix adjust.
Identities = 74/266 (27%), Positives = 112/266 (42%), Gaps = 19/266 (7%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L + P +GA + GV L LDDA A + + Q ++ FPGQ++ + QQ+ F +RF
Sbjct: 10 LDVRPLSGYIGAEIHGVDLREDLDDATIAEIRSTLHQWKVVFPGQNIDHAQQVAFGRRF 69

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G + + + + A + K + + WH D T + ++
Sbjct: 70 GKLTPAHPHEDAPPAGFPEILPIDSRRYARFFGTTKKVTDNGWHTDVTALVNPPAASIL 129

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
A +VP GG T + ++ AAY L E R L + ARHS G+
Sbjct: 130 RAGIVPPYGGDTAWTNLVAAYQELPEQLRDLANGLRARHS-----FGNFPSESE---- 178

Query: 185 YGMDTTATPL---RPLVKVHPETGRPSLLIG----RHAHAIPGMDAAESERFLEGLVDWA 237
YG A PL P+V+VHPETG +L + I G +S R L+ +
Sbjct: 179 YGRKVAANPLVAIHPVVRVHPETGERALFVSPSFTSKDSEIIGFSPKQSRRIIDLDFYEQI 238

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLH 263
+ +W GD+ WDNR H
Sbjct: 239 SRPEFTVRFKWNPGDIAFWDNRATSH 264

>ref|ZP_05226146.1| taurine catabolism dioxygenase TauD/TfdA [Mycobacterium
intracellulare ATCC 13950]
Length = 276

Score = 105 bits (262), Expect = 7e-21, Method: Compositional matrix adjust.
Identities = 84/290 (28%), Positives = 132/290 (45%), Gaps = 28/290 (9%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
++ T L + +G+ + L A+ A Q ++ F G +S++QQ+T
Sbjct: 3 LSTTRLDVDICTPLIGSEIKTDLDTLLSGREAEAIRAILEQRGVVFRRGLQISDEQQVTI 62

Query: 61 AKRFGAI-ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
AK G+I + G G I IS D V Q + + + G++ WH D + P
Sbjct: 63 AKTLGSIVQNEGEGGIYKIS---LDTNVNQRA-----EYLKGSFLWFHFDGSLQPYPN 111

Query: 120 QGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRA-----LVHQRSARHSLVYSQSKLG 173
+ A + GG+T F + AAY+ L EA + +VH SA S Y + ++
Sbjct: 112 LATLLRAMKLSDSGGQTEFCNTYAAYEELPEADKETIAGLRVVH--SAERSQYYVRPEMS 169

Query: 174 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+ + A + T P+V H +GR SLL+G A + + ES L L
Sbjct: 170 YEEIAF-----WQKSPTKSCPMVWTH-RSGRKSLLLGATADYVIDLPVEESRALLARL 221

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
DWA Q V+ H+W GD+++WDN +HRA P+ R+M + LAG
Sbjct: 222 RDWATQPRYVYRHEWRLGDLLMWDNTGTMHRALPYAADSGRLMHRTVLAG 271

>ref|ZP_08197519.1| taurine dioxygenase, TauD/TfdA family [Nocardioidaceae bacterium
Broad-1]
gb|EGD43041.1| taurine dioxygenase, TauD/TfdA family [Nocardioidaceae bacterium
Broad-1]
Length = 315

Score = 105 bits (262), Expect = 7e-21, Method: Compositional matrix adjust.
Identities = 85/284 (29%), Positives = 124/284 (43%), Gaps = 22/284 (7%)

```
Query: 6  LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRF 64
      +++  GA +GA + G+ LA  DD      + +A L+H +L F GQ  L++++Q  FA RF
Sbjct: 19  VRVRRAGARIGAVIEGLRLAEADDTQIQDVRALLRHKVLFFRGQDGLTDEEQSAFAARF 78

Query: 65  GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
      G +      A TV  S      +  AWH D T++  +  +V
Sbjct: 79  GEL-----TTAHPTVNTGSGRVL RVTANAGMAANAWHTDVT FVDRVPAISVL 125

Query: 125  SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
      A +P  GG T +A+  AYD L  +AL  +  A H+  Y  ++  +  A
Sbjct: 126  RAVTLPPYGGTTIWANTAVAYDRLPSPLKALADELWAVHTNSYDYAQRDEEHEQPDA--N 183

Query: 185  YGMDTTAT---PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
      Y  D  A+      P+V+VHPETG  SL++G      G+ +  ES      L D  +
Sbjct: 184  YSRDDFASIHFETRHPVVRVHPETGERSLVLGSEFVKEFDGLTSTESIHLFNLLQDRVTKL 243

Query: 241  PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFK-LPRVMWHSRLAG 283
      W  GDV +WDNR  H A  DF  PR M  +AG
Sbjct: 244  ENTIRWAWQPGDVAMWDNRATQHYAVA-DFDHHPREMRRVTVAG 286
```

```
>ref|NP_252624.1| taurine dioxygenase [Pseudomonas aeruginosa PAO1]
ref|YP_002438647.1| taurine dioxygenase [Pseudomonas aeruginosa LESB58]
ref|ZP_04930151.1| taurine dioxygenase [Pseudomonas aeruginosa C3719]
gb|AAG07322.1|AE004811_5 taurine dioxygenase [Pseudomonas aeruginosa PAO1]
gb|EAZ54270.1| taurine dioxygenase [Pseudomonas aeruginosa C3719]
emb|CAW25768.1| taurine dioxygenase [Pseudomonas aeruginosa LESB58]
      Length = 277
```

Score = 105 bits (262), Expect = 8e-21, Method: Compositional matrix adjust.
Identities = 83/265 (31%), Positives = 117/265 (44%), Gaps = 15/265 (5%)

```
Query: 5  TLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
      +L I P      LG A V+G+ L A LDD G  A+  A L+H +L F  Q L      Q  FA R
Sbjct: 2  SLTIQPISPALGAIVSGIDLGA PLDDTGQRAIEQALLESQVLFVRDQSLERPSQARFAAR 61

Query: 64  FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
      FG +      I  +      Q      D  +  +  N  WH D T++  A GAV
Sbjct: 62  FGD LH-----IHPIYP-SVPEQPEVIVLDTAVTDVRDNAIWHTDVTFLET PALGAV 111

Query: 124  FSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQQAGSA 181
      +A+ +P  GG T +A  AAY+AL  R L+  +A H+  +  +  +  G V +A  A
Sbjct: 112  LAAKQLPPYGGDTLWASSTAAYEALSAPLRRLDGLTATHDIGKSFPRERFG-VTEADLA 170

Query: 182  YIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQA 240
      +      P+V+  HP TGR  L  +      I  ++ AES+  L+ L  A  +
Sbjct: 171  RLEEARLKNPPRSHPVVRTHPVTGRKGLFVSDGFTTRINELEPAESDALLKFLFAHATRP 230

Query: 241  PRVHAHQWAAGDVVVWDNRCLLHRA 265
      +W  DV  WDNR  H A
Sbjct: 231  EFTVRWRWQENDVAFWDNRVTQHYA 255
```

```
>ref|ZP_01367370.1| hypothetical protein PaerPA_01004522 [Pseudomonas aeruginosa
PACS2]
      Length = 277
```

Score = 105 bits (262), Expect = 8e-21, Method: Compositional matrix adjust.
Identities = 83/265 (31%), Positives = 117/265 (44%), Gaps = 15/265 (5%)

Query: 5 TLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+L I P LGA V+G+ L A LDD G A+ A L+H +L F Q L Q FA R
Sbjct: 2 SLTIQPIPALGAIVSGIDLGAPLDDTGQRAIEQALLEHQVLFRRDQSLEPRSQARFAAR 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG + I + Q D + + N WH D T++ A GAV
Sbjct: 62 FGDLH-----IHPIYP-SVPEQPEVIVLDTAVTDVRDNAIWHTDVTFLFETPALGAV 111

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQQAGSA 181
+A+ +P GG T +A AAY+AL R L+ +A H + + + + G V +A A
Sbjct: 112 LAAKQLPPYGGDTLWASSTAAYEALSAPLRRLLDGLTATHDIGKSFPRERFG-VTEADLA 170

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQA 240
+ P+V+ HP TGR L + I ++ AES+ L+ L A +
Sbjct: 171 RLEEARLKNPPRSHPVVRTHPVTGRKGLFVSDGFTTRINELEPAESDALLKFLFAHASRP 230

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRA 265
+W DV WDNR H A
Sbjct: 231 EFTVRWRWQENDVAFWDNRVTQHHA 255

>ref|YP_003732168.1| putative alkylsulfatase (AtsK) [Acinetobacter sp. DR1]
gb|ADI90795.1| putative alkylsulfatase (AtsK) [Acinetobacter sp. DR1]
Length = 317

Score = 105 bits (262), Expect = 8e-21, Method: Compositional matrix adjust.
Identities = 72/274 (26%), Positives = 123/274 (44%), Gaps = 36/274 (13%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L + +GA ++G+HL++ LD + +H A L++ +L F GQ HL + +Q FA+
Sbjct: 12 LHVKKLTGRIGAEISGIHLSSSELDSSVTQFIHDALLEYKVLFFRQGHLDTEQEKFAEL 71

Query: 64 FGA-----IERIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPV 117
FG+ + + G D I + + R +S WH D T++
Sbjct: 72 FGSPVKHPTVPAVDGTD--IFELDSQKGARANS-----WHTDVTFVDA 113

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY-----SQSK 171
+ ++ + ++P GG T +A+ AY+ L E + Q A HS Y +
Sbjct: 114 YPKISILRSLIIPETGGDTTWANTETAYEDLPPELLKQFAEQLVAVHSNEYDYGGPKQNV 173

Query: 172 LGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE 231
+++ ++ +T P+V +HPETG+ SLL+G + G ++S+
Sbjct: 174 PEQLERLKKIFVSTKYETE---HPVVVLPETGKKSLLLGHFFKRLVGFSQSDSQLLFN 229

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L + + QW GDVV+WDNR H A
Sbjct: 230 ILQEKVTRPENTVRWQWQEGDVVIWDNRSTQHHA 263

>gb|ADC34001.1| TfdA-like protein [uncultured bacterium]
gb|ADC34013.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 105 bits (262), Expect = 8e-21, Method: Compositional matrix adjust.
Identities = 69/214 (32%), Positives = 104/214 (48%), Gaps = 27/214 (12%)

Query: 56 QQITFAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPAEDMMKVIVGNMAW 108
QQI FA++FG +ER + + ++N+ ADG V + W
Sbjct: 1 QQIAFAEQFGTLERHMASNRGTVNPLVHIVTNLADGNPSGK-----VASTGW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
H+D ++ P + + A+V+P GG TCFA+M AAY+AL A +A + HS S

Sbjct: 49 HSDKSFRPRPSLATILHAQVMPPDGGETCFANMIAAYEALPGAEGAELDGVVRVVSWEVS 108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTATPL-RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
++++G A A P+ PLV+ PETG +L +G HA G

Sbjct: 109 RARMGITAPAEI-----ADAPPMVHPLVRSIPETGSKALFMGEHAVYFEGQPEEAGR 161

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
LE L A + V+ H+W AGD+++WDNRC+

Sbjct: 162 ARLEKLTAAHAVEERFVYRHKWTAGDLLMWDNRCV 195

>gb|ACX54981.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 93

Score = 105 bits (261), Expect = 9e-21, Method: Compositional matrix adjust.
Identities = 59/96 (61%), Positives = 68/96 (70%), Gaps = 4/96 (4%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYMP+ A+GAVFSA+ VP GG T +ADMRAAYDALDE RA + A HSL YSQ

Sbjct: 1 ADSTYMP LQAKGAVFSAKEVPTHGGETGWADMRAAYDALDEELRAKLEGLAYHSLYYSQ 60

Query: 170 SK-LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET 204
K LG++ +A SA YG+ PLR LVKVHPET

Sbjct: 61 GKVLGYMPKANSA---YGLHEGPPPLRKLKVHPET 93

>ref|NP_824171.1| dioxygenase [Streptomyces avermitilis MA-4680]
dbj|BAC70706.1| putative dioxygenase [Streptomyces avermitilis MA-4680]
Length = 306

Score = 105 bits (261), Expect = 9e-21, Method: Compositional matrix adjust.
Identities = 83/281 (29%), Positives = 133/281 (47%), Gaps = 36/281 (12%)

Query: 12 GATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPG-QHLSNDQQITFAKRFGAIER 69
G+ +GA V G + T+DD + A QH +L+F G + SND + FA+RFG + +

Sbjct: 12 GSAIGAVVAGADFSGTIDDTQVEEIQALDQHLVLVFRGHKDPNSDDLLMFARRFGHVPK 71

Query: 70 IG-----GGDIVAISNVKADGTVRQHSPAEDDMMKVIVGN---MAWHADSTYMPVM 118
G +I+ ISN+ + + K+ VGN M WH D ++ P +

Sbjct: 72 TGLTTGASPDHNEILLISNILDE-----NGQKIGVGNAEWMDWHTDYSFRPRV 119

Query: 119 AQ-GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-----VYSQSK 171
++ G + + E+ P+ GG+T F DM AY++L + R +H ARHSL V +

Sbjct: 120 SRIGFLAAVELPPSGGGQTLFTDMYTAYESLPDDLRLQRLHSYRARHSLRSGYEDVIEEFY 179

Query: 172 LGHVQQAGSAYIGY--GMDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESER 228
G V G + D TAT + L+ +P TGR ++ + I +D S+

Sbjct: 180 QGEVSIIEGPTAKPFVAPEDGTAT-VHQLIARNPRTGRRAYANPLNTRKILELDVTSKE 238

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD 269
L+ L + +AH+W GD+V+WD +H +D

Sbjct: 239 VLQQLFAKPGEPELTIAHEWLPGDIVMWDQLGTVHAKRAFD 279

>ref|ZP_05217892.1| taurine catabolism dioxygenase TauD, TfdA family protein
[Mycobacterium avium subsp. avium ATCC 25291]
Length = 281

Score = 105 bits (261), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 93/291 (31%), Positives = 131/291 (45%), Gaps = 27/291 (9%)

Query: 4 TTLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61

```

      + L IT    ++GA VTG+  A L  DD+   A+  A   + +L+F G +L    Q+ F
Sbjct: 2  SLLTITKLTDSVGA EVTGLDPAALAHDDSVGEAVLDALEDNGVLVFRGLYLDPAAQVAF 61

Query: 62  KRFGAIERIGGG-----DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMP 116
      R G ++   G       I  I+  K+       +  A +D               WH D   P
Sbjct: 62  GRLGEVDHSSDGHHPVPGIYPITL DKSKNASAAYLKATFD-----WHIDGC-TP 109

Query: 117 V----MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
      +      +  V SA  V   GG T FA+  AAYDAL +  +              HSL  SQ +
Sbjct: 110 LGDECPQKATVLSAVRVAERGGETEFANSYAA YDALTDDEKRRFGALRVVHSLEASQRR- 168

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG 232
      V    S +      +  T  PLV  H  +GR SL++G  A  +  GMD  E    LE
Sbjct: 169 --VYPDPSPELVARWRSRRTHEHPLVWTH-RSGRKS LVLGASADYVVGMDLDEGRALLEE 225

Query: 233 LVDWACQAPRVHAHQWAAGDVVVW DNRCLLHRAEPWDFKLPRVMWHSRLAG 283
      L+  A    RV++H W+  GD V+WDNR +LHRA P+D    R M  +  +  G
Sbjct: 226 LLQRATVPERVYSHGWSIGDTVIW DNRGVLHRAAPYDPDSSREMLRTTVLG 276

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>ref|YP_119465.1| putative dioxygenase [Nocardia farcinica IFM 10152]
dbj|BAD58101.1| putative dioxygenase [Nocardia farcinica IFM 10152]
Length = 308

Score = 105 bits (261), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 84/288 (29%), Positives = 129/288 (44%), Gaps = 19/288 (6%)

```

Query: 1  MAQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQI 58
      ++Q+ ++   GA +GA V GV L   LD    A+ AA  +H ++ F GQ HL+ D Q
Sbjct: 4  VSQSAVRVKLG AHIGAVVEGVRLCGDLDPETVTAVRAALHEHKVIFFRGQDHLTEDGQY 63

Query: 59  TFAKRFGAIERIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVM 118
      FA+  G       A   VK+   +H  A               +WH D T++  +
Sbjct: 64  EFAQLLGTPPTPHPTVTSA--GVKSLAIDSRHGRAN-----SWHTDVTTFVDRV 109

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ-- 176
      + ++  AE +P+ GG T +A   AAY++L +  + L   ARH+ +Y  +  +
Sbjct: 110 PKASILRAERLPSYGGSTTWASTVAAYNSLPDPLKRLAEGLRARHTNLYDYAAEAEDRPD 169

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW 236
      +  AY      T      P+V+VHP+TG  +LL+G   I G+ +  ES      D
Sbjct: 170 ENVRAYRREFESTYYETEHPVVEVHPDTGERALLLGHFVKRIVGLPSTESHALFRLFQDR 229

Query: 237 ACQAPRVHAHQWAAGDVVVW DNRCLLHRA-EPWDFKLPRVMWHSRLAG 283
      +      WA GDV +WDNR  H A  + +D    R  +    LAG
Sbjct: 230 VTRLEHTTRWHWAPGDVAIWDNRATQHYAIDDDYDGSEHRLRTRITLAG 277

```

>ref|ZP_07603129.1| Taurine dioxygenase [Streptomyces violaceusniger Tu 4113]
gb|EFN21346.1| Taurine dioxygenase [Streptomyces violaceusniger Tu 4113]
Length = 287

Score = 105 bits (261), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 78/283 (27%), Positives = 122/283 (43%), Gaps = 47/283 (16%)

```

Query: 1  MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQIT 59
      M  + L +TP    LGA +  GV L  L D  F  +H   L H ++ FPGQ HL+ +  I
Sbjct: 1  MPTSELMVTPVSGALGAEIRGVDLT ETLDELFE RVHEL L L GHLVVFFPGQEHLTP EAHIA 60

Query: 60  FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADST 113
      +R G +E      ++ G  +  +  +      +              WH D T
Sbjct: 61  LGRRLGELEVHPFLPKVEGHPEIVVL DADQGAKE-----WHIDVT 102

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Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
+ P ++ +V PA GG T +++ Y+ L E R L+ +A H L Q+
Sbjct: 103 FQPNPPVASILHLQVCPASGGDTMWSNQYLVYETLSEPMRELLDGLTAVHVLNTPQTGEH 162

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEG 232
+ P+V++HPETGR SL + R IP + ES+ L+
Sbjct: 163 SAEH-----PVVRIHPETGRRSLYVTRMWTSHIPQLSRPESDALLQY 204

Query: 233 LVDWACQAPRVHA-HQWAAGDVVVWDNRCLLHRAEPWDFKLPR 274
L + + ++PR + ++W G V +WDNR H A D+ PR
Sbjct: 205 LFEHS-ESPRFNCRYRWQPGAVAMWDNRATQHLAVN-DYTEPR 245

>gb|EGB10818.1| hypothetical protein AURANDRAFT_5093 [Aureococcus anophagefferens]
Length = 275

Score = 104 bits (260), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 91/287 (31%), Positives = 137/287 (47%), Gaps = 28/287 (9%)

Query: 8 ITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRF 65
+ P + LG V G+ L + LDD A+ A H ++ F GQ L+ +QQ+ F KR+G
Sbjct: 2 VEPLSSALGVEVVGLDLRSPLDDDDTVDAITALLDAHLVVCFRGQTSLTPEQQVAFTKRWG 61

Query: 66 AIER--IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM---PVMA 119
A+E +G + + + V + V Q+ + D V N WH D + M PV A
Sbjct: 62 AVEPHPLGSREEIHPAGVP EEVLVAQNRLVDGDS-----VRNDIWHTDLSCMRGRGPV-A 115

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
A+ EV G T FA+ R AY L E +ALV A H+ + H ++AG
Sbjct: 116 YTALLGVEVPREGWGDTLFANTRQAYRGLSEGYKALVDDDLRAVHNTM-----HFERAG 168

Query: 180 SAYIGYGMDDTTATPLRPLVKVHPETGRPSL-LIGRHAHAIPGMDAAESERFLEGLVDWAC 238
+A+ + PLV+ HP TG +L L G + GM ES ++ L+ A
Sbjct: 169 KME---NFTASASSVHPLVRTHPRTGEDALYLSGNFIDRVDGMGRDESRPLVDALIAHAT 225

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFK--LPRVMWHSRLAG 283
+ H+W AGD+V+WDN +H A +D+ + R M + +AG
Sbjct: 226 SPIYTYRHRWRAGDLVMWDNAATMHYAV-FDYAAGMARTMHRTTVAG 271

>ref|ZP_06414085.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EUN1f]
gb|EFC83110.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EUN1f]
Length = 278

Score = 104 bits (260), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 86/285 (30%), Positives = 128/285 (44%), Gaps = 19/285 (6%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWL-QHALLIFPGQHLSNDQQITFAKR 63
++ +TP G LG + GV L A AA L +H ++I+ H+ + + F++
Sbjct: 2 SVTVTPLGPHLGVEIAGVSGGDLPTAEAAAECELLARHGVIYREAHIKDGLVAFSRL 61

Query: 64 FGAI--ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMK-VIVGNMAWHADSTYMPVMAQ 120
G + G ++ I+ + D PA+ D + GN WH D + +
Sbjct: 62 LGEVVPNPTGEHELPEIATITLD-----PAKTDATLAWYRRGNFLWHIDGATDQLPQK 114

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
+ +A V GG T FA AAY+AL EA +A HS +Q + H
Sbjct: 115 ATLLTAREVDPAGGDTEFASTYAAEALPEAEKAADFALQVLHSFAAAQLR-AHPDATDE 173

Query: 181 AYIGYGMDDTTATPLR--PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC 238
+G P+R PLV GR SLL+G A + G+ E E L L+DW+
Sbjct: 174 QKASWGR----VPVRRHPLVWTR-GNGRRSLLL GATAGEVIGLPPEEGEALLARLLDWST 228

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
Q V H+W GD+V+WDN +LHRA P+ R+M + L G
Sbjct: 229 QPQFVLRRHWTGDLVIWDNTGMLHRALPFTATSRRLMHRITTLVG 273

>ref|ZP_06494532.1| taurine catabolism dioxygenase TauD/TfdA [Pseudomonas syringae pv. syringae FF5]
Length = 279

Score = 104 bits (260), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 81/249 (32%), Positives = 122/249 (48%), Gaps = 22/249 (8%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAI--ERIGGGDIVAIS-NVKADGTVRQHSPAEWDD 97
Q +L+FP H S+ +QI F + G E G +I IS +VK + PA
Sbjct: 44 QRGVLVFPQIHFSDAEQIAFTRTLGTFCPEPGDQGNITRISLDVKEN-----PAG--- 93

Query: 98 MMKVIVGNMAWHADSTYM--PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL 155
+ + G++ WH D T P++A ++ S +V + GG T F + +AY+ L A R
Sbjct: 94 -AEFLKGSLYWHIDGTSSDSPILA--SLLSCKVPASWGGNTGFCNTYSAYEGLSSADRQ- 149

Query: 156 VHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHA 215
H S R S L + + G A + M PLV H +GR SL++G A
Sbjct: 150 -HYDSLRLVIHAPWASLLYYNPEPGLAML-EAMQAIGEKEKELPLVWKH-RSGRKSILIGCTA 206

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRV 275
+ G+ A+S R L GL +WA ++H W GD+V+WDN +HRAE +D + R+
Sbjct: 207 QQVVGLSLAQ SARILVGLREWATSEAFSYSHAWQVGDVLIWDNTGTMHRAEAYDPECGRM 266

Query: 276 MWHSRLAGR 284
M ++L G
Sbjct: 267 MHRTKLQGE 275

>gb|ADC34008.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 104 bits (260), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 72/213 (33%), Positives = 103/213 (48%), Gaps = 25/213 (11%)

Query: 56 QQITFAKRFGAIER--IGGGDIVA-----ISNVKADGTVRQHSPAEWDDMMKVIVGNMAW 108
QQI FA++FG +ER + V ++N+ ADG V + W
Sbjct: 1 QQIAFAEQFTLERHVVSNRGTVNPLVHIVTNLGADGKPSGK-----VASTQW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
H+D ++ P + + A V+P GG TCFADM AAY+AL EA +A + HS S
Sbjct: 49 HSDKSFRPQP SLATILHALVMPPQGGETCFADMVAAYEALPEAEKAELAGVRVHWSWGLS 108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER 228
Q+++G + I D PLV+ PETGR +L +G A + G
Sbjct: 109 QARVG--IKVPPEEIADAPDIA---HPLVRTIPETGRKALFMGERAVHLEGQPEDVGR 162

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
LE L A Q V+ H+W GD+++WDNRC+
Sbjct: 163 RLRLTAHAVQERFVYRHKWTLGDLLMWDNRCV 195

>ref|ZP_06308911.1| Taurine catabolism dioxygenase TauD/TfdA [Cylindrospermopsis raciborskii CS-505]
gb|EFA69033.1| Taurine catabolism dioxygenase TauD/TfdA [Cylindrospermopsis raciborskii CS-505]
Length = 304

Score = 104 bits (260), Expect = 1e-20, Method: Compositional matrix adjust.

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
+ +TP +GA V GV L+ L + F AL+ A+L+H +L F Q ++ QQI AKRFG
Sbjct: 1 MNLTPLSEHIGALVEGVDLSNLSEQEFDALYQAYLKHKVLFFRDQGMTPQQQIGLAKRFG 60

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
+ E + + + V + SP G WH D T+ + ++
Sbjct: 61 DLEPV--HPFFPHLDDEEQVVVIETSPGN-----PPGESFWHTDLTWQATPCRC SILQ 111

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-VYSQSKLGHVQQAGSAYIG 184
A+ P GG T + M A + +L + + +A H L + S+ V + G +++
Sbjct: 112 AQHCPPHGGDTIWTSM EAVWSSLTSDDQHTLRGLTATHGLHAFEGSRYDSVNEQGESHVA 171

Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAPRV 243
PLV HPETG + + H I ++ ES + LE L A Q
Sbjct: 172 TVSQGYPPVKHPLVVRHPETGNLTAYVNEQFTHRINELEERESRKRLEQLFALARQPEYQ 231

Query: 244 HAHQWAAGDVVVDNRCLLHRA 265
W G V +W D N C H A
Sbjct: 232 VQFSWQPGSVAIWDNICTQHFA 253

>gb|ACX54974.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 98

Score = 104 bits (260), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 55/98 (56%), Positives = 67/98 (68%), Gaps = 3/98 (3%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYMP+ A+GAVFSAE++P+ GG T +ADMRAAY+ALD+ TRA + A HSL YSQ
Sbjct: 1 ADSTYMP LQAKGAVFSAEIIIPSEGGATGWADMRAAYEALDDDTRARIADLRAHHS LFYSQ 60

Query: 170 SKLGHV---QQAGSAYIGYGMDTTATPLRPLVKVHPET 204
+ G++ Q Y YG LRPLVKVHPET
Sbjct: 61 GRAGYLPSKQNERGGYDMYGYHDEEPSLRPLVKVHPET 98

>gb|ACX54986.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 98

Score = 104 bits (260), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 55/98 (56%), Positives = 66/98 (67%), Gaps = 3/98 (3%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYMPV A+GAVFSAE+VP+ G T +ADMRAAYDA+DE R + ARHSL YSQ
Sbjct: 1 ADSTYMPVQAKGAVFSAEIVPSEGAATGWADMRAAYDAMD EPMRERISAMRARHSLWYSQ 60

Query: 170 SKLGHV---QQAGSAYIGYGMDTTATPLRPLVKVHPET 204
+ G++ + Y YG P+RPLVKVHPET
Sbjct: 61 ERAGYLPSKRNERGGYDQYGYHDLDPVVRPLVKVHPET 98

>ref|NP_962069.1| hypothetical protein MAP3135c [Mycobacterium avium subsp.
paratuberculosis K-10]
gb|AAS05683.1| hypothetical protein MAP_3135c [Mycobacterium avium subsp.
paratuberculosis K-10]
Length = 281

Score = 104 bits (260), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 93/291 (31%), Positives = 130/291 (44%), Gaps = 27/291 (9%)

Query: 4 TTLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
+ L IT ++GA VTG+ A L DD+ A+ A + +L+F G +L Q+ F
Sbjct: 2 SLLTITKLTD SVGA EVTGLDPAALAHDDSVGEAVLDALEDNGVLVFRGLYLDPA A QVAF C 61

Query: 62 KRFGAIERIGGG-----DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
R G ++ G I I+ K+ + A +D WH D P
Sbjct: 62 GRLGEVDHSSDGHHPVPGIYPITLDSKSNASAYLKATFD-----WHIDGC-TP 109

Query: 117 V----MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+ + V SA V GG T FA+ AAYDAL + + HSL SQ +
Sbjct: 110 LGDECPQKATVLSAVRVAERGGETEFANSYAAAYDALTDDEKRRFGALRVVHSLEASQRR- 168

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG 232
V S + + T PLV H +GR SL++G A + GMD E LE
Sbjct: 169 --VYPDPSPELMARWRSRRTHEHPLVWTH-RSGRKS LVLGASADYVVGMDVDEGRALLEE 225

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L+ A RV+ H W+ GD V+WDNR +LHRA P+D R M + + G
Sbjct: 226 LLQRATVPERVYRHGWSIGDTVIWDNRGVLHRAAPYDPDSSREMLRTTVRG 276

>ref|ZP_07795333.1| taurine dioxygenase [Pseudomonas aeruginosa 39016]
gb|EFQ40429.1| taurine dioxygenase [Pseudomonas aeruginosa 39016]
Length = 277

Score = 104 bits (260), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 83/265 (31%), Positives = 116/265 (43%), Gaps = 15/265 (5%)

Query: 5 TLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+L I P LGA V+G+ L A LDD G A+ A L+H +L F Q L Q FA R
Sbjct: 2 SLTIQPIPALGAIVSGIDLGA PLDDTGQRAIEQALLEHQVLFRRDQSLEPRSQARFAAR 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG + I + Q D + + N WH D T++ A GAV
Sbjct: 62 FGD LH-----IHPIYP-SVPEQPEVIVLDTAVTDVRDNAIWHTDVTFLTPALGAV 111

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQQAGSA 181
+A+ +P GG T +A AAY+AL R L+ +A H + + + + G V +A A
Sbjct: 112 LAAKQLPPYGGDTLWASSTAAYEALSAPLRRLLDGLTATHDIGKSFPRERFG-VTEADLA 170

Query: 182 YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQA 240
+ P+V+ HP TGR L + I ++ AES+ L L A +
Sbjct: 171 RLEEARLKNPPRSHPVVRTHPLTGRKGLFVSDGFTTRINELEPAESDALLTFLFAHATRP 230

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRA 265
+W DV WDNR H A
Sbjct: 231 EFTVRWRWQENDVAFWDNRVTQHYA 255

>ref|YP_003490344.1| dioxygenase [Streptomyces scabiei 87.22]
emb|CBG71801.1| putative dioxygenase [Streptomyces scabiei 87.22]
Length = 325

Score = 104 bits (259), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 93/299 (31%), Positives = 134/299 (44%), Gaps = 23/299 (7%)

Query: 3 QTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
+ TL + P +GA + GV LA LDD A + AA L+ ++ F GQ L + QI FA
Sbjct: 13 EDTLDVRPASGHIGADIHGVDLAGPLDDTTVAGIRAALLRWKVVFRRGQRLDHAGQIAFA 72

Query: 62 KRFGAIERI-GGGDIVAISNVKADGTV-----RQH--SPA EWDDMMKVIVGNMAWHADS 112
R G R+ G + + + + T R+H AEW + + WHAD
Sbjct: 73 HRLGEPVRLRARGSVSPAAYPEIETTADRQELGRKHGMDQAEWLERRRHSTLR-GWHADH 131

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
T + AE VP GG T +A++ AY L E R A H L +
Sbjct: 132 TARIDPPALTLLRAERVPPYGGDTTANLATAYAGLSEPVRRFADGLRAEHRL-----GV 186

Query: 173 GHVQQAG-SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFL 230
G++ ++G Y+ + D + P+V+VHPETG L + + I + AES L
Sbjct: 187 GYLARSGDPYLRHLQDHQVASVHPVVRVHPETGERILYVNPYYVEHIVDVSRAESRLLL 246

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAG-RP 285
E V+ + +W G V +WDNR +H A P D PR+M +AG RP
Sbjct: 247 EMFVEQITRPEYTVRFRWEFPGSVALWDNRATVHLA-PSDAAHLDFPRIMHRVMIAGDRP 304

>gb|AD085576.1| PntD [Streptomyces arenae]
Length = 299

Score = 104 bits (259), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 82/289 (28%), Positives = 129/289 (44%), Gaps = 28/289 (9%)

Query: 6 LQITPT-GATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHL-SNDQQITFAK 62
+++TP GA LGA V G + +D + +A + +L+ G S ++ + F +
Sbjct: 1 MEVTPIPGAPLGAVVHGARGVTGDMCKTHLEEIWSALDTYLVVLVRGHETPSYEEFLAFGR 60

Query: 63 RFGAIERIG-----GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTY 114
RFG I + G +I+ +SN+ DG AEW M WH D ++
Sbjct: 61 RFGHIPKTGLTSGAHPEHNEILIVSNLVEDGRKIGVGDAEW-----MGWHTDYSF 110

Query: 115 MPVMAQGAVFSAEVVP-AVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
P ++Q A VP + GG T F DM A Y++L R +H RH+L +
Sbjct: 111 RPRVSQVGFLEAVEVPYSGGETLFTDMYALYESLSPEERRRLHSFRVRHALRTGYEETI 170

Query: 174 HVQQAGSAYIGYGMDTT-----ATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESE 227
+ +G G D + + PL+ +P TGR S+ I + I + +S
Sbjct: 171 EEELQREVTLGEGADRIQPEDGTSTVHPLIARNPRTGRRSVYISTLNTERIVDLAPDDSR 230

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
L+GL+ A + +AH W GD+VVWD +H + +D RVM
Sbjct: 231 ELLDGLLAHAGKPQYTYAHTWQPGDLVVWDQLGTVHAKQAFDPAERRVM 279

>gb|ADC33997.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 104 bits (259), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 72/213 (33%), Positives = 103/213 (48%), Gaps = 25/213 (11%)

Query: 56 QQITFAKRFGAIER--IGGGDIVA-----ISNVKADGTVRQHSPA EWDDMMKVIVGNMAW 108
QQI FA++FG +ER + V ++N+ ADG V + W
Sbjct: 1 QQIAFAEQFGLERHVVSNRGTVNPLVHIVTNLGADGKPSGK-----VASTQW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
H+D ++ P + + A V+P GG TCFADM AAY+AL EA +A + HS S
Sbjct: 49 HSDKSFRPQPSLATILHALVMPPQGGETCFADMIAAYEALPEAEKAELAGVRVHWSWGIS 108

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER 228
Q+++G + I D PLV+ PETGR +L +G A + G
Sbjct: 109 QARVG--IKVPPEEIADAPDMA---HPLVRTIPETGRKALFMGERAVHLEGQPEDVGRA 162

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
LE L A Q V+ H+W GD+++WDNRC+
Sbjct: 163 RLERLTAHAVQERFVYRHKWTLGDLLMWDNRCV 195

>gb|ACX54971.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 98

Score = 104 bits (259), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 55/98 (56%), Positives = 67/98 (68%), Gaps = 3/98 (3%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYMP+ A+GAVFSAE++P+ GG T +ADMRAAY+ALD+ TRA + A HSL YSQ
Sbjct: 1 ADSTYMP LQAKGAVFSAE IIPSEGGATGWADMRAAYEALDDDTRARIADLRAYHSLFYQS 60

Query: 170 SKLGHV---QQAGSAYIGYGMDDTATPLRPLVKVHPET 204
+ G++ Q Y YG LRPLVKVHPET
Sbjct: 61 GRSGYLP SKQNERGGYDMYGYHDEEPSLRPLVKVHPET 98

>emb|CBX81704.1| K03119 taurine dioxygenase [Erwinia amylovora ATCC BAA-2158]
Length = 276

Score = 104 bits (259), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 75/271 (27%), Positives = 119/271 (43%), Gaps = 23/271 (8%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
M T ++TP+ G V GV L ++ A L ++ +L+ QHL+ ++QI F
Sbjct: 1 MKWQTEKLTPS---FGLRVKGVDLKVINHAEEVETLLELIKQYQVLVVAQHLTPPEEQIEF 57

Query: 61 AKRFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADST 113
++ G I ++ ++NV+ +G R + G WH+D
Sbjct: 58 CRKTGTIFPHPLKNTCPWPEMTYVTNVQENGEGARGYPGP-----GFPIWHSDMC 107

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
Y + F AE VP+ GG+T F + AA L + + A +SQ +
Sbjct: 108 YEEHPPRLTTFYAEKVPSEGGKTLFCNTLAACADLPPRLSKTLEDKQA--IFGFSQKLQV 165

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEG 232
Q+ G D L P+++ HP+TGR ++ + H AI GM ESE +L
Sbjct: 166 RCQERGYMLHIEPEDQRPTLHPVLRPHPQTGRKAIYVNWTHDAIVGMSEQSEHYLNV 225

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLH 263
L ++AHQ+ GD+V+WDN LH
Sbjct: 226 LYRHCINPIYLYAHQYQEGDLVIWDNGSTLH 256

>ref|YP_702440.1| alpha-ketoglutarate-dependent taurine dioxygenase [Rhodococcus
jostii RHA1]
gb|ABG94282.1| alpha-ketoglutarate-dependent taurine dioxygenase [Rhodococcus
jostii RHA1]
Length = 288

Score = 103 bits (258), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 81/271 (29%), Positives = 127/271 (46%), Gaps = 26/271 (9%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+L + G GA + G+ +A+ D AA+ +A +H +L+ GQ L + I F +R
Sbjct: 11 SLTLDKFGPHFGAEIIGLDVASATDDEVAAIRSALTEHKVLVLRGQSLGDASHIEFGRR 70

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPA--EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
G + A V G V Q A D+ + WH D T+M G+
Sbjct: 71 GRL-----TAGHPVHDSGDVAQEYVALDSQDNGFADV-----WHTDVTFMKRPPLGS 117

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV---QQAG 179
+ V+P GG T +AD + AY++L R ++ Q +A H + G+ ++ G
Sbjct: 118 ILRPVVLPPHGGDTNWADSQLAYESLSLPVRQMQIDQLTAVHD--GNREFGYLYAQKRG 174

Query: 180 SAYIGYGMDDTA-TPLR-PLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVD 235
+ G + TA P+ P+V+VHPETGR + + G +H I G+ AES L+ L

Sbjct: 175 KGNVWDGEEVTALVPVEHPVVRVHPETGRKGIFVNPFGTSH-IAGVSEAESRGILDFLYA 233

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAE 266

+ + H+W GD+V+WDNR H A

Sbjct: 234 HLTKEHIVRHRWRLGDLVLWDNRSTAHYAN 264

>ref|YP_003592886.1| taurine dioxygenase [Caulobacter segnis ATCC 21756]

gb|ADG10268.1| Taurine dioxygenase [Caulobacter segnis ATCC 21756]

Length = 270

Score = 103 bits (258), Expect = 2e-20, Method: Compositional matrix adjust.

Identities = 80/276 (28%), Positives = 115/276 (41%), Gaps = 30/276 (10%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59

MA L + P +GA + GV L L + F +H A Q+ ++ F Q +S+D

Sbjct: 1 MAYDVLDVKPMTRRIGAEIFGVDLGKPLSNRQFEEIHQALTQYQVIFFRDQEMSHDAHKD 60

Query: 60 FAKRFGAIERIGG----GDIVAIISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115

F ++FG + G D I + AD + V WH+D T

Sbjct: 61 FGRKFGNLAIHSGVPLPDHPEIVAIHADANSK-----FVAGENWHSDLTCD 107

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175

P G++ +V+P GG TCFA M AYD L + +A + SA H V

Sbjct: 108 PEPPLGSILYMKVLPDDGGDTCFASMYWAYDTLSDRMKAYLEGLSAVHD-----ANPV 160

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLV 234

+A I + + P+V+ HP +GR SL + + I G+ AES L L

Sbjct: 161 YKAIFPDIDRKYNCSST---HPIVRTHPVSGRKSLFVNPSYTHIAGLSKAESNAILNFLY 217

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDF 270

A +W V WDNRC H+A WD+

Sbjct: 218 QHASNPDPQVRFRWKPNSVAFWDNRCTWHQAI-WDY 252

>ref|YP_003906658.1| Taurine dioxygenase [Burkholderia sp. CCGE1003]

gb|ADN57367.1| Taurine dioxygenase [Burkholderia sp. CCGE1003]

Length = 310

Score = 103 bits (258), Expect = 2e-20, Method: Compositional matrix adjust.

Identities = 83/276 (30%), Positives = 126/276 (45%), Gaps = 32/276 (11%)

Query: 2 AQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQIT 59

A+ +L I +GA V GV L+ TLD F A+ A H +L F GQ HL + Q

Sbjct: 19 ARASLNIRRLAGRIGAQVEGVTLSPITLDQPTFEAIEKALYTHKVLFFRGQGHLDASQEG 78

Query: 60 FAKRFGAIERIGGGDIVAIISNVKADGTVRQHSPAEWDDMMKVIVGNMA---WHADSTYM 115

FA+RFG A TV H+ + D++ + + A WH D T++

Sbjct: 79 FARRFG-----ETVAHPTVPSHAGSA--DLLDLDSAHGARANSWHTDITFV 122

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY-----SQ 169

+ ++ A +P VGG T +A+ AAY+ + E RA A H+ Y ++

Sbjct: 123 DAYPKLSILRAITIPPVGGDTVWANTAAAYERVPEPLRAFADHARAIHTNAYDYASSHAE 182

Query: 170 SKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF 229

+ +++ +I +T P+V VHP TG +L++G A G+ A +S

Sbjct: 183 ADDTQLKRYREVFISKVYETE---HPVSVHPVTGERTLVLGHFQAQRFAGLSAQDSASL 238

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265

L+ L + + QWA GDV +WDNR H A

Sbjct: 239 LQVLHEHITRLENTVRWQWAEQDVAIWDNRATQHIA 274

>ref|YP_004227685.1| Taurine dioxygenase [Burkholderia sp. CCGE1001]
gb|ADX54625.1| Taurine dioxygenase [Burkholderia sp. CCGE1001]
Length = 310

Score = 103 bits (258), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 84/274 (30%), Positives = 121/274 (44%), Gaps = 28/274 (10%)

Query: 2 AQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQIT 59
A+ +L I +GA + GV L+ LD A F A+ AA H +L F GQ HL + Q
Sbjct: 19 AKASLNIRRVAGRIGAQIEGVRLSPELDQATFEAIEAALHTHKVLFFRGQQHLDDASQEG 78

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA--WHADSTYMPV 117
FA+RFG + A TV H+ + G A WH D T++
Sbjct: 79 FARRFG-----DTVAHPTVPSHAGGSRLDLDSAHGARANSWHTDVTTFVDA 124

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL----- 172
+ +V A +P VGG T +A+ AAY+ L E RA A H+ Y +
Sbjct: 125 YPKVSVLRITIPPVGGDTVWANTAAAYERLPEPLRAFADHARAIHTNAYDYASAHADAD 184

Query: 173 -GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE 231
+++ +I +T P+V+VHP TG +L++G G+ ES L+
Sbjct: 185 DTQLKRYRELFISKVYETE----HPVVRVHPVTGERTLVLGHFVQRFIGLSTQESTALLQ 240

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L + + QWA GDV +WDNR H A
Sbjct: 241 VLHEHITRLENTVRWQWAEGDVAIWDNRATQHYA 274

>ref|YP_553181.1| putative alpha KG dependent 2,4-D dioxygenase [Burkholderia
xenovorans LB400]
gb|ABE33831.1| Putative alpha KG dependent 2,4-D dioxygenase [Burkholderia
xenovorans LB400]
Length = 301

Score = 103 bits (258), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 70/239 (29%), Positives = 111/239 (46%), Gaps = 28/239 (11%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAI-----ERIGGGDIVAISNVKADGTVRQ 89
++ +LIFP Q +++D+ + F+ FG + E I ISN+ D +
Sbjct: 39 RYPVLIFPKQFINDELLAFSANFGPVHTAMSYQTREKEHRLQPKITDISNLGKDNQTFK 98

Query: 90 HSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD 149
M V WH D++Y + A+ + A V GG T FADMRAAYD +
Sbjct: 99 RGDHR---RMNNFVSK-RWHTDASYEAI PARYSFLLAYTVAQRGGETQFADMRAAYDEMP 154

Query: 150 EATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP----LVKVHPETG 205
E R +V S ++++++ G+ + D L P LV+ HP +G
Sbjct: 155 EDLRPVVEDLSCEYNILWARMLSGYTEFP-----DEERAKLPPAQHKLVRQHPVSG 205

Query: 206 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
R +L + HA + E L L+++A Q V+ H+W D+V+WDNR L+HR
Sbjct: 206 RKTLYLSGHATHVVDWPIEGRDLLRELMEFATQPQFVYTHKWHERDLVMWDNRALMHR 264

>ref|YP_639655.1| taurine dioxygenase [Mycobacterium sp. MCS]
ref|YP_938523.1| taurine dioxygenase [Mycobacterium sp. KMS]
ref|YP_001070803.1| taurine dioxygenase [Mycobacterium sp. JLS]
gb|ABG08599.1| Taurine dioxygenase [Mycobacterium sp. MCS]
gb|ABL91733.1| Taurine dioxygenase [Mycobacterium sp. KMS]
gb|ABN98312.1| Taurine dioxygenase [Mycobacterium sp. JLS]
Length = 305

Score = 103 bits (258), Expect = 2e-20, Method: Compositional matrix adjust.

Identities = 79/266 (29%), Positives = 116/266 (43%), Gaps = 21/266 (7%)

```
Query: 7   QITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRF 64
++   GA +GA + GV +   LD       A++ A L+H ++ F GQH L +D Q+ FA+R
Sbjct: 4   RVVKLGANIGARIEGVRVGGLDPVTVTAINEALLEHKVIFFRGQHHLDDGQLAFARRL 63

Query: 65  GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G           +       T R H       D           +WH D T++ + + ++
Sbjct: 64  GTP-----TTAHPVTVSRGHRILPIDSRYD---KANSWHTDVTTFVDRIPKASLL 109

Query: 125  SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVYSQSKLGHVQQAGSAY 182
A   +PA GG T +A   AAYD L   RALV   A H+   Y+   G   +   +
Sbjct: 110  RAVTLPAYGGTTTWASTEAAAYDQLPAPLRALVENLWAVHTNQFDYAADYDGRREALAATE 169

Query: 183  IGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
Y   +   +       P+V++HPETGR   LL+G       G+ AES   L   L +   +
Sbjct: 170  REYREEFVSEYFETEHVPVRIHPETGRRVLLLGHFQVGLGVAESTALLALLQNRVTK 229

Query: 240  APRVHAHQWAAGDVVVWDNRCLLHRA 265
W   GD+ VWDNR   H A
Sbjct: 230  LENTVRWSWEPGDLAVWDNRATQHUYA 255
```

```
>ref|ZP_05521627.1| dioxygenase [Streptomyces lividans TK24]
ref|ZP_06526452.1| dioxygenase [Streptomyces lividans TK24]
gb|EFD64702.1| dioxygenase [Streptomyces lividans TK24]
Length = 315
```

Score = 103 bits (258), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 86/267 (32%), Positives = 112/267 (41%), Gaps = 27/267 (10%)

```
Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ P   T+GA + G   L+   L A       L+ A L+ +L F G HL++DQQ FA +
Sbjct: 47  FEVVPQARTIGAEIRGADLSRPLPALREELNRALLEWKVLFRRGAHLTSDQQQDFAGNW 106

Query: 65  GAIER-----IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
GA+E       G D V +   K DG V +       WH D T+   A
Sbjct: 107  GALETNPLLAAGSSDDV-VRFDKGDGAVPTYE-----NVWHTDVTFRERPA 151

Query: 120  QGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
GAV   VP   GG T +ADM AAYD L   + V   A H +       G + G
Sbjct: 152  LGAVLQLREVPFPGGDTMWADMAAAYDNLPREVKERVDGALAVHDFI-----PGFARFYG 206

Query: 180  SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWAC 238
+   D       P+V+ HPETGR   L +       I G+D ES+R L   L   A
Sbjct: 207  PERLLPHQDLLPPVEHPVVRTHPETGRRMLFVNASF'TTRITGVDRDESRLRLFLFQQAH 266

Query: 239  QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+W   GDV WDNR   H A
Sbjct: 267  VPEYQVRWRWQPGDVAFWDNRATQHUYA 293
```

```
>ref|YP_001757617.1| taurine dioxygenase [Methylobacterium radiotolerans JCM 2831]
gb|ACB26934.1| Taurine dioxygenase [Methylobacterium radiotolerans JCM 2831]
Length = 305
```

Score = 103 bits (258), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 88/292 (30%), Positives = 123/292 (42%), Gaps = 37/292 (12%)

```
Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I       LGA + G+ L+   LDD   AA+ A   H ++ F Q L   +Q F +R
Sbjct: 15  LDIRRVAGRLGAEIRGLALSGDLDDGTVAAIRQALNTHKVVFFRDQDLDEAEQEAFGRR 74
```

Query: 65 GAIERIGGGDIVAISNVKA-----DGTVRQHSPA EWDDMMKVIVGNMAWHADSTY 114
G D+VA V + DG+ + + +WH D T+
Sbjct: 75 G-----DLVAHPTVPSLAGTAGVLDIDGSRGERA-----SSWHTDVTF 112

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
+P ++ A +P GG T +A+ AAY L E R L + A HS VY G
Sbjct: 113 VPAYPALSLRAVTLPPYGGDTLWANTAAAYADLPEPLRDLADKLWALHSNVYDYVG-GR 171

Query: 175 VQQAGSAYIGYGMDDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE 231
V + + Y T T PLV VHPE G SL++G I G+ A+S+ L
Sbjct: 172 VNVSEAGRRRYDEVFTKTVFETEHLVHVHPENGERSLIVGHFIQRILGLTTADSQHLLA 231

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
D A + W GDV +WDNR +HRA + PRV+ + G
Sbjct: 232 IFHDHATRPENTVRWSWRTGDVAIWDNRATVHRAVDYGEAPRVVRRVTIQG 283

>gb|ADC33999.1| TfdA-like protein [uncultured bacterium]
Length = 208

Score = 103 bits (258), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 71/218 (32%), Positives = 105/218 (48%), Gaps = 22/218 (10%)

Query: 56 QQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVG 104
QQI FA+ FG ++ R+ + + ISNV DG + + + M +
Sbjct: 1 QQIAFARAFGLDIGLKKVFKRPNRLKRDESIDISNVADDGRIASLATKK----MYSQLA 56

Query: 105 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHS 164
N WH+DS++ A+ ++ + P GG T FAD+RAAYD L E T+ V A+H+
Sbjct: 57 NQLWHSDDSSFDPPARYSMLYLSNPPKGGETEFA DLRAAYDGLPEDTKREVEGLRAQHN 116

Query: 165 LVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDA 223
++S+ LG P+ PLV+ HP + R L +G H + GM
Sbjct: 117 ALHSRINLGD TDWTEE-----QKNAIPPVEWPLVRTHPGSKRKLLFVG VHTTHVVG MHL 170

Query: 224 AESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
E L L++ A Q V+ H W GD+VVWDNRC+
Sbjct: 171 GEGRLLLAELLEHATQREFVYRHSWRVGD LVVWDNRCV 208

>ref|NP_631553.1| dioxygenase [Streptomyces coelicolor A3(2)]
emb|CAC44685.1| putative dioxygenase [Streptomyces coelicolor A3(2)]
Length = 315

Score = 103 bits (257), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 86/267 (32%), Positives = 112/267 (41%), Gaps = 27/267 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ P T+GA + G L+ L A L+ A L+ +L F G HL++DQQ FA +
Sbjct: 47 FEVVPQARTIGAEIRGADLSRPLPPALREELNRALLEWKVLFFRGAHLTSDQQRDFAGNW 106

Query: 65 GAIER-----IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMA 119
GA+E G D V + K DG V + WH D T+ A
Sbjct: 107 GALETNPLLAAGSSDDV-VRFDKGDGAVPTYE-----NVWHTDVTFRERPA 151

Query: 120 QGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
GAV VP GG T +ADM AAYD L + V A H + G + G
Sbjct: 152 LGAVLQLREVPPFGGDTMWADMAAAYDNLPREVKERVDGALAVHDFI-----PGFARFYG 206

Query: 180 SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWAC 238
+ D P+V+ HPETGR L + I G+D ES+R L L A
Sbjct: 207 PERLLPHQDLLPPVEHPVVRTHPETGRMLFVNASF TTRITGVDRDESDRLRLRFLFQQAH 266

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+W GDV WDNR H A
Sbjct: 267 VPEYQVRWRWQPGDVAFWDNRAHQHYA 293

>ref|ZP_07005112.1| Dioxygenase, TauD/TfdA family [Pseudomonas savastanoi pv. savastanoi NCPPB 3335]
gb|EFH99483.1| Dioxygenase, TauD/TfdA family [Pseudomonas savastanoi pv. savastanoi NCPPB 3335]
Length = 279

Score = 103 bits (257), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 80/253 (31%), Positives = 123/253 (48%), Gaps = 22/253 (8%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAI--ERIGGGDIVAIS-NVKADGTVRQHSPA EWDD 97
Q +L+FP + S+ +QI F + G E G +I IS +VK + PA
Sbjct: 44 QRGVLVFPQINFSDAEQIAFTRTLGTFCPEASDGQNITKISLDVKEN-----PAG--- 93

Query: 98 MMKVIVGNMAWHADSTYMPVMAQGA VFSAE VVP AVGGRTCFADMRAAYDALDEATRALVH 157
+ + G++ WH D T V ++ S +V + GG T F + AAY+AL A +
Sbjct: 94 -AEFLKGS LYWHIDGTSSDVPILASLLSCKVPASWGGNTGFCNTYAA YEALSSADK---- 148

Query: 158 QRSARHSLVYS--QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHA 215
Q R ++++ S L + + G A + M PLV H +GR SL++G A
Sbjct: 149 QHYERLRVIHAPWASLLY NPEPGLAMLK-AMQAIGEKELPLVVRH-RSGRKS LILGCTA 206

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRV 275
+ G A+S + L GL +WA ++H W AGD+V+WDN +HRAE +D R+
Sbjct: 207 QQVVGSSSLAQSAQILVGLREWATAEAFSYSHAWQAGDLVIWDNAGTMHRAEAYDPACGRM 266

Query: 276 MWHSRLAGRPETE 288
M ++L G E
Sbjct: 267 MHRTKLQGE E PFE 279

>ref|ZP_02186917.1| taurine dioxygenase, TauD/TfdA family protein [alpha proteobacterium BAL199]
gb|EDP66099.1| taurine dioxygenase, TauD/TfdA family protein [alpha proteobacterium BAL199]
Length = 304

Score = 103 bits (257), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 89/310 (28%), Positives = 130/310 (41%), Gaps = 43/310 (13%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L P LGA + G+ L++ + DA L + QH +++ GQ ++ D I FA+ F
Sbjct: 2 LTAEPLSRVLGA EIKGLDLSSPIADADREELLTLFWQHKVIVIRGQDVAPDGFIRFAEAF 61

Query: 65 GAIERI-----GGGDIV AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
G IE I +SNV+ DG P D WH+DST+
Sbjct: 62 GTIEPFFISAYNLPTHPIYVLSNVRQDG-----KPIGRDG-----AGTHWHS DSTFTE 110

Query: 117 VMAQGA VFSAE VVP AVGGRTCFADMRAAYDALDEATRALVHQRSA-----RHSLVYS--- 168
+ + VP GG T F + AYD LD+ T+A + R A R VYS
Sbjct: 111 KPSSATLLHGVTVPDRGGDTL FVNTADAYDRLDDETKARIQGRRAIHR YQRKEFVYSGDR 170

Query: 169 ---QSKLGHVQQAGSAYIGYGMDDTTATP-----LRPLVKVHPETGRPSLLIGRH 214
++ +++ + + A+P L P+V+ HP TG L +
Sbjct: 171 TIDDAERTEIERVKALRMAEAAAADAASPTAQR SNQEPDR LHPIVRTHPVTGSKGLYL NDE 230

Query: 215 AHA-IPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRV 273
I G+ E+ L L + A V ++W GDVVVWDN ++H A LP
Sbjct: 231 MTVGIEGIPDEEAVPLLRRLCEVATAPD TVLRYKWRQGDVVVWDNA AVIHSATFTPPDLP 290

Query: 274 RVMWHSRLAG 283
RVM +AG
Sbjct: 291 RVMHRLTIAG 300

>ref|YP_001105490.1| taurine catabolism dioxygenase TauD [Saccharopolyspora erythraea NRRL 2338]
ref|ZP_06564109.1| taurine catabolism dioxygenase TauD [Saccharopolyspora erythraea NRRL 2338]
emb|CAM02565.1| taurine dioxygenase, TauD/TfdA family [Saccharopolyspora erythraea NRRL 2338]
Length = 315

Score = 103 bits (257), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 85/294 (28%), Positives = 131/294 (44%), Gaps = 29/294 (9%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAG-FAALHAAWLQHALLIFPGQ-HLSNDQQIT 59
A + +++ GA +GA V GV L DAG A+ +A L H ++ F Q HL ++ Q+
Sbjct: 14 AGSGVRVVKLGAHIGARVDGVRLLGGDLDACTVEAIRSALLTHKVIFFRDQGHLDDESQVA 73

Query: 60 FAKRFGAIE----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYM 115
FA+ G + + G D I + +D +S A +WH D T++
Sbjct: 74 FARLLGDLTLAHPTVRGRDNANILPIDSD-----YSKAN-----SWHTDVTFFV 116

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS-----Q 169
+ +V A +P GG T +A AAY+ L +ALV A H+ Y +
Sbjct: 117 DRVPAISVLRVAVQLPEYGGTTTWASTVAAEYKLPAPLKALVDSLWAVHTNAYDYAANIDE 176

Query: 170 SKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF 229
+++G V Y + P+V+VHPETG +LL+G + G+ ++ES
Sbjct: 177 TRVGGVDVKFQEYRREFVSNVYETEHPVVRVHPETGERALLLGHFVKRLVGLTSSSEHTL 236

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ L Q W+ GD+ +WDNR H A LPR + LAG
Sbjct: 237 FQLLQSRVTQLENTVRWHWSGDGLAIWDNRATQHYAVADYDDLPRRLHRVTLAG 290

>ref|YP_110629.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei K96243]
ref|YP_337322.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei 1710b]
emb|CAH38065.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei K96243]
gb|ABA52106.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei 1710b]
Length = 292

Score = 103 bits (257), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 79/286 (27%), Positives = 125/286 (43%), Gaps = 31/286 (10%)

Query: 15 LGATVTGVHLATLDDA-GFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG 73
LG V G DA AL AW + Q L + + F++ FG ER
Sbjct: 19 LGTEVYGFDSPPHDAEAVRALIEAWHAGGICRLRRQRLDMAEFVEFSRIFGRPERALNQ 78

Query: 74 D-----IVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGA 122
+ ++ +SN+ +G H ++ WH D Y V +
Sbjct: 79 ERKLTSREDLPELMIVSNILENGVSIGHLGSK-----EAYWHTDMCYTDVPPIAS 128

Query: 123 VFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ A VPA GG T F +M +DAL + R + S +H Y+ +G ++ +
Sbjct: 129 ILYAIEVPARGGNTFEMNMYRVHDALPASLRRQIAGLSIKHDRSYT--AVGELRYGFDSV 186

Query: 183 IGYGMDDTTATP--LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQ 239
+ D T P + P+V+VHP T RP L +GR +A + G+ ESE L+ L +
Sbjct: 187 V----DVTTCPGSIHPVIRVHPVTQRPYLYLGRRLNAYVVGLPVGESEALLDELWRYTRL 242

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
+W GD+++WDNRC +HR + +D R+MW +++ P
Sbjct: 243 DGVTTWTQRWEVGDIMIWDNRCTMHRRDAFDANARRLMWRTQIQADP 288

>ref|ZP_02371424.1| dioxygenase, TauD/TfdA family protein [Burkholderia thailandensis
TXDOH]
Length = 270

Score = 103 bits (257), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 74/272 (27%), Positives = 120/272 (44%), Gaps = 30/272 (11%)

Query: 28 DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGD-----IV 76
D AL AW + Q L + + F++ FG ER + ++
Sbjct: 11 DAEAVRALIEAWHTGGICRLRRQRLDMAEFVEFSRIFGRPERALNQERKLTSREDLPELM 70

Query: 77 AISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRT 136
+SN+ +G H ++ WH D Y V ++ A VPA GG T
Sbjct: 71 IVSNILENGVSIGHLGSK-----EAYWHTDMCYTDVPPITSILYAIEVPACGGNT 120

Query: 137 CFADMRAAYDALDEATRALVHQRSARHSVLVSQSKLGHVQQAGSAYIGYGMDDTTATP--L 194
F +M +DAL + R + S +H Y+ +G ++ + + D T P +
Sbjct: 121 EFMNMYRVHDALPASLRRQIAGLSIKHDRSYT--AVGELRYGFDSVV---DVTTCPGSI 174

Query: 195 RPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P+V+VHP T RP L +GR +A + G+ ESE L+ L + +W GD+
Sbjct: 175 HPPIVRVHPVTQRPYLYLGRRLNAYVVGLPVGESEALLDELWRYTRLDGVTWTQRWEVGDI 234

Query: 254 VVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
++WDNRC +HR + +D R+MW +++ P
Sbjct: 235 MIWDNRCTMHRRDAFDANARRLMWRTQIQADP 266

>ref|NP_792423.1| dioxygenase, TauD/TfdA family [Pseudomonas syringae pv. tomato str.
DC3000]
ref|ZP_03398068.1| dioxygenase, TauD/TfdA family [Pseudomonas syringae pv. tomato T1]
ref|ZP_07252876.1| dioxygenase, TauD/TfdA family protein [Pseudomonas syringae pv.
tomato K40]
gb|AA056118.1| dioxygenase, TauD/TfdA family [Pseudomonas syringae pv. tomato str.
DC3000]
gb|EEB58822.1| dioxygenase, TauD/TfdA family [Pseudomonas syringae pv. tomato T1]
Length = 279

Score = 103 bits (257), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 79/255 (30%), Positives = 118/255 (46%), Gaps = 26/255 (10%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAI--ERIGGGDIVAIS-NVKADGTVRQHSAPAEWDD 97
Q +L+FP H S+ +QI F + G E G +I IS +VK + PA
Sbjct: 44 QRGVLVFPKIHFSDAEQIAFTRTLGTFSPEASDGNITKISLDVKEN-----PAG--- 93

Query: 98 MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH 157
+ + G++ WH D T ++ S +V + GG T F + AAY+AL +A +
Sbjct: 94 -AEFLKGSLSYWHIDGTSSDAPILASLLSCKVPASWGGNTGFCNTYAAYEALGDADKHYRE 152

Query: 158 QRSARH----SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR 213
H SL+Y + G IG PLV H +GR SL++G
Sbjct: 153 SLRVIHAPWASLLYYNPEPLAMLKAMQAIG-----EKELPLVVKH-RSGRKSILIGC 204

Query: 214 HAHAIIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKL 273
A + G A+S + L GL +WA ++H W GD+V+WDN +HRAE +D +
Sbjct: 205 TAQHVVGNSLAQSAQILVGLREWATAEAFSYSHTWQVGDVLDVWDNTGTMHRAEAYDPECG 264

Query: 274 RVMWHSRLAGRPETE 288

R+M ++L G E
Sbjct: 265 RMMHRTKLQGEEPF 279

>ref|ZP_02358219.1| TauD/TfdA family dioxygenase [Burkholderia oklahomensis EO147]
ref|ZP_02365274.1| TauD/TfdA family dioxygenase [Burkholderia oklahomensis C6786]
Length = 283

Score = 103 bits (257), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 81/300 (27%), Positives = 129/300 (43%), Gaps = 36/300 (12%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
MA TL + LG+ V G + L AW + Q L + +
Sbjct: 1 MAYKTL-----SSALGSEVYGFDTPFPYESDAVQTLIDAWHAGGICRLRQQRDLMAEFVE 55

Query: 60 FAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW 108
F++ FG ER + ++ +SN+K +G H A+ W
Sbjct: 56 FSRIFGKPERALNQERKLTSRDDLPELMIVSNIKENGVSIGHLGAK-----EAYW 105

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
H D Y V ++ A VP GG T F +M +DAL + R + S +H Y+
Sbjct: 106 HTDMCYTDPPIASILYAIEVPTRGGDTEFNMNMYRVHDALPASLRKRIAGLSIKHDSRYT 165

Query: 169 QSKLGHVQQAGSAYIGYGMDDTATP--LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAE 225
+G ++ + + D T P + P+V+VHP T RP L +GR +A + G+ E
Sbjct: 166 --AVGELRYGFESVV----DVTTCPSVHPIVRVHPVTRRPYLYLGRRLNAYVVGLPVDE 219

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
SE L+ L + W GD+++WDNRC +HR + +D + R+MW +++ P
Sbjct: 220 SEALLDELWRYTRLGVTWTQHWEVGDIMIWDNRCTMHRRDAFDERARRLMWRTQIQADP 279

>ref|ZP_04700699.1| putative taurine catabolism dioxygenase [Streptomyces albus J1074]
ref|ZP_06589460.1| dioxygenase [Streptomyces albus J1074]
gb|EFE79921.1| dioxygenase [Streptomyces albus J1074]
Length = 315

Score = 103 bits (257), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 84/263 (31%), Positives = 117/263 (44%), Gaps = 21/263 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ P G +GA + G+ L+ L A A L A L+ +L F GQHL++ Q FA+ +
Sbjct: 49 FTLVPQGPLIGAEIRGLDLSRPLTAAVRAELDRALLEWKVLFVRGQHLTSAAQRDFARNW 108

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G +E ++A + A+ VR D +V WH D+T+ A GAV
Sbjct: 109 GELE--TNPLLATGD--AEDVVRF-----DRSQVPTFENVWHTDTTFRENPALGAVL 156

Query: 125 SAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
VP GG T +ADM AAYD L E R V A H + ++ + +
Sbjct: 157 QLREVPPYGGDTLWADMAAAYDNLPEEVRERVEGLRAVHDYLPGFARFTSAEHLAA---- 212

Query: 185 YGMDTTATPLR-PLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPR 242
+T P+ P+V+ HP TGR +L + I G+ ES+R L L A
Sbjct: 213 --FQSTFPPEHPVRRHPVTGRRTLFVNTSFTTTRITGLPQEESDRLLRLLFQQAHPVEY 270

Query: 243 VHAHQWAAGDVVVDNRCLLHRA 265
W AGDV WDNR H A
Sbjct: 271 QVRFHWRAGDVAFWDNRATQHYA 293

>ref|YP_002779396.1| dioxygenase [Rhodococcus opacus B4]
dbj|BAH50451.1| putative dioxygenase [Rhodococcus opacus B4]

Length = 288

Score = 103 bits (257), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 82/270 (30%), Positives = 128/270 (47%), Gaps = 24/270 (8%)

```
Query: 5   TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          +L +   G + GA + G+ +A+   D   A+ +A +H +L+   GQ L +   I F +R
Sbjct: 11  SLTLDKFGPSFGAEILGLDVASATDDEVTAIRSALTEHKVLVLRGQSLDDWGHIEFGRRL 70

Query: 65  GAIERIGGGDIVAIS-NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
          G   R+   G   V   S   NV   +           + D+           WH D T+M   G++
Sbjct: 71  G---RLTAGHPVHDSGNVAREVYALDSKDNFADV-----WHTDVTFMKRPPLGSI 118

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV---QQAGS 180
          V+P   GG T +AD + AY++L   R ++ Q +A H   + G+   ++ G
Sbjct: 119 LRPVVLPPHGGDTNWADSQLAYESLSLPIRQ MIDQLTAVHD---GNREFGYLAQKRGKG 175

Query: 181 AYIGYGMDDTA-TPLR-PLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVDW 236
          I   G + TA   P+   P+V+VHPETGR   + +   G   +H I G+   AES   L+ L
Sbjct: 176 GNIWDGEEVTALAPVEHPVVRVHPETGRKGFVNPFGFTSH-IAGVSEAESRGILDFLYAH 234

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRAE 266
          +   V   H+W   GD+V+WDNR   H A
Sbjct: 235 LTKPEHVVRHRWRLGDLVLWDNRSTAHYAN 264
```

>ref|ZP_05127143.1| taurine dioxygenase [gamma proteobacterium NOR5-3]
gb|EED33690.1| taurine dioxygenase [gamma proteobacterium NOR5-3]
Length = 281

Score = 103 bits (257), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 88/294 (29%), Positives = 130/294 (44%), Gaps = 30/294 (10%)

```
Query: 3   QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
          ++ L+I P   +GA + GV L +   +   A L++ ++ F   Q +S   Q I FA+
Sbjct: 6   KSQLRIEPLTPAIGAEILGVDLGKVTPELVEDVRVALLKYKVVFVRDQQISARQHIDFAR 65

Query: 63  RFGAIERIGGGDIVAISNVKADGTVRQ--HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ 120
          FG +E           A   +AD + +   H P           NM WH+D T+   +
Sbjct: 66  EFGELEIHP-----ATPKNQADPEILRLAHGPD SKGS-----ENM-WHSDVTWREKPSL 113

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQQA 178
          G++ A   VPAVGG T FA+M   AY+ L +AT+   +H R A H +   V+++   ++
Sbjct: 114 GSILRAVEVPVAVGGDTL FANMAMAYERLS DATKEKIHNRIAVHDIARVFAKRLNKRPEEL 173

Query: 179 GSAYIGYGMDDTTATPL--RPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVD 235
          Y           PL   P+V+ HPETG   + + G   I MD   S+   L+ L
Sbjct: 174 HEQY-----PLMEHPVVRTHPETGEQV VYVNGAFTSHIKDMDPQASKSLLD ELYK 223

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG-RPETE 288
          A           +W A +   WDNR   H A   F   RVM   +AG RP E
Sbjct: 224 SAWNPEIQCRFKWRANSIAFWDNRA CQHFAASDYFPAVRVMERVTIAGDRPYFE 277
```

>ref|ZP_04953283.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1710a]
gb|EET02805.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1710a]
Length = 283

Score = 103 bits (257), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 79/286 (27%), Positives = 125/286 (43%), Gaps = 31/286 (10%)

```
Query: 15  LGATVTGVHLATLDDA-GFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG 73
          LG   V G           DA   AL AW   +   Q L   + + F++ FG   ER
```


Sbjct: 10 LGTEVYGFDSPPHDAEAVRALIEAWHAGGICRLRRQRLDMAEFVEFSRIFGRPERALNQ 69

Query: 74 D-----IVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
+ ++ +SN+ +G H ++ WH D Y V +

Sbjct: 70 ERKLTREDLPELMIVSNILENGVSIGHLGSK-----EAYWHTDMCYTDVPPIAS 119

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ A VPA GG T F +M +DAL + R + S +H Y+ +G ++ +

Sbjct: 120 ILYAIEVPARGGNTFEMNMYRVHDALPASLRRQIAGLSIKHDRSYT--AVGELRYGFDSV 177

Query: 183 IGYGMDTTATP--LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQ 239
+ D T P + P+V+VHP T RP L +GR +A + G+ ESE L+ L +

Sbjct: 178 V---DVTTCPGSIHPVIRVHPVTQRPYLYLGRRLNAYVVGLPVGESEALLDELWRYTRL 233

Query: 240 APRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
+W GD+++WDNRC +HR + +D R+MW +++ P

Sbjct: 234 DGVTTWTQRWEVGDIMIWDNRCTMHRRDAFDANARRLMWRTQIQADP 279

>ref|YP_001061907.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei 668]
ref|ZP_02492950.1| dioxygenase, TauD/TfdA family protein [Burkholderia pseudomallei
NCTC 13177]
gb|ABN87967.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 668]
Length = 283

Score = 103 bits (257), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 83/300 (27%), Positives = 130/300 (43%), Gaps = 36/300 (12%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDA-GFAALHAAWLQHALLIFPGQHLSNDQQIT 59
MA TL + LG V G DA AL AW + Q L + +

Sbjct: 1 MAYKTL-----SSALGTEVYGFDSPPHDAEAVRALIEAWHAGGICRLRRQRLDMAEFVE 55

Query: 60 FAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAW 108
F++ FG ER + ++ +SN+ +G H ++ W

Sbjct: 56 FSRIFGRPERALNQERKLTREDLPELMIVSNILENGVSIGHLGSK-----EAYW 105

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
H D Y V ++ A VPA GG T F +M +DAL + R + S +H Y+

Sbjct: 106 HTDMCYTDVPPIASILYAIEVPAHGGNTFEMNMYRVHDALPASLRRQIAGLSIKHDRSYT 165

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAE 225
+G ++ + + D T P + P+V+VHP T RP L +GR +A + G+ E

Sbjct: 166 --AVGELRYGFDSV---DVTTCPGSIHPVIRVHPVTQRPYLYLGRRLNAYVVGLPVGE 219

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
SE L+ L + +W GD+++WDNRC +HR + +D R+MW +++ P

Sbjct: 220 SEALLDELWRYTRLDGVTTWTQRWEVGDIMIWDNRCTMHRRDAFDANARRLMWRTQIQADP 279

>ref|YP_004008831.1| taurine dioxygenase [Rhodococcus equi 103S]
emb|CBH50153.1| putative taurine dioxygenase [Rhodococcus equi 103S]
Length = 295

Score = 103 bits (256), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 82/270 (30%), Positives = 123/270 (45%), Gaps = 24/270 (8%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
++I+ +GA + GV L T D+A FA + A ++ ++ G HL D + A+RFG

Sbjct: 3 IEISALTTAIGAEIRGVDLRTCDDEATFADVRDALHEYQVVFVRGAHLDDADDHLAVARRFG 62

Query: 66 A-----IERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQ 120
I R+ G ++ V +DG SP + WH D T++ +

Sbjct: 63 VPSIFPIARLQGATEPSL-QVISDG---PDSPTAE-----MWHTDVTWISTPPR 108

Sbjct: 111 AVLSAKLLPAFGGDTLWASGIAAYEALSEPLKRLLDGLTATHDFTKS-FPLERFGNTAED 169

Query: 182 YIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
+ + + P P+V+ HP +GR SL + I ++ AESE L+ L A

Sbjct: 170 LLRWEETRSKNPPLSHPVVRTHPVSGRKSLFVSEGFTTKINELEPAESEAILKLLFAHAT 229

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ +W DV WDNR H A

Sbjct: 230 RPEFTIRWRWQENDVAFWWDNRVTQHYA 256

>ref|ZP_07260263.1| dioxygenase, TauD/TfdA family protein [Pseudomonas syringae pv. tomato NCPPB 1108]
Length = 307

Score = 103 bits (256), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 83/281 (29%), Positives = 125/281 (44%), Gaps = 26/281 (9%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAI--ERIGG 72
+GA + L A+ Q +L+FP H S+ +QI F + G E G

Sbjct: 46 IGARIFNSKQELLSGQFAGAIRELLEQRGVLVFPKIHFSDAEQIAFTRTLGTFSPEASDG 105

Query: 73 GDIVAIIS-NVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVA 131
+I IS +VK + PA + + G++ WH D T ++ S +V +

Sbjct: 106 QNITKISLDVKEN-----PAG----AEFLKGSlyWHIDGTSSDAPILASLLSCKVPAS 154

Query: 132 VGGRTCFADMRAAYDALDEATRALVHQRSARH---SLVYSQSKLGHVQQAGSAYIGYGM 187
GG T F + AAY+AL +A + H SL+Y + G IG

Sbjct: 155 WGGNTGFCNTYAAYEALGDADKHRYESLRVIHAPWASLLYNPEPGLAMLKAMQAIG--- 211

Query: 188 DTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQ 247
PLV H +GR SL++G A + G A+S + L GL +WA ++H

Sbjct: 212 ----EKELPLVWKH-RSGRKSILGCTAQHVVGNSLAQSAQILVGLREWATAEAFSYSHT 266

Query: 248 WAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETE 288
W GD+V+WDN +HRAE +D + R+M ++L G E

Sbjct: 267 WQVGDLVIWDNTGTMHRAEAYDPECGRMMHRTKLQGEPEFE 307

>ref|YP_001507682.1| taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EAN1pec]
gb|ABW12776.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EAN1pec]
Length = 281

Score = 103 bits (256), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 87/286 (30%), Positives = 130/286 (45%), Gaps = 20/286 (6%)

Query: 5 TLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T+ P AT+GA V G+ L DDA A+ A ++ +L+F G HL Q+ F++

Sbjct: 4 TITCEPLSATVGAEVKGLDPEWLAHDDAVAGAILDALERYGVLVFRGLHLDPHQTQVAFSQ 63

Query: 63 RFGAIE-RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ- 120
R G I+ G + I V D + ++S A++ + WH D P+ +

Sbjct: 64 RLGEIDYEPGHHVPVSGIYRVTLDKS--KNSSADY-----LKATFEWHMDGC-TPLHGEP 114

Query: 121 ---GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
V SA+ V GG T FA A Y+ L + + HSL SQ ++ V +

Sbjct: 115 PQKATVLSAKEVATSGGETEFASYAGYEMLGDEEKERFGSLHVVSLESSQRRI--VPE 172

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
+ T PLV H GR SL+IG HA + M + L+ L+D

Sbjct: 173 PSVEQLER-WRKRPTSTHPLVWTH-RGGRRSLVIGAHAGHVVDMLDQGRALLQELLDR 230

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

RV+ HQW+ GD V+WDN ++HRA P+ PR + + + G
Sbjct: 231 TAQDRVYRHQWSVGDTVIWDNTGVVHRAAPYASASPRELLRTTVFG 276

>ref|ZP_07230626.1| dioxygenase, TauD/TfdA family protein [Pseudomonas syringae pv.
tomato Max13]
Length = 324

Score = 103 bits (256), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 79/255 (30%), Positives = 118/255 (46%), Gaps = 26/255 (10%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAI--ERIGGGDIVAIS-NVKADGTVRQHSPA EWDD 97
Q +L+FP H S+ +QI F + G E G +I IS +VK + PA
Sbjct: 89 QRGVLVFPKIHFSDAEQIAFTRTLGTFSPEASDQGNITKISLDVKEN-----PAG--- 138

Query: 98 MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH 157
+ + G++ WH D T ++ S +V + GG T F + AAY+AL +A +
Sbjct: 139 -AEFLKGSLSYWHIDGTSSDAPILASLLSCKVPASWGGNTGFCNTYAAAYEALGDADKHRYE 197

Query: 158 QRSARH----SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR 213
H SL+Y + G IG PLV H +GR SL++G
Sbjct: 198 SLRVIHAPWASLLLYNPEPLAMLKAMQAIG-----EKELPLVVKH-RSGRKSILIGC 249

Query: 214 HAHAIIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLP 273
A + G A+S + L GL +WA ++H W GD+V+WDN +HRAE +D +
Sbjct: 250 TAQHVVGNSLAQSAQILVGLREWATAEAFSYSHTWQVGD LVIWDNTGTMHRAEAYDPECG 309

Query: 274 RVMWHSRLAGRPETE 288
R+M ++L G E
Sbjct: 310 RMMHRTKLQGEPPFE 324

>ref|YP_458158.1| alpha-ketoglutarate-dependent taurine dioxygenase [Erythrobacter
litoralis HTCC2594]
gb|ABC63361.1| alpha-ketoglutarate-dependent taurine dioxygenase [Erythrobacter
litoralis HTCC2594]
Length = 281

Score = 103 bits (256), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 83/276 (30%), Positives = 125/276 (45%), Gaps = 31/276 (11%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++ + P+G GAT+ GV L+ LDDA + +AWL H +L F Q + +D F
Sbjct: 2 SMIVEPSGQACGATIRGVLDLGGKLDLITDVRSAWLTHRVLAFAADQSMDDDALERFTLA 61

Query: 64 FGAIER-----IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
G G G+I AI E D+ + N WH+D +++
Sbjct: 62 MGGFGEDPFFDPIPIGRGNIAAILR-----EPDEKAPLFAEN--WHSDWSFLS 106

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVYS-QSKLG 173
G A +P VGG T FAD AA+ AL + + + +A HS L Y+ G
Sbjct: 107 HPPAGTCLLAIEIPPVGGDTLFADQIAAFAALSDEKDKQLRALTAIHS AKLAYAPDGTYG 166

Query: 174 HVQQAGSAYIGYGMDDTTATPLR--PLVKVHPETGRPSLL--IGRHAHAIPGMDAAESERF 229
A + D +A ++ PL++ HPETG ++ +G + I GM AE+
Sbjct: 167 EKDAAGRSMAIRPDESANAMQTHPLIQHPETGEEAIFSTLG-YIIGIEGMAQAEAIAL 225

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
L L W + V+ H W +V+WDNR +LH+A
Sbjct: 226 LSELAQWQSRDEFVYRHHWEPDMLVLWDNRSVLHKA 261

>ref|ZP_05642075.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. tabaci ATCC

11528]
Length = 279

Score = 103 bits (256), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 79/253 (31%), Positives = 122/253 (48%), Gaps = 22/253 (8%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAI--ERIGGGDIVAIS-NVKADGTVRQHSPA EWDD 97
Q +L+FP S+ +QI + G E G +I IS +VK +PA
Sbjct: 44 QRGVLVPQIDFSDAEQIALTRTLGTFCPEASDGNITKISLDVK-----ENPAG--- 93

Query: 98 MMKVIVGNMAWHADSTYMPVMAQGA VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH 157
+ + G++ WH D T V ++ S +V + GG T F + AAY+AL A +
Sbjct: 94 -AEFLKGS LYWHIDGTSSDVPVLASLLSCKVPASWGGNTGFCNTYAAYEALSSADK---- 148

Query: 158 QRSARHSLVYS--QSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHA 215
QR R ++++ S L + + G A + M PLV H +GR SL++G A
Sbjct: 149 QRYERLRVIHAPWASLLYNNPEPGLAMLK-AMQAIGEKEKPLVVRH-RSGRKS LILGCTA 206

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRV 275
+ G+ A+S + L GL +WA ++H W GD+V+WDN +HRAE +D R+
Sbjct: 207 QQVVGVS LAQSAQILVGLREWATAEAFSYSHAWQTGDLVIWDNTGTMHRAEAYDPACGRM 266

Query: 276 MWHSRLAGRPETE 288
M ++L G E
Sbjct: 267 MHRTKLQGE E PFE 279

>ref|ZP_06914719.1| dioxygenase [Streptomyces sviveus ATCC 29083]
gb|EDY58917.2| dioxygenase [Streptomyces sviveus ATCC 29083]
Length = 321

Score = 103 bits (256), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 90/293 (30%), Positives = 128/293 (43%), Gaps = 22/293 (7%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 64
+++ P +GA +TGV LA LDD A+ AA L+ ++ F GQ L + + FA+RF
Sbjct: 14 IEVNPVAGHIGAEITGVDLAGDLDDR VVGAI RA AVL RWKV VFFRGQKLDHAGHVAFARRF 73

Query: 65 G---AIERIGGGDIVAISNVK--AD----GTVRQHSPA EWDDMMKVIVGNMAWHADSTYM 115
G + + G V+ AD G EW + + WH D
Sbjct: 74 GEPVVLKRKGSASPAQFPEVETTADRLELGKFGMEHEEWLQRRRHTLLR-GWHCDHGAR 132

Query: 116 PVMAQGA VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
+ AE VP GG T ++++ AAY L RA V H L +G+
Sbjct: 133 VDPPAATILRAETVPPYGGDTTWSNLAAAYAGLSAPVRAFDGLRVEHRL-----GVGYQ 187

Query: 176 QQAG-SAYIGYMDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGL 233
+ G A + + +D L PLV+VHPETG L + G + I + AES L+ L
Sbjct: 188 PRPGDDANVRHLLDHQVASLHPLVRVHPETGERILYVNGYYVEQIADLSRAESRAILDML 247

Query: 234 VDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283
++ A + +W G V WDNR +H A P D PR M LAG
Sbjct: 248 LEQAVRPEYTVRFRWEPGSVAFWDNRATIH LA-PADNAHLGFPRTMHRVMLAG 299

>ref|YP_340645.1| taurine dioxygenase [Pseudoalteromonas haloplanktis TAC125]
emb|CAI87203.1| putative taurine dioxygenase [Pseudoalteromonas haloplanktis TAC125]
Length = 308

Score = 102 bits (255), Expect = 4e-20, Method: Compositional matrix adjust.

Identities = 82/278 (29%), Positives = 126/278 (45%), Gaps = 23/278 (8%)

```

Query: 6   LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L +TP   +G  V+G  +   L D   A L A W +HA+L+F  Q +S ++QI F++ F
Sbjct: 3   LTVTPLD-NVGVEVSGFDINEPLTDEIKAEKALWYEHAILVFRDQDISPEKQIEFSRIF 61

Query: 65  GAIE----RIGGGDIV-AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMA 119
          G +E   ++   D   +   ++ G + +   A +   + IVG + WH D Y
Sbjct: 62  GPLELHPLKVTTSDKYPELFVLQNGGPMDFQTA FYKG--EEIVGRLDWHMDLHYTARPN 119

Query: 120  QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
          GA+  A VV A  G T F D+  AYDALD+ T+AL+ Q   +S   + + +V  G
Sbjct: 120  HGALLRAVVAAEDGMTGFGDLAKAYDALDDDTKALIEQLEVVYSFSMQRRHMRVYNLDG 179

Query: 180  -----SAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAH---AIP---GMDAAE 225
          +   G   +   P+V  HP +GR  L +   P  G+  E
Sbjct: 180  YEPGPNSPTKPTDIGFPDFSDAAYPMVVTHPISGRKVLEVVEQFLDRVVTPQQFGLSNDE 239

Query: 226  SERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLH 263
          S  LE LV   +   + H+W  GD+V+WDN   +H
Sbjct: 240  SIELLERLVAHVQKPEFTYFHKWREGDMVLWDNWRAMH 277

```

>ref|YP_883118.1| taurine catabolism dioxygenase TauD, TfdA family protein
[Mycobacterium avium 104]
gb|ABK69483.1| taurine catabolism dioxygenase TauD, TfdA family protein
[Mycobacterium avium 104]
Length = 281

Score = 102 bits (255), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 92/291 (31%), Positives = 129/291 (44%), Gaps = 27/291 (9%)

```

Query: 4   TTLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
          + L IT   ++GA VTG+  A L  DD+  A+  A   + +L+F G +L   Q+ F
Sbjct: 2   SLLTITKLTDSVGA EVTGLDPAALAHDDSVGEAVLDALEDNGVLVFRGLYLDPAAQVAF 61

Query: 62  KRFGAIERIGGG-----DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
          R G ++   G   I  I+  K+   +  A +D   WH D  P
Sbjct: 62  GRLGEVDHSSDGHHPVPGIYPITLDKSKNASAAYLKATFD-----WHIDGC-TP 109

Query: 117  V---MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
          +   +  V SA  V   GG T FA+  AYDAL + +   HSL  SQ +
Sbjct: 110  LGDECPQKATVLSAVRVAERGGETEFANSYGAYDALTDDEKQRFGALRVVHSLEASQRR- 168

Query: 173  GHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG 232
          V   S  +   +  T  PLV  H  +GR SL++G  A  + GMD  E   LE
Sbjct: 169  --VYPDPSPELVARWRSRRTHEHPLVWTH-RSGRKS LVLGASADYVVGMDVDEGRALLEE 225

Query: 233  LVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          L+  A   RV+  H W+  GD V+WDNR +LHRA P+D   R M  + + G
Sbjct: 226  LLQRATVPERVYRHGWSIGDTVIWDNRGVLHRAAPYDPDSSREMLRTTVLG 276

```

>ref|YP_001412118.1| taurine dioxygenase [Parvibaculum lavamentivorans DS-1]
gb|ABS62461.1| Taurine dioxygenase [Parvibaculum lavamentivorans DS-1]
Length = 285

Score = 102 bits (255), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 77/269 (28%), Positives = 120/269 (44%), Gaps = 27/269 (10%)

```

Query: 6   LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          ++P   +GA +TG+  L  LD A  +AL  A L   ++ F  Q ++ DQ + FA+ F
Sbjct: 13  FTLSP LPLIGAEITGIDLKPLDTAALSALRQALLDWKVIFFRDQDITTDQHLAFARLF 72

```

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPV 117
G +E + G +++AI++ + D R++ WH+D T+
Sbjct: 73 GELEVHPFAPHKQGYPEVLAITHDR-DRPGRENK-----WHS DVTWREC 115

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
+ G+V A VP VGG T FADM AAYD L E + + A H + ++ + +
Sbjct: 116 PSLGSVLRAIEVPEVGGDTLFDADMYAAYDGLTEEVKEKIDGAVAIHDFAHFRAAM-RARG 174

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDW 236
A I P+V+ HPETGR + + I G++ AES+ L+ L
Sbjct: 175 KSEAEIEEMNRKYPMVEHPVVRTHPETGRKGIYVNVAFQTQHIVGLEKAESDALLKHLQAQ 234

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
A +W + WDNR H A
Sbjct: 235 AAIPYQCRFRWQKNSIAFWDNRSSQHYA 263

>ref|ZP_06846090.1| Taurine dioxygenase [Burkholderia sp. Ch1-1]
gb|EFG66280.1| Taurine dioxygenase [Burkholderia sp. Ch1-1]
Length = 310

Score = 102 bits (255), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 77/268 (28%), Positives = 120/268 (44%), Gaps = 20/268 (7%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L + P +GA V GV L+ L+ A A+ AA ++H ++ F GQ HL + Q FAK
Sbjct: 12 LDLHPVTGRIGAEVRGVRSLGQLEAATVEAIRAALVRHKVIFFRGQTHLQDADQEAFAKL 71

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
G E + + + + H + +WH D T++ Q ++
Sbjct: 72 LG--EPVSHPTVPVVDGTDYLLLELDSHRGGRAN-----SWHTDVTTFVDAYPQASI 119

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG---S 180
+P VGG T +A+ AYD L +AL Q A HS Y + +V + G
Sbjct: 120 LRGVTIPEVGGDTVWANTATAYDDLPPPLKALAEQLWAVHSNEYDYANHANVGERGRDTE 179

Query: 181 AYIGYG---MDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
A+ Y + T P+V+VHPE+G +L++G + G+ + S LE L +
Sbjct: 180 AFRRYREAFVSTRYETEHPVVRVHPESGEKTLILGHFVKSFVGLTPSASAHVLELLQGYV 239

Query: 238 CQAPRVHAHQWAAGDVVVDNRCLLHRA 265
+ + +W GDV +WDNR H A
Sbjct: 240 TRLENIVRWQGTGDVAIWDNRATQHYA 267

>ref|ZP_05226007.1| alpha-ketoglutarate-dependent taurine dioxygenase [Mycobacterium
intracellulare ATCC 13950]
Length = 300

Score = 102 bits (255), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 86/290 (29%), Positives = 123/290 (42%), Gaps = 30/290 (10%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
+ +T G+ +GA + G+ L LDDA + A L H ++ F QH L ++QQ+ FA+
Sbjct: 5 ITVTKLGSRIGARIDGLSLGGHLDDAAVETIRRALLTHKVVFRRHQHLLDDEQQLDFARL 64

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSP-----AEWDDMMKVIVGNMAWHADSTYMPV 117
G I + A +H P +E+ + WH D T+
Sbjct: 65 LG-----TPIGHPAASALAAKHMPVITPIDSEYGKATR-----WHTDVTFAAN 107

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
++ A +P+ GG T +A AAY L E +A+V A H+ Y V

Sbjct: 108 YPAASILRAVTLPSYGGSTLWASTVAAYQHLPEPLKAMVENLWALHTNRYDYVSTEAVMS 167

Query: 178 AGSAYIGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
A + R P+V+VHPETG +LL G G+D ES LE L

Sbjct: 168 MSDAQRAFRQAFKEKPDFRTEHPVVRVHPETGERALLAGDFVRGFVGLDNHESSVLELLQ 227

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA-EPWDFKLPRVMWHSRLAG 283
WA GDV +WDNR HRA + +D + PR+M L G

Sbjct: 228 RRITMPENTIRWAWAPGDVAMWDNRATQHRAIDDYDDQ-PRLMHRITLMG 276

>ref|YP_001074852.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei 1106a]
ref|ZP_02406004.1| dioxygenase, TauD/TfdA family protein [Burkholderia pseudomallei DM98]
ref|ZP_02474301.1| dioxygenase, TauD/TfdA family protein [Burkholderia pseudomallei B7210]
ref|ZP_02509054.1| dioxygenase, TauD/TfdA family protein [Burkholderia pseudomallei BCC215]
ref|ZP_03457012.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 576]
ref|ZP_04521787.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei MSHR346]
ref|ZP_04812264.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1106b]
ref|ZP_04888968.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1655]
ref|ZP_04893943.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei Pasteur 52237]
ref|ZP_04905154.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei S13]
ref|ZP_04967323.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 406e]
gb|ABN93335.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1106a]
gb|EDO86873.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 406e]
gb|EDO90781.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei Pasteur 52237]
gb|EDS88166.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei S13]
gb|EDU09952.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1655]
gb|EEC31511.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 576]
gb|EEP50701.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei MSHR346]
gb|EES22889.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1106b]
Length = 283

Score = 102 bits (255), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 79/286 (27%), Positives = 125/286 (43%), Gaps = 31/286 (10%)

Query: 15 LGATVTGVHLATLDDA-GFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG 73
LG V G DA AL AW + Q L + + F++ FG ER
Sbjct: 10 LGTEVYGFDSFPFHDAEAVRALIEAWHAGGICRLRRQRLDMAEFVEFSRIFGRPERALNQ 69

Query: 74 D-----IVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
+ ++ +SN+ +G H ++ WH D Y V +
Sbjct: 70 ERKLTSREDLPELMIVSNILENGVSIGHLGSK-----EAYWHTDMCYTDVPPIAS 119

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ A VPA GG T F +M +DAL + R + S +H Y+ +G ++ +
Sbjct: 120 ILYAIEVPAHGGNTEFMNMYRVHDALPASLRRQIAGLSIKHDRSYT--AVGELRYGFDSV 177

Query: 183 IGYGMDTTATP--LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQ 239
+ D T P + P+V+VHP T RP L +GR +A + G+ ESE L+ L +
Sbjct: 178 V---DVTTCPGSIHPIVRVHPVTQRPYLYLGRRNLNAYVVGLPVGESEALLDELWRYTRL 233

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
+W GD+++WDNRC +HR + +D R+MW +++ P
Sbjct: 234 DGVTWTQRWEVGDIMIWDNRCTMHRRDAFDANARRLMWRTQIQADP 279

>ref|XP_001216119.1| conserved hypothetical protein [Aspergillus terreus NIH2624]
gb|EAU31760.1| conserved hypothetical protein [Aspergillus terreus NIH2624]

Length = 299

Score = 102 bits (255), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 77/279 (27%), Positives = 130/279 (46%), Gaps = 29/279 (10%)

```
Query: 6   LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          + + P   T GA V   V   +   L D F+ +++A ++ +L+F   L+++   I FAKRF
Sbjct: 14  ISVNPiHPTFGAEVREVDfSKPLTDEVFSEIYSAITKYGLVFRNTGLTDEGHIAFAKRF 73

Query: 65  GAIE-----RIGGGDIVAISNVKADGTVRQ-HSPAewDDMMKVIVGNMAWHAD 111
          G ++                R+   ++ +SNV+ DG++   SP   +           GN  +H D
Sbjct: 74  GELDDITPYLALGRKNRLKYNELFDVSNVEFDGSILDPEsprGQGNK-----GNGLFHVD 128

Query: 112 STYMPVMAQGAVFSAEVV--PAVGGRtCFADMRaAYDAL--DEATRALVHQrsARHSLVY 167
          S++ P   A   ++   +   +   P +GG T FAD R A+D L   D   +   +   A HS+ +
Sbjct: 129 SSFNPRRAGYsLLLSHELPPPGMGGATAFADTRtAFDELpVDLKADLVANDYVAaHSIHh 188

Query: 168 SQSKLGHVQQAGSAYIGYGMdTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMdAAESE 227
          S+                A   + Y M                +V+ H   + R +L I   H H I G+   S+
Sbjct: 189 SRKLAaPEFYADRNPLDYPMGR-----HKMVQRHEPSRRMNLYIAAHIHhIEGLGPEASQ 243

Query: 228 RFLEGLVDWACQAPRVHAHQWA-AGDVVVWdNRCLLHRA 265
          +   +   +   QA V   +W   GD++ WDN C++HRA
Sbjct: 244 KLFDRVFTHCTQAKYVTEVEWKQPGDLIAWDNTCVMHRA 282
```

>ref|YP_003339338.1| taurine dioxygenase [Streptosporangium roseum DSM 43021]
gb|ACZ86595.1| Taurine dioxygenase [Streptosporangium roseum DSM 43021]
Length = 304

Score = 102 bits (255), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 91/289 (31%), Positives = 133/289 (46%), Gaps = 33/289 (11%)

```
Query: 6   LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L+I P G   +GA +TGV L A LD+   A L   A L+   +L F G+ ++   Q   A+ +
Sbjct: 34  LRIRPAGPLIGAEITGVDLGAPLDEELKAELRDALLEWKVLFFRGRRTGADQRRLAEVW 93

Query: 65  GAIERIGGGDIVAISNVKADGTVRQHSPAewDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
          G +E                +S   ++   VR   E   +           WH+D+T+ P   + GAV
Sbjct: 94  GKVE-----TFPFLSKGRSPDVVRFAKHEERPGLENT-----WHSdatWHPTPSMGAVL 142

Query: 125 SAEVVPavGG-RTCFADMRaAYDALDEATRALVHQrsARHSLVYSQSKLGHVQQAGSAYI 183
          A   VPA GG   T ++D+ AAYD LD   ALV   R A H   +   S+LG ++
Sbjct: 143 RAVEVPAGGGGDTIwSDVAAAYDNLDPELaALVDGREAVHHFDWLYSRlGLLE----- 195

Query: 184 GYGMDTTAT---PLR-PLVKVHPETGRPSLLIGR-HAHAIPGMdAAESERFLEGLVDWAC 238
          G   +D                P+R P+V+ HP TGR   + + R   + G++   +           L+D C
Sbjct: 196 GEELDRARADFPpVRHPiVRTHPVTGRKGIFVNRVFTegVVGLEHGAARE----LIDRLC 251

Query: 239 QAPRVHAHQ----WAAGDVVVWdNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          +           +Q   W   G V VWDNR   H A   +           RVM   +AG
Sbjct: 252 RHVETPEYQVRFRWEPGSVAVWdNRATQHYAVNDYYPERRVMERISiAG 300
```

>ref|ZP_02450610.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei 91]
ref|ZP_02458779.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei 9]
ref|ZP_02501145.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei 112]
ref|ZP_03790780.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei Pakistan
9]
gb|EEH28990.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei Pakistan
9]
Length = 270

Score = 102 bits (254), Expect = 6e-20, Method: Compositional matrix adjust.
Identities = 74/272 (27%), Positives = 120/272 (44%), Gaps = 30/272 (11%)

```
Query: 28 DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGD-----IV 76
          D      AL  AW   +      Q L   + + F++ FG  ER   +      ++
Sbjct: 11 DAEAVRALIEAWHAGGICRLRRQRLDMAEFVEFSRIFGRPERALNQERKLTREDLPELM 70

Query: 77 AISNVKADGTVRQHSPAEDWMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGR 136
          +SN+ +G   H   ++          WH D Y V   ++ A VPA GG T
Sbjct: 71 IVSNILENGVSIGHLGSK-----EAYWHTDMCYTDVPPIASILYAIEVPARGGNT 120

Query: 137 CFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATP--L 194
          F +M   +DAL + R   +   S +H   Y+   +G ++   + +   D T P   +
Sbjct: 121 EFMNMYRVHDALPASLRQIAGLSIKHDRSYT--AVGELRYGFDSVV---DVTTCPGSI 174

Query: 195 RPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
          P+V+VHP T RP L +GR +A + G+   ESE L+ L +   +W GD+
Sbjct: 175 HPIVRVHPVTQRPYLYLGRRLNAYVVGLPVGESEALLDELWRYTRLDGVTWTQRWEVVDI 234

Query: 254 VVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
          ++WDNRC +HR + +D   R+MW +++   P
Sbjct: 235 MIWDNRCTMHRDAFDANARRLMWRTQIQADP 266
```

>emb|CAJ89608.1| putative dioxygenase [Streptomyces ambofaciens ATCC 23877]
Length = 312

Score = 102 bits (254), Expect = 6e-20, Method: Compositional matrix adjust.
Identities = 84/266 (31%), Positives = 109/266 (40%), Gaps = 25/266 (9%)

```
Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 64
          + P   T+GA + GV L+ L A   L+ A L+ +L F QHL++DQQ FA +
Sbjct: 44 FDEVPLARTIGAEIRGVDLRPLGAALREELNRALLEWKVLFRAQHLSDDQRAFAGHW 103

Query: 65 GAIER----IGGGDIVAISNVKADGTVRQHSPAEDWMMKVIVGNMAWHADSTYMPVMAQ 120
          G +E      G   +   KAD +   +          WH D T+   A
Sbjct: 104 GRLETNPLLAAGSREDVVRFDKADASTPTYE-----NVWHTDVTFRERPAL 149

Query: 121 GAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
          GAV   VP   GG T +ADM AAYD L   R V   A H +   G + G
Sbjct: 150 GAVLQLREVPPFGGDTLWADMAAAYDNLPREVRDRVDGARAVHDFI-----PGFARFYGP 204

Query: 181 AYIGYGMTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239
          +   D      P+V+ HPETGR L +   I GMD ES+R L L A
Sbjct: 205 ERLIPHQDAFFPVEHPVVRTHPETGRRMLFVNASFTTHTGMDRDESDRLRLFLFQQAHV 264

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
          +W GD+ WDNR H A
Sbjct: 265 PEFQVRFRWQPGDIAFDNRATQHYA 290
```

>ref|YP_001869285.1| taurine catabolism dioxygenase TauD/TfdA [Nostoc punctiforme PCC 73102]
gb|ACC84342.1| Taurine catabolism dioxygenase TauD/TfdA [Nostoc punctiforme PCC 73102]
Length = 304

Score = 102 bits (254), Expect = 6e-20, Method: Compositional matrix adjust.
Identities = 77/272 (28%), Positives = 114/272 (41%), Gaps = 22/272 (8%)

```
Query: 1 MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQH-LSNDQQI 58
          M      I P   +GA + GV+L++ L D   + +   ++H ++ F Q L D Q+
Sbjct: 1 MGSQYFDIKPVAGRIGAEIIGVNLSSNLSDDIISDIRKTLVKHKVIFFRDQQQLDADGQV 60
```

Query: 59 TFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNM-----AWHADST 113
FA+RFG + A TV S E +++ + G +WH D T
Sbjct: 61 AFARRFGEV-----TTAHTPV--PSLPENPEVLDLNYGR TTSRANSWHTDVT 105

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
++ G++ A +P GG T +A+ AY L R L Q A HS Y +
Sbjct: 106 FVDRPPLGSILRALDIPPTGGDTIWANSVTAYQDLPIHLRNLADQLWAVHSNKYDYATAF 165

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+ + AY T L P+V+VHPE+G L IG G+ ES+ L L
Sbjct: 166 DLPEYAKAYRAVFTSTVYETLHPVVRVHPESGERGLFIGGFVRQFRGLSTTESDDILRL 225

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ + +W GDV WDNR H A
Sbjct: 226 QAYITRPENTVRWRWQVGDVAFWDNRATQHYA 257

>ref|YP_001346557.1| taurine dioxygenase [Pseudomonas aeruginosa PA7]
gb|ABR86490.1| taurine dioxygenase [Pseudomonas aeruginosa PA7]
Length = 277

Score = 102 bits (254), Expect = 6e-20, Method: Compositional matrix adjust.
Identities = 90/287 (31%), Positives = 126/287 (43%), Gaps = 18/287 (6%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+L I P LGA V+G+ LA LDD G A+ A L H +L F Q L Q FA
Sbjct: 2 SLTIQPISPALGAIVSGIDLAAPLDDGGQRAIEQALLDHQVLFRRDQSLEPKSQARFAAH 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG + I I A+ Q D + + N WH D T++ A GAV
Sbjct: 62 FGD LH-----IHPIYPSVAE----QPEVIVLDTAVTDVRDNAIWH TDVTFLETPALGAV 111

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQQAGSA 181
A+ +P GG T +A AAY+AL R L+ +A H + + + + G V +A A
Sbjct: 112 LVAKQLPPYGGDTLWASSTAAYEALSAPLRRLDGLTATHDIGKSFPRERFG-VTEADLA 170

Query: 182 YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQA 240
+ P+V+ HP TGR L + I ++ AES+ L+ L A +
Sbjct: 171 RLEEARKLNPPRSHPVVRTHPVTGRKGLFVSDGFTTRINELEPAESDALLKFLFAHATRP 230

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWH--SRLAGRP 285
+W DV WDNR H A D++ R + H + L RP
Sbjct: 231 EFTVRWRWQENDVAFWDNRVTQHYAVD-DYRPQRRVMHRATILGDRP 276

>gb|ADC34019.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 102 bits (254), Expect = 6e-20, Method: Compositional matrix adjust.
Identities = 70/214 (32%), Positives = 105/214 (49%), Gaps = 27/214 (12%)

Query: 56 QQITFAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW 108
QQI FA++FG +ER + ++N+ ADG V + +W
Sbjct: 1 QQIAFAEQFGTLERRIASNRGKTNP L VHIVTNLNADGKPSGK-----VASTSW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
H+D ++ P + A V+P GG TCFA+M AAY+AL A +A + A HS S
Sbjct: 49 HSDKSFRPQPSLATILHALVMPPDGGETCFANMIAAYEALPAAEKAELDGIRAVHSWEIS 108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPL-RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
Q++ G +A I A P+ PLV+ PETG +L +G A G +
Sbjct: 109 QARAGF--KAPPEEIA-----DAPPMAPLVRTIPETGLKALFMGERAVFFEGHPPEEAGQ 161

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
 LE L A + V+ H+W GD+++WDNRC+
 Sbjct: 162 ARLEKLTAHAVEERFVYRHKWTLGDLMLMWDNRCV 195

>ref|ZP_06415360.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EUN1f]
 gb|EFC81811.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EUN1f]
 Length = 277

Score = 102 bits (254), Expect = 6e-20, Method: Compositional matrix adjust.
 Identities = 86/285 (30%), Positives = 128/285 (44%), Gaps = 20/285 (7%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQ-HALLIFPGQHLSNDQQITFAKR 63
 ++ +TP +GA V G+ L D AA A L + +LI+ ++ +D + F++
 Sbjct: 2 SITVTPVSPAVGAEVVGLSGHQLVDRQVAADSLAALDITYGLIYRDANIGDDDLVAFSRL 61

Query: 64 FGAIERIGGGDIVA---ISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
 G + G + + IS V D PA+ D+ WH D V +
 Sbjct: 62 LGDVVVAPMGGGLASHPEISPVSLD-----PAK-SDLANYRRSTFFWHIDGVNDDVPQK 113

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
 ++ +A V GG T FA+ AYDAL + + + HS SQ L H +
 Sbjct: 114 ASLLTARQVADEGGGETEFANTYTYAYDALPDDEKEYLATLRVVHSFAASQ-ILVHPHPSDK 172

Query: 181 AYIGYGMDDTTATPLR--PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC 238
 + P R PL+ +GR SLLIG + G+ A ES L+ L+ W+
 Sbjct: 173 ERAAWNRR----VPSREHPLIWTR-RSGRKSLLIGATTDHVVGLPARESALLDKLLAWST 227

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
 Q V H W GD+V+WDN +LHRA P+ PR+M + LAG
 Sbjct: 228 QESFVLRHWDWRRGDLVIWNTGMLHRLPYQPTAPRLMHRTTLAG 272

>ref|YP_235431.1| taurine catabolism dioxygenase TauD/TfdA [Pseudomonas syringae pv.
 syringae B728a]
 gb|AA37393.1| Taurine catabolism dioxygenase TauD/TfdA [Pseudomonas syringae pv.
 syringae B728a]
 Length = 279

Score = 102 bits (254), Expect = 7e-20, Method: Compositional matrix adjust.
 Identities = 79/250 (31%), Positives = 120/250 (48%), Gaps = 24/250 (9%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMK 100
 Q +L+FP H S+ +QI F + G GD I+ + D VR++ PA +
 Sbjct: 44 QRGVLVFPQIHFSDAEQIAFTRTLGTF-CPEPGDGQNITRISLD--VREN-PAG----AE 95

Query: 101 VIVGNMAWHADSTYM--PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ 158
 + G++ WH D T P++A ++ S +V + GG T F + AAY+ L A +
 Sbjct: 96 FLKGSlyWHIDGTSSDSPILA--SLLSCKVRASWGGNTGFCNTYAAYEGLSSADQQHYDG 153

Query: 159 RSARH----SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH 214
 H SL+Y + G IG PLV H +GR SL++G
 Sbjct: 154 LRVIHAPWASLLYYNPEPGLAMLEAMQVIG-----EKELPLVWKH-RSGRKSLLIGCT 205

Query: 215 AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPR 274
 A + G+ A+S R L GL +WA ++H W GD+V+WDN +HRAE +D + R
 Sbjct: 206 AQQVVGSLAQ SARILVGLREWATSEAFSYSHAWQVGDVLIWNTGTMTMRAEAYDPECGR 265

Query: 275 VMWHSRLAGR 284
 +M ++L G
 Sbjct: 266 MMHRTKLQGE 275

>ref|ZP_06840721.1| Taurine catabolism dioxygenase TauD/TfdA [Burkholderia sp. Ch1-1]
gb|EFG71441.1| Taurine catabolism dioxygenase TauD/TfdA [Burkholderia sp. Ch1-1]
Length = 301

Score = 102 bits (254), Expect = 7e-20, Method: Compositional matrix adjust.
Identities = 69/239 (28%), Positives = 110/239 (46%), Gaps = 28/239 (11%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAI-----ERIGGGDIVAISNVKADGTVRQ 89
++ +LIFP Q +++D+ + F+ FG + E I ISN+ D +
Sbjct: 39 RYPVLIFPKQFINDELLAFSANFGPVHTAMSYQTREKEHRLQPKITDISNLGKDNQTFK 98

Query: 90 HSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD 149
M V WH D++Y + A+ + A V GG T FADMR AYD +
Sbjct: 99 RGDHR---RMNMFVSK-RWHTDASYEAIIPARYSFLLAYTVAQRGGETQFADMREAYDEMP 154

Query: 150 EATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP---LVKVHPETG 205
E R +V S ++++++ G+ + D L P LV+ HP +G
Sbjct: 155 EDLRPVVEDLSCEYNILWARMLSGYTEFP-----DEERAKLPPAQHKLVRHRHPVSG 205

Query: 206 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHR 264
R +L + HA + E L L+++A Q V+ H+W D+V+WDNR L+HR
Sbjct: 206 RKTLYLSGHATHVVDWPIPEGRDLLRELMEFATQPQFVYTHKWHERDLVMWDNRALMHR 264

>ref|ZP_06851972.1| TauD/TfdA family dioxygenase [Mycobacterium parascrofulaceum ATCC
BAA-614]
gb|EFG74695.1| TauD/TfdA family dioxygenase [Mycobacterium parascrofulaceum ATCC
BAA-614]
Length = 281

Score = 102 bits (254), Expect = 7e-20, Method: Compositional matrix adjust.
Identities = 89/288 (30%), Positives = 133/288 (46%), Gaps = 21/288 (7%)

Query: 4 TTLQITPTGATLGATVTGVHLATL---DDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
+ L IT A++GA VTG+ L D G A L A + +L+F G L+ + Q+ F
Sbjct: 2 SLLTITKLTASVGA EVTGLDPGRLPGDPGTGQAVLDA-LEDNGVLVFRGLRLAPEAQVDF 60

Query: 61 AKRFGAIERIGGG--DIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYM--- 115
+ G ++ G + I + + ++S AE ++ WH D
Sbjct: 61 CRLLEGEVDHSADGHPVAGIYPISLNP---KNSSAE-----ILKATFDWHIDGCTPLDD 112

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
+ V SA V GG T FA+ AAYD L + + HSL SQ + H
Sbjct: 113 ECPQKATVLSAVRVAEWGGETEFANSYAAAYDELTDDEKERFGSLRVVHSLEASQRR-AH- 170

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD 235
AG + + T PLV H +GR SL++G A + GMD E L+ L++
Sbjct: 171 PDAGPEQVAR-WRSRRTHEHPLVWTH-RSGRKS LVLGASADYVVGMDLDEGRALLQDLLE 228

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
A +V++H+W+ GD V+WDNR +LHRA P+D R M + + G
Sbjct: 229 RATGPKVYSHEWSVGDTVIWDNRGVLHRAAPYDPASQREMLRTTVLG 276

>ref|ZP_06410990.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EUN1f]
gb|EFC86246.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EUN1f]
Length = 279

Score = 102 bits (253), Expect = 8e-20, Method: Compositional matrix adjust.
Identities = 82/254 (32%), Positives = 112/254 (44%), Gaps = 31/254 (12%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAI---ERIGGGDIVAISNVKADGTVRQHSPAEDD 97

```

      +H +L+F   +L   Q+ F +R G +   +   D   I   +   D   PA   +
Sbjct: 41  EHGVLFLFRELNLNDYATQVAFCRRLGELLTFPKTPPLDFPEIMEINWD-----PA--NP 91

Query: 98  MMKVIVGNMAWHADSTYMP-VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV 156
          GN AWH D   P   + +V S   VV   GG T FA   AAYDAL
Sbjct: 92  RSDYFRGNTAWHLDGALDPGNPPKASVMSGGVVTDSGGETEFASTYAAYDAL----- 143

Query: 157 HQRSARHSLVYSQSKLGHVQQA--GSAYIGYGMDDTTATPLRPLVKVHP-----ETGRPSL 209
          SA+   + + ++ H +A   AY   +   A   +   K HP   E+GR SL
Sbjct: 144 ---SAQEKEEFGLKLRVIHTLEAILRPAYPNPTPEQRADWAKRPAKEHPLVWQHESGRRSL 200

Query: 210 LIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD 269
          + G   I GMD AE   L+ L   A   RV   H W   GD+V+WDNR L+HR P+D
Sbjct: 201 VFGSTTSHIAGMDEAEGRALLDELERRATTPDRVLQHTWTQGDMVIWDNRGLVHRVRPFD 260

Query: 270 FKLPRVMWHSRLAG 283
          +PR M+ + LAG
Sbjct: 261 PAVPRRMYRTTLAG 274

```

>gb|ACX54970.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 98

Score = 102 bits (253), Expect = 8e-20, Method: Compositional matrix adjust.
Identities = 58/99 (58%), Positives = 67/99 (67%), Gaps = 5/99 (5%)

```

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
          ADSTYM V A GAVF+AE+VP   GG T FADMRAAYDALD+ATR + + +A HS YS
Sbjct: 1   ADSTYMRVQAMGAVFTAIEIVPDDGGDTGFADMRAAYDALDDATREQIDRLAAYHSRRYSM 60

Query: 170 SKLG-HVQQAGS---AYIGYGMDDTTATPLRPLVKVHPET 204
          +   HV Q   +   GYG DT   PLRPL+KVHPET
Sbjct: 61  DRADLHVSQENADRYQLYGYGADTEP-PLRPLIKVHPET 98

```

>gb|ADC33993.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 102 bits (253), Expect = 9e-20, Method: Compositional matrix adjust.
Identities = 69/214 (32%), Positives = 103/214 (48%), Gaps = 27/214 (12%)

```

Query: 56  QQITFAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW 108
          QQI FA++FG +ER   +   + ++N+ ADG   V + +W
Sbjct: 1   QQIAFAEQFGTLERHIASNRGKTNPVLHIVTNLNADGKPSGK-----VASTSW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
          H+D ++ P   +   + A V+P GG TCFA+M AAY+AL A +A +   A HS S
Sbjct: 49  HSDKSFRPQPSLATILHALVMPPDGGGETCFANMIAAYEALPAAEKAELDGIRAVHSWEIS 108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
          Q++ G   A   A P+ PLV+ PETG +L +G A   G   +
Sbjct: 109 QARAGFKAPAEI-----ADAPPMSHPLVRTIPETGLKALFMGERAVFFEGHPEEVGQ 161

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
          LE L   A +   V+ H+W GD+++WDNRC+
Sbjct: 162 ARLEKLTAHAVEERFVYRHKWTLGDLLMWDNRCV 195

```

>ref|ZP_07309248.1| taurine dioxygenase [Streptomyces griseoflavus Tu4000]
gb|EFL37617.1| taurine dioxygenase [Streptomyces griseoflavus Tu4000]
Length = 321

Query: 170 SKLGHV---QQAGSAYIGYGMDTTATPLRPLVKVHPET 204
+ G++ Q Y YG LRPLVKVHPET
Sbjct: 61 DRAGYMPSKONESGGYDOYGYHDMEPSLRPLVKVHPET 98

>ref|YP_001824503.1| putative taurine catabolism dioxygenase [Streptomyces griseus subsp. griseus NBRC 13350]
dbj|BAG19820.1| putative taurine catabolism dioxygenase [Streptomyces griseus subsp. griseus NBRC 13350]
Length = 307

Score = 101 bits (252), Expect = 9e-20, Method: Compositional matrix adjust.
Identities = 83/266 (31%), Positives = 114/266 (42%), Gaps = 27/266 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ P G +GA + GV L+ LD A A L A L+ +L F QHL++ QQ FA +
Sbjct: 41 FRLVPLGRVIGAEHLGVDLRPLDAAALRAELDRALLEWKVLFVRDQHLTSRQQRAFAGYW 100

Query: 65 GAIER---IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
G +E + GD ++ + D V WH D T+ A G
Sbjct: 101 GELETNPLLATGDDPEVARL-----DRTAVPTFENVWHTDVTFRERPALG 145

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
AV VP GG T +ADM AAYD L E + + A H + S+ ++
Sbjct: 146 AVLQLREVPPPTGGDTLWADMAAAYDNLP EEVKERIEGARAVHDFIPGFSRFYPPER---- 201

Query: 182 YIGYGMTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQA 240
+ D P+V+ HP TGR ++ + I G + ES+R L L A A
Sbjct: 202 -LAPHQDRFPFVEHPVRRHPVTGRRTIFVNASFTTRIVGFEREESDRLLRLLFQQA-HA 259

Query: 241 PRVHAH-QWAAGDVVVWDNRCLLHRA 265
P W AGDV WDNR H A
Sbjct: 260 PEFQVRFSWRAGDVAFWDNRATQHIA 285

>ref|ZP_01078548.1| Probable taurine catabolism dioxygenase [Marinomonas sp. MED121]
gb|EAQ63339.1| Probable taurine catabolism dioxygenase [Marinomonas sp. MED121]
Length = 270

Score = 101 bits (252), Expect = 9e-20, Method: Compositional matrix adjust.
Identities = 70/264 (26%), Positives = 113/264 (42%), Gaps = 15/264 (5%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
+QI +GA V GV+LA DA F A++ AW Q+ ++ P Q ++ ++ + A RFG
Sbjct: 1 MQIERLTPNIGAMVHGVNLAICSDAEFEAVYQAWYQNGVIFLPDQKMTPEEHLKIASRFG 60

Query: 66 AIERIGG--GDIV AISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
+ + ++ V TVR +P E WH D T+ ++ ++
Sbjct: 61 ELAPVHPFFPNVKEAPQVSIVETVRGKAPLE-----SFWHTDLTWQKRPSKASL 109

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-VYSQSKLGHVQQAGSAY 182
A+ +P VGG T + MRA ++AL E ++ + Q HSL + K +
Sbjct: 110 LHAQHLPEVGGDTIWCSMRAVFNALSEEDKSSIRQLKTMHSLHAFENIKTDEINADWHKD 169

Query: 183 IGYGMTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAP 241
+ P+V PETG L I + ++ +S L+ L A QA
Sbjct: 170 VIKTAAANPPVEHPMVTKL PETGEEILFINEQFTRFVISLNNTKSRALLDRLFALARQAE 229

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRA 265
+W + +WDNR H A
Sbjct: 230 YQVRFKWQPNTLAIWDNRSTQHIA 253

>ref|ZP_05218298.1| alpha-ketoglutarate-dependent taurine dioxygenase [Mycobacterium avium subsp. avium ATCC 25291]
Length = 297

Score = 101 bits (252), Expect = 1e-19, Method: Compositional matrix adjust.

Query: 56 QQITFAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW 108
 QQI FA++FG +ER + + +N+ ADG V + W
 Sbjct: 1 QQIAFAEQFGTLERHVASNRGTANPLVHIVTNLGADGKPSGK-----VASTQW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
H+D ++ P + + A V+P GG TCFADM AY+AL EA + + HS S
Sbjct: 49 HSDKSFRPQPSLATILHALVMPPDGGETCFADMITAYEALPEAEKVELAGVRVHWSGLS 108

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER 228
Q+++G + I D + PLV+ PETGR +L +G A + G
Sbjct: 109 QARVG--IKVPPEEIVDAPDMS---HPLVRTIPETGRKALFMGERAVHLEGQPEDVGRA 162

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
LE L A Q V+ H+W GD+++WDNRC+
Sbjct: 163 RLERLTAHAVQERFVYRHKWTLGDLLMWDNRVCV 195

>gb|ACX54982.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 98

Score = 101 bits (252), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 58/99 (58%), Positives = 66/99 (66%), Gaps = 5/99 (5%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYM V A GAVF+AE+VP GG T FADMRAAYDALD+ATR + +A HS YS
Sbjct: 1 ADSTYMRVQAMGAVFTAIEIVPDDGGDTGFADMRAAYDALDDATREQIDSLAAYHSRRYSM 60

Query: 170 SKLG-HVQQAGS---AYIGYGMDTTATPLRPLVKVHPET 204
+ HV Q + GYG DT PLRPL+KVHPET
Sbjct: 61 DRADLHVSQENADRYQLYGYGADTEP-PLRPLIKVHPET 98

>ref|YP_001508006.1| taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EAN1pec]
gb|ABW13100.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EAN1pec]
Length = 279

Score = 101 bits (252), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 90/281 (32%), Positives = 130/281 (46%), Gaps = 25/281 (8%)

Query: 12 GATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSDNDQQITFAKRFGAIER 69
G +GA V G+ L D +A A ++ L+F G ++ Q+ F +R G +
Sbjct: 10 GEKVGAEVLGIDADRLNDQDLPSACLTALEENGALLFRGLNIDPATQVAFCRRLGELIS 69

Query: 70 IGGG---DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY-MPVMAQGAVFS 125
DI I+ + D + H AE+ GN+AWH D + + +V +
Sbjct: 70 FPTSPPYDIPEINEINWDPS---HPRAEY-----FRGNVAWHIDGALDHDIPPKASVMT 120

Query: 126 AEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 185
AEVV GG T FA AAYD L +A + +R A +++++ + V+ A
Sbjct: 121 AEVVTEQGGETEFASTYAAYYDDLTDAAK----ERFADLRVIHTLEAI--VRPAYPNPTPE 174

Query: 186 GM-DTTATPLR--PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPR 242
+ D P R PLV H +GR SL+ G I GM + L+ L + A R
Sbjct: 175 QLADWAKRPSREHPLVWQH-RSGRRSLVFGSTTSHIVGMSREDGRALLDELEERATAPNR 233

Query: 243 VHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
V +H W AGD+V+WDNR L+HR P+D PR M LAG
Sbjct: 234 VFSHSWTAGDMVIWDNRGLVHRVRPFDQTEPRRMRITLAG 274

>ref|ZP_01627520.1| alpha-ketoglutarate-dependent taurine dioxygenase [marine gamma
proteobacterium HTCC2080]
gb|EAW39827.1| alpha-ketoglutarate-dependent taurine dioxygenase [marine gamma
proteobacterium HTCC2080]
Length = 282

Score = 101 bits (252), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 80/273 (29%), Positives = 123/273 (45%), Gaps = 27/273 (9%)

```
Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L +T + A+ GA++TGV L   L +   A + + WLQH ++ FP Q LS +   ++ F
Sbjct: 3   LTVTASQASCGASITGVDLTQNLSEDSIAEIRSHWLQHKVVAFPNQRLSPEDLERVSQYF 62

Query: 65  GAI-ERIGGGDIVAISNV-----KADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM 118
          G I E   G I   N+   KAD T               +   +H+D ++MP+
Sbjct: 63  GEIGEDPFFGHIDGYPNICAIRQKADETT-----IFAETFHSDWSFMPPIP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVYS-QSKLGHV 175
          + + +P GG T FAD   A+D + ++ R V   +A HS L Y+   G
Sbjct: 109 PAATMLLSITIPPHGGDTLFDQVKAFDEMPDSLRLRERVENLTAIHSALGYAPDGAYGDQ 168

Query: 176 QQAG--SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEG 232
          Q+   S I           T   PLV+ H ETG+ +L   + +   M+   ++ L
Sbjct: 169 DQSNGRSMTIKPSESARETCNHPLVRTHRETKKALFSSAAYIQSFSDMNLETAQALLME 228

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          L +   Q   ++ HQW   +V+WDNR LLH A
Sbjct: 229 LYQYQTQEQLYRHHQWQPNMLVMWDNRSLHAA 261
```

>gb|ADC34017.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 101 bits (252), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 72/207 (34%), Positives = 102/207 (49%), Gaps = 13/207 (6%)

```
Query: 56  QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM 115
          QQI FA++FG +ER   VA + KA+ V   +   D   V + WH+D ++
Sbjct: 1   QQIAFAEQFGLERH-----VASNRKANPLVHIVTNLGPDKPSGKVASTQWHSKSF 55

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
          P +   + A V+P GG TCFA+M AAY+AL A +A +   HS   SQ++ G
Sbjct: 56  PQPSLATILHALVMPPDGGETCFANMIAAYEALPAAEKAALDGVRRVHVSWEISQARAG-- 113

Query: 176 QQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
          A   I           A P+ PLV+ PETGR +L +G A   G   LE L
Sbjct: 114 TPAPPEEIA-----DAPPMSHPLVRTIPETGRKALFMGERAVFFEGHPPEAGRARLEKLT 168

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCL 261
          A +   V+ H+W GD+++WDNRC+
Sbjct: 169 AHAVEERFVYRHKWTLGDLLMWDNRCV 195
```

>ref|YP_003116441.1| Taurine dioxygenase [Catenulispora acidiphila DSM 44928]
gb|ACU74600.1| Taurine dioxygenase [Catenulispora acidiphila DSM 44928]
Length = 307

Score = 101 bits (252), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 91/294 (30%), Positives = 129/294 (43%), Gaps = 38/294 (12%)

```
Query: 5   TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAK 62
          T+ +TP   +GA ++G+ L   +   FA L A L+ +L F GQ ++ + FA
Sbjct: 38  TVTVTPCTRLIGAQISGIDLGEPAVEVFAELDRALLEFKVLFFRGQSRVTAARHRDFAG 97

Query: 63  RFGAIE---RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMA 119
          +G +E   + GD+ I V+ + + R+   V N+ WHAD T+   A
Sbjct: 98  MWGELEIHPFLPQGDVAEI--VRFEKSEREAG-----VENV-WHADVTWREKPA 143
```

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY-----SQSKLG 173
G+V A VP GG TCFADM AAYD L E +A + R A H KL
Sbjct: 144 LGSVLRAVEVPEAGGDTCTCFADMAAAYDCLPEQVKARIEGRVAVHDFTLPGIGMDPDCLK 203

Query: 174 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
+Q+ A P+V+ HP TGR +L + I G+ ESE L+
Sbjct: 204 EMQEKYPVAV-----EHPVVRTHPTGRRTLFVNAIFTTHIVGLPEQESEELLKV 252

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
L A +W G + WDNR + H A F RVM + + G RP
Sbjct: 253 LFRQASVPEYQVRFKWEPGSIAFWDNRAVQHYAVSDYFPRRRVMERAAILGDRP 306

>ref|YP_003411151.1| Taurine dioxygenase [Geodermatophilus obscurus DSM 43160]
gb|ADB76780.1| Taurine dioxygenase [Geodermatophilus obscurus DSM 43160]
Length = 322

Score = 101 bits (252), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 78/255 (30%), Positives = 115/255 (45%), Gaps = 14/255 (5%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERIGGG 73
GA V GV LA+ DA A+ A H +L F GQH L D QI +R G +
Sbjct: 53 FGARVHGVDLASATDAQVRAIRTAALAAHKVLFSSGQHALHPDGQIALGRRRLGDVTE---- 108

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVG 133
S+ G +H D ++ WH D T++ G+V A V+P G
Sbjct: 109 -----SHPVVPVGVDEEHPEIYALDSASGGFADV-WHTDVTFVRRPPLGSVLRAVVLPTG 162

Query: 134 GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATP 193
G T +AD++ AY++L E + L Q A H ++A + + G
Sbjct: 163 GDTQWADLQLAYESLSEPLQRLADQLVAVHDGTREFGYYLAQREARTKWEQEQQFQALVPV 222

Query: 194 LRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251
P+V++HPETGR L + G +H + + AES L+ + + H+W+ G
Sbjct: 223 EHPVVRIPHETGRKGLFVNPGFVSH-LKDVSDAESRYLLDLFYAHITKPEHIVRHRWSVG 281

Query: 252 DVVVWDNRCLLHRAE 266
DVV+WDNR +H A
Sbjct: 282 DVVMWDNRSTVHYAN 296

>ref|YP_004084309.1| taurine dioxygenase [Micromonospora sp. L5]
gb|ADU10158.1| Taurine dioxygenase [Micromonospora sp. L5]
Length = 287

Score = 101 bits (252), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 84/260 (32%), Positives = 115/260 (44%), Gaps = 46/260 (17%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIE----- 68
LGA V G+ L TL D GFA +H L+H ++ GQ L+ + F +RFG +E
Sbjct: 16 LGAEVHGIDLNTLTDEGFALIHDLKKHQQVFLAGQTGLTPQAHVAFGRRFGEVELHPYL 75

Query: 69 -RIGG-GDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
R+ G +IV I + ADG KV V WH D T+ +V
Sbjct: 76 PRLDGHPEIIVVIDS--ADGG-----KVDV----WHTDMTFHQSPPIASVLHL 116

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG 186
+P VGG T + + Y+AL R L+ +A H I G
Sbjct: 117 IQLPEVGGDTMWTNQYRVYEALSAPMRDILLDGLTAIH-----VIRIG 158

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
+ T+ P+V+VHPETGR SL + R IP + ES+ LE L ++
Sbjct: 159 TEFTSRAEHPVVRVHPETGRRLSYVNRLFTSHIPQLTRNESDALLEHLFTFSESPQFTCR 218

Query: 246 HQWAAGDVVVWDNRCLLHRA 265
++W GDV VWDNR H A
Sbjct: 219 YRWRTGDVAVWDNRVTQHYA 238

>ref|YP_001412109.1| taurine dioxygenase [Parvibaculum lavamentivorans DS-1]
gb|ABS62452.1| Taurine dioxygenase [Parvibaculum lavamentivorans DS-1]
Length = 289

Score = 101 bits (251), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 81/285 (28%), Positives = 129/285 (45%), Gaps = 15/285 (5%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++ + P + GA +TG+ L+ L A +H AW HA++ FP Q L++D+ F +
Sbjct: 10 SIHVKNPNASGFGAEITGLDLSKPLPPDVLAEVHRAWADHAVVWFPDQPLTHDELEAFTLQ 69

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
G G +A + + P E K WH+D ++ +
Sbjct: 70 IGPFF---GHDPFIAPMEGRPHILELRREPNE-----KARNFGAGWHSWDSFQEEPPAATI 121

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVY-SQSKLGHVQQAGS 180
++V P VGG T +AD AYDAL + + ++ +A HS L Y ++ ++ +
Sbjct: 122 LHSKVTPPVGGDTLYADCTRAYDALSDMKVLSGLTAVHSAALPYGTGIFAQEKEQRT 181

Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
I + T PLV+ HP TGR +L + + I M ES L L +
Sbjct: 182 MKIIVSKEAEKTCPHPLVRTHPVTGRKALYVSPVYTVGIESMTHEESAAILGFLYTHMTK 241

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRAE-PWDFKLPRVMWHSRLAG 283
V+ H+W + +WDNRC LH A+ +D L RVM + +AG
Sbjct: 242 DEFVYRHKWRENMLTMWDNRCTLHFADGGYDGHLL-RVMHRTTVAG 285

>ref|YP_002278025.1| taurine dioxygenase [Rhizobium leguminosarum bv. trifolii WSM2304]
gb|ACI58925.1| Taurine dioxygenase [Rhizobium leguminosarum bv. trifolii WSM2304]
Length = 309

Score = 101 bits (251), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 73/269 (27%), Positives = 115/269 (42%), Gaps = 29/269 (10%)

Query: 8 ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFG 65
+ P +GA + GV L L DA AA++ L+H ++ F Q HL + +Q FA+R G
Sbjct: 16 VIPLTGRVGAEIKGVRLGGDLSATVAAINQLLLKHKVIFFRDQGHLEDSEQEAFAFARLG 75

Query: 66 AI-----ERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
+ G I+ + + + G Q WH D T++
Sbjct: 76 DLVPHTQGPVAGTASILNLDSSRGGGRADQ-----WHTDVTTFVDAY 117

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG--HVQ 176
+ +V V+PA GG T +++ AAY++L + L A HS Y + +
Sbjct: 118 PKFSVLRGVVIPAAGGDTIWSNTHAAYESLPAPLKLLAENLWAIHSNAYDYAAVRPRATA 177

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW 236
+ + T P+V+VHPETG SLL+G + G+ ++S + E +
Sbjct: 178 EEKKHFEEVFTSTIYETEHPVVRVHPETGERSLLLGNFVQRLVGLSKSDSAKLYEVFQSY 237

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+W AGDV +WDNR H A
Sbjct: 238 VTAPENTVRWRWRAGDVAIWDNRATQHYA 266

>ref|YP_761331.1| TauD/TfdA family dioxygenase [Hyphomonas neptunium ATCC 15444]
gb|ABI78212.1| dioxygenase, TauD/TfdA family [Hyphomonas neptunium ATCC 15444]
Length = 278

Score = 101 bits (251), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 79/275 (28%), Positives = 117/275 (42%), Gaps = 31/275 (11%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAA-LHAAWLQHALLIFPGQHLSNDQQITFAKR 63
TL +TP+ GA V G+ L+ AA + WL+H +L FP Q+LS+D F
Sbjct: 2 TLTVTTPSDMACGAQVRGLDLSKPVTTDLAAEIRDIWLKHQVLCFPEQNLSDDDLERFTLA 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA-----WHADSTYMPV 117
FG GD I+ + R+H A +K G + WH+D ++
Sbjct: 62 FGPF-----GDDPFIPIPG----RKHIIA-----VKRAAGETSPIFAESWHSWDSFQVK 107

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
QG +P GG T F + A + E R + + A HS + S G
Sbjct: 108 PPQGTCLYGITIPPEGGDTLFVNQYKALAEMPEDLRRRIEGKKAVHSAKNAYSPKG---M 164

Query: 178 AGSAYIGYGMDTTATP-----LRPLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFL 230
G+ G MD A+ P ++ HPETGR SL + + GM+ E +
Sbjct: 165 YGAGDKGRSMDIRASDEAEAAANTHPFIRTHPETGRESLFGCAGYIVGVEGMEQQEGWDLI 224

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ W + + H+W G +++WDNRC LH A
Sbjct: 225 TEVYRWQTRPEFQYRHRWEKGMLLMWDNRCTLHMA 259

>ref|YP_001240347.1| putative dioxygenase [Bradyrhizobium sp. BTAi1]
gb|ABQ36441.1| putative dioxygenase [Bradyrhizobium sp. BTAi1]
Length = 228

Score = 101 bits (251), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 87/276 (31%), Positives = 111/276 (40%), Gaps = 75/276 (27%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
+Q+ P G LGA V L + DD FA+ A L+H +L+ GQ LS F++RFG
Sbjct: 16 IQVIPMGKALGAEACNVDLKSFDDWAFASFMRRALLKHQVLLVRGQRLSERDIAVFSRRFG 75

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
HAD Y
Sbjct: 76 -----HADLAYTSPSTLS---- 88

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 185
G R F + AAYDAL A R S++ H++ A
Sbjct: 89 -----GDRLTFCSLYAYDALSPALR-----SRVAHLKIRHLAAEAN 125

Query: 186 GMDTT-ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRV 243
G TT A+ + PLV HP+TGR L +G HAI G+D AES+ L+ L A +
Sbjct: 126 GCHTTFASAVHPLVAPHDPDTGRSMLALGHRHHAIAGLDRAESDALLDDLWQIAERPEFT 185

Query: 244 HAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHS 279
AH GD VVWD RC +HR E D LPR +WHS
Sbjct: 186 WAHTCRPGDFVVWDTRCTIHRREASD--LPR-LWHS 218

>ref|YP_001895833.1| Taurine dioxygenase [Burkholderia phytofirmans PsJN]
gb|ACD16609.1| Taurine dioxygenase [Burkholderia phytofirmans PsJN]
Length = 310

Score = 101 bits (251), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 76/272 (27%), Positives = 122/272 (44%), Gaps = 28/272 (10%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L I P +GA + GV L++ L+ A A+ AA ++H ++ F GQ HL + Q FA+
Sbjct: 12 LDIHPVTGRIGAEIRGVRLSSQLEAATVEAIRAALIRHKVIFFRGQTHLQDADQEAFA 71

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
G E + + + + H + + WH D T++ Q ++
Sbjct: 72 LG--EPVSHPTVPVVDGTDYLLLELDSHRGGRAN-----SWHTDVT FVDAYPQASI 119

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG---- 179
+PAVGG T +A+ AY+ L +AL Q A HS Y + V + G
Sbjct: 120 LRGV TIPAVGGDTVWANTATAYEDLPPLKALADQLWAVHSNDYDYANHTSVGERGRDAE 179

Query: 180 -----SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
A++ +T P+V+VHPE+G +L++G + G+ + S LE L
Sbjct: 180 AIRRHREAFVSTRYETE----HPVVRVHPESGEKTLILGHFVKS FVGLAPSASAHLELL 235

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ + + +W AGDV +WDNR H A
Sbjct: 236 QGYVTRHENIVRWRWQAGDVAIWDNRATQHYA 267

>ref|YP_002978144.1| Taurine dioxygenase [Rhizobium leguminosarum bv. trifolii WSM1325]
gb|ACS58605.1| Taurine dioxygenase [Rhizobium leguminosarum bv. trifolii WSM1325]
Length = 309

Score = 101 bits (251), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 73/269 (27%), Positives = 116/269 (43%), Gaps = 29/269 (10%)

Query: 8 ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFG 65
+ P +GA + G+ L L DA AA++ L+H ++ F Q HL + +Q +FA+R G
Sbjct: 16 VVPLTGRVGAEIRGIRLGGDLSDATVAAINQLLLKHKVIFFRDQDHLGDSEQESFARRLG 75

Query: 66 AI-----ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM 118
+ G I+ + + + G Q WH D T++
Sbjct: 76 DLVPHPTQGPVAGTASILNLDSSRGGGRADQ-----WHTDVT FVDAY 117

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
+ +V V+PA GG T +++ AAY++L + + L A HS Y + + A
Sbjct: 118 PKFSVLRGVVIPAAGDTIWSNTHAAYESLPASLKLADNLWAIHSNAYDYAAVRPRATA 177

Query: 179 GSA--YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW 236
+ T P+V+VHPETG SLL+G + G+ ++S + E +
Sbjct: 178 DEKKHFEEVFTSTIYETEHPVVRVHPETGERSLLLGNFVQRLVGLSKSDSAKLYEVFQSY 237

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
W AGDV +WDNR H A
Sbjct: 238 VTAPENTVRWHWRAGDVAIWDNRATQHYA 266

>ref|ZP_08156958.1| taurine dioxygenase [Rhodococcus equi ATCC 33707]
gb|EGD21685.1| taurine dioxygenase [Rhodococcus equi ATCC 33707]
Length = 295

Score = 101 bits (251), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 81/270 (30%), Positives = 123/270 (45%), Gaps = 24/270 (8%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
++I+ +GA + GV L T D+A FA + A ++ ++ G HL D + A+RFG
Sbjct: 3 IEISALTTAIGAEIRGVLDLRTCDEATFADVRDALHEYQVVFVRGAHL DADDHLAVARRFG 62

Query: 66 A-----IERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ 120
I R+ G ++ V +DG SP + WH D T++ +

Sbjct: 63 VPSIFPIARLQGATEPSL-QVISDG---PDSPTAE-----MWHTDVTWISTPPR 108

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH---SLVYSQSKLGHVQQ 177
A+ EV+P GG T +A M AA+DAL + ++ H S V S + GH

Sbjct: 109 YALLCGEVIPDAGGDTLWASMTAAHDALSPTMQNMLAGLEVEHTTDSFVESILERGHDS 168

Query: 178 AGSAYIGYGMDTTA-TPLRPLVKVHPETGRPSLLIGRHA-HAIPGMDAAESERFLEGLVD 235
A T T + PL++ HPE GR L IG + + I GM ES+ L L +

Sbjct: 169 QAQALADRLRATYPRTVVHPLIRTHPENGRRLFIGGPSMNRIKGMRRDESDALLGFLRN 228

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
+ +W+ GD+ +WD R +HRA

Sbjct: 229 YVTDERFQCRWRWSPGDLAIWDERSTMHRA 258

>ref|YP_883488.1| alpha-ketoglutarate-dependent taurine dioxygenase [Mycobacterium
avium 104]
gb|ABK64579.1| alpha-ketoglutarate-dependent taurine dioxygenase [Mycobacterium
avium 104]
Length = 297

Score = 101 bits (251), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 85/287 (29%), Positives = 120/287 (41%), Gaps = 27/287 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
+ +T G+ +GA V GV L LDDA + A L H ++ F QH L + +Q+ FA+

Sbjct: 5 ITVTKLGSRIGARVDGVRGGDLDDATVEQIRALLTHKVIFFRHQHLLDDSRQLEFARL 64

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSP-----AEWDDMMKVIVGNMAWHADSTYMPV 117
G I + A +H P +E+ + WH D T+

Sbjct: 65 LG-----TPIGHPAASALAAKHLPVITPIDSEYGKATR-----WHTDVTFAAN 107

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
++ A +P+ GG T +A AAY L E R L A H+ Y + +

Sbjct: 108 YPAASILRAVTLPSYGGSTLWASTVAAYQQLPEPLRHLTENLWALHTNRYDYVRNDPMD 167

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
A+ P+V+VHPETG +LL G G+D ES LE L

Sbjct: 168 TQRAFRQAFKPDFRTEHPVVRVHPETGERALLAGDFVRGFVGLDGHESSVLELLQRR 227

Query: 238 CQAPRVHAHQWAAGDVVVDNRCLLHRA-EPWDFKLPRVMWHSRLAG 283
WA GDV +WDNR HRA + +D + PR+M L G

Sbjct: 228 TMPENTVRWSWAPGDVAMWDNRATQHRAIDDYDDQ-PRLMHRITLMG 273

>ref|YP_003836819.1| taurine dioxygenase [Micromonospora aurantiaca ATCC 27029]
gb|ADL47243.1| Taurine dioxygenase [Micromonospora aurantiaca ATCC 27029]
Length = 287

Score = 100 bits (250), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 83/260 (31%), Positives = 115/260 (44%), Gaps = 46/260 (17%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIE----- 68
LGA V G+ L TL D GFA +H L+H ++ GQ L+ + F +RFG +E

Sbjct: 16 LGAEVHGIDLNTLTDEGFALIHDLKKHQQVFLAGQTGLTPQAHVAFGRRFGEVELHPYL 75

Query: 69 -RIGG-GDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
R+ G +IV I + ADG KV V WH D T+ ++

Sbjct: 76 PRLDGHPEIVVIDS--ADGG-----KVDV----WHTDMTFHQSPPIASILHL 116

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG 186
+P VGG T + + Y+AL R L+ +A H I G

Sbjct: 117 IQLPEVGGDTMWTNQYRVYEALSAPMRDLLDGLTAIH-----VIRIG 158

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
+ T+ P+V+VHPETGR SL + R IP + ES+ LE L ++
Sbjct: 159 TEFTSRAEHPVVRVHPETGRRSLYVNRLFTSHIPQLTRNESDALLEHLFTFSESPQFTCR 218

Query: 246 HQWAAGDVVVDNRCLLHRA 265
++W GDV VWDNR H A
Sbjct: 219 YRWRTGDVAVWDNRVTQHYA 238

>gb|ADC34012.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 100 bits (250), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 71/213 (33%), Positives = 102/213 (47%), Gaps = 25/213 (11%)

Query: 56 QQITFAKRFGAIER--IGGGDIVA-----ISNVKADGTVRQHSPAEWDDMMKVIVGNMAW 108
QQI FA++FG +ER + V ++N+ ADG V + W
Sbjct: 1 QQIAFAEQFGTLERHVSNRGTVNPLVHIVTNLGADGKPSGK-----VASTQW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
H+D ++ P + + A V+P GG TCFADM AAY+AL EA +A + HS S
Sbjct: 49 HSDKSFRPQPSLATILHALVMPPQGGETCFADMVAAYEALPEAEKAELAGVRVHWSWGLS 108

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER 228
Q+++G + I D LV+ PETGR +L +G A + G
Sbjct: 109 QARVG--IKVPPEEIADAPDIAHL---LVRTIPETGRKALFMGERAVHLEGQPEDVGRA 162

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVDNRCL 261
LE L A Q V+ H+W GD+++WDNRC+
Sbjct: 163 RLERLTAHAVQERFVYRHKWTLGDLLMWDNRCV 195

>ref|NP_902525.1| taurine dioxygenase [Chromobacterium violaceum ATCC 12472]
gb|AAQ60523.1| taurine dioxygenase [Chromobacterium violaceum ATCC 12472]
Length = 277

Score = 100 bits (250), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 81/271 (29%), Positives = 118/271 (43%), Gaps = 27/271 (9%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+LQ+T LGA V G+ LA LDD AL A L+H +L F GQ ++ QQ FA R
Sbjct: 2 SLQLTRLSPALGAVVEGIDLARPLDDERRRALSEALLRHQVLFRRGQDITPLQQRNFAVR 61

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
FG + + +I+ + D + N WH D T++
Sbjct: 62 FGDLHTHIYPQHPDAREIMVLDTDAVD-----LQDNAVWHTDVTTFIE 104

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
GAV +A +P +GG T +A AAY+AL + +A + SA H S +
Sbjct: 105 TPPLGAVLAARQLPELGGDTLWASGIAAYEALSASLKARLDGLSAVHDFAKSFPLARYGL 164

Query: 177 QAGSAYIGYGMDTTATPL-RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
P+ PLV++HPE+GR +L + A+ + AE + L+ L
Sbjct: 165 TDDRRRWDETRRKHPPIHPLVRIHPESGRRALFVSEGFTVAVNDLPEAEGQALLQFLF 224

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
+ +W GDV WDNRC +H A
Sbjct: 225 AHQSRPEFSIRRWQPGDVAFWDNRCTIHYA 255

>ref|YP_345986.1| taurine dioxygenase [Pseudomonas fluorescens Pf0-1]
gb|ABA71997.1| alpha-ketoglutarate-dependent taurine dioxygenase [Pseudomonas

fluorescens Pf0-1]
Length = 280

Score = 100 bits (250), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 81/268 (30%), Positives = 121/268 (45%), Gaps = 19/268 (7%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
++L ITP + LGA ++GV ++ L+ A+ A L+ +L F Q + QQ FA
Sbjct: 2 SSLNITPLSSALGAQISGVDISQPLNQEQRDAIEQALLKFQVLFNRNQPPIEPSQQARFAH 61

Query: 63 RFGAIERIGGGDIVAI-SNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
FG + I I NV V D + + N WH D T++P A G
Sbjct: 62 YFGDLH-----IHPIYPNVPEQPEV-----LILDTAVTDVRDNAIWHTDVTFPLPTPAMG 110

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQAG 179
AV SA+++P GG T +A AAY+AL +AL+ +A H + + G+ QA
Sbjct: 111 AVLSAKLLPEFGGDTLWASGIAAYEALSAPMKALLEGLTATHDFTRSFPLERYGNTQPAL 170

Query: 180 SAYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
+ + PL P+++ HP +GR SL + I + ESE L+ L A
Sbjct: 171 AQW--EEARRKNPPLSHPVIRTHPVSGRRSLFVNEGFTSKINELSETESEAVLKFLFAHA 228

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ +W D+ WDNH H A
Sbjct: 229 TRPEFTIRWRWQKDDIAFWDNRVTHYA 256

>ref|YP_001504833.1| taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EAN1pec]
gb|ABW09927.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EAN1pec]
Length = 278

Score = 100 bits (250), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 84/284 (29%), Positives = 126/284 (44%), Gaps = 25/284 (8%)

Query: 9 TPTGATLGATVTGVHLATLDDAGFAA-LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAI 67
TP A +G +TGV L AA A Q+ ++++ H+ + + + F++ G +
Sbjct: 6 TPLSAHVGLEITGVCGRDLPTPSAAADCLKALEQYGVVVYREAHIGDQELVAFSRLLEGEV 65

Query: 68 --ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMK-VIVGNMAWHADSTYMPVMAQGAVF 124
G I+ + D PA+ D + GN WH D + + +
Sbjct: 66 APNPTGEHQFPEIATITLD-----PAKTDVRAWYRQGNFLWHIDGATEELPQKATLL 118

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
+A V GG T FA AAYDAL E + + HS +Q + A+
Sbjct: 119 TAREVDPKGGDTEFASTYAAAYDALPEEEKERLAGLRVVHSFAAAQQR-----AHPE 169

Query: 185 YGMDTTATPLRPLVKVHP-----ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
D A R V+ HP TGR SLL+G A + G+ A E + L+ L+DW+ Q
Sbjct: 170 ATEDQRAAWARVPVREHPLVWTRRTGRRSLLLGATAGEVIGIPADEGQALLKRLLDWSTQ 229

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
V H+W GD+V+WDN +LHRA P+ R+M + L G
Sbjct: 230 PRFVLRHRWRLGDLVIWDNTGMLHRATPFAATSRLMHRTTLVG 273

>ref|YP_003009527.1| Taurine dioxygenase [Paenibacillus sp. JDR-2]
gb|ACS99440.1| Taurine dioxygenase [Paenibacillus sp. JDR-2]
Length = 309

Score = 100 bits (249), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 73/267 (27%), Positives = 113/267 (42%), Gaps = 24/267 (8%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62

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      T   + P G +GA + GV L   +       A L H A L+ +L F Q +++++QQ+ FAK
Sbjct: 40 TLFTLKPLGPVIGAEIEGVDLKEQVSPEVKAELHRALEWKVLFFRNQDITSEQQLNFAK 99

Query: 63 RFGAIER---IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
      ++G +E   + G+   I+   + D ++                               WH D ++   +
Sbjct: 100 QWGELENHPFLPKGEAAEITRFEKDANMKGQE-----NNWHTDVSWRLEPS 145

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
      GAV   VP   GG T +ADM AAYD L EA + ++ +A H   + +
Sbjct: 146 LGAVLRLSEVPPQGGDTLWADMGAAYDNLPEAVKERINGLTAIHDFTPTFGR-----NMP 200

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
      +                               P+V+ HPETGR +L +           I G+D E E+ L+ L A
Sbjct: 201 PELLAQKQAEFPAAEHPVVRTHPETGRKTLFVNPIFTTRIVGLDEEEGEKLLQYLFRQAE 260

Query: 239 QAPRVHAHQWAAAGDVVVWDNRCLLHRA 265
      W   + +WDNR   H A
Sbjct: 261 IPEYQVRFNWEKNSIGLWDNRATQHYA 287

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>ref|XP_572683.1| 2,4-dichlorophenoxyacetate alpha-ketoglutarate dioxygenase
  [Cryptococcus neoformans var. neoformans JEC21]
ref|XP_773666.1| hypothetical protein CNBH1210 [Cryptococcus neoformans var.
  neoformans B-3501A]
gb|EAL19019.1| hypothetical protein CNBH1210 [Cryptococcus neoformans var.
  neoformans B-3501A]
gb|AAW45376.1| 2,4-dichlorophenoxyacetate alpha-ketoglutarate dioxygenase,
  putative [Cryptococcus neoformans var. neoformans JEC21]
Length = 312

```

Score = 100 bits (249), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 80/288 (27%), Positives = 130/288 (45%), Gaps = 32/288 (11%)

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Query: 5   TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      T+ TP   T A   +GV   +       ++ +LIF   L++ + + + F
Sbjct: 2   TINYTPLHPTFVAEASGVDFDNITPEVVEEIKKGLAKYGVLFIRKGTGLNDKKHVEMSSFF 61

Query: 65 GA-----IERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIV--GNMAWHA 110
      G                               I R+   ++ +SNV A+G + Q +           + I+ GN +H
Sbjct: 62 GELDDVKPYNKLGRINRLAYDELFDVSNVDAEGNIFQPT-----GQRAIINRGNTIFHC 115

Query: 111 DSTYMPVMAQGAVFSAEVVPA--AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
      DS++ P A   ++ A +P   GG T FAD R AYD L E   + +       HS +S
Sbjct: 116 DSSFNPRRAGYSLLLAHELPPAGTGGNTEFADTRTAYDDLPEERKETIKDWVLWHSQHHS 175

Query: 169 QSKLGHVQQAGSAYIGY-GMDTTATPL--RPLVKVHPETGRPSLLIGRHAHAIPGMDAAE 225
      +   V   G   +       T+ P   LV+VH +GR +L I HA+ I   +
Sbjct: 176 R----RVANPGEPLLDQEKFLPTSHPFKGKHLVQVHEPSGRTNLYIANHAYKIESLPLEH 231

Query: 226 SERFLEGLVDWACQAPR-VHAHQWAA-GDVVVWDNRCLLHRAEPWDFK 271
      + ++ L+D C +PR V + +W   GD+V+WDN C++HRA P F+
Sbjct: 232 GQAEIKTLLD-HCSSPRYVCSVEWKNDGDLVIWDNTCVMHRAVPGAFE 278

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>ref|ZP_03498565.1| Taurine dioxygenase [Rhizobium etli Kim 5]
Length = 309

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Score = 100 bits (249), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 73/269 (27%), Positives = 115/269 (42%), Gaps = 29/269 (10%)

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Query: 8   ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRF 65
      I P   +GA + G+ L   L DA +A++   L+H ++ F Q HL + +Q FA+R G
Sbjct: 16   IVPLTGRVGAEIKGIRLGGELSDATVSAINQLLLKHKVIFFRDQGHLLDPEQEAFAARLG 75

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Query: 66 AI-----ERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
+ G I+ + + + G Q WH D T++
Sbjct: 76 DLVPHTQGPPIAGTASILNLDSSRGGGRADQ-----WHTDVTTFVDAY 117

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAYDALDEATRALVHQRSARHSLVYSQSKLG--HVQ 176
+ +V V+PA GG T +++ AAY++L + L A HS Y + +
Sbjct: 118 PKFSVLGRGVVIPAAGGDTIWSNTHAAYESLAAPLKLLADNLWAIHSNAYDYAAVRPRATA 177

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW 236
+ + T P+V+VHPETG SLL+G + G+ ++S R E +
Sbjct: 178 EEKKHFEEVFTSTIYETEHPVVRVHPETGERSLLLGNFVQRLVGLSKSDSARLYEVFQSY 237

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
+W AGDV +WDNR H A
Sbjct: 238 VTAPENTVRWRWRAGDVAIWDNRATQHYA 266

>ref|NP_217923.1| dioxygenase [Mycobacterium tuberculosis H37Rv]
ref|NP_338038.1| dioxygenase, putative [Mycobacterium tuberculosis CDC1551]
ref|NP_857080.1| dioxygenase [Mycobacterium bovis AF2122/97]
ref|YP_979555.1| putative dioxygenase [Mycobacterium bovis BCG str. Pasteur 1173P2]
ref|YP_001284793.1| putative dioxygenase [Mycobacterium tuberculosis H37Ra]
ref|YP_001289368.1| dioxygenase [Mycobacterium tuberculosis F11]
ref|ZP_02550985.1| hypothetical dioxygenase [Mycobacterium tuberculosis H37Ra]
ref|ZP_03417624.1| dioxygenase [Mycobacterium tuberculosis 02_1987]
ref|ZP_03430292.1| dioxygenase [Mycobacterium tuberculosis EAS054]
ref|ZP_03434487.1| dioxygenase [Mycobacterium tuberculosis T85]
ref|ZP_03533983.1| dioxygenase [Mycobacterium tuberculosis GM 1503]
ref|ZP_03538655.1| dioxygenase [Mycobacterium tuberculosis T17]
ref|YP_002646516.1| putative dioxygenase [Mycobacterium bovis BCG str. Tokyo 172]
ref|YP_003033454.1| dioxygenase [Mycobacterium tuberculosis KZN 1435]
ref|ZP_04927333.1| hypothetical protein TBCG_03349 [Mycobacterium tuberculosis C]
ref|ZP_04982062.1| hypothetical dioxygenase [Mycobacterium tuberculosis str. Haarlem]
ref|ZP_05142958.1| dioxygenase [Mycobacterium tuberculosis '98-R604 INH-RIF-EM']
ref|ZP_05219309.1| putative dioxygenase [Mycobacterium tuberculosis KZN 4207]
ref|ZP_05765935.1| dioxygenase [Mycobacterium tuberculosis CPHL_A]
ref|ZP_05770007.1| dioxygenase [Mycobacterium tuberculosis T46]
ref|ZP_05774263.1| dioxygenase [Mycobacterium tuberculosis K85]
ref|ZP_06434681.1| dioxygenase [Mycobacterium tuberculosis T46]
ref|ZP_06438849.1| dioxygenase [Mycobacterium tuberculosis CPHL_A]
ref|ZP_06444892.1| dioxygenase [Mycobacterium tuberculosis KZN 605]
ref|ZP_06451972.1| dioxygenase [Mycobacterium tuberculosis T17]
ref|ZP_06456366.1| dioxygenase [Mycobacterium tuberculosis K85]
ref|ZP_06506613.1| dioxygenase [Mycobacterium tuberculosis 02_1987]
ref|ZP_06514914.1| dioxygenase [Mycobacterium tuberculosis EAS054]
ref|ZP_06518945.1| dioxygenase [Mycobacterium tuberculosis T85]
ref|ZP_06522967.1| conserved hypothetical protein [Mycobacterium tuberculosis GM 1503]
ref|ZP_06801511.1| dioxygenase [Mycobacterium tuberculosis 210]
ref|ZP_06953848.1| dioxygenase [Mycobacterium tuberculosis KZN 4207]
ref|ZP_06962186.1| dioxygenase [Mycobacterium tuberculosis KZN R506]
ref|ZP_07416083.1| dioxygenase [Mycobacterium tuberculosis SUMu001]
ref|ZP_07420811.1| dioxygenase [Mycobacterium tuberculosis SUMu002]
ref|ZP_07424616.1| dioxygenase [Mycobacterium tuberculosis SUMu003]
ref|ZP_07428986.1| dioxygenase [Mycobacterium tuberculosis SUMu004]
ref|ZP_07433493.1| dioxygenase [Mycobacterium tuberculosis SUMu005]
ref|ZP_07437684.1| dioxygenase [Mycobacterium tuberculosis SUMu006]
ref|ZP_07441896.1| dioxygenase [Mycobacterium tuberculosis SUMu008]
ref|ZP_07446082.1| dioxygenase [Mycobacterium tuberculosis SUMu007]
ref|ZP_07482182.1| dioxygenase [Mycobacterium tuberculosis SUMu009]
ref|ZP_07486526.1| dioxygenase [Mycobacterium tuberculosis SUMu010]
ref|ZP_07490747.1| dioxygenase [Mycobacterium tuberculosis SUMu011]

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ref|ZP_07495298.1| dioxygenase [Mycobacterium tuberculosis SUMu012]
ref|ZP_07817279.1| dioxygenase [Mycobacterium tuberculosis KZN V2475]
sp|P65075.1|Y3406_MYCTU RecName: Full=Uncharacterized dioxygenase Rv3406/MT3514
sp|P65076.1|Y3440_MYCBO RecName: Full=Uncharacterized dioxygenase Mb3440
emb|CAB01017.1| PROBABLE DIOXYGENASE [Mycobacterium tuberculosis H37Rv]
gb|AAK47852.1| dioxygenase, putative [Mycobacterium tuberculosis CDC1551]
emb|CAD95627.1| PROBABLE DIOXYGENASE [Mycobacterium bovis AF2122/97]
emb|CAL73465.1| Probable dioxygenase [Mycobacterium bovis BCG str. Pasteur 1173P2]
gb|EAY58641.1| hypothetical protein TBCG_03349 [Mycobacterium tuberculosis C]
gb|EBA43575.1| hypothetical dioxygenase [Mycobacterium tuberculosis str. Haarlem]
gb|ABQ75231.1| putative dioxygenase [Mycobacterium tuberculosis H37Ra]
gb|ABR07766.1| hypothetical dioxygenase [Mycobacterium tuberculosis F11]
dbj|BAH27748.1| putative dioxygenase [Mycobacterium bovis BCG str. Tokyo 172]
gb|ACT26559.1| dioxygenase [Mycobacterium tuberculosis KZN 1435]
gb|EFD15096.1| dioxygenase [Mycobacterium tuberculosis T46]
gb|EFD19264.1| dioxygenase [Mycobacterium tuberculosis CPHL_A]
gb|EFD22807.1| dioxygenase [Mycobacterium tuberculosis KZN 605]
gb|EFD45148.1| dioxygenase [Mycobacterium tuberculosis K85]
gb|EFD49147.1| dioxygenase [Mycobacterium tuberculosis T17]
gb|EFD55251.1| dioxygenase [Mycobacterium tuberculosis 02_1987]
gb|EFD63552.1| dioxygenase [Mycobacterium tuberculosis EAS054]
gb|EFD75111.1| conserved hypothetical protein [Mycobacterium tuberculosis GM 1503]
gb|EFD79143.1| dioxygenase [Mycobacterium tuberculosis T85]
gb|EFO73321.1| dioxygenase [Mycobacterium tuberculosis SUMu001]
gb|EFP13718.1| dioxygenase [Mycobacterium tuberculosis SUMu002]
gb|EFP17899.1| dioxygenase [Mycobacterium tuberculosis SUMu003]
gb|EFP21789.1| dioxygenase [Mycobacterium tuberculosis SUMu004]
gb|EFP25370.1| dioxygenase [Mycobacterium tuberculosis SUMu005]
gb|EFP29247.1| dioxygenase [Mycobacterium tuberculosis SUMu006]
gb|EFP33106.1| dioxygenase [Mycobacterium tuberculosis SUMu007]
gb|EFP37057.1| dioxygenase [Mycobacterium tuberculosis SUMu008]
gb|EFP41780.1| dioxygenase [Mycobacterium tuberculosis SUMu009]
gb|EFP45644.1| dioxygenase [Mycobacterium tuberculosis SUMu010]
gb|EFP49592.1| dioxygenase [Mycobacterium tuberculosis SUMu011]
gb|EFP53203.1| dioxygenase [Mycobacterium tuberculosis SUMu012]
gb|EGB27082.1| dioxygenase [Mycobacterium tuberculosis CDC1551A]
Length = 295

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Score = 100 bits (249), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 78/262 (29%), Positives = 114/262 (43%), Gaps = 14/262 (5%)

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Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
+ + G+ +GA + GV L LD A + AA L H ++ F GQH L + +Q+ FA
Sbjct: 5 ITVKKLGSRIGAQIDGVRLGGDLDPAAVNEIRAALLAHKVVFVRGQHQLDDAEQLAFAGL 64

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
G IG +A+++ D + +E+ + WH D T+ +V
Sbjct: 65 LGT--PIGHPAALAD---DAPIITPINSEFGKANR-----WHTDVTFAANYPAASV 112

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
A +P+ GG T +A+ AAY L E + L A H+ Y + A A+
Sbjct: 113 LRAVSLPSYGGSTLWANTAAAYAELPEPLKCLTENLWALHTNRYDYVTTKPLTAAQRAFR 172

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRV 243
P+V+VHPETG +LL G + G+D+ ES E L
Sbjct: 173 QVFEKPDFRTEHPVVRVHPETGERTLLAGDFVRSFVGLDSHESRVLFEVLQRRITMPENT 232

Query: 244 HAHQWAAGDVVVWDNRCLLHRA 265
WA GDV +WDNR HRA
Sbjct: 233 IRWNWAPGDVAIWDNRATQHRA 254

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>gb|ACX54969.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein

[uncultured bacterium]
Length = 98

Score = 100 bits (249), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 55/98 (56%), Positives = 64/98 (65%), Gaps = 3/98 (3%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYMP+ A+GAVFSAE+VP T +ADMRAAYDALD+ TR V SA HSL YSQ
Sbjct: 1 ADSTYMP LQAKGAVFSAEIVPEGRAPTGWADMRAAYDALDDETRLRVEGMSAYHSLFYSQ 60

Query: 170 SKLGHV---QQAGSAYIGYGMDDTTATPLRPLVKVHPET 204
+ G++ + Y YG LRPLVKVHPET
Sbjct: 61 DRAGYMP SKKNESGGYDQYGYHMEPSLRPLVKVHPET 98

>ref|YP_001869111.1| taurine catabolism dioxygenase TauD/TfdA [Nostoc punctiforme PCC 73102]
gb|ACC84168.1| Taurine catabolism dioxygenase TauD/TfdA [Nostoc punctiforme PCC 73102]
Length = 287

Score = 100 bits (249), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 81/296 (27%), Positives = 131/296 (44%), Gaps = 30/296 (10%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T ++I+P A LG VT + + + L A +LIF Q LS+ + + F+
Sbjct: 7 TKVKISPIDAPLGTIVTDLDASQAI APEVILQLKQALDRHILIFKDKLSDKELLNFSL 66

Query: 63 RFGAIERIGGGDIVAISNVKADGT-VRQHSPA EWDDMMKVI-----VGNMAWHADST 113
FGA+ V +D T V P E ++ + G + +H+D
Sbjct: 67 YFGAL-----FVPSDETPVLASKPGETPVVIPISNVDGGYTGTGELTFHSDHK 114

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
+ P + G++ A +P+ GG T + + AY+ALDE T+ +R A L+ L
Sbjct: 115 WTPTSSGSLLYALEIPSQGGNTYWLNTNLAYEALDETTK----ERIADLQLITYNPFLR 170

Query: 174 HVQQAGSAYIGYGMDDTTATPL--RPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFL 230
S Y +P+ PLV+ HPE+G+ L + + G++ E + +
Sbjct: 171 DRNAPRSLYRLDKTIPLISPIFPHPLVRTHPESGKKHLYLDAATEVEVVGLEPEEESKLI 230

Query: 231 EGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
E L Q + H+W+ GD+V WDN+ LH + +D RV+ LAG RP
Sbjct: 231 EQLRQHNLNPKFYQQHKWSVGDIVYWDNQATLHYRQAFDPNERRVLKRVSLAGSRP 286

>ref|ZP_03421998.1| dioxygenase [Mycobacterium tuberculosis 94_M4241A]
ref|ZP_07014298.1| hypothetical dioxygenase [Mycobacterium tuberculosis 94_M4241A]
gb|EFI31977.1| hypothetical dioxygenase [Mycobacterium tuberculosis 94_M4241A]
Length = 295

Score = 100 bits (249), Expect = 3e-19, Method: Compositional matrix adjust.
Identities = 78/262 (29%), Positives = 114/262 (43%), Gaps = 14/262 (5%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
+ + G+ +GA + GV L LD A + AA L H ++ F GQH L + +Q+ FA
Sbjct: 5 ITVKKLGSRIGA QIDGVRLGGDLDPAAVNEIRAALLAHKVVFRRGQHQLDDAEQLAFAGL 64

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVI VGNMAWHADSTYMPVMAQGAV 123
G IG +A+++ D + +E+ + WH D T+ +V
Sbjct: 65 LGT--PIGHPAALAD---DAPIITPINSEFGKANR-----WHTDVTFAANYPAASV 112

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
A +P+ GG T +A+ AAY L E + L A H+ Y + A A+

Sbjct: 113 LRAVSLPSYGGSTLWANTAAAYAELPEPLKCLTENLWALHTNRYDYVTTKPLTAAQRAFR 172
Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRV 243
P+V+VHPETG +LL G + G+D+ ES E L
Sbjct: 173 QVFEKPDFRTEHPVVRVHPETGERTLLAGDFVRSFVGLDSHESRVLFVFLQRRITMPENT 232
Query: 244 HAHQWAAGDVVVWDNRCLLHRA 265
WA GDV +WDNR HRA
Sbjct: 233 IRWNWAPGDVAIWDNRATQHRA 254

>ref|ZP_02414516.1| dioxygenase, TauD/TfdA family protein [Burkholderia pseudomallei
14]
Length = 270

Score = 100 bits (248), Expect = 3e-19, Method: Compositional matrix adjust.
Identities = 74/272 (27%), Positives = 119/272 (43%), Gaps = 30/272 (11%)

Query: 28 DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGD-----IV 76
D AL AW + Q L + + F+ FG ER + ++
Sbjct: 11 DAEAVRALIEAWHAGGICRLRRQRLDMAEFVEFSLIFGRPERALNQRKLTSSREDLPELM 70
Query: 77 AISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRT 136
+SN+ +G H ++ WH D Y V ++ A VPA GG T
Sbjct: 71 IVSNILENGVSIGHLGSK-----EAYWHTDMCYTDVPPIASILYAIEVPAHGGNT 120
Query: 137 CFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP--L 194
F +M +DAL + R + S +H Y+ +G ++ + + D T P +
Sbjct: 121 EFMNMYRVHDALPASLRRQIAGLSIKHDSYR--AVGELRYGFDSVV---DVTTCPGSI 174
Query: 195 RPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P+V+VHP T RP L +GR +A + G+ ESE L+ L + +W GD+
Sbjct: 175 HPIVRVHPVTQRPYLYLGRRLNAYVVGLPVGESEALLDELWRYTRLDGVTWTQRWEVGDI 234
Query: 254 VVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
++WDNRC +HR + +D R+MW +++ P
Sbjct: 235 MIWDNRCTMHRRDAFDANARRLMWRTQIQADP 266

>gb|ADC34033.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 100 bits (248), Expect = 3e-19, Method: Compositional matrix adjust.
Identities = 71/213 (33%), Positives = 102/213 (47%), Gaps = 25/213 (11%)

Query: 56 QQITFAKRFGAIER--IGGGDIVA-----ISNVKADGTVRQHSPAEDMMKVIVGNMAW 108
QQI FA++FG +ER + V ++N+ ADG V + W
Sbjct: 1 QQIAFAEQFGTLERHVSNRGTVNPLVHIVTNLADGKPSGK-----VASTQW 48
Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
H+D ++ P + + A V+P GG TCFADM AAY+AL EA +A + HS S
Sbjct: 49 HSDKSFRPQP SLATILHALVMPPQGGETCFADMVAAYEALPEAEKAEAGVRVHWSGLS 108
Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER 228
Q+++G + I D LV+ PETGR +L +G A + G
Sbjct: 109 QARVG--IKVPPEEIIADAPDIAHL---LVRTIPETGRKALFMGERAVHLEGQPEDVGRA 162
Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
LE L A Q V+ H+W GD+++WDNRC+
Sbjct: 163 RLERLTAHAGQERFVYRHKWTLGDLLMWDNRV 195

>ref|YP_002947816.1| Taurine dioxygenase [Variovorax paradoxus S110]

gb|ACS22550.1| Taurine dioxygenase [Variovorax paradoxus S110]
Length = 290

Score = 100 bits (248), Expect = 3e-19, Method: Compositional matrix adjust.
Identities = 87/289 (30%), Positives = 134/289 (46%), Gaps = 20/289 (6%)

```
Query: 6  LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      +++ P      GA +TG+ ++ L      + AW H+++ FP Q L++ + F +F
Sbjct: 9  IRVRPQPHAFGAEITGLSISRPLPAPVLDEVKKAHAAHVSFVFPDQPLTHSELEAFTLQF 68

Query: 65  GAIERIGGGD--IVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
      G      G D  IV I +      +R+  E D+ K +      WH+D ++      G
Sbjct: 69  GEF----GVDPYIVPIEDHPHILELRR----EADE--KAVNFGAQWHSDFSQEEPPAGT 118

Query: 123  VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVYSQSKL-GHVQQAG 179
      + ++V P VGG T +AD  AYD L + + L+  A HS + Y + L      +
Sbjct: 119  ILHSKVTPPVGGDTLYADGYRAYDELSDTMKRLLDGLVAIHSAGMPYKDGFLFAKETETR 178

Query: 180  SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
      S I      D T  PLV++HP T R +L + +  I GM  ES  L L
Sbjct: 179  SMKIVVSEDADKTWPHPLVRLHPVTRRKALYVSPVYTQGIEMTRGESAALLGYLYQHMV 238

Query: 239  QAPRVHAHQWAAGDVVVWDNRCLLHRAE-PWDFKLPRVMWHSRLAG-RP 285
      +  V+ H+WA  + +WDNRC LH A+ +D L RVM + +AG RP
Sbjct: 239  RDEYVYRHRWAPNMLTLWDNRCTLHNADGGYDGH-L-RVMHRTTIAGERP 286
```

>ref|YP_001985889.1| taurine dioxygenase protein [Rhizobium etli CIAT 652]
gb|ACE93626.1| putative taurine dioxygenase protein [Rhizobium etli CIAT 652]
Length = 309

Score = 100 bits (248), Expect = 3e-19, Method: Compositional matrix adjust.
Identities = 73/269 (27%), Positives = 115/269 (42%), Gaps = 29/269 (10%)

```
Query: 8  ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRF 65
      + P      +GA + G+ L  L DA AA++  L+H ++ F Q HL + +Q FA+R G
Sbjct: 16  VVPLTGRVGAEIKGIRLGGELSDATVAAINQLLLKHKVIFFRDQGHLLDSEQEAFAARRLG 75

Query: 66  AI-----ERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
      +      G  I+ + + + G  Q      WH D T++
Sbjct: 76  DLVPHTQGPVSGTASILNLDSSRGGGRADQ-----WHTDVTFTVDAY 117

Query: 119  AQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
      + +V  V+PA GG T +++  AAY++L  + L  A HS Y + +  A
Sbjct: 118  PKFSVLRGVVIPAAGGDTIWSNTHAAYESLPAPLKLLADNLWAIHSNAYDYAAVRPRATA 177

Query: 179  GSA--YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW 236
      +      T      P+V+VHPETG  SLL+G  + G+ ++S + E  +
Sbjct: 178  EEKRHFEEVFTSTIYETEHPVVRVHPETGERSLLGNFVQRLVGVSKSDSAKLYEVFQSY 237

Query: 237  ACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      +W AGDV +WDNR  H A
Sbjct: 238  VTPENTVRWRWRAGDVAIWDNRATQHYA 266
```

>ref|YP_496820.1| taurine dioxygenase [Novosphingobium aromaticivorans DSM 12444]
gb|ABD25986.1| Taurine dioxygenase [Novosphingobium aromaticivorans DSM 12444]
Length = 316

Score = 100 bits (248), Expect = 3e-19, Method: Compositional matrix adjust.
Identities = 85/282 (30%), Positives = 133/282 (47%), Gaps = 24/282 (8%)

```
Query: 3  QTTLQITPTGATLGATVTGVHLATLDDAG-FAALHAAWLQHALLIFPGQH-LSNDQQITF 60
```



```

      + L I P   T+GA + GV L+   DAG   A+   A ++H ++ F GQ   L + +   F
Sbjct: 14  NSPLDIVPVTGTIGAEIRGVTLSGDL DAGTVQA IKDAVVRHKVVFFRGQKDLDDARHEGF 73

Query: 61  AKRFGAIERIGGGDIVAISNVK-ADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMA 119
      A   FG           + VA   V   A+G+           E D   K           +WH D T++
Sbjct: 74  ASLFG-----EPVAHPTVPVAEGS---RYLLELDS--KEGYAASSWHTDVTTFVDSYP 120

Query: 120  QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
      +G++   A   VP   GG T +A+   AY++L E+ R LV+   A H+ +Y   + + + +
Sbjct: 121  KGSILRAITVPEAGGDTVWANGETAYESLPESLRQLVNNLWAVHTNLYDYAAVLNAPKGD 180

Query: 180  SA---YIGYGMDTTATPL----RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG 232
      + +           A+ +           P+V+VHP +G+ SLL+G           G++ A+S R   +
Sbjct: 181  ETERERVNFHKSVFASTVYETEHPVVRVHPVSGQRSLLLGHFVKQFVGLNQADSSRLFQI 240

Query: 233  LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPR 274
      L D   +   V   +W   GDV   WDN+   HRA   DF L R
Sbjct: 241  LQDHITRPENVVRWRWQPGDVAFWDNQSTQHRAVA-DFGLQR 281

```

>ref|YP_001684358.1| taurine dioxygenase [Caulobacter sp. K31]
gb|ABZ71860.1| Taurine dioxygenase [Caulobacter sp. K31]
Length = 295

Score = 100 bits (248), Expect = 3e-19, Method: Compositional matrix adjust.
Identities = 78/269 (28%), Positives = 120/269 (44%), Gaps = 22/269 (8%)

```

Query: 6   LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      L +TP G   LGA ++ V L   L   AA+ AA L+H ++ F   Q +S++   + F + F
Sbjct: 18  LTVTPAGPVLGAEISSVDLRQPLAPEIVA AIRAALLRHKVVFVRDQDISHEDHVRFGRYF 77

Query: 65  GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV 117
      G +E           G +I+ I   ADG   +           +++++ ++           WH D T+ P
Sbjct: 78  GDLEGHVPVTAHVPGFPEILLIE--AADGMKLR-----EEIVPLVRVANKWHTDVTFRPA 129

Query: 118  MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
      + G V   +P +GG T FAD   A Y   L +A +A +   A H ++   QS   V +
Sbjct: 130  PSMGGVLRMRQMPPLGGDTLFDATAAIYRDLPDALKARIADLQA EHDIL--QSYGYRVDE 187

Query: 178  AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
      A   +           A   P+V+ HPETG   L + +           I G+   E+ R L   L+D
Sbjct: 188  AKRQELRAAHPVQA---HPVVRTHPETGEKHLFVNKVFTTRILGLPEDEAARLLADLLDR 244

Query: 237  ACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      +W   +V   WDNR   H A
Sbjct: 245  VKTPEYQVRFRWTPNAIVFWDNRATQHYA 273

```

>ref|YP_004019382.1| taurine catabolism dioxygenase TauD/TfdA [Frankia sp. Eu11c]
gb|ADP83512.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. Eu11c]
Length = 277

Score = 100 bits (248), Expect = 3e-19, Method: Compositional matrix adjust.
Identities = 81/283 (28%), Positives = 129/283 (45%), Gaps = 16/283 (5%)

```

Query: 5   TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWL-QHALLIFPGQHLSNDQQITFAKR 63
      ++ ++P   A +G +TG+   L D   AA   +L +H ++I+   H+ +   + ++
Sbjct: 2   SVTVSPISAEVGVQITGLAGHQLADPAVAADTRKYLDEHGVVIYREAHIGDADLVALSRL 61

Query: 64  FG--AIERIGGGD-IV AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ 120
      G   +   +GG +   +S +   D   PA+   +   G   WH D   V +
Sbjct: 62  LGEVVVAPMGGE EEFPEVSAISLD-----PAQ-SALAA YRTGTFTYWHIDGANDLV PQK 113

```

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
+ +A V GG T FA++ AAY+ L +A HS +Q +L H S
Sbjct: 114 ATLLTALEVATEGGDTEFANLYAAAYEGLSAEDKARFADLRVVSFAATQ-RLAHPD--AS 170

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
+ + + PLV GR SLL+G A I G+ ES L+ L+DWA Q
Sbjct: 171 DKVRASWEKVPSREHPLVWTR-RNGRKSLLVGATADHIVGLPEDESALLDRLLDWATQP 229

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
HQW+ GD+V+WDN +LHRA+P+ R+M + L G
Sbjct: 230 RFSLRHQWSRGDLVIWDNTGILHRAQPYTALSRRMLMHRITLVG 272

>gb|ADO34971.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ADO34972.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ADO34973.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 98

Score = 99.8 bits (247), Expect = 4e-19, Method: Compositional matrix adjust.
Identities = 55/98 (56%), Positives = 65/98 (66%), Gaps = 3/98 (3%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYMP+ A+GAVFSAE+VP T +ADMRAAY+ALD+ TRA V SA HSL YSQ
Sbjct: 1 ADSTYMP LQAKGAVFSAEIVPEGRAPTGWADMRAAYEALDDETRARVESLSAYHSLFYSQ 60

Query: 170 SKLGHV---QQAGSAYIGYGMDDTTATPLRPLVKVHPET 204
++ G++ Y YG LRPLVKVHPET
Sbjct: 61 ARAGYMP SKTNESGGYDQYGYHMDPSLRPLVKVHPET 98

>ref|ZP_06474456.1| Taurine dioxygenase [Frankia symbiont of Datisca glomerata]
gb|EFD28791.1| Taurine dioxygenase [Frankia symbiont of Datisca glomerata]
Length = 308

Score = 99.8 bits (247), Expect = 4e-19, Method: Compositional matrix adjust.
Identities = 84/298 (28%), Positives = 128/298 (42%), Gaps = 41/298 (13%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ + P GA + GV L+ LDDA A + +A L+ ++ F Q + + +QI F RF
Sbjct: 10 IDVRPLSGHTGAEIHGVDLSQLDDATIAEIRSALLRWKVVFVRDQSIGHAEQIAFGARF 69

Query: 65 GAIERI-----GGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYM 115
G I G I+ I + + + + + I + WH D T +
Sbjct: 70 GKITPAHPHEDAPPEGFPQILPIDSRRYEKKFGK-----RKITYDNGWHTDVTAL 119

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
G++ A++VP GG T + ++ AAY L E RA A+HS +S L
Sbjct: 120 VNPPAGSILRADIVPPYGGDTAWTNLVAAYQGLPEELRAFADGLRAKHS--FSPRL--- 174

Query: 176 QQAGSAYIGYGMDDTTATPL---RPLVKVHPETGRPSLLIG---RHAHAIPGMDAAESER 228
AG+ YG + PL P+V+VHPETG +L + + I G +S R
Sbjct: 175 --AGTP---YGEKIASNPLLAHPVVRVHPETGERALFVSPTFTSGENEIIGFSTRQSHR 229

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFK--LPRVMWHSRLAG 283
L+ + + +W+ GDV WDNR H P D RV++ L G
Sbjct: 230 ILDLFYEQIARPEYTVRFRWSPGDVAFWWDNRATAHLG-PSDLNHLDFDRVLYRITLEG 286

>ref|YP_001683423.1| taurine dioxygenase [Caulobacter sp. K31]
gb|ABZ70925.1| Taurine dioxygenase [Caulobacter sp. K31]

Length = 270

Score = 99.8 bits (247), Expect = 4e-19, Method: Compositional matrix adjust.
Identities = 83/282 (29%), Positives = 118/282 (41%), Gaps = 42/282 (14%)

```
Query: 1  MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
      M   L + P   +GA + GV L   L + F   +H A   Q+ +L F   Q +++D
Sbjct: 1  MTYDVLVDKPMTRRIGAEIFGVDLGQPLSNRQFEEVHQALTQYQVLFVRDQEMTHDAHKA 60

Query: 60  FAKRFGAIERIGG-----GDIVAINVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS 112
      F ++FG +   G           +IVAI           H+ A+   K + G   WH+D
Sbjct: 61  FGRKFGLAIHSGVPGLPEHPEIVAI-----HADAD----SKFVAGE-NWHS DL 104

Query: 113  TYMPVMAQGA VFSAE VVPAVGGR TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
      T P   G++   +V+P   GG TCFA M AAY+ L +   +A +   SA H
Sbjct: 105  TCDPEPPLGSILYMKVLPDDGGDTCFASMYAAYETLSDRMKAYLEGLSAVH----- 155

Query: 173  GHVQQAGSAYIGYGMD---TTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESER 228
      A   Y   D   T   P+V+ HP +GR SL +   +   I G+   AES
Sbjct: 156  ----DANPVYKAIFPDIDRTYNCSTHPIVRTHPVSGRKS L FVNPSYTTTHIAGVSKAESAA 211

Query: 229  FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDF 270
      L L A   +W   V WDNRC H+A WD+
Sbjct: 212  ILGFLYQHASNPDFQVRFRWRKNSVAFWDNRCTWHQAI-WDY 252
```

>ref|YP_439438.1| TauD/TfdA family dioxygenase [Burkholderia thailandensis E264]
gb|ABC36162.1| dioxygenase, TauD/TfdA family [Burkholderia thailandensis E264]
Length = 281

Score = 99.8 bits (247), Expect = 4e-19, Method: Compositional matrix adjust.
Identities = 73/262 (27%), Positives = 115/262 (43%), Gaps = 21/262 (8%)

```
Query: 15  LGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
      LGA + G+ + L   +   +H LL+FPGQ LS +QQ+   + FG +E
Sbjct: 10  LGAEIRGIDFSQPLSSQTRDDIIGLLSEHQLLVFPQGRLSCEQQVAACRDFGELEPHPM T 69

Query: 69  --RIGGGDIVAINVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA VFSA 126
      ++ +SNV DG   +   ++           WH+D Y+   A+   F A
Sbjct: 70  TNTSSFPEMTIVSNVTTDGKPVGYPTPPFE-----LWHS DL CYLEHPAKMTFFYA 119

Query: 127  EVVPAVGGR TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG 186
      E VP   G T FA+M AAY+ L +   ++ +   R+A SL   S +   ++ G
Sbjct: 120  ESVPDAGD TWFANMFAAYETLPDELKSAIDGRNAIFSL--DSSLVKRCRKIGFDLNIAE 177

Query: 187  MDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
      D T   P V+ HP T R S+ +   H   I G   ES+ L+ +   ++
Sbjct: 178  DDFKPTVSHPAVRTHPHTRRRSIFVNWAHTDRIEGYSHEESDEILDRIFAHCRNEDFIYR 237

Query: 246  HQWAAGDVVVWDNRCLLHRAEP 267
      H++   D+V+WDN L+H   P
Sbjct: 238  HRYTNEDLVIWDNASLIHTNSP 259
```

>ref|ZP_02370755.1| dioxygenase, TauD/TfdA family protein [Burkholderia thailandensis
TXDOH]
ref|ZP_02384640.1| dioxygenase, TauD/TfdA family protein [Burkholderia thailandensis
Bt4]
ref|ZP_05590823.1| TauD/TfdA family dioxygenase [Burkholderia thailandensis E264]
Length = 276

Score = 99.8 bits (247), Expect = 5e-19, Method: Compositional matrix adjust.
Identities = 73/262 (27%), Positives = 115/262 (43%), Gaps = 21/262 (8%)

Query: 15 LGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
LGA + G+ + L + +H LL+FPGQ LS +QQ+ + FG +E
Sbjct: 5 LGAEIRGIDFSQPLSSQTRDDIIGLLSEHQLLVFPGQRLSCEQQVAACRDFGELEPHPM 64

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
++ +SNV DG + ++ WH+D Y+ A+ F A
Sbjct: 65 TNTSSFPEMTIVSNVTTDGKPGVGYTPPPFE-----LWHS DLCYLEHPAKMTFFYA 114

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG 186
E VP G T FA+M AAY+ L + ++ + R+A SL S + ++ G
Sbjct: 115 ESVPDAHGD TWFANMFAAYETLPDELKSAIDGRNAIFSL--DSSLVKRCRKIGFDLNIAE 172

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
D T P V+ HP T R S+ + H I G ES+ L+ + ++
Sbjct: 173 DDFKPTVSHPAVRTHPHTRRRSIFVNWAHTDRIEGYSHEESDEILDRIFAHCRNEDFIYR 232

Query: 246 HQWAAGDVVVWDNRCLLHRAEP 267
H++ D+V+WDN L+H P
Sbjct: 233 HRYTNEDLVIWDNASLIHTNSP 254

>ref|ZP_06062866.1| taurine catabolism dioxygenase TauD/TfdA [Acinetobacter johnsonii SH046]
gb|EEY96645.1| taurine catabolism dioxygenase TauD/TfdA [Acinetobacter johnsonii SH046]
Length = 288

Score = 99.4 bits (246), Expect = 5e-19, Method: Compositional matrix adjust.
Identities = 77/271 (28%), Positives = 115/271 (42%), Gaps = 33/271 (12%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG-----DIVAISN 80
L A +H +LIF Q L + Q + FA FG+I R D+V +SN
Sbjct: 19 LKQALAEHLILIFKNQTLDDLQYLAFASYFGSIFRPSADNPVLASQTD TGVPDPVVPVSN 78

Query: 81 VKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFAD 140
G H G + HAD + P+ + G++ A +P GG+T + +
Sbjct: 79 AVQGQNYTGH-----GELTPHADHQWTPPLPSFGSLLYALELPQDGGQTSWFN 125

Query: 141 MRAAYDALDEATRALVHQRS--ARHSLVYSQSKLGHVQQAGSAYIGYGMDDTA--TPLRP 196
AYDAL + + + Q + V +QS G+ S Y + T P
Sbjct: 126 TIKAYDALPDDVKQIDQLQLITYNPFVRAQSNTGNTGYGDSPPYRFKQPILGHTYHPH 185

Query: 197 LVKVHPETGRPSL-LIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HPE+GR +L L R + +D +E + L + + HQW GD+V
Sbjct: 186 LVRTHPESGRKALWLNTRSEVELLNVD DSEGSELIAALRAHILKPEFRYKHQWETGDIVF 245

Query: 256 WDNRCLLHRAEPWDFKLPRVMWHSRLA-GRP 285
WDN+ LH P+ R++ LA GRP
Sbjct: 246 WDNQVTLHSRRPFPVDQRRLLKRISLAGGRP 276

>ref|ZP_06192658.1| hypothetical protein SOD_h00590 [Serratia odorifera 4Rx13]
gb|EFA14626.1| hypothetical protein SOD_h00590 [Serratia odorifera 4Rx13]
Length = 282

Score = 99.4 bits (246), Expect = 5e-19, Method: Compositional matrix adjust.
Identities = 85/291 (29%), Positives = 125/291 (42%), Gaps = 33/291 (11%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 64
L+ITP G +GA V V LA L D F L+ A L+H +L F Q ++ QQ A RF
Sbjct: 5 LKITPLGPYIGALVENNVLARPLGDGQFEQLYHALLKHQVLFERNQIPITPLQQRDLAGR 64

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIV-----GNMAWHADSTYM 115
G + I V T D+ ++IV N WH D T++
Sbjct: 65 GDLH-----IHPVYPHAT-----DVEEIIIVLDTHDDNPPDNDNWHTDVTFI 105

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
QGA+ +A+ +P+ GG T +A AAY+AL E R L+ A H S + H+
Sbjct: 106 ENPPQGAILAAKTLPSPGGDTLWASGIAAYEALSEPFRQLLAGLKAHEDFTKSFPEHKHL 165

Query: 176 QQAGSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
+ + + + P L P+V+ HP +GR +L + I + ESE L
Sbjct: 166 -SSEEEHQRWQVAKQKNPPLLHPVVRTHPVSQRQALFVNEGFTTRIVDLAPKESEALLNF 224

Query: 233 LVDWACQAPRVHAHQWAAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + +W D+ +WDNR H A R+M + + G
Sbjct: 225 LFAHITKPEFQVRWRWQEDDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|ZP_06271905.1| Taurine dioxygenase [Streptomyces sp. ACTE]
gb|EFB68071.1| Taurine dioxygenase [Streptomyces sp. ACTE]
Length = 299

Score = 99.4 bits (246), Expect = 5e-19, Method: Compositional matrix adjust.
Identities = 83/266 (31%), Positives = 120/266 (45%), Gaps = 17/266 (6%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRF 64
L +TP G + GA + G+ L LDD AL A +++ +L GQ L + QI F +R
Sbjct: 13 LPLTPLGPSFGAEIRGIDLGRLLDDQVLALREALVRYKLVFVRGQDGLDDAAQIEFGRR 72

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G + G V S D +S D+ + WH D T++ +V
Sbjct: 73 GEVTV---GHPVHDSR---DVAPEVYSLDSQDNGFADV-----WHTDVTFVRRPPAISVL 121

Query: 125 SAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH--SLVYSQSKLGHVQQAGSAY 182
A V+P GG T +AD + AY +L RA V +A H + + H Q G+ +
Sbjct: 122 RAVVLPPTGGDTNWADSQLAYASLSPGLRAYVDTLTAVHDGTREFGYLAQHRQGRGNLW 181

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVDWACQA 240
G A P+V+VHPE+GR L + G +H + G+ ES L+ L +
Sbjct: 182 EGEVFTLAPVEHPVVRVHPESGRKGLFVNPGFTSHIV-GVSEHESRGILDILYAHLT KP 240

Query: 241 PRVHAHQWAAAGDVVVWDNRCLLHRAE 266
V H+W GDV +WDNR H A
Sbjct: 241 EHVVRHRWQPGDVTLDNRSTAHYAN 266

>ref|ZP_06711045.1| taurine dioxygenase [Streptomyces sp. e14]
gb|EFF94167.1| taurine dioxygenase [Streptomyces sp. e14]
Length = 287

Score = 99.4 bits (246), Expect = 6e-19, Method: Compositional matrix adjust.
Identities = 81/270 (30%), Positives = 119/270 (44%), Gaps = 25/270 (9%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQ-QITFAKRF 64
+ ITP G + GA + G+ LA LDD AL A ++H +L GQ +D QI F +R
Sbjct: 1 MPITPLGPSFGAEIHGIDLARLDDHEILALREALVRHKLVFVRGQDTLDDAAQIEFGRR 60

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G + + + D +S D+ + WH D T++ +V
Sbjct: 61 GEVT-----VGHPVHDSGDVAPEVYSLDSQDNGFADV-----WHTDVTFVARPPAISVL 109

Query: 125 SAEVVPAVGGRTCFADMRAAYDALDEATRA-----LVHQRSARHSLVYSQSKLGHVQQA 178
A V+P GG T +AD + AY++L RA VH S +Q + G
Sbjct: 110 RAVVLPPTGGDTNWADSQLAYESLSPGLRAHIDTLTAVHDGSREFGYLAQRRKGR---- 165

Query: 179 GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVDW 236
G+ + G P+V+VHPE+GR L + G +H + G+ ES L+ L
Sbjct: 166 GNLWEGEVFTLKPVEHPVVRVHPESGRKGLFVNPGFTSHIV-GVSEHESRGLLDILYAH 224

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRAE 266
+ V H+W GDV +WDNR H A
Sbjct: 225 LTKPEHVVRHRWQRGDVALWDNRSTAHYAN 254

>ref|ZP_08224952.1| putative taurine catabolism dioxygenase [Streptomyces cf. griseus
XylebKG-1]
Length = 307

Score = 99.4 bits (246), Expect = 6e-19, Method: Compositional matrix adjust.
Identities = 82/267 (30%), Positives = 116/267 (43%), Gaps = 29/267 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ P G +GA + GV L+ LD A A L A L+ +L F QHL++ QQ FA +
Sbjct: 41 FRLVPLGRVIGAEHLGVDLSRPLDAAALRAELDRALLEWKVLFVRDQHLTSRQQRAFAGYW 100

Query: 65 GAIER---IGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQG 121
G +E + GD ++ + D V WH D T+ A G
Sbjct: 101 GELETNPLLATGDDPEVARL-----DRTAVPTFENVWHTDVTFRERPALG 145

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
AV VP GG T +ADM AAYD L + + V A H + ++ ++ +
Sbjct: 146 AVLQLREVPPPTGGDTLWADMAAAYDNLPDEVKERVEGARAVHDFIPGFARFSPPERLAH 205

Query: 182 YIGYGMDTTATPLR-PLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239
+ P+ P+V+ HP TGR ++ + I G + ES+R L L A
Sbjct: 206 QEEF-----PPVEHPVVRHRPVTGRRTFVNASFTTRIVGFEREESDRLLRLLFQQA-H 258

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
AP W AGDV WDNR H A
Sbjct: 259 APEFQVRFSWRAGDVAFWDNRATQHYA 285

>ref|ZP_06412415.1| Taurine dioxygenase [Frankia sp. EUN1f]
gb|EFC84794.1| Taurine dioxygenase [Frankia sp. EUN1f]
Length = 320

Score = 99.4 bits (246), Expect = 6e-19, Method: Compositional matrix adjust.
Identities = 91/289 (31%), Positives = 125/289 (43%), Gaps = 22/289 (7%)

Query: 2 AQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQIT 59
A T Q+TP +GA V GV L LD A+ AA LQH ++ F GQ HL QI
Sbjct: 15 ALTITQLTPR---IGAIVDGVRLGGDLADTVTAIRAAALQHRVIFFRGQDHLDTATQIA 71

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMA 119
FA+ G + + + G H E D G AWH D T+
Sbjct: 72 FARLLGPLTQ-----AHPTQAPLAGEPLVH---ELDASRGGGRAG--AWHTDVTFTDRPP 120

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS---QSKL-GH 174
++ A VP GG T +++ AAY L R L + A H+ + +S L G
Sbjct: 121 AFSILRAVTVPPQGGDTLWSNTVAAYHELPAELRELAEKLRHHTNQHDYGLRESDLA GL 180

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
Q+ ++ + T P+V++HPETG PSL+G I G+ ++S L
Sbjct: 181 PQEIIDRFLEFRSVEFETE-HPVVRHPETGEPSSLLGGFVKQIKGLSPSQSTNLLRTFG 239

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
D + QW GDV +WDNR H A PRV+ +AG

Sbjct: 240 DAVARPENTVRWQWKTGDVAIWDNRSTQHYAVNDYNDAPRVVHRVTVAG 288

>ref|NP_631410.1| dioxygenase [Streptomyces coelicolor A3(2)]
emb|CAB92200.1| probable dioxygenase [Streptomyces coelicolor A3(2)]
Length = 328

Score = 99.4 bits (246), Expect = 6e-19, Method: Compositional matrix adjust.
Identities = 90/295 (30%), Positives = 126/295 (42%), Gaps = 22/295 (7%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T +++ P +GA + GV LA LD A AA+ +A L+ ++ F Q L + + FA+
Sbjct: 19 TGIEVEPVAGHIGAEIRGVDLAAGLDAAQVAARSAVLRWKVVFVRDQRLDHAGHVAFAR 78

Query: 63 RFG--AIERIGGGDIVAISNVKAD-----GTVRQHSPA EWDDMMKVIVGNMAWHADST 113
FG + R G ++ G EW + + WH D
Sbjct: 79 LFGEPPVLP RR GKASPA GFPEIETTADRLELGGRFGMEHDEWLRRRRHTL-LRGWHCDHG 137

Query: 114 YMPVMAQGA VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
V AE VP GG T +A++ AAY L RALV A H L +G
Sbjct: 138 ARVDPPAATVLAETVPPYGGDTTANLAAAYAGLSAPLRALVDTLRAEHRL-----GVG 192

Query: 174 HVQQAG-SAYIGYGMDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLE 231
+ + G AY+ + + + PLV+VHPETG L + G + I G+ ES LE
Sbjct: 193 YQPRPGDDAYVRHLLHHQTATVHPLVRVHPETGERVLFVNGYYVEQIAGLSRPESAAILE 252

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283
LV+ A + +W G V WDNR +H A P D PR M L G
Sbjct: 253 LLVEQATRPEYTVRFRWEPGSAFVWDNRATIH LA-PGDHAHL DHPRTMHRVMLTG 306

>ref|ZP_01896407.1| Probable taurine catabolism dioxygenase [Moritella sp. PE36]
gb|EDM69259.1| Probable taurine catabolism dioxygenase [Moritella sp. PE36]
Length = 272

Score = 99.0 bits (245), Expect = 6e-19, Method: Compositional matrix adjust.
Identities = 75/265 (28%), Positives = 111/265 (41%), Gaps = 15/265 (5%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
T+QI P +GA + V L +D F A++ AW H ++ F Q LS QQ+T A RF
Sbjct: 2 TMQIEPLTPHIGALIHVLDLVHCNDTTFEAVYQAWFTHQVIFVFREQVLSPPQQQLTIAARF 61

Query: 65 GAIERIGG--GDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
G +E + V TV+ P E WH D T+ ++ +
Sbjct: 62 GELEPTHPFFPHVAQAPQVSIETVKGPPL E-----SFWHTDLTWRQQPSKAS 110

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV-YSQSKLGHVQQAGSA 181
V A+ VP GG T + M A + L E + L+ + SA H+L + + + +
Sbjct: 111 VLHAQHVP HCGGDTLWCSTAVFRQLPEQDKILLRRLSAMHALFAFDGIESSEITEDWQQ 170

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQA 240
+ T P++ HP+TG L I I GM+ +S L L A Q
Sbjct: 171 DVLA VSATNPPVSHPVITRHPDTGEEILFINEQFTRYIIGMNRDDSNALLAKLFAMARQP 230

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRA 265
+W A + +WDNR H A
Sbjct: 231 EYQVRFKWQANSLAIWDNRSTQHYA 255

>ref|ZP_07300902.1| taurine dioxygenase [Streptomyces hygroscopicus ATCC 53653]
gb|EFL29271.1| taurine dioxygenase [Streptomyces hygroscopicus ATCC 53653]
Length = 300

Score = 99.0 bits (245), Expect = 6e-19, Method: Compositional matrix adjust.
Identities = 85/292 (29%), Positives = 128/292 (43%), Gaps = 35/292 (11%)

```
Query: 4   TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
          T   I   G   +GA V GV L+ LD A + +++A L+H L+F Q L + Q+ FA
Sbjct: 5   TGFDIRRIGGRIGAEVLGVALSDDLDPALVSDINSALLEHKALVFRDQQQLDDAAQLRFAS 64

Query: 63  RFG-----AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM 115
          FG           + + G   +I V A+ +R +               WH D T++
Sbjct: 65  LFGELTTAHTPTVPSVDGQP--SILPVNAEEGIRANR-----WHTDVTTFV 106

Query: 116  PVMAQGA VFSAEVVP AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
          + +           VVP GG T A+ AAY L + R L + A H+ Y +
Sbjct: 107  RSPPKVSTLRGIVVPPYGGNTLIANAGAA YQDL PQPLRELADKLWAVHTNDYDYAAPPKD 166

Query: 176  QQAG---SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG 232
          ++A   +I   T           P+V+VHPE+G L IG A + G+ +ES L
Sbjct: 167  EKAAEHRKR FISRKYRTA----HPVVRVHPESGERGLFIGGFAQSF IGLGPSES RDLLRI 222

Query: 233  LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG 283
          + + +   W+ GDVVV+DNR H A P D+ LPR++ +AG
Sbjct: 223  FQSYVIRPENIVRIAWSPGDVVVFDNRITQH YA-PDDYGDLPRL LHRVTVAG 273
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>ref|YP_001106845.1| taurine dioxygenase, 2-oxoglutarate-dependent [Saccharopolyspora
erythraea NRRL 2338]
emb|CAM03920.1| taurine dioxygenase, 2-oxoglutarate-dependent [Saccharopolyspora
erythraea NRRL 2338]
Length = 279
```

Score = 99.0 bits (245), Expect = 6e-19, Method: Compositional matrix adjust.
Identities = 76/273 (27%), Positives = 111/273 (40%), Gaps = 43/273 (15%)

```
Query: 1   MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFP-GQHLSNDQQIT 59
          M +   + P   LGA V GV L L D+ F A+   L+H +L FP   L
Sbjct: 1   MNENRFDVRPVSGALGAEVRGVPLDALTDSDFTAVRELLEHLVLFFPDAAAGLEPGAHKA 60

Query: 60  FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST 113
          F +RFG +E           ++ G D + + + +   Q + A+               WH D T
Sbjct: 61  FGRRFGELEVHPFLPKLP GHDELVLVDLSE-----QGARAD-----VWHTDVT 102

Query: 114  YMPVMAQGA VFSAEVVP AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
          + P   +V   P GG T +++ AY+AL R L+ +A H +
Sbjct: 103  FSPSPPIASVLQLVECPSPSGGDTMWSNQYLAYEALSAPVRELLDGLTAVHVFKHPNGSFR 162

Query: 174  HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
          +           P+V+ HPETGR SL + R H IP + ES+ L
Sbjct: 163  SEAE-----HPVVR AHPETGRRSLYVNRMFTHRIPQLTPGESDALLRQ 205

Query: 233  LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          L + +   RV ++W G V VWDNR H A
Sbjct: 206  LFEVSESPQRVCRYRWVPGAVAVWDNRVTQH YA 238
```

```
>ref|YP_002129572.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Phenylobacterium
zucineum HLK1]
gb|ACG77143.1| alpha-ketoglutarate-dependent taurine dioxygenase [Phenylobacterium
zucineum HLK1]
Length = 286
```

Score = 99.0 bits (245), Expect = 7e-19, Method: Compositional matrix adjust.
Identities = 84/286 (29%), Positives = 125/286 (43%), Gaps = 19/286 (6%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+++ P GA V G+ L+ L + AAW +HA+L FP Q LS D F +
Sbjct: 8 IEVRPQPTGFGAEVRGLDLSRPLPPGVLEQVKAARHAVLAFPNQPLSLDALEAFTLQI 67

Query: 65 GAIERIGGGDIVAISNVKADGTVRQ--HSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGA 122
G G+ I + V + P E K WH+D ++
Sbjct: 68 GPF-----GEDPFIKPMGHPNVLELRREPDE-----KATNFGAGWHSDFSQARPPAAT 117

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG---HVQQAG 179
+ +E+VP VGG T F D AY+AL + ++ A HS + G +
Sbjct: 118 ILRSEIVPPVGGDTLFCDGARAYEALSPTFQRMLEGLRAVHSATRAYGTKGVFARETEKR 177

Query: 180 SAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
+ I + A+ PLV+ HP TGR +L + + I G+ ES+ L L
Sbjct: 178 TMEIIVSPEADASLTHPLVRTHPVTGRKALYVSPVYTTGIEGLTVEESQAILGFLFAHMT 237

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRAE-PWDFKLPRVMWHSRLAG 283
+ V+ H+W G V++WDNRC H AE +D L RVM + +AG
Sbjct: 238 KEAFVYRHKWRPGMVLMDNRCTAHFAEGGYDGH-LVMHRTTVAG 282

>ref|YP_003102078.1| taurine dioxygenase [Actinosynnema mirum DSM 43827]
gb|ACU38232.1| Taurine dioxygenase [Actinosynnema mirum DSM 43827]
Length = 281

Score = 99.0 bits (245), Expect = 7e-19, Method: Compositional matrix adjust.
Identities = 74/273 (27%), Positives = 113/273 (41%), Gaps = 51/273 (18%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFP-GQHLSNDQQITFAKR 63
T Q+ P ++GA V GV L+T+DD F +H ++H +L FP L+ + F R
Sbjct: 6 TFQVRPVSIGSIGAEVYGVLDLSTVDDEQFKEIHDLLVRHLVLFPEAGGLTPEAHQAFGSR 65

Query: 64 FGAIE-----RIGGGDIVAI----SNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADST 113
FG +E ++ G + + + KAD WH D +
Sbjct: 66 FGELEVHPFLPKLEGHEHIVVLDSDKGAKAD-----VWHTDVS 103

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
Y+ +V + P GG T +++ AY+AL E R L+ +A H + Q
Sbjct: 104 YVKHPPITSVLQITLTPEAGGDTMWSNQYLAYEALSEPMRELLEGTASHVFAHPQGTG- 162

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
+ P+V+VHP +GR SL + R I + ES LE
Sbjct: 163 -----RSEVEHPVVRVHPVSGRKSlyVNRMFtkRILQLSRGESAAALLEH 206

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L + + R ++WA G V +WDNR H A
Sbjct: 207 LFEVSESPQRTCRYRWAPGAVAMWDNRATQHya 239

>ref|YP_003133666.1| Probable taurine catabolism dioxygenase [Saccharomonospora
viridis
DSM 43017]
gb|ACU96839.1| Probable taurine catabolism dioxygenase [Saccharomonospora viridis
DSM 43017]
Length = 308

Score = 99.0 bits (245), Expect = 7e-19, Method: Compositional matrix adjust.
Identities = 77/276 (27%), Positives = 120/276 (43%), Gaps = 35/276 (12%)

Query: 3 QTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITF 60
+T + +T G +GA + GV L LD+A A + AA L+H ++ F QH L + Q F
Sbjct: 8 RTDISVTKIGGNIGARIDGVWLGGLDDEATVARIRAALLEHKVVFFRQQHLLDAGQQAF 67

Query: 61 AKRFG-----AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST 113
+ G + +G G+I+ I AE+ +WH+D T
Sbjct: 68 GRLLGELTQPHPTVRSVGLGNILPID-----AEYGRAN-----SWHSDVT 107

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS--- 170
++ + +V A +P GG T +A+ AY L ++ +AL + A H+ +Y S
Sbjct: 108 FVDRIPAFSLRAVTIPPYGGSTVWANTATAYANLPDSLKALAEKLWAVHTNLYDYSRHV 167

Query: 171 ---KLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
++G + Y P+V+VHPETG LL+G + G+ +AES
Sbjct: 168 DERRIGGIDVKERDYRDEFRSEVYETEHPVVRVHPETGERVLLLGHFVKHLVGLSSAESN 227

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH 263
L + QW GDV +WDNR H
Sbjct: 228 VIFNLLQARITRLENTVRWQWRPGDVAIWDNRATQH 263

>gb|ADC34047.1| TfdA-like protein [uncultured bacterium]
Length = 191

Score = 99.0 bits (245), Expect = 8e-19, Method: Compositional matrix adjust.
Identities = 65/211 (30%), Positives = 102/211 (48%), Gaps = 25/211 (11%)

Query: 56 QQITFAKRFGAIERI----GGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHAD 111
QQI FA+R+G I G D I +K +P E + VGN AWH D
Sbjct: 1 QQIAFARRWGNHYFPLSPGLPDHPEILEIKK-----TPEEEKN-----VGN-AWHTD 47

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
+ P A + A+ VP GG T F++ AAY++L A + ++ S++
Sbjct: 48 QMFAPKPAMATMLYAKEVPRYGGDTMFSNQYAAYESLSSAMQQMLAGLKTVC SVL----- 102

Query: 172 LGHVQQAGSAYIGYG-MDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFL 230
V+ +G Y +++ + PL++ HPETGR +L IG HA + GM ES+ L
Sbjct: 103 --DVRNSGGNYNADAPVNSKTVSMHPLIRTHPETGRRALYIGNHARSFDMTEESKPLL 160

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
+ L+ + + + +W G + +WDNRC+
Sbjct: 161 DYLIQHSTRPETICRFRWRPGSMIAIWDNR CV 191

>ref|YP_710871.1| putative taurine dioxygenase [Frankia alni ACN14a]
emb|CAJ59264.1| putative taurine dioxygenase [Frankia alni ACN14a]
Length = 308

Score = 99.0 bits (245), Expect = 8e-19, Method: Compositional matrix adjust.
Identities = 77/275 (28%), Positives = 117/275 (42%), Gaps = 38/275 (13%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ + P GA + G+ L LDDA A + +A Q ++ F QH+ + QQ+ F +RF
Sbjct: 11 IDVRPLSGHTGAEIHGIDLREELDDATVAEIRSALHQWKVFFRDQHIDHAQQVAFGRRF 70

Query: 65 GAI-----ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM 115
G + +G +I+ I + + V A +D+ WH D T +
Sbjct: 71 GRLTPAHPHEEAPPVGFPEILPIDSRRY-AKVFGKRKATYDN-----GWHTDVTAL 120

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
++ +V+P GG T + ++ AAY+ L E R L ARHS G+
Sbjct: 121 VNPPTASILRGDVIPPYGGDTAWTNLVAAAYEGLPEPLRNADGLRARHS-----FGNF 173

Query: 176 QQAGSAYIGYGMDTTATPL---RPLVKVHPETGRPSLLIGRHAHA----IPGMDAAESER 228
YG A PL P+V+VHPETG +L + A I G +S +
Sbjct: 174 PSDSE----YGRRVAANPLVAIHPVVRVHPETGERALFVSPSFTAKDGEIIGFSPKQSRQ 229

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH 263
L+ D ++ +W GDV WDNR H
Sbjct: 230 ILDVFYDQISRSEFTVRFKWNQGDVAFWDNRATAH 264

>ref|YP_001563031.1| taurine dioxygenase [Delftia acidovorans SPH-1]
gb|ABX34646.1| Taurine dioxygenase [Delftia acidovorans SPH-1]
Length = 282

Score = 98.6 bits (244), Expect = 8e-19, Method: Compositional matrix adjust.
Identities = 79/274 (28%), Positives = 123/274 (44%), Gaps = 28/274 (10%)

Query: 6 LQITPTGATLGATVTGVHLA--TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++I P +GA + GV LA DDA F+ + AA L+H +L Q L+ + + FA+R
Sbjct: 1 MRIEPMTCIGAELLGVRDLADAVRDDALFSEIRAALLRHKVLFLRDQGLTRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E VA S+ + G VR + +P + +D + +WH D+T+ G
Sbjct: 61 FGELE----DHPVAGSDPEHPGLVRIYRTPETQPNDRYE-----NSWHCDATWREAPPMSG 111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V P VGG T +A+M AY+ L +A +AL+ ARHS+ + +++ +
Sbjct: 112 VLHCVECPVGGDTLWANMALAYERLPDAVKALIAPLRARHSIECTFGAAMPIERRLALK 171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LEGLVD 235
Y P+V+ HPETG L + + R GL+
Sbjct: 172 AQY-----PDAEHPVVRTHPETGEKVLVFNNGFTTHTNFHTPANVRVGQDFTQGASGLLQ 226

Query: 236 WACQAPRVHAHQ---WAAGDVVVWDNRCLLHRA 265
+ + +Q W AG V +WDNR H A
Sbjct: 227 YLIGQAIIPEYQVRWRWRAGSVAIWDNRATQHYA 260

>ref|YP_003329314.1| TauD [Sinorhizobium meliloti]
gb|ABA55987.1| TauD [Sinorhizobium meliloti]
Length = 317

Score = 98.6 bits (244), Expect = 8e-19, Method: Compositional matrix adjust.
Identities = 75/276 (27%), Positives = 117/276 (42%), Gaps = 43/276 (15%)

Query: 8 ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFG 65
+ P +GA V GV L L D AA++ L++ ++ F GQ HL +Q FA+R G
Sbjct: 16 VVPLTGRVGAIEVRGVRLGGDLSDVAIAAINQLLLKYKVIFFRQGEHLDEVEQELFARRLG 75

Query: 66 AI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM 118
+ G I+ + + + G Q WH D T++
Sbjct: 76 DLVPHPTQGPTAGTASILNLDSSRGGGRADQ-----WHTDVTFVDAY 117

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY-----SQ 169
+ +V V+P GG T +++ AAY++L + L A HS Y S
Sbjct: 118 PKFSVLRGVVIPTAGGDTIWSNTHAAYESLPAPLKLLADNLWAIHSNAYDYAAVRPRASA 177

Query: 170 SKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF 229
+ H ++ ++ I Y + P+V+VHPETG SLL+G + G+ ++S +
Sbjct: 178 EEKKHFEEVFTSTI-YETE-----HPVVRVHPETGEKSLLLGNFVQRLVGLSKSDSAKL 230

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
E + W AGDV +WDNR H A
Sbjct: 231 YELFQSYVTAPENTVRWHWQAGDVAIWDNRATQHYA 266

>ref|YP_002129780.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Phenylobacterium
zucineum HLK1]
gb|ACG77351.1| alpha-ketoglutarate-dependent taurine dioxygenase [Phenylobacterium
zucineum HLK1]
Length = 289

Score = 98.6 bits (244), Expect = 9e-19, Method: Compositional matrix adjust.
Identities = 81/273 (29%), Positives = 124/273 (45%), Gaps = 23/273 (8%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
M+Q+ LQI LGA ++GV L+ L D AA+ A ++H ++ F GQ L+ ++Q+
Sbjct: 1 MSQS-LQIRRIAGALGAEISGVLDLSQDLPDQTIAAIRRALVEHQVIFFRGQALTPERQVA 59

Query: 60 FAKRFGAIE---RIGG--GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTY 114
F RFG + + G G + +K + +V G WH+D ++
Sbjct: 60 FGARFGPLNVHPFVAGMAGQPAVMEIIK-----EPQDRVNFGG-GWHS DMSF 105

Query: 115 MPVMAQGA VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
+ + G++ A VP GG T FA AA++AL + + +A HS S GH
Sbjct: 106 LERPSIGSILYAVEVPDFGGDTL FASQA AFEALSPGLQKTLEGLNAVHSASREYSARGH 165

Query: 175 VQQAGSAY-IGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEG 232
Q SA + + P+V VHPETGR +L + I G ES+ L+
Sbjct: 166 SAQKRSAMSVAEADGYVGEYVHPVVLVHPETGRKALYVNPFAFTLRIDGWSKRESKPLLDY 225

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L + + +W G V WDNR + H A
Sbjct: 226 LFEHSRYEGFTCRFRWEPGSVAFWDNRSVWHFA 258

>ref|ZP_01616036.1| putative dioxygenase [marine gamma proteobacterium HTCC2143]
gb|EAW33119.1| putative dioxygenase [marine gamma proteobacterium HTCC2143]
Length = 300

Score = 98.6 bits (244), Expect = 9e-19, Method: Compositional matrix adjust.
Identities = 82/291 (28%), Positives = 121/291 (41%), Gaps = 35/291 (12%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
A+ +T +LGA V G++LA D + QH +L FP Q LS D+ + F
Sbjct: 10 AENLWDVTRLAGSLGAEVRGINLAQATDITDITEVQRLNQHMLVFFPAQFLSEDEHVAFG 69

Query: 62 KRFGAIERIGGGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQG 121
FG +E G ++ + +R D+ WH D T+ A
Sbjct: 70 AHFGPLE--GHPNL TNADSHPKLFELRASQGGVADE-----WHTDITFQE QPALM 117

Query: 122 AVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
++ P GG T + ++ A+DAL + + SA H A
Sbjct: 118 SILKMVKCPESGGDTMWTNLCDAFDALSPMQEMCMGLSALHD-----A 161

Query: 182 YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQA 240
+ D A + P+V++HPETGR +L + H I M A ES+ L L W Q+
Sbjct: 162 HPHDRADKMA--IHPVVR IHPETGRKALYVNEHFTRRIVEMSAVESDSVLRFLTRWV-QS 218

Query: 241 PRVHA-HQWAAGDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLAG-RPETEG 289
PR + W G + +WDNRC H DF R++ + G RPE G
Sbjct: 219 PRFTVRYHWTEGAIGMWDNRCTQHYVLN-DFSEERIIQRVTVMGDRPEGPG 268

>ref|YP_001700840.1| putative taurine dioxygenase [Mycobacterium abscessus ATCC 19977]
emb|CAM60186.1| Putative taurine dioxygenase [Mycobacterium abscessus]
Length = 310

Score = 98.2 bits (243), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 84/297 (28%), Positives = 127/297 (42%), Gaps = 38/297 (12%)

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Query: 4   TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQ-QITFAK 62
          + L++   G  +GA + GV L  +D A  +A++ A L+H ++ F GQH  +D+ Q  FAK
Sbjct: 3   SDLRVVKLGENIGARIDGVRLGEVDTATASAINAMLEHKVVFFRGQHHVDDEVQFAFAK 62

Query: 63  RFGAIER-----IGGGDIVAIS-NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV 117
          G          +   D+  +  +  +  G   Q                      WH D T++
Sbjct: 63  SMGIPTTPHPTLTSSDVKVLPI DSEEGGRANQ-----WHTDVTTFVDR 104

Query: 118  MAQGAVFSAE VVP AVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVYSQSKLGHV 175
          + + ++   A  +P  GG T +   AAY  L  +  +  L   A H+   Y+Q   V
Sbjct: 105  IPKASILRAVELPPYGGTTTWTSTVAAYRQLPKPLQDLADNLWAMHNNQFDYTQVDPKAV 164

Query: 176  QQ-----AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE-- 227
          +          +GS Y+   T          P+V+VHPETG  +LL+G   I  + A+ES+
Sbjct: 165  AELLAKAGSGSKYVREFGATHFETHHPVVRVHPETGEKALLLGNFVKRILDVSASESQAL 224

Query: 228  -RFLLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVRMWSRLAG 283
          R  +  V W      R      W  GDV +WDNR  H A          PR M      LAG
Sbjct: 225  FRMFQDRVTWLENTIR---WSWELGDVAMWMDNRATQHYAISDYGDQPRRMHRVTLAG 278

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>ref|ZP_01065145.1| Probable taurine catabolism dioxygenase [Vibrio sp. MED222]
gb|EAQ53613.1| Probable taurine catabolism dioxygenase [Vibrio sp. MED222]
Length = 271

Score = 98.2 bits (243), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 72/269 (26%), Positives = 119/269 (44%), Gaps = 25/269 (9%)

```

Query: 6   LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
          L+I          +GA + GV LAT          ++ A + H ++   Q LS +Q +  A+RFG
Sbjct: 2   LKIEQVTPHIGARIHGVDLATCSVTELDEVYQALISHQVIFLGDQILSPEQHLMIAERFG 61

Query: 66  AIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM 118
          +E          R+   V++   T R ++P E                      WH D T+  V
Sbjct: 62  QLELAHPFFPRVESAPQVSVIE-----TTRGNAPME-----SYWHTDLTWRKVP 105

Query: 119  AQGA VFSAE VVP AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV-YSQSKLGHVQQ 177
          ++ ++   A+ +P+  GG T +   M A +D+LDE  +  +   SA HSLV +  +  ++
Sbjct: 106  SKASLLHAQHIPPSTGGDTIWCSMTAVFDSLDEDMKVKLRLGLSATHSLVAFEGVEPDQIEL 165

Query: 178  AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDW 236
          +          + P+V+ HPETG+ +L I          I  +D  ES+  L  L  +
Sbjct: 166  DWHKSLLKTAQQNPPVIHPVQSHPETGKETLYINEQFTRYINELDRQESDILLNQLFEI 225

Query: 237  ACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          A  +          +W  G  +  +WDNR  H A
Sbjct: 226  ARRPEFQVRFKWDKGSMAIWDNRVTQHYA 254

```

>ref|ZP_01812660.1| Probable taurine catabolism dioxygenase [Vibrionales bacterium
SWAT-3]
gb|EDK29869.1| Probable taurine catabolism dioxygenase [Vibrionales bacterium
SWAT-3]
Length = 271

Score = 98.2 bits (243), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 70/269 (26%), Positives = 122/269 (45%), Gaps = 25/269 (9%)

```

Query: 6   LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
          L+I P          +GA + G++L+   ++   ++ A + + ++ F  Q LS +Q +  AKRFG

```

Sbjct: 2 LKIEPITPHIGARIHGLNLSGCSESELEDDVYQALVTYQVVFDEQSLSPEQHLALAKRFG 61

Query: 66 AIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVM 118
+ E R+ V++ T R ++P E WH D T+ +

Sbjct: 62 ELEPAHPFFPRVERAPQVSVIE-----TTRGNAPME-----SYWHTDLTWREL 105

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV-YSQSKLGHVQQ 177
++ ++ A+ VP VGG T + M A +D+LDE+ + + SA HSLV + + ++

Sbjct: 106 SKASLLHAQHVPDVGDTIWCSMTAVFDSLDESMKDKLRGLSATHSLVAFEGLESDQIEL 165

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDW 236
+ PLV++HPETG+ +L I I ++ E + L L +

Sbjct: 166 DWHSKLLKTAQENPPVKHPLVQLHPETGKETLYINEQFTRYINELEREEDGALLSQLFEI 225

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ +W G + +WDNR H A

Sbjct: 226 TRRPEYQVRFKWNKGSMAIWDNRVTQHYA 254

>ref|ZP_05521780.1| dioxygenase [Streptomyces lividans TK24]
ref|ZP_06526600.1| dioxygenase [Streptomyces lividans TK24]
gb|EFD64850.1| dioxygenase [Streptomyces lividans TK24]
Length = 328

Score = 98.2 bits (243), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 89/295 (30%), Positives = 125/295 (42%), Gaps = 22/295 (7%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T +++ P +GA + GV LA LD A AA+ +A L+ ++ F Q L + + FA+

Sbjct: 19 TGIEVEPVAGHIGAEIRGVDLAAGLDAAQVAARSAVLRWKVVFRRDQRLDHAGHVAFA 78

Query: 63 RFG---AIERIGGGDIVAISNVKAD-----GTVRQHSPAEDDDMMKVIVGNMAWHADST 113
FG + R G ++ G EW + + WH D

Sbjct: 79 LFGPEVVLPRRGKASPAGFPEIETTADRLELGGFRGMEHDEWLRRRRHTL-LRGWHCDHG 137

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
V AE VP GG T +A++ AAY L RA V A H L +G

Sbjct: 138 ARVDPPAATVLAETVPPYGGDTTANLAAAYAGLSAPLRAFVDTLRAEHRL-----GVG 192

Query: 174 HVQQAG-SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLE 231
+ + G AY+ + + + PLV+VHPETG L + G + I G+ ES LE

Sbjct: 193 YQPRPGDDAYVRHLLHHQTATVHPLVRVHPETGERVLFVNGYYVEQIAGLSRPESAAILE 252

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283
LV+ A + +W G V WDNR +H A P D PR M L G

Sbjct: 253 LLVEQATRPEYTVRFRWEPGSAFWDNRATIHLa-PGDHAHLDPRTMHRVMLTG 306

>ref|YP_442487.1| dioxygenase, TauD/TfdA [Burkholderia thailandensis E264]
ref|ZP_02388151.1| dioxygenase, TauD/TfdA [Burkholderia thailandensis Bt4]
ref|ZP_05586956.1| dioxygenase, TauD/TfdA [Burkholderia thailandensis E264]
gb|ABC36290.1| dioxygenase, TauD/TfdA [Burkholderia thailandensis E264]
Length = 292

Score = 98.2 bits (243), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 83/268 (30%), Positives = 121/268 (45%), Gaps = 20/268 (7%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAG-FAALHAAWLQHALLIFPGQ-HLSNDQQITFAK 62
TL+I P T+GA V LA + ++G + A L++ +L F Q LS + QI F K

Sbjct: 3 TLEIRPLSGTIGAQVRNRTLAVGVESGRVDEIRQALLRYKVLFFTNQPDLSVETQIAFGK 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E K DG Q +D + ++ WH D + +

Sbjct: 63 LFGELE-----TNFPSFTAKPDG---QPEVTVFDGAVSTGRASI-WHTDLSIAKTPSAMG 113

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ--SKLGHVQQAGS 180
+ + PA GG T +AD+ AAY AL +A + + A H ++ Q + G Q G

Sbjct: 114 ILCVKETPASGGDTMWADLEAAYAALSPGMQAFLEGQRAVHDMMPQYQRPQAFQTQGR 173

Query: 181 AYIGYGMDDTTAT--PLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWA 237
+ MD + P+V+VHPETGR L + + I G +AES L L

Sbjct: 174 S----DMDLSEVFGAHPVVRVHPETGRKCLFVNPFLTSHITGFHSAESATILNYLYALM 229

Query: 238 CQAPRVHAHQWAAGDVVVDNRCLLHRA 265
+ V W+ GDV +WDNRC +H A

Sbjct: 230 ERPQYVVRWHWSNGDVALWDNRCTMHTA 257

>ref|YP_472514.1| putative taurine dioxygenase protein [Rhizobium etli CFN 42]
gb|ABC93787.1| putative taurine dioxygenase protein [Rhizobium etli CFN 42]
Length = 309

Score = 98.2 bits (243), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 71/262 (27%), Positives = 113/262 (43%), Gaps = 29/262 (11%)

Query: 15 LGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGAI----- 67
+GA + G+ L L DA AA++ L+H ++ F Q HL + +Q FA+R G +

Sbjct: 23 VGAEIKGIRLGGELSDATVAAINQLLLKHKVIFFRDQGHLLDDSEQEAFARRLGDLPVHPT 82

Query: 68 --ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQQAVFS 125
G I+ + + G Q WH D T++ + +V

Sbjct: 83 QGPVSGTASILNLDSSRGGGRADQ-----WHTDVTTFVDAYPKFSVLR 124

Query: 126 AEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG--HVQQAGSAYI 183
V+PA GG T +++ AAY++L + L A HS Y + + + +

Sbjct: 125 GVVIPAAGGDTIWSNTHAAYESLPAPLKLLADNLWAIHSNAYDYAAVRPRATAEKKHFE 184

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRV 243
T P+V+VHPETG SLL+G + G+ ++S + E +

Sbjct: 185 EVFTSTIYETEHPVVRVHPETGERSLLLGNFVQRLVGLSKSDSAKLYEVFQSYVTAPENT 244

Query: 244 HAHQWAAGDVVVDNRCLLHRA 265
+W AGDV +WDNR H A

Sbjct: 245 VRWRWRAGDVAIWDNRATQHYA 266

>gb|ACF98187.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[uncultured bacterium 1114]
Length = 280

Score = 98.2 bits (243), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 80/269 (29%), Positives = 115/269 (42%), Gaps = 20/269 (7%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
+ +TL I + LGA + G+ L+ LD A + AA L+H ++ F Q ++ Q +

Sbjct: 2 LRNSTLTIERISAGALGAEINGLDLSQDLGEIVAQIRAALLEHLVVFVRDQTMTPQQLVA 61

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMA 119
F +RFG V VK + + KV G + WH+D+TY+

Sbjct: 62 FGRRFGMP-----VEYPFVKGTPEAPEVIEVLKLEHEKVNFGGI-WHSDTTYLAEP 112

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
G++ A VP GG T FA+M AY++L R L+ +A S S V +

Sbjct: 113 MGSMLLAAEVPPFGGDTLFANMFLAYESLSARMRELLDGLTA-----ISSAKADVSRTR 167

Query: 180 SAYI----GYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLV 234

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      I   G G T       P+V+ HPE+GR L +   H       GM A ESE L L
Sbjct: 168 EDRIASNPGGGAKTVYEAHPVVRTHPESGRKGLYVNIAHTVRFGGMTAESEPLLAFLF 227

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLH 263
      +           +W G + WDNH H
Sbjct: 228 RHQTKPEFTCRFRWQPGSLAFWDNRSTQH 256

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>emb|CAK48578.1| unnamed protein product [Aspergillus niger]
Length = 311

Score = 97.8 bits (242), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 84/280 (30%), Positives = 131/280 (46%), Gaps = 28/280 (10%)

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Query: 5   TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
      TL P   TLGA   GV + + DA   L AA ++ +L+F   L + +   FA++
Sbjct: 19  TLTFRPLHPTLGAECGVDFSKPVPDAVIEQLRAAMAKNGILVFRATGLDDARHTAFARQ 78

Query: 64  FG-----AIERIG-----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHA 110
      G       A+ + G       G+++ I NV DG +   S   W       +++ G   +H
Sbjct: 79  LGPEMVDSAVGKPGVPNRLDPKGELMDIGNVDGDGRIL--STTSWRS--QLLRGTRLFHV 134

Query: 111 DSTYMPVMAQGAVFSAEVP--AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
      D +Y   A ++ A +P   GG T FAD R AY L E T+ +   HSL+ S
Sbjct: 135 DGSYFQRRAGYSLLRHQLPFRGTGGATAFADTRTAYADLAEETKNEIQNHVLWHSMLQS 194

Query: 169 QSKLGHVQQAGSAYIGYMDTTATP--LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAES 226
      + LG   A ++ + AT       LV++H + R +L +G HA+ I G   A+S
Sbjct: 195 R-YLG----APENWLIRLLPEAATSRGRHQLVQLHKPSNRMNLYLGSHAYQIDGWSRADS 249

Query: 227 ERFLEGLVDWACQAPRVHAHQWA-AGDVVVWDNRCLLHRA 265
      + +E L+ A Q   V   W   GD+++WDN C++HR+
Sbjct: 250 KPVEALMRHASQDKYVLTVDWQNNGDMIMWDNTTCVMHRS 289

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>ref|YP_004018287.1| taurine catabolism dioxygenase TauD/TfdA [Frankia sp. Eu1lc]
gb|ADP82417.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. Eu1lc]
Length = 275

Score = 97.8 bits (242), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 83/274 (30%), Positives = 125/274 (45%), Gaps = 21/274 (7%)

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Query: 15  LGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGG 72
      +GA V V + + DD   A   A ++ +L+F   ++ ++ QI F ++ G + +I G
Sbjct: 13  VGEVVDVDVDRMLHDDDLPTACLRALAEENGVLFLFRELNIDDEAQIAFGRKLGRLAQIPG 72

Query: 73  ---GDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHAHASTYMPVMAQGAVFSAEVP 129
      +++ IS   A+   Q+ P+           N WH D +   + A+ A+ SA V+
Sbjct: 73  YRSPEVMEISFDPANPNA-QYFPS-----NDHWHFDGSMDDIPAKAALMSARVI 120

Query: 130 PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDT 189
      GG T FA   AYDAL + +           H+   Q +   Q +   +
Sbjct: 121 TDEGGETEFASTYVAYDALSDDEEKDRFAGLRILHTFESIQR--TYQDPTPEQLEDWAS 177

Query: 190 TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWA 249
      PLV H E+GR SL+ G A + GMD ES   L L +   RV H W+
Sbjct: 178 WEDREHPLVWEH-ESGRSLVFGASAARVIGMDVEESRALLADLERRSTAPDRVLRHSWS 236

Query: 250 AGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
      GD+V+WDN L+HRA P+D   PR M + LAG
Sbjct: 237 VGD LVIWNLGLVHRACPFDRTPRRMHRITTLAG 270

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>ref|ZP_05225744.1| taurine catabolism dioxygenase TauD, TfdA family protein
[Mycobacterium intracellulare ATCC 13950]
Length = 280

Score = 97.8 bits (242), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 90/295 (30%), Positives = 130/295 (44%), Gaps = 30/295 (10%)

Query: 6 LQITPTGATLGATVTGVHLATL-DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L IT ++GA V G+ L DD+ AA+ A + +L+F G HL Q+ F +
Sbjct: 4 LTITKLTESVGAEVAGLGPTTELADDSVGAAVLDALEDNGVLVFRGLHLDPAQVGFRCRL 63

Query: 65 GAIERIGGG--DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM---PVMA 119
G ++ G + I + D + +++ A + + WH D
Sbjct: 64 GEVDHSSDGHHPVAGIYPITLDKS--KNASAAAY-----LKATFDWHIDGCTPLGDECPQ 115

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDAL-DE-----ATRALVHQRSARHSLVYSQSKLG 173
+ V SA V GG T FA+ AAYD L DE T +VH A VY
Sbjct: 116 KATVLSAVRVAEWGGETEFANSYAAAYDDLDEEKQRFGLRVVHSLASQRRVYPDPSP 175

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
VQ+ S T PLV H +GR SL++G A + GM+ E L+ L
Sbjct: 176 QVQRWRS-----RRTHEHPLVWTH-RSGRKSLVLGASADYVVGMELEDEGRALLDEL 225

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETE 288
+ A +V++H W+ GD V+WDNR +LHRA P+D R M + + G E
Sbjct: 226 LARATTPEKVYSHSWSGDVTIWDNRGVLHRAAPYDPDSQREMLRTTVLGDEPIE 280

>ref|ZP_02374281.1| dioxygenase, TauD/TfdA [Burkholderia thailandensis TXDOH]
Length = 292

Score = 97.8 bits (242), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 83/268 (30%), Positives = 121/268 (45%), Gaps = 20/268 (7%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAG-FAALHAAWLQHALLIFPGQ-HLSNDQQITFAK 62
TL+I P T+GA V LA + ++G + A L++ +L F Q LS + QI F K
Sbjct: 3 TLEIRPLSGTIGAQVRNRTLAVGVESGRVDEIRQALLRYKVLFFTNQPDLSVETQIAFGK 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E K DG Q +D + ++ WH D + +
Sbjct: 63 LFGELE-----TNFPSFTAKPDG---QPEVTVFDGAVSTGRASI-WHTDLSIAKTPSAMG 113

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ--SKLGHVQQAGS 180
+ + PA GG T +AD+ AAY AL +A + + A H ++ Q + G Q G
Sbjct: 114 ILCVKETPASGGDTMWADLEAAYAALSPGMQAFLEGQRAVHDMMPQYARPGAFQTQGR 173

Query: 181 AYIGYGMDDTTAT--PLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWA 237
+ MD + P+V+VHPETGR L + + I G +AES L L
Sbjct: 174 S----DMDLSEVFGEHPVVRVHPETGRKCLFVNPFLTSHITGFHSAESATILNYLYALM 229

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ V W+ GDV +WDNRC +H A
Sbjct: 230 ERPQYVVRWHWSNGDVALWDNRCTMHTA 257

>ref|XP_002152412.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase, putative [Penicillium marneffei ATCC 18224]
gb|EEA19475.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase, putative [Penicillium marneffei ATCC 18224]
Length = 336

Score = 97.8 bits (242), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 77/284 (27%), Positives = 128/284 (45%), Gaps = 23/284 (8%)

Query: 6 LQITPT-GATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
L + P + GA V+G++ L DA L ++A++IF +L ND+ + F++
Sbjct: 9 LTVAPILNNSFGAEVSGINWDQVPLPDATIKTLITLQNKYAIIFRNTNLDNDRHVAFSQ 68

Query: 63 RFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST 113
+ GA+E R+ + +SN++ADG+V + W + GN WH DS
Sbjct: 69 QLGALELNPVWGNTTRVNNQYLFVDVSNLEADGSAKRGSRRAHSL----GNALWHTDSA 124

Query: 114 YMPVMAQGA VFSAEVVPVAVG-GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+ A+ ++ A VP G G+T FAD R A+ LDE + + H L +S+
Sbjct: 125 FNQHRAKYSLLLAHSVPGEKGKGTTFADTRRAWRELDEERKGELKDVVVEHELWHSRRLA 184

Query: 173 GHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAE---SERF 229
+ + G A LV+ P + + HA + D E S++
Sbjct: 185 APEEYSELTPPEERGKKPPA--YHRLVQRTPNGEEETFFLAHAHAKRLFSKDGEELDSQKK 242

Query: 230 LEGLVDWACQAPRVHAHQW-AAGDVVVWDNRCLLHRAEPWDFKL 272
+ L+ Q +W +AGD++ WDNR +HRA +D K+
Sbjct: 243 IWDLIAHCTQDKYTFVAEWKSAGDLMWWDNRQSMHRASAYDEKM 286

>ref|ZP_02363324.1| dioxygenase, TauD/TfdA [Burkholderia oklahomensis C6786]
Length = 292

Score = 97.8 bits (242), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 81/266 (30%), Positives = 122/266 (45%), Gaps = 16/266 (6%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAG-FAALHAAWLQHALLIFPGQ-HLSNDQQITFAK 62
TL+I P T+GA V LA + ++G + A L++ +L F Q LS + QI F K
Sbjct: 3 TLEIRPLSGTIGAQRNCTLAGVVESGRVDEIRQALLRYKVLFFTNQPDLSVETQIAFGK 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E D + + K DG Q +D + ++ WH D + +
Sbjct: 63 LFGELET----DFPSFT-AKPDG---QPEVTVF DGAVSTGRASI-WHTDLSIAKRPSAMG 113

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ--SKLGHVQQAGS 180
+ + P GG T +AD+ AAY AL +A + + A H ++ Q + G Q G
Sbjct: 114 ILCVKETPDSSGDTMWADLEAAYAALSPGMQAFLEGQRAVHDMMPQYAERPGAFQTQGR 173

Query: 181 AYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQ 239
+ + + P+V+VHPETGR L + + I G +AES L L +
Sbjct: 174 SDMD--LSNVFGAEHPVVRVHPETGRKCLFVNPFLTSHITGFHSAESAMILNHL YALMER 231

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
V W+ GDV +WDNRC +H A
Sbjct: 232 PQYVVRWHWSNGDVALWDNRCTMHTA 257

>ref|YP_001511156.1| taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EAN1pec]
gb|ABW16250.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EAN1pec]
Length = 277

Score = 97.8 bits (242), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 85/289 (29%), Positives = 130/289 (44%), Gaps = 23/289 (7%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQH-ALLIFPGQHLSNDQQIT 59
M TT +ITP T + + G L D G A A L+ +++F + ++ +
Sbjct: 1 MGTTRKITPNTGTGTEFSGLKGTQLV---DKGVADDALAALEETGVVVFSEADIDDES LVA 57

Query: 60 FAKRFGAIERI--GGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV 117
FA+ G + + G I I + D+ Q A + + WH D T V
Sbjct: 58 FARLLGNVLPLPMGSHKIKEIQRITRDAS--QSKLAAYRE-----ATFYWHIDGTTGEV 109

Query: 118 MAQGAVFSAEVVPA-VGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ--SKLGH 174
+ + +A + G T FA+ AAY+AL + +A + A HS SQ +
Sbjct: 110 PDKATLLTARRISGDPEGDTEFANTYAAEALSDEEKAQLEGVRALHSFTASQLVANPNP 169

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
+ +A+ D T +P+V GR SLL+G A + G+ A E L+ L+
Sbjct: 170 SPEERA--DRNPTREQPIVWTR-RNGRKSLLVGSTAGEVVGLPADEGRALLDRLL 223

Query: 235 DWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
DWA Q V H+W GD+V+WDN +LHRA P+ R+M + LAG
Sbjct: 224 DWATQPQFVLRHRWTQGDVLIWDNTGMLHRALPYGPSSSRMLMHRASLAG 272

>ref|YP_003594362.1| taurine dioxygenase [Caulobacter segnis ATCC 21756]
gb|ADG11744.1| Taurine dioxygenase [Caulobacter segnis ATCC 21756]
Length = 295

Score = 97.4 bits (241), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 78/272 (28%), Positives = 123/272 (45%), Gaps = 28/272 (10%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L +TP G LGA ++G+ L A L AA+ AA L++ ++ F Q +S + + F + F
Sbjct: 18 LTVTPAGTVLGAEISGIDLRAPLKPEIVAIRAALLRYKVFFRDQDISYEDHVRFGRYF 77

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPV 117
G +E G +I+ I ADG + +D++ ++ WH D T+
Sbjct: 78 GDLEGHPVTSHVPGFPEILHIE--AADGMKLR-----EDIVPIVRAANKWHTDVTFREA 129

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS KLGHVQQ 177
+ G V +P +GG T FAD A Y L + + +A H ++ QS V +
Sbjct: 130 PSMGGVLRMRQMPPLGGDTLFADTAAIYRDLPPKLKDQIADLTAEHDII--QSYGYRVDE 187

Query: 178 AGSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
A + A P + P+V+ HPETG L + + I G+ E++ L L+
Sbjct: 188 AKRQEL-----RAAYPPMVHPVVRTHPETGEKHLFVNKVFTTRILGLPEDEAKALLNELL 242

Query: 235 DWACQAPRVHAH-QWAAGDVVWDNRCLLHRA 265
D +AP +W +V WDNH H A
Sbjct: 243 D-RVKAPEYQVRFRWTPNAIVFWDNRATQHYA 273

>ref|YP_857443.1| taurine dioxygenase [Aeromonas hydrophila subsp. hydrophila ATCC 7966]
gb|ABK38038.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aeromonas hydrophila subsp. hydrophila ATCC 7966]
Length = 284

Score = 97.4 bits (241), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 80/277 (28%), Positives = 121/277 (43%), Gaps = 35/277 (12%)

Query: 4 TTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
+L ITP G +GA ++G+ LA LD+ FA L A L H +L F Q ++ QQ A
Sbjct: 3 NSLHITPLGPHIGAEISGISLAGPLDEGQFAQLQQALLTHQVLFVRDQIPITPRQQRALAN 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIV-----GNMAWHADST 113
RFG + V H+P + ++IV N WH D T
Sbjct: 63 RFGDLH-----IHPVYPHAP----EAEEIIVLDTHDDNPPDNDNWHDTVT 103

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS KLGL 173
++ A+ +A+ +P VGG T +A AA++ L + L+ A H +++S
Sbjct: 104 FIETPPALAILAAKQLPPVGGDTLWASGIAAFEGLSPLRQLLTGLEAEHD--FTKSFPA 161

Query: 174 HVQQAGSAYIGYGMDDTA--TPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERF 229
H A A + A PLR P+++ HP +GR +L + +P + A ESE
Sbjct: 162 HRHNASPAEYQRWQEAARHPPLRHPVIRTHPLSGRQALFVNEGFTTTLRLPDLPQAESEAL 221

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE 266
L L + +W D+ +WDNR H A
Sbjct: 222 LTFLFRHVTKPEYQVRWRWREHDIAIWDNRVTQHYAN 258

>gb|ADY81776.1| putative alkylsulfatase [Acinetobacter calcoaceticus PHEA-2]
Length = 302

Score = 97.4 bits (241), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 74/288 (25%), Positives = 118/288 (40%), Gaps = 28/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
+ + P +GA + GV L++ L+ + + L+H ++ F Q HL++ +Q FA+
Sbjct: 14 IDVIPLAGRIGAQINGVELSSNLNSEVLNQIRQSLEHKVIFFRNQEHLTDQEKEFAEL 73

Query: 64 FG-----AIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPV 117
G + G + + + DG WH D T++
Sbjct: 74 LGQPISHPTVPVAEGSTYIFELDSRHDGRAD-----VWHTDVTFVSN 115

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVYSQSKLGHV 175
+ ++ A P GG T +A+ AAYD L E + L +Q A H+ Y +
Sbjct: 116 YPKISILRAVTTPNRGGDTTWANTEAAYDELPEPLKLLANQLRAIHTNDFDYGGFRPSAS 175

Query: 176 QQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD 235
+ + T PLV+VHPETG+ +L++G+ G+ A ES + E D
Sbjct: 176 DEVVKRHQKIFASTVYEAHPLVRVHPETGKRTLILGQFFKRFVGLTAKESNKLFEIFQD 235

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ W GDV +WDNR H A R+M LAG
Sbjct: 236 RITKPENTIRWTWKDGDVAIWDNRATQHLAVNDYGNALRIMRRVTLAG 283

>ref|YP_001260806.1| taurine catabolism dioxygenase TauD/TfdA [Sphingomonas wittichii
RW1]
gb|ABQ66668.1| Taurine catabolism dioxygenase TauD/TfdA [Sphingomonas wittichii
RW1]
Length = 282

Score = 97.1 bits (240), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 79/269 (29%), Positives = 116/269 (43%), Gaps = 20/269 (7%)

Query: 9 TPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA- 66
TP +G+ V G+ L+ + + L A +++ PGQ + + + FA FG
Sbjct: 6 TPLAPAIGSVVEGLDLSDRMSEPTMRRLLALLFDRGVVVIPGQTIDDAAYVRFASFVFGTP 65

Query: 67 ----IERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGA 122
I D AI + D +PA D G + WH+DS+Y V
Sbjct: 66 LDFFIPEHRNADFPAAIRINNDPA----TPAAMRD-----GAVHWHSDSSYESVPGCVT 115

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ + P GG T FA AAY L EATRA + ARH L + G + +
Sbjct: 116 MLFGKEAPDQGGETHFASTSAAYADLPEATRARIIDGLVARHELGRAPWIEGETRPDPN-- 173

Query: 183 IGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPR 242
T P PLV VHP TGR + A+AI GMD AE+ + L + +
Sbjct: 174 --RPPRKTDAPSHPLVMVHPVTGRKGIFSGTAYAIIDGMDDAEATALIRELREHVAKPAY 231

Query: 243 VHAHQWAAGDVVVWDNRCLLHRAEPWDFK 271
+++ GD+V+WDN +H A P ++

Score = 97.1 bits (240), Expect = 3e-18, Method: Compositional matrix adjust.

Identities = 73/266 (27%), Positives = 110/266 (41%), Gaps = 24/266 (9%)

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Query: 2   AQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
          + TT +T G +GA + G+ L+ + D      + +A H + F GQ L ++ Q F
Sbjct: 20  SATTPTVTRLGKNIGAVIEGIDLSDGIDTDEVEFIRFIRALATHKAVGFRGQFLDDESQYAF 79

Query: 61  AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ 120
          R G              +A V + G              D + +      +WH D +++ + +
Sbjct: 80  TSRIGT-----PTLAHPTVHSTGL-----DRLVIEGAANSWHTDVSFVDRVPK 122

Query: 121  GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
          +V A +P GG T FA+ AAY+AL E R L      A HS Y +      +
Sbjct: 123  ISVLRAVTLPPYGGSTLFAANTVAAYNALPEPLRVLADSLWATHSNEYDYAN---SHDSNK 179

Query: 181  AYIGYGMTDTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
          Y + T P      P+V +HPETG SLL+G      G+ E      + D
Sbjct: 180  DKTEYHREFTRVPFETEHVPVHLHPETGERSLLLGHFVQGFGLGLKTREFHDLFDIFQDRI 239

Query: 238  CQAPRVHAHQWAAGDVVVWDNRCLLH 263
          + V + W GDVV+WDN H
Sbjct: 240  TRPDNVFSWDWQEGDVVLWDNHATQH 265

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>ref|ZP_05096186.1| Taurine catabolism dioxygenase TauD, TfdA family [marine gamma
proteobacterium HTCC2148]
gb|EEB77493.1| Taurine catabolism dioxygenase TauD, TfdA family [marine gamma
proteobacterium HTCC2148]
Length = 297

```

Score = 97.1 bits (240), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 87/271 (32%), Positives = 126/271 (46%), Gaps = 21/271 (7%)

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Query: 5   TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
          +++T +G + GA V GV L+ L      A + AWLQH +L FPGQ LS+D F
Sbjct: 20  NIEVTASGQSCGAEVRGVDLSRELAPTIVAQIREAWLQHQLVSFPGQSLSDDDLRLFTLC 79

Query: 64  FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGA 122
          FG      GD I+ + T R+H A D + +      WH+D ++ QG
Sbjct: 80  FGPF-----GDDPFIAPI----TGRKHIIAVQRDAGETTSLFAEQWHSDFSQARPPQGT 130

Query: 123  VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
          +P GG T FAD AA A+ ++ R + + A HS + S G + A A
Sbjct: 131  CLYGVTIPTGGDTLFAAQVAAAAAMPKSLRDKLEGKRAVHSAIMGYSPAGILGDADKA- 189

Query: 183  IGYGMTD-----TATPLRPLVKVHPETGRPSLL--IGRHAHAIPGMDAAESERFLEGLV 234
          G MD      AT ++ HPETGR S+L +G + I G++ E L L
Sbjct: 190  AGRSMDIRPSDAAATQSHLIIFSHPETGRDSILGTVG-YMIGIEGLEGEERALLTELY 248

Query: 235  DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          +W +      + H W G +++WDNR +LH A
Sbjct: 249  EWQTREEFRYRHHWEQGTLLMWDNRVLHSA 279

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>ref|YP_002417336.1| putative taurine catabolism dioxygenase [Vibrio splendidus LGP32]
emb|CAV18911.1| Probable taurine catabolism dioxygenase [Vibrio splendidus LGP32]
Length = 271

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Score = 97.1 bits (240), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 71/269 (26%), Positives = 121/269 (44%), Gaps = 25/269 (9%)

```

Query: 6   LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
          L+I      +GA + GV+LAT      ++ A + H ++ Q LS +Q + A+RFG
Sbjct: 2   LKIEQVTPHIGAQIHGVNLTATCSVTELDEVYQALITHQVIFLGDQVLSPEQHLMIAERFG 61

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Query: 66 AIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM 118
+E R+ V++ T R ++P E WH D T+ V
Sbjct: 62 KLEPAHPFFPRVESAPQVSVE-----TTRGNAPME-----SYWHTDLTWRKVP 105

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV-YSQSKLGHVQQ 177
++ ++ A+ +P+ GG T + M A +++LDE +A + SA HSLV + + ++
Sbjct: 106 SKASLLHAQHIPPSTGGDTIWCSMTAVFESLDEDMKAKLRGLSATHSLVAFEGVESDQIEL 165

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDW 236
+ + P+V+ HPETG+ +L I I +D +S+ L L +
Sbjct: 166 DWHSLLKTAQKNPPVIHPVVQSHPETGKETLYINEQFTRYINELDRQSDVLLYQLFEI 225

Query: 237 ACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
A + +W G + +WDNR H A
Sbjct: 226 ARRPEFQVRFKWDKGSMAIWDNRVTQHYA 254

>emb|CAY27324.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 96.7 bits (239), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 52/125 (41%), Positives = 73/125 (58%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRA YDALD+ T+ +V HS ++S++K+G + P+R
Sbjct: 1 TEFADMRA GYDALDDETKDIVEDLVCEHSQIFSRKMGFTDLTPEERERF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+VHP TGR SL + HA +I G E++ FL L + A Q V+AH+W+ GD+V
Sbjct: 55 QRLVRVHPVTGRKSLFLASHAGSILGWVPPEAQTFMLDLTEIATQRQFVYAHEWSVGDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|YP_605995.1| taurine dioxygenase [Pseudomonas entomophila L48]
emb|CAK13178.1| taurine dioxygenase, 2-oxoglutarate-dependent [Pseudomonas
entomophila L48]
Length = 277

Score = 96.7 bits (239), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 81/269 (30%), Positives = 123/269 (45%), Gaps = 23/269 (8%)

Query: 5 TLQITPTGATLGATVTGVHLA---TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
+L +TP LGA ++GV ++ T++ A+ A LQH +L F Q ++ +QQ FA
Sbjct: 2 SLTVTPLSPALGAQISGVDISREITVEQRD--AIEQALLQHQVLFRRDQPITPEQQARFA 59

Query: 62 KRFGAIERIGGGDIVAI-SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ 120
RFG + I I NV V D + + N WH D T++P A
Sbjct: 60 ARFGDLH-----IHPIYPNPVETPQV-----LILDTAVTDVRDNAVWHTDVTFPLTPAL 108

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQ 178
GAV SA+ +PA GG T +A AA++AL R ++ +A H + + G +
Sbjct: 109 GAVLSAKQLPAYGGDTLWASGIAAFEALSAPLREMLDGLTATHDFTKSFPLERFGTTPED 168

Query: 179 GSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
+ + + PL P+V+ HP +GR +L + I ++ ESE L+ L
Sbjct: 169 LARWEATRRNN--PPLSHPVVRTHPVSGRKALFVNEGFTTRINELNEQESEALLKLLFAH 226

Query: 237 ACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
A + +W DV WDNR H A

Sbjct: 227 ATRPEFSIRWRWQENDVAFWDNRVTQHFA 255

>ref|YP_905004.1| taurine catabolism dioxygenase, TauD [Mycobacterium ulcerans Agy99]
ref|YP_001849453.1| taurine catabolism dioxygenase, TauD [Mycobacterium marinum M]
gb|ABL03533.1| taurine catabolism dioxygenase, TauD [Mycobacterium ulcerans Agy99]
gb|ACC39598.1| taurine catabolism dioxygenase, TauD [Mycobacterium marinum M]
Length = 298

Score = 96.7 bits (239), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 80/265 (30%), Positives = 110/265 (41%), Gaps = 17/265 (6%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
+ + G+ +GA V GV L A LD A + AA L+H ++ F QH L + QQ+ FA
Sbjct: 5 ITVKKLGSRIGAQVDGVSLGADLDAAAVDQIRAALLEHKVIFFRNQHHLLDDQQQLQFAGL 64

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
G IG A + D + +EW + WH D T+ ++
Sbjct: 65 LGT--PIGH---PAAAAALPDAPIITPINSEWGKANR-----WHTDVTFAANYPAASI 112

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
A +P GG T +A+ AY L E + LV A H+ Y VQ
Sbjct: 113 LRAVTLPNYGGSTLWANTATAYAELPEPLKCLVENLWALHTNRYDYVANEAVQALTDTTQ 172

Query: 184 GYGMDDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
+ R P+V+VHPETG +LL G G+D+ ES E L
Sbjct: 173 AFRQAFQKPDFRTEHPVVRVHPETGERTLLAGDFVRGVGLDSQESSALFELLQRRITSP 232

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRA 265
W +GDV +WDNR HRA
Sbjct: 233 ENTIRWNWESGDVAIWDNRATQHRA 257

>ref|YP_003771048.1| taurine dioxygenase [Amycolatopsis mediterranei U32]
gb|ADJ50646.1| taurine dioxygenase [Amycolatopsis mediterranei U32]
Length = 306

Score = 96.7 bits (239), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 81/265 (30%), Positives = 112/265 (42%), Gaps = 24/265 (9%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGF-AALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ P G +GA V GV L A L+ A L+ +L F Q +++ QQ FA +
Sbjct: 39 FTLRPLRLIGAEVDGVDLGAPVGADLREELNHALLEWKVLFVRDQRITSAQQRAFAANW 98

Query: 65 GAIER---IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
G +E I GD A++ + + + WH D T+ P A G
Sbjct: 99 GELETNPFIPRGDDDAVTRFERTAAAMPGE-----NIWHTDVTWRPAPALG 144

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
+V VP VGG T +ADM AAYD L E RA + +A H + G + + A
Sbjct: 145 SVLRRLIEVPPVGGDTMWADMAAAYDNLPEDVRARIDGLTAVHDYL-----PGFDRFSDPA 199

Query: 182 YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQA 240
+ D P+V+ HPETGR +L + + I G+D ES+R L L A
Sbjct: 200 LLAQWQDRFPPEHPVVRTHPETGRRTLFVNQAFTHIAGLDRTESDRLRLRYLFLQAHTP 259

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRA 265
W V WDNR H A
Sbjct: 260 EFQVRFSWRPNSVAFWDNRATQHYA 284

>ref|YP_257415.1| taurine dioxygenase [Pseudomonas fluorescens Pf-5]
gb|AA95680.1| alpha-ketoglutarate-dependent taurine dioxygenase [Pseudomonas

fluorescens Pf-5]
 Length = 279

Score = 96.7 bits (239), Expect = 3e-18, Method: Compositional matrix adjust.
 Identities = 80/267 (29%), Positives = 120/267 (44%), Gaps = 19/267 (7%)

```
Query: 5   TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
          +L ITP + LGA + G+ ++ L      A+  A L+H +L F  Q ++  QQ  FA
Sbjct: 2   SLTITPLSSALGAQIGGIDISQPLSIEHRDAIEQALLKHQVLFFRNQPVTPQQQARFAAC 61

Query: 64  FGAIERIGGGDIVAI-SNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
          FG +      I  I  NV      V      AE D      +  N  WH D T++P  A GA
Sbjct: 62  FGD LH-----IHPIYPNVPEQPEVLILDTAETD-----VRDNAIWHTDVTF LPTPALGA 110

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQAGS 180
          V SA+++P  GG T +A  AAY+AL E  + L+  +A H      +  + G+  +  +
Sbjct: 111 VLSAKLLPEFGGDTLWASGIAAYEALSEPMKNLLQGLTATHDFTKSFPLERFGNTTEDLA 170

Query: 181 AYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
          +      PL  P+++ HP +GR SL +      I  +  +ES  L+ L  A
Sbjct: 171 RW--EETRRKNPPLSHPVIRTHPVSGRKS L FVNDGFTTRINELSESESAAILQLLFAHAT 228

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          +      +W  D+  WDNR  H A
Sbjct: 229 RPEFTIRWRWQENDIAFWDNRV TQHYA 255
```

>ref|ZP_06917085.1| taurine catabolism dioxygenase [Streptomyces sviveus ATCC 29083]
 gb|EDY57975.1| taurine catabolism dioxygenase [Streptomyces sviveus ATCC 29083]
 Length = 298

Score = 96.7 bits (239), Expect = 3e-18, Method: Compositional matrix adjust.
 Identities = 85/286 (29%), Positives = 120/286 (41%), Gaps = 25/286 (8%)

```
Query: 6   LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          ++I      A +GA V GV LA  LD+  AAL  A  H  L+F  HL ++ Q  FA+ F
Sbjct: 4   IEIRKVTANIGAQVFGVDLAEP LDEETAALRDALNTHKALVFS DVHLDDEGQQAFARHF 63

Query: 65  GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA---WHADSTYMPVMAQG 121
          G +      A  V A      P + +      G  A  WH D T++  Q
Sbjct: 64  GDL-----TTAHTVTPAVD GAPNVL PVDSE-----GGRAANHWHTDVTFVLNPPQA 109

Query: 122 AVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS----QSKLGHVQQ 177
          +  +  +P  GG T  A+  AAY  L E  R L      A H+  Y      +  L  Q
Sbjct: 110 STLRLSLTIPPYGGETLIANSAAAYRDLPEPLRRLADDLWAEHTNDYDYAVPEETLDEEQ 169

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
          A  A      +  P+V+VHP TG  L IG  A  I G+  ES + L+ L  +
Sbjct: 170 ARRAQF---TSIKYRTVHPVVRVHPLTGERGLF IGGAQRIVGLSTGESRKL LLDLQSYV 226

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          +  +  H+W+  +V++DNR  H A      LPR +  +AG
Sbjct: 227 TRPENLLRHRWSENQLVLF DN RITQHYAVDNYDGLPRRLHRVT VAG 272
```

>ref|XP_003195730.1| 2,4-dichlorophenoxyacetate alpha-ketoglutarate dioxygenase
 [Cryptococcus gattii WM276]
 gb|ADV23943.1| 2,4-dichlorophenoxyacetate alpha-ketoglutarate dioxygenase,
 putative [Cryptococcus gattii WM276]
 Length = 312

Score = 96.7 bits (239), Expect = 4e-18, Method: Compositional matrix adjust.
 Identities = 74/288 (25%), Positives = 128/288 (44%), Gaps = 32/288 (11%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
T+ TP T A +GV + + ++ +L+F L++ + ++ F
Sbjct: 2 TINYTPLHPTFVAEASGVDFNNITPEVVEEIKEGMAYGVLFVRKTGLNDKNHVMESRLF 61

Query: 65 GA-----IERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIV--GNMAWHA 110
G I R+ ++ +SNV +G + Q + + I+ GN +H
Sbjct: 62 GELDDVKPYNALGRINRLAYDELFDVSNVDPEGNIFQPT-----GQRAIINRGNTVDFHC 115

Query: 111 DSTYMPVMAQGAVFSAEVP--AVGGRTCFADMRAAYDALDEATRALVHQRSARH-SLVY 167
DS++ P A ++ A +P GG T FAD R AY+ L E H+R+ + L +
Sbjct: 116 DSSFNPRRAGYSLLLAHELPPAGTGGNTEFADTRTAYNDLPEE-----HKRAIKDWVLWH 170

Query: 168 SQSKLGHVQQAGSAYIG-YGMDTTATPL--RPLVKVHPETGRPSLLIGRHAHAIPGMDAA 224
SQ V G + T+ P LV++H +GR +L I HA+ + +
Sbjct: 171 SQHHSRRVANPGEPLDQKKFLPTSHPFQKHKLQVQIHEPSGRNTLYIANHAYKVESLPLE 230

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAA-GDVVVWDNRCLLHRAEPWDFK 271
+ + ++ L+D V + +W GD+V+WDN C++HRA P F+
Sbjct: 231 QGQAEIKALLDHCSSPNYVCSVEWKNNGDLVIWDNTCVMHRAVPGAFE 278

>ref|ZP_08138776.1| taurine dioxygenase [Pseudomonas sp. TJI-51]
gb|EGB99951.1| taurine dioxygenase [Pseudomonas sp. TJI-51]
Length = 277

Score = 96.7 bits (239), Expect = 4e-18, Method: Compositional matrix adjust.
Identities = 82/267 (30%), Positives = 121/267 (45%), Gaps = 19/267 (7%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+L ITP LGA ++GV ++ + A A+ A LQH +L F Q ++ +QQ FA R
Sbjct: 2 SLTITPLSPALGAQISGVDISRDITAAQRDAIEQALLQHQLVFFRDQPINPEQQARFAAR 61

Query: 64 FGAIERIGGGDIVAI-SNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG + I I NV V D + + N WH D T++P A GA
Sbjct: 62 FGDH-----IHPIYPNPVDPDPQV-----LVLDTAVTVDVRDNAVWHTDVTFLPTPALGA 110

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQAGS 180
V SA+ +PA GG T +A AA++AL R ++ +A H + + G + +
Sbjct: 111 VLSAKQLPAYGGDTLWASGIAAFEALSAPLRGMLDGLTATHDFTKSFPLERFGTTAEDLA 170

Query: 181 AYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
+ + PL P+V+ HP +GR +L + I + ESE L+ L A
Sbjct: 171 RWEATRRNN--PPLSHPVVRTHPVSGRKALFVNEGFTTRINELSELESEALLKLLFAHAT 228

Query: 239 QAPRVHAHQWAAAGDVVVWDNRCLLHRA 265
+ +W DV WDN H A
Sbjct: 229 RPEFSIRWRWQEHDFWFDNRVTQHFA 255

>ref|YP_003732176.1| putative alkylsulfatase [Acinetobacter sp. DR1]
gb|ADI90803.1| putative alkylsulfatase [Acinetobacter sp. DR1]
Length = 302

Score = 96.7 bits (239), Expect = 4e-18, Method: Compositional matrix adjust.
Identities = 74/288 (25%), Positives = 118/288 (40%), Gaps = 28/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
+ + P +GA + GV L++ L+ + + L+H ++ F Q HL++ +Q FA+
Sbjct: 14 IDVIPLAGRIGAQINGVELSSNLNPEVLNQIRQSLLEHKVIFFRNQEHLDQEQEKFAEL 73

Query: 64 FG-----AIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPV 117
G + G + + + DG WH D T++

Sbjct: 74 LGQPISHPTVPVAEGSTYIFELDSRHDGRAD-----VWHTDVTTFVSN 115

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVYSQSKLGHV 175
+ ++ A P GG T +A+ AAYD L E + L +Q A H+ Y +

Sbjct: 116 YPKISILRAVTTTPNRGGDTTWANTEAAYDELPEPLKLLANQLRAIHTNDFDYGGFRPSAS 175

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD 235
+ + T PLV+VHPETG+ +L++G+ G+ A ES + E D

Sbjct: 176 DEVVKRHQKIFASTVYEAHPLVRVHPETGKRTLILGQFFKRFVGLTAKESNKLFEIFQD 235

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ W GDV +WDNR H A R+M LAG

Sbjct: 236 RITKPENTIRWTWKDGDVAIWDNRATQHLAVNDYGNALRIMRRVTLAG 283

>ref|ZP_03270351.1| Taurine dioxygenase [Burkholderia sp. H160]
gb|EDZ98062.1| Taurine dioxygenase [Burkholderia sp. H160]
Length = 315

Score = 96.3 bits (238), Expect = 4e-18, Method: Compositional matrix adjust.
Identities = 78/288 (27%), Positives = 127/288 (44%), Gaps = 16/288 (5%)

Query: 3 QTTLQITPTGATLGATVTGVHLA--TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
+ L+I+P A +GA ++GV+L LD A+ AA L+ ++ F Q LS++Q + F+

Sbjct: 9 EAELRISPLSAHIGAEISGVYLTRPLDQKQIQAIRAALLKWRVVFREQLSHEQHVAFS 68

Query: 62 KRFGAIERIG---GGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVM 118
+FG + +G G + + + +R+ + E +++ G WH D T

Sbjct: 69 AQFGELT-VGHPVFGHVEGHPQIYSISKLRRAFRFEGPPLLRPWTG---WHTDVTAAVNP 124

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
++ +P GG T + ++ AY+ L E R V H Q G

Sbjct: 125 PFASILRGVTIPPYGGDTQWTNLVIAYEKLSEPLRKFDGLRGVHRFAPPQGAAG----- 179

Query: 179 GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
A++ T PLV+VHPETG +L + I G+ ES+ LE L +

Sbjct: 180 TEAFVAAVEQHTLVSEHPLVRVHPETGERALYVSPGFLKQIVGVTPRESQLLELLWEHV 239

Query: 238 CQAPRVHAHQWAAGDVVVDNRCLLHRA--EPWDFKLPRVMWHSRLAG 283
+ +W AG V WDNR H A + +D R ++ + L G

Sbjct: 240 TRPEFTVFRWEAGSVAFWDNRRTAHLAPTDFDLDFDRQLYRTTLVG 287

>gb|EGD02376.1| Taurine catabolism dioxygenase TauD/TfdA [Burkholderia sp. TJI49]
Length = 282

Score = 96.3 bits (238), Expect = 4e-18, Method: Compositional matrix adjust.
Identities = 83/275 (30%), Positives = 124/275 (45%), Gaps = 30/275 (10%)

Query: 6 LQITPTGATLGATVTGVHLA--TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++I P +GA +TGV+LA DDA FA + AA L+H ++ Q ++ + FA+R

Sbjct: 1 MRIEPLTCAIGAEITGVNLADAARDALFAEIRAALLKHKVVFLRNQDIARADHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E V + + G VR + SP +D + WHAD+T+ + GA

Sbjct: 61 FGELE----DHPVVGCDPENPLVRIYKSPDAPNDHYE-----NGWHADATWREIPQMG 111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAQAGSAY 182
V P VGG T +A+M AY+ L + L+ ARHS+ ++ G V

Sbjct: 112 VLRCVECPVGGDTMWANMVLAYEKLPRHVKDLIAPLARHSI---EATFGAVMPIDKRL 168

Query: 183 IGYGMDDTTATPLRPLVKVHPETGRPSLLI-GRHAHA-----PGMDAAESERFLEG---LV 234
A P+V+ HPETG L + G H PG + + F G L+

Sbjct: 169 ALKARFPDAE--HPVVRTHPETGEKVLFCVGFTHFTNYHNPG-NVRVGQDFTRGASDLL 225

Query: 235 DWACQAPRVHAHQ----WAAGDVVVWDNRCLLHRA 265

+ + +Q W GD+ +WDNR H A

Sbjct: 226 QYLISQAAIPEYQVRWRWRQGDIAIWDNRATQHYA 260

>pdb|10IJ|C Chain C, Crystal Structure Of The Alkylsulfatase Atsk, A Non-Heme
Fe (Ii) Alphaketoglutarate Dependent Dioxygenase In
Complex With Alphaketoglutarate
Length = 301

Score = 96.3 bits (238), Expect = 4e-18, Method: Compositional matrix adjust.
Identities = 81/290 (27%), Positives = 125/290 (43%), Gaps = 32/290 (11%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63

L + P +GA + GV L+ LD A A+ AA ++H ++ F GQ HL + Q FAK

Sbjct: 15 LDVHPVAGRIGAEIRGVKLSFDLDAATVEAIQAALVRHKVIFFRGQTHLDDQSQEGFAKL 74

Query: 64 FGAIERIGGGDIVAISN----VKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119

G E + + + ++ DG Q + +WH D T++

Sbjct: 75 LG--EPVAHPTVPVVDGTRYLLQLDGAQGQRA-----NSWHTDVTTFVEAYP 118

Query: 120 QGAVFSAEYVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----G 173

+ ++ + V PA GG T +A+ AAY L E R L + A HS Y + L

Sbjct: 119 KASILRSVVAPASGGDTVWANTAAAYQELPEPLRELADKLWAVHSNEYDYASLKPDIIDPA 178

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233

+++ + +T P+V+VHP +G +L +G I G A+S+ L

Sbjct: 179 KLERHRKVFTSTVYETE----HPVVRVHPISGERALQLGHFVKRIKGYSLADSQHLFAVL 234

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ +W AGDV +WDNR H A PR++ LAG

Sbjct: 235 QGHVTRLENTVRWRWEAGDVAIWDNRATQHYAVDDYGTQPRIVRRVTLAG 284

>pdb|10IH|A Chain A, Crystal Structure Of The Alkylsulfatase Atsk, A Non-Heme
Fe(Ii) Alphaketoglutarate Dependent Dioxygenase

pdb|10IH|B Chain B, Crystal Structure Of The Alkylsulfatase Atsk, A Non-Heme
Fe(Ii) Alphaketoglutarate Dependent Dioxygenase

pdb|10IH|C Chain C, Crystal Structure Of The Alkylsulfatase Atsk, A Non-Heme
Fe(Ii) Alphaketoglutarate Dependent Dioxygenase

pdb|10IH|D Chain D, Crystal Structure Of The Alkylsulfatase Atsk, A Non-Heme
Fe(Ii) Alphaketoglutarate Dependent Dioxygenase

pdb|10II|A Chain A, Crystal Structure Of The Alkylsulfatase Atsk, A Non-Heme
Fe(Ii) Alphaketoglutarate Dependent Dioxygenase In
Complex With Iron And Alphaketoglutarate

pdb|10II|B Chain B, Crystal Structure Of The Alkylsulfatase Atsk, A Non-Heme
Fe(Ii) Alphaketoglutarate Dependent Dioxygenase In
Complex With Iron And Alphaketoglutarate

pdb|10II|C Chain C, Crystal Structure Of The Alkylsulfatase Atsk, A Non-Heme
Fe(Ii) Alphaketoglutarate Dependent Dioxygenase In
Complex With Iron And Alphaketoglutarate

pdb|10II|D Chain D, Crystal Structure Of The Alkylsulfatase Atsk, A Non-Heme
Fe(Ii) Alphaketoglutarate Dependent Dioxygenase In
Complex With Iron And Alphaketoglutarate

pdb|10IJ|B Chain B, Crystal Structure Of The Alkylsulfatase Atsk, A Non-Heme
Fe (Ii) Alphaketoglutarate Dependent Dioxygenase In
Complex With Alphaketoglutarate

pdb|10IJ|D Chain D, Crystal Structure Of The Alkylsulfatase Atsk, A Non-Heme
Fe (Ii) Alphaketoglutarate Dependent Dioxygenase In
Complex With Alphaketoglutarate

pdb|1VZ4|A Chain A, Fe-Succinate Complex Of Atsk

pdb|1VZ4|D Chain D, Fe-Succinate Complex Of Atsk
pdb|1VZ5|A Chain A, Succinate Complex Of Atsk
pdb|1VZ5|B Chain B, Succinate Complex Of Atsk
pdb|1VZ5|C Chain C, Succinate Complex Of Atsk
pdb|1VZ5|D Chain D, Succinate Complex Of Atsk
gb|AAD31784.1|AF126201_2 putative alkylsulfatase [*Pseudomonas putida*]
Length = 301

Score = 96.3 bits (238), Expect = 4e-18, Method: Compositional matrix adjust.
Identities = 81/290 (27%), Positives = 125/290 (43%), Gaps = 32/290 (11%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L + P +GA + GV L+ LD A A+ AA ++H ++ F GQ HL + Q FAK
Sbjct: 15 LDVHPVAGRIGAEIRGVKLSPLDLAATVEAIQAALVRHKVIFFRGQTHLDDQSQEGFAKL 74

Query: 64 FGAIERIGGGDIVAISN----VKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
G E + + + ++ DG Q + +WH D T++
Sbjct: 75 LG--EPVAHPTVPVVDGTRYLLQLDGAQGQRA-----NSWHTDVTFVEAYP 118

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----G 173
+ ++ + V PA GG T +A+ AAY L E R L + A HS Y + L
Sbjct: 119 KASILRSVVAPASGGDTVWANTAAAYQELPEPLRELADKLWAVHSNEYDYASLKPDIIDPA 178

Query: 174 HVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
+++ + +T P+V+VHP +G +L +G I G A+S+ L
Sbjct: 179 KLERHRKVFTSTVYETE----HPVVRVHPISGERALQLGHFVKRIKGYSLADSQHLFAVL 234

Query: 234 VDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPVMMWHSRLAG 283
+ +W AGDV +WDNR H A PR++ LAG
Sbjct: 235 QGHVTRLENTVRWRWEAGDVAIWDNRATQHYAVDDYGTQPRIVRRVTLAG 284

>ref|YP_619823.1| putative alpha-ketoglutarate-dependent taurine dioxygenase [Plasmid QKH54]
emb|CAJ43305.1| putative alpha-ketoglutarate-dependent taurine dioxygenase [Plasmid QKH54]
Length = 298

Score = 96.3 bits (238), Expect = 4e-18, Method: Compositional matrix adjust.
Identities = 76/262 (29%), Positives = 109/262 (41%), Gaps = 12/262 (4%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
+++TPT +GA V + L L D GFA L A L H ++ DQ ++ A
Sbjct: 20 IRVTPPTTGAIGADVENLDLTRLSDGEFAELRQALLAHKVIFI-----RDQALSVDLER 73

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
+ +G AD H E + + G AWH D T+ +
Sbjct: 74 VTQHLGEFGREPYVTCMADHPHVHVKEASEKAPFVFGG-AWHTDWTQERPPAFTLLY 132

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVYSQSKLGHVQQAGSAYI 183
+P GG TC+A++ AY+ L +AL+ A HS + Y + H + I
Sbjct: 133 GHDIPPYGGDTCYANLALAYEWLSPGMQALLENLDAVHSPMAYGVNA-KHNALLENMAI 191

Query: 184 GYGMDTTATPL-RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAP 241
YG DT+A PLV HPETG+ L I + I G+ ES L+ L A
Sbjct: 192 NYGSDTSADERSHPLVTRHPETGKKVLFINPAYTTGIKGLRTEESRPLLDYLFKLATSEA 251

Query: 242 RVHAHQWAAGDVVVDNRCLLH 263
+W G + +WDNR H
Sbjct: 252 FTCRMRWRQGTLAIWDRNSTWH 273

>ref|ZP_06834222.1| taurine dioxygenase [*Gluconacetobacter hansenii* ATCC 23769]

gb|EFG84595.1| taurine dioxygenase [Gluconacetobacter hansenii ATCC 23769]
Length = 317

Score = 96.3 bits (238), Expect = 4e-18, Method: Compositional matrix adjust.
Identities = 73/271 (26%), Positives = 118/271 (43%), Gaps = 18/271 (6%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ PTG +GA V G+ L LD A A L A LQH +L F Q +++ +Q+ F++ F
Sbjct: 7 FTVIPTGPVIGAEVLGIDLKNPLDTATIAGLRQALLQHKVLFRRNPITDAEQVRFSSRYF 66

Query: 65 G-----AIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVG-----NMAWHADSTY 114
G I+ G + N+K+ +R++ ++ + G + WH D T+
Sbjct: 67 GQVTPAHPIKNGLVGQPEVMENIKSLKALRENILSDVEQQQLRANGRHFRSRGWHTDITF 126

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
+ + +P GG T + D+ A Y++L + R + SA H ++
Sbjct: 127 VANPTSISFLRGIEIPEFGGDTAWVDLEALYNSLSDTLRGFLDGLSAVHGRDDARIGFPL 186

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL 233
+ Y G + PLV++HPETGR SL + IP + ES+ L L
Sbjct: 187 PPRRDGRYNGAFLAE-----HPLVRIHPETGRSSLFLSPGFIRYIPALRQGESDTLLSFL 241

Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLH 263
++ + A W + VWDNR H
Sbjct: 242 IEELAGRIDLQARFHWTPHSLAVWDNRATAH 272

>pdb|10IJ|A Chain A, Crystal Structure Of The Alkylsulfatase Atsk, A Non-Heme
Fe (Ii) Alphaketoglutarate Dependent Dioxygenase In
Complex With Alphaketoglutarate
pdb|10IK|A Chain A, Crystal Structure Of The Alkylsulfatase Atsk, A Non-Heme
Fe (Ii) Alphaketoglutarate Dependent Dioxygenase In
Complex With Fe, Alphaketoglutarate And
2-Ethyl-1-Hexanesulfuric Acid
pdb|10IK|D Chain D, Crystal Structure Of The Alkylsulfatase Atsk, A Non-Heme
Fe (Ii) Alphaketoglutarate Dependent Dioxygenase In
Complex With Fe, Alphaketoglutarate And
2-Ethyl-1-Hexanesulfuric Acid
Length = 301

Score = 96.3 bits (238), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 81/290 (27%), Positives = 125/290 (43%), Gaps = 32/290 (11%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L + P +GA + GV L+ LD A A+ AA ++H ++ F GQ HL + Q FAK
Sbjct: 15 LDVHPVAGRIGAEIRGVKLSPLDLAATVEAIQAALVRHKVIFFRGQTHLDDQSQEGFAKL 74

Query: 64 FGAIERIGGGDIVAISN-----VKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
G E + + + ++ DG Q + +WH D T++
Sbjct: 75 LG--EPVAHPTVPVVDGTRYLLQLDGAQQQRA-----NSWHTDVTTFVEAYP 118

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----G 173
+ ++ + V PA GG T +A+ AAY L E R L + A HS Y + L
Sbjct: 119 KASILRSVAPASGGDTVWANTAAAYQELPEPLRELADKLWAVHSNRYDYASLKPDDIPA 178

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHHAHAIPGMDAAESERFLEGL 233
+++ + +T P+V+VHP +G +L +G I G A+S+ L
Sbjct: 179 KLERHRKVFTSTVYETE-----HPVVRVHPISGERALQLGHFVKRIKGYSLADSQHLFAVL 234

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAG 283
+ +W AGDV +WDNR H A PR++ LAG
Sbjct: 235 QGHVTRLENTVRWRWEAGDVAIWDNRATQHYAVDDYGTQPRIVRRVTLAG 284

>ref|ZP_07283312.1| dioxygenase [Streptomyces sp. AA4]
gb|EFL11681.1| dioxygenase [Streptomyces sp. AA4]
Length = 308

Score = 96.3 bits (238), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 82/263 (31%), Positives = 113/263 (42%), Gaps = 24/263 (9%)

Query: 8 ITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
+ P G +GA ++GV L A + A L+ A L+ +L F QH+++ QQ FA +G
Sbjct: 43 LRPLGRVIGAEISGVDLGAPVSPRLRAELNRALLEWKVLFVRDQHITSQQQRAFAANWGE 102

Query: 67 IER---IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
+E I GD +D VR A + WH D T+ P A G+V
Sbjct: 103 LETNPFIPRGD-----SDEVVRFTRTAGMPGYENI-----WHTDVTWRPNPALGSV 148

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
VP +GG T +ADM AAYD L R + +A H V G + +
Sbjct: 149 LRLVEVPPIGGDTMWADMAAAYDNLPAVVRERIDGLTAVHDFV-----PGFDRFTDPDLL 203

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPR 242
D P+V+ HPETGR +L + + I G+D ES+R L L A
Sbjct: 204 AQWQDAYPPVEHPVVRTHPETGRRTLFFVNQAFTHIVGLDRGESDRLRLRYLFLQAHTPEF 263

Query: 243 VHAHQWAAGDVVVWDNRCLLHRA 265
+W V WDNR H A
Sbjct: 264 QVRFRWEPDSVAFWDNRATQHYA 286

>ref|YP_001505977.1| taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EAN1pec]
gb|ABW11071.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EAN1pec]
Length = 277

Score = 95.9 bits (237), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 86/292 (29%), Positives = 128/292 (43%), Gaps = 29/292 (9%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQ-HALLIFPGQHLSNDQQIT 59
MA T +I+P +G + G+ L D AA L+ H ++++ H+ +D +
Sbjct: 1 MAVTVTEISPE---VGVEIAGLAGHQLADPAVAADCQVLLERHGVVVYRETHVGDDDLVA 57

Query: 60 FAKRFG--AIERIGGGDI-VAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
F++ G + +GG D IS + D PAE + G WH D
Sbjct: 58 FSRLLGQVVAPVGGTDTHPEISKITLD-----PAE-SVLAAYRRGTFFFWHIDGANDE 109

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ + + +A V GG T FA+ AAY+AL +A + + HS SQS
Sbjct: 110 LPQKATLLTAHQVSDEGGDTEFANTYAAEALSDAEKEQFAKL RVVHSFAASQSL----- 164

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHP-----ETGRPSLLIGRHAHAIPGMDAAESERFLE 231
A T A R + HP +GR SLL+G + G A ES L+
Sbjct: 165 ----AEPDASERTRALWARVPAREHPLVWTRRSGRSSLLVGATTDHVVGWPADESRLALD 220

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L++W+ Q V H W GD+V+WDN +LHRA P+ R+M + L G
Sbjct: 221 RLLEWSTQPRFVLRHHWHRGDLVIWDNTGMLHRAIPYTATSRRLMHRRTTLVG 272

>ref|YP_003114519.1| Taurine dioxygenase [Catenulispora acidiphila DSM 44928]
gb|ACU72678.1| Taurine dioxygenase [Catenulispora acidiphila DSM 44928]
Length = 315

Score = 95.9 bits (237), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 75/276 (27%), Positives = 121/276 (43%), Gaps = 20/276 (7%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
M + L I+ +GA ++G+ LA L++ AA+ AA L+H ++ F Q L + QI
Sbjct: 1 MPENQLTISRVRIGRIGAEISGIDLAEPLEEHTVAAIRAALLEHKVVFFRAQLRDHGSQIA 60

Query: 60 FAKRFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMA-WHADS 112
FA++FG + E I + D +++ + K + WH D
Sbjct: 61 FARQFGELTHAHPHEDAPPEQFPQILTIDPDYRQKYGEDFRQEYRKRQYSYFSGWHTDV 120

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-VYSQSK 171
T G++ AE VP GG T + ++ AAY+ L + L A H + ++ +
Sbjct: 121 TAAVNPPAGSILRAEAVPEFGGDTQWTNLAAAYEGLSAPLQRLAESLRAVHRFRIPAE 180

Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERF 229
++ + + P+V+VHPETG L + G H + G+ A ES R
Sbjct: 181 SKRAERVNANLL-----IAEHPVVRVHPETGERVLFVNPGFTDHIV-GLSAVESRRV 231

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L+ + + +W AGDV WDNR H A
Sbjct: 232 LDLFYEHLTRPEYTVRFRWRAGDVAFWDNRATAHLA 267

>ref|YP_046264.1| putative alkylsulfatase [Acinetobacter sp. ADP1]
emb|CAG68442.1| putative alkylsulfatase [Acinetobacter sp. ADP1]
Length = 302

Score = 95.9 bits (237), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 74/288 (25%), Positives = 118/288 (40%), Gaps = 28/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
+ + P +GA + GV L++ L+ + + L+H ++ F Q HL++ +Q FA+
Sbjct: 14 IDVIPLAGRIGAQINGVELSSHLNPEVLNQIRQSLLEHKVIFFRNQEHLTDQEKEKFAEL 73

Query: 64 FG-----AIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPV 117
G + G + + + DG WH D T++
Sbjct: 74 LGQPISHPTVPVAEGSTYIFELDSRHDGRAD-----VWHTDVTTFVSN 115

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVYSQSKLGHV 175
+ ++ A P GG T +A+ AAYD L E + L +Q A H+ Y +
Sbjct: 116 YPKISILRAVTTPHRGDDTTWANTEAAYDELPEPLKLLANQLRAIHTNDFDYGGFRPSAS 175

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD 235
+ + T PLV+VHPETG+ +L++G+ G+ A ES + E D
Sbjct: 176 DEVVVKRHQKIFASTVYEAHPLVRVHPETGKRTLILGQFFKRFVGLTAKESNKLFEIFQD 235

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ W GDV +WDNR H A R+M LAG
Sbjct: 236 RITKPENTIRWTWKDGDVAIWDNRATQHLAVNDYGNALRIMRRVTLAG 283

>ref|ZP_02468961.1| dioxygenase TauD/TfdA family protein [Burkholderia thailandensis
MSMB43]
Length = 281

Score = 95.9 bits (237), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 73/262 (27%), Positives = 114/262 (43%), Gaps = 21/262 (8%)

Query: 15 LGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
LGA + G+ + L + +H LL+FPGQ LS +QQI FG +E
Sbjct: 10 LGAEIRGIDFSKPLSSQARDDVIGLLSEHQLLVFPGQRLSCEQQIAACGAFGELEPHPM 69

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
++ +SNV +DG + ++ WH+D Y+ A+ F A

Sbjct: 70 TNTSSFPEMTIVSNVTSDGKPVGYTPPPFE-----LWHS DLCYLEHPAKMTFFYA 119

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG 186
E VP G T FA+M AY+ L + +A + + A SL S + ++ G

Sbjct: 120 ESVPDAHGDWTFANMFRAYETLPDELKAAIDGKRAVFSL--DSSLVKRCRKIGFDLNIAE 177

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
D T P V+ HP T + S+ + H I G ES+ L+ + ++

Sbjct: 178 DDFKPTVSHPAVRTHPHTRQRSIFVNWAHTDRIEGYSPEESDEILDRIFAHCRNEDFIYR 237

Query: 246 HQWAAGDVVVWDNRCLLHRAEP 267
H++A D+V+WDN L+H P

Sbjct: 238 HRYANEDLVIWDNASLIHTNSP 259

>ref|YP_759632.1| TauD/TfdA family dioxygenase [Hyphomonas neptunium ATCC 15444]
gb|ABI75797.1| dioxygenase, TauD/TfdA family [Hyphomonas neptunium ATCC 15444]
Length = 279

Score = 95.9 bits (237), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 88/299 (29%), Positives = 115/299 (38%), Gaps = 33/299 (11%)

Query: 6 LQITP-TGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+QITP TGA GA +TGV + L F A+ A+ H ++ F Q LS + I FA+RF

Sbjct: 1 MQITPLTGA--GAEITGVDIRALTAPQFDAVRQAYADHGVIFFRDQSLSEEDHIAFARRF 58

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSP---AEWDDMMKVIVGNMAWHADSTYMPVMAQ 120
G I N+ + P + K +G WH D +Y A

Sbjct: 59 GPI-----NINRFFLAHERYPEIALVLKEKEQKTNIGG-GWHTDHSYDAEPAM 105

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ----RSARHSLVYSQSKLGHVQ 176
G+V A +P GG T FA M AYD LD TR + SA+H

Sbjct: 106 GSVLVARQLPDEGGDTWFASMYTAYDTLADTRNEIDSLRAVHSAKHIFGSQTDNFYKAN 165

Query: 177 QAGSAYIGY--GMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGL 233
+ IG D P+V HP +G+ +L + I G S L L

Sbjct: 166 EDTGGRIGNTAAADVLEDVAHPVVITHPLSGKKALYVNPFAFTTRIAGYSDEASSALLMRL 225

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL 292
A H +W G V WDNR W + + RL R EG AL

Sbjct: 226 YAHAMNPDHAHRFKWQPGSVAFWDNRAT-----WHWAMNDYHGERRLMHRITIEGCAL 278

>ref|YP_458641.1| alpha-ketoglutarate-dependent taurine dioxygenase [Erythrobacter
litoralis HTCC2594]
gb|ABC63844.1| alpha-ketoglutarate-dependent taurine dioxygenase [Erythrobacter
litoralis HTCC2594]
Length = 270

Score = 95.9 bits (237), Expect = 6e-18, Method: Compositional matrix adjust.
Identities = 77/251 (30%), Positives = 103/251 (41%), Gaps = 10/251 (3%)

Query: 16 GATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDI 75
G V+GV LA+ DA + + +H + +F Q S + I F KR+G I DI

Sbjct: 6 GVEVSGVQLASCTDAEMEDIKQSIYEHGVAVFRDQEFSDQEDHIRFGKRWGGI-----DI 59

Query: 76 VAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGGR 135
+ D E D+ + AWH D +Y + A G+V A +P GG

Sbjct: 60 NNYFPLDDDYGEIAIVKKEADESTNI---GGAWHTDHSYDQIPAMGSVLVARDLPPSGGD 116

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T +A M AAYDAL + +A + A H+ + G Q G D +

Sbjct: 117 TEWAHMGAAAYDALPDDLKAEIEGLEAFHTADHVYKTDGLYAQTDMGKNLRGQDLKTGAHV 176

Query: 196 PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
P+V HP TGR L + I G ES LE L A QW G V
Sbjct: 177 PVVIRHPHTGRKLLYVNSAFTINIVGKTREESLPLEKLYAAALTGDNQRLQWKPGTVA 236

Query: 255 VWDNRCLLHRA 265
+WDNR H A
Sbjct: 237 IWDNRRTWHNA 247

>ref|YP_001666503.1| taurine dioxygenase [Pseudomonas putida GB-1]
gb|ABY96167.1| Taurine dioxygenase [Pseudomonas putida GB-1]
Length = 277

Score = 95.9 bits (237), Expect = 6e-18, Method: Compositional matrix adjust.
Identities = 80/267 (29%), Positives = 119/267 (44%), Gaps = 19/267 (7%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+L ITP LGA ++GV ++ + A+ A LQH +L F Q ++ +QQ FA R
Sbjct: 2 SLTITPLSPALGAQISGVDISRDISAQARDAIEQALLQHQLVFFRNQPINPEQQARFAAR 61

Query: 64 FGAIERIGGGDIVAI-SNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG + I I NV V D + + N WH D T++P A GA
Sbjct: 62 FGD LH-----IHPIYPNV PETPQV-----LVLD TAVTDVRDNAVWHTDVTFLPTPALGA 110

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQAGS 180
V SA+ +PA GG T +A AA++AL R ++ +A H + + G + +
Sbjct: 111 VLSAKQLPAYGGDTLWASGIAAFEALSVPLREMLDGLTATHDFTKSFPLERFGTTPEDLA 170

Query: 181 AYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
+ + PL P+V+ HP +GR +L + I + ES+ L L A
Sbjct: 171 RWEATRRNN--PPLSHPVVRTHPVSGRKALFVNEGFTTTRINELSEDESALLRLLFAHAT 228

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ +W DV WDNR H A
Sbjct: 229 RPEFSIRWRWQENDVAFWDNRV TQHFA 255

>ref|ZP_01770198.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 305]
gb|EBA45341.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 305]
Length = 327

Score = 95.9 bits (237), Expect = 6e-18, Method: Compositional matrix adjust.
Identities = 73/262 (27%), Positives = 114/262 (43%), Gaps = 21/262 (8%)

Query: 15 LGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
LGA + G+ + L + +H LL+FPGQ LS +QQI FG +E
Sbjct: 56 LGAEIRGIDFSKPLSSQARDDVIGLLSEHQLLVFPGQRLSCEQQIAACGAFGELEPHPMPT 115

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
++ +SNV +DG + ++ WH+D Y+ A+ F A
Sbjct: 116 TNTSSFPEMTIVSNVTS DGKPVGYPTPPFE-----LWHS D L CYLEHPAKMTFFYA 165

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 186
E VP G T FA+M AY+ L + +A + + A SL S + ++ G
Sbjct: 166 E SVPDAHGD TWFANMFRAYETLPDELKAAIDGKHAVFSL--DSSLVKRCRKIGFDLNIAE 223

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
D T P V+ HP T + S+ + H I G ES+ L+ + ++
Sbjct: 224 DDFKPTVSHPAVRTHPHTRQRSIFVNWAHTDRIEGYSPEESDEILDRIFAHCRNEDFIYR 283

Query: 246 HQWAAGDVVVWDNRCLLHRAEP 267
H++A D+V+WDN L+H P

Sbjct: 284 HRYANEDLVIWDNASLIHTNSP 305

>ref|ZP_06414132.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EUN1f]
gb|EFC83067.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EUN1f]
Length = 277

Score = 95.9 bits (237), Expect = 6e-18, Method: Compositional matrix adjust.
Identities = 84/288 (29%), Positives = 133/288 (46%), Gaps = 21/288 (7%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
M TT +ITP T + +TG L +D A AA + +++F + ++ + F
Sbjct: 1 MGITTRKITPNTGTEFSGLTGTQL--VDKGVAADALAALEESGVVVFREADIDDES LVAF 58

Query: 61 AKRFGAIERI--GGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
+ G + + GG + I + D + Q A + + WH D T V
Sbjct: 59 GRLGLDVLPLPMGGHRLKEIQRITRDAS--QSKLAAYRE-----ATFYWHIDGTTGEVP 110

Query: 119 AQGAVFSA-EVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ--SKLGHV 175
+ + +A ++ + G T FA+ AAY+AL + +A + A HS SQ +
Sbjct: 111 DKATLLTARQISGSTEGDTEFANTYAAAEALSDEDKASLEGVRALHSFTASQLVANPDPS 170

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD 235
+ +A+ D T +P+V GR SLL+G A + G+ A E L+ L+D
Sbjct: 171 PEERA AW-----DRNP TREQPVVWTR-RNGRKSLLVGSTAGEVVGLPADEGRALLDRLLD 224

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAG 283
WA Q V H+W GD+V+WDN +LHRA P+ R+M + LAG
Sbjct: 225 WATQPQFVLRHRWTQGD LVIWDNTGMLHRALPYGPTSSRLMHRASLAG 272

>dbj|BAC00965.1| alpha-ketoglutarate-dependent dioxygenase [Pseudomonas putida]
Length = 277

Score = 95.9 bits (237), Expect = 7e-18, Method: Compositional matrix adjust.
Identities = 81/267 (30%), Positives = 119/267 (44%), Gaps = 19/267 (7%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+L ITP LGA ++GV ++ + A+ A LQH +L F Q ++ QQ FA R
Sbjct: 2 SLTITPLSPALGAQISGVDISRITAERDAIEQALLQHQLVFFRDQPINPQQARFAAR 61

Query: 64 FGAIERIGGGDIVAI-SNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG + I I NV V D + + N WH D T++P A GA
Sbjct: 62 FGD LH-----IHPIYPNPVETPQV-----LILDTAVTDVRDNAVWHTDVTFLPTPALGA 110

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQAGS 180
V SA+ +PA GG T +A AA++AL R ++ +A H + + G + +
Sbjct: 111 VLSAKQLPAYGGDTLWASGIAAFEALSAPLREMLDGLTATHDFTKSFPLERFGTTPEDLA 170

Query: 181 AYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
+ + PL P+V+ HP +GR +L + I + ESE L+ L A
Sbjct: 171 RWEATRRNN--PPLSHPVVRTHPVSGRKALFVNEGFTTTRINELSELESEALLKLLFAHAT 228

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ +W DV WDN R H A
Sbjct: 229 RPEFSIRWRWQENDVAFWDNRVTQHFA 255

>gb|ADI06110.1| Taurine dioxygenase [Streptomyces bingchenggensis BCW-1]
Length = 292

Score = 95.9 bits (237), Expect = 7e-18, Method: Compositional matrix adjust.
Identities = 89/295 (30%), Positives = 133/295 (45%), Gaps = 39/295 (13%)

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>ref|YP_001062636.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei 668]
ref|YP_001075592.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei 1106a]
ref|ZP_03450844.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 576]
ref|ZP_03795808.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pakistan
9]
ref|ZP_04811238.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1106b]
ref|ZP_04896769.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pasteur
52237]
ref|ZP_04967966.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 406e]
gb|ABN88130.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 668]
gb|ABN92814.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 1106a]
gb|EDO87545.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 406e]
gb|EDO93607.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pasteur
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52237]
gb|EEC38656.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 576]
gb|EEH23813.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pakistan 9]
gb|EES21863.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1106b]
Length = 327

Score = 95.9 bits (237), Expect = 7e-18, Method: Compositional matrix adjust.
Identities = 73/262 (27%), Positives = 114/262 (43%), Gaps = 21/262 (8%)

Query: 15 LGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
LGA + G+ + L + +H LL+FPGQ LS +QQI FG +E
Sbjct: 56 LGAEIRGIDFSEPLSSQARDDVIGLLSEHQLLVFPQGRLSCEQQIAACGAFGELEPHPM 115
Query: 69 --RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
++ +SNV +DG + ++ WH+D Y+ A+ F A
Sbjct: 116 TNTSSFPEMTIVSNVTSBGKPVGYPTPPFE-----LWHS DLCYLEHPAKMTFFYA 165
Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG 186
E VP G T FA+M AY+ L + +A + + A SL S + ++ G
Sbjct: 166 ESVPAHAGDTWFANMFRAYETLPDELKAAIDGKHAVFSL--DSSLVKRCRKIGFDLNI 223
Query: 187 MDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
D T P V+ HP T + S+ + H I G ES+ L+ + ++
Sbjct: 224 DDFKPTVSHPAVRTHPHTRQRSIFVNWAHTDRIEGYSPEESDEILDRIFAHCRNEDFIYR 283
Query: 246 HQWAAGDVVWVWDRNRCLLHRAEP 267
H++A D+V+WDN L+H P
Sbjct: 284 HRYANEDLVIWDRNASLIHTNSP 305

>gb|ADW07602.1| Taurine dioxygenase [Streptomyces flavoviridis ATCC 33331]
Length = 296

Score = 95.5 bits (236), Expect = 7e-18, Method: Compositional matrix adjust.
Identities = 87/286 (30%), Positives = 126/286 (44%), Gaps = 31/286 (10%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T+ +TP LGA VTG+ L+ L D L A+L H +L+F Q ++ +Q FA R
Sbjct: 22 TISVTPVTPVLGA EVTGLDLSQELTDRQEKELVHAFLAHHVLVFRDQDITPEQHKRFAAR 81
Query: 64 FGAIERIG---GGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQ 120
FG + + G I ++A R I GN WHAD T +
Sbjct: 82 FGELHPVALAAEGSDPHILEIRATKESR-----AIAGN-GWHADGTADTDPSL 128
Query: 121 GAVFSAEVP--AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
G++ +P GG T FA+M AY+ L A R+ + SA H + G A
Sbjct: 129 GSMLEYITEIPEGSGGDTL FANMHLAYELLSPAMRSFLDGLSALHDGALPWATAGQTPPA 188
Query: 179 GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVDWA 237
Y + T P+V +HPETGR L + G + I + ES+ L+ L
Sbjct: 189 -----DYDIPRTE--HPVVVLHPETGRKLLFVNGPYTSHITQLARPESDALLQMLYAH 240
Query: 238 CQAPRVHAH-QWAAGDVVWVWDRNRCLLHRAEPWDFKLPRVMWHSRLA 282
+ P + +W +V WDNRC+ H A WD+ P + R+A
Sbjct: 241 ARTPLLQCRIRWQPRTL VFDNRVQHHAH-VWDY-FPHGRYGRVA 284

>ref|ZP_02406873.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei
DM98]
Length = 276

Score = 95.5 bits (236), Expect = 7e-18, Method: Compositional matrix adjust.
Identities = 73/262 (27%), Positives = 114/262 (43%), Gaps = 21/262 (8%)

Query: 15 LGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
LGA + G+ + L + +H LL+FPQG LS +QQI FG +E
Sbjct: 5 LGAEIRGIDFSKPLSSQARDDVIGLLSEHQLLVFPGQRLSCEQIIAACGAFGELEPHPM 64

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA VFSA 126
++ +SNV +DG + ++ WH+D Y+ A+ F A
Sbjct: 65 TNTSSFPEMTIVSNVTS DGKPVGYTPPF E-----LWHS D L C Y L E H P A K M T F F Y A 114

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 186
E VP G T FA+M AY+ L + +A + + A SL S + ++ G
Sbjct: 115 ESVPDAHGD TWFANMFRAYETLPDELKAAIDGKHAVFSL--DSSLVKRCRKIGFDLNIAE 172

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
D T P V+ HP T + S+ + H I G ES+ L+ + ++
Sbjct: 173 DDFKPTVSHPAVRTHPHTRQRSIFVNWAHTDRIEGYSPEESDEILDRIFAHCRNEDFIYR 232

Query: 246 HQWAAGDVVVWDNRCLLHRAEP 267
H++A D+V+WDN L+H P
Sbjct: 233 HRYANEDLVIWDNASLIHTNSP 254

>ref|ZP_02356184.1| dioxygenase, TauD/TfdA [Burkholderia oklahomensis EO147]
Length = 292

Score = 95.5 bits (236), Expect = 7e-18, Method: Compositional matrix adjust.
Identities = 80/266 (30%), Positives = 122/266 (45%), Gaps = 16/266 (6%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAG-FAALHAAWLQHALLIFPGQ-HLSNDQQITFAK 62
TL+I P T+GA V LA + ++G + A L++ +L F Q LS + QI F +
Sbjct: 3 TLEIRPLSGTIGAQVRNRTL AGVVESGRVDEIRQALLRYKVLFFTNQPDLSVETQIAFGR 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E D + + K DG Q +D + ++ WH D + +
Sbjct: 63 LFGELET----DFPSFT-AKPDG--QPEVTVF DGAVSTGRASI-WHTDLSIAKRPSAMG 113

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ--SKLGHVQQAGS 180
+ + P GG T +AD+ AAY AL +A + + A H ++ Q + G Q G
Sbjct: 114 ILCVKETPDSSGDTMWADLEAAYAALSPGMQAFLEGQRAVHDMMPQYAERPGAFQTQGR 173

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQ 239
+ + + P+V+VHPETGR L + + I G +AES L L +
Sbjct: 174 SDMD--LSNVFGAEHPVVRVHPETGRKCLFVNPFLTSHITGFHSAESAMILNHL YALMER 231

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
V W+ GDV +WDNRC +H A
Sbjct: 232 PQYVVRWHWSNGDVALWDNRCTMHTA 257

>ref|YP_003942972.1| Taurine dioxygenase [Enterobacter cloacae SCF1]
gb|ADO49688.1| Taurine dioxygenase [Enterobacter cloacae SCF1]
Length = 282

Score = 95.5 bits (236), Expect = 7e-18, Method: Compositional matrix adjust.
Identities = 83/295 (28%), Positives = 126/295 (42%), Gaps = 28/295 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 64
L ITP+G +GA V+GV L L D F L+ A L+H ++ Q ++ QQ A RF
Sbjct: 5 LHITPSGPFIGAEVSGVDLTRPLSDNQFEQLYHAML RHQVVFLEQAITPQQRALALRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM 118
G + G + + + + D +P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPHADGVVEEIIVLDTHTND-----NPPDNDN-----WHTDVTFTIDTP 108

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Query: 15  LGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
          LGA + G+   + L           +           +H LL+FPGQ LS +QQI      FG +E
Sbjct: 10  LGAEIRGIDFSEPLSSQARDDVIGLLSEHQLLVFPGQRLSCEQQIAACGAFGELEPHPMPT 69
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Query: 69 --RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA VFSA 126
++ +SNV +DG + ++ WH+D Y+ A+ F A
Sbjct: 70 TNTSSFP EMTIVSNVTS DGKPVGYPTPPFE-----LWHS D L C Y L E H P A K M T F F Y A 119

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG 186
E VP G T FA+M AY+ L + +A + + A SL S + ++ G
Sbjct: 120 ESVPDAHGDTWFANMFRAYETLPDELKAAIDGKHAVFSL--DSSLVKRCRKIGFDLNIAE 177

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
D T P V+ HP T + S+ + H I G ES+ L+ + ++
Sbjct: 178 DDFKPTVSHPAVRTHPHTRQRSIFVNWAHTDRIEGYSPEESDEILDRIFAHCRNEDFIYR 237

Query: 246 HQWAAGDVVVWDNRCLLHRAEP 267
H++A D+V+WDN L+H P
Sbjct: 238 HRYANEDLVIWDNASLIHTNSP 259

>ref|ZP_02403488.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei DM98]
Length = 292

Score = 95.5 bits (236), Expect = 8e-18, Method: Compositional matrix adjust.
Identities = 81/268 (30%), Positives = 121/268 (45%), Gaps = 20/268 (7%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFA-ALHAAWLQHALLIFPGQ-HLSNDQQITFAK 62
TL+I P T+GA V LA + ++G A + A L++ +L F Q LS + QI F +
Sbjct: 3 TLEIRPLSGTIGAQVCNRTLADVDES GRADEIRQALLRYKVLFFTNQPELSVETQIAFGR 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E K DG Q +D + ++ WH D + +
Sbjct: 63 LFGELE-----TNFPSFTAKPDG---QPEVTVFDGAVSTGRASI-WHTDLSIAKTPSAMG 113

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ--SKLGHVQQAGS 180
+ + P GG T +AD+ AAY AL +A + + A H ++ Q + G Q G
Sbjct: 114 ILCVKETPDSGGDTMWADLEAAYAALSPGMQAFLEGQRAVHDMMTTPQYARPGAFQTRGR 173

Query: 181 AYIGYGMDDTTAT--PLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWA 237
+ MD + P+V+VHPETGR L + + + G +AES L L
Sbjct: 174 S----DMDLSEVFGEAHPVVRVHPETGRKCLFVNPFLLTSHLVGFHSAESATILNYLYALM 229

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ V W+ GDV +WDNRC +H A
Sbjct: 230 ERPQYVVRWHWSRGDVALWDNRCTMHTA 257

>ref|ZP_02451448.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei
91]
ref|ZP_02493780.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei
NCTC 13177]
Length = 276

Score = 95.5 bits (236), Expect = 8e-18, Method: Compositional matrix adjust.
Identities = 73/262 (27%), Positives = 114/262 (43%), Gaps = 21/262 (8%)

Query: 15 LGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
LGA + G+ + L + +H LL+FPQG LS +QOI FG +E
Sbjct: 5 LGAEIRGIDFSEPLSSQARDDVIGLLSEHQLLVFPQGRLSCEQQIAACGAFGELEPHPM 64

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA VFSA 126
++ +SNV +DG + ++ WH+D Y+ A+ F A
Sbjct: 65 TNTSSFP EMTIVSNVTS DGKPVGYPTPPFE-----LWHS D L C Y L E H P A K M T F F Y A 114

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG 186

E VP G T FA+M AY+ L + +A + + A SL S + ++ G
Sbjct: 115 ESVPDAHGDTWFANMFRAYETLPDELKAAIDGKHAVFSL--DSSLVKRCRKIGFDLNIAE 172
Query: 187 MDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
D T P V+ HP T + S+ + H I G ES+ L+ + ++
Sbjct: 173 DDFKPTVSHPAVRTHPHTRQRSIFVNWAHTDRIEGYSPEESDEILDRIFAHCRNEDFIYR 232
Query: 246 HQWAAGDVVVWDNRCLLHRAEP 267
H++A D+V+WDN L+H P
Sbjct: 233 HRYANEDLVIWDNASLIHTNSP 254

>ref|YP_001618162.1| taurine dioxygenase [Sorangium cellulosum 'So ce 56']
emb|CAN97682.1| Taurine dioxygenase [Sorangium cellulosum 'So ce 56']
Length = 316

Score = 95.5 bits (236), Expect = 8e-18, Method: Compositional matrix adjust.
Identities = 83/289 (28%), Positives = 120/289 (41%), Gaps = 21/289 (7%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L + P +GA + GV L L A A+ LQ ++ F Q +SN+Q +TF + F
Sbjct: 15 LDVRPLTPVIGAEIHGVDLRKPLAPATVQAIEQTLLQWKVIFFREQDISNEQLLTFGRTF 74
Query: 65 GAIER-----IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
G + +G + I KA H K WH D T++
Sbjct: 75 GPLTPAHPIALGLPEHPEIWERKAAEYKENHRSDLSIPTAKPPRDYKGWHIDITFVANPN 134
Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
+ ++ +P GG T +++++ AYD L +ALV A H S G
Sbjct: 135 RYSILRGVEIPPYGGDTLWSNLECAYDGLSPTIKALVDGLQAVHRTSSYDS-----G 186
Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVDWA 237
G L PLV+VHP TGR SL + G +H + G+ ES+ L+ L D
Sbjct: 187 EPRPGRKATGPFAALHPLVRVHPRTGRKSLFVNPGTTSHIV-GLRERESQALLDMLADEV 245
Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283
+ +W + VWDN+ H A P D F LPRV+ +AG
Sbjct: 246 TRPEYAVRFRWTPNAIAVWDNQATAH-AGPIDYAHFDLPRVVRITVAG 293

>ref|YP_003563776.1| alpha-ketoglutarate-dependent taurine dioxygenase [Bacillus
megaterium QM B1551]
gb|ADE70342.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Bacillus
megaterium QM B1551]
Length = 311

Score = 95.1 bits (235), Expect = 9e-18, Method: Compositional matrix adjust.
Identities = 75/274 (27%), Positives = 115/274 (41%), Gaps = 35/274 (12%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T I P +GA + G+ L+ L L+ A+L+ +L F Q ++++Q + FAK
Sbjct: 39 TFFSIKPLTPIIGAIEGLDLKPLAKEVQEELNRAFLEWKVLFVRNQEITSEQHLAFAK 98
Query: 63 RFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST 113
+G +E + +IV S + G WHAD T
Sbjct: 99 LWGDLEVHPFYKPPASQEQAKEIVQFSRNQKQGG-----SENVVHADVT 141
Query: 114 YMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
+ A+ +V VP VGG T +ADM AAYD L E+ + + A H S
Sbjct: 142 FRESPAKASVLRLLIEVPPVGGDTLWADMAAAYDNLPESIKKQIEHLKAIHDFTPS---FA 198
Query: 174 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH--AHAIPGMDAAESERFLE 231
H+ Q + + A P+V+ HPETGR +L + H + G++ +E E+ L+

Sbjct: 199 HLLQPDELK-AFQREFPAVE-HPIVRTHPETGRKTLFVNSSFTTHVV-GLEHSEGEQLLQ 255

Query: 232 GLVDWACQAPRVHAHQWAAAGDVVVWDNRCLLHRA 265

L A +W + WDNR H A

Sbjct: 256 SLFRQAHVPEYQVRFRWEVNSIAFWDNRRATQHVA 289

>ref|XP_001801431.1| hypothetical protein SNOG_11187 [Phaeosphaeria nodorum SN15]
gb|EAT81686.1| hypothetical protein SNOG_11187 [Phaeosphaeria nodorum SN15]
Length = 314

Score = 95.1 bits (235), Expect = 9e-18, Method: Compositional matrix adjust.
Identities = 76/289 (26%), Positives = 122/289 (42%), Gaps = 26/289 (8%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59

M T L P AT A GV A L + +L+F L + + +

Sbjct: 1 MVSTRLTFDPLHATFAAKCLGVDFQAALPAKTVEEIRCGLATYGVLFVRHAQLDDARHVA 60

Query: 60 FAKRFGAIE----RIGGG-----DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNM 106

FA + G ++ I G ++ +SN+ DG + + ++ +GN

Sbjct: 61 FAAQLGELDDSTPYIKAGRKHRLAPYTELFDVSNLDDGNIVSTDLSRF----QLGLGNG 116

Query: 107 AWHADSTYMPVMAQGAVFSAEVVP--AVGGRTCFADMRAAYDALDEATRALVHQRSARHS 164

+H DS + P A +V A +P GG T FAD R AY LDE T+ + HS

Sbjct: 117 LFHVDSAFNPRRAGYSVLRAHELPPKGTGATAFADTRTAYADLDEVTKGRIKDHVVSLS 176

Query: 165 LVYSQSKLGHVQQAGSAYI-GYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDA 223

L +S+ + ++ G + LV+ H +GR +L I HAH I G+

Sbjct: 177 LWHSRR---LAAPDCEFLQGMKPEEHFMARHRLVQTHEASGRNTNLYIAHHAHHIDGLSQ 232

Query: 224 AESERFLEGLVDWACQAPRVHAHQWAA-GDVVVWDNRCLLHRAEPWDFK 271

+ + L+ A Q +W + GD+++WDN C++H A F+

Sbjct: 233 DVGQEVIRNLLSHATQEKYTIEVEWESNGDIIWDNTTCVMHAARRGAFE 281

>ref|ZP_04690003.1| dioxygenase [Streptomyces ghanaensis ATCC 14672]
ref|ZP_06580790.1| conserved hypothetical protein [Streptomyces ghanaensis ATCC 14672]
gb|EFE71251.1| conserved hypothetical protein [Streptomyces ghanaensis ATCC 14672]
Length = 324

Score = 95.1 bits (235), Expect = 9e-18, Method: Compositional matrix adjust.
Identities = 91/292 (31%), Positives = 128/292 (43%), Gaps = 20/292 (6%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64

+++ P +GA VTGV LA LD+A AA+ AA L+ ++ F GQ L + + A+RF

Sbjct: 17 VEVPRVAGHIGAEVTGVDLAGDLDEAVVAAIRAAVLRWKVVFVRGQRLDHAGHVALARRF 76

Query: 65 G---AIERIGGG---DIVAISNVKADGTVRQHSPAEWDD--MMKVIVGNMAWHADSTYMP 116

G + R G D I + E D+ + WH D

Sbjct: 77 GEPVVLPRRGKASPPDFPEIETTADRLELGGFRGMEHDEWLRRRRHTLLRGWHCDHGARGV 136

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-VYSQSKLGHV 175

+ AE VP GG T +++ AAY L R + A H L V QS+ G

Sbjct: 137 DPPAATILRAETVPPYGGDTTWSNLAAAYAGLSAPVREFADRLRAEHLGVGYQSRPGD- 195

Query: 176 QQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLV 234

AY+ + +D PLV+VHPETG L + G + I G+ ES L+ L+

Sbjct: 196 ----DAYVRHLLDRQTASEHPLVRVHPETGERVLYVNGYYVEQITGLSRPESAAVLQMLL 251

Query: 235 DWACQAPRVHAHQWAAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283

+ A + +W G V WDNR +H A P D PR+M LAG

Sbjct: 252 EQATRPEYTVRFRWEPGSVAFWDNRRATIHVA-PGDTAHLDPHPRIMHRVMLAG 302

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>ref|YP_108822.1| putative sulfur metabolism-related protein [Burkholderia
pseudomallei K96243]
ref|YP_334048.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei 1710b]
ref|YP_993448.1| dioxygenase, TauD/TfdA [Burkholderia mallei SAVP1]
ref|YP_001029119.1| dioxygenase, TauD/TfdA [Burkholderia mallei NCTC 10229]
ref|YP_001080957.1| dioxygenase, TauD/TfdA [Burkholderia mallei NCTC 10247]
ref|YP_001066827.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei 1106a]
ref|ZP_01763717.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 305]
ref|ZP_02265463.1| dioxygenase, TauD/TfdA family [Burkholderia mallei PRL-20]
ref|ZP_02412027.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei 14]
ref|ZP_02448147.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei 91]
ref|ZP_02456323.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei 9]
ref|ZP_02471884.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei B7210]
ref|ZP_02482359.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei 7894]
ref|ZP_02490549.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei NCTC 13177]
ref|ZP_02498679.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei 112]
ref|ZP_02506689.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei BCC215]
ref|ZP_03457090.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 576]
ref|ZP_03794512.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pakistan
9]
ref|YP_002897334.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei MSHR346]
ref|ZP_04816826.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1106b]
ref|ZP_04891024.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei 1655]
ref|ZP_04897975.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei Pasteur 52237]
ref|ZP_04904443.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei S13]
ref|ZP_04949460.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1710a]
ref|ZP_04964591.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei 406e]
ref|ZP_04974306.1| dioxygenase TauD/TfdA family [Burkholderia mallei 2002721280]
emb|CAH36229.1| putative sulfur metabolism-related protein [Burkholderia
pseudomallei K96243]
gb|ABA48168.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei 1710b]
gb|ABM51215.1| dioxygenase, TauD/TfdA [Burkholderia mallei SAVP1]
gb|ABN02045.1| dioxygenase, TauD/TfdA family [Burkholderia mallei NCTC 10229]
gb|ABN89084.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 1106a]
gb|ABO05696.1| dioxygenase, TauD/TfdA family [Burkholderia mallei NCTC 10247]
gb|EBA50731.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 305]
gb|EDK85181.1| dioxygenase TauD/TfdA family [Burkholderia mallei 2002721280]
gb|EDO84391.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei 406e]
gb|EDO94813.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei Pasteur 52237]
gb|EDS87455.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei S13]
gb|EDU12008.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei 1655]
gb|EEC31405.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 576]
gb|EEH25073.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pakistan 9]
gb|ACQ96121.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei MSHR346]
gb|EES27451.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1106b]
gb|EES46464.1| dioxygenase, TauD/TfdA family [Burkholderia mallei PRL-20]
gb|EET06479.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1710a]
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Length = 292

Score = 95.1 bits (235), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 81/268 (30%), Positives = 121/268 (45%), Gaps = 20/268 (7%)

```
Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFA-ALHAAWLQHALLIFPGQ-HLSNDQQITFAK 62
TL+I P T+GA V LA + ++G A + A L++ +L F Q LS + QI F +
Sbjct: 3 TLEIRPLSGTIGAQVRNRTLADVVESGRADEIRQALLRYKVLFFTNQPELSVETQIAFGR 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIIVGNMAWHADSTYMPVMAQGA 122
FG +E K DG Q +D + ++ WH D + +
Sbjct: 63 LFGELE-----TNFPSFTAKPDG---QPEVTVFDGAVSTGRASI-WHTDLSIAKTPSAMG 113

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ--SKLGHVQQAGS 180
```

```

      +   + P  GG T +AD+ AAY AL   +A +   + A H ++ Q   + G Q G
Sbjct: 114 ILCVKETPDSSGGDTMWADLEAAYAALSPGMQAFLEGQRAVHDMMTPQYAQRPGAFQTRGR 173

Query: 181 AYIGYGMDDTTAT--PLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWA 237
      +       MD +       P+V+VHPETGR L +       + + G +AES L L
Sbjct: 174 S----DMDLSEVFGAEHPVVRVHPETGRKCLFVNPFLTSHLVGFHSAESATILNYLYALM 229

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      +   V   W+ GDV +WDNRC +H A
Sbjct: 230 ERPQYVVRWHWSRGDVALWDNRCTMHTA 257

```

>ref|ZP_02485616.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei
7894]
Length = 281

Score = 95.1 bits (235), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 73/262 (27%), Positives = 114/262 (43%), Gaps = 21/262 (8%)

```

Query: 15  LGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
      LGA + G+   + L       +       +H LL+FPGQ LS +QQI       FG +E
Sbjct: 10  LGAEIRGIDFSEPLSSQARDDVIGLLSEHQLLVFPQGRLSCEQQIAACGAFGELEPHPM 69

Query: 69  --RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
      ++ +SNV +DG   +       ++       WH+D Y+   A+   F A
Sbjct: 70  TNTSSFPEMTIVSNVTSDGKPVGYPTPPFE-----LWHS DLCYLEHPAKMTFFYA 119

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 186
      E VP   G T FA+M AY+ L +   +A +   + A SL   S +   ++ G
Sbjct: 120 ESVPAHAGDTWFANMFRAYETLPDELKAAIDGKHAVFSL--DSSLVKRCRKIGFDLNIAE 177

Query: 187 MDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
      D   T   P V+ HP T + S+ +   H   I G   ES+ L+ +       ++
Sbjct: 178 DDFKPTVSHPAVRTHPHTRQRSIFVNWAHTDRIEGYSPEESDEILDRVFAHCRNEDFIYR 237

Query: 246 HQWAAGDVVVWDNRCLLHRAEP 267
      H++A D+V+WDN L+H P
Sbjct: 238 HRYANEDLVIWDNASLIHTNSP 259

```

>ref|YP_001666482.1| taurine dioxygenase [Pseudomonas putida GB-1]
gb|ABY96146.1| Taurine dioxygenase [Pseudomonas putida GB-1]
Length = 301

Score = 95.1 bits (235), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 84/286 (29%), Positives = 120/286 (41%), Gaps = 24/286 (8%)

```

Query: 6   LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
      L I P       +GA + GV L A LD A   A+ AA +QH ++ F Q HL + Q FAK
Sbjct: 15  LDIHPVAGRIGAEIRGVRLSADLDAATVEAIQAALVQHKVIFFREQTHLDDQSQEGFAKL 74

Query: 64  FGAIERIGGGDIVAISN----VKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
      G E +   + +       ++ DG   Q +       +WH D T++
Sbjct: 75  LG--EPVAHPTVPVVDGTSYLLQLDGAEGQRA-----NSWHTDVTFVDAYP 118

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG-HVQQA 178
      + ++   + V P  GG T +A+ AAY L E R L + A HS Y + +   V A
Sbjct: 119 KASILRSVVAPTSGGDTVWANTAAAYQELPEPLRELADKLWAVHSNEYDYASIKPDVDPA 178

Query: 179 G-SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
      Y       T       P+V+VHP +G +L +G   I G   A+S+   L
Sbjct: 179 KLERYRKVFTSTVYETEHPVVRVHPISGERALQLGHFVKRIKGYSLADSQHLFAVLQGHV 238

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Query: 238 CQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W GDV +WDNR H A PRV+ LAG
Sbjct: 239 TRLENTVRWRVQVGDVAIWDNRATQHYAVDDYGTQPRVVRVTLAG 284

>ref|YP_002799405.1| Taurine dioxygenase protein [Azotobacter vinelandii DJ]
gb|AC078430.1| Taurine dioxygenase protein [Azotobacter vinelandii DJ]
Length = 318

Score = 95.1 bits (235), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 84/292 (28%), Positives = 123/292 (42%), Gaps = 22/292 (7%)

Query: 2 AQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A + +TP +GA V GV L+ L A A+ AA L+ +L F QHL + QQ+ F
Sbjct: 14 AAEAIIVTPLSLYIGAQVDGVDLRPLPSAQREAIRAALLRWKVLFFHDQHLDDHAQQVAF 73

Query: 61 AKRFG--AIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
++FG + G + + + G R A + D +++ WH D +
Sbjct: 74 GRQFGEPTVGHVPVFGHVEGHPEIYSVG--RDRFKARFTDE-RLVRPWSGWHTDVSAALNP 130

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
A+ +P GG T + D+ AAY+ L RA V H +
Sbjct: 131 PAAAILRGVDIPPYGGDTQWTDLVAAYNGLSPTLRAFVDGLRGEHRFTTPPE-----G 182

Query: 179 GSAYIGYGMDDTTATPL---RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLV 234
A G+ PL PLV+VHPETG +L + I G+ ESE+ LE L
Sbjct: 183 AEARPGFSEPLAVRPLVSEHPLVRVHPETGEKALFVSPFTLKRIVGLSPRESEQLLELLF 242

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDF---KLPRVMWHSRLAG 283
+ A + +W G + WDNR H+ P D LPR ++ L G
Sbjct: 243 EHAIRPEYTVRFKWRPGSLAFWDNRVTAHQF-PSDIHATDLPRQLYRITLVG 293

>ref|YP_335290.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei 1710b]
ref|ZP_04899972.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei S13]
gb|ABA52694.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1710b]
gb|EDS82984.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei S13]
Length = 327

Score = 95.1 bits (235), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 73/262 (27%), Positives = 114/262 (43%), Gaps = 21/262 (8%)

Query: 15 LGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
LGA + G+ + L + +H LL+FPGQ LS +QQI FG +E
Sbjct: 56 LGAEIRGIDFSKPLSSQARDDVIGLLSEHQLLVFPGQCLSCEQQIAACGAFGELEPHPM 115

Query: 69 --RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
++ +SNV +DG + ++ WH+D Y+ A+ F A
Sbjct: 116 TNTSSFPEMTIVSNVTSKGKPVGYPTPPFE-----LWHS DLCYLEHPAKMTFFYA 165

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 186
E VP G T FA+M AY+ L + +A + + A SL S + ++ G
Sbjct: 166 ESVPAHAGDTWFANMFRAYETLPDELKAAIDGKHAVFSL--DSSLVKRCRKIGFDLNI 223

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
D T P V+ HP T + S+ + H I G ES+ L+ + ++
Sbjct: 224 DDFKPTVSHPAVRTHPHTRQRSIFVNWAHTDRIEGYSPEESDEILDRIFAHCRNEDFIYR 283

Query: 246 HQWAAGDVVVDNRCLLHRAEP 267
H++A D+V+WDN L+H P
Sbjct: 284 HRYANEDLVIWDNASLIHTNSP 305

>ref|ZP_04954431.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1710a]
gb|EET03953.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1710a]
Length = 281

Score = 94.7 bits (234), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 73/262 (27%), Positives = 114/262 (43%), Gaps = 21/262 (8%)

Query: 15 LGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
LGA + G+ + L + +H LL+FPGQ LS +QQI FG +E
Sbjct: 10 LGAEIRGIDFSKPLSSQARDDVIGLLSEHQLLVFPGQCLSCEQQIAACGAFGELEPHPM 69

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA VFSA 126
++ +SNV +DG + ++ WH+D Y+ A+ F A
Sbjct: 70 TNTSSFPEMTIVSNVTS DGKPVGYPTPPFE-----LWHS DLYC LEHPAKMTFFYA 119

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG 186
E VP G T FA+M AY+ L + +A + + A SL S + ++ G
Sbjct: 120 ESVPDAHGD TWFANMFRAYETLPDELKAAIDGKHAVFSL--DSSLVKRCRKIGFDLNIAE 177

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
D T P V+ HP T + S+ + H I G ES+ L+ + ++
Sbjct: 178 DDFKPTVSHPAVRTHPHTRQRSIFVNWAHTDRIEGYSPEESDEILDRIFAHCRNEDFIYR 237

Query: 246 HQWAAGDVVVWDNRCLLHRAEP 267
H++A D+V+WDN L+H P
Sbjct: 238 HRYANEDLVIWDNASLIHTNSP 259

>emb|CAY27239.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 94.7 bits (234), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 51/124 (41%), Positives = 69/124 (55%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFADMRAAYDALDDETKVEIEDMICEHSLMYSRDSLGLD-----YTDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV++HP GR SL + HA AI GM E+ L L + A + V+ H+WA D+V+
Sbjct: 56 RLVRIHPVHGRKSLYLSSHAGAIKMSVPEARLLLRDLTEHATKPEFVYVHKWALHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>ref|ZP_07674287.1| taurine dioxygenase, TauD/TfdA family [Ralstonia sp. 5_7_47FAA]
gb|EFP67403.1| taurine dioxygenase, TauD/TfdA family [Ralstonia sp. 5_7_47FAA]
Length = 318

Score = 94.7 bits (234), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 79/271 (29%), Positives = 118/271 (43%), Gaps = 30/271 (11%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L++ +G V + L A L + FA+L+AA L++ +L F Q HL +DQ F KR
Sbjct: 16 LRVRRVAGHIGGEVLDLKLGADLAEDTFASLYAALLKYKVLFFRDQQHLDDQHQAFGKR 75

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA V 123
FG I VA V A + D K +WH D T++ + ++
Sbjct: 76 FGRI-----VAHPTVPAPTGTQLFEL----DASKGGGRADSWHTDVTFLDAFPKVS I 123

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ-----SKLGH 174

```
>emb|CAY27432.1| alpha-KG-dehydrogenase [uncultured bacterium]
      Length = 119
```

Score = 94.7 bits (234), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 52/124 (41%), Positives = 69/124 (55%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T FADMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFADMRAAYDALDDETKVEIEDMICEHSLMYSRGSLGFLD-----YTDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP TGR SL + HA AI G E+ L L++ A Q V+AH+W D+V+
Sbjct: 56 RLVRTHPSTGRKSLYLASHAGAIVGWVPPEARALLRDLIEHATQRFVYAHEWKQWDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>ref|YP_004005470.1| taurine dioxygenase [Rhodococcus equi 103S]
ref|ZP_08154648.1| taurine dioxygenase [Rhodococcus equi ATCC 33707]
emb|CBH46785.1| putative taurine dioxygenase [Rhodococcus equi 103S]
gb|EGD24222.1| taurine dioxygenase [Rhodococcus equi ATCC 33707]
Length = 305

Score = 94.7 bits (234), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 76/278 (27%), Positives = 113/278 (40%), Gaps = 25/278 (8%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T ++ P +GA + GV L L A L+ ++ F Q ++ Q FA+
Sbjct: 37 TQFEVRPVTPFIGAEIHGVDLRDPSPAEIEELRRALLEWKVVFVRDQQITGTQHRDFARH 96

Query: 64 FGAIE---RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQ 120
+G +E + G++ + + + + SP WH D T+
Sbjct: 97 WGELEVHPLLPQGEVPEVVFHFERG-----EDSPG-----TENIWHVDVTWQKRPL 142

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
G+V A VP GG T +ADM AYD L + + + R A H V S + ++ +
Sbjct: 143 GSVLRALLEVPPAGGDTLWADMGNAYDCLSDVEKIEGRVAVHDFVPSFGRSMSPEKLAA 202

Query: 181 AYIGYGMTTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
M P+ P+V++HPETGR +L + IP MD E E L L D A
Sbjct: 203 -----MQEQFPPVEHPIVRIHPETGRRTLFVNSLFTTHIPDMDPVEGEALLRHLFDQAK 256

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
+W + WDNR H A F RVM
Sbjct: 257 VPDFQCRFRWQPNSIAFWDNRATQHYAASDYFPHRRVM 294

>ref|YP_004236558.1| taurine dioxygenase [Acidovorax avenae subsp. avenae ATCC 19860]
gb|ADX47991.1| Taurine dioxygenase [Acidovorax avenae subsp. avenae ATCC 19860]
Length = 318

Score = 94.4 bits (233), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 85/297 (28%), Positives = 122/297 (41%), Gaps = 42/297 (14%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
L+I LG V + L A LDDA L AA ++H +L F GQH L + + F +R
Sbjct: 16 LRIRRVAGALGGEVLDELASAGLDDATIGHLTAALVRHKVLFVRGQHQLDDARHQAFGER 75

Query: 64 FG-----AIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPV 117
G + G I + K G +WH D T++
Sbjct: 76 LGRTVSHPTVPAREGTRIFELDASKGGGRAD-----SWHTDVTFLDA 117

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS-----LVYS 168


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      + + A VPA GG T +A+ AAY+ L E + L A HS LV
Sbjct: 118 FPKYGILRAVTVPAYGGDTVWANTAAAYERLPEDLKRLADSLWAVHSNNYDYGADRLVVD 177

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER 228
      +++L H + ++ + Y + PLV VHP +G +LL+G I G + ES R
Sbjct: 178 ETRLRHHRDVFASEV-YEAE-----HPLVHVHPVSGERALLLGHFIIQRIQGSSTESAR 230

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
      E L + + W DV +WDNR H A + PRV+ + G P
Sbjct: 231 LFELLQNRVTRLENTVRWSWRQNDVAIWDNRATQHIAVNDYGRQPRVRRVTVHGDP 287

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>ref|ZP_08207133.1| taurine dioxygenase [Novosphingobium nitrogenifigens DSM 19370]
gb|EGD60811.1| taurine dioxygenase [Novosphingobium nitrogenifigens DSM 19370]
Length = 271

Score = 94.4 bits (233), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 74/273 (27%), Positives = 116/273 (42%), Gaps = 23/273 (8%)

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Query: 1 MAQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
      M ++ + P +GA V+GV L LD+ A + A+ +H ++ F Q + +D I
Sbjct: 1 MPYQSITVAPVTPVIGAEVSGVDLTRPLDETQIAEIKRAFAEHLVIFFRDQPVGHDDHIR 60

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMA 119
      A+ FG + + V + D V WH+D +
Sbjct: 61 LARYFGGVHIAPSTAPWQVPGVPEVTIIHA-----DENSTFVAGEDWHSMDSCDDAPP 113

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
      G++ +P VGG T F++M AAYDAL + +A + +A H V LG G
Sbjct: 114 LGSILYLHTIPPVGGDTVFSNMYYAAYDALSDRMKAYLDGLTAVHDAV-----LGF---GG 165

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
      G + + P+++ HPETGR ++ + R I G+ ES L L +
Sbjct: 166 ITPEGMKLPRNS--HPVIRTHPETGRKAIFVNRGFTTRIEGVDPDIESRSILSYLYE-HV 221

Query: 239 QAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDF 270
      Q P+ +W + WDNRC H A WD+
Sbjct: 222 QHPQFQCRFRWQPHSIAFWDNRCAQHSAL-WDY 253

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>ref|YP_001480784.1| taurine dioxygenase [Serratia proteamaculans 568]
gb|ABV43656.1| Taurine dioxygenase [Serratia proteamaculans 568]
Length = 282

Score = 94.4 bits (233), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 79/285 (27%), Positives = 119/285 (41%), Gaps = 21/285 (7%)

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Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      L ITP G +GA V V+LA L D F L+ A L+H +L Q ++ QQ A RF
Sbjct: 5 LNITPLGPYIGALVENVNLRPLGDBGQFEQLYHALLKHQVLFRLNQIPITPLQQRNLAGRF 64

Query: 65 GAIE----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
      G + D+ I + H+P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPQAADVKEIIVLD----THDHNPPDNDN-----WHTDVTFIENPPL 110

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV-QQAG 179
      GA+ +A+ +P+ GG T +A AAY+AL E R L+ A H S + H +
Sbjct: 111 GAILAAKTL PSTGGDTLWASGIAAYEALSEPFRLLAGLKAEHDFTKSFPEHKHRGSEEE 170

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
      + L P+V+ HP +GR +L + I + ES+ L L
Sbjct: 171 RQRWQVAVQKNPPLLHPVVRTHPVSGRQALFVNEGFTTRIVDLAPKESDALLNLFLEFAHIT 230

```

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W D+ +WDNR H A R+M + + G
Sbjct: 231 KPEFQVRWRWQENDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|YP_003280552.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
CNB-2]
gb|ACY35256.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
CNB-2]
Length = 329

Score = 94.4 bits (233), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 78/284 (27%), Positives = 121/284 (42%), Gaps = 14/284 (4%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+++TP A +GA ++GV+L L A + +A L+ ++ F QHLS++QQI F+++F
Sbjct: 27 IRVTPQSAHIGALISGVNLKQALSAAEVHTIRSALLRWKVIFFRDQHLSHEQQIAFSRQF 86

Query: 65 GAIERIGGGDIVA-ISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
G E G + + ++ +H A WHAD T ++
Sbjct: 87 G--ELTPGHPVFGHVEGFPELYSIAKHRKANRHSGQAEQRPWTGWHADVTAAHNPPAASI 144

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
+P GG T + ++ AAY+AL +A + H Q A Y+
Sbjct: 145 LRGVTTIPPYGGDTQWTNLAAAYEALSRPLQAFLQGLRGEHRFSAPQGA-----TASQEYL 199

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPR 242
D T PLV +HPETG L I +I + ES LE L + A +
Sbjct: 200 DLVRDNTLISEHPLVTIHPETGEKVLVYISPGFLKSIVELSTRESRVLLELLWEHAVSSEF 259

Query: 243 VHAHQWAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283
+W G + WDNR H A P D + R ++ + L G
Sbjct: 260 TVRFKWEPSGLAFWDNRSTAHVA-PQDIFALEFDRQLYRTTLVG 302

>ref|ZP_07046181.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
S44]
gb|EFI59988.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
S44]
Length = 329

Score = 94.0 bits (232), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 79/285 (27%), Positives = 121/285 (42%), Gaps = 14/285 (4%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ITP A +GA ++GV+L L A + +A L+ ++ F QHLS++QQI F+ +F
Sbjct: 27 IRITPQSAHIGALISGVNLKQALSAAEVHTIRSALLRWKVIFFRDQHLSHEQQIAFSHQF 86

Query: 65 GAIERIGGGDIVA-ISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
G E G + + ++ +H A WHAD T ++
Sbjct: 87 G--ELTPGHPVFGHVEGFPELYSIAKHRKANRHSGQAEQRPWTGWHADVTAAHNPPAASI 144

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
+P GG T + ++ AAY+AL + +A + H Q A Y+
Sbjct: 145 LRGVTTIPPYGGDTQWTNLAAAYEALSKPLQAFLQGLRGEHRFSAPQGA-----TASQEYL 199

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPR 242
D T PLV +HPETG L I +I + ES LE L + A +
Sbjct: 200 DLVRDNTLISEHPLVTIHPETGEKVLVYISPGFLKSIVELSTRESRVLLELLWEHAVSSEF 259

Query: 243 VHAHQWAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAGR 284
+W G + WDNR H A P D + R ++ + L G
Sbjct: 260 TVRFKWEPSGLAFWDNRSTAHVA-PQDIFALEFDRQLYRTTLVGE 303

>emb|CAY27303.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27391.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27488.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 94.0 bits (232), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 52/125 (41%), Positives = 72/125 (57%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALD+ T+A + RHS +YS+ KLG V+ + P+R
Sbjct: 1 TEFADMRAAYDALDDRTKADIENLVCRHSNMYSRGKLGLEFTEDEERAVF-----RPVR 54

Query: 196 PL-VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
L V+ HP +GR SL + HA I GM ++ L L ++A + P V++H W D+V
Sbjct: 55 QLLVRRHPVSGRKSFLSAHAGEIEGMPTPQARMMLLLDTEFATREPFVYSHVWRVNDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|YP_118167.1| putative taurine dioxygenase [Nocardia farcinica IFM 10152]
dbj|BAD56803.1| putative taurine dioxygenase [Nocardia farcinica IFM 10152]
Length = 312

Score = 94.0 bits (232), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 80/287 (27%), Positives = 125/287 (43%), Gaps = 17/287 (5%)

Query: 5 TLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T+ + P +GA +TGV L L D A+ +A + +L F QH+ + + F++R
Sbjct: 13 TVHVPVAVAGHIGADITGVDLREPLTDPQVEAITSALHTYKVLFFRDQHIGHAEHVAFSRR 72

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FGA+ D A ++ V + + K N WH D + + ++
Sbjct: 73 FGAVTPSHPYDDDAPTDYPEILAVDTRLYEKRFGRKASYTNQ-WHTDVSPLINPPAASI 131

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
AE+ P GG T + ++ AAY+ L E+ R V A H + G + A S
Sbjct: 132 LRAEIAPERGGDTRWTNLVAAEHLPESLRRFVDGLQAEH-----RFGGSRPAWSTDS 184

Query: 184 GYGMDTTATPL--RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
Y A PL P+V+VHP TG +L + I G+ A+S+ L L D
Sbjct: 185 DYAKKVAAAPLVTEHPVVRVHPVTGERALFVNPGFTTRIVGLTPAQSDAVLRLFLDHLAD 244

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283
+ +W G + WDNR H A P D + RV++ + L G
Sbjct: 245 PAFTVSFRWRPGSIAFWDNRATAHLA-PSDIDHLDVTRVLYRTTLEGG 290

>emb|CAY27532.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 94.0 bits (232), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 71/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYD+LD+ T+ L+ HS +YS+++LG + + P+R
Sbjct: 1 TEFADMRAAYDSLQDQTKDLIEDLVCEHSQIYSRARLGFTDFSPEELERFK-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + H +I G A E+ L L + A Q V+ H+WA GD+V

Sbjct: 55 QRLVRTHPSTGRKSLYLASHIGSIIGWSAPEATLLMLDLTEIATQREFVYPHEWAVGDIV 114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>emb|CAY27285.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 94.0 bits (232), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 49/124 (39%), Positives = 69/124 (55%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T F DMRAAYDALD+ T+ + + HSL+YS+ LG + Y + + L+
Sbjct: 1 TEFGBMRAAYDALDDETKVEIEDMTCEHSLMYSRGSLGFLD-----YTDEEKEMSKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV++HP GR SL + HA AI GM E+ L L + A + V+ H+W D+V+
Sbjct: 56 RLVRIHPVHGRKSLYLSSHAGAIGMSVPEARLLLLRDLTEHATKPEFVYVHKWTLHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>ref|ZP_07965125.1| TfdA family Taurine catabolism dioxygenase TauD [Segniliparus
rugosus ATCC BAA-974]
gb|EFV13673.1| TfdA family Taurine catabolism dioxygenase TauD [Segniliparus
rugosus ATCC BAA-974]
Length = 306

Score = 94.0 bits (232), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 77/269 (28%), Positives = 115/269 (42%), Gaps = 30/269 (11%)

Query: 4 TTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFA 61
T +++T G +GA + GV L + A+ A L H ++ F GQ HL ++ Q FA
Sbjct: 3 TAIRVTKLGEHIGARIDGVRLGGDVAPETVEAIRRAMLAHKVVFVRGQGHLDDEAQKFA 62

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVI---VGNMA--WHADSTYMP 116
G H A D + I G A WH D T+
Sbjct: 63 DLLGT-----RTTAHPVAPLDQEIVPIDSATGARANQWHTDVTFC 103

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ ++ A V+PA GG TC+A+ AY+ L R L + A H+ + + +
Sbjct: 104 RPPKASLLRAVVLPAHGGSTCWANTAVAYERLPAPLRRLADELWAEHTSQFDYAAPNARE 163

Query: 177 QAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW 236
+ +A+ T PLV+VHPETG SLL+G A I G+ ++ES+ + D
Sbjct: 164 ELAAAWSAIDFATE---HPLVRVHPETGERSLLLGNFAKRILGVSSSESQALIRLFQDR 219

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ W GD+ +WDNR H A
Sbjct: 220 ITRLEHTVRWNWEPGDLAMWDNRATQHYA 248

>ref|YP_001863223.1| taurine dioxygenase [Burkholderia phymatum STM815]
gb|ACC76177.1| Taurine dioxygenase [Burkholderia phymatum STM815]
Length = 282

Score = 94.0 bits (232), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 77/274 (28%), Positives = 119/274 (43%), Gaps = 28/274 (10%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++I ++GA +TGV LA DD FA + AA L+H +L Q ++ Q + FA+R
Sbjct: 1 MRIEQLTCSIGAELTGVDLADAVHDDGLFAEIRAALLKHRVLFRLDQEITRAQHVAFAARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E +A S+ + G VR + +P + +D + AWH D+T+ G
Sbjct: 61 FGELE----DHPIAGSDPEHPGLVRIYKTPDQPNDRYE-----NAWHTDATWRAAPPFGC 111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V P VGG T +A+M AY+ L E + + ARHS+ S +++ +
Sbjct: 112 VLRCVECPVPGGDTMWANMVLAYENLPEHVKTQIADLRARHSIEASFGAAMPIEKRHALK 171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG-----LVD 235
Y P+V+ HPETG L + E RF + L+
Sbjct: 172 AQY-----PDAEHPVVRTHPETGEKVLVFNFTTFTNYHTPERVRFQDANPGASMLLS 226

Query: 236 WACQAPRVHAHQ---WAAGDVVVWDNRCLLHRA 265
+ V +Q W + +WDNR H A
Sbjct: 227 YLVSQAYVPEYQVRWRWRKNSIAIWDNRSTQHYA 260

>ref|YP_003989699.1| Taurine dioxygenase [Geobacillus sp. Y4.1MC1]
gb|ADP75088.1| Taurine dioxygenase [Geobacillus sp. Y4.1MC1]
Length = 310

Score = 94.0 bits (232), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 75/263 (28%), Positives = 115/263 (43%), Gaps = 18/263 (6%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ P +GA + GV L + A L+ A L+ +L F Q ++++QQ FA+ +
Sbjct: 41 FEVKPLSPIIGAEIIGVDLREPITPELQAEINRALLEWKVLFFRNQKITSEQQRAFARLW 100

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G +E I + + R H ++++ WHAD T+ A+ AV
Sbjct: 101 GELEVHPFYPIEEGQSKEIVRFSRDKQGGFENI-----WHADVTFRANPAKAAVL 151

Query: 125 SAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
VP VGG T +ADM AAYD L + + + +A H S S L ++
Sbjct: 152 RLIEVPPVGGDTLWADMGAAYDNLPEIKERIDNLTAIHDFTPSFSLMTPEELAIAKQKE 211

Query: 185 YGMDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPR 242
+ P+ P+V+ HPETGR +L + I G++ ESE+ L+ L A
Sbjct: 212 F-----PPVEHPVVRTHPETGRKTLFVNPAFTTRIVGLEPEESEKLLQYLFRQAHIPY 265

Query: 243 VHAHQWAAGDVVVWDNRCLLHRA 265
W V WDNR H A
Sbjct: 266 QVRFHWEKDTVAFWDNRATQHYA 288

>ref|NP_887599.1| putative dioxygenase [Bordetella bronchiseptica RB50]
emb|CAE31551.1| putative dioxygenase [Bordetella bronchiseptica RB50]
Length = 289

Score = 93.6 bits (231), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 89/285 (31%), Positives = 130/285 (45%), Gaps = 18/285 (6%)

Query: 6 LQITP-TGATLGATVTGVHLATLDDAGFA-ALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
LQ P T LG V GV L A A L A W +HA+L+ Q L + A
Sbjct: 9 LQTRPLTQHGLGIEVRGVDLGAELPAQVARTLRALWSEHAVLVVRDQRLDPPGFLRAAGV 68

Query: 64 FGAI--ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
FG I +++G ++ + GT+ D + V N +H D + G
Sbjct: 69 FGEILPQQLGK--FSLPDYPLVGTISSRDLPIRDGKLHVRGEN--YHTDHSNFPREPPMG 123

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
+ A +P+ GG T F D+RAAYD L E T+A + S R VY S+ + +A
Sbjct: 124 TMLHAIELPSHGGDTQFVDVRAAYDDLPEQTKARIA--SLRSDHVESSR---SPRKMAA 178

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVDWACQ 239
A+ +PLV VHP +GRP+L + GR + G+ E + L + A Q
Sbjct: 179 LTPQQRAEAASSSQPLVIVHPVSGRPALYLNTGR-MEGVDGLPEDEGFALINMLYEHAHQ 237

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRAE-PWDFKLPRVMWHSRLAG 283
+ HQW GD V+WDNR ++H+A +D + R ++ L G
Sbjct: 238 PRYEYRHQWRKGDFVLWDNRSMVHQANADFPQELRFLYRLMLKG 282

>ref|YP_001751827.1| taurine dioxygenase [Pseudomonas putida W619]
gb|ACA75458.1| Taurine dioxygenase [Pseudomonas putida W619]
Length = 277

Score = 93.6 bits (231), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 80/269 (29%), Positives = 121/269 (44%), Gaps = 23/269 (8%)

Query: 5 TLQITPTGATLGATVTGVHLA---TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
+L +TP LGA ++GV ++ T++ A+ A LQH +L F Q ++ +QQ FA
Sbjct: 2 SLTVTPLSPALGAQISGVDISREITVEQRD--AIEQALLQHQLVFFRDQPITPEQQAHAFA 59

Query: 62 KRFGAIERIGGGDIVAI-SNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
RFG + I I NV V D + + N WH D T++P A
Sbjct: 60 ARFGDLH-----IHPIYPNPVQTPQV-----LILDTAVTDVRDNAVWHTDVTFLPTPAL 108

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQA 178
GAV SA+ +PA GG T +A AA+ AL R ++ +A H + + G +
Sbjct: 109 GAVLSAKQLPAYGGDTLWASGIAAFQALSAPLREMLDGLTAMHDFTKSFPLERFGTTPED 168

Query: 179 GSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
+ + + PL P+++ HP +GR +L + I + ESE L+ L
Sbjct: 169 LARWEATRRNN--PPLSHPVIRTHPVSGRKALFVNEGFTTRINELSELESEALLKLLFAH 226

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
A + +W DV WDNH H A
Sbjct: 227 ATRPEFSIRWRWQENDVAFWDNRVTHQHA 255

>ref|YP_884597.1| alpha-ketoglutarate-dependent taurine dioxygenase [Mycobacterium
smegmatis str. MC2 155]
gb|ABK72553.1| alpha-ketoglutarate-dependent taurine dioxygenase [Mycobacterium
smegmatis str. MC2 155]
Length = 312

Score = 93.6 bits (231), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 82/281 (29%), Positives = 117/281 (41%), Gaps = 31/281 (11%)

Query: 12 GATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE-- 68
G TLGA ++GV L L A F L A ++ +L F Q +S D A++FG +E
Sbjct: 49 GTTLGAQISGVDLTRPLAGAVFDELRTALHEYKVLFFRDQPMSADAHAAALARQFGPLEVH 108

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
A++ + D V + AWH D T+ P + A+ A
Sbjct: 109 PLLPANSAESALARFQKDANVSGY-----ENAWHHDVTRWRPEPSILAILHA 154

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG 186
VP +GG T FADM AAYD+LD+ T+A + + A H Y L ++ +
Sbjct: 155 IEVPPIGGDTLFDADMYAAYDSLDDETKAEIDRLDAHDFTYLRLGLVPDEKIAELQAHAHP 214

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH 246
T P+V HP TGR L + R A L+D C+ H
Sbjct: 215 PVT-----HPVVCTHPITGRRHLYVNR---MFVSHIAGYPHDTGRALLDRLCRTADAPEH 266

Query: 247 Q---WAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
Q WA V +WNR + H A + R+M + + G
Sbjct: 267 QVRFRWAPDSVAIWDNRVQHYAASGYWPHTRIMERASVTG 307

>emb|CAY27276.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 93.6 bits (231), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 50/124 (40%), Positives = 68/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFADMRAAYDALDDETKVEIEDMICEHSLMYSRGSGLGFLD-----YTDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV++HP GR SL + HA AI GM E+ L L + A + V+ H+W D+V+
Sbjct: 56 RLVRIHPVHGRKSLYLSSHAGAIKGSVPEARLLLRNLTEHATKPEFVYVHKWTLHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>emb|CAY27521.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 93.6 bits (231), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 53/124 (42%), Positives = 72/124 (58%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALDE TRA V + HSL++S+ +G SA+ ++ L+
Sbjct: 1 TEFADMRAAYDALDERTRAEEVEELICEHSLHSGAIGF-----SAFTPEEIEGFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP TGR SL + H I G E+ F+ L++ A Q V+AH+W D+V+
Sbjct: 56 RLVRFHPATGRKSLFLSAHIGTIIGWPQPEAMAFIRDLEHATQPQFVYHRWTQHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>emb|CAY27476.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27547.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 93.6 bits (231), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 55/125 (44%), Positives = 71/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALDEAT+A Q HSL++S+ LG + T P+R
Sbjct: 1 TEFADMRAAYDALDEATKAETEQLVCEHSLMFSRGALGFSD-----LSKEERTMFRPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I G E+ FL +V+ A Q V++H+W D+V
Sbjct: 55 QRLVRTHPVTGRKSLFLSAHAGGIVGWPVPEARAFLRDMVEHATQPRFVYSHKWRQWDLV 114

Query: 255 VWDNR 259

+WDNR
Sbjct: 115 MWDNR 119

>ref|NP_742398.1| taurine dioxygenase [Pseudomonas putida KT2440]
gb|AAN65862.1|AE016214_7 alpha-ketoglutarate-dependent taurine dioxygenase
[Pseudomonas
putida KT2440]
Length = 277

Score = 93.6 bits (231), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 80/267 (29%), Positives = 118/267 (44%), Gaps = 19/267 (7%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+L ITP LGA ++GV ++ + A+ A LQH +L Q ++ +QQ FA R
Sbjct: 2 SLTITPLSPALGAQISGVDISRDIAEERDAIEQALLQHQLVFLRDQPINPEQQARFAAR 61

Query: 64 FGAIERIGGGDIVAI-SNVKADGTVRQHSPEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG + I I NV V D + + N WH D T++P A GA
Sbjct: 62 FGD LH-----IHPIYPNVDP TPQV-----LVLDTAVTDVRDNAVWHTDVTFLPTPALGA 110

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQAGS 180
V SA+ +PA GG T +A AA++AL R ++ +A H + + G Q +
Sbjct: 111 VLSAKQLPAYGGDTLWASGIAAFEALSAPLREMLDGLTATHDFTKSFPLERFGTTPQDLA 170

Query: 181 AYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
+ + PL P+V+ HP +GR +L + I + ES+ L L A
Sbjct: 171 RWEATRRNN--PPLSHPVVRTHPVSGRKALFVNEGFTTRINELSESDALLRLLFAHAT 228

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ +W DV WDNR H A
Sbjct: 229 RPEFSIRWRWQENDVAFWDNRVTQHFA 255

>ref|YP_103265.1| dioxygenase, TauD/TfdA [Burkholderia mallei ATCC 23344]
ref|ZP_00440417.1| dioxygenase, TauD/TfdA family [Burkholderia mallei GB8 horse 4]
ref|ZP_04884616.1| dioxygenase, TauD/TfdA [Burkholderia mallei ATCC 10399]
ref|ZP_04906581.1| dioxygenase TauD/TfdA family [Burkholderia mallei FMH]
ref|ZP_04915641.1| dioxygenase TauD/TfdA family [Burkholderia mallei JHU]
gb|AAU48166.1| dioxygenase, TauD/TfdA [Burkholderia mallei ATCC 23344]
gb|EDK56885.1| dioxygenase TauD/TfdA family [Burkholderia mallei FMH]
gb|EDK57139.1| dioxygenase TauD/TfdA family [Burkholderia mallei JHU]
gb|EDP88970.1| dioxygenase, TauD/TfdA [Burkholderia mallei ATCC 10399]
gb|EEP86043.1| dioxygenase, TauD/TfdA family [Burkholderia mallei GB8 horse 4]
Length = 292

Score = 93.6 bits (231), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 81/268 (30%), Positives = 120/268 (44%), Gaps = 20/268 (7%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFA-ALHAAWLQHALLIFPGQ-HLSNDQQITFAK 62
TL+I P T+GA V LA + ++G A + A L++ +L F Q LS + QI F +
Sbjct: 3 TLEIRPLSGTIGAQVRNRTLADVVESSGRADEIRQALLRYKVLFFTNQPELSVETQIAFGR 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E K DG Q +D + ++ WH D + +
Sbjct: 63 LFGELE-----TNFPSFTAKPDG---QPEVTVFDGAVSTGRASI-WHTDLSIAKTPSAMG 113

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ--SKLGHVQQAGS 180
+ + P GG T +AD+ AAY AL +A + + A H ++ Q G Q G
Sbjct: 114 ILCVKETPDSSGDTMWADLEAAYAALSPGMQAFLEGQRAVHDMMPQYAQHPGAFQTRGR 173

Query: 181 AYIGYGMDDTTAT--PLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWA 237
+ MD + P+V+VHPETGR L + + + G +AES L L

Sbjct: 174 S---DMDLSEVFGAEHPVVRVHPETGRKCLFVNPFLTSHLVGFHSAESATILNYLYALM 229

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ V W+ GDV +WDNRC +H A

Sbjct: 230 ERPQYVVRWHWSRGDVALWDNRCTMHTA 257

>ref|YP_003187897.1| alpha-ketoglutarate-dependent taurine dioxygenase [Acetobacter
pasteurianus IFO 3283-01]
dbj|BAH99517.1| alpha-ketoglutarate-dependent taurine dioxygenase [Acetobacter
pasteurianus IFO 3283-01]
dbj|BAI02570.1| alpha-ketoglutarate-dependent taurine dioxygenase [Acetobacter
pasteurianus IFO 3283-03]
dbj|BAI05616.1| alpha-ketoglutarate-dependent taurine dioxygenase [Acetobacter
pasteurianus IFO 3283-07]
dbj|BAI08665.1| alpha-ketoglutarate-dependent taurine dioxygenase [Acetobacter
pasteurianus IFO 3283-22]
dbj|BAI11713.1| alpha-ketoglutarate-dependent taurine dioxygenase [Acetobacter
pasteurianus IFO 3283-26]
dbj|BAI14759.1| alpha-ketoglutarate-dependent taurine dioxygenase [Acetobacter
pasteurianus IFO 3283-32]
dbj|BAI17805.1| alpha-ketoglutarate-dependent taurine dioxygenase [Acetobacter
pasteurianus IFO 3283-01-42C]
dbj|BAI20789.1| alpha-ketoglutarate-dependent taurine dioxygenase [Acetobacter
pasteurianus IFO 3283-12]
Length = 314

Score = 93.6 bits (231), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 73/262 (27%), Positives = 116/262 (44%), Gaps = 17/262 (6%)

Query: 9 TPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAI 67
TP +GA V+GV+LA +L + L L+H +L F Q+++ QQ FA+RFG +
Sbjct: 33 TPLSPAIGAIVSGVNLAQSLTAKTESRLRELLLRHQVLFRRNQNITPRQQRNFAQRFGPL 92

Query: 68 ERIGGGDIVA-ISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
+ VA + + T E +D+ N WH D T+ GAV +A
Sbjct: 93 HQHPIYPTVADVPEIIVLDT-----EQNDLK----DNALWHTDVTFSQTPLGAVLAA 141

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS--QSKLGHVQQAGSAYIG 184
+P GG T +A AAYDAL + + + +A H +S S+ G + ++
Sbjct: 142 RHLPPSGGDTLWASATAAYDALSDGMKLRLEHLTALHDFTHSFPLSRFGRTEAEKQKWL- 200

Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRV 243
+ P++++HPET + ++ + + G++ ES L L +
Sbjct: 201 RTREQQPPVEHPVIRIHPETNKRAIFVNEGFTTEVCGLEIEESAALLRFLFQHLSKPEFS 260

Query: 244 HAHQWAAGDVVVWDNRCLLHRA 265
W GDV WDNR H A
Sbjct: 261 VRWTWREGDVAFWDNRAQHYA 282

>ref|YP_001059547.1| dioxygenase, TauD/TfdA [Burkholderia pseudomallei 668]
gb|ABN82873.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 668]
Length = 292

Score = 93.6 bits (231), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 80/268 (29%), Positives = 122/268 (45%), Gaps = 20/268 (7%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFA-ALHAAWLQHALLIFPGQ-HLSNDQQITFAK 62
TL+I P T+GA V LA + ++G A + A L++ +L F Q LS + QI F +
Sbjct: 3 TLEIRPLSGTIGAQVRNRTLADVVESGRADEIRQALLRYKVLFFTNQPELSVETQIAFGR 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122

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          FG +E          A      + + TV          +D +      ++ WH D +      +
Sbjct: 63  LFGELE-TNFPSFTAKPEGQPEVTV-----FDGAVSTGRASI-WHTDLSIAKTPSAMG 113

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ--SKLGHVQQAGS 180
          +   + P   GG T +AD+ AAY AL      +A +   + A H ++ Q   + G   Q   G
Sbjct: 114 ILCVKETPDSSGDTMWADLEAAYAALSPGMQAFLEGQRAVHDMMPQYARPGAFQTRGR 173

Query: 181 AYIGYGMDDTAT--PLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWA 237
          +       MD +          P+V+VHPETGR L +          + + G +AES L L
Sbjct: 174 S---DMDLSEVFGAEHPVVRVHPETGRKCLFVNPFLTSHLVGFHSAESATILNYLYALM 229

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          +   V       W+ GDV +WDNRC +H A
Sbjct: 230 ERPQYVVRWHWSRGDVALWDNRCTMHTA 257

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>gb|ADR57960.1| TauD [Pseudomonas putida BIRD-1]
Length = 277

Score = 93.6 bits (231), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 81/267 (30%), Positives = 118/267 (44%), Gaps = 19/267 (7%)

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Query: 5   TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
          +L ITP   LGA ++GV L+   +       A+   A LQH +L   Q ++ +QQ FA R
Sbjct: 2   SLTITPLSPALGAQISGVDLSRDISAEERDAIEQALLQHQVLFRLDQPINPEQQARFAAR 61

Query: 64  FGAIERIGGGDIVAI-SNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
          FG +       I I NV       V       D +   + N WH D T++P A GA
Sbjct: 62  FGD LH-----IHPIYPNVDP TPQV-----LVLD TAVTDVRDNAVWHTDVTF LPTPALGA 110

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQAGS 180
          V SA+ +PA GG T +A   AA++AL   R ++   +A H   +   + G   Q   +
Sbjct: 111 VLSAKQLPAYGGDTLWASGIAAFEALSAPLREMLDGLTATHDFTKSFPLERFGTTPQDLA 170

Query: 181 AYIGYGMDDTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
          +   +   PL P+V+ HP +GR +L +       I +   ES+ L L A
Sbjct: 171 RWEATRRNN--PPLSHPVVRTHPVSGRKALFVNEGFTTRINELSELESDALLRLLFAHAT 228

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          +       +W   DV   WDNR   H A
Sbjct: 229 RPEFSIRWRWQEHDVAFWDNRVTQHFA 255

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>ref|YP_002799353.1| TauD/TfdA family taurine catabolism dioxygenase [Azotobacter vinelandii DJ]
gb|AC078378.1| taurine catabolism dioxygenase, TauD/TfdA family [Azotobacter vinelandii DJ]
Length = 287

Score = 93.2 bits (230), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 80/275 (29%), Positives = 115/275 (41%), Gaps = 23/275 (8%)

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Query: 5   TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
          TL+ITP   T+GA V+GV L L A   L A LQ+ +L F QHLS +QQ+ FA+
Sbjct: 12  TLEITPLEPTIGA EVSGVDLKKPLSPAQRDLKALLLQYKVLFFRDQHL SREQQVAFARH 71

Query: 64  FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
          FG +       +       + A + D ++       WH+D++++ GAV
Sbjct: 72  FGELYVHPTSKQPDERFPEVHQIIASEARARYGDALR-----GRWHS DTSWLLEPTYGAV 126

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
          +P GG T +AD   Y L + +A +       H+ S +G
Sbjct: 127 LRPLDLPPAGGDTIWADSGLVYRGLPDDVKARIDDLVYVHNFKPSLDAVG-----F 177

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Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPR 242
Y + + PLV+ HPETG L I I G ES ++ L+ P
Sbjct: 178 DYPLVS-----HPLVRTHPETGEDVLFINFSMPYILGWSPEESRELVDYLLK-EFSTPE 231

Query: 243 VHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
H +W G + WDNR LH PRVM
Sbjct: 232 YHVRFKWREGSLAFWDNRSSLHYPVHNYGDYPRVM 266

>ref|YP_002396447.1| taurine dioxygenase [Escherichia coli ED1a]
emb|CAR06605.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli
ED1a]
Length = 283

Score = 93.2 bits (230), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 78/289 (26%), Positives = 125/289 (43%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA +TG L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQITGADLTRPLSDNQFEQLYHAVLRHHVVFLRDQAITPQQQRALAQR 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIQTP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T +A AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWASGIAAYEALSVPFRQLLSGLRAEHDFRKSFPEYKY-RKT 167

Query: 179 GSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + + P L P+V+ HP TG+ +L + I + ESE L G +
Sbjct: 168 EAEHQRWREAVAKNPPLLHPVVRTHPVTGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M+ + + G
Sbjct: 227 AHITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMYRATILG 275

>ref|YP_001412266.1| taurine dioxygenase [Parvibaculum lavamentivorans DS-1]
gb|ABS62609.1| Taurine dioxygenase [Parvibaculum lavamentivorans DS-1]
Length = 271

Score = 93.2 bits (230), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 80/285 (28%), Positives = 117/285 (41%), Gaps = 39/285 (13%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
M L + P A +GA + G+ L+ L + +H A +QH ++ F Q L + +
Sbjct: 1 MDYEVLTVKPMSTARIGAEIEGIDLSEPLSNKVIDEVHTALMQHQVIFFRDQELDHVRHKE 60

Query: 60 FAKRFGAIERIGG-----GDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
+ FG + G +IVAI D+ K + G WH+D
Sbjct: 61 LGRAFGELAIHSGVAGLADHPEIVAIHA-----DEKSKFVAGE-NWHS DL 104

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
T + G++ VVP VGG T FA M AAY+AL + + A H + +
Sbjct: 105 TCNEIPPMSILYLPVVPEVGGDTMFASMYAAEALSPGMQTYLDGLYAVHDGEHVYRPI 164

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLE 231
V + P+V+ HP TGR + + + I G+ AES+ LE
Sbjct: 165 --VNDPNKRF-----PCNTHPVVRTHPVTGRKGIFVNPSYTTTEIVGLGKAESDGVLE 214

Query: 232 GLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRV 275

L C P H +W V WDNRC H A WD+ P+V
Sbjct: 215 MLYK-HCANPNFHVFRWPKSVAFWDNRCTWHLAV-WDY-FPQV 256

>emb|CAY27235.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27237.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27241.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27243.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27247.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27251.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27253.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27258.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 93.2 bits (230), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 50/124 (40%), Positives = 68/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFADMRAAYDALDDETKVEIEDMICEHSLMYRSGSLGFLD-----YTDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV++HP GR SL + HA AI GM E+ L L + A + V+ H+W D+V+
Sbjct: 56 RLVRIHPVHGRKSLYLSSHAGAIKMSVPEARLLLRDLTEHATKPEFVYVHKWTLHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>emb|CAY27510.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 93.2 bits (230), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 52/124 (41%), Positives = 67/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALD+ T+A + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFADMRAAYDALDDETKAEIEDLVCEHSLMYRSGSLGFLD-----YSDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP GR SL + HA AI GM E L L + A Q V+ H+W D+V+
Sbjct: 56 RLVRTHPAHGRKSLYLSSHAGAIKMSVPEGRLLLRDLNEHATQLEFVYVHKWKLHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>ref|YP_701701.1| taurine dioxygenase [Rhodococcus jostii RHA1]
gb|ABG93543.1| probable taurine dioxygenase [Rhodococcus jostii RHA1]
Length = 318

Score = 93.2 bits (230), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 78/299 (26%), Positives = 129/299 (43%), Gaps = 35/299 (11%)

Query: 2 AQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A T L++ P +GA ++G+ L L D A + A ++ +L F Q + + +QI F
Sbjct: 15 ADTALEVRPVAGHIGAEISGIDLRKELADNEVAQVRDALHRYKVLFFRDQEIGHAEQIAF 74

Query: 61 AKRFGAIERI-----GGGDIVAIISNVKADGTVRQHSPAEDDMMKVIVGNMAWHAD 111
+++FG + G I+A+ + K + + K + WH D
Sbjct: 75 SRKFGDVTSPHPYDDEAPEGFQILAVDSRKYEKFRG-----KKYSYDNKWHTD 124

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
T + G + A +VP GG T + ++ AAY+ L ++ + LV A H +
Sbjct: 125 VTALINPPAGTILRAHIVPEQGQDQTWNLVAAIEGLPDSLKGLVDGLRAEH-----R 177

Query: 172 LGHVQQAGSAYIGYGMDDTTATPL---RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESE 227
G + Y + T PL P+V+VHP TG +L + I G+ ++S+
Sbjct: 178 FGGRHPQWAEEDSSYALKTRENPLVTEHPVVRVHPVTGERALFVTPGFTSRIVGVSPSQSD 237

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283
R L+ L +WA G + WDNR H A P D + RV++ + L G
Sbjct: 238 RLLDLLFAEVTNPAYTVRFRWAPGSLAFWDNRATAHLA-PTDLHDLDVTRVLYRTTLEG 295

>ref|ZP_03426827.1| dioxygenase [Mycobacterium tuberculosis T92]
Length = 274

Score = 93.2 bits (230), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 72/240 (30%), Positives = 103/240 (42%), Gaps = 13/240 (5%)

Query: 27 LDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERIGGGDIVAISNVKADG 85
LD A + AA L H ++ F GQH L + +Q+ FA G IG +A+++ D
Sbjct: 6 LDPAAVNEIRAALLAHKVVFRRGQHQLDDAEQLAFAGLLGT--PIGHPAAIALAD---DA 60

Query: 86 TVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAY 145
+ +E+ + WH D T+ +V A +P+ GG T +A+ AAY
Sbjct: 61 PIITPINSEFGKANR-----WHTDVTFAANYPAASVLRVSLPSYGGSTLWANTAAAY 113

Query: 146 DALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETG 205
L E + L A H+ Y + A A+ P+V+VHPETG
Sbjct: 114 AELPEPLKCLTENLWALHTNRYDYVTTKPLTAAQRAFRQVFEKPDFRTEHPVVRVHPETG 173

Query: 206 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
+LL G + G+D+ ES E L WA GDV +WDNR HRA
Sbjct: 174 ERTLLAGDFVRSFVGLDSHESRVLFVLRITMPENTIRWNWAPGDVAIWDNRATQHRA 233

>emb|CAY27216.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 92.8 bits (229), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 54/128 (42%), Positives = 71/128 (55%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALD+AT+A V HS+VYS+ ++G A + A LR
Sbjct: 1 TEFADMRAAYDALDDATKAIVEDLVTEHSIVYSREQIGFNDYA-----EGNADRLR 51

Query: 196 P----LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251
P LV HP TGR SL + H I G E+ F+ L++ A Q V++H+W
Sbjct: 52 PVQHRLVITHPVTGRKSLYLSSHIGGIVGWPMPEARAFIRDIEHATQPEFVYSHKWRVN 111

Query: 252 DVVVDNR 259
D+V+WDNR
Sbjct: 112 DMVMWDNR 119

>gb|ACX54985.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ACX54988.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ACX54989.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 89

Score = 92.8 bits (229), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 53/95 (55%), Positives = 62/95 (65%), Gaps = 6/95 (6%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYMPV A+ ++ SA VV GG T +ADMRAA DALD R+ V SA HS+ YSQ
Sbjct: 1 ADSTYMPVSAKASMLSARVVTTKGGETEWADMRAALDALDTEARSRVADLSAYHSIAYSQ 60

Query: 170 SKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPET 204
++ G +GYGMD A LRPLVKVHPET
Sbjct: 61 AQAGFESD-----LGYGMDEAAQ-LRPLVKVHPET 89

>emb|CAY27268.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 92.8 bits (229), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 50/124 (40%), Positives = 68/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFADMRAAYDALDDETKVEIEDMICEHSLMYSRGSLSGLFD-----YTDEEKEMFEPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV++HP GR SL + HA AI GM E+ L L + A + V+ H+W D+V+
Sbjct: 56 RLVRIHPVHGRKSLYLSSHAGAIKMSVPEARLLLRDLTEHATKPEFVYVHKWTLHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>emb|CAY27440.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 92.8 bits (229), Expect = 5e-17, Method: Compositional matrix adjust.
Identities = 53/125 (42%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALDE T+A + HSL+YS+ LG + + T TP+R
Sbjct: 1 TEFADMRAAYDALDEKTKAEAEDLACEHSLIYSRGTGLGFTE-----LSEEEKKTFTTPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 254
LV+ HP TGR SL + H I G E+ F+ L + A Q +AH+W D+V
Sbjct: 55 QRLVRTHPVTGRKSLYLSSHIGTIVGWPMPEARAFIRDLTEHATQPRFTYAHKWRQFDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|YP_002768378.1| dioxygenase [Rhodococcus erythropolis PR4]
dbj|BAH35639.1| putative dioxygenase [Rhodococcus erythropolis PR4]
Length = 281

Score = 92.8 bits (229), Expect = 5e-17, Method: Compositional matrix adjust.
Identities = 80/278 (28%), Positives = 117/278 (42%), Gaps = 14/278 (5%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
+ T +TPT T+GA ++G+ L+ L D + L A L+ +L F Q + +
Sbjct: 2 LPYTRFTLTPTTPTIGAEISGIQLSGQLSDETMSELRRALLEWKVLFVRDQTIDRSEHRD 61

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119

FA R+G++E+ +AD D M + N WH D ++ +
Sbjct: 62 FASRWGSLEQHPFFKYTQPGQSEADIVTLAK-----DAMTGGVENN--WHNDVSWHEFPS 114

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
AV A VP VGG T +AD AAY+ L E + + Q A H + S K H+ +
Sbjct: 115 FAAVLRAVEVPPVGGDTLWADTGAAYELLPEGIKERIDQLVAEHDWINSFGK--HMDPST 172

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWAC 238
A + P+V+V PETGR L + I G+ AES+ L L
Sbjct: 173 VAKLRPQFPAVR--HPVVRVIPETGRKVLVFNLSFTQRIVGVSSEADELLTLRYRHVH 229

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
+ +W + WDNR H A F RVM
Sbjct: 230 RPEFQVRLKWRNTTIAFWDNRTCQHYAASDYFPARRVM 267

>emb|CAY27211.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 92.8 bits (229), Expect = 5e-17, Method: Compositional matrix adjust.
Identities = 55/125 (44%), Positives = 70/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALDE T+ LV HS +YS+ LG + P+R
Sbjct: 1 TEFADMRAAYDALDEETKDLVADLVCEHSQLYSRQLLGFTDFTEERERF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA +I G E+ FL+ L + A Q V+AH+W GD+V
Sbjct: 55 QRLVRTHPTVGRKSLYLSSHAGSIVGWPVPEARAFLKDLNEHATQREFVYHRWRVGDV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>emb|CAY27305.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 92.8 bits (229), Expect = 5e-17, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 71/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALD+ T+A + RHS +YS+ KLG V+ + P+R
Sbjct: 1 TEFADMRAAYDALDDRTKADIENLVCRHSNMYSRGKLGVEFTDEERAVF-----RPVR 54

Query: 196 PL-VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
L V+ HP +GR SL + H I GM ++ L L ++A + P V++H W D+V
Sbjct: 55 QLLVRRHPVSGRKSFLSAHVGEIEGMPTPQARMLLLDLTFATREPFVYSHVWRVNDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>emb|CAJ89754.1| putative dioxygenase [Streptomyces ambofaciens ATCC 23877]
Length = 329

Score = 92.8 bits (229), Expect = 5e-17, Method: Compositional matrix adjust.
Identities = 88/292 (30%), Positives = 127/292 (43%), Gaps = 20/292 (6%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+++ P +GA + GV LA LD A AA+ AA L+ ++ F QHL + + FA+ F
Sbjct: 22 IEVEPAAGHIGAEIHGVDLAGGLDAAQVAAVRAAVLRWKVFFRQHLHDHAGHVAFARLF 81

Query: 65 G---AIERIGGGDIVAISNVKAD-----GTVRQHSPA EWDDMMKVIVGNMAWHADSTYM 115
G + R G ++ G EW + + WH D
Sbjct: 82 GDPVTLPRRGKASPAGFPEIETTADRLELGGFRFGMEHDEWLRRRRRTL-LRGWHCDHGAR 140

Query: 116 PVMAQGA VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
+ AE VP GG T +++ AAY L RA V A H L +G+
Sbjct: 141 VDPPAATILRAETVPPYGGDTTWSNLAAAYAGLSAPMRAFDGLRAEHL-----GVGYQ 195

Query: 176 QQAG-SAYIGYGMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGL 233
+ G AY+ + +D + PLV+VHPETG L + G + I G+ ES LE L
Sbjct: 196 PRPGDDAYVRHLLDHQTSVHPLVRVHPETGERVLFVNGYVVEQIVGLSRPESA AAVLELL 255

Query: 234 VDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKL--PRVMWHSRLAG 283
++ A + +W G V WDNR +H A + L PR M LAG
Sbjct: 256 LEHATRPEYTVRFRWQPGSVAFWDNRATIH LAPS DNAHLDPRTMHRVMLAG 307

>emb|CAY27393.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 92.8 bits (229), Expect = 5e-17, Method: Compositional matrix adjust.
Identities = 54/125 (43%), Positives = 70/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYD LDEAT+A Q HSL++S+ LG + T P+R
Sbjct: 1 TEFADMRAAYDGLDEATKAETEQLVCEHSLMFSRGALGFS DLSKEER-----TMFRPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I G E+ FL +V+ A Q V++H+W D+V
Sbjct: 55 QRLVRTHPVTGRKSLFLSTHAGGIVGWVPPEARAF LRDMVEHATQPRFVYSHKWRQWDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|YP_608305.1| dioxygenase, TauD [Pseudomonas entomophila L48]
emb|CAK15507.1| putative dioxygenase, TauD [Pseudomonas entomophila L48]
Length = 289

Score = 92.8 bits (229), Expect = 5e-17, Method: Compositional matrix adjust.
Identities = 86/297 (28%), Positives = 131/297 (44%), Gaps = 52/297 (17%)

Query: 7 QITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
++TP +GA + GV L+ L A + A+L++ +L+F QHL +Q F + FG
Sbjct: 27 RLTPV---IGA EIGGV DLSRPLAAEQ LAEIRRAFLNHVLFVRDQHLDVEQHKA FGRLFG 83

Query: 66 AIERIG----GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQG 121
+ + GD + ++A+ R V WH D T + G
Sbjct: 84 ELRALPLDDIDGDDPELVVIRANAQSR-----FVAGETWHTDGTADLEPSMG 130

Query: 122 AVFSAEVVPVAVG--GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
++ + PA+G G T FA+M A + L A +A + +A H
Sbjct: 131 SMLYVKETPAIGTGGDTL FANMHLALEMLSPAMQAFLGTLTAIHD-----GE 177

Query: 180 SAYIGY----GMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGL 233
+ GY G+ T P+V HP+TGRPSL + G +H + + A ES+ L L
Sbjct: 178 MPWKGYTPPPGLPKTE---HPVVVRHPQTGRPSL FVNSGFTSHIV-QLSAGESQMLLNLL 233

Query: 234 VDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSR---LAGRPE 286
D + P + +WA G +V WDNRC H A WD+ P + R L GRP+
Sbjct: 234 FDLVAREPVLSCRVRWAPGTLVFWDNRC TQHHAV-WDY-FPHSRYGERVTILGGRPQ 288

>ref|YP_296355.1| taurine dioxygenase [Ralstonia eutropha JMP134]
gb|AAZ61511.1| Taurine dioxygenase [Ralstonia eutropha JMP134]
Length = 282

Score = 92.4 bits (228), Expect = 6e-17, Method: Compositional matrix adjust.
Identities = 78/274 (28%), Positives = 120/274 (43%), Gaps = 28/274 (10%)

Query: 6 LQITPTGATLGATVTGVHLA--TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+Q+ +LGA + GV+LA DD FA + A LQH +L Q++S + FA+R
Sbjct: 1 MQVKQITCSLGAELVGVNLADAVRDDGLFAEIRALLLQHRVLFRLDQNISRADHVAFAARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E VA S+ + G VR + +P + +D + AWH+D+T+ GA
Sbjct: 61 FGELE----DHPVAGSDPEHPGLVRIYKTPDQPNDRYE-----NAWHSDDTTWREAPQFGA 111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V P VGG T +A+M AY+ L E +A + ARHS+ S +++ +
Sbjct: 112 VLRCVECPVGGDTMWANMALAYERLPEHIKAQIADLRARHSIEASFGAAMPIEKRLALK 171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE-----GLVD 235
Y P+V+ HPETG L + A RF + L+
Sbjct: 172 AQY-----PDAEHPVVRTHPETGEKILYVNAFTTHTFTNFHTANRVRFGQDANPGAPDLLR 226

Query: 236 WACQAPRVHAHQ---WAAGDVVVWDNRCLLHRA 265
+ + +Q W + +WDN H A
Sbjct: 227 YLISQAYIPEYQVRWRWEPNSMAIWDNTATQHYA 260

>gb|ACX54996.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 89

Score = 92.4 bits (228), Expect = 6e-17, Method: Compositional matrix adjust.
Identities = 53/95 (55%), Positives = 62/95 (65%), Gaps = 6/95 (6%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYMPV A+ ++ SA VV GG T +ADMRAA DALD R+ V SA HS+ YSQ
Sbjct: 1 ADSTYMPVSAKASMLSARVVTTKGGETEWADMRAALDALDPEARSRVADLSAHSIAYSQ 60

Query: 170 SKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPET 204
++ G +GYGMD A LRPLVKVHPET
Sbjct: 61 AQAGFESD-----LGYGMDEAAQ-LRPLVKVHPET 89

>ref|YP_257356.1| taurine catabolism dioxygenase TauD [Pseudomonas fluorescens Pf-5]
gb|AA95621.1| taurine dioxygenase, TauD/TfdA family [Pseudomonas fluorescens
Pf-5]
Length = 301

Score = 92.4 bits (228), Expect = 6e-17, Method: Compositional matrix adjust.
Identities = 79/265 (29%), Positives = 114/265 (43%), Gaps = 18/265 (6%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L I P +GA + GV L+ LD A A+ A +Q+ ++ F GQ HL + Q F+
Sbjct: 15 LDIHPVAGRIGAEIRGVQLSGDLDAATVEAIRQALVQYKVIFFRQTHLDDQSQEAFSHL 74

Query: 64 FGAIERIGGGDIVAISNVKA-DGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
G + VA V DGT E D +WH D T++ + +
Sbjct: 75 LG-----EPVAHPTVPVRDGT---RYLMELDGAQGQRAN--SWHTDVTTFVDAYPKAS 121

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVYSQSKLGHVQQAGS 180

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      + + V PA GG T +A+  AY+ L   R L +  A HS   Y+ +K   +
Sbjct: 122 ILRSVVAPASGGDTVWANTATAYNELSAELRELADKLWAVHSNEYDYAGAKPDVSAE KLE 181

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
      Y      T      P+V+VHPE+G  SL++G      I G  A+S      L      +
Sbjct: 182 RYRKVFTSTVFETEHPIVRVHPESGEKSLVLGHFVKRIKGYSQADSAHLFGLLQSHVTRL 241

Query: 241 PRVHAHQWAAAGDVVVWDNRCLLHRA 265
      +W+AGDV +WDNR   H A
Sbjct: 242 ENTVRWRWSAGDVAIWDNRSTQHYA 266

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>emb|CAY27418.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 92.4 bits (228), Expect = 6e-17, Method: Compositional matrix adjust.
Identities = 52/125 (41%), Positives = 71/125 (56%), Gaps = 7/125 (5%)

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Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
      T F DMRAAYDALD+AT+A +      HSL++S+  LG +      +      T P+R
Sbjct: 1   TEFGDMRAAYDALDDATKAEIEDLVCEHSLIFSRGSLGFTE-----LSEEEERATFRPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDVV 254
      LV+ HP TGR SL +  H AI G   E+  FL  L++ A Q   V++H+W   D+V
Sbjct: 55  QRLVRAHPVTGRKSLFLSSHGGAILGWPVPEARAFRLDLMEHATQPQFVYSHKWRQWDLV 114

Query: 255 VWDNR 259
      +WDNR
Sbjct: 115 MWDNR 119

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>ref|YP_001563037.1| taurine dioxygenase [Delftia acidovorans SPH-1]
gb|ABX34652.1| Taurine dioxygenase [Delftia acidovorans SPH-1]
Length = 281

Score = 92.4 bits (228), Expect = 6e-17, Method: Compositional matrix adjust.
Identities = 89/298 (29%), Positives = 127/298 (42%), Gaps = 46/298 (15%)

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Query: 7   QITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      QITP      +GA ++GVHL  A  D A FA + AA L H +L F  Q ++  + + FA RF
Sbjct: 5   QITPA---IGAEISGVHLGDAARDAALFADIRAALLTHRVLFRRDQDITRAEHVAFASRF 61

Query: 65  GAIERIGGGDIVAISNVKADGTVRQH---SPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
      G +E      VA S+ +  G VR +      P +++      WH D + P  A G
Sbjct: 62  GPLE----DHPVAGSDPEHPGLVRIYRSDDPHSYEN-----TWHC DGLWRPNPAMG 108

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
      AV      P +GG T + +M  AY+ L E      S + S+  ++K G      G+
Sbjct: 109 AVLRCIECPPIGGDTIWVNMVKAYEELPE-----SIKRSIGGLRAKAGIEHTFGAV 159

Query: 182 YIGYGMDDTTAT---PLR-PLVKVHPETGRPSLLIGRH-----AHAIP-----GMDAAES 226
      A+   P+  P+V+ HPETG  L +G      ++ P      G+D A
Sbjct: 160 MAPEARARLASEHPPVEHPVVRTHPETGEKLLFVGAGFSTHFVNYSTPENVRHGIDKAPG 219

Query: 227 ERFLEGLVDWACQAPRVHAH-QWAAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
      L +      P      W  GDV VWDNR  H A      +  PR M  + + G
Sbjct: 220 AALLMNYLISRATIEYQVRWSWKPGDVAVWDNRSTQHYALNDYYPAPRRMERAGIVG 277

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>emb|CAY27497.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 92.4 bits (228), Expect = 7e-17, Method: Compositional matrix adjust.

Identities = 51/124 (41%), Positives = 66/124 (53%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRA YDALD+ TRA + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFGDMRAGYDALDDETRAIEDMVCEHSLMYSRGSGLGFLD-----YTDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP GR SL + HA AI GM E+ L L + A Q V+ H+W D+V+
Sbjct: 56 RLVRTHPVHGRKSLYLSSHAGAIQGMSPPEARLLLRDLTEHATQPEFVYVHKWTLHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>emb|CAY27456.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 92.4 bits (228), Expect = 7e-17, Method: Compositional matrix adjust.
Identities = 53/125 (42%), Positives = 70/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALD T+A V + HSL++S+ +G Q + P+R
Sbjct: 1 TEFADMRAAYDALDARTKAEVEELVCEHSLHSGAIGFTQFTPEEIEINF-----RPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 254
LV+ HP+TGR SL + HA AI G E+ FL L + A Q V++H W D+V
Sbjct: 55 QRLVTRHPQTGRKSLFLSSHAGAIEGWTIPEARSFLRDLTEHATQREFVYSHPWQRHDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>gb|EGB71242.1| TfdA family protein Taurine catabolism dioxygenase TauD
[Escherichia coli TW10509]
Length = 283

Score = 92.4 bits (228), Expect = 7e-17, Method: Compositional matrix adjust.
Identities = 78/288 (27%), Positives = 122/288 (42%), Gaps = 27/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA +TGV L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQITGVDLTRPLSDNQFEQLYHAVLRHQVFLREQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQQA 178
GA+ +A+ +P+ GG T ++ AAY+AL R L+ A H S + + +
Sbjct: 109 PAGAILAAKELPSTGGDTLWSSGIAAYEALSVPFRRQLLSGLCAEHDFRKSFPPEYKYRKTE 168

Query: 179 GSAYIGYGMDDTTATP-LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
+ P L P+V+ HP TG+ +L + I + ESE L G +
Sbjct: 169 EEHQRWHEAVAKNPPLHPVVRTHPVTGKQALFVNEGFTTRIVDVSEKESEALL-GFLFA 227

Query: 237 ACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G
Sbjct: 228 HITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>gb|ACX54987.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein

[uncultured bacterium]
gb|ACX54999.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 89

Score = 92.4 bits (228), Expect = 7e-17, Method: Compositional matrix adjust.
Identities = 53/95 (55%), Positives = 62/95 (65%), Gaps = 6/95 (6%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
ADSTYMPV A+ ++ SA VV GG T +ADMRAA DALD R+ V SA HS+ YSQ
Sbjct: 1 ADSTYMPVSAKASMLSARVVTTKGGETEWADMRAALDALDPEARSRVADLSAYHSIAYSQ 60

Query: 170 SKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET 204
++ G +GYGMD A LRPLVKVHPET
Sbjct: 61 AQAGFESD-----LGYGMDEAAQ-LRPLVKVHPET 89

>gb|ACG80557.1| TfdA [uncultured bacterium]
Length = 119

Score = 92.4 bits (228), Expect = 7e-17, Method: Compositional matrix adjust.
Identities = 53/127 (41%), Positives = 68/127 (53%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT--- 192
T F DMRAAYDALD+ T+A + HSL+YS+ LG ++ Y D A
Sbjct: 1 TEFGDMRAAYDALDDDTKAEIEDMICEHSLMYSRGSLG-----FLDYTDDEKAMFKP 52

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
L+ LV+ HP R SL + HA AI GM E+ L L + A Q VH H+W D
Sbjct: 53 VLQRLVTRHPVHRRKSLYLSSHAGAIKMSMPEARLLLLRDLTEQATQREFVHIHKWTVDH 112

Query: 253 VVVWDNR 259
+V+WDNR
Sbjct: 113 LVMWDNR 119

>emb|CAY27485.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 92.4 bits (228), Expect = 7e-17, Method: Compositional matrix adjust.
Identities = 54/125 (43%), Positives = 70/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRAAYDALDEAT+A Q HSL++S+ LG + T P+R
Sbjct: 1 TEFGDMRAAYDALDEATKAETEQLVCEHSLMFSRGALGFSDLKEER-----TMFRPV 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 254
LV+ HP TGR SL + HA I G E+ FL +V+ A Q V++H+W D+V
Sbjct: 55 QRLVTRHPVTGRKSLFLSAHAGGIVGWPVEARAFLRDMVEHATQPRFVYSHKWRQWDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>emb|CAY27277.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 92.4 bits (228), Expect = 7e-17, Method: Compositional matrix adjust.
Identities = 49/124 (39%), Positives = 68/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+

Sbjct: 1 TEFADMRAAYDALDDETKVEIEDMICEHSLMYSRGSLGFLD-----YTDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV++HP GR SL + HA AI GM E+ + L + A + V+ H+W D+V+

Sbjct: 56 RLVRIHPVHGRKSLYLSSHAGAIKMSVPEARLLMRDLTEHATKPEFVYVHKWTLHDLVM 115

Query: 256 WDNR 259
WDNR

Sbjct: 116 WDNR 119

>gb|ABR27343.1| TfdA [uncultured bacterium]
Length = 118

Score = 92.4 bits (228), Expect = 7e-17, Method: Compositional matrix adjust.
Identities = 51/122 (41%), Positives = 66/122 (54%), Gaps = 5/122 (4%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPL 197
FADMRAAYDALD+ T+A + HSL+YS+ LG + Y + L+ L

Sbjct: 2 FADMRAAYDALDDETKAEIEDLICEHSLMYSRGSLGFLD-----YTDEEKEMFKPVLQRL 56

Query: 198 VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWD 257
V+ HP GR SL + HA AI GM E L L + A Q V+ H+W D+V+WD

Sbjct: 57 VRTHPAHGRKSLYLSSHAGAIRGMSMEGRLLLRDLTEHATQPEFVYVHRWTVHDLVMWD 116

Query: 258 NR 259
NR

Sbjct: 117 NR 118

>emb|CAY27526.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 92.0 bits (227), Expect = 8e-17, Method: Compositional matrix adjust.
Identities = 52/127 (40%), Positives = 70/127 (55%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTAT--- 192
T FADMRAAYDALD+ T+A + HSL+YS+ LG ++ Y + A

Sbjct: 1 TEFADMRAAYDALDDETKAEIEDMICEHSLMYSRGSLG-----FLDYSDEEKAMFKP 52

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
L+ LV+ HP GR SL + HA AI GM E+ L L + A + V+ H+W D

Sbjct: 53 VLQRLVTRHPVHGRKSLYLSSHAGAIKMSVPEARLLLRDLTEHATKPEFVYVHKWTLHD 112

Query: 253 VVVWDNR 259
+V+WDNR

Sbjct: 113 LVMWDNR 119

>gb|ADC34016.1| TfdA-like protein [uncultured bacterium]
Length = 198

Score = 92.0 bits (227), Expect = 8e-17, Method: Compositional matrix adjust.
Identities = 60/207 (28%), Positives = 97/207 (46%), Gaps = 10/207 (4%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
QQI FA+R G I V +G + + + +G WH D +Y

Sbjct: 1 QQIAFARRLGRI-----VVNKFFPENGAHPEIAEVRKEKEQRTNIGG-GWHTDHSYD 51

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
P+ A G++ A +P GG T FA++ AAYDAL + + + A+HS + + G

Sbjct: 52 PIPALGSILVARELPESGGDTMFANLYAAYDALSDGLKRTLSTLRKHSNRHLYGENGLY 111

Query: 176 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
+++ A G + + + P+V HPE+GR +L + H G A+S L+ L
Sbjct: 112 RKSDLASQLKGPEGVSDAVHPVWITHPESGRRALYVNPGLHFEWSEADSRPLLKHLV 171

Query: 235 DWACQAPRVHAHQWAAGDVVWDNRCL 261
+ A + +WA G + WDNRC+
Sbjct: 172 EHASRPEFTCRFRWAPGSIAFWDNRV 198

>ref|YP_003598515.1| alpha-ketoglutarate-dependent taurine dioxygenase [Bacillus megaterium DSM 319]
gb|ADF40165.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Bacillus megaterium DSM 319]
Length = 311

Score = 92.0 bits (227), Expect = 9e-17, Method: Compositional matrix adjust.
Identities = 75/275 (27%), Positives = 115/275 (41%), Gaps = 37/275 (13%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T I P +GA + G+ L+ L L+ A+L+ +L F Q +++Q + FAK
Sbjct: 39 TFFSIKPLTPIIGAEIEGLDLKPLAKEVQEELNRAFLEWKVLFRRNQAITSEQHLAFK 98

Query: 63 RFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADST 113
+G +E + +IV S + G WHAD T
Sbjct: 99 LWGDLEVHPFYKPASQEQAKEIVQFSRNQKQGG-----SENVWHADVT 141

Query: 114 YMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
+ A+ +V VP VGG T +ADM AAYD L E+ + + A H S
Sbjct: 142 FRENPAKASVLRLEVEPPVGGDTLWADMAAAYDNLPESIKKQIEHLKAIHDFTPS---FA 198

Query: 174 HVQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH--AHAIPGMDAAESERFLE 231
H+ Q + + A P+V+ HPETGR +L + H + G++ +E E+ L+
Sbjct: 199 HLLQPDELE-AFQREFPAVK-HPIVRTHPETGRKTLFVNSSFTTHVV-GLHSEGEQLLQ 255

Query: 232 GLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
L P +W + WDNR H A
Sbjct: 256 YLFR-QVHVPEYQVFRFRWEVNSIAFWDNRATQHYA 289

>ref|ZP_02144821.1| dioxygenase, TauD/TfdA family protein [Phaeobacter gallaeciensis BS107]
gb|EDQ13282.1| dioxygenase, TauD/TfdA family protein [Phaeobacter gallaeciensis BS107]
Length = 278

Score = 92.0 bits (227), Expect = 9e-17, Method: Compositional matrix adjust.
Identities = 78/292 (26%), Positives = 122/292 (41%), Gaps = 33/292 (11%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
+ I P LGA + G + +D F+A+ A+ +++++ GQ + FA+RFG
Sbjct: 1 MDILPMTGGLGAEILGADIRSED--FSAIRDAFAEYSVIVLRGQTAGPGDHLAFARRFG 58

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNM-----AWHADSTYMPV 117
+ NV R P E + ++ WH D +Y
Sbjct: 59 PV-----NVN-----RFFKPVEGHPEIATVLKEKDQTEAVGEGWHTDHSYDQE 101

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHV 175
A G++ A +P GG T F M AAY+AL E R + +A HS V+ + +
Sbjct: 102 PAMGSILHAIEMPPYGGDTLFSMGAAYEALSEPMMRFLDGLTAVHSSRHVFGAAAMDS- 160

Query: 176 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
+ S +G T P+V HP +GR L + I G++ ES L ++
Sbjct: 161 EAVKSGRLGNAEAAATQDVRHPVWITHPLSGRRGLFVNPFVTTRIEGLNPEESSALL-AML 219

Query: 235 DWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
CQ P +W AGD+ +WDNR H+A R+M + G P
Sbjct: 220 YAHCCQQPEFQCRVRWRAGDITMWDNRATRHKAINDYHGFRRLMHRVTVEGGP 271

>gb|AAS64583.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
Length = 119

Score = 92.0 bits (227), Expect = 9e-17, Method: Compositional matrix adjust.
Identities = 53/127 (41%), Positives = 70/127 (55%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTAT--- 192
T FADMRAAYDALD+ T+A + HSL+YS+ LG ++ Y + A
Sbjct: 1 TEFADMRAAYDALDDDTKAEIEDMICEHSLMYSRGS LG-----FLDYSEEEKAMFKP 52

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
L+ LV+ HP R SL + HA AI GM E+ L L + A Q V+AH+W D
Sbjct: 53 VLQRLVRTHPVHRRKSLYLSSHAGAIQGMSVPEARLLLRDLTEHATQREFVYAHKWTLLHD 112

Query: 253 VVVWDNR 259
+V+WDNR
Sbjct: 113 LVMWDNR 119

>ref|YP_729160.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Ralstonia
eutropha H16]
emb|CAJ95795.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Ralstonia
eutropha H16]
Length = 280

Score = 92.0 bits (227), Expect = 9e-17, Method: Compositional matrix adjust.
Identities = 77/291 (26%), Positives = 121/291 (41%), Gaps = 28/291 (9%)

Query: 6 LQITPTGATLGATVTGVHLA--TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++ P +GA V+GV LA DDA FA + + L H +L Q +S + FA+R
Sbjct: 1 MRAQPLTCNIGAEVSGVSLADAARDDALFAEIKSLLLLTHKVLFLRDQEISRADHVAFAARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQQGAV 123
FG +E VA S+ G V+ + + ++ ++H D ++ G V
Sbjct: 61 FGELE----DHPVAGSDPDHPGLVQIYRSKRENYEN-----SYHTDGSWRETPPMGCV 110

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
P VGG T + +M AAY+ L E + + A+HS+ +S ++ S
Sbjct: 111 LRCIECPVGGDTIWNMAAAYEHLPEETIKQRIAGLRKHSIEHSFGAAMSPEKRASLAA 170

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LEG 232
Y M P+V+ HPETG +L + + E+ R+ L
Sbjct: 171 QYPMVE-----HPVVRTHPETGEKALYVCGFSTHFANFHTPENVRVYQDKTPGASHLLNY 225

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L+ A +W V +WDNRC H A + PR M + + G
Sbjct: 226 LISQAAIPEYQVRFRWPNSVAIWDNRCTQHAYVDYWPAPRKMERAAIIG 276

>ref|YP_004016993.1| taurine dioxygenase [Frankia sp. Eu1lc]
gb|ADP81123.1| Taurine dioxygenase [Frankia sp. Eu1lc]
Length = 261

Score = 91.7 bits (226), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 81/277 (29%), Positives = 114/277 (41%), Gaps = 41/277 (14%)

Query: 7 QITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65

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      I P      LGA V GV LA +DDA  AL AA+ +H +L+F  Q L+ D  +  + F
Sbjct: 9  DIRPASVPLGAEEVVGVDLAGGVDDATAEALRAAFWKHKVLVFRDQDLAPDAHVRVRIFD 68

Query: 66  A-----IERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
          + R      +V + N++  G                      AWH  T+
Sbjct: 69  EPFDHPQWLYRHEDNRLVYVFNLEKAGNA-----AAWHVGGTWRNPP 110

Query: 119  AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
          + +VVP +GGRT +AD++AAYD L E  + L+  +A          V A
Sbjct: 111  FTIESLTYQVPEIGGRTLWADLQAAYDGLSEPFKQLLESVNA-----VYNA 157

Query: 179  GSAYIGYGMD-TTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
          Y      T T      P+V+ H  TGR  L +  A  + G+  AE E  L  L+  A
Sbjct: 158  DPGDGTYNRPVPTETVEHPVVRTHRHTGRKGLFLSASALRLTGVSPAEGEALLPFLLAHA 217

Query: 238  CQAPRVHAHQWAAGDVVWVDNRCLLHRAEPWDFKLPR 274
          +  W  GD V+WDN+  H A  D+  PR
Sbjct: 218  SSPNYTVSFGWKPGDFVIWDNQATWHYAVN-DYDGPR 253

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>ref|ZP_05001574.1| taurine dioxygenase [Streptomyces sp. Mgl]
gb|EDX26085.1| taurine dioxygenase [Streptomyces sp. Mgl]
Length = 325

Score = 91.7 bits (226), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 79/268 (29%), Positives = 112/268 (41%), Gaps = 25/268 (9%)

```

Query: 4  TTLQITPTGATLGATVTGVHLATLDDAG-FAALHAAWLQHALLIFPGQ-HLSNDQQITFA 61
      +T  IT  G  +GA + G+ LA  AG  A +  A L H ++ F GQ HL  FA
Sbjct: 20  STTSITRLGGRIGAEELGGIRLAGDLPAGTVAEIRGALLAHKVVFRRGQDHLDEAGHEAFA 79

Query: 62  KRFGAIERIGGGDIVAISNVKADGT----VRQHSPAEDDMMKVIVGNMAWHADSTYMPV 117
      + GA      +  +  ADG      + H A  +          WH D T++P
Sbjct: 80  RLLGA-----PVAHPTVPSADGRYALGIDSHHGARANQ-----WHTDVTTFVPA 122

Query: 118  MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH--V 175
      +V A  +P  GG T +A+  AY  L E  R L  A H+  Y  + L  +
Sbjct: 123  YPAFVSLRAVTIPPYGGNTLWANTATAYAHLPEPLRVLADSLRAVHTNEYDYAALKPDAL 182

Query: 176  QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD 235
      +A + Y      T      P+V+VHPETG  +LL+G  I G+  +S  ++
Sbjct: 183  PEALAQYREVFTSTKFLTEHPVVRVHPETGERTLLLGNFVQRIKGLTGQDSRALIDLFQP 242

Query: 236  WACQAPRVHAHQWAAGDVVWVDNRCLLH 263
      +          QW AGDV +WDNR  H
Sbjct: 243  HVERPENTVRWQWRAGDVAIWDNRATQH 270

```

>ref|ZP_07742091.1| putative taurine catabolism dioxygenase [Vibrio caribbenthicus ATCC BAA-2122]
gb|EFP97503.1| putative taurine catabolism dioxygenase [Vibrio caribbenthicus ATCC BAA-2122]
Length = 276

Score = 91.7 bits (226), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 70/266 (26%), Positives = 115/266 (43%), Gaps = 19/266 (7%)

```

Query: 6  LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
      L+I      +GA V  V LA  + F  ++ A+L H ++  Q+LS  +  +  A+RFG
Sbjct: 2  LEIERLTPHIGAYVRNVDLARCSQSDFDQVYQAFNLHQVIFVDQQNLSPEHLLLAERFG 61

Query: 66  AIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMA----WHADSTYMPVMAQG 121

```


Sbjct: 62 +E + NVK+ + +++ GN WH D T+ ++
QLEPVHPF----FPNVKSHQIC-----IIETTRGNQPLESIWHTDLTWKTPSKC 108

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
++ A+ VP+VGG T + M A +D+L+ + + SA HSL ++ H

Sbjct: 109 SLLHAQHVPVSVGGDTIWCSMTAVFDSLEPDLQQQLRDMSAIHSMTAFENIEEHDVTLDWQ 168

Query: 182 YIGYGMDTTATPL-RPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQ 239
P+ P+V VHPET + +L I I M S++ L+ L A +

Sbjct: 169 KKVIETSQKYPPVTHPMVHVHPETQKETLFINEQFTRQIENMSPDSSQKLLDQLFAHARR 228

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
+W G + +WDNR H A

Sbjct: 229 PEFQVRLKWKKGTLAIWDNRVTQHYA 254

>ref|ZP_01039422.1| Taurine dioxygenase [Erythrobacter sp. NAP1]
gb|EAQ29893.1| Taurine dioxygenase [Erythrobacter sp. NAP1]
Length = 285

Score = 91.7 bits (226), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 81/290 (27%), Positives = 127/290 (43%), Gaps = 36/290 (12%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAG-FAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
TL I P +GA + G+ L + A A + AA L++ ++ F Q L+ + I FA+

Sbjct: 14 TLDIRPLTPAIGAEIHGIDLGAPNVAERIAEVRALLKYGVIFFRDQDLTQEAHIAFARH 73

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA-----WHADSTYMPV 117
FG +E + Q +P +++++ G + WH+D T+

Sbjct: 74 FGELE-----IHPATPKDQANP----EVLRIAHGPKSRGQENNWHSDDVTWREE 117

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARH--SLVYSQSKLGHV 175
+ G++ A VP GG T FA+M AY+ L E + +A H S V+++ +LG

Sbjct: 118 PSLGSILLAREVPECGDITLFANMHLAYERLSEQMQRFCESLTAVHDISRVFAK-RLGKA 176

Query: 176 QQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGL 233
+ + P+R P+++ HPETG + + I G+ A ES L+ L

Sbjct: 177 PE-----DLHEKYPPMRHPVIRTHPETGERVIYVNTAFTSHIEGLSAKESAWLLDHL 228

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
A +W AG V WDNR H A F RVM +AG

Sbjct: 229 YATAKDVEIQCRFRWQAGSVAFWDNRVCQLAVSDYFPARRVMERVITIAG 278

>gb|ACG80551.1| TfdA [uncultured bacterium]
gb|ACG80572.1| TfdA [uncultured bacterium]
gb|ACG80573.1| TfdA [uncultured bacterium]
gb|ACG80579.1| TfdA [uncultured bacterium]
gb|ACG80585.1| TfdA [uncultured bacterium]
Length = 119

Score = 91.7 bits (226), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 52/128 (40%), Positives = 70/128 (54%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DMRAAYDALD+AT+A + HS+V+S+ ++G A + A LR

Sbjct: 1 TEFGDMRAAYDALDDATKAEIENLVTEHSIVFSREQIGFTDYA-----EGNADKLR 51

Query: 196 P----LVKVHPETGRPSLLIGRHHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251
P LV HP TGR SL + H I G E+ F+ L++ A Q V+AH+W

Sbjct: 52 PVQHRLVITHPVTGRKSLYLSSHIGGIVGWFPPEARAFIRDLEHATQRRFVYAHEWRVN 111

Query: 252 DVVVWDNR 259

D+V+WDNR
Sbjct: 112 DLVMWDNR 119

>ref|ZP_07576719.1| Taurine catabolism dioxygenase TauD/TfdA [Sphingobium
chlorophenolicum L-1]
gb|EFN08850.1| Taurine catabolism dioxygenase TauD/TfdA [Sphingobium
chlorophenolicum L-1]
Length = 323

Score = 91.7 bits (226), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 79/296 (26%), Positives = 120/296 (40%), Gaps = 19/296 (6%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++ P A G + G +L LDDA A+H AW+ +L+F + Q+ +
Sbjct: 7 VIERRPLEAPFGVEIVGANLTRELDDATRKAIHDAWIDAGILLFRDVRNDDMAQMLSTI 66

Query: 64 FGAIERIGGGDI-----VAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYM 115
FG +E D+ + ++ D + R + D + + G + WH D ++M
Sbjct: 67 FGEMEPAAATADLNDPVNQFMMTLAYDPQDPSGRPNPFYRVDGIDRA--GWLGHWDQSF 124

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLG 173
P + +GAV G T F D AYD L +A + + + + G
Sbjct: 125 PTIVRGAVLRMTTEPARTMGETGFIDAIQAYDRLSPQMQRARIEGLEVVYEFNPDFCSGQFG 184

Query: 174 HVQQAGSAYIGY---GMDTTATPL-RPLVKVHPETGRPSL-LIGRHAHAIPGMDAAESE 227
+ IG G P+ PLV ETGR L L HA +PGMD ES+
Sbjct: 185 FPKDIERLNIGATVKAGSHYDFPPVHPLVITQRETGRKVLKLSPMHARYVPGMDKEESD 244

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L L + + HQW D+VVWDN ++H A R + +AG
Sbjct: 245 ALLTELAEHLGDPAHAYFHQWQENDMVVWDNRIVHSANGVPLDCKRTARRTTIAG 300

>gb|ACG80584.1| TfdA [uncultured bacterium]
Length = 119

Score = 91.7 bits (226), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 52/126 (41%), Positives = 70/126 (55%), Gaps = 13/126 (10%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRP- 196
FADMRAAYDALD+AT+A + HS+V+S+ ++G A + A LRP
Sbjct: 3 FADMRAAYDALDDATKAEIENLVTEHSIVFSREQIGFTDYA-----EGNADKLPRV 53

Query: 197 ---LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
LV HP TGR SL + H I G E+ F+ L++ A Q V+AH+W D+
Sbjct: 54 QHRLVITHPVTGRKSLYLSSHIGGIVGWPVPEARAFVRDLMEHATQRQFVYAHEWRVNDL 113

Query: 254 VVWDNR 259
V+WDNR
Sbjct: 114 VMWDNR 119

>emb|CAY27274.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 91.7 bits (226), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 49/124 (39%), Positives = 67/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFGDMRAAYDALDDETKVEIEDMICEHSLMYSRGSLSGLD-----YTDEEKEMFKPALQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV++HP GR SL + HA AI GM E+ L L + A + V+ H+W D+V+
Sbjct: 56 RLVRIHPVHGRKSLYLSSHAGAIKMSVPEARLLLLRDLTEHATKPEFVYVHKWTPHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>ref|YP_322991.1| taurine catabolism dioxygenase TauD/TfdA [Anabaena variabilis ATCC
29413]
gb|ABA22096.1| Taurine catabolism dioxygenase TauD/TfdA [Anabaena variabilis ATCC
29413]
Length = 321

Score = 91.7 bits (226), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 82/303 (27%), Positives = 130/303 (42%), Gaps = 42/303 (13%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
M +++ P +GA + GV L+T L D + A L+ ++ F Q++ + QI
Sbjct: 1 MGKYKHIEVKPVSGFIGAEIGGVDLSTHLQDETIQEIRKALLKWKVVFFRNQNIDHAAQIA 60

Query: 60 FAKRFGAI-----ERIGG-GDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHA 110
F RFG + E I G I+ I S E + ++ WH
Sbjct: 61 FTGRFGEVTYAHPHEDEPIEGYSQILPID-----RSRYERRNGLRRSSYESRWHT 110

Query: 111 DSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL----- 165
D T G++ A VP++GG T + ++ AAY+ L R L + A H
Sbjct: 111 DVTAAINPPAGSILRAVNVPSIGGDTQWTNLVAAYEGLSAPVRELADKLKAEHRFNARLR 170

Query: 166 VYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDA 223
+ S SK+ Q+ + I + P+V+VHPETG +L + G +H I +
Sbjct: 171 LPSNSKIA--QRIANPI-----VSIHPVVRVHPETGERALFVNPGFTSH-ILDVSP 219

Query: 224 AESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSR 280
ESE LE + + +W GD+ WDNR H A P D ++ RV++ +
Sbjct: 220 QESELLLELFFNQITKPAYTTRFRWNNGDIAFWDNRATAHLA-PQDLDHLEVERVLYRTT 278

Query: 281 LAG 283
+ G
Sbjct: 279 ITG 281

>emb|CAY27255.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27264.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 91.7 bits (226), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 49/124 (39%), Positives = 67/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFADMRAAYDALDDETKVEIEDMICEHSLMYSRGSLGFLD-----YTDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV++HP GR SL + HA AI GM E+ L L + A + V+ H+W D+V+
Sbjct: 56 RLVRIHPVHGRKSLYLSSHAGAIKMSVPEARLLLLRDLTEHATKPEFVYVHKWTLHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

```
>ref|YP_668361.1| taurine dioxygenase [Escherichia coli 536]
ref|ZP_03035003.1| taurine dioxygenase [Escherichia coli F11]
ref|ZP_07181787.1| taurine dioxygenase [Escherichia coli MS 200-1]
gb|ABG68462.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli
536]
gb|EDV65797.1| taurine dioxygenase [Escherichia coli F11]
gb|EFJ58786.1| taurine dioxygenase [Escherichia coli MS 200-1]
gb|EGB79938.1| taurine dioxygenase [Escherichia coli MS 60-1]
Length = 283
```

Score = 91.7 bits (226), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 78/289 (26%), Positives = 124/289 (42%), Gaps = 29/289 (10%)

```
Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA +TG L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQITGADLTRPLSDNQFEQLYHAVLRHQVFLRDQAITPQQQRALAQR 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIQTP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T +A AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWASGIAAYEALSVPFRQLLSGLRAEHDFRKSFPYKY-RKT 167

Query: 179 GSAYIGYGMTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + + P L P+V+ HP TG+ +L + I + ESE L G +
Sbjct: 168 EAEHQWRWEAVAKNPPLHPVVRTHPVTGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 275
```

```
>ref|ZP_02884967.1| Taurine dioxygenase [Burkholderia graminis C4D1M]
gb|EDT09399.1| Taurine dioxygenase [Burkholderia graminis C4D1M]
Length = 315
```

Score = 91.7 bits (226), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 77/286 (26%), Positives = 124/286 (43%), Gaps = 16/286 (5%)

```
Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++Q+ P A +GA + GV L LD A + AA L+ ++ F Q L+++Q I F+ +
Sbjct: 11 SIQVNPLSAHIGAEIHGVDLTQKLDARQVAEIRAALLRWRVVFREQFLTHEQHIAFSAQ 70

Query: 64 FGAIERIG---GGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
FG + +G G + + + + RQ + E +++ G WH D T
Sbjct: 71 FGELT-VGHPVFGHVDGHAIEYSISKYRQATRFEGQTLRPWTG--WHTDVTAAVNPPW 126

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 180
++ +P GG T + ++ AAY L RA V H G
Sbjct: 127 ASILRGVTIPPYGGDTQWTNLMAAYQKLSAPLRAFVDGLRGLHRFAPPAGASG-----TE 181

Query: 181 AYIGYGMTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239
A++ PLV+VHPETG +L + +I G+ ES+ LE L + +
Sbjct: 182 AFVKAVEQRILVTEHPLVRVHPETGERALYVSPSFLKSIVGVTPRESQALLELLWEHVTR 241

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA--EPWDFKLPRVMWHSRLAG 283
+W AG V WNR H A + +D + R ++ + L G
Sbjct: 242 PEFTVRFKWEAGSVAFWDNRATAHLAPSDIFDLEFDRQLYRTTLVG 287
```

```
>ref|YP_002327887.1| taurine dioxygenase [Escherichia coli O127:H6 str. E2348/69]
```

ref|ZP_07622676.1| taurine dioxygenase [Escherichia coli H299]
emb|CAS07856.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli
O127:H6 str. E2348/69]
dbj|BAI53872.1| taurine dioxygenase [Escherichia coli SE15]
gb|EFZ76740.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli
RN587/1]
Length = 283

Score = 91.7 bits (226), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 78/289 (26%), Positives = 124/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA +TG L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQITGADLTRPLSDNQFEQLYHAVLRHQVVFRLRDQAITPQQQRALAQR 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIQTP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T +A AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWASGIAAYEALSVPFRQLLSGLRAEHDFRKSFPYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + + P L P+V+ HP TG+ +L + I + ESE L G +
Sbjct: 168 EAEHQWRWEAVAKNPPLLHPVVRTHPVTGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|ZP_06069264.1| taurine catabolism dioxygenase TauD/TfdA [Acinetobacter lwoffii
SH145]
gb|EEY90259.1| taurine catabolism dioxygenase TauD/TfdA [Acinetobacter lwoffii
SH145]
Length = 321

Score = 91.3 bits (225), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 80/306 (26%), Positives = 125/306 (40%), Gaps = 40/306 (13%)

Query: 6 LQITP-TGATLGATVTGVHLATLDDA-GFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++I P T LGA V G+ + L A +H +LIF Q L + Q + F+
Sbjct: 29 IKIVPQTDQALGAVVFGDLARKAQSSSETILQLKQALAEHLILIFKQQSLDDLQYLAFSTY 88

Query: 64 FGAIERIGGG-----DIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWH 109
FG+I R G D+V +SN G H G + H
Sbjct: 89 FGSIFRPGADTPVLAAQSDSGVPPDVVPVSNVAVGQGDYTG-----GELTPH 135

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRS--ARHSLVY 167
D + P+ + ++ A +P GG+T + + AYDAL++ T+A + Q + V
Sbjct: 136 TDHQWTPPLPSFASLLYAIELPQNGGQTSWINTIKAYDALNKETKAQIDQLQLITYNPFVR 195

Query: 168 SQSKLGHVQQAQSA-----YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPG 220
Q G + + + A P PLV+ HPE+GR +L + H +
Sbjct: 196 RQKTRDQADDQGYGNSPLYRFKDPILSHAYP-HPLVRTHPESGRKALWLNTHTHEVELVN 254

Query: 221 MDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSR 280
D + + L + + + H W GD+V WDN+ LH P+ R++
Sbjct: 255 YDDQAGSQLIAKLREHISKPEFAYEHHEIGDIVFWDNQVTLHSRRPFPADQRRLK 314

Query: 281 LAG-RP 285
LAG RP

Sbjct: 315 LAGSRP 320

>emb|CAY27260.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 91.3 bits (225), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 49/124 (39%), Positives = 68/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAY+ALD+ T+ + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFADMRAAYEALDDETKVEIEDMICEHSLMYSRGSLSGLD-----YTDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV++HP GR SL + HA AI GM E+ L L + A + V+ H+W D+V+
Sbjct: 56 RLVRIHPVHGRKSLYLSSHAGAIKMSVPEARLLLRDLTEHATKPEFVYVHKWTLHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>emb|CAY27350.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 91.3 bits (225), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 55/125 (44%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALDEAT+ VH RHS ++S+ LG + + P+R
Sbjct: 1 TEFADMRAAYDALDEATKREVHDLVCRHSQIFSRGILGFTDFTEEERVKWA-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I G E+ FL L + A Q V+AH W D+V
Sbjct: 55 QRLVRRHPTTGRLSLYLASHAGEIEGWVPPEARAFRLDLNEHATQRQFVYAHVWRLHDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|YP_003298992.1| Taurine dioxygenase [Thermomonospora curvata DSM 43183]
gb|ACY96954.1| Taurine dioxygenase [Thermomonospora curvata DSM 43183]
Length = 293

Score = 91.3 bits (225), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 80/287 (27%), Positives = 115/287 (40%), Gaps = 27/287 (9%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
++ G +GA + G L D ++ L+H LIF L FA RFGA
Sbjct: 3 KVVRIIGRIGAEIIGADLTDPDAFPTEEINRLLLEHKALIFRDAGLDEAGHRDFAARFGA 62

Query: 67 IERI-----GGGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQG 121
+ R + + V AD R + WH D T++ +
Sbjct: 63 LTRAHPTVPSAEGLEVLAVDADTGHAN-----VWHTDVTFTVTPPKI 106

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
+ A +P GG T A+ AAY L E R L + A HS Y + +
Sbjct: 107 STLRAIKLPPYGGDTLIANAAAAYRDLPEPLRELADRLWAVHSNAYDYATPAKSAEYRRV 166

Query: 182 YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAP 241
+ T P+V+ HPETG +L IG A I G+ ES L L + +
Sbjct: 167 FTSKVYQTA----HPVREHPETGERTLFIGGFAQRIVGLSGTESRDILRILQSYVTRPE 222

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAGRPET 287
+ +W GD+VV+DNR H A P D+ PR++ +AG P T
Sbjct: 223 NIVRVVRWNVGDLVVFNDNRITQHYA-PDDYDDRPRLLRITVAGGPVT 268

>ref|YP_004154990.1| taurine dioxygenase [Variovorax paradoxus EPS]
gb|ADU36879.1| Taurine dioxygenase [Variovorax paradoxus EPS]
Length = 317

Score = 91.3 bits (225), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 76/269 (28%), Positives = 114/269 (42%), Gaps = 19/269 (7%)

Query: 3 QTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITF 60
L I +GA V GV L+ L F ++ AA L+H +L F GQ HL + QQ F
Sbjct: 16 NNELDIVRQAGHIGAEVVRGRLSGELQPEVFRSIIKAAALLKHKVLFRRGQQHLLDQAQQAF 75

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQ 120
+ +G E + + ++ K +H +WH D T+ Q
Sbjct: 76 GRLWG--ELVPHPTVPSMDGTLKLELDSRHGGRA-----NSWHTDVTFEVAYPQ 122

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY----SQSKLGHVQ 176
++ A V+PA GG T +A+ AAY++L + +AL + A H Y S+
Sbjct: 123 VSILRAVVIPAYGGDTVWANTVAAYESLSDDLKALADRLRAVHGNDYDYAASRQPADLAD 182

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW 236
+ Y P+V+VHPETG SL++G + G +S+ L L
Sbjct: 183 EGVKRYKEVFTRRLLEAEHPVVRVHPETGERSLVLGHFVKRLVGHSTYDSQHLLSVLQSH 242

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ +W GDV +WDNR H A
Sbjct: 243 VHRLENTVRWRWTQGDVAIWDNRATQHYA 271

>ref|YP_457842.1| taurine dioxygenase [Erythrobacter litoralis HTCC2594]
gb|ABC63045.1| Taurine dioxygenase [Erythrobacter litoralis HTCC2594]
Length = 289

Score = 91.3 bits (225), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 82/290 (28%), Positives = 126/290 (43%), Gaps = 38/290 (13%)

Query: 6 LQITPTGATLGATVTGVHLATLD-DAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I P +GA + + L D A+ AA L+ ++ F Q L+ DQ I FA+ F
Sbjct: 18 LDIRPLTPAIGAEIHDIDLGAGDVGDSIPAIRAALLKFGVIFFRDQDLTQDQHIAFARHF 77

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMA-----WHADSTYMPVM 118
G +E V Q +P +++++ G + WH+D T+
Sbjct: 78 GKLE-----VHPATPRDQPNP----EVLRIAHGPKSRGQENNWHSDDVTWREKP 121

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH--SLVYSQSKLGHVQ 176
+ G++ A VP VGG T FA+M A++ L R +A H S V+++ +LG
Sbjct: 122 SLGSILLAREVPEVGGDTLAFANMHLAFERLSPKMREFCEGLTAVHDISRVFAK-RLGKTP 180

Query: 177 QAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGL 233
+ + P+R P+++ HPETG + + G +H I G+ ES L+ L
Sbjct: 181 EE-----LHEKYPPMRHPVIRTHPETGERVVYVNNGFTSH-IEGLSPDESRLWLLDHL 231

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
A +W AG + WDNR H A F RVM +AG
Sbjct: 232 YKTAWDVEIQCRFRWKAGSIAFWDNRVCQHLAVSDYFPAKRVMERVTIAG 281

>ref|YP_345946.1| taurine dioxygenase [Pseudomonas fluorescens Pf0-1]

gb|ABA71957.1| putative taurine dioxygenase [Pseudomonas fluorescens Pf0-1]
Length = 306

Score = 91.3 bits (225), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 76/264 (28%), Positives = 112/264 (42%), Gaps = 16/264 (6%)

```
Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
          L I P   +GA + GVHL+ LD A   A+   A+Q+ ++ F Q L + +Q FA
Sbjct: 15  LDIHPVAGRIGAEIRGVHLSGELDAATVEAIQQALIQYKVVFREQTQLDDQRQEAF AHL 74

Query: 64  FGAIERIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGAV 123
          G       + VA   V +   R       + + +       +WH D T++   + ++
Sbjct: 75  LG-----EPVAHPTVPSREGTRYLLELDGAEGQRA----NSWHTDVTFVDAYPKASI 122

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS--KLGHVQQAGSA 181
          + V PA GG T +A+   AY+ L   R L + A HS Y + K   +
Sbjct: 123 LRSVVAPAFGGDTLWANTATAYNELPTELRELADKLVAHVSNEYDYAAVKPDVSAEKLER 182

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAP 241
          Y       T       P+V+VHP +G SLL+G       I G   A+S       L   +
Sbjct: 183 YRKIFTSTVYETEHPPVRVHPISGEKSLLLGHFVKRIKGYSAHLSAHLFGLLQSHVIRQE 242

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRA 265
          V   +W AGDV +WNR   H A
Sbjct: 243 NVVRWRWKAGDVVAIWDNRSTQHYA 266
```

>ref|ZP_06413046.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EUN1f]
gb|EFC84131.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EUN1f]
Length = 278

Score = 91.3 bits (225), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 84/275 (30%), Positives = 115/275 (41%), Gaps = 38/275 (13%)

```
Query: 28  DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTV 87
          DD   A   A   ++ +L+F   HL ++ Q+ F +R G + R   G   +   +   +   +
Sbjct: 28  DDEFDPACLALAEYGVLLFREIHLDDAEQVEFCRRLGELARFRGYRLPEVMEINFEPSN 87

Query: 88  RQHSPAEDMMKVIVGNMAWHADSTY---MPVMAQGAVFSAEVVPAVGGRTCFADMRAA 144
          R   AE+       N WH D       P A   V +A VV   GG T FA   AA
Sbjct: 88  RN---AEY-----FRSNDGWHIDGCLDGGPPRA--GVLARVVADHGGGETEFASSYAA 136

Query: 145 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPL-----RPLVK 199
          Y+AL +A +   +   H+   Q +       +Y   D T   L   RP +
Sbjct: 137 YEALSDAEKEQYAKLRVVHTFEAVQRR-----SY-----PDPTPKQLAEWASRP-TR 182

Query: 200 VHP-----ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
          HP       +GR SL+ G A I GMD E   L L   A   V H W+ GD V
Sbjct: 183 EHPLVWEQRSGRRSLVFGHTASHIVGMDRDEGRALLAELEARATTPDNVLRHSWSVGDTV 242

Query: 255 VWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEG 289
          +WNR LLHRA +D   PR M   + L G   +G
Sbjct: 243 IWDNRGLLHRACAFDRTRPRTMHRTTLLGDEPIQG 277
```

>ref|ZP_07289824.1| taurine dioxygenase [Streptomyces sp. C]
gb|EFL18193.1| taurine dioxygenase [Streptomyces sp. C]
Length = 313

Score = 91.3 bits (225), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 82/261 (31%), Positives = 111/261 (42%), Gaps = 27/261 (10%)

```
Query: 12  GATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGAIER 69
```


Sbjct: 17 G +GA + GV L L A + AA L H ++ F Q HL FA R
GGRIGAEIGGVRLGGDLAAETVAEVRAALLAHKVVFVRDQDHLDEASHEAFA-----R 69

Query: 70 IGGGDIVAISNVKADGT----VRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGA VFS 125
+ G + + ADG + H A + WH D T++P ++

Sbjct: 70 LLGTPVAHPTVPSADGRYALGIDSHHGARANQ-----WHTDVTFPAYPAFSILR 119

Query: 126 AEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH--VQQAGSAYI 183
A +P GG T +A+ AY L E RAL A HS Y + L + +A + Y

Sbjct: 120 AVTIPPYGGDTLWANTATAYSHLPEPLRALADGLRAVHSNEYDYAALKPDALPEALAQYR 179

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRV 243
TT PLV+VHPETG +LL+G I G+ +S R L L ++P

Sbjct: 180 EVFTSTTFLTEHPLVRVHPETGERTLLLGNFVQRIQGLTGRDS-RVLVDLFQAHVESPEN 238

Query: 244 HAH-QWAAGDVVVWDNRCLLH 263
QW AGDV +WDNR H

Sbjct: 239 TVRWQWRAGDVVAIWDNRATQH 259

>ref|YP_841739.1| taurine catabolism dioxygenase [Ralstonia eutropha H16]
emb|CAJ97009.1| probable taurine catabolism dioxygenase [Ralstonia eutropha H16]
Length = 320

Score = 91.3 bits (225), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 83/265 (31%), Positives = 115/265 (43%), Gaps = 19/265 (7%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L I P +GA + GV L L A FAA+ AA L+H +L F Q HL + Q FA+

Sbjct: 14 LDIHPVAGRIGAEIRGVALHGDLPPATFAAIRAALLRHKVLFFRDQVHLDDAAQQGFARL 73

Query: 64 FGAIERIGGGDIVAISNVKA-DGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG D V V + DGT E D +WH D T+ +

Sbjct: 74 FG-----DTPHPTVPSRDGT---QLLELDSQHGGGRAN--SWHTDVTFDLAYPAVS 119

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVYSQSKLGHVQQAGS 180
V A VPA GG T +A+ AAY L E R L + A H+ Y+ +++ +

Sbjct: 120 VLRAVTVPAAGGDTVWANTAAAYQDLPEPLRELADKLWALHTNDYDYAATRVNPSDEGLK 179

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
Y P+V+VHPETG +L++G + +A+S + L +

Sbjct: 180 RYRELFTSALYETEHPVVRVHPETGERTILVLGHFVKLLDYSSADS AHLIAVLQGHVHRL 239

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRA 265
+W AGDV +WDNR H A

Sbjct: 240 ENTVRWRWRAGDVVAIWDNRATQHYA 264

>ref|ZP_07042961.1| taurine dioxygenase [Comamonas testosteroni S44]
gb|EFI63307.1| taurine dioxygenase [Comamonas testosteroni S44]
Length = 293

Score = 91.3 bits (225), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 78/265 (29%), Positives = 114/265 (43%), Gaps = 31/265 (11%)

Query: 12 GATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE-- 68
G +GA V + LA L L AA L+H L+ ++ DQ + A+ FG E

Sbjct: 11 GPRIGAEVPQLDLADPLSAQTLQELEAALLRHEALVLHVPDMTPDQHLAIARHFGEAEVH 70

Query: 69 ----RIGGG--DIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGA 122
+G G I I + D DM WH D +++P

Sbjct: 71 TFYPNLGQGYEQITVIDSKLGDRA-----DM-----WHHDESFLSPPIVT 111

Query: 123 VFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK-LGHVQQAGSA 181
+ A ++P GG TC+ M +AYDAL + + SA H + + L H
Sbjct: 112 MTHARILPPTGGDTCTWISMTSAYDALSPQMKQYLDGLSAWHDMSPMATAALQHIGICTHER 171

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQA 240
Y+ + L P+V+VHP TGR +L + + I G+ AES L L Q
Sbjct: 172 YVEV-VGQNRRLHPMVRVHPLTGRKALYVSPTYVTHIDGLPQAESRAILAYLHAHCMQV 230

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRA 265
+ H+WA GD+V+WDNR ++H A
Sbjct: 231 EFLFKHRWALGDMVIWDNRSVVHNA 255

>emb|CAY27406.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 91.3 bits (225), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 52/125 (41%), Positives = 68/125 (54%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALD T+A V HSL++S+ +G + + P+R
Sbjct: 1 TEFADMRAAYDALDARTKAEVEDLVCLHSLMFSRQAIGFTELTEQEIAAFK-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA AI G E+ FL L + A Q V++H W D+V
Sbjct: 55 QRLVRTHPVTGRKSLFLSSHAGAIEGWTVPPEARMLRDLTEHATQREFVYSHAWQPFDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|YP_003980365.1| alpha-ketoglutarate-dependent taurine dioxygenase 1
[Achromobacter
xylosoxidans A8]
gb|ADP17650.1| alpha-ketoglutarate-dependent taurine dioxygenase 1 [Achromobacter
xylosoxidans A8]
Length = 291

Score = 90.9 bits (224), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 81/275 (29%), Positives = 122/275 (44%), Gaps = 31/275 (11%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L+ P LGA + G+ L+ L D F + AA +H ++ F Q L+ Q I F+ RF
Sbjct: 7 LETQPIAGALGAEIRGIDLSRPLSDDQFDDVRAALHEHLVVFRRDQQLTPQQHIDFSSRF 66

Query: 65 GAIERI-----GGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPV 117
G + + G I+ + K++ T R + G + WH D +Y
Sbjct: 67 GELLEVPFVRALDGHPTILPVMKGKSETTRR-----LFGGL-WHTDMSYAE 112

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
G+ V+P GG T +A+M AYDAL + + ++ A HS V S G V
Sbjct: 113 PPLGSALYGRVIPPYGGDTMWANMYRAYDALSDKLKQILDGLGAVHSAVRSYGAGGAVVN 172

Query: 178 AGSAYIGYGMDT-----TATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFL 230
G + MD + + P+V+VHP TG+ +L + G + GM ESE L
Sbjct: 173 NGDP--AHKMDVRTDDRAASEVVHPVVRVHPATGKKALYVNGTYTLRFDMGTQEESPELL 230

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ L A + +W G + +WDNRC H A
Sbjct: 231 QFLYRHAARPEFTCRFRWTPGSLALWDNRCTQH LA 265

>ref|ZP_06707925.1| taurine dioxygenase [Streptomyces sp. e14]
gb|EFF91047.1| taurine dioxygenase [Streptomyces sp. e14]
Length = 300

Score = 90.9 bits (224), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 79/291 (27%), Positives = 120/291 (41%), Gaps = 34/291 (11%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+++I A +GA V G L+ LD A AA+ A H L+F G HL + Q FA+
Sbjct: 2 SIEIRKVTARIGAQVLGADLSRPLDAATVAAIREALNTHKALVFDGVHLDDAGQEAFARH 61

Query: 64 FG-----AIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADST 113
FG A+E G +++ + + + WH D T
Sbjct: 62 FGDLTTHAHTVPFAVE--GAPNVLPVDSERGRAN-----HWHTDVT 99

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS-KL 172
++ Q + + +P GG T AD AAY L E R L A H+ Y +
Sbjct: 100 FVLNPPQASTLRSITIPPYGGETLIADAAAAYRDLPEPLRRLADTLWAEHTNDYDYAVPE 159

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG 232
+ + +A T P+V+VHP TG L IG A + G+ ES + L+
Sbjct: 160 ESIDEDKAAQRAQFTSITYRTAHPVVRVHPLTGERGLFIGGFAQRVVGLSVPESTRKILDL 219

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + + V +W+ +V++DNR H A LPR + +AG
Sbjct: 220 LQSYVTRPENVLRRWRWSENQLVLFNDRITQHYAIDNYDGLPRRLNRVTVAG 270

>emb|CAY27542.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 90.9 bits (224), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 70/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DMRAAYDALD+AT+A + HSL++S+ LG + + T P+R
Sbjct: 1 TEFGLDMRAAYDALDDATKAEIEDLVCEHSLIFSRGSLGFTE-----LSEERATFRPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + H I G E+ FL L++ A Q V++H+W D+V
Sbjct: 55 QRLVRAHPVTGRKSLFLSSHGGTILGWVPPEARAFRLDLMEHATQPQFVYSHKWRQWDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|ZP_08120023.1| taurine dioxygenase [Pseudonocardia sp. P1]
Length = 290

Score = 90.9 bits (224), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 84/282 (29%), Positives = 121/282 (42%), Gaps = 36/282 (12%)

Query: 2 AQTTLQITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
A T+ P T+GA + V L AT DDA FA L A L+H +L Q+++ Q +
Sbjct: 5 AAPTIIHAELTCTIGAELHDVDLGAATRDDALFAELRALLLRHKVLFLRDQNITGGQHVA 64

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQH----SPAEDDMMKVIVGNMAWHADSTYM 115
A+RFG +E V S+ + G VR + SP E + A+H D+T+
Sbjct: 65 LARRFGDLE----DHPVLGSDPEHPGLVRIYKDLDSPPEHYEN-----AFHCDATWR 112

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
G V PAVGG T + DM AAY L + +A + ARHS+ S +

Sbjct: 113 ENPPMGCVLHCVETPAVGGDTIWVDMAAAYARLPDEVKARIGGLRARHSIEASFGAAMPI 172

Query: 176 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF----- 229
+Q + + P+V+ HPETG L + + ++ RF

Sbjct: 173 EQRHELHRRF-----PDAEHPVVRTHPETGEKVLFFVNGFTTHLVNYHTPDNVRFGIDYAP 227

Query: 230 -----LEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
L+ L+ A AP +W G V +WDNR H A

Sbjct: 228 GASALLQYLISQAT-APEYQVRWRWTPGSVAIWDRSTQHYA 268

>ref|YP_001265603.1| taurine dioxygenase [Pseudomonas putida F1]
gb|ABQ76419.1| Taurine dioxygenase [Pseudomonas putida F1]
Length = 291

Score = 90.9 bits (224), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 79/267 (29%), Positives = 118/267 (44%), Gaps = 19/267 (7%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+L ITP LGA ++GV ++ + A+ A LQH +L Q ++ +QQ FA R

Sbjct: 16 SLTITPLSPALGAQISGVDISRDISAERDAIEQALLQHQLFLRDQPINPEQQARFAAR 75

Query: 64 FGAIERIGGGDIVAI-SNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG + I I NV V D + + N WH D T++P A GA

Sbjct: 76 FGD LH-----IHPIYPNVDPDPQV-----LVLDTAVTDVRDNAVWHTDVTFLPTPALGA 124

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQAGS 180
V SA+ +PA GG T +A AA++AL R ++ +A H + + G + +

Sbjct: 125 VLSAKQLPAYGGDTLWASGIAAFEALSAPLREMLGGLTATHDFTKSFPLERFGTTPEDLT 184

Query: 181 AYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
+ + PL P+V+ HP +GR +L + I + ES+ L L A

Sbjct: 185 RWEATRRNN--PPLSHPVVRTHPVSGRKALFVNEGFTTRINELSELESDALLRLLFAHAT 242

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ +W DV WDNR H A

Sbjct: 243 RPEFSIRWRWQEHDVAFWDNRVTQHFA 269

>emb|CAY27281.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 90.9 bits (224), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 53/127 (41%), Positives = 68/127 (53%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTAT--- 192
T FADMRAAYDALD T+A + HSL+YS+ LG ++ Y + A

Sbjct: 1 TEFADMRAAYDALDNDTKAEIEGMICEHSLMYSRGS LG-----FLDYSDEEKAMFKP 52

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
L+ LV+ HP R SL + HA AI GM E+ L L + A Q VH H+W D

Sbjct: 53 VLQRLVRTHPVHRRKSLYLSSHAGAIKGSMPPEARLLLLRDLTEHATQPEFVHVHKWTVHD 112

Query: 253 VVVWDNR 259
+V+WDNR

Sbjct: 113 LVMWDNR 119

>ref|YP_539419.1| taurine dioxygenase [Escherichia coli UTI89]
ref|YP_851548.1| taurine dioxygenase [Escherichia coli APEC O1]
ref|YP_002390194.1| taurine dioxygenase [Escherichia coli S88]
ref|ZP_04538123.1| taurine dioxygenase [Escherichia sp. 3_2_53FAA]
gb|ABE05888.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli

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UT189]
gb|ABI99833.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli
APEC O1]
emb|CAR01715.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli
S88]
gb|EEH85111.1| taurine dioxygenase [Escherichia sp. 3_2_53FAA]
gb|ADE90240.1| taurine dioxygenase [Escherichia coli IHE3034]
gb|ADN72465.1| taurine dioxygenase [Escherichia coli UM146]
gb|EFU49220.1| taurine dioxygenase [Escherichia coli MS 110-3]
gb|EFU58846.1| taurine dioxygenase [Escherichia coli MS 16-3]
gb|EGB48885.1| TfdA family protein Taurine catabolism dioxygenase TauD
[Escherichia coli H252]
gb|EGB54265.1| TfdA family protein Taurine catabolism dioxygenase TauD
[Escherichia coli H263]
Length = 283

```

Score = 90.9 bits (224), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 78/289 (26%), Positives = 124/289 (42%), Gaps = 29/289 (10%)

```

Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L ITP G +GA +TG L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5   LSITPLGPYIGAQITGADLTRPLSDNQFEQLYHAVLRHHVVFRLRDQAITPQQQRALAQR 64

Query: 65  GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYPMVM 118
          G + G D + + + D +P + D+ WH D T++
Sbjct: 65  GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIQTP 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
          GA+ +A+ +P+ GG T +A AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWASGIAAYEALSVPFRRQLLSGLRAEHDFRKSFPEYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
          + + + P L P+V+ HP TG+ +L + I + ESE L G +
Sbjct: 168 EAEHQWRWEAVAKNPPLLHPVVRTHPVTGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          P +W D+ +WDNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

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```

>gb|ACG80564.1| TfdA [uncultured bacterium]
Length = 118

```

Score = 90.9 bits (224), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 52/125 (41%), Positives = 67/125 (53%), Gaps = 11/125 (8%)

```

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---PL 194
          F DMRAAYDALD+ T+A + HSL+YS+ LG ++ Y D A L
Sbjct: 2   FGDMAAYDALDDDTKAEIEDMICEHSLMYSRGSLG-----FLDYTDDEKAMFKPVL 53

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
          + LV+ HP R SL + HA AI GM E+ L L + A Q VH H+W D+V
Sbjct: 54 QRLVRTHPVRHRRKSLYLSSHAGAIKMSPEARLLLRDLTEHATQREFVHIHKWTVHDLV 113

Query: 255 VWDNR 259
          +WDNR
Sbjct: 114 MWDNR 118

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>ref|YP_888161.1| alpha-ketoglutarate-dependent taurine dioxygenase [Mycobacterium
smegmatis str. MC2 155]
gb|ABK75482.1| alpha-ketoglutarate-dependent taurine dioxygenase [Mycobacterium
smegmatis str. MC2 155]

```

Length = 299

Score = 90.9 bits (224), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 76/273 (27%), Positives = 118/273 (43%), Gaps = 39/273 (14%)

```
Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
          + +T GA +GA + GV +   L A  +A++AA L+H ++ F GQ HL +   Q+ FA+
Sbjct: 3   VTVTKLGAHIGARIDGVRVGGDLSPATVSAINAALLEHKVIFFSQDHLDDAGQLEFAEL 62

Query: 64  FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNM---AWHADSTYMPVMA 119
          G                               TV  + AE  + + I               +WH D T++ +
Sbjct: 63  LGT-----PTVAHPPTLAEGAEQLLPIDSRYDKANSWHTDVTTFVDRIIP 104

Query: 120  QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY-----SQSKL 172
          + ++ A  +P+ GG T +A   AAY L   R L   A H+ +   S  +
Sbjct: 105  KASLLRAVTLPSYGGTTAWASTEAAQQLPAPLRLTLADNLWAVHTNRFDYADSAISAEQR 164

Query: 173  GHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG 232
          G+ Q+ S Y Y ++           P+V+VHPETG   LL+G   + G+   ES
Sbjct: 165  GYRQRFESDY--YEVE-----HPVVRVHPETGERVLLLGHFVKFSFVGLKDTESAALFRL 216

Query: 233  LVDWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
          D  +           W GD+ +WDNR   H A
Sbjct: 217  FQDRITRLENTVRWSWKPGLAIWDNRATQHYA 249
```

>emb|CAY27454.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 90.9 bits (224), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 52/125 (41%), Positives = 70/125 (56%), Gaps = 7/125 (5%)

```
Query: 136  TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR 195
          T FADMRAAYD LDE T+A +           HSL++S+ LG   + +   +   P+R
Sbjct: 1   TEFADMRAAYDTLDERTKAEIEDLVCEHSLMFSRGLLGFTAMSEAEREMF-----RPVR 54

Query: 196  P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
          LV+ HP TGR SL +   HA   I G   E+   FL L++ A Q   V++HQW   D+V
Sbjct: 55  QRLVRTHPVTGRKSLFLSAHAGTIVGWPVPEARAFLRDLIEHATQPQLVYSHQWRQWDLV 114

Query: 255  VWDNR 259
          +WDNR
Sbjct: 115  MWDNR 119
```

>emb|CAY27352.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 90.9 bits (224), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 54/125 (43%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

```
Query: 136  TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR 195
          T FADMRAAYDALDEAT+ VH   +HS ++S+ LG   + +   P+R
Sbjct: 1   TEFADMRAAYDALDEATKREVHDLVCQHSQIFSRGILGFTDFTDEERVKWA-----PVR 54

Query: 196  P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
          LV+ HP TGR SL +   HA   I G   E+   FL L + A Q   V+AH W   D+V
Sbjct: 55  QRLVRRHPTTGRLSLYLASHAGGIEGWPVPEARAFLRDLTEHATQRFVYAHVWRLHDLV 114

Query: 255  VWDNR 259
          +WDNR
Sbjct: 115  MWDNR 119
```

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
 LV+ HP+TGR SL + HA AI G E+ FL L + A Q V++H W D+V+
 Sbjct: 56 RLVRTHPOTGRKSLFLSSHAGAIEGWTIPEARSFLRDLTEHATQREFVYSHPWROHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>ref|ZP_06728473.1| taurine dioxygenase [Acinetobacter haemolyticus ATCC 19194]
gb|EFF81838.1| taurine dioxygenase [Acinetobacter haemolyticus ATCC 19194]
Length = 291

Score = 90.9 bits (224), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 72/274 (26%), Positives = 112/274 (40%), Gaps = 30/274 (10%)

Query: 3 QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
+ TL I +++GA + V L T+D+ + A L H ++ F Q L+ Q A+
Sbjct: 10 EMTLNIEIIKSSIGAIHVDLNTVDENTTQQIQQALLDHHVIFFRNQQLAPQAQELAR 69

Query: 63 RFGA-----IERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST 113
FG+ +E + +I+ + + K D + N WH D T
Sbjct: 70 GFGSLHIHPFPTVENVP--EIIVLDSWKQD-----LRDNELWHTDVT 110

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
+ G V A +P VGG T ++ AA+ LD+A + + +A H + S
Sbjct: 111 FSKNPPLGCVLQAIKIPPVGGDTLWSSGVAAAFAGLDQALQEKLKGLTATHDIRQSFPIER 170

Query: 174 HVQQ-AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLE 231
Q + + P+V+ HP TG+P L + I +D ES L+
Sbjct: 171 FAQNDVERKKLEETFKRNPVVPVVRTHPVTGQPILFVSEGFTTRINELDEVESAELLQ 230

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L A QW GDV +WDNRC H+A
Sbjct: 231 YLFAHATHEQFHLRWQWQEGDVAIWDNRCTQHKA 264

>emb|CAY27270.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 90.5 bits (223), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 49/124 (39%), Positives = 67/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFADMRAAYDALDDETKVEIEDMICEHSLMYSRGSGLGFLD-----YTDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV++HP R SL + HA AI GM E+ L L + A + V+ H+W D+V+
Sbjct: 56 RLVRIHPVHDRKSLYLSSHAGAIKMSVPEARLLLLRDLTEHATKPEFVYVHKWTLHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>ref|YP_001262589.1| taurine catabolism dioxygenase TauD/TfdA [Sphingomonas wittichii
RW1]
gb|ABQ68451.1| Taurine catabolism dioxygenase TauD/TfdA [Sphingomonas wittichii
RW1]
Length = 313

Score = 90.5 bits (223), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 81/291 (27%), Positives = 124/291 (42%), Gaps = 24/291 (8%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIER----- 69
+GA +T D A AL A+ H +L+FP S D + ++ FG ++

Sbjct: 12 VGARITLDPARIGDPALTDALRRAFADHGVLLFPRIQTSPDIHVALSRCFGTLQVHPV NK 71

Query: 70 ---IGGGDIVAISNVKAD--GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G ++V +S G + H A + + + G + WH D +YM + G++

Sbjct: 72 NQVEGFPEVVDMSYTPPSRPGDLSYH--AVYRIEGREL AGWLPWHFDLSYMAEINHGSML 129

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
A VP GGRT F D Y+ L + + + + K + + A A +

Sbjct: 130 RALEVPPEGGRTGFM DRIRLYELLPPDDLKRRIEGLGVVYRFQPDMMKRRYCRPADMALVA 189

Query: 185 YGM-----DTTATPL-RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
M D P+ P+V +TGR L + A I GMD E + L

Sbjct: 190 PSMKAGMFDGVDLDRDFPPVHPMVYTERDTGRKVLNVAPLFAVGIAGMD DPEGDALLGA 249

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
++D C A + HQWAAGD+++WDN +H AE PR M + LAG

Sbjct: 250 VIDHCCTADFAYFHQWAAGDMILWDNWRAMHSAEGVPPHYPRMQRTSLAG 300

>ref|XP_002342012.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase, putative [Talaromyces stipitatus ATCC
10500]

gb|EED24625.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase, putative [Talaromyces stipitatus ATCC
10500]
Length = 341

Score = 90.5 bits (223), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 78/287 (27%), Positives = 131/287 (45%), Gaps = 26/287 (9%)

Query: 1 MAQTTLQITPT---GATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGHLSND 55
M +L + P + GA V+GV ++ +A A L ++ +LIF L N

Sbjct: 20 MQYGS LTVIPVLRSEDSVFGEVSGVDWNRSIPEATVAQLVELQDKYGV LIFRETGLDNA 79

Query: 56 QQITFAKRFGA-----IERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIV 103
+ I F+++ GA +R+G + + N++ D T+ + W +

Sbjct: 80 RHIAFSQQLGAELVNPFYYGRENDRLGEPLLFVGNIEMDRTL VKPDSRRWHHSL---- 135

Query: 104 GNMAWHADSTYMPVMAQGAVFSAEVVPVAVGGR-TCFADMRAAYDALDEATRALVHQRSAR 162
GN WH DS+Y ++ ++ + P GG T FAD R AY L + + +

Sbjct: 136 GNALWHTDSSYHQRRSKYSILLSHGNPVGKGSWTHFADTRRAYADLPD TKKKEIEDLVVE 195

Query: 163 HSLVYSQSKLGHVQQAGSAYIGYGM DTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMD 222
H L +S+ KL G+ + + + LV+ P+ GR +L + HA I G

Sbjct: 196 HDLWHSR-KLASPIVYGNP-LPHELA AKPPAYHRLVQKAPD-GRQTLYLAAHAKLILGWS 252

Query: 223 AAESERFLEGLVDWACQAPRVHAHQWAAG-DVVVWDNRCLLHRAEPW 268
ES++ + L+D Q+ V + +W +G D+V WDN R +HRA P+

Sbjct: 253 FEESQKLIWELIDHCTQSEYVFSMEWLSGGDMVWWDNRQSMHRANPY 299

>emb|CAY27395.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27512.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 90.5 bits (223), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 52/125 (41%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM DTTATPLR 195
T FADMRAAYDALD T+A + HSL++S+ LG + + T P+R

Sbjct: 1 TEFADMRAAYDALDGD TKAEIEGLVCEHSLIFSRGSLGFTE-----LSEAERTMFKPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254

LV+ HP TGR SL + H I G E+ FL LV+ A Q V++H+W D+V
Sbjct: 55 QRLVRTHPVTGRKSLFLSSHGGTIVGWPVPEARAFRLDLVEHATQRRFVYSHKWRQWDLV 114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>ref|YP_003339620.1| taurine dioxygenase [Streptosporangium roseum DSM 43021]
gb|ACZ86877.1| Taurine dioxygenase [Streptosporangium roseum DSM 43021]
Length = 301

Score = 90.5 bits (223), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 74/261 (28%), Positives = 111/261 (42%), Gaps = 15/261 (5%)

Query: 8 ITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRF 65
I+P +GA V+GV L L + AA L+H ++ F GQ HL Q+ FA G
Sbjct: 6 ISPVAGRIGAEVSGVRLGGDLPAETVQEIRAALLRHKVIFFRGQEHLDERGQVAFAGLLG 65

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
+ A V A ++ + KV WH D T++ +V
Sbjct: 66 DL-----TTAHTPTVPALNGNSSILDLDYSNGHKV----DRWHTDVTTFVDRPPLASVLR 114

Query: 126 AEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ--QAGSAYI 183
A VP GG T +A+ AY+ L + LV A H+ + +++ + Y
Sbjct: 115 AVTVPPAGGDTLWANTVTAYENLPQELTRLVEGLRAVHTNQFDYARIATSDDPERTRKYA 174

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRV 243
T P+V+VHPETG S+L+G A + G+ A S + + + Q
Sbjct: 175 EVFTSTVFETEHPVVRVHPETGERSILLGDFAKRVVGLPADISATLIRLVQEQVTQVENT 234

Query: 244 HAHQWAAGDVVVWDNRCLLHR 264
+W+ GDV +WDNR HR
Sbjct: 235 VRWRWSPGDVAIWDNRATQHR 255

>gb|ACG80562.1| TfdA [uncultured bacterium]
Length = 119

Score = 90.5 bits (223), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 52/127 (40%), Positives = 68/127 (53%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTAT--- 192
T F DMRAAYDALD+ T+A + HSL+YS+ LG ++ Y + A
Sbjct: 1 TEFCDMRAAYDALDDDTKAEIEDMICEHSLMYSRSLG-----FLDYTDEEKAMFKP 52

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
L+ LV+ HP R SL + HA AI GM E+ L L + A Q VH H+W D
Sbjct: 53 VLQRLVRTHPVHRRKSLYLSSHAGAIQGMSPPEARLLLLRNLTTEHATQREFVHVHKWTLHD 112

Query: 253 VVVWDNR 259
+V+WDNR
Sbjct: 113 LVMWDNR 119

>gb|ABL97729.1| taurine dioxygenase [uncultured marine bacterium EB0_39H12]
Length = 261

Score = 90.5 bits (223), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 67/260 (25%), Positives = 112/260 (43%), Gaps = 36/260 (13%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF--AIERIGG 72
+GA ++ ++L L + +L +++++F Q L+ A +G +I +

Sbjct: 9 IGAELSNINLNDLSKDEVHMIKKYFLDYSVIVFRNQSLAPKDLKDIAFWGGASIHVPFK 68

Query: 73 G-----DIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE 127
G +I+ I N + H+ N WH+D T+ + +

Sbjct: 69 GIEGHPEIIEIRNYGE----KYHT-----NAHWHSVDVTFEETPPDATLLYSI 111

Query: 128 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 187
VP GG T F+ AYD L ++ + + A HS LG + +G

Sbjct: 112 EVPKEGGDTLFFSSQYLAYDELKTDLKSCSLADKKAIHS-----NLGVLMLSGG-----DT 160

Query: 188 DTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH 246
T P+ + HPETG+ +L + I MD+ ES++ LE L A ++ H

Sbjct: 161 KNAKTVEHPVPFREHPETGKKALYVTEAFVKEIKNMDSNESQKILEYLYRHASNEDIYIRH 220

Query: 247 QWAAGDVVVWDNRCLLHRAE 266
+W+ GD+VVWDNR + H AE

Sbjct: 221 KWSGDGLVVWDNRSVQHYAE 240

>ref|YP_001267994.1| taurine dioxygenase [Pseudomonas putida F1]
gb|ABQ78810.1| Taurine dioxygenase [Pseudomonas putida F1]
gb|ADR60295.1| Taurine dioxygenase [Pseudomonas putida BIRD-1]
Length = 282

Score = 90.5 bits (223), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 78/274 (28%), Positives = 111/274 (40%), Gaps = 28/274 (10%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+ I +GA V+GV+LA DD FA L LQH +L QH S + + FA+R

Sbjct: 1 MHIEQLTCAIGAEVSGVNLADAIHDELFAQLRQQLLQHRVLFRLDQHFSAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHS-PAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E VA S+ + G V+ + P + +D + AWH D+T+ G

Sbjct: 61 FGELE----DHPVAGSDPEHPGLVQIYKRPDQPNDRYE-----NAWHTDATWREAPPMSGC 111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V P VGG T +A+M AY+ L +A + ARHS+ ++ G

Sbjct: 112 VLRCVECPVGGDTLWANMVLAYENLPNDVKARIEDLRARHSI---EASFGAAMPLDKRL 168

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LE 231
A P+V+ HPETG L + + RF L

Sbjct: 169 ALKAQFPDAE--HPVVRTHPETGEQVLFVNAFTTHFSNYHTPQRVRFQDANPGAGDLLR 226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L+ A +W V +WDNR H A

Sbjct: 227 YLISQAYLPEYQVRWRWKPNVSAIWDNRSTQHIA 260

>ref|YP_002008631.1| taurine dioxygenase, 2-oxoglutarate-dependent [Cupriavidus taiwanensis LMG 19424]
emb|CAQ72579.1| taurine dioxygenase, 2-oxoglutarate-dependent [Cupriavidus taiwanensis LMG 19424]
Length = 321

Score = 90.5 bits (223), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 83/265 (31%), Positives = 115/265 (43%), Gaps = 19/265 (7%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L I P +GA + GV L L A FAA+ AA L+H +L F Q HL + Q FA+

Sbjct: 15 LDIHPVAGRIGAEIRGVALHGDLPATFAAIRAALLRHKVLFVRDQVHLDAAQQGFARL 74

Query: 64 FGAIERIGGGDIVAISNVKA-DGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG D V V + DGT E D +WH D T+ +

Sbjct: 75 FG-----DTPHPTVPSRDGT---QLLELDSQHGGGRAN--SWHTDVTFDLAYPAVS 120

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVYSQSKLGHVQQAGS 180
V A VPA GG T +A+ AAY L E R L + A H+ Y+ +++ +

Sbjct: 121 VLRAVTVPAAGGDTVWANTAAAYQDLPEPLRELADKLWALHTNDYDYAATRVNPSDEGLK 180

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
Y P+V+VHPETG +L++G + +A+S + L +

Sbjct: 181 RYREVFTSALYETEHPPVVRVHPETGERTLVLGHFVKLLDYASADSAHLIAVLQGHVHRL 240

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRA 265
+W AGDV +WDNR H A

Sbjct: 241 ENTVRWRWRAGDVAIWDNRATQHYA 265

>ref|YP_701700.1| taurine dioxygenase [Rhodococcus jostii RHA1]
gb|ABG93542.1| probable taurine dioxygenase [Rhodococcus jostii RHA1]
Length = 313

Score = 90.1 bits (222), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 88/299 (29%), Positives = 132/299 (44%), Gaps = 39/299 (13%)

Query: 4 TTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T L+I P +GA V+GV LA LD+A A L A L H +L F Q L + QI F++

Sbjct: 12 TELRIAPIAGYIGA EVSGVDLAGDLDEAAARLRQALLDHKVLFFRDQPLDHAAQIRFSR 71

Query: 63 RFGAIERI-----GGGDIVAI SNVK--ADGTVRQHSPA EWDDMMKVIVGNMAWHAD 111
FG + G +I+ + + K A G R++S A + WH D

Sbjct: 72 HF GKVT PAHPYDYNAP EGYPEI LEVDSRKYAARGGARKYSYANF-----WHTD 119

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
+ + +E+VP VGG T + ++ AAY L E+ + V A H +

Sbjct: 120 VSALVNPPAITFLRSELVPDVGDTAWTNLAAAYANLPESLKT FVDGLRAEH-----R 172

Query: 172 LGHVQQAGSAYIGYGMDDTTATPL--RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESE 227
G Q+ A + T P+ P+V+VHPETG L + I G+ A+S+

Sbjct: 173 FGGRQKRWEAGSDAEQNVTTKPIVTEHPVVRVHPETGERGLFVTPGFTSRILGVSPAQSD 232

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283
R L+ L + +W + VWDNR H A P D + RV++ + + G

Sbjct: 233 RILDLLFEEVTNPAYTVRVRWQNN SIGVDNRITAH LA-PADLDHLDVVRVLYRTTVEG 290

>ref|ZP_02509143.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei BCC215]
Length = 346

Score = 90.1 bits (222), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 83/271 (30%), Positives = 118/271 (43%), Gaps = 30/271 (11%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQ-QITFA 61
L I P +GA V G+ L + +D F + A L H ++ F QH +D+ Q FA

Sbjct: 61 LSIRPLSGHIGAEVQGIQLGSQMAPNDIRF--ITQALLTHRVIFFRRQHHLDDRAQELFA 118

Query: 62 KRFGAIER---IGGGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM 118
+ FG I + +GG AI + + R +S WH D T+

Sbjct: 119 QAFGEIVKHPTMGGKTGSAILELHSH EGGGRANS-----WHTDVT FGLRP 162

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY----SQSKLGH 174
+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H

Sbjct: 163 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSSLQDLVDKLWAVHGNDFDY AASRVELLH 222

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234

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      A      Y      T      P+V++HPETG  SLL+G +A      D  +S R  E  L
Sbjct: 223 DPVAKEYRKKYAAQVIKTE-HPVVQIHPETGKSLLLGHYAQRVFQYDTHDSNRLYEILQ 281

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      +      WAAGDV +WDNR  H A
Sbjct: 282 AHITRLENTVRWHWAAGDVAIWDNRSTQHYA 312

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>ref|ZP_07576777.1| Taurine catabolism dioxygenase TauD/TfdA [Sphingobium
chlorophenolicum L-1]
gb|EFN08908.1| Taurine catabolism dioxygenase TauD/TfdA [Sphingobium
chlorophenolicum L-1]
Length = 343

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Score = 90.1 bits (222), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 78/279 (27%), Positives = 120/279 (43%), Gaps = 22/279 (7%)

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Query: 6  LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      L++      +  GA + GV L+  LDDA AA+  W++  LL+      +  ++ Q+  ++ F
Sbjct: 29  LKVRALSSGFGAEIMGVDLRPLDDATAAAIRDIWIEAGLLLRDPNADDEAQMRLSRLF 88

Query: 65  GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIV-----GNMAWHADSTY 114
      G +E      D+  +N      ++ PA  DD  +      G + WH D ++
Sbjct: 89  GEMEPAAATADMNDPNNQFM--MTLKYDPA--DDKPRFQTDYHFGGHDRAGYIPWHWDQSF 144

Query: 115  MPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKL 172
      MP + +GAV  E  A  GRT F D  AY+ L  +  +      + V  + Q  K
Sbjct: 145  MPTIVRGAVLRMEQPAAQLGRTGFIDAIEAYERLSPEMKDRIDGMEVVYHFVTDFLQCKY 204

Query: 173  G---HVQQAGSAYIGYGMDDTTATPL-RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESE 227
      G  ++      G      P+  P+V  ETGR +L I  A  I GMD AES+
Sbjct: 205  GVPADLRALPRDTPSGGAKYDFPPVVPVITQRETGRKALKISPLQAQYILGMDRAESD 264

Query: 228  RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE 266
      L  L      + H W  D++VWDN  ++H AE
Sbjct: 265  TLLAELAHLTDERHAYFHDWQKNDMLVWDNRMIHHA 303

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>emb|CAY27536.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

```

Score = 90.1 bits (222), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 51/124 (41%), Positives = 70/124 (56%), Gaps = 5/124 (4%)

```

Query: 136  TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
      T F DMRAAYDALD AT+A +      HSL+YS+ +LG      SA++      A  +
Sbjct: 1  TEFGDMRAAYDALDAATKAEIEDLVCEHSLIYSRGQLGF-----SAFLPDERVAMAPVRQ 55

Query: 196  PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
      LV++HP TGR SL + H  I G  E+  F+  L++ A Q  V+ H+W  D+V+
Sbjct: 56  RLVRIHPVTGRKSLFLAAHIGTILGWPQPEAMAFIRDLMEHATQPQFVYVHKWTLHDLVM 115

Query: 256  WDNR 259
      WDNR
Sbjct: 116  WDNR 119

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>ref|ZP_04899281.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei S13]
gb|EDS82293.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei S13]
Length = 294

```

Score = 90.1 bits (222), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 83/271 (30%), Positives = 118/271 (43%), Gaps = 30/271 (11%)

Query: 6 LQITPTGATLGATVTGVHLATL---DDAGFAALHAAWLQHALLIFPGQHLSNDQ-QITFA 61
L I P +GA V G+ L + +D F + A L H ++ F QH +D+ Q FA
Sbjct: 9 LSIRPLSGHIGAEVQGIQLGSQMAPNDIRF--ITQALLTHRVIFRRQHHLDDRAQELFA 66

Query: 62 KRFGAIER---IGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
+ FG I + +GG AI + + R +S WH D T+
Sbjct: 67 QAFGEIVKHPTMGGKTGSAILELHSHEGGRANS-----WHTDVTFLGRP 110

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY---SQSKLGH 174
+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
Sbjct: 111 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSSLQDLVDKLVAVHGNDFDYAASRVELLH 170

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
A Y T P+V++HPETG SLL+G +A D +S R E L
Sbjct: 171 DPVAKEYRKKYAAQVIKTE-HPVVQIH PETGEKSLLLGHYAQRQFVQYDTHDSNRLYEILQ 229

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
+ WAAGDV +WDNR H A
Sbjct: 230 AHITRLENTVRWHWAAGDVAIWDNRSTQHYA 260

>ref|ZP_01626396.1| taurine dioxygenase [marine gamma proteobacterium HTCC2080]
gb|EAW40919.1| taurine dioxygenase [marine gamma proteobacterium HTCC2080]
Length = 273

Score = 90.1 bits (222), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 74/271 (27%), Positives = 115/271 (42%), Gaps = 33/271 (12%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWL-QHALLIFPGQHLSNDQQITFAKRF 64
+Q+ LGA + GV L + + + L +H +L F Q + QQ A F
Sbjct: 1 MQVKRIAGALGAEIKGVDLGQILTPEISIVIRDLLNEHEVLFFRQQAIEPAQQRDLAAIF 60

Query: 65 GAIE-RIGGGDIVAISNVKA-DGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
G ++ G + I V + TV + S E WH+D T+
Sbjct: 61 GPLQTHPAYGTVAGIPEVMILESTVDKPKSKIE-----VWHSMDTFRQHPPSVT 108

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS-KLGHVQQAGSA 181
V V+P VGG T FA M +AYDAL E + + A H ++Q + + G
Sbjct: 109 VLRGMVIPNVGGDTLFASTMSAYDALSEGKVVYLEGLVAVHD--FAQGFRESLAEPGGRE 166

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIG---RHAHAIPGMDAAESERFLEGLVDWA 237
+G ++ P+V+VHPETG+ L + H +P ++++ L+D+
Sbjct: 167 RLGAALEENPPVRHPVVQVHPETGKKVLFVNALFTTHIEGLPPLESS-----ALLDFL 219

Query: 238 CQAPRVHAH----QWAAGDVVVDNRCLLHR 264
CQ + H QW VV+WDNR H+
Sbjct: 220 CQHAALPEHTCRFQWTPDSVVLWDNRSTQHK 250

>ref|YP_001751848.1| taurine dioxygenase [Pseudomonas putida W619]
gb|ACA75479.1| Taurine dioxygenase [Pseudomonas putida W619]
Length = 301

Score = 90.1 bits (222), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 86/286 (30%), Positives = 124/286 (43%), Gaps = 24/286 (8%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L I P +GA + GV L A LD A AA+ AA +Q+ ++ F GQ HL + Q FAK
Sbjct: 15 LDIQPVAGRIGAQIRGVKLSADLDAATVAAIQAALVQYKVIFFRQQAHLDDLSDQEGFAKL 74

Query: 64 FGAIERIGGGDIVAISN----VKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
G E + + + ++ DG Q + +WH D T++

Sbjct: 75 LG--EPVAHPTVPVVDGTSYLLQLDGAEGQRA-----NSWHTDVTTFVDAYP 118

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG-HVQQA 178
+ ++ + V PA GG T +A+ AAY L E R L + A HS Y + + V A

Sbjct: 119 KASILRSVVPASGGDTVWANTAAAYQELPEPLRELADKLWAVHSNEYDYASIKPDVDP 178

Query: 179 G-SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
Y T P+V+VHP +G +L +G I G A+S+ L

Sbjct: 179 KLERYRKVFTSTVYETEHFVVRVHPISGERALQLGHFVKRIKGYSLADSQHLFALLQGHV 238

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W AGDV +WDNR H A PR++ LAG

Sbjct: 239 ARLENTVRWRWEAGDVAIWDNRATQHYAVDDYGTQPRIVRRVTLAG 284

>emb|CAY27306.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 90.1 bits (222), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 68/125 (54%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALD+ T+A + RHS +YS+ KLG + P+R

Sbjct: 1 TEFADMRAAYDALDDRTKADIENLVCRHNSMYSRGKLGGLADFTEEERRVFK-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + H I GM ++ L L ++A + P V++H W D V

Sbjct: 55 QRLVRRHPVTGRKSLFLSAHVGEIEGMPTPQARMLLLDLTEFATREPFVYSHVWRLNDFV 114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>ref|ZP_08196821.1| taurine dioxygenase, TauD/TfdA family [Nocardiodaceae bacterium
Broad-1]
gb|EGD43820.1| taurine dioxygenase, TauD/TfdA family [Nocardiodaceae bacterium
Broad-1]
Length = 310

Score = 90.1 bits (222), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 75/274 (27%), Positives = 110/274 (40%), Gaps = 18/274 (6%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L + G +GA + GV L+ L A + AA L+H ++ F GQ HL + QI F +R

Sbjct: 12 LTVHKVGGGRIGAHIDGVTLSGDLPAETIAEIRAAILKHKVVFVRGQDHLDDRTQIAFGER 71

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
G + A TV S + +WH D T++ ++

Sbjct: 72 LGPL-----TTAHPTVNTGSARVLT LKANRGMAANSWHTDVTTFVDRPPAFSI 118

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
+P GG T +A+ AY+ L +ALV A HS Y + +

Sbjct: 119 LRGAIEPEYGGNTVWANTVTAYERLHPQLKALVDDLWAVHSNDYDYVRPDEAESTDDVAA 178

Query: 184 GYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
+ +T R P V++HPETG +L++G G++ ES L D

Sbjct: 179 RKREEFVSTIYRTEHPAVRIHPETGERALVLGHFVKHFTGLNQKESATLFNLLQDRV TAL 238

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPR 274
W GDV +WDNR H A +LPR

Sbjct: 239 ENTVRWHWQQGDVAIWDNRATQHYAVADFDELPR 272

>emb|CAY27531.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 90.1 bits (222), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 50/124 (40%), Positives = 69/124 (55%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALD T+AL+ HS ++S+ LG ++ + A +
Sbjct: 1 TEFADMRAAYDALDAKTKALIEDLVCEHSRIFSKGALGF-----SFTEEEVKAFAPVRQ 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP+TGR SL + HA I G E+ L L + A Q V++H+W GD+V+
Sbjct: 55 RLVTRTHPKTGRKSLYLSSHAGRIVGWPVPEAMLLLRELTEHATQREFVYSHKWRVGDLM 114

Query: 256 WDNR 259
WDNR
Sbjct: 115 WDNR 118

>ref|ZP_02406094.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei DM98]
Length = 381

Score = 90.1 bits (222), Expect = 4e-16, Method: Compositional matrix adjust.
Identities = 83/271 (30%), Positives = 118/271 (43%), Gaps = 30/271 (11%)

Query: 6 LQITPTGATLGATVTGVHLATL---DDAGFAALHAAWLQHALLIFPGQHLSNDQ-QITFA 61
L I P +GA V G+ L + +D F + A L H ++ F QH +D+ Q FA
Sbjct: 96 LSIRPLSGHIGAEVQGIQLGSQMAPNDIRF--ITQALLTHRVIFFRQHHLDDRAQELFA 153

Query: 62 KRFGAIER---IGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
+ FG I + +GG AI + + R +S WH D T+
Sbjct: 154 QAFGEIVKHPTMGGKTGSAILELHSHEGGRANS-----WHTDVTFLGRP 197

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY---SQSKLGH 174
+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
Sbjct: 198 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSSLQDLVDKLWAVHGNDFDYAASRVLLH 257

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
A Y T P+V++HPETG SLL+G +A D +S R E L
Sbjct: 258 DPVAKEYRKKYAAQVIKTE-HPVVQIHPTETGEKSLLLGHYAQRQFVQYDTHDSNRLYEILQ 316

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ WAAGDV +WDNR H A
Sbjct: 317 AHITRLENTVRWHWAAGDVVAIWDNRSTQHYA 347

>ref|ZP_03450440.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 576]
gb|EEC38252.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 576]
Length = 381

Score = 90.1 bits (222), Expect = 4e-16, Method: Compositional matrix adjust.
Identities = 83/271 (30%), Positives = 118/271 (43%), Gaps = 30/271 (11%)

Query: 6 LQITPTGATLGATVTGVHLATL---DDAGFAALHAAWLQHALLIFPGQHLSNDQ-QITFA 61
L I P +GA V G+ L + +D F + A L H ++ F QH +D+ Q FA
Sbjct: 96 LSIRPLSGHIGAEVQGIQLGSQMAPNDIRF--ITQALLTHRVIFFRQHHLDDRAQELFA 153

Query: 62 KRFGAIER---IGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
+ FG I + +GG AI + + R +S WH D T+
Sbjct: 154 QAFGEIVKHPTMGGKTGSAILELHSHEGGRANS-----WHTDVTFLGRP 197

Query: 119 AQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVY----SQSKLGH 174
+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
Sbjct: 198 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSSLQDLVDKLWAVHGNDFDYAASRVELLH 257

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
A Y T P+V++HPETG SLL+G +A D +S R E L
Sbjct: 258 DPVAKEYRKKYAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRFVQYDTHDSNRLYEILQ 316

Query: 235 DWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
+ WAAGDV +WDNR H A
Sbjct: 317 AHITRLENTVRWHWAAGDVAIWDNRSTQHYA 347

>gb|ACG80549.1| TfdA [uncultured bacterium]
Length = 119

Score = 90.1 bits (222), Expect = 4e-16, Method: Compositional matrix adjust.
Identities = 52/128 (40%), Positives = 69/128 (53%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DMRAAYDALD+AT+A + HS+V+S+ ++G A + A LR
Sbjct: 1 TEFGDMRAAYDALDDATKAEIENLVTEHSIVFSREQIGFTDYA-----EGNADKLR 51

Query: 196 P----LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251
P LV HP TGR SL + H I G E+ F+ L++ A Q V+AH+W
Sbjct: 52 PVQHRLVITHPVTGRKSLYLSSHIGGIVGWVPPEARAFIRDLMEHATQRRFVYAHEWRVN 111

Query: 252 DVVVDNR 259
D V+WDNR
Sbjct: 112 DPVMWDNR 119

>ref|NP_900474.1| taurine dioxygenase [Chromobacterium violaceum ATCC 12472]
gb|AAQ58480.1| probable taurine dioxygenase [Chromobacterium violaceum ATCC 12472]
Length = 280

Score = 90.1 bits (222), Expect = 4e-16, Method: Compositional matrix adjust.
Identities = 78/272 (28%), Positives = 121/272 (44%), Gaps = 24/272 (8%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ P T+G +TGV L DA F L A QH LL+ G L+ +QQ+ A++F
Sbjct: 1 MRFNPLFPPTIGTELTGVTTFNDILSDALFPELDHALRQHQLLVIRGLQLTPEQQLLLARKE 60

Query: 65 G-----AIERIGGGD---IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
G + R D ++ SN DG + VGN WH DS++
Sbjct: 61 GHPIPFVMSRYHHPDHPMISSNEVKDGK-----PLGVARVGNF-WHQDSSFTQ 109

Query: 117 VMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYS-QSKLGHV 175
A + +P G T FA Y L E + + ARH++ + + HV
Sbjct: 110 DPAAYTMLYGINIPPRSGDTLFASAIIDLRLPEEWKRRRIAGLQARHTVSKRFRIRAEHV 169

Query: 176 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
+ + T L PLV++ ++G+P L + + + G+D A S+ FL+ L+
Sbjct: 170 GLSIAELNEVIAQEHPVLHPLVQIDQDSGQPYLYASKEYVDEVGLDRASSDEFDLD-LI 228

Query: 235 DWACQAP-RVHAHQWAAGDVVWDNRCLLHRA 265
D Q P V+ H+W GD+++W R LH A
Sbjct: 229 DRLTQDPAHVYVHRWQPGDLLIWKTRTALHAA 260

>ref|YP_002383757.1| taurine dioxygenase [Escherichia fergusonii ATCC 35469]
emb|CAQ90146.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia
fergusonii ATCC 35469]

Query:	4	TTLQITPTIGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSDNQGITFAK	62
		T + P G +GA + G L L A + A L+ +L F GQH S QQ FA+	
Sbjct:	43	TLFDVVPLGPVIGAEIRGADLTRPLAPAVREEIDRALLEWKVLFRRGQHPSPAQQRAFAR	102
Query:	63	RFGAIER---IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA	119
		+G +E + GD ++ R +P+ WH D T+ A	
Sbjct:	103	NWGELETNPLLAAGDDPEVARFD-----RSSAPS-----FENVWHTDVTFRERPA	147
Query:	120	QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG	179
		GAV VP GG T +ADM +AYD L + + A H V ++ ++	
Sbjct:	148	LGAVLHLREVPPYGGDTMWADMASAYDNLAPEVKERLEGARAVHDFVPGFARFTPEER--	205

Query: 180 SAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWAC 238
I + D P+V+ HP TGR L + I G D ES+R L L A
Sbjct: 206 --LIPF-QDRFPPVEHPVVRTHPVTGRRLMFVNTSFTTRIVGWDRDESDRMLRLLFQQA 262

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
W AGDV WDNR H A
Sbjct: 263 VPEYQVRFTWRAGDVAFWDNRRATQHYA 289

>emb|CAY27459.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 89.7 bits (221), Expect = 4e-16, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR 195
T F DMRAAYDALD+A +A + Q HSL++S+ LG + + P+R
Sbjct: 1 TEFGDMRAAYDALDDAMKAEIEQVVCESLMFSGALGFSE-----LNEQEAMFRPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I E+ FL L++ A Q V++HQW D+V
Sbjct: 55 QRLVRTHPVTGRKSLFLSAHAGGIVNWPVEARAFRLDLIEHATQPQLVYSHQWQQWDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>emb|CAY27444.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 89.7 bits (221), Expect = 4e-16, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR 195
T F DMRAAYD LDE T+A + HSL++S+ LG + + + P+R
Sbjct: 1 TEFGDMRAAYDTLDERTKAEIEDLVCEHSLMFSGLLGFTAMSEAEREMF-----RPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I G E+ FL L++ A Q V++HQW D+V
Sbjct: 55 QRLVRTHPVTGRKSLFLSAHAGTIVGWPVPEARAFRLDLIEHATQPQSVYSHQWRQWDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|ZP_06656271.1| taurine dioxygenase [Escherichia coli B185]
gb|EFF06653.1| taurine dioxygenase [Escherichia coli B185]
Length = 283

Score = 89.7 bits (221), Expect = 4e-16, Method: Compositional matrix adjust.
Identities = 75/288 (26%), Positives = 121/288 (42%), Gaps = 27/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFRLDQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYPMV 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFTIETP 108

Query: 119 AQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178

Query:	138	FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPL	197
		F DMRAAYDAL + T+A + HSL+YS+ LG V Y L+ L	
Sbjct:	2	FGDMRAAYDALHDETKAEIEDLVCEHSLMYSRGSGLGFVD-----YTDEEKQMFKPVLQRL	56
Query:	198	VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDVVVWD	257
		V+ HP GR SL + HA AI GM E L L + A Q V+ HQW D+V+WD	
Sbjct:	57	VRTHPVHGRKSLYLSSHAGAIRGMSVPEGRLLLRDLTEHATQPEFVYVHQWTVHDLVMWD	116

Query: 258 NR 259
NR
Sbjct: 117 NR 118

>ref|ZP_07447356.1| taurine dioxygenase [Escherichia coli NC101]
gb|EFM54365.1| taurine dioxygenase [Escherichia coli NC101]
Length = 283

Score = 89.7 bits (221), Expect = 4e-16, Method: Compositional matrix adjust.
Identities = 77/289 (26%), Positives = 123/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA +TG L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQITGADLTRPLSDNQFEQLYHAVLRHHVFLRDQAITPQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIQTP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T +A AAY+ L R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWASGIAAYEVLVSVFPRQLLSGLRAEHDFRKSFPYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + + P L P+V+ HP TG+ +L + I + ESE L G +
Sbjct: 168 EAEHQRWREAVAKNPPLHPVVRTHPVTGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|ZP_03504692.1| Taurine dioxygenase [Rhizobium etli Brasil 5]
Length = 313

Score = 89.7 bits (221), Expect = 4e-16, Method: Compositional matrix adjust.
Identities = 76/273 (27%), Positives = 114/273 (41%), Gaps = 32/273 (11%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
+ + P +GA + G+ L L DA AA++ L+H ++ F Q HL + Q FA+R
Sbjct: 17 IDVVPLTGRVGAEIKGIRLGGLSDATVAAVNQLLKHKVIFFRDQGHLLDDSAQEAFAFARR 76

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMP 116
G + G I+ + + + G Q WH D T++
Sbjct: 77 LGDLVPHTQGPVSGTASILNLDSSRGGGRADQ-----WHTDVTTFVD 118

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH-- 174
+ +V V+PA GG T +++ AAY++L + L A HS Y + +
Sbjct: 119 AYPKFSVLRGVVIPAAGGDTIWSNTHAAYESLPAPLKLLADNLWAIHSNAYDYAAVRPRA 178

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER-FLEGL 233
+ + T P+V+VHPETGR + R + PG E R L GL
Sbjct: 179 TAEKKHFEEVFTSTIYETEHPVVRVHPETGR-KIAAARQFRSAPGRPLEERLRQTLRGL 237

Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
AP +W AGDV +WDNR H A
Sbjct: 238 PILTFTAPENTVRWRWRAGDVVAIWDNRATQHYA 270

>gb|ACG80568.1| TfdA [uncultured bacterium]
gb|ACG80586.1| TfdA [uncultured bacterium]

Length = 119

Score = 89.7 bits (221), Expect = 4e-16, Method: Compositional matrix adjust.
Identities = 51/122 (41%), Positives = 63/122 (51%), Gaps = 5/122 (4%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPL 197
F DMRAAYDAL + T+A + HSL+YS+ LG V Y L+ L
Sbjct: 3 FGDMRAAYDALHDETKAEIEDLVCEHSLMYSRGSLGFVD-----YTDEEKQMFKPVLQRL 57

Query: 198 VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVD 257
V+ HP GR SL + HA AI GM E L L + A Q V+ HQW D+V+WD
Sbjct: 58 VRTHPVHGRKSLYLSSHAGAIRGMSVPEGRLLLRDLTEHATQPEFVYVHQWTVHDLVMWD 117

Query: 258 NR 259
NR
Sbjct: 118 NR 119

>ref|YP_001240769.1| putative dioxygenase [Bradyrhizobium sp. BTAi1]
gb|ABQ36863.1| Putative dioxygenase [Bradyrhizobium sp. BTAi1]
Length = 316

Score = 89.7 bits (221), Expect = 4e-16, Method: Compositional matrix adjust.
Identities = 77/267 (28%), Positives = 116/267 (43%), Gaps = 29/267 (10%)

Query: 8 ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRF 65
++ A +GA + V L+ L DA ++ LQH ++ F GQ HL + +Q FAKR G
Sbjct: 23 VSRLSARIGAEIRNVRLSGDLPDALVKEINDLLLQHRVIFFRGQDHLDDAEQERFAKRLG 82

Query: 66 AIERIGGGDIVAISNVKA-DGTVRQHSAPAEWDDMMKVIVGNMA--WHADSTYMPVMAQGA 122
D+V V A GT S E D G A WH D T++ + A
Sbjct: 83 -----DLVPHTVGAIKGTA---SILELDSGRG---GGRADSWHTDVTTFVDAYPKAA 128

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY-----SQSKLGHVQ 176
V V+P GG T +++ AAY L + L + A HS Y S++ +
Sbjct: 129 VLRGVVPIEFGGDTIWSNTAAAYQDLPAQLADELWAVHSNAYDYAATRSRATEDR 188

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW 236
+ G +T P+V+VHPETG +LL+G G+ A+ ++ + +
Sbjct: 189 HFEEVFTGTIYETE---HPVVRVHPETGERTLLLGNFVQRFVVGIRKADGQKLFDFQSY 244

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLH 263
+W GD+ +WDNR H
Sbjct: 245 ITAPENTVRWRWKQGDIAIWDNRATQH 271

>ref|YP_605974.1| alkylsulfatase AtsK [Pseudomonas entomophila L48]
emb|CAK13157.1| Alkylsulfatase AtsK [Pseudomonas entomophila L48]
Length = 301

Score = 89.7 bits (221), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 81/286 (28%), Positives = 119/286 (41%), Gaps = 24/286 (8%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L I P +GA + G+ L A L A+ AA +Q+ ++ F Q HL + Q FA+
Sbjct: 15 LDIQPVAGRIGAEIRGIKLSADLAPETIDAIQAALVQYKVIFFRAQEHLDDQGQEAFAQL 74

Query: 64 FGAIERIGGGDIVAISN----VKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
G E I + + ++ DG Q + +WH D T++
Sbjct: 75 LG--EPIAHPTVPVVDGTSYLLQLDGAEGQRA-----NSWHTDVTTFVDAYP 118

Query: 120 QGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG-HVQQA 178
+ ++ + V PA GG T +A+ AAY L E R L A HS Y + + V A

Sbjct: 119 KASILRSVAPASGGDTVWANTAAAYQELPEPLRVLADTLWAVHSNEYDYASVKPDVDP 178
Query: 179 G-SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
Y T P+V+VHP +G +L +G I G A+S+ L
Sbjct: 179 KLERIRKVFSTSTVYETHPVVRVHPISGERALQLGHFVKRIKGYSLADSQHLFALLQGHV 238
Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W AGDV +WDR H A PR++ LAG
Sbjct: 239 TRLENTVRWRWQAGDVAIWDRATQHYAVDDYGTQPRIVRRVTLAG 284

>ref|YP_001895727.1| Taurine dioxygenase [Burkholderia phytofirmans PsJN]
gb|ACD16503.1| Taurine dioxygenase [Burkholderia phytofirmans PsJN]
Length = 315

Score = 89.7 bits (221), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 77/286 (26%), Positives = 122/286 (42%), Gaps = 16/286 (5%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++Q+TP A +GA + GV L LD A + AA L+ ++ F Q L+++Q + F+ +
Sbjct: 11 SIQVTPLSAHIGAEIHGVDLTQKLDARQIAEIRAALLKWRVVFREQLTHEQHVAFSAQ 70
Query: 64 FGAIERIG---GGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQ 120
FG + +G G + V + R+ + E + + G WH D T
Sbjct: 71 FGELT-LGHPVFGHVDGYPEVYSISKYRKATRFEGQTLQRPWTG---WHTDVTAAALNPPW 126
Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
++ +P GG T + ++ AAY L R V H G
Sbjct: 127 ASILRGVTIPPYGGDTQWTNLVAAYQKLSAPLRGFVDGLRGLHRFTPPAGASG-----TE 181
Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239
A+ T PLV+VHPETG +L + +I G+ ES+ LE L + +
Sbjct: 182 AFNKAVEQRTLVTHEPLRVHPETGERALVSPSFLKSIVGVSPRESQVLELLLEWHVTR 241
Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA--EPWDFKLPRVMWHSRLAG 283
+W AG V WDR H A + +D + R ++ + L G
Sbjct: 242 PEFTVRFKWEAGSVAFWDRATAHLAPTDFDLEFDRQLYRTTLVG 287

>emb|CAY27222.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 89.7 bits (221), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 50/124 (40%), Positives = 69/124 (55%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALD T+AL+ HS ++S+ LG ++ + A +
Sbjct: 1 TEFADMRAAYDALDARTKALIEDLVCEHSRIFSKGALGF-----SFTEEEVKAFAPVRQ 54
Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP+TGR SL + HA I G E+ L L + A Q V++H+W GD+V+
Sbjct: 55 RLVRTHPKTGRKSLYLSSHAGRIVGWPVPEAMLLRELTEHATQREFVYSHKWRVGDLM 114
Query: 256 WDR 259
WDR
Sbjct: 115 WDR 118

>ref|YP_001629701.1| taurine dioxygenase [Bordetella petrii DSM 12804]
emb|CAP41431.1| taurine dioxygenase [Bordetella petrii]
Length = 214

Score = 89.7 bits (221), Expect = 5e-16, Method: Compositional matrix adjust.

Identities = 55/215 (25%), Positives = 104/215 (48%), Gaps = 35/215 (16%)

```
Query: 6   LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          +I   + +GA + GV L A +D+  FA +   WL++ +L+F GQ L+N+Q + F+ RF
Sbjct: 3   FEIRRLSSGIGAEIIGVDLSADIDEKTFQIEKCWLENVILLFRGQKLNNEQHVRF SARF 62

Query: 65  GA-----IERIGGGD---IVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM 115
          G           I+R+   D   I+ + ++   + +R                               VG   WH+D ++
Sbjct: 63  GKLDEHDDIKRLRDPDHHEILPVL SIPGEKRLR-----VG-AQWHS DMSHS 107

Query: 116  PVMAQGA VFSAEVVPAVGGR TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
          + ++   E +P +GG T F +M  AY+ L E+ + L+   H + ++ +G
Sbjct: 108  LCPPKASLLRCEEIPPLGGDTMFGNMYLAYERLSESMKRLDDLWCVDMTIAKH NIGQY 167

Query: 176  QQAGSAYIGYGMDTTATPL-RPLVKVHPETGRPSL 209
          +           +           P+ +P++++HPETG+  L
Sbjct: 168  NE-----VRKRQPPVAQPIIRIHPETGKKGL 193
```

>emb|CAY27374.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 117

Score = 89.4 bits (220), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 50/123 (40%), Positives = 70/123 (56%), Gaps = 7/123 (5%)

```
Query: 136  TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
          T FADMRAAYDALD+ T+A +   RHS +YS+ KLG V+   +   P+R
Sbjct: 1   TEFADMRAAYDALDDRTKAD IENLVCRHSNMYSRGKLGLEFTDEERAVF-----RPVR 54

Query: 196  PL-VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
          L V+ HP +GR SL + HA I GM ++   L L ++A + P V++H W   D+V
Sbjct: 55  QLLVRRHPVSGRKSFLSAHAGEIEGMPTPQARMLLLDLTEFATREPFVYSHVVRVNDLV 114

Query: 255  VWD 257
          +WD
Sbjct: 115  MWD 117
```

>emb|CAY27503.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 89.4 bits (220), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

```
Query: 136  TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
          T F DMRAAYD LDE T+A +   HSL++S+ LG   + +   +   P+R
Sbjct: 1   TEFGDMRAAYDTLDERTKAEIEDLVCEHSLMFSRGLLGFTAMSEAEREMF-----RPVR 54

Query: 196  P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
          LV+ HP TGR SL + HA I G   E+ FL L++ A Q   V++HQW   D+V
Sbjct: 55  QRLVRTHPVTGRKSFLSAHAGTIVGWPVPEARAFRLDLIEHATQPQLVYSHQWRQWDLV 114

Query: 255  VWDNR 259
          +WDNR
Sbjct: 115  MWDNR 119
```

>gb|AAP21654.1| Shy7 [Streptomyces hygrosopicus subsp. yingchengensis]
Length = 251

Score = 89.4 bits (220), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 78/255 (30%), Positives = 114/255 (44%), Gaps = 37/255 (14%)

Query: 19 VTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQI---TFAKRFGAIERIG-- 71
+TG+ LA +DDA L A+ +H +L+F GQHL+ +Q + FA+ F +
Sbjct: 1 MTGIDLAAGVDDATAEELRRAFREHKVLFVRGQHLTPEQHVEAVRIFAEPFDHPTAVKDP 60

Query: 72 GGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTY-MPVMAQGAVFSAEVVP 130
+V NV+ G WH + PV A ++ + EVVP
Sbjct: 61 AHPLVYPYNVQHTGKAS-----TWHIGGLWRKPVFAIESL-TYEVVP 101

Query: 131 AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTT 190
A+GG T +AD++AAYD L E + L+ A VY + + Q + +
Sbjct: 102 ALGGHTLWADLQAAYDDLSEPFKELLESVGA---VYDANAGNYAQGSKREAV-----E 151

Query: 191 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA 250
T P+V HPETGR L I A + G+ + E + L+ L+ A W A
Sbjct: 152 ETVEHPVVLTHPETGRKGLFISTALSGLTGVTSQEGKVLDDHLLRHASSPDYTIIRFGWNA 211

Query: 251 GDVVVWDNRCLLHRA 265
GD V+WDNR H A
Sbjct: 212 GDFVLWDNRATWHYA 226

>emb|CAY27355.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 89.4 bits (220), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 52/124 (41%), Positives = 68/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T FADMRAAYDALD+ +A HS ++S++ LG S + A +
Sbjct: 1 TEFADMRAAYDALDDEAKAECEENLVCEHSQFLSRAILGF-----SDFTEEEERRKFAPVRQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDVVV 255
LV+ HP TGR SL + HA I G E+ FL LV+ A Q V++HQW GD+V+
Sbjct: 56 VLVTRTHPVTRKSLYLSSHAGGIEGWPVPEARAFLRDLVEHATQRQFVYSHQWRVGDLM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>ref|YP_295812.1| taurine dioxygenase [Ralstonia eutropha JMP134]
gb|AAZ60968.1| Taurine dioxygenase [Ralstonia eutropha JMP134]
Length = 281

Score = 89.4 bits (220), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 83/295 (28%), Positives = 123/295 (41%), Gaps = 40/295 (13%)

Query: 7 QITPTGATLGATVTGVHLAT--LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
QITP +GA ++GV+L D A FA + AA L+H +L F Q ++ + FA F
Sbjct: 5 QITPA---IGAEISGVNLGEGARDPALFAEIKAAALLKHRVLFRRKQEIIRADHVAFAFAF 61

Query: 65 GAIERIGGGDIVAISNVKAD---GTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
G +E D + +V R +P +++ ++H D + P A
Sbjct: 62 GKLE-----DHPVVGSPDHPGLVKVYRSDNPHSYEN-----SYHCDGLWRPNPAM 107

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
GAV P +GG T + +M AYD L E + ++ AR S+ +S G V +
Sbjct: 108 GAVLRCLCEPEIGGDTIWNMVKAYDELPEEIKRKINGLRARASIEHS---FGAVMTPE 164

Query: 181 AYIGYMDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIP-----GMDAAESERF 229
D A P+V+ HPETG L +G ++ P G+D +
Sbjct: 165 R-AKLAQDHPAVE-HPVVRTHPETGEKILFVGASFTTHFTNYSTPDNVRHGIDKSPGASL 222

Query: 230 LEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + P W GDV VWDNR H A + PR M + + G
Sbjct: 223 LLNYLTSRATIPEYQVRWAWQEGDVAVWDNRSTQHYAVNDYYPAPRKMERAGIVG 277

>ref|ZP_07500810.1| taurine dioxygenase [Escherichia coli M605]
Length = 283

Score = 89.4 bits (220), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 77/289 (26%), Positives = 123/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA +TG L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQITGADLTRPLSDNQFEQLYHAVLRHQVFLRDQAITPQQQRALAQR 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIQTP 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T +A AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWASGIAAYEALSVPFRQLLSGLRAEHDFRKSFPYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + + P L P+V+ HP G+ +L + I + ESE L G +
Sbjct: 168 EAEHQWRWEAVAKNPPLLHPVVRTHPVGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|ZP_06354055.1| taurine dioxygenase [Citrobacter youngae ATCC 29220]
gb|EFE07953.1| taurine dioxygenase [Citrobacter youngae ATCC 29220]
Length = 283

Score = 89.4 bits (220), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 78/287 (27%), Positives = 118/287 (41%), Gaps = 25/287 (8%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA +TG LA L D F L+ A L+H ++ Q ++ QQ A RF
Sbjct: 5 LNITPLGPYIGAQITGADLARPLSDNQFEQLYHAVLRHQVFLREQVITPQQQRALALRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIDTP 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + Q
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSSPFRQLLSGLRAEHDFRKSFPQYKYRQTP 168

Query: 179 GSAYIGYGMDDTTATP-LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
P L P+V+ HP +G+ +L + I + ESE L L
Sbjct: 169 EEHQRWLDAVAKHPPLLHPVVRTHPVSQKQALFVNEGFTTRIVDVTEKESEALLSFLFAH 228

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W DV +WDNR H A R+M + + G
Sbjct: 229 ITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>emb|CAY27334.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 89.4 bits (220), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 52/125 (41%), Positives = 67/125 (53%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T FADMRAAYDALDE R + HS +YS+ KLG + P+R
Sbjct: 1 TEFADMRAAYDALDEWLRNQIEDLVCLHSNMYSRGKLGADFTDEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I GM E+ L L ++A + P V++H W D+V
Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMMLLLDLTEFATREPFVYSHAWRVNDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>emb|CAY27463.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 89.4 bits (220), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 68/125 (54%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T F DMRAAYDA DE T+A + HSL+YS+ LG + + T TP+R
Sbjct: 1 TEFGDMRAAYDAPDEKTKAEAE DLACEHSLIYSRGTLGFTE-----LSEEERKTFTPV 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + H I G E+ F+ L + A Q+ +AH+W D+V
Sbjct: 55 QRLVRTHPVTGRKSLYLSSHIGTIVGWMPPEARAFIRDLEHATQSRFTYAHKWRQFDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|YP_714407.1| putative taurine dioxygenase [Frankia alni ACN14a]
emb|CAJ62855.1| Putative taurine dioxygenase [Frankia alni ACN14a]
Length = 262

Score = 89.4 bits (220), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 82/274 (29%), Positives = 110/274 (40%), Gaps = 31/274 (11%)

Query: 7 QITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
I P LGA V GV LA +DDA AL A+ QH +L+F QHLS D + + F
Sbjct: 10 DIRPASPVLGAEEVVGVDLAGGVDDATAEALREAFWQHKVLVFRDQHLSPPDAHVQAVRIFD 69

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAE--WDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
+ +H +D ++ G WH T+
Sbjct: 70 -----EPFDHPKWLYRHEDNRLVYDFQLEKAGGASTWHVGGTWRTPPFHLES 116

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
+ +VVP +GGRT +AD++AAYD L E + L+ SA V A
Sbjct: 117 LTYQVVPDIGNRTLWADLQAAYDGLSEPFQHLLLESVSA-----VYNADPGDG 163

Query: 184 GYGMD-TTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPR 242
Y T T P+V+ H TGR L + A + G+ AE L L+ A
Sbjct: 164 TYNRPPVTETVEHPVVRTHRHTGRKGLFLSSALRLTGVGPAEGAALLPFLAHASSPNY 223

Query: 243 VHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
+ W GD V WDN H A D+ PRV
Sbjct: 224 TVSFGWKPGDFVTWDLATWHFAVN-DYDGPRVY 256

```
>ref|ZP_04896195.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pasteur
52237]
gb|EDO93033.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pasteur
52237]
```

Length = 294

Score = 89.4 bits (220), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 83/271 (30%), Positives = 117/271 (43%), Gaps = 30/271 (11%)

```
Query: 6   LQITPTGATLGATVTGVHLATL---DDAGFAALHAAWLQHALLIFPGQHLSND-QQITFA 61
          L I P   +GA V G+ L +   +D F + A L H ++ F QH +D Q FA
Sbjct: 9   LSIRPLSGHIGAEVQGIQLGSQMAPNDIRF--ITQALLTHRVIFFRRQHHLDDLAQELFA 66

Query: 62  KRFGAIER---IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM 118
          + FG I +   +GG AI + +   R +S                               WH D T+
Sbjct: 67  QAFGEIVKHPTMGKKTGSAILELHSHEGGRANS-----WHTDVTFGLRP 110

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY---SQSKLGH 174
          + +V A +P GG T +A+ AAY L + + LV + A H +   S+ +L H
Sbjct: 111 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSSLQDLVDKLVAVHGNDFDYAASRVELLH 170

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
          A       Y       T   P+V++HPETG SLL+G +A       D +S R E L
Sbjct: 171 DPVAKEYRKKYAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRQFVQYDTHDSNRLYEILQ 229

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
          +           WAAGDV +WDNR H A
Sbjct: 230 AHITRLENTVRWHWAAGDVAIWDNRSTQHYA 260
```

>ref|YP_001412108.1| taurine dioxygenase [Parvibaculum lavamentivorans DS-1]
gb|ABS62451.1| Taurine dioxygenase [Parvibaculum lavamentivorans DS-1]
Length = 276

Score = 89.4 bits (220), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 76/282 (26%), Positives = 118/282 (41%), Gaps = 13/282 (4%)

```
Query: 6   LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
          +++      GA V G LA L ++ A+ A++ + ++ F Q+L+ + I FA+R+G
Sbjct: 4   IEVRKMTGGCGAEVLGADLAKLSNSDMEAVRQAYVDYGVVFFRDQNLTPEDHIAFARRWG 63

Query: 66  AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
          I       +V       +       E + + + G WH D +Y A G+V
Sbjct: 64  DI-----VVRNFFFTPTQNPLIAEVRKEKEQTVNIGGG---WHTDHSYDAEPAMGSVLV 113

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 185
          A +P GG T FA M AA+DAL + + A HS + G + +
Sbjct: 114 ARELPDEGGDTMFASMYAAWDALTPGLKKTLEGLRAVHSNAHVFGAAGFYKNSDQKGFK 173

Query: 186 GMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVDWACQAPRV 243
          G + + + P+V HP +GR +L + G H G ES+ L+ L A +
Sbjct: 174 GENLVSEAVHPVVVTHPLSGRKALYVNPGFTH-FEGWSWLESKPLLDYLFABAARPEFT 232

Query: 244 HAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
          QW G V WDNR H A R+M +AG P
Sbjct: 233 CRFQWRDGSVAFWDNRATWHYAVNDYHGERRLMHRITIAGAP 274
```

>ref|ZP_06066452.1| taurine dioxygenase [Acinetobacter junii SH205]
gb|EEY94283.1| taurine dioxygenase [Acinetobacter junii SH205]
Length = 281

Score = 89.4 bits (220), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 72/273 (26%), Positives = 111/273 (40%), Gaps = 32/273 (11%)

```
Query: 5   TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          TL I       T+GA + V L T+D+ + A L H + F Q L+ Q A+ F
```

Sbjct: 2 TLNIEVIKPTIGAIHVDLNTVDENTTQQIQQALLDHHEIFFRNQQQLAPQAQAEELARGF 61

Query: 65 GA-----IERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
G+ +E + +I+ + + K D + N WH D T+

Sbjct: 62 GSLHIHPIFPTVENVP--EIIVLDSWKQD-----LRDNELWHTDVTFS 102

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLG 173
G V A +P VGG T ++ AA+ ALD++ + + +A H + Y +

Sbjct: 103 QNPPLGCVLQAIKIPVGGDTLWSSGVAAFAALDQSLQQLKGLTATHDIRQSYPIERFA 162

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
H + + P+V+ HP TG+ L + I +D +ES L+

Sbjct: 163 H-NDVERKKLEETFKRNPVPHVVRTHPVTGQSILFVSEGFTTRINELDESESAELLQY 221

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L A QW GDV +WDNRC H+A

Sbjct: 222 LFAHATHEQFHLRWQWQEGDVAIWDNRCTQHKA 254

>ref|YP_072200.1| taurine dioxygenase [Yersinia pseudotuberculosis IP 32953]
ref|YP_653194.1| taurine dioxygenase [Yersinia pestis Antiqua]
ref|YP_649809.1| taurine dioxygenase [Yersinia pestis Nepal516]
ref|YP_001161506.1| taurine dioxygenase [Yersinia pestis Pestoides F]
ref|ZP_01917492.1| putative taurine dioxygenase [Yersinia pestis CA88-4125]
ref|YP_001402883.1| taurine dioxygenase [Yersinia pseudotuberculosis IP 31758]
ref|NP_671259.2| taurine dioxygenase [Yersinia pestis KIM 10]
ref|NP_991584.2| taurine dioxygenase [Yersinia pestis biovar Microtus str. 91001]
ref|YP_001608011.1| taurine dioxygenase [Yersinia pestis Angola]
ref|ZP_02223665.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia
pestis
biovar Orientalis str. F1991016]
ref|ZP_02228556.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia
pestis
biovar Orientalis str. IP275]
ref|ZP_02231419.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia
pestis
biovar Antiqua str. E1979001]
ref|ZP_02239180.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia
pestis
biovar Antiqua str. B42003004]
ref|ZP_02304630.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia
pestis
biovar Antiqua str. UG05-0454]
ref|ZP_02310582.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia
pestis
biovar Orientalis str. MG05-1020]
ref|ZP_02317412.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia
pestis
biovar Mediaevalis str. K1973002]
ref|ZP_02333537.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia
pestis
FV-1]
ref|YP_001719027.1| taurine dioxygenase [Yersinia pseudotuberculosis YPIII]
ref|YP_001874317.1| taurine dioxygenase [Yersinia pseudotuberculosis PB1/+]
ref|YP_002345269.1| taurine dioxygenase [Yersinia pestis CO92]
ref|ZP_04456500.1| putative taurine dioxygenase [Yersinia pestis Pestoides A]
ref|ZP_04460202.1| putative taurine dioxygenase [Yersinia pestis biovar Orientalis
str. PEXU2]
ref|ZP_04462280.1| putative taurine dioxygenase [Yersinia pestis biovar Orientalis
str. India 195]
ref|ZP_04519686.1| putative taurine dioxygenase [Yersinia pestis Nepal516]
ref|ZP_06205285.1| taurine dioxygenase [Yersinia pestis KIM D27]
ref|YP_003566332.1| putative taurine dioxygenase [Yersinia pestis Z176003]

emb|CAH22957.1| putative taurine dioxygenase [Yersinia pseudotuberculosis IP 32953]
gb|ABG20209.1| taurine dioxygenase [Yersinia pestis Nepal516]
gb|ABG15249.1| putative taurine dioxygenase [Yersinia pestis Antiqua]
emb|CAL18870.1| putative taurine dioxygenase [Yersinia pestis C092]
gb|ABP38534.1| taurine dioxygenase [Yersinia pestis Pestoides F]
gb|EDM40249.1| putative taurine dioxygenase [Yersinia pestis CA88-4125]
gb|ABS46369.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia
pseudotuberculosis IP 31758]
gb|ABX86880.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia pestis
Angola]
gb|EDR30701.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia pestis
biovar Orientalis str. IP275]
gb|EDR37410.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia pestis
biovar Orientalis str. F1991016]
gb|EDR42912.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia pestis
biovar Antiqua str. E1979001]
gb|EDR49923.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia pestis
biovar Antiqua str. B42003004]
gb|EDR58844.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia pestis
biovar Orientalis str. MG05-1020]
gb|EDR63018.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia pestis
biovar Antiqua str. UG05-0454]
gb|EDR65143.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia pestis
biovar Mediaevalis str. K1973002]
gb|ACA66574.1| Taurine dioxygenase [Yersinia pseudotuberculosis YPIII]
gb|ACC90860.1| Taurine catabolism dioxygenase TauD/TfdA [Yersinia
pseudotuberculosis PB1/+]
gb|EE074798.1| putative taurine dioxygenase [Yersinia pestis Nepal516]
gb|EE082489.1| putative taurine dioxygenase [Yersinia pestis biovar Orientalis
str. India 195]
gb|EE086456.1| putative taurine dioxygenase [Yersinia pestis biovar Orientalis
str. PEXU2]
gb|EE092408.1| putative taurine dioxygenase [Yersinia pestis Pestoides A]
gb|ACY57071.1| putative taurine dioxygenase [Yersinia pestis D106004]
gb|ACY60859.1| putative taurine dioxygenase [Yersinia pestis D182038]
gb|EFA47492.1| taurine dioxygenase [Yersinia pestis KIM D27]
gb|ADE63070.1| putative taurine dioxygenase [Yersinia pestis Z176003]
gb|ADV96891.1| putative taurine dioxygenase [Yersinia pestis biovar Medievalis
str. Harbin 35]
Length = 282

Score = 89.4 bits (220), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 79/292 (27%), Positives = 125/292 (42%), Gaps = 30/292 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L +TP G +GA V +++A L D+ F L+ L+H +L F Q ++ QQ A RF
Sbjct: 5 LIVTPLGPHIGALVENINIAHPLGDSQFEQLYHVLLKHQVLFRRNPITPLQORDLAGRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + + + + D +P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPHTQECEEIIVLDTADD-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH--VQ 176
GA+ +A+ +P GG T ++ AAYDAL + L+ A H S + H
Sbjct: 109 PLGAILAAKQLPTTGGDTLWSSGIAAYDALSAFPKQLLAGLQAEDFTKSFPEKHRTTP 168

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ ++ G + L P+++ HP +GR +L + I G+ ESE L G +
Sbjct: 169 EEHQRWLQ-GKEKNPPLLHPVIRTHPVSGRQALFVNEGFTTRIIGLSKSEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
P +W DV +WDNR H A RVM + + G RP
Sbjct: 227 AHTTKPEFQVRWRWQDDVAIWDNRVTQHYANADYLPQRRVMHRATILGDRP 278

>emb|CAY27414.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 89.4 bits (220), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 51/124 (41%), Positives = 66/124 (53%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALD+ T+A + HSL+YS+ LG + Y L+
Sbjct: 1 TEFADMRAAYDALDDDTKAEIEDLVCEHSLMYSRGSLGFTE-----YTDDEKQMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP R SL + HA AI GM E+ L L + A Q V+ H+W D+V+
Sbjct: 56 RLVRTHPVHRRKSLYLSSHAGAILGMSVPEARLLLRDLTEHATQPEFVYVHKWTLHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>gb|ACG80555.1| TfdA [uncultured bacterium]
gb|ACG80561.1| TfdA [uncultured bacterium]
Length = 119

Score = 89.4 bits (220), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 50/124 (40%), Positives = 65/124 (52%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRA YDALD+ T+A + HSL+YS+ LG + Y L+
Sbjct: 1 TEFGDMRAGYDALDDETAEIEDMICEHSLMYSRGSLGFLE-----YTDEEKQLFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP GR SL + HA AI GM E+ L L + A Q V+ H+W D+V+
Sbjct: 56 RLVRTHPVHGRKSLYLSSHAGAIKGMTMPEARLLLRDLNEHATQPEFVYVHKWTLHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>ref|ZP_04889621.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 1655]
gb|EDU10605.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 1655]
Length = 294

Score = 89.4 bits (220), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 83/271 (30%), Positives = 117/271 (43%), Gaps = 30/271 (11%)

Query: 6 LQITPTGATLGATVTGVHLATL---DDAGFAALHAAWLQHALLIFPGQHLSND-QQITFA 61
L I P +GA V G+ L + +D F + A L H ++ F QH +D Q FA
Sbjct: 9 LSIRPLSGHIGAEVQGIQLGSQMAPNDIRF--ITQALLTHRVIFFRRQHHLDDLAQELFA 66

Query: 62 KRFGAIER---IGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
+ FG I + +GG AI + + R +S WH D T+
Sbjct: 67 QAFGEIVKHPTMGGKTGSAILLEHSHEGGRANS-----WHTDVTFTGLRP 110

Query: 119 AQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVY---SQSKLGH 174
+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
Sbjct: 111 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSSLQDLVDKLWAVHGNDFDYAASRVELLH 170

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
A Y T P+V++HPETG SLL+G +A D +S R E L
Sbjct: 171 DPVAKYRKKYAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRVQYDTHDSNRLYEILQ 229

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ WAAGDV +WDNR H A
Sbjct: 230 AHITRLENTVRWHWAAGDVVAIWDNRSTQHYA 260

>gb|EGC08562.1| TfdA family protein Taurine catabolism dioxygenase TauD
[Escherichia fergusonii B253]
Length = 283

Score = 89.4 bits (220), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 76/288 (26%), Positives = 121/288 (42%), Gaps = 27/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPHIGALISGADFTRPLSDNQFEQLYHAVLRHQVFLREQAITPQQQRVLAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPHAAGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQ 176
GA+ +A+ +P+ GG T +A AAY+AL R L++ A H + + K +
Sbjct: 109 PAGAILAAKELPSTGGDTLWASGIAAYEALSAPFRQLLNGLQAEHDFRKSFPYKFRKTE 168

Query: 177 QAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + + L P+V+ HP +GR +L + I + A ESE L L
Sbjct: 169 EEHQRW-REAVAKNPPLHPVVRTHPVSGRHALFVNEGFTTRIVDVTAKESEMLLAFLFA 227

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ W DV +WDNR H A R+M + + G
Sbjct: 228 HITKPEFQVRWCWQPNDVAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|ZP_01908082.1| taurine dioxygenase [Plesiocystis pacifica SIR-1]
gb|EDM78974.1| taurine dioxygenase [Plesiocystis pacifica SIR-1]
Length = 282

Score = 89.4 bits (220), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 75/268 (27%), Positives = 105/268 (39%), Gaps = 29/268 (10%)

Query: 7 QITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
I P +GA V GV L A L L AA L H +L F Q +S + A+ FG
Sbjct: 4 SIHPLTPPVGAEVVRGVDLRAPLSAEQSEFLEAALLAHGVLFFRDQDISPADHLALARA 63

Query: 66 -----AIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMA 119
+ + G D V I V D + + WH D T++
Sbjct: 64 EPVPHPSFSPVPGFDVNILRVTPDEEPKIDT-----WHTDMTFLEAPP 107

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
G++ A V+ GG T F AAYD+L + + A HS + H
Sbjct: 108 LGSILRARVLTECGDGLFGSTIAAYDSLPTMKRRLEGLRAAHSFTHG---FRHSLAEP 164

Query: 180 SAYIGYGMDDTATPLR--PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 236
A A P R P+V+VHP +G+P L + R I + ES+ L L +
Sbjct: 165 DASPRLRAAKAHPVRVHPVVRVHPRSGKPGFLVNRLFTTHILDLPERESDLSLLAYLYEH 224

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
Q +W+ + WDNRC +HR
Sbjct: 225 LEQPEHTCRFRWSPNAIAFWDNRCTIHR 252

>ref|ZP_04746502.1| putative dioxygenase [Mycobacterium kansasii ATCC 12478]

Length = 296

Score = 89.0 bits (219), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 75/262 (28%), Positives = 108/262 (41%), Gaps = 13/262 (4%)

```
Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
          + +   G+ +GA + GV L   LD A   +   A L H ++ F   QH L + QQ+ FA
Sbjct: 5   IAVQKLGSRIGAQMMDGVRLLGGDLDPAEVDQIRKALLTHKVIFFRSQHHLDDQQQLAFAGL 64

Query: 64  FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
          GA               I + A   +++P               +   N   WH D T+   +V
Sbjct: 65  LGA-----PIGHPAAAMLAENAPIITPINSEYGKANR-WHTDVTFAANYPSASV 113

Query: 124  FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
          A +P   GG T +A+   AAY+ L E   + L   A H+   +   + +A A+
Sbjct: 114  LRAVTLPGYGGSTLWANTAAAYEGLPEPLKCLTENLWALHTNRHDYLAHAEPLTEAQRHR 173

Query: 184  GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRV 243
          P+V+VHPETG   +LL G               G+D+ ES   E L
Sbjct: 174  QAFQKPDFQTEHPVVRVHPETGERTLLAGSFVRNFVGLDSHESSVLFELLQRRITAPENT 233

Query: 244  HAHQWAAGDVVWVDNRCLLHRA 265
          W   GDV +WDNR   HRA
Sbjct: 234  IRWNWERGDAIWDNRATQHRA 255
```

>emb|CAY27209.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27387.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 89.0 bits (219), Expect = 7e-16, Method: Compositional matrix adjust.
Identities = 50/124 (40%), Positives = 69/124 (55%), Gaps = 6/124 (4%)

```
Query: 136  TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
          T FADMRAAYDALD T+AL+   HS ++S+ LG   ++   +   A   +
Sbjct: 1   TEFADMRAAYDALDGKTKALIEGLVCEHSRIFSKGALGF-----SFTEEEVKAFAPVRQ 54

Query: 196  PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
          LV+ HP+TGR SL +   HA   I G   E+   L L + A Q   V++H+W   GD+V+
Sbjct: 55  RLVTRHPKTKGRKSLYLSSHAGRIVGWPVPEAMLLRELTEHATQREFVYSHKWRVGDLMV 114

Query: 256  WDNR 259
          WDNR
Sbjct: 115  WDNR 118
```

>gb|EGB79347.1| taurine dioxygenase [Escherichia coli MS 57-2]
Length = 283

Score = 89.0 bits (219), Expect = 7e-16, Method: Compositional matrix adjust.
Identities = 77/289 (26%), Positives = 123/289 (42%), Gaps = 29/289 (10%)

```
Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L ITP G   +GA +TG L   L D F   L+ A L+H ++   Q ++   QQ   A+RF
Sbjct: 5   LSITPLPGYIGAQITGADLTRPLSDNQFELYHAVLRHQVVFRLDQAITPQQQRALAQRF 64

Query: 65  GAIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
          G +               G D + + +   D   +P + D+               WH D T++
Sbjct: 65  GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIQTP 108

Query: 119  AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
          GA+ +A+ +P+ GG T +A   AAY+AL   L+   A H   S   +   + ++
Sbjct: 109  PAGAILAAKELPSTGGDTLWASGIAAYEALSVPFHQLLSGLRAEHDFRKSFPEYKY-RKT 167
```

Query: 175 VQQAGSAYIGYGMDTTATPLRLPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
A Y T P+V++HPETG SLL+G +A D +S R E L

Sbjct: 258 DPVAKEYRKKYAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRQFVQYDTHDSNRLYEILQ 316

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ WAAGDV +WDNR H A

Sbjct: 317 AHITRLENTVRWHWAAGDVAIWDNRSTQHYA 347

>emb|CAY27340.1| alpha-KG-dehydrogenase [uncultured bacterium]

emb|CAY27461.1| alpha-KG-dehydrogenase [uncultured bacterium]

emb|CAY27549.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 119

Score = 89.0 bits (219), Expect = 7e-16, Method: Compositional matrix adjust.

Identities = 51/125 (40%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195

T FADMR AYD LD TRA + HSL+YS+ +G + + P+R

Sbjct: 1 TEFADMRNAYDTLDAKTRAQIENLVCEHSLIYSRSGSMGFTE-----LTEDERAMMKPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254

LV+ HP TGR SL + HA I G ES FL L + A Q V+ H+W D+V

Sbjct: 55 QRLVRTHPVTGRKSLYLSSHAGTIVGWLVPESRDFLRDLNEHATQRENVYIHRWRQFDLV 114

Query: 255 VWDNR 259

+WDNR

Sbjct: 115 MWDNR 119

>ref|YP_402198.1| taurine dioxygenase [Shigella dysenteriae Sd197]

ref|ZP_07680623.1| alpha-ketoglutarate-dependent taurine dioxygenase [Shigella dysenteriae 1617]

gb|ABB60709.1| taurine dioxygenase [Shigella dysenteriae Sd197]

gb|EFP71583.1| alpha-ketoglutarate-dependent taurine dioxygenase [Shigella dysenteriae 1617]

Length = 283

Score = 89.0 bits (219), Expect = 8e-16, Method: Compositional matrix adjust.

Identities = 74/288 (25%), Positives = 122/288 (42%), Gaps = 27/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLI FPGQHLSNDQQITFAKRF 64

L ITP G +GA ++G L +L D F L+ A L+H ++ Q ++ QQ A+RF

Sbjct: 5 LSITPLGPYIGAQISGADLTRSLSDNQFELYHAVLRHQVVFRLDQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118

G + G D + + + D +P + D+ WH D T++

Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178

GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++

Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235

+ + P L P+V+ HP +G+ +L + I + ESE L L

Sbjct: 168 EEEHQRWREAVAKNPPLHPVVRTHPVSQKQALFVNEGFTTRIVDVSEKESEALLSFLFA 227

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ +W D+ +WDNR H A R+M + + G

Sbjct: 228 HITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHQATILG 275

>ref|ZP_04382578.1| alpha-ketoglutarate-dependent taurine dioxygenase [Rhodococcus erythropolis SK121]

gb|EEN89971.1| alpha-ketoglutarate-dependent taurine dioxygenase [Rhodococcus

erythropolis SK121]
Length = 317

Score = 89.0 bits (219), Expect = 8e-16, Method: Compositional matrix adjust.
Identities = 82/288 (28%), Positives = 119/288 (41%), Gaps = 15/288 (5%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
+ T +TPT T+GA ++G+ L+ L D + L A L+ +L F Q + +
Sbjct: 38 LPYTRFTTLPTTPTTIGAEISGISLSGQLSDETMSELRRALLEWKVLFRRDQTIERSEHRD 97

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
FA R+G++E+ +AD D M + N WH D ++ +
Sbjct: 98 FASRWGSLEQHPFFKYTQPGQSEADIVTLAK-----DAMTGGVENN--WHNDVSWHEFPS 150

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
AV A VP VGG T +AD AAY+ L E + + A H + S K H+ +
Sbjct: 151 FAAVLRAVEVPPVGGDTLWADTGAAYELLPEGIKERIDNLVAEHDWINSFGK--HMDPST 208

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWAC 238
A + P+V+V PETGR L + I G+ AES L L
Sbjct: 209 VAKLRPQFPAVR--HPVVRVIPETGRKVLVFNLSFTQRIVGVPEAESNELLTLLYRHVH 265

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
+ +W + WDNR H A F RVM + G RP
Sbjct: 266 RPEFQVRLKWRTDTIAFWDNRTCQHYAASDYFPARRVMDRISIVGDRP 313

>ref|YP_002869897.1| putative taurine dioxygenase [Pseudomonas fluorescens SBW25]
emb|CAY46487.1| putative taurine dioxygenase [Pseudomonas fluorescens SBW25]
Length = 301

Score = 89.0 bits (219), Expect = 8e-16, Method: Compositional matrix adjust.
Identities = 75/268 (27%), Positives = 111/268 (41%), Gaps = 24/268 (8%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L I P +GA + G+ L+ LD A A+ A +Q+ ++ F Q HL + Q FA
Sbjct: 15 LDIHPVAGRIGAEIRGIRLSGDLDAATVEAIQQALVQYKVVFREQTHLDDQSQEAF AHL 74

Query: 64 FGAIERIGGGDIVAISNVK----ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
G E I + + DGT Q + + WH D T++
Sbjct: 75 LG--EPIAHPTVPVRDGTFRFLMELDGTGRQRANS-----WHTDVTTFVDAYP 118

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
+ +V + + P GG T +A+ +AY+ L RAL A HS Y + L A
Sbjct: 119 KASVLRSLAPKSGGDTVWANTSSAYNDLSVELRALADNLWAVHSNEYDYAALKPDVSAE 178

Query: 180 --SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
AY T P+V+VHP +G +LL+G + G A+S + L
Sbjct: 179 RLEAYRKVFTSTVYETEHPVVRVHPVSGEKTLLLGHFVKRLKGYSQADSTQLFNLLQSHV 238

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ +W GDV +WDNR H A
Sbjct: 239 TRLENTVRWRWNTGDVAIWDNRATQHYA 266

>gb|ACG80565.1| TfdA [uncultured bacterium]
Length = 118

Score = 89.0 bits (219), Expect = 8e-16, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 66/125 (52%), Gaps = 11/125 (8%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTAT---PL 194
F DMRAAYDALD+ T+A + HSL+YS+ LG ++ Y D A L

Sbjct: 2 FGDMAAYDALDDDTKAEIEDMICEHSLMYSRGSLG-----FLDYTDDEKAMFKPVL 53

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
+ L + HP R SL + HA AI GM E+ L L + A Q VH H+W D+V

Sbjct: 54 QRLXRTHPVHRRKSLYLSSHAGAIKMSMPEARLLLRDLTEHATQREFVHIHKWTVHDLV 113

Query: 255 VWDNR 259
+WDNR

Sbjct: 114 MWDNR 118

>ref|YP_002401497.1| taurine dioxygenase [Escherichia coli 55989]
emb|CAU96250.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli 55989]
Length = 283

Score = 89.0 bits (219), Expect = 8e-16, Method: Compositional matrix adjust.
Identities = 75/289 (25%), Positives = 123/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF

Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVFLRDQTITPQQQRALAQR 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++

Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L++ A H S + + ++

Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLNGLRAEHDFRKSFPPEYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L G +

Sbjct: 168 EEEHQRWREAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G

Sbjct: 227 AHITKPEFQVRWRWQPNDIAIWDNRVTVQHYANADYLPQRRIMHRATILG 275

>ref|YP_001454351.1| taurine dioxygenase [Citrobacter koseri ATCC BAA-895]
gb|ABV13915.1| hypothetical protein CKO_02809 [Citrobacter koseri ATCC BAA-895]
Length = 283

Score = 89.0 bits (219), Expect = 8e-16, Method: Compositional matrix adjust.
Identities = 78/289 (26%), Positives = 123/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA V+G L L D F L+ A L+H ++ Q ++ QQ A+RF

Sbjct: 5 LSITPLGPYIGALVSGADLTRPLSDNQFEQLYHAVLRHQVFLREQAITPQQQRALAQR 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G + + + + D +P + D+ WH D T++

Sbjct: 65 GDLHIHPVYPHAEGVEEIIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQ 176
GA+ +A+ +P+ GG T +A AAYDAL E R L+ A H + + K

Sbjct: 109 PAGAILAAKELPSSGGDTLWASGIAAYDALSEPFRQLLSGLRAEHDFRKSFPPEYKYRKT 168

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ ++ + L P+V+ HP +G+ +L + I + ESE L G +

Sbjct: 169 EEHQRWLE-AVAKHPPLLHPVVRTHPVSGKLALFVNEGFTTRIVDVTEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W DV +WDNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWQPDDVAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|YP_003451475.1| taurine dioxygenase [Azospirillum sp. B510]
dbj|BAI74931.1| taurine dioxygenase [Azospirillum sp. B510]
Length = 283

Score = 88.6 bits (218), Expect = 9e-16, Method: Compositional matrix adjust.
Identities = 75/268 (27%), Positives = 111/268 (41%), Gaps = 13/268 (4%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
+A TL +TP +GA V G+ L L D+ AAL A + H +L F Q L+ Q
Sbjct: 4 IALPTLVLTVPVSPAIGARVEGLDLTRPLSDSEAAALERALVAHQVLFENQPLTPQAQRA 63

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
FA RFG + V H+P++ N WH D T +
Sbjct: 64 FAARFGQLHVHPIYPKVPEQPEIMVLDTGPHNPSD-----NDVWHTDVTCIENPP 113

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
S +++P VGG T +A AAY+ L E R L+ A H S + H
Sbjct: 114 AIVALSGKLIPPVGGDTVWASNIAAYNGLSEPIRRLLEPLKALHDFTRSFPEWRHNGDPE 173

Query: 180 S-AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWA 237
+ A + + P+++ HP +G +L + + I G+ ES L+ L D
Sbjct: 174 THARWKAAREKHPPVHVPVIRTHPVSGAKALFVNENFTSRIVGLSDRESAAILDFLYDHY 233

Query: 238 CQAPRVHAHQWAAGDVVVDNRCLLHRA 265
+ +W D+V+WDNR H A
Sbjct: 234 SRPEFTVRWRWKTDDLVLWDNRSTQHYA 261

>emb|CAY27424.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 88.6 bits (218), Expect = 9e-16, Method: Compositional matrix adjust.
Identities = 51/127 (40%), Positives = 68/127 (53%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT--- 192
T F DMRAAYDALD+ T+A + HSL+YS+ LG ++ Y + A
Sbjct: 1 TEFMDMRAAYDALDDETKAEIEDMICEHSLMYSRGSGLG-----FLDYSDEEKAMFKP 52

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
L+ LV+ HP R SL + HA AI GM E+ L L + A Q V+ H+W D
Sbjct: 53 VLQRLVIRTHPVHRRKSLYLSSHAGAIQGMSPPEARLLLLRDLTEHATQREFVYVHKWTLHD 112

Query: 253 VVVDNR 259
+V+WDNR
Sbjct: 113 LVMWDNR 119

>ref|ZP_06907775.1| taurine dioxygenase [Streptomyces pristinaespiralis ATCC 25486]
gb|EDY64309.2| taurine dioxygenase [Streptomyces pristinaespiralis ATCC 25486]
Length = 305

Score = 88.6 bits (218), Expect = 9e-16, Method: Compositional matrix adjust.
Identities = 79/278 (28%), Positives = 113/278 (40%), Gaps = 34/278 (12%)

Query: 5 TLQITPTGATLGATVTGVHLA--TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
++++ P TLGA ++GV LA DD F + L++ +L Q +S + + FA+
Sbjct: 23 SIEVEPLTCTLGAEISGVSLADAARDDDLFTTEIKGLLLRYKVLFLRDQDISRAEHVAFAR 82

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQH----SPAEDDDMMKVIVGNMAWHADSTYMPVM 118
RFG +E VA S+ G VR + SPAE + A H D T+
Sbjct: 83 RFGELE----DHPVAGSDPDHPGLVRIYKDLDSPAEHYEN-----ALHTDGTWREN 130

Query: 119 AQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
+ GAV P VGG T + DM AY+ L E R + ARHS+ ++ G V
Sbjct: 131 SMGAVLRCSVESPPVGGDTIWVDMQAAYNRLPEHIRTQIEDLRARHSI---EATFGAVLPE 187

Query: 179 GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF----- 229
+ A P+V+ HPETG L + + RF
Sbjct: 188 EKRHALKAQFPDAE--HPVVRTHPETGEKILFVNAFTTHFVNYHTPRNVRFQDYAPGSG 245

Query: 230 --LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L L+ A +W V +WDNR H A
Sbjct: 246 LLLNYLISQAAVPEYQVRFRWRKNSVAIWDNRSTQHYA 283

>ref|YP_002411171.1| taurine dioxygenase [Escherichia coli UMN026]
ref|ZP_06647579.1| tauD [Escherichia coli FVEC1412]
ref|ZP_06988980.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli FVEC1302]
ref|ZP_07118595.1| taurine dioxygenase [Escherichia coli MS 198-1]
emb|CAR11623.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli UMN026]
emb|CBG33235.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli 042]
gb|EFF02361.1| tauD [Escherichia coli FVEC1412]
gb|EFI21716.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli FVEC1302]
gb|EFJ71941.1| taurine dioxygenase [Escherichia coli MS 198-1]
Length = 283

Score = 88.6 bits (218), Expect = 9e-16, Method: Compositional matrix adjust.
Identities = 75/288 (26%), Positives = 121/288 (42%), Gaps = 27/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA +TG L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQITGADLTRPLSDNQFEQLYHAVLRHQVFLREQAITPQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPEYKY-RKT 167

Query: 179 GSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L L
Sbjct: 168 EEEHQRWREAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALLSFLFA 227

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLAG 283
+ +W D+ +WDNR H A R+M + + G
Sbjct: 228 HITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>gb|ACG80581.1| TfdA [uncultured bacterium]
gb|ACG80582.1| TfdA [uncultured bacterium]
Length = 118

Score = 88.6 bits (218), Expect = 9e-16, Method: Compositional matrix adjust.
Identities = 51/123 (41%), Positives = 66/123 (53%), Gaps = 7/123 (5%)

gb|EEA20041.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase, putative [Penicillium marneffeii ATCC 18224]
Length = 337

Score = 88.6 bits (218), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 75/272 (27%), Positives = 121/272 (44%), Gaps = 22/272 (8%)

Query: 12 GATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAI--- 67
+ GA V+GV + A L A ++ +LIF L N + I F+++ G
Sbjct: 40 NSAFGAEVSGVDWENPVPAETVAQLVALQDKYGVLFRETGLDNARHIAFSQQLGESLEV 99

Query: 68 -----ERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVM 118
+R+G + + N++ D T+ ++ W + GN WH DS+Y
Sbjct: 100 NPFYYGRENDRLGEPFLFDVGNIELDRTLKVNESRRWHHSL---GNALWHTDSSYHQQR 155

Query: 119 AQGAVFSAEVVPAVGGR-TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
++ ++ + P GG T FAD R AY L E + + H L +S+ KL
Sbjct: 156 SKYSILLSHGPNVKGGSWTHFADTRRAYADLPETKKKEIEDLIVEHDLWHSR-KLASPIV 214

Query: 178 AGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
G + + + LV+ P GR +L + HA I G ES++ + L+D
Sbjct: 215 YGDP-LPHELAACKPPAYHRLVQTAP-NGRRTLYLAHAHAKLILGQSFEESQKLIWELIDHC 272

Query: 238 CQAPRVHAHQWAAG-DVVVDNRCLLHRAEPW 268
Q V + +W +G D+V WDNR +HRA P+
Sbjct: 273 TQPKYVFSMEWLSGGDMVWVDNRQSMHRANPY 304

>gb|EGC96200.1| taurine dioxygenase [Escherichia fergusonii ECD227]
Length = 283

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 76/288 (26%), Positives = 121/288 (42%), Gaps = 27/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPHIGALISGADFTPLSDNQFEQLYHAVLRHQVFLREQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPHAAGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQ 176
GA+ +A+ +P+ GG T +A AAY+AL R L++ A H + + K +
Sbjct: 109 PAGAILAAKELPSTGGDTLWASGIAAYEALSAPFRQLLNGLQAEHDFRKSFPPEYKFRKTE 168

Query: 177 QAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + + L P+V+ HP +GR +L + I + A ESE L L
Sbjct: 169 EDHQRW-REAVAKNPPLLHPVVRTHPVSGRHALFVNEGFTTRIVDVTAKESEMLLAFLFA 227

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ W DV +WDNR H A R+M + + G
Sbjct: 228 HITKPEFQVRWCWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|ZP_07966578.1| TfdA family Taurine catabolism dioxygenase TauD [Segniliparus
rugosus ATCC BAA-974]
gb|EFV12195.1| TfdA family Taurine catabolism dioxygenase TauD [Segniliparus
rugosus ATCC BAA-974]
Length = 310

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 75/267 (28%), Positives = 113/267 (42%), Gaps = 29/267 (10%)

Query: 8 ITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
+ P T+GA ++GV L+ L A L A L+ +L F Q ++ + FA +G
Sbjct: 38 LVPASPTIGAEISGVRLSGGLAPEVLAE LRRLLEWKVLFVRDQDIARQEHREFAALWGG 97

Query: 67 IERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA-----WHADSTYMPVMAQ 120
+E+ +R H + D++ + +MA WH D T+ P +
Sbjct: 98 LEQ-----HPFMRYHGKQDDVDVVS LAKNDMAAGTENVWHNDVTWRPDPSF 143

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
AV A VP +GG T ++D AYD L + + + A H + S ++ Q+
Sbjct: 144 AAVLRAVEVPDLGGDTMWSDTAVAYDLLPDLGLKERIDHLEAEHDWIQSFGRMMPEQEIER 203

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
+ T P+V+V PETGR L + R I GMD A+S LE L
Sbjct: 204 LRPDFPPVT-----HPVVRVIPETGRRVLFVNRVFTTRIVGMDEAQSRELLEDLY-LRMN 257

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
P +W V +WDNR H A
Sbjct: 258 RPEFQVRLRWQPNTVAMWDNRNRTCQHYA 284

>emb|CAY27257.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 70/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALD+A +A + Q HSL++S+ LG + + P+R
Sbjct: 1 TEFADMRAAYDALDDAMKAEIEQVVCESL MFSRGALGFSE-----LNEQEQAMFRPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I E+ FL L++ A Q V++H+W D+V
Sbjct: 55 QRLVRTHPVTGRKSLFLSAHAGGIVNWPPEARAFLRDLMEHATQPRFVYSHKWRQWDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>emb|CAY27430.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALDE + + HS +YS+ KLG T + P+R
Sbjct: 1 TEFADMRAAYDALDERLKQQIEDLVCLHSNMYSRGKLGLADFTDEER-----TASKPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I GM E L L ++A + V++H W D V
Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEGRMLLLDLTEFATREQFVYSHMWRVNDVF 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|ZP_06860409.1| alpha-ketoglutarate-dependent taurine dioxygenase [Citromicrobium
bathyomarinum JL354]
Length = 279

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 82/296 (27%), Positives = 116/296 (39%), Gaps = 30/296 (10%)

```
Query: 6  LQITPTGATLGATVTGVHLA--TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
      +Q+T      G  + GV LA  T D A      + A  +H  + +F  Q      + I FA+
Sbjct: 3  MQMTALAPHCVEIRGVQLAEATGDAALLDEIRTAVWEHGVALFRDQDFGPQEHIAFARA 62

Query: 64  FGAIERIGGGDI-----VAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV 117
      +G I+      +      +A+  +AD T      +G  WH D +Y  +
Sbjct: 63  WGGIDINNYFPLTDAFPEIAVVGKRADQTTN-----IGG-GWHTDHSYDQI 107

Query: 118  MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQ 177
      A G++  A  +P  GG T FA M AAYDAL + + +  A HS  + S  G+  Q
Sbjct: 108  PAMGSILVARELPPTGGDTLFAHMGAAAYDALSDDLKTEIEGLEAFHSADHVYSPDGYAQA 167

Query: 178  AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDW 236
      A      G  T      P+  HP+TGR  L +      I G  ES  L+ L
Sbjct: 168  TDMAESLRGQMMTTGARHPVAIRHPQTGRKLLYVNAAFTHIVGRTREESMPLLQRLFAT 227

Query: 237  ACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL 292
      A  A      +W  G V  +WDNR      W  +      H+R  R      G AL
Sbjct: 228  ALSADNTARVEWQPGSVAIWDNRRT-----WHMAMNDYQGHARTMHRITLTGEAL 277
```

>emb|CAY27220.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 49/124 (39%), Positives = 69/124 (55%), Gaps = 6/124 (4%)

```
Query: 136  TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
      T FADMRAAYDALD  T+AL+      HS ++S+  LG      ++  +  A  +
Sbjct: 1   TEFADMRAAYDALDAKTALIEDLVCEHSRIFSKGALGF-----SFTEEEVKAFAPVRQ 54

Query: 196  PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
      LV+  HP+TGR SL +  +A  I G  E+  L  L + A Q  V++H+W  GD+V+
Sbjct: 55  RLVRTHPKTGRKSLYLSSYAGRIVGWVPEAMLLLLRELTEHATQREFVYSHKWRVGDVLM 114

Query: 256  WDNR 259
      WDNR
Sbjct: 115  WDNR 118
```

>ref|YP_001262249.1| taurine catabolism dioxygenase TauD/TfdA [Sphingomonas wittichii
RW1]
gb|ABQ68111.1| Taurine catabolism dioxygenase TauD/TfdA [Sphingomonas wittichii
RW1]
Length = 317

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 77/280 (27%), Positives = 124/280 (44%), Gaps = 30/280 (10%)

```
Query: 8  ITPTGATLGATVTGVHLATLDDAGF-AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
      +TP+G  +  + G+  A L DA      L+  W++H L++F G  S++  I  ++ FG
Sbjct: 9  LTPSGEAI--QIHGLERAHLTDAAVREELNRLWIRHGLVVFGRMDDSDELHIELSRVFGP 66

Query: 67  IE----RIGGGDI--VAISNVKADGTVRQHSPAEWDDMMKVIVGN-----MAWHADSTYM 115
      +  + G  D  + I+NV      Q+ P  + + + G      + H D Y
Sbjct: 67  FQLHPIKQGNTPSRLEITNV-----QYEPGGENGNVYTVNGVDLGGWLPLHFDLVYF 119

Query: 116  PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL-DEATR-----ALVHQRSARHSLVYSQ 169
      +  G  +      V+P  G T F D  AAY+ L DE  R      +V+      S  + +
```

Sbjct: 120 DKNVHGGLLRPRVIPPEMGGTVFLDKIAAYETLPDELKRRAEGLEVVDYFYMDISTMKNS 179

Query: 170 SKLGHVQQAGSAY--IGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAES 226
+ + G + I D+ + PLV E+GR L + A + G+D AE

Sbjct: 180 VDDIRLVRMGKKFRDIQQREDSYPRSIHPLVYAQKESGRKMLNLSPWFADELLGLDKAEG 239

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAE 266
+ L LV P++H H+W GD+V+WDN +LH AE

Sbjct: 240 DALLGELVRHTLSHPQIHVHRWTPGDIVLWDNRMLHGAE 279

>emb|CAY27328.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27336.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27385.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 67/125 (53%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR 195
T FADMRAAYDALDE + + HS +YS+ KLG + P+R

Sbjct: 1 TEFADMRAAYDALDEWLKNQIEDLVCLHSNMYSRGKLGADFTDEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I GM E+ L L ++A + P V++H W D+V

Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMMLLLDLTEFATREPFVYSHAWRVNDLV 114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>ref|ZP_05434206.1| taurine dioxygenase [Shigella sp. D9]
Length = 283

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 75/289 (25%), Positives = 122/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF

Sbjct: 5 LSITPQGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFRLDQTITPQQORALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++

Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++

Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPEYKY-RKT 167

Query: 179 GSAYIGYGMTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L G +

Sbjct: 168 EEEHQRWREAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G

Sbjct: 227 AHITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>emb|CAY27323.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.

Identities = 50/123 (40%), Positives = 68/123 (55%), Gaps = 7/123 (5%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRP- 196
FADMRAAYDALDE T+A V HSL++S++ +G + + P+R
Sbjct: 3 FADMRAAYDALDERTKAEVQDLVCEHSLLSRAAVGFTFTPEEVANF-----RPVRQR 56

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVW 256
LV+ HP +GR SL + HA I G E+ FL L + A Q V++H W D+V+W
Sbjct: 57 LVRTHPASGRKSLFLSSHAGTIVGWTVPERSFLRDLTEHATQREFVYSHAWRQHDLMVW 116

Query: 257 DNR 259
DNR
Sbjct: 117 DNR 119

>emb|CAY27290.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27292.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27553.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 52/125 (41%), Positives = 68/125 (54%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T FADMRAAYDALD+ T+A V HSL+YS+ +G + + P+R
Sbjct: 1 TEFADMRAAYDALDDRTKAEVAGLVCEHSLLYSRQAVGFTDFTPEEISNF-----QPVR 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
PLV+V TGR SL + HA I G ES FL L++ A + V++H W D+V
Sbjct: 55 HPLVRVQKATGRKSLFLSAHAGVIVGWSVPESRAFLRDLIEHATRPEFVYSHSWRQHDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>emb|CAY27363.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 54/124 (43%), Positives = 68/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T FADMRAAYDALD+ TRA Q HS ++S++ LG S + A +
Sbjct: 1 TEFADMRAAYDALDDETRAECQLICEHSQLFSRAILGF-----SDFTDEERRNFAPVQQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP TGR SL + HA AI G E+ FL L + A Q V+AH W D+V+
Sbjct: 56 RLVRHPVTGRRSLFLASHAGAILGWPVPEARAFRLDLTEHATQRRFVYAHVWKQWDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>emb|CAY27228.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27321.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 66/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195

Sbjct: 1 T FADMRAAYDALDE + + HS +YS+ KLG + P+R
TEFADMRAAYDALDERLKNQIEDLVCLHSNMYSRGKLGGLADFTDEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I GM E+ L L ++A + P V++H W D V

Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMMLLLDLTEFATREPFVYSHVWRLNDFV 114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>ref|YP_001846143.1| taurine catabolism dioxygenase [Acinetobacter baumannii ACICU]
gb|ACC56796.1| Probable taurine catabolism dioxygenase [Acinetobacter baumannii
ACICU]
Length = 293

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 67/273 (24%), Positives = 109/273 (39%), Gaps = 32/273 (11%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I T+GA + + L L++ + A L H ++ F Q L+ Q A+ F

Sbjct: 7 NLNIEVIKPTIGAIHNDLNALNEQTTQQIQQALLDHQVIFFRKQQQLAPQAQADLARSF 66

Query: 65 G-----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
G +IE + +++ + + K D + N WH D T+

Sbjct: 67 GTLHVHPPIYPSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFS 107

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLG 173
G V A +P VGG T ++ AA+ L + + +A H + + +

Sbjct: 108 KTPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQRKLRGLTATHDIRKSFPLELFA 167

Query: 174 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
H ++ + + P+V+ HP TG P L + I + ESE+ L

Sbjct: 168 HNEEEREKLLQ-TFKRNPPVHPVVRTHPTGEPLLFVSEGFTTRINELPEQESEQLLNF 226

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L + A Q +W GDV +WDNRC H+A

Sbjct: 227 LFEHATQEQFHLRRKWQGDVAIWDNRCTQHKA 259

>gb|AAS64597.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
Length = 119

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 50/124 (40%), Positives = 65/124 (52%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDAL++ TR + HSL+YS+ LG + Y L+

Sbjct: 1 TEFADMRAAYDALNDETRTEIEDMICEHSLMYSRGSGLFLD-----YTEEEKQMFKPVQLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP GR SL + HA I GM E+ L L + A Q V+ H+W D+V+

Sbjct: 56 RLVTRTHPVHGRKSLYLSSHAGGIIGMSVPEARVLLRDLNEHATQPEFVYVHKWTLHDLVM 115

Query: 256 WDNR 259
WDNR

Sbjct: 116 WDNR 119

>ref|ZP_02149378.1| alpha-ketoglutarate-dependent taurine dioxygenase [Phaeobacter
gallaeciensis 2.10]
gb|EDQ09090.1| alpha-ketoglutarate-dependent taurine dioxygenase [Phaeobacter

gallaeciensis 2.10]
Length = 278

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 77/292 (26%), Positives = 121/292 (41%), Gaps = 33/292 (11%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
+ I P LGA + G + +D F+A+ A+ +++++ GQ + FA+RFG
Sbjct: 1 MDILPMTGGLGAEILGADIRSED--FSAIRDAFAEYSVIVLRGQTAGPGDHLAFARRFG 58

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNM-----AWHADSTYMPV 117
+ NV R P E + ++ WH D +Y
Sbjct: 59 PV-----NVN-----RFFKPVEGHPEIATVLKEKDQTEAVGEGWHTDHSYDQE 101

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHV 175
A ++ A +P GG T F M AAY+AL E R + +A HS V+ + +
Sbjct: 102 PAMVSILHAIEMPPYGGDTLFFVSMGAAYEALSEPMMRFLDGLTAVHSSRHVFGAAAMDS- 160

Query: 176 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
+ S +G T P+V HP +GR L + I G++ ES L ++
Sbjct: 161 EAVKSGRLGNAEAATQDVRHPVVITHPLSGRRGLFVNPVFTTRIEGLNTEESSALL-AML 219

Query: 235 DWACQAPRVHAH-QWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
CQ P +W AGD+ +WDNR H+A R+M + G P
Sbjct: 220 YAHCQQPEFQCRVRWRAGDITMWDNRATWHKAINDYHGFRLMHRVTVEGGP 271

>gb|AAS64589.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
Length = 119

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 50/124 (40%), Positives = 65/124 (52%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DMRAAYDAL++ TR + HSL+YS+ LG + Y L+
Sbjct: 1 TEFMDMRAAYDALNDETRTEIEDMICEHSLMYRSGSLGFLD-----YTEEEKQMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP GR SL + HA I GM E+ L L + A Q V+ H+WA D+V+
Sbjct: 56 RLVRTHPVHGRKSLYLSSHAGGIIGMSVPEARVLLRDLNEHATQPEFVYVHKWALHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>gb|EFZ56791.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli
LT-68]
Length = 283

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 75/289 (25%), Positives = 123/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQISGADLTRLPLSDNQFEQLYHAVLRHQVFLRDQAITPQQRALAQR 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + +

Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGLIAAYEALSVPFRQLLSGLRAEHDFRKSFPPEYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + + I + ESE L G +

Sbjct: 168 EEEHQWRWEAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTNTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G

Sbjct: 227 AHITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|YP_587247.1| taurine catabolism dioxygenase TauD/TfdA (2-oxoglutarate-dependent)
[Cupriavidus metallidurans CH34]
gb|ABF11978.1| taurine catabolism dioxygenase TauD/TfdA (2-oxoglutarate-dependent)
[Cupriavidus metallidurans CH34]
Length = 299

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 83/284 (29%), Positives = 121/284 (42%), Gaps = 48/284 (16%)

Query: 6 LQITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++I P A++GA + GV L A DD F + AA L+H +L Q +S + + FA+R

Sbjct: 1 MRIEPMASIGAEVLGVRLSDAIHDDGLFDEIRAALLRHKVLFLRDQDISRAEHVAFAR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHS-PAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E VA S+ G V+ + P + D + AWH D+T+ G

Sbjct: 61 FGGLE----DHPVAGSHPDHPGLVQIYKRPDQPMDDRYE----NAWHTDATWREAPPLGC 111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V P +GG T +A+M AY+ L + + ARHS+ S +++ +

Sbjct: 112 VLRCVESPEIGGDTMWANMVLAYENLPAHVKTQIAGLRARHSIEASFGAAMPIEKRLALK 171

Query: 183 IGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMD----AAESER 228
Y P P+V+VHPETG L + AH G D A E R

Sbjct: 172 AQY-----PDPEHPVVRVHPETGEKVLVFNFTTTHFSNFHTPAHVRYGQDYNPGAGELLR 226

Query: 229 FL-----EGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
+L E V W +W A + +WDNR H A

Sbjct: 227 YLISQAFIPEYQVRW-----RWKANSMAIWDNRSTQHYA 260

>ref|ZP_07516225.1| taurine dioxygenase [Escherichia coli TA143]
Length = 283

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 76/289 (26%), Positives = 122/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA +TG L L D F L+ A L+H ++ Q ++ QQ A+RF

Sbjct: 5 LSITPLGPYIGAQITGADLTRPLSDNQFEQLYHAVLRHQVFLREQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHS-PAEWDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++

Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFTIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++

Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGLIAAYEALSVPFRQLLSGLRAEHDFRKSFLLEYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L G +

Sbjct: 168 EEEHQWRWEAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>gb|AAS64590.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
Length = 119

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 51/127 (40%), Positives = 67/127 (52%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTAT--- 192
T F DMRAAYDALD+ T+ + HSL+YS+ LG ++ Y + A
Sbjct: 1 TEFADMRAAYDALDDTKTEIEDMICEHSLMYSRGSLG-----FLDYTDEEKAMFKP 52

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
L+ LV+ HP R SL+ HA AI GM E+ L L+ A Q VH H+W D
Sbjct: 53 VLQRLVRTHPVHRRKSLYLSSHAGAIQMSIPEARLLLLRDLTEHATQPEFVHVHKWTLHD 112

Query: 253 VVVWDNR 259
+V+WDNR
Sbjct: 113 LVMWDNR 119

>ref|YP_294247.1| taurine dioxygenase [Ralstonia eutropha JMP134]
gb|AAZ59403.1| Taurine dioxygenase [Ralstonia eutropha JMP134]
Length = 299

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 77/273 (28%), Positives = 117/273 (42%), Gaps = 26/273 (9%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+++ P A++GA + G++LA DD FA + AA LQH +L Q +S + + FA+R
Sbjct: 1 MRVEPLTASIGAEVLGLNLADAIHDDDLFAEIRAALLQHKVLFRLDQDISRAEHVAFER 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG +E VA S+ + G V+ + + D M AWH D+T+ G V
Sbjct: 61 FGQLE----DHPVAGSHPQYPGLVQIYK--QPDQPMDRYEN--AWHTDATWREAPPMGCV 112

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
PAVG T +A+M AY+ L + + ARHS+ S +++ +
Sbjct: 113 LRCVEGPAVGADTMWANMVLAYENLPAHVKTEIAGLRARHSIEASFGAAMPIEKRLALKE 172

Query: 184 GYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LEG 232
Y P P+V++HPETG L + A R+ L
Sbjct: 173 QY-----PDPEHPVVRIPHETGEKVLVFNATTHFTNFHTAAHVRYGQDYNPGGADLLRY 227

Query: 233 LVDWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
LV A +W + +WDNR H A
Sbjct: 228 LVSQAFIPEYQVRWRWKPNSMAIWDNRSTQHYA 260

>emb|CAY27551.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 52/127 (40%), Positives = 68/127 (53%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTAT--- 192
T FADMRAAYDALD T+A + HSL+YS+ LG ++ Y + A
Sbjct: 1 TEFADMRAAYDALDNDTKAEIDDMICEHSLMYSRGSLG-----FLDYTDEEKAMFKP 52

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252

L+ LV+ HP R SL + HA AI GM E+ L L + A Q V+ H+W D
Sbjct: 53 VLQRLVRTHPVHRRKSLYLSSHAGAIQGMSPPEARLLLRDLTEHATQPEFVYVHKWTLHD 112

Query: 253 VVVWDNR 259
+V+WDNR

Sbjct: 113 LVMWDNR 119

>ref|ZP_02380861.1| Taurine dioxygenase [Burkholderia ubonensis Bu]
Length = 282

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 76/274 (27%), Positives = 117/274 (42%), Gaps = 28/274 (10%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+++ P +GA ++GV LA DD FA + A L+H +L Q ++ + + FA+R
Sbjct: 1 MRVEPLTCAIGAELSGVSLADAVHDDGLFAEIRALLLKHRLVFLRDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E VA S+ + G VR + SP + +D + AWH+D+++ G
Sbjct: 61 FGELE----DHPVAGSDPEHPGLVRIYKSPDQPNDRYE-----NAWHSASWRVAPPFGC 111

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V P VGG T +A+M AY+ L + + ARHS+ S + + +
Sbjct: 112 VLRCVACPPVGGDTMWANMALAYENLPGHVKRQIDGLRARHSIEASFGAAMPIDKRLALK 171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LE 231
Y P+V+ HPETG L + E RF L+
Sbjct: 172 TQY-----PDAEHPVVRTHPETGEKILYVNAFTTHTFTNFTPERVRFQDANPGAGQLLQ 226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L+ A +WA V +WDNR H A
Sbjct: 227 YLISQAYIPEYQVRWRWAKHSVAIWDNRSTQHYA 260

>ref|ZP_03049591.1| taurine dioxygenase [Escherichia coli E110019]
gb|EDV88435.1| taurine dioxygenase [Escherichia coli E110019]
Length = 283

Score = 88.2 bits (217), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 75/288 (26%), Positives = 120/288 (41%), Gaps = 27/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVFLRDQTITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + +
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPEYKYRKTE 168

Query: 179 GSAYIGYGMDDTTATP-LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
+ P L P+V+ HP +G+ +L + I + ESE L G +
Sbjct: 169 EEHQRWHEAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALL-GFLFA 227

Query: 237 ACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G
Sbjct: 228 HITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 275

```
>ref|YP_001457202.1| taurine dioxygenase [Escherichia coli HS]
ref|ZP_03028556.1| taurine dioxygenase [Escherichia coli B7A]
ref|ZP_03046235.1| taurine dioxygenase [Escherichia coli E22]
ref|ZP_03061361.1| taurine dioxygenase [Escherichia coli B171]
ref|YP_002291665.1| taurine dioxygenase [Escherichia coli SE11]
ref|YP_002385844.1| taurine dioxygenase [Escherichia coli IAI1]
ref|YP_003220350.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli
0103:H2 str. 12009]
ref|ZP_07098522.1| taurine dioxygenase [Escherichia coli MS 107-1]
ref|ZP_07140078.1| taurine dioxygenase [Escherichia coli MS 182-1]
ref|ZP_07223377.1| taurine dioxygenase [Escherichia coli MS 78-1]
ref|ZP_07520973.1| taurine dioxygenase [Escherichia coli TA271]
ref|ZP_07591888.1| Taurine dioxygenase [Escherichia coli W]
ref|ZP_07689331.1| taurine dioxygenase [Escherichia coli MS 145-7]
gb|ABV04819.1| taurine dioxygenase [Escherichia coli HS]
gb|EDV62962.1| taurine dioxygenase [Escherichia coli B7A]
gb|EDV81757.1| taurine dioxygenase [Escherichia coli E22]
gb|EDX29416.1| taurine dioxygenase [Escherichia coli B171]
dbj|BAG75914.1| taurine dioxygenase [Escherichia coli SE11]
emb|CAQ97240.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli
IAI1]
dbj|BAI29216.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli
0103:H2 str. 12009]
gb|EFK02991.1| taurine dioxygenase [Escherichia coli MS 182-1]
gb|EFK50264.1| taurine dioxygenase [Escherichia coli MS107-1]
gb|EFK71052.1| taurine dioxygenase [Escherichia coli MS 78-1]
gb|EFN38256.1| Taurine dioxygenase [Escherichia coli W]
gb|EFO58825.1| taurine dioxygenase [Escherichia coli MS 145-7]
gb|ADT73978.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli W]
gb|EFW76187.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli
EC4100B]
gb|EFZ70177.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli
1357]
gb|ADX52053.1| Taurine dioxygenase [Escherichia coli KO11]
gb|EGB41602.1| TfdA family protein Taurine catabolism dioxygenase TauD
[Escherichia coli H120]
gb|EGB85854.1| taurine dioxygenase [Escherichia coli MS 117-3]
gb|EGC10767.1| TfdA family protein Taurine catabolism dioxygenase TauD
[Escherichia coli E1167]
Length = 283
```

Score = 87.8 bits (216), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 75/289 (25%), Positives = 122/289 (42%), Gaps = 29/289 (10%)

```
Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFLRDQTITPQQORALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRRQLLSGLRAEHDFRKSFPPEYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L G +
Sbjct: 168 EEEHQRWREAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 275
```

>ref|ZP_06877015.1| taurine dioxygenase [Pseudomonas aeruginosa PAb1]
Length = 216

Score = 87.8 bits (216), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 68/211 (32%), Positives = 96/211 (45%), Gaps = 14/211 (6%)

```
Query: 5   TLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
          +L I P   LGA V+G+ L A LDDAG A+ A L+H +L F Q L   Q FA R
Sbjct: 2   SLTIQPISPALGAIVSGIDLGAPLDDAGQRAIEQALLEHQVLFRRDQSLEPRSQARFAAR 61

Query: 64  FGAIERIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGAV 123
          FG +       I +       Q       D + + N WH D T++ A GAV
Sbjct: 62  FGDH-----IHPIYP-SVPEQPEVIVLDTAVTDVRDNAIWHDTVTFLETPALGAV 111

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQQAGSA 181
          +A+ +P GG T +A AAY+AL R L+ +A H + + + + G V +A A
Sbjct: 112 LAAKQLPPYGGDTLWASSTAAYEALSAPLRRLDGLTATHDIGKSFPRERFG-VTEADLA 170

Query: 182 YIGYGMDDTTATPLRPLVKVHPETGRPSLLIG 212
          +                P+V+ HP TGR L +
Sbjct: 171 RLEEARKLNPPRSHPVVRTHPLTGRKGLFVS 201
```

>ref|YP_586764.1| taurine dioxygenase 2-oxoglutarate-dependent [Cupriavidus metallidurans CH34]
gb|ABF11495.1| taurine dioxygenase, 2-oxoglutarate-dependent [Cupriavidus metallidurans CH34]
Length = 280

Score = 87.8 bits (216), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 78/296 (26%), Positives = 121/296 (40%), Gaps = 33/296 (11%)

```
Query: 6   LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
          +Q+ P   ++GA + GV +A + DD FA + A L+H +L F Q +S   + FAKR
Sbjct: 1   MQVNPLTCSIGAELAGVSIADVARDTLFAEIKALLKHRVLFRRDQDISRADHVAFAKR 60

Query: 64  FGAIERIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGAV 123
          FG +E       VA S + G + + + D       +H D+++ +GAV
Sbjct: 61  FGDLE----DHPVANSVPEHPGLIEIYKSEKRDHFEN-----TYHTDASWRACPPKGAV 110

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
          P VGG T + +M AY L E + + A+H + +S + ++
Sbjct: 111 LRCISCPDVGDDTIWVNMVEAYKHLPEDIKVKIAGLRKXGIEHSFGAIMTTEEREEL-- 168

Query: 184 GYGMDDTTATPL--RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----L 230
          PL P+V+ HPETG L +G +       E+ RF       L
Sbjct: 169 -----VRKNPLVDHPVVRTHPETGEKILYVGPFSTHFINYHTPENVRFGQDKTPGASLLL 223

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
          L+ A       +W V +WDN H A + PR M + + G RP
Sbjct: 224 NYLISQAAIPEYQVRFRWKPNVALWDNVSTQHYAVSDYWPAPRRMERATIKGDRP 279
```

>gb|EFX23899.1| taurine dioxygenase [Escherichia coli O55:H7 str. 3256-97 TW 07815]
Length = 283

Score = 87.8 bits (216), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 75/289 (25%), Positives = 122/289 (42%), Gaps = 29/289 (10%)

```
Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF
```

Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFLRDQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++

Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++

Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPEYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L G +

Sbjct: 168 EEEHQRWREAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G

Sbjct: 227 VHITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|ZP_06840794.1| Taurine dioxygenase [Burkholderia sp. Chl-1]
gb|EFG71514.1| Taurine dioxygenase [Burkholderia sp. Chl-1]
Length = 282

Score = 87.8 bits (216), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 74/273 (27%), Positives = 116/273 (42%), Gaps = 26/273 (9%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++ P +GA + GV+LA DD FA + AA L+H +L Q++S + + FA+R

Sbjct: 1 MRAEPLTCAIGAELIGVNLADAVDDDGLFAEIRAALLKHRVLFRLDQNISRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG +E VA S+ + G VR + + + AWHAD+T+ GAV

Sbjct: 61 FGELE----DHPVAGSDPEHPGLVRIYKNQDQPNDRY----ENAWHADATWREAPQFGAV 112

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
P VGG T +A+M AY L + + + ARHS+ S +++ +

Sbjct: 113 LRCVECPVGGDTMWANMVLAYGNLPDHIKTQIADLRARHSIEASFGAAMPIEKRLALKA 172

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE-----GLVDV 236
+ P+V+ HPETG L + E RF + L+ +

Sbjct: 173 QF-----PDAEHPVVRTHPETGEKVLVNAFTTHTFTNYHTPERVRFQDANPGAGDLLRY 227

Query: 237 ACQAPRVHAHQ---WAAGDVVVDNRCLLHRA 265
+ +Q W + +WDNR H A

Sbjct: 228 LISQAYIPEYQVRWRWKPNISAIWDNRSTQHYA 260

>ref|ZP_01765614.1| taurine dioxygenase [Burkholderia pseudomallei 305]
gb|EBA49401.1| taurine dioxygenase [Burkholderia pseudomallei 305]
Length = 451

Score = 87.8 bits (216), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 83/271 (30%), Positives = 117/271 (43%), Gaps = 30/271 (11%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSND--QQITFA 61
L I P +GA V G+ L + +D F + A L H ++ F QH +D Q FA

Sbjct: 166 LSIRPLSGHIGAEVQGIQLGSQMAPNDIRF--ITQALLTHRVIFFRRQHHLDDLAQELFA 223

Query: 62 KRFGAIER---IGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
+ FG I + +GG AI + + R +S WH D T+

Sbjct: 224 QAFGEIVKHPTMGGKTGSAILELHSHEGGRANS-----WHTDVTFLGRP 267

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY---SQSKLGH 174

+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
Sbjct: 268 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSSLQDLVDKLWAVHGNDFDYAASRVLLH 327

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
 A Y T P+V++HPETG SLL+G +A D +S R E L
Sbjct: 328 DPVAKEYRKKYAAQVIKTE-HPVVQIHPEPETGEKSLLLGHYAQRQFVQYDTHDSNRLYEILQ 386

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 + WAAGDV +WDNR H A
Sbjct: 387 ARITRLENTVRWHWAAGDVAIWDNRSTQHYA 417

>ref|ZP_06473474.1| Taurine dioxygenase [Frankia symbiont of Datisca glomerata]
gb|EFD29839.1| Taurine dioxygenase [Frankia symbiont of Datisca glomerata]
Length = 314

Score = 87.8 bits (216), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 77/289 (26%), Positives = 128/289 (44%), Gaps = 23/289 (7%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 L + P T+GA ++GV L L D + A L++ ++ F Q L+ ++ FA+RF
Sbjct: 15 LAVRPLQPTTIGAEISGVDLRYPLTDEVRDQIRATILKYKVFFRDQELTREEHEAFARRF 74

Query: 65 GAIERIGGGDIVAISNVKADGT-VRQHSAPAEWDDMMKVIV---GNMAW---HADSTYMPV 117
 G + G +++ T + + + A++ D + + +W H D+++ V
Sbjct: 75 GPLYPHPSGPKAPLND SAGRATSIHRIAAADFKDYERARATADADESWDAYHTDTSWRLV 134

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
 GAV A +P +GG T + D AY+AL + + + R H +
Sbjct: 135 PTWGAVLRAVTLDPDIGGDTIWVDAGLAYNALSDDVKERLAGRHVTHDF-----RD 184

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLVDW 236
 A +A +GY + P+V+VH ETG L + H +I G+D +ES L ++D
Sbjct: 185 ALNA-VGYDYPIVS---HPVVRVHRETGEKILWVNFTQHPSILGLDRSESRELLTLVLDQ 240

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
 + W G V WDNR +H A PRV+ +A P
Sbjct: 241 YRKPEHQVRFSWRPGSVAFWDNRATVHYAVRNYGDFPRVLERILIAEEP 289

>ref|YP_003682823.1| Taurine dioxygenase [Nocardiosis dassonvillei subsp.
dassonvillei
DSM 43111]
gb|ADH70317.1| Taurine dioxygenase [Nocardiosis dassonvillei subsp. dassonvillei
DSM 43111]
Length = 308

Score = 87.8 bits (216), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 75/280 (26%), Positives = 115/280 (41%), Gaps = 42/280 (15%)

Query: 4 TTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFA 61
 T L + P +GA ++GV L LD A A++ AA L H ++ F Q HL+++ Q FA
Sbjct: 10 TDSLRLPVAGRIGAEISGVRLGPDLDGATVASIRAALLAHKVFFRDQRHLTDETQAGFA 69

Query: 62 KRFGAIER-----IGGGD--IVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADS 112
 G + GGD ++ I + + +WH D
Sbjct: 70 ALLGPLTTPHPTTGAAGGDHHLVLPIDSERGKAN-----SWHTDV 109

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY----- 167
 T++ Q +V A +P GG T +A+ AY L + + L A H+ Y
Sbjct: 110 TFVDRPPQASVLRVHLPPRGGDTVWANTATAYQDLPQLKDLADGLRAVHTNDYDYAAV 169

Query: 168 --SQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAE 225

+ G +++ A++ T P+V+VHPETG L +G A G+ + +
Sbjct: 170 APERPTGDLRKRYEAFVSTLFKTE-----HPVVRVHPETGERVLFGLGHFAQHFTGLSSKD 225

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

 + L +A W GDV VWDNR H A
Sbjct: 226 FHHLFDLLQQRVTRAENTVRWSWREGDVAVWDNRATQHYA 265

>ref|NP_752410.1| taurine dioxygenase [Escherichia coli CFT073]
gb|AAN78954.1|AE016756_137 Alpha-ketoglutarate-dependent taurine dioxygenase
[Escherichia coli
CFT073]
Length = 283

Score = 87.8 bits (216), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 77/289 (26%), Positives = 123/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 L IT G +GA +TG L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITSLGPYIGAQITGADLTRPLSDNQFEQLYHAVLRHHVVFLRDQTITPQQRALAQR 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
 G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIQTP 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
 GA+ +A+ +P+ GG T +A AA+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWASGIAAYEALSVPFRRQLLSGLRAEHDFRKSFPYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
 + + + P L P+V+ HP TG+ +L + I + ESE L G +
Sbjct: 168 EAEHQRWREAVAKNPPLHPVVRTHPVTGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
 P +W D+ +WDNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|YP_003592890.1| taurine dioxygenase [Caulobacter segnis ATCC 21756]
gb|ADG10272.1| Taurine dioxygenase [Caulobacter segnis ATCC 21756]
Length = 285

Score = 87.8 bits (216), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 73/268 (27%), Positives = 110/268 (41%), Gaps = 30/268 (11%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIER----- 69
 GA ++G+ LA+ DA + + +H + GQ ++ D + F RFG E
Sbjct: 16 FGAEISGIDLASAPDAALDQVVDTFHRHGAIALRGQKMPDDLRFGRFGDPEDHTQTR 75

Query: 70 ---IGGGDIVAISNVKADGT-VRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
 G I +SN DG + H+ + WH D +Y P +
Sbjct: 76 FTLPGYPKIFILSNRVVDGKPIGAHN-----DGVGWHTDYSYKPEPVMLTMLY 123

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY--SQSKLGHVQQAGSAYI 183
 A VP G T AD AA++AL +AL+ HS + + + G Q
Sbjct: 124 AVEVPDEGSDTLLADGCAAWNALPADKQALLEGRLHHSYKHFMATRQFGQQQTLSPLE 183

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLL--IGRHAHAIPGMDAAESERFLEGLVDWACQAP 241
 D PL++ HP GR +L G I GM L+ LV++ +
Sbjct: 184 AANPDVE----HPLIRTHPADGRKALWPSTGTVTEVI-GMPGPAGLALLDELVEFMTEER 238

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRAEPWD 269
 V+ H+W GD+++WDNRC LH +D

Sbjct: 239 FVYRHKWRVGDLLMWDNRCTLHTGTLYD 266

>gb|ADC34024.1| TfdA-like protein [uncultured bacterium]
Length = 202

Score = 87.8 bits (216), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 61/209 (29%), Positives = 94/209 (44%), Gaps = 10/209 (4%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM 115
QQI FA+ FG I+ ++ + GTVR+ + + GN WH D ++
Sbjct: 1 QQIAFAQGFG EIDVDPTAGMLPVP GPYPEIGTVRKEP-----EQTRNTGGN--WHTDHSFD 53

Query: 116 PVMAQGA VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
P+ G++ A +P GG T FA M AAYDAL + + + +A H+ + + L
Sbjct: 54 PIPPLGSILVARDLPDTGGDTL FASMYAAYDALSDGLKKTLEGMNAVHAKTRAF AALPKE 113

Query: 176 QQAGSAYIGYGMDDTTAT--PLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEG 232
+Q +A A + P+V HPE+GR L + + G ES L+
Sbjct: 114 RQVSAAEHAEIQARFAARDAIHPVVP RHPESGRRLLFVNPNYTTRFEGWTEQESAPLLDY 173

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
L A + + QW G + WDNRC+
Sbjct: 174 LYRHAARPEFTYRFQWREGSIAFWDNRCV 202

>ref|NP_821782.1| taurine catabolism dioxygenase [Streptomyces avermitilis MA-4680]
dbj|BAB69377.1| putative oxidoreductase [Streptomyces avermitilis]
dbj|BAC68317.1| putative taurine catabolism dioxygenase [Streptomyces avermitilis
MA-4680]
Length = 296

Score = 87.8 bits (216), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 76/271 (28%), Positives = 107/271 (39%), Gaps = 28/271 (10%)

Query: 12 GATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIG 71
G +GATV G AT DA AAL + + + GQ LS + + KR G E
Sbjct: 8 GTAIGATVEGFDHATASDADIAALKSTVYTKKIAVLKGQDLSPQEFLELGKRLGRPETYY 67

Query: 72 G-----GDIV AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA V 123
+I SNV +G + V WHAD +MP +
Sbjct: 68 EPMYHHPEVTEIFVSSNVPENGK-----QIGVPKTKGFWHADYQFMPDPFGITL 116

Query: 124 FSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-VYSQSKLGHVQQAGSAY 182
+V+P T F DM AYD L E + + RHS+ Y + + V + S
Sbjct: 117 IYPQVIPRQNRGTYFIDMGRAYDRLPEDLKKEIGGTYCRHSVRKYFKIRPHDVYRPISEI 176

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLL-----IGRHAHAIPGMDAAESERFLE--GLV 234
I T ++P HP TG L IG +D +R + G +
Sbjct: 177 IEEVERKTPAVVQPTTFTHPMTGETVLYISEGFTIGVEDQDGEPLDDELLKRLFQATGQL 236

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
D + +H + GD++VWDNR L+HRA
Sbjct: 237 DETFEHDNIHLQSFEQGDLLVWDNRSLIHRA 267

>ref|NP_286110.1| taurine dioxygenase [Escherichia coli O157:H7 EDL933]
ref|NP_308449.1| taurine dioxygenase [Escherichia coli O157:H7 str. Sakai]
ref|ZP_02774840.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4113]
ref|ZP_02781904.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4401]
ref|ZP_02786567.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4501]
ref|ZP_02793313.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4486]
ref|ZP_02801346.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4196]

ref|ZP_02808228.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4076]
 ref|ZP_02811208.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC869]
 ref|ZP_02825245.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC508]
 ref|YP_001726209.1| taurine dioxygenase [Escherichia coli ATCC 8739]
 ref|ZP_03070945.1| taurine dioxygenase [Escherichia coli 101-1]
 ref|ZP_03083951.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4024]
 ref|ZP_03248934.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4206]
 ref|ZP_03257088.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4045]
 ref|ZP_03263279.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4042]
 ref|YP_002269009.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4115]
 ref|ZP_03441846.1| taurine dioxygenase [Escherichia coli O157:H7 str. TW14588]
 ref|YP_003037478.1| taurine dioxygenase [Escherichia coli BL21-Gold(DE3)pLysS AG]
 ref|YP_003043545.1| taurine dioxygenase [Escherichia coli B str. REL606]
 ref|YP_003076385.1| taurine dioxygenase [Escherichia coli O157:H7 str. TW14359]
 ref|ZP_05938128.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli O157:H7 str. FRIK2000]
 ref|ZP_05948588.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli O157:H7 str. FRIK966]
 ref|YP_003498093.1| Taurine dioxygenase [Escherichia coli O55:H7 str. CB9615]
 ref|ZP_06935240.1| taurine dioxygenase [Escherichia coli OP50]
 ref|ZP_07121300.1| taurine dioxygenase [Escherichia coli MS 84-1]
 ref|ZP_07145752.1| taurine dioxygenase [Escherichia coli MS 187-1]
 ref|ZP_07207646.1| taurine dioxygenase [Escherichia coli MS 124-1]
 ref|ZP_07784639.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli 1827-70]
 gb|AAG54718.1|AE005216_6 taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli O157:H7 str. EDL933]
 dbj|BAB33845.1| taurine dioxygenase [Escherichia coli O157:H7 str. Sakai]
 gb|ACA78882.1| Taurine dioxygenase [Escherichia coli ATCC 8739]
 gb|EDU32111.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4196]
 gb|EDU54047.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4113]
 gb|EDU68373.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4076]
 gb|EDU74379.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4401]
 gb|EDU80839.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4486]
 gb|EDU86468.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4501]
 gb|EDU92177.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC869]
 gb|EDU95796.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC508]
 gb|EDX38156.1| taurine dioxygenase [Escherichia coli 101-1]
 gb|EDZ75999.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4206]
 gb|EDZ81245.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4045]
 gb|EDZ84838.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4042]
 gb|ACI38041.1| taurine dioxygenase [Escherichia coli O157:H7 str. EC4115]
 gb|ACI70550.1| taurine dioxygenase [Escherichia coli]
 gb|ACI70551.1| taurine dioxygenase [Escherichia coli]
 gb|ACI70552.1| taurine dioxygenase [Escherichia coli]
 gb|ACI70553.1| taurine dioxygenase [Escherichia coli]
 gb|EEC30407.1| taurine dioxygenase [Escherichia coli O157:H7 str. TW14588]
 emb|CAQ30839.1| taurine dioxygenase monomer, subunit of taurine dioxygenase [Escherichia coli BL21(DE3)]
 gb|ACT30293.1| Taurine dioxygenase [Escherichia coli 'BL21-Gold(DE3)pLysS AG']
 gb|ACT38009.1| taurine dioxygenase [Escherichia coli B str. REL606]
 gb|ACT42217.1| taurine dioxygenase [Escherichia coli BL21(DE3)]
 gb|ACT70309.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli O157:H7 str. TW14359]
 gb|ADD55109.1| Taurine dioxygenase [Escherichia coli O55:H7 str. CB9615]
 gb|EFJ88205.1| taurine dioxygenase [Escherichia coli MS 84-1]
 gb|EFK25293.1| taurine dioxygenase [Escherichia coli MS 187-1]
 gb|EFK70768.1| taurine dioxygenase [Escherichia coli MS 124-1]
 emb|CBI99927.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli ETEC H10407]
 gb|EFQ02245.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli

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1827-70]
gb|EFU36154.1| taurine dioxygenase [Escherichia coli MS 85-1]
gb|EFW67418.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli
0157:H7 str. EC1212]
gb|EFX08073.1| taurine dioxygenase [Escherichia coli 0157:H7 str. G5101]
gb|EFX29929.1| taurine dioxygenase [Escherichia coli 055:H7 str. USDA 5905]
gb|EFX32203.1| taurine dioxygenase [Escherichia coli 0157:H7 str. LSU-61]
gb|EGB34804.1| TfdA family protein Taurine catabolism dioxygenase TauD
[Escherichia coli E1520]
gb|EGB58918.1| TfdA family protein Taurine catabolism dioxygenase TauD
[Escherichia coli H489]
gb|EGB67429.1| TfdA family protein Taurine catabolism dioxygenase TauD
[Escherichia coli TA007]
gb|EGD64918.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli
0157:H7 str. 1044]
gb|EGD69838.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli
0157:H7 str. 1125]
Length = 283

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Score = 87.8 bits (216), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 75/289 (25%), Positives = 122/289 (42%), Gaps = 29/289 (10%)

Query:	6	LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQOITFAKRF	64
		L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF	
Sbjct:	5	LSITPLPGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFRLRDQAITPQQQRALAQRF	64
Query:	65	GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM	118
		G + G D + + + D +P + D+ WH D T++	
Sbjct:	65	GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP	108
Query:	119	AQGAVFSAEVPVAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA	178
		GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++	
Sbjct:	109	PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRLQLSGLRAEHDFRKSFPPEYKY-RKT	167
Query:	179	GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD	235
		+ + P L P+V+ HP +G+ +L + I + ESE L G +	
Sbjct:	168	EEEHQRWREAVAKNPPLLHPVVRTHPVSQKQALFVNEGFTTRIVDVSEKESEALL-GFLF	226
Query:	236	WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG	283
		P +W D+ +WDNR H A R+M + + G	
Sbjct:	227	AHITKPEFOVRWRWOPNDIAIWDNRVTOHYANADYLPORRIMHRATILG	275

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>ref|YP_004017356.1| taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EuIlc]
gb|ADP81486.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EuIlc]
      Length = 304
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Score = 87.8 bits (216), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 82/270 (30%), Positives = 114/270 (42%), Gaps = 18/270 (6%)

Query:	10	PTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIER	69
		P G V G++LA + D ++L L+H ++ P Q L DQ I A RFG R	
Sbjct:	32	PLSDRFGVEVRGLNLANVTDEDESSSLRGLLLRHGVVAVPDQILDPDQHIALAARFG---R	88
Query:	70	IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIIVGNMAWHADSTYMPVMAQGAVFSAEIVV	129
		+ V +A ++ WD G AWH+ YMP A V V	
Sbjct:	89	VTPSSAVIPGLNRAYPQIKVIDSRRWDG-----GLDAWHSVMQYMPEPAAVLVLYLRVA	142
Query:	130	PAVGGRCTCFADMRAAYDALDEATRA-LVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM	188
		P G + +AYDALD +A L R H+ + +++ G	
Sbjct:	143	PPGGTTLRWLSRESAYDALDPDLKARLRGVRGVHHAPALDE---YLRAFGPGRWNGRTI	198
Query:	189	TTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH	246

T P+ P+V+VHPETGR L I A+ G+ AA+ R LE LVD ++
Sbjct: 199 TRVDPVEHPVVRVHPETGRLGLFIDPWSTQALVGVPAAGRRLLERLVDHLTSPEHEASY 258

Query: 247 QWAAGDVVWDNRCLLHRAEPWDFKLPRVM 276

G VV+ D R L RA D PR++
Sbjct: 259 PAEPGTVVLVDMRSTLMRAT--DAPGPRIL 286

>ref|NP_414902.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli str. K-12 substr. MG1655]
ref|AP_001019.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli str. K-12 substr. W3110]
ref|YP_001729277.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli str. K-12 substr. DH10B]
ref|YP_001742500.1| taurine dioxygenase [Escherichia coli SMS-3-5]
ref|ZP_03003383.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli

53638]
ref|YP_002925457.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli BW2952]
ref|ZP_05437876.1| taurine dioxygenase [Escherichia sp. 4_1_40B]
ref|ZP_06652354.1| tauD [Escherichia coli B354]
ref|ZP_07100549.1| taurine dioxygenase [Escherichia coli MS 119-7]
ref|ZP_07132906.1| taurine dioxygenase [Escherichia coli MS 115-1]
ref|ZP_07162132.1| taurine dioxygenase [Escherichia coli MS 116-1]
ref|ZP_07170093.1| taurine dioxygenase [Escherichia coli MS 175-1]
ref|ZP_07189032.1| taurine dioxygenase [Escherichia coli MS 69-1]
ref|ZP_07189322.1| taurine dioxygenase [Escherichia coli MS 196-1]
ref|ZP_07247099.1| taurine dioxygenase [Escherichia coli MS 146-1]
ref|ZP_07496368.1| taurine dioxygenase [Escherichia coli H736]
ref|ZP_07612080.1| taurine dioxygenase [Escherichia coli H591]
sp|P37610.3|TAUD_ECOLI RecName: Full=Alpha-ketoglutarate-dependent taurine dioxygenase;

AltName: Full=2-aminoethanesulfonate dioxygenase;
AltName: Full=Sulfate starvation-induced protein 3;
Short=SSI3

pdb|1GQW|A Chain A, TaurineALPHA-Ketoglutarate Dioxygenase From Escherichia Coli
pdb|1GQW|B Chain B, TaurineALPHA-Ketoglutarate Dioxygenase From Escherichia Coli
pdb|1GY9|A Chain A, TaurineALPHA-Ketoglutarate Dioxygenase From Escherichia Coli
pdb|1GY9|B Chain B, TaurineALPHA-Ketoglutarate Dioxygenase From Escherichia Coli
pdb|1OS7|A Chain A, Crystal Structure Of Taud With Iron, Alpha-Ketoglutarate And Taurine Bound At Ph 7.5
pdb|1OS7|B Chain B, Crystal Structure Of Taud With Iron, Alpha-Ketoglutarate And Taurine Bound At Ph 7.5
pdb|1OS7|C Chain C, Crystal Structure Of Taud With Iron, Alpha-Ketoglutarate And Taurine Bound At Ph 7.5
pdb|1OS7|D Chain D, Crystal Structure Of Taud With Iron, Alpha-Ketoglutarate And Taurine Bound At Ph 7.5
pdb|1OTJ|A Chain A, Crystal Structure Of Apo (Iron-Free) Taud
pdb|1OTJ|B Chain B, Crystal Structure Of Apo (Iron-Free) Taud
pdb|1OTJ|C Chain C, Crystal Structure Of Apo (Iron-Free) Taud
pdb|1OTJ|D Chain D, Crystal Structure Of Apo (Iron-Free) Taud
dbj|BAA12841.1| dioxygenase [Escherichia coli]
gb|AAB18091.1| dioxygenase [Escherichia coli str. K-12 substr. MG1655]
gb|AAC73471.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli str. K-12 substr. MG1655]
dbj|BAE76149.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli str. K12 substr. W3110]
gb|ACB01499.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli

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str. K-12 substr. DH10B]
gb|ACB19431.1| taurine dioxygenase [Escherichia coli SMS-3-5]
gb|EDU66415.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli
53638]
gb|ACR65621.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli
BW2952]
gb|ACX40864.1| Taurine dioxygenase [Escherichia coli DH1]
gb|EFF14176.1| tauD [Escherichia coli B354]
gb|EFI88168.1| taurine dioxygenase [Escherichia coli MS 196-1]
gb|EFJ65171.1| taurine dioxygenase [Escherichia coli MS 175-1]
gb|EFJ79538.1| taurine dioxygenase [Escherichia coli MS 69-1]
gb|EFJ99868.1| taurine dioxygenase [Escherichia coli MS 115-1]
gb|EFK16072.1| taurine dioxygenase [Escherichia coli MS 116-1]
gb|EFK48251.1| taurine dioxygenase [Escherichia coli MS 119-7]
gb|EFK89376.1| taurine dioxygenase [Escherichia coli MS 146-1]
dbj|BAJ42211.1| taurine dioxygenase [Escherichia coli DH1]
gb|EFU97320.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli
3431]
gb|EGB39333.1| TfdA family protein Taurine catabolism dioxygenase TauD
[Escherichia coli E482]
Length = 283

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Score = 87.8 bits (216), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 74/288 (25%), Positives = 121/288 (42%), Gaps = 27/288 (9%)

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Query: 6  LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5  LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFRLRQAITPQQQRALAQR 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHD FRKSFPEYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L L
Sbjct: 168 EEEHQRWREAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALLSFLFA 227

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPVRVMWHSRLAG 283
+ +W D+ +WDNR H A R+M + + G
Sbjct: 228 HITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

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>ref|ZP_04627176.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia
bercovieri ATCC 43970]
gb|EEQ07932.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia
bercovieri ATCC 43970]
Length = 278

```

Score = 87.8 bits (216), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 78/287 (27%), Positives = 123/287 (42%), Gaps = 29/287 (10%)

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Query: 8  ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
+TP G +GA V +++A L D F L+ A L+H +L F Q ++ QQ A RFG
Sbjct: 3  VTPLGPHIGALVENINIARPLGDGQFEQLYHALLKHQVLFVRNQIPITPLQQRELAGRFGD 62

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMA 119
+ +I+ + +P + D+ WH D T++
Sbjct: 63 LHIHPVYPHTKECEEIIVLD-----THDNNPPDNDN-----WHTDVTFIDHPP 105

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Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS--QSKLGHVQQ 177
GA+ +A+ +PA GG T ++ AAYDAL + L+ A H +S + K +
Sbjct: 106 LGAILAAKQLPATGGDTLWSSGVAAYDALSAFQKQLLAGLRAEHDFAHSPFEHKNRGTP 165

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
++ + L P+V+ HP TGR +L + I + A ES+ L L
Sbjct: 166 EHQRWL-LAKERNPPLLHPVVRTHPVTGRQALFVNEGFTTRIVDLSAKESDAILRLLFAH 224

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
A + +W DV +WDNR H A RVM + + G
Sbjct: 225 ATKPEFQVRWRWQQDDVAIWDNRVTQHYANADYLPQRRVMHRATILG 271

>ref|ZP_02493042.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei NCTC 13177]
Length = 381

Score = 87.8 bits (216), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 82/271 (30%), Positives = 116/271 (42%), Gaps = 30/271 (11%)

Query: 6 LQITPTGATLGATVTGVHLATL---DDAGFAALHAAWLQHALLIFPGQHLSND-QQITFA 61
L I P +GA V G+ L + +D F + A L H ++ F QH +D Q FA
Sbjct: 96 LSIRPLSGHIGAEVQGIQLGSQMAPNDIRF--ITQALLTHRVIFRRQHHLDDLAQELFA 153

Query: 62 KRFGAIER---IGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
+ FG I + +GG AI + + R +S WH D T+
Sbjct: 154 QAFGEIVKHPTMGKGTGSAILELHSHEGGRANS-----WHTDVTFLRLP 197

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY----SQSKLGH 174
+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
Sbjct: 198 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSSLQDLVDKLWAVHGNDFDYAASRVLLH 257

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
A Y T P+V++HPETG SLL+G +A D +S R E L
Sbjct: 258 DPVAKEYRKYAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRQVQYDTHDSNRLYEILQ 316

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
+ WA GDV +WDNR H A
Sbjct: 317 AHITRLENTVRWHWATGDVAIWDNRSTQHYA 347

>ref|YP_555387.1| taurine dioxygenase [Burkholderia xenovorans LB400]
gb|ABE36037.1| Taurine dioxygenase [Burkholderia xenovorans LB400]
Length = 315

Score = 87.8 bits (216), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 76/285 (26%), Positives = 121/285 (42%), Gaps = 14/285 (4%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++Q+ P A +GA + GV L LD + A + AA L+ ++ F Q L+++Q + F+ +
Sbjct: 11 SIQVKPLSAHIGAEHLHGVDLTKLDPSEVAQIRAALLRWRVFFREQFLTHEQHVAFSAQ 70

Query: 64 FG--AIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
FG + G + V + R+ + E +++ G WH D T
Sbjct: 71 FGEPTLGHVPFGHVDGHPEVYSISKYRKATRFEGQALLRPWTG--WHTDVTAAALNPPWA 127

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
++ +P GG T + ++ AY+ L RA V H G A
Sbjct: 128 SILRGVTIPPYGGDTQWTNLALAYEKLAPLRAFVDGLRGVHRFTTPAGASG-----TEA 182

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQA 240
++ PLV+VHPETG L + +I G+ ESE LE L + A +
Sbjct: 183 FVKAVEQRLVTEHPLVRVHPETGERVLYVSPSFLKSIVGVTPRESEALLELLWEHATRP 242

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRA--EPWDFKLPRVMWHSRLAG 283
+W AG V WDNR H A + +D R ++ + L G
Sbjct: 243 EFTVRFKWEAGSVAFWDNRATAHLAPTDFDLDFDRQLYRTTLVG 287

>ref|YP_587420.1| taurine dioxygenase [Cupriavidus metallidurans CH34]
gb|ABF12151.1| taurine dioxygenase [Cupriavidus metallidurans CH34]
Length = 281

Score = 87.8 bits (216), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 80/296 (27%), Positives = 126/296 (42%), Gaps = 42/296 (14%)

Query: 7 QITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
QITP +GA ++GV++ A D A FA + AA L+H +L F Q ++ + FA F
Sbjct: 5 QITPA---IGAEISGVNIGEAAARDPAVFAEIRAALLKHRVLFRRKQEI TRADHVAFASGF 61

Query: 65 GAIERIGGGDIVAISNV-KADGTV---RQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQ 120
G +E D + +V G V R +P +++ ++H D + P A
Sbjct: 62 GKLE-----DHPVVGSPDYPGLVKVYRSDNPHSFEN-----SYHCDGLWRPNPAM 107

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
GAV P +GG T + +M AY+ L + ++ + AR S+ +S + +
Sbjct: 108 GAVLRCLCEPEIGGDTIWNMVKAYEELPDEIKSKIDGLRARASIEHSFGAVMTPENRAK 167

Query: 181 AYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGRH-----AHAIPGMDAAESER 228
+ P+ P+V++HPETG L +G A+ G+D +
Sbjct: 168 -----LAQDHPPVEHPVVRIPHETGEKILFVGASFTHFTNYSTPANVRHGIDKSPGAS 221

Query: 229 FLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + P W GDV VWDNR H A + PR M + + G
Sbjct: 222 LLLNYLTSRATIEYQVRWAWQEGDVAVWDNRSTQHYAVNDYYPAPRKMERAGIVG 277

>ref|ZP_07506274.1| taurine dioxygenase [Escherichia coli M718]
Length = 283

Score = 87.8 bits (216), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 74/288 (25%), Positives = 121/288 (42%), Gaps = 27/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFELYHAVLRHQVFLRDQAITPQQQRALAQR 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPPEYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L L
Sbjct: 168 EEEHQRWREAVAKNPPLHPVVRTHPVSQKQALFVNEGFTTRIVDVSEKESSEALLSFLFA 227

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W D+ +WDNR H A R+M + + G
Sbjct: 228 HITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|YP_003227485.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli
O26:H11 str. 11368]

ref|YP_003232936.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli
O111:H- str. 11128]
dbj|BAI23745.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli
O26:H11 str. 11368]
dbj|BAI34385.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli
O111:H- str. 11128]
gb|EFZ63951.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli
1180]
Length = 283

Score = 87.8 bits (216), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 75/289 (25%), Positives = 122/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVFLRDQTIAPQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPPEYKY-RKT 167

Query: 179 GSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L G +
Sbjct: 168 EEEHQRWREAVAKNPPLHPVVRTHPVSQKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|ZP_07965013.1| TfdA family Taurine catabolism dioxygenase TauD [Segniliparus
rugosus ATCC BAA-974]
gb|EFV13761.1| TfdA family Taurine catabolism dioxygenase TauD [Segniliparus
rugosus ATCC BAA-974]
Length = 317

Score = 87.8 bits (216), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 72/266 (27%), Positives = 113/266 (42%), Gaps = 22/266 (8%)

Query: 7 QITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRF 64
Q+ + +GA +TGV L A L A+ A L H +++F GQ HL + Q FA++
Sbjct: 19 QLRKLTSDIGAEITGVRLGADLGAQTALAIRQAVLDHKVVVFRGQDHLDDAGQRAFAEQL 78

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G + T+R + ++ + +WH D T++ +V
Sbjct: 79 GPL-----TLGHPTLRSRTEGAILEVNSEHGRSDSWHTDVTTFVDSPPAFSVL 125

Query: 125 SAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQ 177
+P GG T +A+ +AY+ L E R L A H+ Y ++ G ++
Sbjct: 126 RPVALPEYGGTTAWANTTSAYNRLPEPLRLLAESLRAVHTNRYDYARTHERDAHEGQDEE 185

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAAHAIPGMDAAESERFLEGLVDWA 237
G A P+V+VHPETG +LL+G+ I + +ES+ L D
Sbjct: 186 KGRAQYEEFRSVQYETEHPPVVRVHPETGERTLLLGQFVSHILDLKPSESDAVYRILQDRI 245

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLH 263
+ W+ GDV VWDNR H
Sbjct: 246 TKLENTVRWHWSLGDVAVWDNRATQH 271

>emb|CAY27347.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 87.4 bits (215), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 52/128 (40%), Positives = 72/128 (56%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALD+AT+A HSL++S+ +LG + + D +R
Sbjct: 1 TEFADMRAAYDALDDATKAETGLVCEHSLMFSREQLG-----FTEFSPDEREA-MR 51

Query: 196 P----LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251
P LV+ HP TGR SL + H +I G E+ F+ L++ A Q V+AH+W
Sbjct: 52 PVRQRLVRTHPVTGRKSLFLAAHIGSIVGWVPPEARAFIRDLMEHATQPRFVYHRWQQW 111

Query: 252 DVVVWDNR 259
D+V+WDNR
Sbjct: 112 DLVMWDNR 119

>ref|ZP_04002432.1| taurine dioxygenase [Escherichia coli 83972]
ref|ZP_07178571.1| taurine dioxygenase [Escherichia coli MS 45-1]
ref|ZP_07196515.1| taurine dioxygenase [Escherichia coli MS 185-1]
ref|ZP_07511126.1| taurine dioxygenase [Escherichia coli TA206]
gb|EEJ49179.1| taurine dioxygenase [Escherichia coli 83972]
gb|EFJ55037.1| taurine dioxygenase [Escherichia coli MS 185-1]
gb|EFJ91086.1| taurine dioxygenase [Escherichia coli MS 45-1]
gb|ADN45051.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli
ABU 83972]
gb|EFU53513.1| taurine dioxygenase [Escherichia coli MS 153-1]
Length = 283

Score = 87.4 bits (215), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 77/289 (26%), Positives = 123/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L IT G +GA +TG L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITSLGPYIGAQITGADLTRPLSDNQFEQLYHAVLRHHVVFLRDQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFTIQT 108

Query: 119 AQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T +A AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWASGIAAYEALSVFPFRQLLSGLRAEHDFRKSFPEYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + + P L P+V+ HP TG+ +L + I + ESE L G +
Sbjct: 168 EAEHQRWREAVAKNPPLLHPVVRTHPVTGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>emb|CAY27376.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 117

Score = 87.4 bits (215), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 49/123 (39%), Positives = 68/123 (55%), Gaps = 6/123 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195

Sbjct: 1 T FADMRAAYDALD T+AL+ HS ++S+ LG ++ + A +
TEFADMRAAYDALDGKTKALIEDLICEHSRIFSKGALGF-----SFTEEEVKAFAPVRQ 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP+TGR SL + HA I G E+ L L + A Q V++H+W GD+V+

Sbjct: 55 RLVTRHPKTGRKSLYLSSHAGRIVGWPVPEAMLLRELTEHATQREFVYSHKWRVGDLMV 114

Query: 256 WDN 258
WDN

Sbjct: 115 WDN 117

>gb|EFW49871.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Shigella
dysenteriae CDC 74-1112]
Length = 283

Score = 87.4 bits (215), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 72/271 (26%), Positives = 116/271 (42%), Gaps = 29/271 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF

Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVFLRDQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++

Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++

Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPEYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L G +

Sbjct: 168 EEEHQRWREAVAKNPPLHPVVRTHPVSQKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
P +W D+ +WDNR H A

Sbjct: 227 AHITKPEFQVRWRWQPNDAIWDNRVTQHYA 257

>emb|CAY27457.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 87.4 bits (215), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 51/128 (39%), Positives = 65/128 (50%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALDE + + HS +YS+ KLG + D T +

Sbjct: 1 TEFADMRAAYDALDERLKHKIEDLVCLHSNMYSRGKLG-----LADFTDEERTAFK 51

Query: 196 P----LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251
P LV+ HP TGR SL + HA I GM E L L ++A + V++H W

Sbjct: 52 PVRQRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEGRMLLLDLTEFATREQFVYSHMWRVN 111

Query: 252 DVVVWDNR 259
D V+WDNR

Sbjct: 112 DFVMWDNR 119

>gb|ACG80563.1| TfdA [uncultured bacterium]
Length = 119

Score = 87.4 bits (215), Expect = 2e-15, Method: Compositional matrix adjust.

Identities = 49/124 (39%), Positives = 65/124 (52%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR 195
T F DMRAAYDALD+ T+A + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFCDMRAAYDALDDETKAEIDDLVCEHSLMYSRGS LGFTE-----YTDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP R SL + HA I GM E L L + A Q+ V+ H+W D+V+
Sbjct: 56 RLVTRHPVHRRKSLYLSSHAGKIVGMSVPEGRLLLRDLNEHATQSEFVYVHKWKLHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>ref|ZP_03541010.1| Taurine dioxygenase [Comamonas testosteroni KF-1]
gb|EED65296.1| Taurine dioxygenase [Comamonas testosteroni KF-1]
Length = 282

Score = 87.4 bits (215), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 78/276 (28%), Positives = 118/276 (42%), Gaps = 32/276 (11%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+QI P +GA + V LA DD FA + AA L+H +L Q +S + + FA+R
Sbjct: 1 MQINPLTCAIGAELVDVQLADALRDDGLFAEIKAAALKHKVLFRLRHQRISRAEHVGFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E V S+ G V+ + +P + D + +WH D+T+ V G
Sbjct: 61 FGELE----DHPVVGSDPDHPLGLVQIYKTPDKPLDRYE-----NSWHCDATWREVPPMGC 111

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQQAGS 180
V P VGG T +A+M AY+ L + ++ ARHS+ + + H + A
Sbjct: 112 VLRCVECPVVGDDTMWANMALAYEMLPSHIKDVIAPLARHSIECTFGAAMPAHKRLALK 171

Query: 181 AYIGYGMTTATPLRPLVKVHPETGRPSLLIG-----RHAHAIPGMDAAE-SERF 229
A P+V+ HPETG L + A+ G D + S
Sbjct: 172 AQFPDAE-----HPVVRTHPETGEKVLVSVSGFTTHFTNFHTPANVRVGQDFTQGSSSL 224

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L+ L+ A +W G + +WDNR H A
Sbjct: 225 LQFLISQAAIPEYQVRWRWEPGSIWIWDNRATQHIA 260

>emb|CAY27469.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 87.4 bits (215), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 50/124 (40%), Positives = 68/124 (54%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR 195
T FADMRAAYDALD T+AL+ HS ++S+ LG ++ + A +
Sbjct: 1 TEFADMRAAYDALDGETKALIEDLVCEHSRIFSKGALGF-----SFTEEEVKAFAPVRQ 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP+TGR SL + HA I G E+ L L + A Q V +H+W GD+V+
Sbjct: 55 RLVTRHPKTRKSLYLLSHAGRIVGWPVEAMLLRELTEHATQREFVFSHKWRVGDVLM 114

Query: 256 WDNR 259
WDNR
Sbjct: 115 WDNR 118

>ref|ZP_07300800.1| TauD/TfdA family taurine dioxygenase [Streptomyces hygroscopicus]

ATCC 53653]
gb|EFL29169.1| TauD/TfdA family taurine dioxygenase [Streptomyces hygroscopicus
ATCC 53653]
Length = 320

Score = 87.4 bits (215), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 73/263 (27%), Positives = 118/263 (44%), Gaps = 23/263 (8%)

Query: 8 ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
+ G +GA ++GV L LD+A AA+ AA L+H ++ F QH + A+ A
Sbjct: 15 VEKIGGRIGAVISGVRLGGDLDEATVAAIRAAALEHKVVFVRDQHHL-----AESHEA 68

Query: 67 IERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
R+ G + + ADG R P + + + WH D T++P ++ A
Sbjct: 69 FGRLLGEPVAHPTVPSADG--RYAFPIDNEHGGRA---NQWHTDVTVPAYPAFSILRA 122

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRAL-----VHQRSARHSLVYSQSKLGHVQQAGS 180
EV+P GG T +++ AAY L E R L VH ++ + +++ +
Sbjct: 123 EVIPPYGGNTLWSNTAAAYAHLEPLRVLADSLRGVHTNDYDYAATRPDASAAALERHLT 182

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
+ T P+V+VHPETG +L++G + G + +S ++ L +
Sbjct: 183 VFTAIFKQTE---HPVVRVHPETGERTLILGNFVQKLSGFNGRDSRALIDVLQSHIERP 238

Query: 241 PRVHAHQWAAGDVVVWDNRCLLH 263
QW AGDV +WDNR H
Sbjct: 239 ENTIRWQWRAGDVAIWDNRATQH 261

>ref|NP_706204.1| taurine dioxygenase [Shigella flexneri 2a str. 301]
ref|NP_835990.1| taurine dioxygenase [Shigella flexneri 2a str. 2457T]
ref|YP_687911.1| taurine dioxygenase [Shigella flexneri 5 str. 8401]
gb|AAN41911.1| taurine dioxygenase [Shigella flexneri 2a str. 301]
gb|AAP15795.1| taurine dioxygenase [Shigella flexneri 2a str. 2457T]
gb|ABF02606.1| taurine dioxygenase, 2-oxoglutarate-dependent [Shigella flexneri 5
str. 8401]
gb|ADA72596.1| Taurine dioxygenase [Shigella flexneri 2002017]
gb|EFS11128.1| alpha-ketoglutarate-dependent taurine dioxygenase [Shigella
flexneri 2a str. 2457T]
Length = 283

Score = 87.4 bits (215), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 75/289 (25%), Positives = 122/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFELYHAVLRHQVVFRLRDQAITPQQORALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSWLRAEHDFRKSFPYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L G +
Sbjct: 168 EEEHQRWREAVAKNPPLHHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>emb|CAY27528.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 87.4 bits (215), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 52/127 (40%), Positives = 69/127 (54%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTAT--- 192
T FADMRAAYDALD+ T+A + HSL+YS+ LG ++ Y + A
Sbjct: 1 TEFADMRAAYDALDDDTKAEIEDMICEHSLMYSRGS LG-----FLDYTDEEKAMFKP 52

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
L+ LV+ HP R SL + HA AI GM E L L + A + V+AH+W D
Sbjct: 53 VLQRLVRTHPVHRRKSLYLSSHAGAIQGMSVPEGRLLLRDLNEHATRPEFVYAHKWT LHD 112

Query: 253 VVVWDNR 259
+V+WDNR
Sbjct: 113 LVMWDNR 119

>emb|CAY27367.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 87.4 bits (215), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 50/124 (40%), Positives = 67/124 (54%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T FADMRAAYDALD T+AL+ HS ++S+ LG G + A +
Sbjct: 1 TEFADMRAAYDALDAKTKALIEDLVCEHSRIFSKGALGFSFTEGE-----LKAFAFVRQ 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ H +TGR SL + HA I G E+ L L + A Q V++H+W GD+V+
Sbjct: 55 RLVRTHRKTRKSLYLTSHAGRIVGWPVPEAMLLRELTEHATQREFVYSHKWQVGD LVM 114

Query: 256 WDNR 259
WDNR
Sbjct: 115 WDNR 118

>gb|AAS64588.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
Length = 119

Score = 87.4 bits (215), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 49/124 (39%), Positives = 64/124 (51%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T F DMRAAYDAL++ TR + HSL+YS+ LG + Y L+
Sbjct: 1 TEFADMRAAYDALNDETRTEIEDMICEHSLMYSRGS LGFLD-----YTEEEKQMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP GR SL + HA I GM E+ L L + A Q V+ H+W D+V+
Sbjct: 56 RLVRTHPVHGRKSLYLSSHAGGIIGMSVPEARVLLRDLNEHATQPESVYVHKWTLHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>ref|ZP_06787243.1| taurine dioxygenase [Acinetobacter sp. 6014059]
gb|ADX03573.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Acinetobacter
baumannii 1656-2]
gb|ADX92074.1| taurine dioxygenase [Acinetobacter baumannii TCDC-AB0715]

Length = 293

Score = 87.4 bits (215), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 67/273 (24%), Positives = 109/273 (39%), Gaps = 32/273 (11%)

```
Query: 5   TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L I   T+GA + + L L++   + A L H ++ F Q L+   Q   A+ F
Sbjct: 7   NLNIEVIKPTIGAIHNLNIDLNALNEQTQQIQQALLDHQVIFFRKQQLAPQAQADLARSF 66

Query: 65  G-----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
          G           +IE +   +++ + + K D               + N   WH D T+
Sbjct: 67  GTLHVHPYPSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFS 107

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLG 173
          G V   A +P VGG T ++   AA+ L   + +   +A H +   + +
Sbjct: 108 KTPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQRKLRGLTATHDIRKSFPLERFA 167

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
          H ++   +               + P+V+ HP TG P L +   I   +   ESE+ L
Sbjct: 168 HNEEEREKLLQ-TFKRNPVVPVVRTHPVTGEPLLFVSEGFTTRINELPEQESEQLLNF 226

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          L + A Q           +W   GDV +WDNRC   H+A
Sbjct: 227 LFEHATQEQFHLRWKQDGDVAIWDNRCTQHKA 259
```

```
>gb|ACI70549.1| taurine dioxygenase [Escherichia coli]
gb|EFX12863.1| taurine dioxygenase [Escherichia coli O157:H- str. 493-89]
gb|EFX17668.1| taurine dioxygenase [Escherichia coli O157:H- str. H 2687]
          Length = 283
```

Score = 87.4 bits (215), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 75/289 (25%), Positives = 122/289 (42%), Gaps = 29/289 (10%)

```
Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L ITP G +GA ++G L   L D F L+ A L+H ++   Q ++   QQ   A+RF
Sbjct: 5   LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVFLRDQAITPQQORALAQRF 64

Query: 65  GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM 118
          G +               G D + + +   D           +P + D+               WH D T++
Sbjct: 65  GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFTIETP 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
          GA+ +A+ +P+ GG T +   AAY+AL   R L+   A H   S   + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHYFRKSFPEYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
          + +               P L P+V+ HP +G+ +L +   I   +   ESE L G +
Sbjct: 168 EEEHQRWREAVAKNPPLHPVVRTHPVSQKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          P           +W   D+ +WDNR   H A               R+M   + + G
Sbjct: 227 AHITKPEFQVRWRWPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275
```

```
>emb|CAY27525.1| alpha-KG-dehydrogenase [uncultured bacterium]
          Length = 119
```

Score = 87.0 bits (214), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

```
Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQAGSAYIGYGMDDTTATPLR 195
          T FADMRAAYD LDE T+A +   HSL++S+ LG   + +   +   P+R
```

Sbjct: 1 TEFADMRAAYDTLDERTKAEIEDLVCEHSLMFSRGLLGFTAMSEAEREMF-----RPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I G E+ L L++ A Q V++HQW D+V

Sbjct: 55 QRLVVRTHPVTGRKSLFLSAHAGTIVGWPVPEARASLRDLIEHATQPQLVYSHQWRQWDLV 114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>ref|ZP_02486273.1| taurine dioxygenase [Burkholderia pseudomallei 7894]
Length = 272

Score = 87.0 bits (214), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 81/290 (27%), Positives = 116/290 (40%), Gaps = 32/290 (11%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
++TP LGA V V L+ DA + AA H +L F GQ LS + FA FG

Sbjct: 3 RLTPA---LGAIVDDVDLSNATDALRDDIRAALAHQVLFRRGQRLSAARHRDFAAGFGD 59

Query: 67 I-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
+ +I+ + N D + N WH D T+

Sbjct: 60 LHVHPIYPSHPDAREIMVLDNAVFD-----LQDNAIWHTDVTFTETPP 102

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQ 177
+ ++ +A +P GG T + AAYDAL E +A + +A+H + + G V

Sbjct: 103 RASILAAHTLPETGGDTLWGSFGAAYDALSERVKAQLDGLTAQHDFTKSFPLKRFG-VTA 161

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
A T + P+V+ HPETGR +L + I G+ E L L

Sbjct: 162 EDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNEGFTTEIDGLPEEEGAALLRFLFAH 221

Query: 237 ACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
+ +W GDV WDNR +H A K RVM + + G RP

Sbjct: 222 QSRPEFTLRWRWQPGDVAFWDNRSTIHYAVNDYGKAHRVMHRATIVGDRP 271

>emb|CAY27478.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 87.0 bits (214), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 49/124 (39%), Positives = 68/124 (54%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DMRAAYDALD T+AL+ HS ++S+ LG ++ + A +

Sbjct: 1 TEFGLMRAAYDALDGKTKALIEDIVCEHSRIFSKGALGF-----SFSEEEVKAFAPVRQ 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 255
LV+ HP+TGR SL + HA I G E+ L L + A Q V++H+W GD+V+

Sbjct: 55 RLVVRTHPKTGRKSLYLSSHAGRIVGWPVPEAMLLRELTEHATQREFVYSHKWRVGDLM 114

Query: 256 WDNR 259
WDNR

Sbjct: 115 WDNR 118

>ref|YP_001412268.1| taurine catabolism dioxygenase TauD/TfdA [Parvibaculum
lavamentivorans DS-1]
gb|ABS62611.1| Taurine catabolism dioxygenase TauD/TfdA [Parvibaculum
lavamentivorans DS-1]
Length = 284

Score = 87.0 bits (214), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 73/276 (26%), Positives = 110/276 (39%), Gaps = 29/276 (10%)

```
Query: 6  LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
          L+ P      G + V L T      + + + ++ Q + D ++F FG
Sbjct: 7  LRTRPLMPGFGVEIFDVLDLKTAGSDARQKVVDLFHANGAILLRQDMDPDDLMSFIGLFG 66

Query: 66 AIER-----IGGGDIVAISNVKADGT-VRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
          E      G I +SN DG + H+      + WH D +Y
Sbjct: 67 EAEDHTQTQFTLPGYSKIFLLSNKIVDGKPIGAHNDG-----VGWHTDYSYKE 114

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
          + A VP G T AD+ AAYD+L +A + HS + S +
Sbjct: 115 EPVMCTMLYAVEVPDEGSDTLADLCAAYDSLPRERQAQLDGLVLHHSYQHLMS----TR 170

Query: 177 QAGSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL 233
          Q G + M A P PLV+ HP GR +L + I GM E++ ++ L
Sbjct: 171 QFGRMELSEEM-KAANPDVFHPLVRTHPADGRKALWVSTGTVKGIVGMPDDEAQAIDEL 229

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD 269
          V++ P VH H+W GD+++WDNRC LH +D
Sbjct: 230 VEFVTSEPFVHRHKWHVGDILMWDNRCTLHTGTVFD 265
```

>ref|ZP_04900578.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei S13]
gb|EDS83590.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei S13]
Length = 277

Score = 87.0 bits (214), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 84/303 (27%), Positives = 119/303 (39%), Gaps = 49/303 (16%)

```
Query: 4  TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
          T L +T LGA V V L+ DA + AA H +L F GQ LS + FA
Sbjct: 2  TRLTLRLTPALGAIVDDVDLSNATDALRDDIRAALAHHQVLFRRGQRLSAAHRDRFAAG 61

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
          FG + +I+ + N D + N WH D T+
Sbjct: 62 FGDLVHVPPIYSPHDAREIMVLDAVFD-----LQDNAIWHTDVTFTE 104

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGH 174
          + ++ +A +P GG T + AAYDAL E +A + +A+H + + G
Sbjct: 105 TPTRASILAHAHTLPETGGDTLWGSFGAAYDALSERVKAQLDGLTAQHDFTKSFPLKRF- 163

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR---HAHAIPGMDAAESERFL 230
          V A T + P+V+ HPETGR +L + +P + A RFL
Sbjct: 164 VTAEDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNEGFTTEIDELPEEEGAALLRFL 223

Query: 231 -----EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          E + W +W GDV WDNR +H A K RVM + + G
Sbjct: 224 FAHQSRPEFTLRW-----RWQPGDVAFWDNRSTIHYAVNDYGKAHRVMHRATIVG 273

Query: 284 -RP 285
          RP
Sbjct: 274 DRP 276
```

>ref|YP_001008090.1| taurine dioxygenase [Yersinia enterocolitica subsp.
enterocolitica
8081]
emb|CAL13964.1| putative taurine dioxygenase [Yersinia enterocolitica subsp.
enterocolitica 8081]

Length = 282

Score = 87.0 bits (214), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 76/289 (26%), Positives = 124/289 (42%), Gaps = 29/289 (10%)

```
Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L +TP G  +GA +  V++A  L D+ F  L+ A L+H +L F  Q ++  QQ  A RF
Sbjct: 5   LVVTPGLPHIGALIENTVNIARPLGDSQFEQLYHALLKHQVLFRRNPITPLQQORDLAGRF 64

Query: 65  GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV 117
          G +                +I+ +                ++P + D+                WH D T++
Sbjct: 65  GDLHIHPVYPHAKECEEIIVLD-----THDNNPPDNDN-----WHTDVTFIET 107

Query: 118  MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
          GA+ +A+ +P  GG T ++  AAY+AL  + L+  A H  +S  + H  +
Sbjct: 108  PPLGAILAAKQLPTTGGDTLWSSGIAAYEALSVPFKQLLAGLQAEHDFTHSFPEKH-RA 166

Query: 178  AGSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
          + + +  P  L P+V+ HP +GR +L +  I +  ES+  L  L
Sbjct: 167  TPEDHQRWLLAKEKNPPLLHPVVRTHPVSGRQALFVNEGFTTRIVDLSEKESDALLRFLF 226

Query: 235  DWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          A +  +W  DV +WDNR  H A  RVM  + + G
Sbjct: 227  AHATKPEFQVRWRWQPDDVAIWDNRVTQHYANADYLPQRRVMHRATILG 275
```

>gb|AAT41922.1| putative dioxygenase [Fremyella diplosiphon Fd33]
Length = 320

Score = 87.0 bits (214), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 80/303 (26%), Positives = 128/303 (42%), Gaps = 42/303 (13%)

```
Query: 1   MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
          M+  +++ P  +GA + GV L+  L D  A +  A L+  ++ F  Q++ +  QI
Sbjct: 20  MSNKHIEVKPVAGHIGAEIGGVDLRPLSDKAVAEIRQALLKWKVIFFRNQIDHAAQIA 79

Query: 60  FAKRFGAI-----ERIGG-GDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHA 110
          F  RFG +  E I G  +I+ I  S  E  + ++  WH
Sbjct: 80  FTSRFGEVTYAHPHEDEPIEGFAEILPID-----RSRYERKNGLRRSSYENRWHT 129

Query: 111  DSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL----- 165
          D T +  G++  A  VP+ GG T + ++ AAY+ L  +AL  A+H
Sbjct: 130  DVTAVVNPAGSILRAVNVPSPFGGDTQWTNLVAAYEGLSAPVKALADTLKAQHFFNARLR 189

Query: 166  VYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDA 223
          + S SKL  A  + P+V+VHPETG  +L +  G  +H I  +
Sbjct: 190  LSSSSKLAKRIAANP-----QVSIHPVVRVHPETGERALFVNPGFTSH-ILDVSP 238

Query: 224  AESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDF---KLPRVMWHSR 280
          ES+  LE  +  +  GD+  WDNR  H A P D  ++ RV++ +
Sbjct: 239  QESDLLLELFFNQITKPAYTTRFHGNGDIAFWDNRATAHLA-PQDLDHIEVERVLYRTT 297

Query: 281  LAG 283
          + G
Sbjct: 298  ITG 300
```

>gb|EGB60776.1| TfdA family protein Taurine catabolism dioxygenase TauD
[Escherichia coli M863]
Length = 283

Score = 87.0 bits (214), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 75/289 (25%), Positives = 123/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++GV L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQISGVDLTRPLSDNQFEQLYHAVLRHQVVFVREQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVM 118
G + G + + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVEEIIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRLLSGLRAEHDFRKSFPYKY-RKT 167

Query: 179 GSAYIGYGMDDTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L G +
Sbjct: 168 EEEHQWRWEAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|YP_003270569.1| taurine dioxygenase [Haliangium ochraceum DSM 14365]
gb|ACY18676.1| Taurine dioxygenase [Haliangium ochraceum DSM 14365]
Length = 272

Score = 87.0 bits (214), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 74/257 (28%), Positives = 110/257 (42%), Gaps = 20/257 (7%)

Query: 13 ATLGAATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIG 71
A LGA V+GV L LDD A + L+H +L F Q L+ Q + FA+RFG E +G
Sbjct: 8 AALGAEVSGVDLTQPLDDDALAIVRGGLLEHQVLFREQUALTPAQHLAFARRFG--EPVG 65

Query: 72 GGDIVAISNVKADGTVRQ--HSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV 129
+ A + P + D WH D T++ G++ V+
Sbjct: 66 HPAYPHVDGYPAINILENTPERPPKID-----TWHTDMTFLERPPLGSILRGVVI 115

Query: 130 PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAAGSAYIGYGMDDT 189
P GG T +A + A+DAL + + A HS + + + G + +
Sbjct: 116 PR-GGDTQWASLALAWDALARMQRYLEGLEALHSFAHG-FRHSLEPGGFERLERAVRD 173

Query: 190 TATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-Q 247
P+++VHPE+GR +L + R I G+ AES L G + + P +
Sbjct: 174 NPPVRHPVMRVHPESGRKALFVNRLFTTHIDGLSEAESRAVL-GFLFGHLETPEFSCRFR 232

Query: 248 WAAGDVVVDNRCLLHR 264
W V WDNR LHR
Sbjct: 233 WRPDSVAFWDNRITLHR 249

>ref|ZP_02902232.1| taurine dioxygenase [Escherichia albertii TW07627]
gb|EDS92198.1| taurine dioxygenase [Escherichia albertii TW07627]
Length = 283

Score = 87.0 bits (214), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 75/289 (25%), Positives = 121/289 (41%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++GV L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPQGPYIGAQISGVDLTRPLSDNQFEQLYHAVLRHQVVFVREQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++

Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+ L R L+ A H S + ++

Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGLAAYETLSVPFRQLLSGHRAEHDFRKSFPYK-SRKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L G +

Sbjct: 168 EEEHQWRWREAAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G

Sbjct: 227 THITKPEFQVRWRWPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>emb|CBY29263.1| alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia enterocolitica subsp. palearctica Y11]
Length = 282

Score = 87.0 bits (214), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 76/289 (26%), Positives = 124/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L +TP G +GA + V++A L D+ F L+ A L+H +L F Q ++ QQ A RF

Sbjct: 5 LVVTPGLPHIGALIENTVNIARPLGDSQFEQLYHALLKHQVLFFRNQPITPLQQRDLAGRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPV 117
G + +I+ + ++P + D+ WH D T++

Sbjct: 65 GDLHIHPVYPHAKECEEIIVLD-----THDNPPDNDN-----WHTDVTFIET 107

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 177
GA+ +A+ +P GG T ++ AAY+AL + L+ A H +S + H +

Sbjct: 108 PPLGAILAAKQLPTTGGDTLWSSGIAAYEALSAPFKQLLAGLRAEHDFTHSFPEHKKH-RA 166

Query: 178 AGSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
+ + + P L P+V+ HP +GR +L + I + ES+ L L

Sbjct: 167 TPEDHQRWLLAKEKNPPLLHPVVRTHPVSGRQALFVNEGFTTRIVDLSEKESDALLRFLF 226

Query: 235 DWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
A + +W DV +WDNR H A RVM + + G

Sbjct: 227 AHATKPEFQVRWRWQDDVAIWDNRVTQHYANADYLPQRRVMHRATILG 275

>ref|ZP_05827549.1| alpha-ketoglutarate-dependent taurine dioxygenase [Acinetobacter baumannii ATCC 19606]
gb|EEX05167.1| alpha-ketoglutarate-dependent taurine dioxygenase [Acinetobacter baumannii ATCC 19606]
Length = 293

Score = 87.0 bits (214), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 68/276 (24%), Positives = 111/276 (40%), Gaps = 38/276 (13%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I T+GA + + L L++ + A L H ++ F Q L+ Q A+ F

Sbjct: 7 NLNIEVIKPTIGAIHIDIDLNALNEQTQQIQQALLDHQVIFFRKQQLAPQAQADLARSF 66

Query: 65 G-----AIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYM 115
G +IE + +++ + + K D + N WH D T+

Sbjct: 67 GTLHVHPIYPSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFS 107

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLG 173
G V A +P VGG T ++ AA+ L + + +A H + + +

Sbjct: 108 KTPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQRLRLGLTATHDIRKSFPLELFA 167

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR----HAAHAIPGMDAAESERF 229
H ++ + + P+V+ HP TG P L + H + +P ESE+
Sbjct: 168 HNEEEREKLLQ-TFKRNPPVHPVVRTHPVTGEPLLFVSEGFTTHINELP---EQESEQL 223

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L L + A Q +W GDV +WDNRC H+A
Sbjct: 224 LNFLFEHATQEQFHLRWKQDGDVAIWDNRCTQHKA 259

>ref|ZP_05824825.1| alpha-ketoglutarate-dependent taurine dioxygenase [Acinetobacter
sp. RUH2624]
gb|EEW99810.1| alpha-ketoglutarate-dependent taurine dioxygenase [Acinetobacter
sp. RUH2624]
Length = 293

Score = 87.0 bits (214), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 68/276 (24%), Positives = 111/276 (40%), Gaps = 38/276 (13%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I T+GA + + L L++ + A L H ++ F Q L+ Q A+ F
Sbjct: 7 NLNIEVIKPTIGAIHIDIDLNALNEQTTQIQQALLDHQVIFFRKQQLAPQVQADLARSF 66

Query: 65 G-----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
G +IE + +++ + + K D + N WH D T+
Sbjct: 67 GTLHVHPIYPSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFS 107

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLG 173
G V A +P VGG T ++ AA+ L + + +A H + + +
Sbjct: 108 KTPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQQKLRGLTATHDIRKSFPPLERFA 167

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR----HAAHAIPGMDAAESERF 229
H ++ + + P+V+ HP TG P L + H + +P ESE+
Sbjct: 168 HNEEEREKLLQ-TFKRNPPVHPVVRTHPVTGEPLLFVSEGFTTHINELP---EQESEQL 223

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L L + A Q +W GDV +WDNRC H+A
Sbjct: 224 LNFLFEHATQEQFHLRWKQDGDVAIWDNRCTQHKA 259

>ref|YP_003606990.1| Taurine dioxygenase [Burkholderia sp. CCGE1002]
gb|ADG17479.1| Taurine dioxygenase [Burkholderia sp. CCGE1002]
Length = 282

Score = 87.0 bits (214), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 73/274 (26%), Positives = 121/274 (44%), Gaps = 28/274 (10%)

Query: 6 LQITPTGATLGATVTGVHLA--TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+++ ++GA +TGV++A DD FA + +A L+H +L Q ++ + + FA+R
Sbjct: 1 MRVEQLTYSIGAEELTGVNVAHAHDDGLFAEIRSALLKHRVLFRLDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E VA S+ + G VR + +P + +D + AWHAD+T+ GA
Sbjct: 61 FGELE----DHPVAGSDPENPLVRIYKTPDQPNDRYE-----NAWHADATWREKPPQFGA 111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V P VGG T +A+M AY+ L +A + ARHS+ S +++ +
Sbjct: 112 VLRCVECPVGGDTMWANMVLAYENLPAYVKAQIADLRARHSIEASFGAAMPIEKRLALK 171

Query: 183 IGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE-----GLVD 235
+ P+V+ HPET L + E RF + L+
Sbjct: 172 AQF-----PDAEHPVVRTHPETEEKVLVFSFTSHFTNFHTPERVRFQDANPGAGDLLR 226

Query: 236 WACQAPRVHAHQ---WAAGDVVVWDNRCLLHRA 265
+ + +Q W + +WDNR H A
Sbjct: 227 YLISQAYIPEYQVRWRWQKNSIAIWDNRSTQHYA 260

>emb|CAY27436.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 87.0 bits (214), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 50/127 (39%), Positives = 70/127 (55%), Gaps = 12/127 (9%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH--VQQAGSAYIGYGMDDTTATP 193
T F DMRAAYDALD T+AL+ HS ++S+ LG ++ A++ P
Sbjct: 1 TEFQDMRAAYDALDAKTALIEDLVCEHSRIFSKGTGLGFSFTEELKAFV-----P 51

Query: 194 LRP-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
+R LV+ H +TGR SL+ HA I G E+ L L + A Q V++H+W GD
Sbjct: 52 VRQILVRTHRKTGRKSLYLSSHAGRIVGPVPEAMLLRELTEHATQREFVYSHKWQVGD 111

Query: 253 VVVWDNR 259
+V+WDNR
Sbjct: 112 LVMWDNR 118

>gb|ABO11873.2| taurine dioxygenase [Acinetobacter baumannii ATCC 17978]
Length = 289

Score = 87.0 bits (214), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 68/276 (24%), Positives = 111/276 (40%), Gaps = 38/276 (13%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I T+GA + + L L++ + A L H ++ F Q L+ Q A+ F
Sbjct: 7 NLNIEVIKPTIGAIHIDIDLNALNEQTQQIQQALLDHQVIFFRKQQLAPQAQADLARSF 66

Query: 65 G-----AIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYM 115
G +IE + +++ + + K D + N WH D T+
Sbjct: 67 GTLHVHPIYPSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFS 107

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLG 173
G V A +P VGG T ++ AA+ L + + +A H + + +
Sbjct: 108 KTPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQQKLRGLTATHDIRKSFPLELFA 167

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR----HAHAIPGMDAAESERF 229
H ++ + + P+V+ HP TG P L + H + +P ESE+
Sbjct: 168 HNEEEREKLLQ-TFKRNPPVVPVVRTHPVTGEPLLFVSEGFTTHINELP---EQESEQL 223

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L L + A Q +W GDV +WDNRC H+A
Sbjct: 224 LNFLFEHATQEQQFHLRWKQDGDVAIWDNRCTQHKA 259

>ref|ZP_08155918.1| taurine dioxygenase [Rhodococcus equi ATCC 33707]
gb|EGD22704.1| taurine dioxygenase [Rhodococcus equi ATCC 33707]
Length = 319

Score = 87.0 bits (214), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 81/285 (28%), Positives = 119/285 (41%), Gaps = 34/285 (11%)

Query: 4 TTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T+ ++P T+GA ++G+ L+ L + A L A L+ +L F Q + FA+
Sbjct: 40 TSFVSVPTPTIGAEISGIRLSGNLSERTLAELRRALLEWKVLFVRDQDIERSDHRGFAQ 99

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGA 122

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      +G +E+      +      AD      D+M      N WH D T+      + A
Sbjct: 100 LWGDLEQHPFFKYIQPGQTDADVVTLAK-----DVM TSGFEN-NWHNDVTWSEHPSFAA 152

Query: 123 VFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQAGSAY 182
      V A +P VGG T +AD AAYD L + R + +A H V++
Sbjct: 153 VLRAVEIPPVGGDTLWADTGAAYDLLPQDIRDRIDHLAAEHDWVHA----- 198

Query: 183 IGYGM-DTTATPLR-----PLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEG 232
      G GM + + LR      P+V+V PETGR L +      I G+D AES+ L
Sbjct: 199 FGAGMPEDSVAALRPEFPVPVQHPVVRVIPETGRRVLFVNVSFTRRILGVDTAESDELLRM 258

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
      L Q P      +W + +WDNR H A + RVM
Sbjct: 259 LYR-HIQRPEFQVRLRWQPNTIALWDNRTCQHYAASDYYPARRVM 302

```

>ref|ZP_02501235.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 112]
Length = 393

Score = 87.0 bits (214), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 84/273 (30%), Positives = 119/273 (43%), Gaps = 35/273 (12%)

```

Query: 6 LQITPTGATLGATVTGVHLATL---DDAGFAALHAAWLQHALLIFPGQHLSNDQ-QITFA 61
      L I P      +GA V G+ L +      +D F + A L H ++ F QH +D+ Q FA
Sbjct: 109 LSIRPLSGHIGAEVQGIQLGSQMAPNDIRF--ITQALLTHRVIFFRRQHHLDDRAQELFA 166

Query: 62 KRFGAIER---IGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADSTYM--P 116
      + FG I + +GG AI + + R +S      WH D T + P
Sbjct: 167 QAFGEIVKHPTMGKGTGSAILELHSHEGGRANS-----WHTDVTCLRPP 210

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY----SQSKL 172
      ++ V A +P GG T +A+ AAY L + + LV + A H + S+ +L
Sbjct: 211 KLS---VLRALALPDAGDTVWANTVAAYQHLPSSLQDLVDKLWAVHGNDFDYAASRVEL 267

Query: 173 GHVQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG 232
      H A Y T P+V++HPETG SLL+G +A D +S R E
Sbjct: 268 LHDVPAKEYRKKYAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRVQYDTHDSNRLYEI 326

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      L + WAAGDV +WDNR H A
Sbjct: 327 LQAHITRLENTVRWHWAAGDVVAIWDNRSTQHYA 359

```

>ref|ZP_02510493.1| taurine dioxygenase [Burkholderia pseudomallei BCC215]
Length = 272

Score = 87.0 bits (214), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 79/287 (27%), Positives = 114/287 (39%), Gaps = 31/287 (10%)

```

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
      ++TP LGA V V L+ DA + AA H +L F GQ LS + FA FG
Sbjct: 3 RLTPA---LGAIVDDVDLSNATDALRDDIRAALAHQVLFRRGQRLSAARHRDFAAGFGD 59

Query: 67 I-----ERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADSTYMPVMA 119
      +      +I+ + N D      + N WH D T+
Sbjct: 60 LHVHPIYPSHPDAREIMVLDNAVFD-----LQDNAIWHTDVTFTETPP 102

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQ 177
      + ++ +A +P GG T + AAYDAL E +A + +A+H + + G V
Sbjct: 103 RASILAAHTLPETGGDTLWGSFGAAYDALSERVKAQLDGLTAQHDFTKSFPLKRFG-VTA 161

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236

```

```

      A      T  +   P+V+ HPETGR +L  +      I G+   E   L  L
Sbjct: 162 EDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNEGFTTEIDGLPEEEGAALLRFLFAH 221

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
      +      +W  GDV  WDNR  +H A      K  RVM  + + G
Sbjct: 222 QSRPEFTLRWRWQPGDVAFWDNRSTIHYAVNDYGKAHRVMHRATIVG 268

```

```

>ref|ZP_04560819.1| taurine dioxygenase [Citrobacter sp. 30_2]
gb|EEH91795.1| taurine dioxygenase [Citrobacter sp. 30_2]
      Length = 283

```

Score = 86.7 bits (213), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 78/290 (26%), Positives = 120/290 (41%), Gaps = 26/290 (8%)

```

Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      L ITP G  +GA +TG  L   L D  F  L+ A L+H ++   Q ++  QQ  A RF
Sbjct: 5   LSITPLGPYIGAQITGADLTRPLSDNQFEQLYHAVLRHQVVFLRQQVITPQQQRALALRF 64

Query: 65  GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
      G +      G + + + +  D      +P + D+      WH D T++
Sbjct: 65  GDLHIHPVYPHAEGVEEIIVLDTHTND-----NPPDNDN-----WHTDVTFTIDTP 108

Query: 119 AQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
      GA+ +A+ +P+ GG T +   AAY+AL E  R L+   A H   S  + + +
Sbjct: 109 PAGAILAAKELPSAGDTLWTSGIAAYEALSEPFRQLLSGLRAEHDFRKSFEYKYRKTP 168

Query: 179 GSAYIGYGMDDTTATP-LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
      P L P+V+ HP  +G+ +L  +      I  +   ESE  L  L
Sbjct: 169 EEHQRWLDAVAKHPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVTEKESEALLSFLFAH 228

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
      +      +W  DV +WDNR  H A      R+M  + + G RP
Sbjct: 229 ITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILGDRP 278

```

```

>emb|CAY27287.1| alpha-KG-dehydrogenase [uncultured bacterium]
      Length = 119

```

Score = 86.7 bits (213), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 66/125 (52%), Gaps = 7/125 (5%)

```

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAAGSAYIGYGMDDTTATPLR 195
      T FADMRAAYDALDE  + +   HS +YS+ KLG      +      P+R
Sbjct: 1   TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLGADFTEEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
      LV+ HP TGR SL +  HA  I GM  E+   L  L ++A + P V++H W   D V
Sbjct: 55  QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMMLLLDLTEFATRDPYVYSHVWRLNDFV 114

Query: 255 VWDNR 259
      +WDNR
Sbjct: 115 MWDNR 119

```

```

>gb|AAS64596.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
      Length = 119

```

Score = 86.7 bits (213), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 49/124 (39%), Positives = 64/124 (51%), Gaps = 5/124 (4%)

```

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAAGSAYIGYGMDDTTATPLR 195
      T F DMRAAYDAL++ TR  +      HSL+YS+ LG  +      Y      L+

```

Sbjct: 1 TEFGDMRAAYDALNDETRTEIEDMICEHSLMYSRGSLGFLD-----YTEEEKQMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP GR SL + HA I GM E+ L L + A Q V+ H+W D+V+

Sbjct: 56 RLVRTHPVHGRKSLYLSSHAGGIIGMSVPEARVLLRDLNEHATQPEFVYVHKWTLHDLM 115

Query: 256 WDNR 259
WDNR

Sbjct: 116 WDNR 119

>ref|YP_001461543.1| taurine dioxygenase [Escherichia coli E24377A]
gb|ABV18165.1| taurine dioxygenase [Escherichia coli E24377A]
Length = 283

Score = 86.7 bits (213), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 74/288 (25%), Positives = 120/288 (41%), Gaps = 27/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAALQHALLIFFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF

Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVFLRDQAITPQQQRALAQR 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++

Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++

Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPEYKY-RKT 167

Query: 179 GSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ L + I + ESE L L

Sbjct: 168 EEEHQRWREAVAKNPPLLHPVVRTHPVSGKQVLFVNEGFTTRIVDVSEKESEALLSFLFA 227

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W D+ +WDNR H A R+M + + G

Sbjct: 228 HITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|ZP_04698014.1| putative taurine catabolism dioxygenase [Streptomyces roseosporus
NRRL 15998]
ref|ZP_04713212.1| putative taurine catabolism dioxygenase [Streptomyces roseosporus
NRRL 11379]
ref|ZP_06588916.1| taurine dioxygenase [Streptomyces roseosporus NRRL 15998]
gb|EFE79377.1| taurine dioxygenase [Streptomyces roseosporus NRRL 15998]
Length = 311

Score = 86.7 bits (213), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 87/290 (30%), Positives = 120/290 (41%), Gaps = 33/290 (11%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFA-ALHAALQHALLIFFPGQH-LSNDQQITFAKR 63
LQI P GA + GV L A L A L+ ++ F GQ+ + D Q+ +

Sbjct: 43 LQIEPLTPHFGAVIGGVDLTRPVTGTLADELRLQALLEWKVIFFRGQNGFTPDHQLALSGL 102

Query: 64 FGAIER---IGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQ 120
+G E IS + D K WH+D ++M +

Sbjct: 103 WGPPEPNPFFATTGTAGISRLAKDA-----KAAGNKNIWSDHSFMANPSL 148

Query: 121 GAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 180
GAV A VPAVGG T +ADM AAYD L E + + +A H S L + +Q +

Sbjct: 149 GAVLRAVEVPAVGDTMWADMAAAYDNLPEDLKERIEDLTAVHDWEASWGALMNEEQKAA 208

Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239


```
>ref|YP_001603688.1| alpha-ketoglutarate-dependent taurine dioxygenase
      [Gluconacetobacter diazotrophicus PAL 5]
ref|YP_002277264.1| Taurine dioxygenase [Gluconacetobacter diazotrophicus PAL 5]
emb|CAP57402.1| Alpha-ketoglutarate-dependent taurine dioxygenase
      [Gluconacetobacter diazotrophicus PAL 5]
gb|ACI52649.1| Taurine dioxygenase [Gluconacetobacter diazotrophicus PAL 5]
      Length = 318
```

Score = 86.7 bits (213), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 71/266 (26%), Positives = 116/266 (43%), Gaps = 24/266 (9%)

```
Query: 8  ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
      +T  G  +GA + G+ L+  L +  A ++ A L++ ++ F  Q L +  Q      RFG
Sbjct: 14  LTRLGGNIGAEIHGITLSPDLSEQDVAFVYKAMLEYKVIFFRQQSLDSAGQEQLGARFGT 73

Query: 67  IERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA--WHADSTYMPVMAQGAVF 124
      +      +  +  A GT      +K  G  A  WHAD T+M  +  ++
Sbjct: 74  L-----VAHPTVASAKGTNHIFE-----LKAQKGRAANTWHADMTFMATYPKASIL 119

Query: 125  SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV-YSQSKLGHVQQAGSAYI 183
      +      GG T +A+  AY AL +  + L +  A H+  Y  + L  V +  +I
Sbjct: 120  RSVHTAPYGGATLWANTATAYQALPQPLQELADKLWAIHTNDDYDHTDL--VVERDWDIFI 177

Query: 184  GYGMDTTATPL----RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
      +  +  A  +      PLV+VHPETG  SL++G  +  +  +S  L+  +  +  +
Sbjct: 178  RWSANVFAARIFETRHLVRVHPETGEKSLILGNFVKRLVDFNLPDSRALLDLFLSYVTR 237

Query: 240  APRVHAHQWAAGDVVVWDNRCLLHRA 265
      W  GDV +WDNR  LHRA
Sbjct: 238  PENTITWHWQPGDVAMWDNRALHRA 263
```

>ref|YP_842033.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Ralstonia
eutropha H16]
emb|CAJ97303.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Ralstonia
eutropha H16]
Length = 282

Score = 86.7 bits (213), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 72/273 (26%), Positives = 116/273 (42%), Gaps = 26/273 (9%)

```
Query: 6  LQITPTGATLGATVTGVHLATLD-DAG-FAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
      +  P  T+GA ++GV LA  DAG F  + A  LQH +L  Q ++  +  + FA+R
Sbjct: 1  MHAEPLTCTIGAELSGVSLADASRDAGLFTEIKALLLQHKVLFRLDQDITRAEHVAFARR 60

Query: 64  FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
      FG +E      V  S+ +  G V+ +  +  KV  ++H D+T+  G  V
Sbjct: 61  FGELE----DHPVVGSDPEHPGLVQIYKSPD----SKVEHYENSFHCDATWRQAPPMGCV 112

Query: 124  FSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
      PAVGG T + +M  AY  L +  +A +  A+HS+ ++  ++  +
Sbjct: 113  LRCVETPAVGDDTIWVNMGEAYRRLPQDIKARIEGLRAKHSIEHTFGANMPPEKRAALAA 172

Query: 184  GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE-----GLVDW 236
      + M      P+V+  HPETG  L +      +  RF +      L+  +
Sbjct: 173  QFPMVE-----HPVVRTHPETGEKVLVFNASTSHFANYHRDDVVRFGKDFMPGAGDLLHY 227

Query: 237  ACQAPRVHAHQ---WAAGDVVVWDNRCLLHRA 265
      C  +  +Q  W  V +WDNRC  H  A
Sbjct: 228  LCAQAEIPEYQVRWRWKKNSVAIWDNRCTQHYA 260
```

>emb|CAY27499.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.7 bits (213), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 67/125 (53%), Gaps = 7/125 (5%)

```
Query: 136  TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
      T F  DMRAAYDALD+ T+A V      HSL+YS+  +G      +      P+R
Sbjct: 1  TEFGBMRAAYDALDDRTKAEVAGLVCEHSLLSYRQAVGFTDFTPEEISNF-----QPVR 54
```

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
PLV+V TGR SL + HA I G ES FL L++ A + V++H W D+V
Sbjct: 55 HPLVRVQKATGRKSLFLSAHAGVIVGWSVPESRAFLRDLIEHATRPEFVYSHSWRQHDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|YP_004005855.1| taurine dioxygenase [Rhodococcus equi 103S]
emb|CBH47170.1| taurine dioxygenase [Rhodococcus equi 103S]
Length = 299

Score = 86.7 bits (213), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 79/277 (28%), Positives = 115/277 (41%), Gaps = 32/277 (11%)

Query: 5 TLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
L P ++GA V GV L + DDA FA L + L+H +L F Q +S + + A+
Sbjct: 17 NLDARPLTCSIGAEVDGVDLGEVSRDDALFAELKSRLLLEHKVLFRRDQDMSRAEHVALAQ 76

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGA 122
RFGA+E V S+ + G VR + + D + A+H D+T+ G
Sbjct: 77 RFGALE---DHPVVGSDPEHPGLVRIYK--DLDSAPEAF--ENAYHCDATWRVNPMPGC 128

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V PAVGG T + +M AY L E + + ARHS+ S ++Q
Sbjct: 129 VLRCVEGPAVGGDTIWNMALAYARLPERVKERIEGLRARHSIEASFGARLPQIEQRLEL- 187

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA-- 240
+ P+V+VHPETG L + + AE+ R +D+A A
Sbjct: 188 ----KERFPDAEHPVVRVHPETGEKILFVNSFTTHLTNFHTAENVR---SGIDYAPGAGD 240

Query: 241 -----PRVHAH-QWAAGDVVVWDNRCLLHRA 265
P +W V +WDNR H A
Sbjct: 241 LLRYLQTQATIPEYQVRWRWTKNSVAIWDNRSTQHYA 277

>ref|ZP_06414550.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EUN1f]
gb|EFC82603.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EUN1f]
Length = 277

Score = 86.7 bits (213), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 78/282 (27%), Positives = 116/282 (41%), Gaps = 20/282 (7%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQ-HALLIFPGQHLSNDQQITFAKRFGA 66
++P +G V G+ L D AA A L+ H ++++ ++ + + F++ G
Sbjct: 5 VSPISPEVGVEVAGLRGHQLVDPAAAAECQALLEKHGVVVYRELNIDDADLVAFSRMLGT 64

Query: 67 IERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
+ G I + V PAE + G WH D + + + +A
Sbjct: 65 VVVAPTGGIEGLPEVSKITL----DPAE-SVLAAYRKGTFFWHIDGANDELPQKATLLTA 119

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 186
V GG T FA+ AAYDAL + +A HS SQ A
Sbjct: 120 RQVSDEGGDTEFANTYAAAYDALTDDEKAQFATLRVVSFAASQRL-----AEPDAS 170

Query: 187 MDTTATPLRPLVKVHP-----ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAP 241
T A R + HP +GR SLL+G + G ES L+ L+ W+ Q
Sbjct: 171 EKTRALWARVPSREHPLVWTRRSRGRKSLLVGATTSHVVGWPEEESRALLDRL LAWSTQPR 230

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
V H W GD+V+WDN +LHRA P+ R+M + L G

Sbjct: 231 FVLRHHWRPGDLVIWDNTGMLHRAIPYTATSRRLMHRTTLVG 272

>gb|ACG80570.1| TfdA [uncultured bacterium]
Length = 119

Score = 86.7 bits (213), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 50/128 (39%), Positives = 64/128 (50%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T F DMRAAYDALDE + + HS +YS+ KLG + D T +
Sbjct: 1 TEFGDMRAAYDALDERLKQQIEDLVCLHSNMYSRGKLG-----LADFTDEERTAFK 51

Query: 196 P----LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251
P LV+ HP TGR SL + HA I GM E L L ++A + V++H W
Sbjct: 52 PVRQRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEGRMLLLDLTEFATREQFVYSHMWRVN 111

Query: 252 DVVVWDNR 259
D V+WDNR
Sbjct: 112 DFVMWDNR 119

>ref|ZP_06056572.1| alpha-ketoglutarate-dependent taurine dioxygenase [Acinetobacter
calcoaceticus RUH2202]
gb|EEY77871.1| alpha-ketoglutarate-dependent taurine dioxygenase [Acinetobacter
calcoaceticus RUH2202]
Length = 293

Score = 86.7 bits (213), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 69/275 (25%), Positives = 108/275 (39%), Gaps = 36/275 (13%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I T+GA + + L L++ + A L H ++ F Q L+ Q A+ F
Sbjct: 7 NLNIEVIKPTIGAIHIDIDLNALNEQTQQIQQALLDHQVIFFRKQQLAPQAQADLARSF 66

Query: 65 GA-----IERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
G+ IE + +++ + + K D + N WH D T+
Sbjct: 67 GSLHVVHPIYPSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFS 107

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYD---ALDEATRALVHQRSARHSLVYSQSK 171
G V A +P VGG T ++ AA+ L + R L R S + +
Sbjct: 108 KNPLGCVLQAIKIPVGGDTLWSNTAAFKGLPLELQDKLRGLTATHDIRKS--FPLER 165

Query: 172 LGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL 230
H ++ + + P+V+ HP TG P L + I + ESE+ L
Sbjct: 166 FAHNEEECEKLLQ-TFKRNPPVHPVVRTHPVTGEPLLFVSEGFTTRINELSEQESEQLL 224

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L + A Q +W GDV +WDNRC H+A
Sbjct: 225 NFLFEHATQEKFHLRWKQDGDVAIWDNRCTQHKA 259

>emb|CAY27249.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27262.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27293.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.7 bits (213), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 66/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T FADMRAAYDALDE + + HS +YS+ KLG + P+R
Sbjct: 1 TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLGGLADFTEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I GM E+ L L ++A + P V++H W D V
Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMLLLLDLTEFATRDPFVYSHVWRLNDFV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|ZP_04640756.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia
mollaretii ATCC 43969]
gb|EEQ10707.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia
mollaretii ATCC 43969]
Length = 276

Score = 86.7 bits (213), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 78/290 (26%), Positives = 124/290 (42%), Gaps = 30/290 (10%)

Query: 8 ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
+TP G +GA V +++A L D F L+ A L+H +L F Q ++ QQ A RFG
Sbjct: 1 MTPLGPYIGAVVENINIRPLGDGQFEQLYHALLKHQVLFERNQPITPLQRELAGRFGD 60

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
+ +I+ + ++P + D+ WH D T++
Sbjct: 61 LHIHPVYPHTKECEEIIVLD-----THDNNPPDNDN-----WHTDVTFIENPP 103

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS--QSKLGHVQQ 177
GA+ +A+ +PA GG T ++ AAY+ L + L+ A H +S + K +
Sbjct: 104 LGAILAAKQLPATGGDTLWSSGIAAYETLSAPFKQLLAGLRAEHDFAHSPFEHKNRGTP 163

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
++ + L P+V+ HP TGR +L + I + A ES+ L L
Sbjct: 164 EHQRWL-LAKENNPPLLHPVVRTHPVTGRQALFVNEGFTTRIVDLSAKESDAILRFLFAH 222

Query: 237 ACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
A + +W DV +WDNR H A RVM + + G RP
Sbjct: 223 ATKPEFQVRWRWQQDDVAIWDNRVTQHYANADYLPQRRVMHRATILGDRP 272

>gb|ACG80580.1| TfdA [uncultured bacterium]
Length = 119

Score = 86.7 bits (213), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 50/128 (39%), Positives = 64/128 (50%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DMRAAYDALDE + + HS +YS+ KLG + D T +
Sbjct: 1 TEFCDMRAAYDALDERLKQQIEDLVCLHSNMYSRGKLG-----LADFTDEERTAFK 51

Query: 196 P----LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251
P LV+ HP TGR SL + HA I GM E L L ++A + V++H W
Sbjct: 52 PVRQRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEGRMLLLDLTEFATREQFVYSHMWRVN 111

Query: 252 DVVVDNR 259
D V+WDNR
Sbjct: 112 DFVVDNR 119

>ref|YP_003611636.1| taurine dioxygenase [Enterobacter cloacae subsp. cloacae ATCC
13047]
gb|ADF60687.1| taurine dioxygenase [Enterobacter cloacae subsp. cloacae ATCC
13047]

Length = 282

Score = 86.7 bits (213), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 75/288 (26%), Positives = 123/288 (42%), Gaps = 27/288 (9%)

```
Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L ITP G +GA V+G+ + L D F L+ A L+H ++ Q ++ QQ A RF
Sbjct: 5   LTITPLGPYIGAQVSGLDVTRPLSDNQFEQLYHAVLRHQVVFLREQAITPQQQRALALRF 64

Query: 65  GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM 118
          G + + + + D +P + D+ WH D T++
Sbjct: 65  GDLHIHPVYPHAEGVEEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119  AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
          GA+ SA+++P GG T +A AA++AL R L+ A H S + + ++
Sbjct: 109  PAGAILSAKLLPETGGDTLWASGIAAFEALSAPFRTLLSGLRAEHDFKKSFEQYKY-RKT 167

Query: 179  GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
          + + + P L P+V+ HP TG+ +L + I + ESE L L
Sbjct: 168  EAEHQRWQEAVAKHPPLLHPVVRTHPVTGKQALFVNEGFTTRIVDVTEKESEALLRFLFA 227

Query: 236  WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          + +W D+ +WDNR H A R+M + + G
Sbjct: 228  HITKPEFQVRWRWQENDLAIWDNRVTQHYANADYLPQRRIMQRATILG 275
```

>gb|ADY81414.1| taurine dioxygenase [Acinetobacter calcoaceticus PHEA-2]
Length = 293

Score = 86.7 bits (213), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 66/273 (24%), Positives = 109/273 (39%), Gaps = 32/273 (11%)

```
Query: 5   TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L I T+GA + + L L++ + A L H ++ F Q L+ Q A+ F
Sbjct: 7   NLNIEVIKPTIGAIHIDIDLNALNEQTTQQIQQALLDHQVIFFRKQQLAPQAQADLARSF 66

Query: 65  G-----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
          G +IE + +++ + + K D + N WH D T+
Sbjct: 67  GTLHVHPPIYPSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFS 107

Query: 116  PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLG 173
          G V A +P VGG T ++ AA+ L + + +A H + + +
Sbjct: 108  KTPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQQLRGLTATHDIRKSFPLELFA 167

Query: 174  HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
          H ++ + + P+V+ HP TG P L + I + ESE+ L
Sbjct: 168  HNEEEREKLLQ-TFKRNPPVHPVVRTHPVTGEPLLFVSEGFTTRINELPEQESEQLLNF 226

Query: 233  LVDWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
          L + A Q +W GD+ +WDNRC H+A
Sbjct: 227  LFEHATQEQFHLRWKWQDGDIAIWDNRCTQHKA 259
```

>ref|YP_111581.1| taurine dioxygenase [Burkholderia pseudomallei K96243]
ref|YP_001076170.1| taurine dioxygenase [Burkholderia pseudomallei 1106a]
ref|ZP_01768758.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 305]
ref|ZP_03456606.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 576]
ref|ZP_03791681.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei Pakistan 9]
ref|ZP_04813042.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 1106b]

ref|ZP_04893420.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei Pasteur 52237]
ref|ZP_04968854.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 406e]
emb|CAH39048.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia
pseudomallei K96243]
gb|ABN93706.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 1106a]
gb|EBA46669.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 305]
gb|EDO88031.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 406e]
gb|EDO90258.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei Pasteur 52237]
gb|EEC31743.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 576]
gb|EEH27989.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei Pakistan 9]
gb|EES23667.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 1106b]
Length = 277

Score = 86.7 bits (213), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 81/293 (27%), Positives = 115/293 (39%), Gaps = 29/293 (9%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T L +T LGA V V L+ DA + AA H +L F GQ LS + FA
Sbjct: 2 TRLTLRLTPALGAIVDDVDLSNATDALRDDIRAALAHQVLFRRGQRLSAARHRDFAAG 61

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
FG + +I+ + N D + N WH D T+
Sbjct: 62 FGD LHVHP IYSPHDAREIMVLDNAVFD-----LQDNAIWHTDVTFTTE 104

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSILV--YSQSKLGH 174
+ ++ +A +P GG T + AAYDAL +A + +A+H + + G
Sbjct: 105 TPRASILAAHTLPETGGDTLWGSFGAAYDALSGRVKAQLDGLTAQHDFTKSFPLKRF- 163

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL 233
V A T + P+V+ HPETGR +L + I G+ E L L
Sbjct: 164 VTAEDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNEGFTTEIDGLPEEEGAALLRFL 223

Query: 234 VDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
+ +W GDV WDNR +H A K RVM + + G RP
Sbjct: 224 FAHQSRPEFTLRWRWQPGDVAFWDNRSTIHYAVNDYGKAHRVMHRATIVGDRP 276

>emb|CAY27279.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27295.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.7 bits (213), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 66/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSILVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALDE + + HS +YS+ KLG + P+R
Sbjct: 1 TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLGADFTEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I GM E+ L L ++A + P V++H W D V
Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMLLLLLTFEATRDPPFVYSHIWRNLDFV 114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>ref|ZP_05968819.1| taurine dioxygenase [Enterobacter cancerogenus ATCC 35316]
gb|EFC55760.1| taurine dioxygenase [Enterobacter cancerogenus ATCC 35316]
Length = 282

Score = 86.7 bits (213), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 77/289 (26%), Positives = 123/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA V G+ + L D F L+ A L+H ++ Q +S QQ A+RF
Sbjct: 5 LIITPLGPNIGAQVAGLDVTRPLSDNQFEQLYHAVLRHQVFLREQAISPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVM 118
G + G + + + + D +P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPHAEGVEEIIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P GG T +A AA++AL RAL+ A H S + + + +
Sbjct: 109 PAGAILAAKQLPETGGDTLWASGIAAFEALSAPFRALLSGLRAEHDFKKSFEYKY-RNS 167

Query: 179 GSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP TG+ +L + I + ESE L G +
Sbjct: 168 DEEHQRWQEAVAKHPPLLHPVVRTHPVTGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G
Sbjct: 227 AHITRPEFQVRWRWQENDLAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>emb|CAY27540.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.7 bits (213), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 47/124 (37%), Positives = 66/124 (53%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADM AYDALD T+ + HS +YS+ +LG + + ++
Sbjct: 1 TEFADM PGAYDALDSETKDEIEDLVCEHSQIYSRQQLGFTDFTEEERVRF-----KPVIQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 255
LV+ HP TGR SL + HA I G E+ FL+ L + A Q V++H+W GD+V+
Sbjct: 56 RLVRTHTPTTGRKSLYLSSHAGGIVGWVPEARAFKDLNEHATQRFVYSHKWRVGDVLM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>emb|CAY27507.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.7 bits (213), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 48/125 (38%), Positives = 66/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DMRAAYD LD T+A + HSL+YS+ LG + + + TP+R
Sbjct: 1 TEFGDMRAAYDGLDTKTKAEIEDLVCEHSLIYSRGTLGFTELSDEERRMF-----TPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + H I G E+ F+ L + A Q ++H+W D+V
Sbjct: 55 QRLVRAHPVTGRKSLYLSSHIGTIVGWPMPEARAFIRDLTEHATQKQFTYSHKWRQYDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|YP_001683427.1| taurine catabolism dioxygenase TauD/TfdA [Caulobacter sp. K31]
gb|ABZ70929.1| Taurine catabolism dioxygenase TauD/TfdA [Caulobacter sp. K31]
Length = 287

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 76/277 (27%), Positives = 113/277 (40%), Gaps = 30/277 (10%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
L I+ GA + + L + DA + AA+ +H ++ GQ ++ D + F RFG
Sbjct: 9 LTISELKPGFGAQIHDIDLPSSSDAEIDKVVAAFHRHGAVVLRGQDMTPDDLRFIFGRFG 68

Query: 66 AIER-----IGGGDIVAISNVKADGT-VRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
E G I +SN DG + H+ + WH D +Y P
Sbjct: 69 DAEDHTQTRFTLPGYPKIFILSNRVVDGKPLGAHN-----DGVGWHTDYSYKP 116

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY--SQSKLGH 174
+ A VP G T AD AA++AL +A + S HS + + + G
Sbjct: 117 EPVMLTMLYAVEVPDEGSDTLLADGCAAWNALSPKQAEELLPLSLHHSYKHFMATRQFGQ 176

Query: 175 VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLL--IGRHAHAIPGMDAAESERFLEG 232
Q D PL++ HP GR +L G I G E L+
Sbjct: 177 QQTLSPELEAANPDVE----HPLIRTHPADGRKALWPSTGTVTEVI-GKPGPEGLALLDE 231

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD 269
LV++ V+ H+WA GD+++WDNRC LH +D
Sbjct: 232 LVEFMTGDDEFVYRHKWAKGDLMLWDNRCTLHTGTLYD 268

>ref|YP_003280390.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
CNB-2]
gb|ACY35094.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
CNB-2]
Length = 282

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 77/274 (28%), Positives = 116/274 (42%), Gaps = 28/274 (10%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 63
+QI P +GA + V LA DD FA + A L+H +L Q +S + + FA+R
Sbjct: 1 MQINPLTCAIGAELVDVQLADALRDDGLFAEIKTALLKHKVFLRRQSSISRAEHVGFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E V S+ + G V+ + +P + D + +WH D+T+ V G
Sbjct: 61 FGELE----DHPVVGSDPEHPGLVQIYKTPDKPLDRYE-----NSWHCDATWREVPPMGC 111

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSGLGHVQQAGSAY 182
V P VGG T +A+M AY+ L + ++ ARHS+ + G A
Sbjct: 112 VLRCVECPVGGDTMWANMALAYEMLPSHIKDVIAPLRARHSI---ECTFGAAMPAQKRL 168

Query: 183 IGYGMDTATPLRPLVKVHPETGRPSLLIG-----RHAHAIPGMDAAE-SERFLE 231
A P+V+ HPETG L + A+ G D + S L+
Sbjct: 169 ALKAQFPDAE--HPVVRTHPETGEKVLVFSGFTTHFTNFHTPANVRVQDFTQGSSSLQ 226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L+ A +W G + +WDNR H A
Sbjct: 227 FLISQAAIPEYQVRWRWEPGSIAIWDNRATQHYA 260

>emb|CAY27543.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 51/127 (40%), Positives = 69/127 (54%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTA--TP 193
T FADMRAAYD LD+ T+A + HSL+YS+ LG ++ + D P
Sbjct: 1 TEFADMRAAYDDLDEETKAEIEPMICEHSLMYSRGSLG-----FLDFTEDKRMFKP 52

Query: 194 LR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
+R LV+ HP TGR SL + HA AI G E+ L L + A V+ H+W+ D
Sbjct: 53 VRQKLVRAHPVTGRKSLYLSSHAGAILGYTMPEARIIILRDLTEHATSPKYVYTHKWSQWD 112

Query: 253 VVVWDNR 259
+V+WDNR
Sbjct: 113 LVMWDNR 119

>emb|CAY27472.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 51/124 (41%), Positives = 65/124 (52%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRA YDALDE T+ALV HS +YS+ LG + + A +
Sbjct: 1 TEFGDMRAGYDALDEETKALVRDLVCEHSQIYSRGVLGFTE-----FTEEERRKNAPVPQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP TGR SL + HA I G E+ L L + A Q V+AH+W D+V+
Sbjct: 56 RLVRRHPTGRSLFLSSHAGTIVGWPVPEARALLRDLTEHATQREFVYHRWRQYDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>ref|YP_295875.1| taurine dioxygenase [Ralstonia eutropha JMP134]
gb|AAZ61031.1| Taurine dioxygenase [Ralstonia eutropha JMP134]
Length = 303

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 73/280 (26%), Positives = 118/280 (42%), Gaps = 35/280 (12%)

Query: 4 TTLQITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
+++++ P T+GA ++ V+L A DD A + A L+H +L F Q ++ Q + FA
Sbjct: 19 SSIRVEPLTCTIGAELSNVNLGAAEDDGQMAEIRALLKHRVLFRRDQDITRAQHVAFA 78

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQH----SPAEWDDMMKVIVGNMAWHADSTYMPV 117
RFG +E V S+ G V+ + SP E ++ +WH D+T+
Sbjct: 79 SRFGKLE----DHPVVGSHPDYPGLVQIYKTPDSPPERNEN-----SWHTDATWREK 126

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
G V P VGG T + +M AY+ L E + + ARHS+ S +++
Sbjct: 127 PPLGCVLRICPPVGGDTMWVNMVEAYNQLPEEIKTKIGSLRARHSIEASFGAAMPIEK 186

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERF----- 229
+ Y P+V++HPETG L + G + + RF
Sbjct: 187 RLALKAQY-----PDAEHPVVRIHPETGEKVLVNGSFTHFTNYPANVRFGLDKSPG 241

Query: 230 LEGLVDWACQAPRVHAHQ---WAAGDVVVWDNRCLLHRA 265

L+++ + +Q W V WDNR H A
Sbjct: 242 ASNLLNYLTSQAMIPEYQVRFWRKKNSVAFWDNRSTQHYA 281

>ref|XP_381837.1| hypothetical protein FG01661.1 [Gibberella zeae PH-1]
Length = 380

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 75/263 (28%), Positives = 112/263 (42%), Gaps = 25/263 (9%)

Query: 14 TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG 73
T+G V GV L++L DAG L + ++ F Q + D I+ A +FG G
Sbjct: 103 TIGTEVEGVQLSSLSDAGKDELARYVAERKVVAFRNQDFA-DLPISSEALKFGGY---FGR 158
Query: 74 DIVAISNVKADGTVRQH-----SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE 127
+ ++ +G H ++D K V ++AWH+D TY
Sbjct: 159 HHIHPTSGSPEGHPEIHLVHRSAGDKSYEDFFKTRVSSVAWHSIDITYEQPPGTTFLYVL 218
Query: 128 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 187
P GG T FA+ AY+ L + L+H A HS + + +A + G
Sbjct: 219 DNPDTGGDTLFAANTVEAYNRLSPTFQKLLHGLKATHSGI-----EQVNASVKKGS 268
Query: 188 DTTATPL---RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRV 243
P+ P+V+ HP TG SL + + +I G+ ES+ L L +
Sbjct: 269 IKRREPVVNEHPIVRTHPVTGEKSLYVNPQFTRSIIVGLKKEESDAILNFLFEHIAWGADF 328
Query: 244 HAH-QWAAGDVVVWDNRCLLHRA 265
HA +WA G VVVWDNR + H A
Sbjct: 329 HARVKWAKGTVVVWDNRSVQHTA 351

>emb|CAY27483.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 53/125 (42%), Positives = 67/125 (53%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALD+ T+A V HSL+YS+S +G + P+R
Sbjct: 1 TEFADMRAAYDALDDRTKAEVAGLVCEHSLLYSRSVAVGFTDFTPEEVSNF-----QPVR 54
Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+V TGR SL + HA I G ES FL L + A Q V++H W D+V
Sbjct: 55 HRLVRVQKATGRKSLFLSAHAGVIVGWSVPESRAFLRDLTEHATQREFVYSHAWRQHDLV 114
Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|ZP_07617352.1| taurine dioxygenase [Escherichia coli TA280]
Length = 283

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 74/288 (25%), Positives = 121/288 (42%), Gaps = 27/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVFLRDQAITPLQQRALAQR 64
Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFTIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPEYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L L
Sbjct: 168 EEEHQRWREAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALLSFLFA 227

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W D+ +WDNR H A R+M + + G
Sbjct: 228 HITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>emb|CAY27448.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 49/124 (39%), Positives = 65/124 (52%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAAGSAYIGYGMDDTTATPLR 195
T F DMRAAYDALD+ +A + HSL+YS+ LG Y + L+
Sbjct: 1 TEFADMRAAYDALDDEMKAIEDLICEHSLMYSRGSLGFTD-----YSDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP GR SL + HA A+ GM E L L + A + V+AH+W D+V+
Sbjct: 56 RLVRTHPVHGRKSLYLSSHAGAVRGMSVPEGRLLLRDLNEHATRPEFVYAHKWTLHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>ref|YP_001704936.1| putative dioxygenase [Mycobacterium abscessus ATCC 19977]
emb|CAM64282.1| Putative dioxygenase [Mycobacterium abscessus]
Length = 316

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 70/264 (26%), Positives = 115/264 (43%), Gaps = 23/264 (8%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
+ + G +GA V G+ L L A+ A + +L+F QH L + Q FA
Sbjct: 15 ITVEKLGEHIGARVNGIELRGDLSADRVEAIRLALAINKVLVFTQHHLLDAGQYAF-- 72

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
R+ G + V++ GT +++ + WH D T++ + + +V
Sbjct: 73 -----RLLGEPTLPHPTVRSHGT-----ELLNLEGAANGWHTDVTFFVDRIKASV 117

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY----SQSKLGHVQQA 179
+P+ GG T +A AAY+ L + R+LV A H+ +Y S + G +
Sbjct: 118 LRPVTLPSYGGATTWASTVAAAYQLPKPLRSLVDDLWATHTNLYDYASSGASGGVSAERR 177

Query: 180 SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
+AY + + P+V+VHPETG SLL+G+ + + +AE + L +
Sbjct: 178 AAYYTEFTSSRYETVHPVVRVHPETGERSLLLGQFVKSFQDLPSAEFASLFLQLQARITK 237

Query: 240 APRVHAHQWAAGDVVVDNRCLLH 263
W GDV +WDNR H
Sbjct: 238 LENTFRWNWRLGDVAIWDNRATQH 261

>ref|NP_106571.1| hypothetical protein mll5998 [Mesorhizobium loti MAFF303099]
dbj|BAB52357.1| mll5998 [Mesorhizobium loti MAFF303099]

Length = 295

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 71/257 (27%), Positives = 110/257 (42%), Gaps = 31/257 (12%)

Query: 13 ATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGAIERI 70
A +GA + V L A L D AA++ L+H ++ F Q HL + Q FA RFG +
Sbjct: 21 ARIGAEIRNVKLSADLPDRITAAINGLVLEHKVVFVRDQGHLLDAGQERFALRFGKLSPY 80

Query: 71 --GGGDIVAIISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV 128
G I I + D G WH D + M + AV
Sbjct: 81 PEGTTPYIDIDTARGD-----TGAYVWHIDWSCMDAYPKIAVLRGVT 122

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 188
+P VGG T +++ AAY L + L ++ A HS S +++ + G ++
Sbjct: 123 IPLVGGDTVWSNTAAAYLDLPLPLQLRLANELWAVHSFPGS-----YLRSSSTEPNTGPMIE 177

Query: 189 TTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQW 248
T P+V+VHPETG +L++G + G+ + +R L+ +W
Sbjct: 178 TE---HPVVRVHPETGERTLVLGYYVTRFVGVISKYDGRLLDLFESHVTAQENTVRWKW 233

Query: 249 AAGDVVVWDNRCLLHRA 265
GD+ +WDNR +H A
Sbjct: 234 KEGDIAIWDNRATMHCA 250

>ref|ZP_07303772.1| taurine catabolism dioxygenase [Streptomyces viridochromogenes DSM

40736]

gb|EFL32141.1| taurine catabolism dioxygenase [Streptomyces viridochromogenes DSM 40736]

Length = 297

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 79/283 (27%), Positives = 120/283 (42%), Gaps = 19/283 (6%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++I A +GA V GV + LD+ + AL A H L+F + L + Q F + F
Sbjct: 3 IEIHKVTANIGARVEGVDITRPLDEETYALREALNAHKALVFDAEGLDDAGQQAQFVRHF 62

Query: 65 GAIERIGGGDIVAIISNVKADGTVRQHSPAEWDDMMKVIVGNMA--WHADSTYMPVMAQGA 122
G I A V A P + + G A WH D T++ Q +
Sbjct: 63 GDI-----TTAHTVPAVDGAPNVLPVDSEG-----GRAANHWHTDVTFLNPPQAS 109

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS-KLGHVQQAGSA 181
+ VP GG T A AAY L ++ R+L A H+ Y + V +A
Sbjct: 110 SLRSITVPPYGGETLIASSAAAYRNLPDSLRLADTLWAEHTNDYDYAVPEESVDDEQAA 169

Query: 182 YIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAP 241
+ P+V+VHP TG L IG A I G+ ES + L+ L + +
Sbjct: 170 RRAQFTSIKYRTVHPVVRVHPLTGERGLFIGGFAQRIVGLSPGESRKILDLLQAYVTRPE 229

Query: 242 RVHAHQWAAAGDVVVWDNRCLLHRA-EPWDFKLPRVMWHSRLAG 283
+ H+W+ +V++DNR H A + +D + PR + +AG
Sbjct: 230 NILRHRWSPNQLVLFNDRITQHYAVDNYDGR-PRRLHRVTVAG 271

>ref|YP_001345668.1| hypothetical protein PSPA7_0272 [Pseudomonas aeruginosa PA7]

gb|ABR84054.1| hypothetical protein PSPA7_0272 [Pseudomonas aeruginosa PA7]

Length = 300

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 78/283 (27%), Positives = 121/283 (42%), Gaps = 18/283 (6%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQ-QITFAKR 63
L I P +GA + GV L+ LD A A+ AA ++H ++ F GQ +DQ Q FA
Sbjct: 14 LDIQPVAGRIGAEIRGVTLSEGLDAATVEAIQAALVRHKVIFFRGQSQLEDDQTQEAF AHL 73

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA V 123
G + VA V + R + + + +WH D T++ + ++
Sbjct: 74 LG-----EPVAHPTVPSREGTRFLLLELDGAEGRR A-----NSWHTDVT FVEAYPKASI 121

Query: 124 FSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL---GHVQQAGS 180
+ V P GG T +A+ +AY L R L + A HS Y + + V+Q +
Sbjct: 122 LRSV VAPESGGDTVWANTASAYADLPAELRELADRLWAVHSNEYDYAGVKPSASVEQLEN 181

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
Y T P+V+VHP++G +LL+G + G+ +S L +
Sbjct: 182 -YRKVFTSTVYETEHPVVRVHPQSGERTLLLGHFVKRLKGLSQHDSAHLFAVLQGHVTRL 240

Query: 241 PRVHAHQWAAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+W AGDV +WDNR H A PR++ L G
Sbjct: 241 ENTVRWRWQAGDVAIWDNRATQHAYAIDDYGNQPRMVRRVTLGG 283

>ref|XP_001383599.2| hypothetical protein PICST_43041 [Scheffersomyces stipitis CBS 6054]
gb|ABN65570.2| predicted protein [Scheffersomyces stipitis CBS 6054]
Length = 383

Score = 86.3 bits (212), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 76/270 (28%), Positives = 108/270 (40%), Gaps = 15/270 (5%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN--DQQI 58
A T ++ LG+ V G+ L+ LDD G L Q + IF Q S+ + +
Sbjct: 78 ANGTHKVKVKTPKLGSEVHGIQLSQLDDKGKNDLALFLAQRGV AIFRDQDFSSYGPEFAV 137

Query: 59 TFAKRFGAIE-RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV 117
+ K FG + G + T R S E D + N+ WH+D +Y
Sbjct: 138 EYKGKYGPLHVHPTSGSPEGFPQLHI--TFRGASQNELDSAFETR TNNIGWHS DVS YELN 195

Query: 118 MAQGA VFSAEV VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
Q FS P GG T FAD + AY L + ++ H L S+ + H+ Q
Sbjct: 196 PPQITFFSVLEGPESGGDTIFADTQEAYKRLSPTMQKML---EGLHVLHTSEDQ-AHINQ 251

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDW 236
A G + + PLV+ HP T L + R I + ESE LE L +
Sbjct: 252 AAG---GICRRAPVSNIHPLVRQHPVTKEKFLFLNREFGR RIVELKEE ESENLLLEFLFNH 308

Query: 237 ACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
A + W VV+WDNR +H A
Sbjct: 309 VESAHDQLRANWEPNTTVLWDNRRTVHSA 338

>emb|CAY27338.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.3 bits (212), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 49/125 (39%), Positives = 67/125 (53%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FAD+RAAYDAL+E + + HS +YS+ KLG + P+R
Sbjct: 1 TEFADIRAAAYDALEGLKNQIEDLVCLHSNMYSRGKLG LADFTDEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDVV 254
LV+ HP TGR SL + HA I GM E+ L L ++A + P V++H W D+V

Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMLLLLDLTEFATREPFVYSHAWRVNDLV 114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>ref|YP_001063217.1| taurine dioxygenase [Burkholderia pseudomallei 668]
gb|ABN86658.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 668]
Length = 335

Score = 86.3 bits (212), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 81/293 (27%), Positives = 115/293 (39%), Gaps = 29/293 (9%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T L +T LGA V V L+ DA + AA H +L F GQ LS + FA
Sbjct: 60 TRLTLTRLTPALGAIVDDVDLSNATDALRDDIRAALAHHQVLFRRGQRLSAARHRDFAAG 119

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMP 116
FG + +I+ + N D + N WH D T+
Sbjct: 120 FGDLHVHPIYPSHPDAREIMVLDNAVFD-----LQDNAIWHTDVTFTTE 162

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSIV--YSQSKLGH 174
+ ++ +A +P GG T + AAYDAL +A + +A+H + + G
Sbjct: 163 TPPRASILAAHTLPETGGDTLWGSFGAAYDALSGRVKAQLDGLTAQHDFTKSFPLKRFG- 221

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL 233
V A T + P+V+ HPETGR +L + I G+ E L L
Sbjct: 222 VTAEDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNEGFTTEIDGLPEEEGAALLRFL 281

Query: 234 VDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
+ +W GDV WDNR +H A K RVM + + G RP
Sbjct: 282 FAHQSRPEFTLRWRWQPGDVAFWDNIRSTIHYAVNDYGKAHRVMHRATIVGDRP 334

>emb|CAY27534.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.3 bits (212), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 51/128 (39%), Positives = 69/128 (53%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSIVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALD+AT+A + HS+V+S+ ++G + A LR
Sbjct: 1 TEFADMRAAYDALDDATKAEIEDLVTEHSIVFSREQIGFSDYEAAH-----ADKLR 51

Query: 196 P----LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251
P LV HP TGR SL + H I G E+ F+ L++ A Q V+ H+W
Sbjct: 52 PVRHRLVVTHPVTGRKSLFLAAHIGTILGWPQPEAMAFIRDLMEHATQPQFVYVHRWTRH 111

Query: 252 DVVVWDNR 259
D+V+WDNR
Sbjct: 112 DLVMWDNR 119

>gb|ADZ44154.1| taurine dioxygenase [Yersinia enterocolitica subsp. palearctica
105.5R(r)]
Length = 282

Score = 86.3 bits (212), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 76/288 (26%), Positives = 120/288 (41%), Gaps = 27/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64

Sbjct: 5 L +TP G +GA + V++A L D+ F L+ A L+H +L F Q ++ QQ A RF
LVVTPLGPHIGALIENTVNIARPLGDSQFEQLYHALLKHQVLFERNQIPITPLQQRDLAGRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPV 117
G + +I+ + ++P + D+ WH D T++

Sbjct: 65 GDLHIHPVYPHAKECEEIIVLD-----THDNNPPDNDN-----WHTDVTFIET 107

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
GA+ +A+ +P GG T ++ AAY+AL + L+ A H +S + H

Sbjct: 108 PPLGAILAAKQLPTTGGDTLWSSGIAAYEALSAPFKQLLAGLRAEHDFTHSFPEHKHRAT 167

Query: 178 AGSAYIGYGMDTTATP-LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
P L P+V+ HP +GR +L + I + ES+ L L

Sbjct: 168 PEDHQRWLLAKEKNRPLLHPVVRTHPVSQRQALFVNEGFTTRIVDLSEKESDALLRFLFA 227

Query: 236 WACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
A + +W DV +WDNR H A RVM + + G

Sbjct: 228 HATKPEFQVRWRWQQDDVAIWDNRVTQHYANADYLPQRRVMHRATILG 275

>ref|ZP_06690679.1| conserved hypothetical protein [Acinetobacter sp. SH024]
gb|EFF87311.1| conserved hypothetical protein [Acinetobacter sp. SH024]
Length = 293

Score = 86.3 bits (212), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 66/273 (24%), Positives = 109/273 (39%), Gaps = 32/273 (11%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I T+GA + + L L++ + A L H ++ F Q L+ Q A+ F

Sbjct: 7 NLNIEVIKPTIGAIHIDIDLNALNEQTQQIQQALLDHQVIFFRKQQLAPQAQADLARSF 66

Query: 65 GA-----IERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYM 115
G+ IE + +++ + + K D + N WH D T+

Sbjct: 67 GSLHVVHPIYPSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFS 107

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLG 173
G V A +P VGG T ++ AA+ L + + +A H + + +

Sbjct: 108 KTPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQQKLRGLTATHDIRKSFPLERFA 167

Query: 174 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
H ++ + + P+V+ HP TG P L + I + ESE+ L+

Sbjct: 168 HNEEEREKLLQ-TFKRNPPVHPVVRTHPVTGEPLLFVSEGFTTRINELPEQESEQLLDF 226

Query: 233 LVDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
L A Q +W GD+ +WDNRC H+A

Sbjct: 227 LFKHATQEQFHLRWKQDGDIAIWDNRCTQHKA 259

>ref|ZP_07046346.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
S44]
gb|EFI60153.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
S44]
Length = 282

Score = 86.3 bits (212), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 77/274 (28%), Positives = 116/274 (42%), Gaps = 28/274 (10%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+QI P +GA + V LA DD FA + A L+H +L Q +S + + FA+R

Sbjct: 1 MQINPLTCAIGAELVDVQLADALRDDGLFAEIKTALLKHKVLFLLRRQSSISRAEHVGFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E V S+ + G V+ + +P + D + +WH D+T+ V G

Sbjct: 61 FGELE----DHPVIGSDPEHPGLVQIYKTPDKPLDRYE-----NSWHCDATWREVPPMGC 111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V P VGG T +A+M AY+ L + ++ ARHS+ + G A

Sbjct: 112 VLRCVECPVPGGDTMWANMALAYEMLPSHIKDVIAPLRARHSI---ECTFGAAMPAQKRL 168

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIG-----RHAHAIPGMDAAE-SERFLE 231
A P+V+ HPETG L + A+ G D + S L+

Sbjct: 169 ALKAQFPDAE--HPVVRTHPETGEKVLFFVSGFTTHTFTNFHTPANVRVGQDFTQGSSSLLQ 226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L+ A +W G + +WDNR H A

Sbjct: 227 FLISQAAIPEYQVRWRWEPGSAIWDNRATQHYA 260

>ref|ZP_04624706.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia kristensenii ATCC 33638]
gb|EEP90807.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Yersinia kristensenii ATCC 33638]
Length = 276

Score = 86.3 bits (212), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 75/287 (26%), Positives = 123/287 (42%), Gaps = 29/287 (10%)

Query: 8 ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
+TP G +GA V +++A L D+ F L+ A L+H +L F Q ++ QQ A RFG

Sbjct: 1 MTPLGPYIGALVENINIARPLGDSQFEQLYHALLKHQVLFVRNQPITPLQQRDLAQRFGD 60

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
+ +I+ + ++P + D+ WH D T++

Sbjct: 61 LHIHPVYPHAKECEEIIVLD-----THDNNPPDNDN-----WHTDVTFIENPP 103

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
GA+ +A+ +P GG T ++ AAY+AL + L+ A H V+S + H +

Sbjct: 104 LGAILAAKQLPTTGGDTLWSSGIAAYEALSAPFKQLLAGLRAEHDFVHSFPEKH-RATP 162

Query: 180 SAYIGYGMDDTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
+ + + P L P+V+ HP +GR SL + I + ES+ L L

Sbjct: 163 EDHQRWLLAKEKNPPLLHPVVRTHPVSGRQSLFVNEGFTTRIVDLSDKESDALLRFLFAH 222

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W DV +WDNR H A R+M + + G

Sbjct: 223 TTKPEFQVRWRWQQDDVAIWDNRVTQHYANADYLPQRRIMHRATILG 269

>ref|YP_001504880.1| taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EAN1pec]
gb|ABW09974.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. EAN1pec]
Length = 279

Score = 86.3 bits (212), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 74/284 (26%), Positives = 123/284 (43%), Gaps = 18/284 (6%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWL-QHALLIFPGQHLSNDQQITFAKRF 64
+++T +GA ++G L + AA A L ++ +L++ H+ + + F++

Sbjct: 3 IEVTRLAPEIGAEISGYTGRDLVNEAAAAACKAALDRYGVLVYREVHIEDGDLVRFSLRL 62

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVG---NMAWHADSTYMPVMAQ 120
G V + V G + + D V+ G N WH D + +

Sbjct: 63 GE-----VVVPKVNDPGEHPEIARITLDPEKSVLAGYRQGNFLWHIDGATDELDPQK 113

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
+ +A V GG T FA+ AAY+AL + +A + HS +Q ++ + A

Sbjct: 114 ATLLTAREVDPAGGDTEFANTYAAEALSDEEKAEIADLQVVHSFAIAQ-RIAYPDAADK 172

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
+ + T + PLV GR SLLIG A + G L+ L+ W+
Sbjct: 173 QRASW--EKVPTRVHPLVWTRA-NGRKSLLIGATAGMVVGRSEDRGRITLLDRLLQWSTSP 229

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR 284
HQW GD+V+WDN +LHRA P++ R+M + L G+
Sbjct: 230 RFTLRHQWRRGDLVIWDNTGVLHRLPFEPTSRRMLMHRITTLVGQ 273

>gb|EFW59470.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Shigella
flexneri CDC 796-83]
Length = 283

Score = 86.3 bits (212), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 71/271 (26%), Positives = 115/271 (42%), Gaps = 29/271 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVFLRDQAITPQQQRALAQR 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGITAYEALSVPFRQLLSGLRAEHDFRKSFPYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L G +
Sbjct: 168 EEEHQRWREAVAKNPPLHHPVVRTHPVSQKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
P +W D+ +WDNR H A
Sbjct: 227 AHITKPEFQVRWRWQPNDIAIWDNRVTQHYA 257

>emb|CAY27434.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.3 bits (212), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 49/125 (39%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAAGSAYIGYGMDDTTATPLR 195
T F DMRAAYDALDE + + + HS +YS+ KLG + + + P+R
Sbjct: 1 TEFADMRAAYDALDERLKQIEELVCLHSNMYSRGKLGTEFSDEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I GM E L L ++ Q V++H W D V
Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEGRMLLLDLTEFGTQHGFVYSHTWRVNDV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>emb|CAY27283.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.3 bits (212), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 49/124 (39%), Positives = 65/124 (52%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR 195
T FADMRAAYDALDE + + HS +YS+ KLG + + +
Sbjct: 1 TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLGADSTEEERRVF-----KSVRQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP TGR SL + HA I GM E+ L L ++A + P V++H W D V+
Sbjct: 56 RLVRHPVTGRKSLFLSAHAGEIEGMSIPEARMLLLDLTEFATRDPFVYSHVWRLNDFVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>gb|AAT51233.1| PA0193 [synthetic construct]
Length = 301

Score = 86.3 bits (212), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 78/283 (27%), Positives = 120/283 (42%), Gaps = 18/283 (6%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L I P +GA + GV L+ LD A A+ AA ++H ++ F Q HL + Q FA
Sbjct: 14 LDIRPVAGRIGAEIRGVTLSGELDAATVEAIQAALVRHKVIFFRDQSHLDDQTQEAF AHL 73

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
G + VA V + R + + + +WH D T++ + ++
Sbjct: 74 LG-----EPVAHPTVPSREGTRFLLLELDGAEGRR-----NSWHTDVTFFVEAYPKASI 121

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL---GHVQQAGS 180
+ V P GG T +A+ +AY L R L + A HS Y + + V+Q +
Sbjct: 122 LRSVVAPESSGGDTVWANTASAYADLPAELRELADRLWAVHSNEYDYAGVKPSASVEQLEN 181

Query: 181 AYIGYGMTTATATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
Y T P+V+VHP++G +LL+G + G+ +S L +
Sbjct: 182 -YRKVFTSTVYETEHPVVRVHPQSGERTLLLGHFVKRLKGLSQHDSAHLFVAVLQGHVTRL 240

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+W AGDV +WDNR H A PRV+ L G
Sbjct: 241 ENTVRWRWQAGDVAIWDNRATQHYAIDDYGDQPRVVRVTLGG 283

>ref|ZP_06842052.1| Taurine dioxygenase [Burkholderia sp. Ch1-1]
gb|EFG70277.1| Taurine dioxygenase [Burkholderia sp. Ch1-1]
Length = 315

Score = 85.9 bits (211), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 75/286 (26%), Positives = 121/286 (42%), Gaps = 16/286 (5%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++++TP A +GA + GV L LD A + AA L+ ++ F Q L++ Q + F+ +
Sbjct: 11 SIEVTPLSAHIGAEIHGVDLTQKLDARQIAEIRAALLKWRVVFVFREQFLTHGQHVAFSAQ 70

Query: 64 FGAIERIG---GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ 120
FG + +G G + V + R+ + E + + G WH D T
Sbjct: 71 FGELT-LGHPVFGHVEGHPEVYSISKYRKATRFEGQTLQRPWTG---WHTDVTAAVNPPW 126

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
++ +P GG T + ++ AAY L R+ V H G
Sbjct: 127 ASILRGVTIPPYGGDTQWTNLVAAYQKLSAPLRSFVDSLRLGIHRFTPPAGASG-----TQ 181

Query: 181 AYIGYGMTTATATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239
A++ PLV+VHPETG +L + +I G+ ES+ LE L + +
Sbjct: 182 AFLEAVEQRVLVTEHPLVRVHPETGERALVSPSFLKSIVGVSPRESQVLELLWEHVTR 241

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA--EPWDFKLPRVMWHSRLAG 283
+W AG V WDNR H A + +D R ++ + L G
Sbjct: 242 PEFTVRFKWQAGSVAFWDNRATAHLAPTDIFDLDFDRQLYRTTLVG 287

>ref|ZP_01617748.1| Taurine dioxygenase [marine gamma proteobacterium HTCC2143]
gb|EAW30341.1| Taurine dioxygenase [marine gamma proteobacterium HTCC2143]
Length = 288

Score = 85.9 bits (211), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 72/279 (25%), Positives = 111/279 (39%), Gaps = 41/279 (14%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAA-LHAAWLQHALLIFPGQHLSNDQQIT 59
MA + +GA +TG+ L A L L +L F Q++S +Q ++
Sbjct: 12 MASYDFSVKKLTPNIGALITGIDLTGASQEICAQLKEVLLDAKVLFFRDQNISLEQHMS 71

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGN-----MAWHAD 111
FA+ FG +E V +P D +++ + WH+D
Sbjct: 72 FARHFGDLE-----VHPFAPTHKDHPEVLVLSHGKDSKGTENFWHSD 113

Query: 112 STYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQ 169
T+ + G++ A+ VP GG T FADM AY+ L + + V R A H V+ +
Sbjct: 114 VTWRKEPSLGSILRAKRPETGGDTLAFADMYVAYENLSDEVKEKVEGRIAIHDFGRVFR 173

Query: 170 SKLGHVQQAGSAYIGYGMDTTATPL--RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAES 226
+ +Q PL P+++ HPETGR ++ + +I MD AES
Sbjct: 174 NLTEEKREQEMK-----RKYPLSEHPVIRTHPETGRKAIYVNTAFTDSIKDMDKAES 224

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L L A +W + WDNR H A
Sbjct: 225 AALLAHLAQAANTPEYQCRFKWQPNISIAFWDNRSCQHYA 263

>emb|CAY27438.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 85.9 bits (211), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 50/125 (40%), Positives = 63/125 (50%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DMR AYD LD TRA + HSL+YS+ G + + P+R
Sbjct: 1 TEFGDMRNAYDTLDAKTRAQIENLVCEHSLIYSRGSTGFTE-----LTEDERAMMKPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I G ES FL L + A Q V+ H+W D+V
Sbjct: 55 QRLVRTHPVTGRKSLYLSSHAGTIVGWLVPESRDFLRDLNEHATQRENVYIHRWRQFDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|NP_248883.1| hypothetical protein PA0193 [Pseudomonas aeruginosa PA01]
ref|YP_002437802.1| putative alkylsulfatase [Pseudomonas aeruginosa LESB58]
ref|ZP_04930892.1| hypothetical protein PACG_03650 [Pseudomonas aeruginosa C3719]
gb|AAG03583.1|AE004457_4 hypothetical protein PA0193 [Pseudomonas aeruginosa PA01]
gb|EAZ55011.1| hypothetical protein PACG_03650 [Pseudomonas aeruginosa C3719]
emb|CAW24921.1| putative alkylsulfatase [Pseudomonas aeruginosa LESB58]
Length = 300

Score = 85.9 bits (211), Expect = 6e-15, Method: Compositional matrix adjust.
Identities = 78/283 (27%), Positives = 120/283 (42%), Gaps = 18/283 (6%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L I P +GA + GV L+ LD A A+ AA ++H ++ F Q HL + Q FA
Sbjct: 14 LDIRPVAGRIGAEIRGVTLSEGLDAATVEAIQAALVRHKVIFFRDQSHLDDQTQEAFHL 73

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
G + VA V + R + + + +WH D T++ + ++
Sbjct: 74 LG-----EPVAHPTVPSREGTRFLELDGAEGRA----NSWHTDVTTFVEAYPKASI 121

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL---GHVQQAGS 180
+ V P GG T +A+ +AY L R L + A HS Y + + V+Q +
Sbjct: 122 LRSVVAPESSGGDTVWANTASAYADLPAELRELADRLWAVHSNEYDYAGVKPSASVEQLEN 181

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
Y T P+V+VHP++G +LL+G + G+ +S L +
Sbjct: 182 -YRKVFTSTVYETEHPVVRVHPQSGERTLLLGHFVKRLKGLSQHDSAHFLFAVLQGHVTRL 240

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+W AGDV +WDNR H A PRV+ L G
Sbjct: 241 ENTVRWRWQAGDVAIWDNRATQHYAIDDYGDQPRVVRVTLGG 283

>ref|YP_001909093.1| taurine dioxygenase [Erwinia tasmaniensis Et1/99]
emb|CAO98227.1| Taurine dioxygenase, 2-oxoglutarate-dependent (Taurine dioxygenase)
[Erwinia tasmaniensis Et1/99]
Length = 279

Score = 85.9 bits (211), Expect = 6e-15, Method: Compositional matrix adjust.
Identities = 76/291 (26%), Positives = 124/291 (42%), Gaps = 33/291 (11%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++I G +GA V+ ++L+ L DA F L+ A ++H +L Q L+ QQ A RF
Sbjct: 5 IRIQALGPHIGALVSDINLSRPLSDAQFEQLYHALIRHQVLFRLDQPLTPHQQRQLASRF 64

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIV-----GNMAWHADSTYM 115
G + V H+P D+ ++IV N WH D T++
Sbjct: 65 GDLHI-----HPVYPHAP----DVEEIIIVLDTHDDNPPDNDNWHTDVTFI 105

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
GA+ +A+ +PA GG T +A AA+DAL +AL+ H S + +
Sbjct: 106 ETTPAGAILAAKQLPASGGDTLWASGIAAWDALAPLQALLDGLQGEHDFRKSQFQYKY- 164

Query: 176 QQAGSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
+ + + + P L P+V+ HP +G+ +L + + G+ ES+ L
Sbjct: 165 RSSAEHQQRWQAVAKNPPVLHPVVRTHPVSGKKALFVNEGFTTRLIGLKEKESDALLNF 224

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + +W DV +WDNR H A R+M + + G
Sbjct: 225 LFAHITKPDFQVRWRWQDDVAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|YP_002319044.1| taurine dioxygenase [Acinetobacter baumannii AB0057]
ref|YP_002325944.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Acinetobacter
baumannii AB307-0294]
ref|ZP_06781894.1| taurine dioxygenase [Acinetobacter sp. 6013113]
ref|ZP_06796981.1| taurine dioxygenase [Acinetobacter sp. 6013150]
ref|ZP_07226239.1| taurine dioxygenase [Acinetobacter baumannii AB056]
ref|ZP_07239996.1| taurine dioxygenase [Acinetobacter baumannii AB059]
gb|ACJ41061.1| taurine dioxygenase [Acinetobacter baumannii AB0057]
gb|ACJ56370.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Acinetobacter
baumannii AB307-0294]
Length = 293

Score = 85.9 bits (211), Expect = 6e-15, Method: Compositional matrix adjust.

Identities = 67/276 (24%), Positives = 111/276 (40%), Gaps = 38/276 (13%)

```
Query: 5   TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L I      T+GA +  + L L++      + A L + ++ F Q L+  Q  A+ F
Sbjct: 7   NLNIEVIKPTIGAIHNDLNALNEQTTQQIQQALLDYQVIFFRKQQLAPQAQADLARSF 66

Query: 65   G-----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
          G      +IE +   +++ + + K D      + N WH D T+
Sbjct: 67   GTLHVHPIYPSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFS 107

Query: 116  PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLG 173
          G V A  +P VGG T ++   AA+ L   + +   +A H +   + +
Sbjct: 108  KTPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQQLRGLTATHDIRKSFPLERFA 167

Query: 174  HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR----HAHAIPGMDAAESERF 229
          H ++      +      + P+V+ HP TG P L +      H + +P      ESE+
Sbjct: 168  HNEEEREKLLQ-TFKRNPVVPVVRTHPVTGEPLLFVSEGFTTHINELP---EQESEQL 223

Query: 230  LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          L L + A Q      +W GDV +WDNRC H+A
Sbjct: 224  LNFLFEHATQEQFHLRWKQDGDVAIWDNRCTQHKA 259
```

>emb|CAY27317.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 85.9 bits (211), Expect = 6e-15, Method: Compositional matrix adjust.
Identities = 49/125 (39%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

```
Query: 136  TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
          T FADMRAAYDALD+AT+A V      HS+V+S+ ++G A      G + P++
Sbjct: 1   TEFADMRAAYDALDDATKAIVEDLVTEHSIVFSREQIGFSDYAS-----GNEERLRPVQ 54

Query: 196  -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
          LV HP +GR SL + H I G E+ + L++ A Q V+ H+W D+V
Sbjct: 55  HRLVITHPVSGRKSLEYLSSHIGGIVGWPVPEARALIRDLMEHATQRQFVYTHEWRVNDLV 114

Query: 255  VWDNR 259
          +WDNR
Sbjct: 115  MWDNR 119
```

>gb|ADC34007.1| TfdA-like protein [uncultured bacterium]
Length = 193

Score = 85.9 bits (211), Expect = 6e-15, Method: Compositional matrix adjust.
Identities = 69/219 (31%), Positives = 99/219 (45%), Gaps = 39/219 (17%)

```
Query: 56   QQITFAKRFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGN 105
          QQI FAKR+G I      + G +IV      K D TV      GN
Sbjct: 1   QQIAFAKRWGEIHLHPMPCLPDNPGIIEIVK---KEDDTV-----AFGGN 43

Query: 106  MAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL 165
          WH D +      A+ + A+ VPA GG T +A++ AYD+L + +A++
Sbjct: 44  --WHTDQMFDTDPARVTMLYAKQVPAAGGDTLYANLYQAYDSLSDGMKAMIGD----- 94

Query: 166  VYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGRH--AHAIPGMD 222
          + + S+ ++ +      MD A + PLV+VHPETGR +L I      I GM
Sbjct: 95  LRTISQYDKKKRPAFMTPTEMDVPAPVEHPLVRVHPETGRKALYISYEGITRRIAGMT 154

Query: 223  AAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
          AES L L++ A +      +W G +VVWDNRC+
Sbjct: 155  EAESRPILSYLLNHAIRPEFTCRFRWQVQVSLVVWDNRCLV 193
```

>emb|CAY27442.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 85.9 bits (211), Expect = 6e-15, Method: Compositional matrix adjust.
Identities = 48/124 (38%), Positives = 65/124 (52%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR 195
T FADMRA +D+LD T+AL HS +YS+ LG + + L+
Sbjct: 1 TEFADMRAAGWDSLDLPETQALCEDLICEHSQIYSRQILGFTDFTEEERVRF-----KPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP TGR SL + HA I G E+ L L + A Q V++H+W GD+V+
Sbjct: 56 RLVRTHTPTGRKSLYLSSHAGGIVGWPVPEAMLLRELTEHATQREFVYSHKWQVGDLM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>gb|ADC34045.1| TfdA-like protein [uncultured bacterium]
Length = 198

Score = 85.9 bits (211), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 68/217 (31%), Positives = 92/217 (42%), Gaps = 30/217 (13%)

Query: 56 QQITFAKRFG-----AIERIGGGDIVAISNV----KADGTVRQHSPA--WDDMMKVIVG 104
QQI FA+RFG R IS V K DG SPA+ W G
Sbjct: 1 QQIAFARRFGEPDDNKTRTRNPHFPEISTVINKPKLDG-----SPADAHW-----G 47

Query: 105 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS 164
WH+D+++ + VP VGG T FA+M AY+ L + + L+ H
Sbjct: 48 GSDWHSASFKLAPTGITLLHGVAVPPVGGDTQFANMYLAYETLSGMMKKLISGLEGVH- 106

Query: 165 LVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAA 224
V + L H M T PLV+VHPETGR SL +G I GM
Sbjct: 107 -VQKEKLLDHSTPERLEESRRSM----TIAHPLVRVHPETGRKSLYVGEKVQLIAGMTPE 161

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
ES ++ L A + ++ HQ D+++W+N C
Sbjct: 162 ESRPLIDFLCTHARRPQFIYRHQMKQEDLLMWNNPCF 198

>ref|YP_309357.1| taurine dioxygenase [Shigella sonnei Ss046]
gb|AAZ87122.1| taurine dioxygenase, 2-oxoglutarate-dependent [Shigella sonnei Ss046]
gb|EFZ49963.1| alpha-ketoglutarate-dependent taurine dioxygenase [Shigella sonnei 53G]
Length = 283

Score = 85.9 bits (211), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 74/289 (25%), Positives = 122/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L++ ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRYQVFLRDQAITPQQQRALAQR 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178

GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPPEYKY-RKT 167
Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L G +
Sbjct: 168 EEEHQWRWEAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226
Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>emb|CAN89617.1| putative taurine dioxygenase [Streptomyces collinus]
Length = 307

Score = 85.9 bits (211), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 80/275 (29%), Positives = 116/275 (42%), Gaps = 26/275 (9%)

Query: 4 TTLQITPTGATLGATVTGVHLA--TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
T++++ +GA + GV++A DD FA + + L+H +L Q LS + + FA
Sbjct: 24 TSIEVERLTCAIGAELRGVNIADAVRDDLFAEIKSLLEHRVLFRLDQDLSRAEHVAFA 83
Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
RFGA+E VA S+ G VR + E D + A H D T+ + G
Sbjct: 84 SRFGALE----DHPVAGSDPDHPGLVRIYK--ELDSAPEHY--ENALHTDGTWRVNPMSG 135
Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
AV P VGG T + DM AAYD L +A + ARHS+ ++ G V
Sbjct: 136 AVLHCVESPPVGGDTIWVDMVAAYDRLPAHVKAQIAGLRARHSI---EASFGAVMPEEKR 192
Query: 182 YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG-----LV 234
+ A P+V+ HPETG L + + RF + L+
Sbjct: 193 IALHEQYPDAE--HPVVRTHPETGEKILFVNAFTTHTNFHTPANVRFGQDYAPGASHLL 250
Query: 235 DWACQAPRVHAHQ---WAAGDVVVWDNRCLLHRA 265
+ V +Q W G V +WDNR H A
Sbjct: 251 SYLISQAAVPEYQVRWRWTPGSVAIWDNRSTQHYA 285

>ref|ZP_07952776.1| TfdA family Taurine catabolism dioxygenase TauD
[Enterobacteriaceae
bacterium 9_2_54FAA]
gb|EFV38957.1| TfdA family Taurine catabolism dioxygenase TauD [Enterobacteriaceae
bacterium 9_2_54FAA]
Length = 282

Score = 85.9 bits (211), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 76/281 (27%), Positives = 116/281 (41%), Gaps = 13/281 (4%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I P +GA V+ ++L+ L DA F L+ A L+H +L Q ++ QQ A RF
Sbjct: 5 LTIQPLSPAIGAVVSNLNLRLSDAQFEQLYHALLKHQVLFAREQVITPLQQRELASRF 64
Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G + + A G E D N WH D T++ GA+
Sbjct: 65 GDLH-----IHPVYPHAAGV---EEIIELDTHHDNPPDNDNWHTDVTFIENPPLGAIL 114
Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
+A+ VP VGG T ++ AAY+AL + L+ A H S + H++
Sbjct: 115 AAKRVPEVGGDTLWSSGIAAYEALSPQLKVLLSGLQAEHDFEKSFPPEKHRLRSEEEHQWR 174
Query: 185 YGMDDTTATP-LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPR 242
P L P+V+ HP +GR +L + + G+ E E L+ L +

Sbjct: 175 LQAKRQHPPLLHPVVRTHPVSQRQALFVNEGFTTTLVGIPQQEGEALLQFLFRHTTKPEF 234

Query: 243 VHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+W D+ +WDNR H A R+M + + G

Sbjct: 235 QVRWRWQQDDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>emb|CAY27492.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 85.9 bits (211), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 50/125 (40%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195

T FADMRAAYDALDE + + HS +YS+ KLG + P+R

Sbjct: 1 TEFADMRAAYDALDERLKHRIEDLVCLHSNMYSRGKLGLTDFDDESAF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254

LV+ HP TGR SL + HA I GM E L L ++A + V++H W D+V

Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEGRMLLLDLTEFATRDEFVYSHAWRVDDL 114

Query: 255 VWDNR 259

+WDNR

Sbjct: 115 MWDNR 119

>emb|CAY27309.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 85.5 bits (210), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 48/125 (38%), Positives = 70/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195

T FADMRAAYDAL T+A + HS ++S+ ++G A + P+R

Sbjct: 1 TEFADMRAAYDALPAETKAEIEDLVCEHSQIFSRQQIGFFDLAEERARF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254

+V+ HP TGR S + HA AI G E+ FL L++ A + V++H+W+ GD+V

Sbjct: 55 QCMVRTHPVTGRKSAYLASHAGAIVGWVPPEARIFLRDLIEHATREFVYSHKWSVGDLV 114

Query: 255 VWDNR 259

+WDNR

Sbjct: 115 MWDNR 119

>gb|EFW79602.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. glycinea
str. B076]

gb|EFW85432.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. glycinea
str. race 4]

Length = 289

Score = 85.5 bits (210), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 86/298 (28%), Positives = 128/298 (42%), Gaps = 48/298 (16%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62

T ++TP +GA V GV L+ L + A+L++ +L+F QHL+ +Q F +

Sbjct: 24 TVNRLTPI---IGAEEVGGVDLSQPLSAKQLTEIRRAFLENHVLVFRDQHLTVEQHKAFGR 80

Query: 63 RFG-----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV 117

FG +E I G D + V+A+ R WH D T

Sbjct: 81 LFGPLRALPVESIDGDDPELVV-VRANAQSR-----FAAGELWHTDGTADLE 126

Query: 118 MAQGAVFSAEVPVAV--GGRTCFCADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175

```

      + G++   + PA+  GG T FA+M  A + L  A +A + + +A H           G +
Sbjct: 127 PSMGSMLYVKETPAIGTGGDTLGFANMHLAIEMLSPAMQAFLGELTAIHD-----GEI 178

Query: 176 QQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEG 232
      + GY               P+V  HPETGR SL +  G  +H + + A ES  L
Sbjct: 179 -----PWKGYQPPANLPKSEHPVVVRHPETGRRSLFVNSGFTSHIV-QLSAGESRTLLNM 232

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSR---LAGRPE 286
      L D  + P +      +W      +V WDNRC  H A  WD+  P  +  R  L GRP+
Sbjct: 233 LFDLIAREPSLSCRVRWEPNTLVFWDNRCTQHHAH-WDY-FPHSRYGERVTILGGRPK 288

```

>emb|CAY27416.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 85.5 bits (210), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 50/125 (40%), Positives = 68/125 (54%), Gaps = 7/125 (5%)

```

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
      T F DMRAAYD LDE T+A +      HSL++S+  LG  + +      +      P+R
Sbjct: 1   TEFWDMRAAYDTLDERTKAEIEDLICEHSLMFSRGLLGFTAMSEAEREMF-----RPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
      LV+ HP T R SL +  HA  I G      E+  FL  L++ A Q  V++HQW  D+V
Sbjct: 55  QRLVRTHPVTRRKSFLSLAHAGTIVGWPVPEARAFRLDLIEHATQPQLVYSHQWRQWDLV 114

Query: 255 VWDNR 259
      +WDNR
Sbjct: 115 MWDNR 119

```

>ref|YP_273987.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. phaseolicola
1448A]
gb|AAZ36278.1| dioxygenase, TauD/TfdA family [Pseudomonas syringae pv.
phaseolicola 1448A]
Length = 286

Score = 85.5 bits (210), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 86/298 (28%), Positives = 128/298 (42%), Gaps = 48/298 (16%)

```

Query: 4   TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
      T  ++TP      +GA V GV L+  L      +  A+L++ +L+F  QHL+ +Q  F +
Sbjct: 21  TVNRLTPI---IGAEEVGGVDLSQPLSAKQLTEIRRAFLENHVLVFRDQHLTVEQHKAFAFR 77

Query: 63  RFG-----AIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPV 117
      FG      +E I G D  +  V+A+  R      WH D T
Sbjct: 78  LFGPLRALPVESIDGDDPELVV-VRANAQSR-----FAAGELWHTDGTADLE 123

Query: 118 MAQGAVFSAEVPVAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
      + G++   + PA+  GG T FA+M  A + L  A +A + + +A H           G +
Sbjct: 124 PSMGSMLYVKETPAIGTGGDTLGFANMHLAIEMLSPAMQAFLGELTAIHD-----GEI 175

Query: 176 QQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEG 232
      + GY               P+V  HPETGR SL +  G  +H + + A ES  L
Sbjct: 176 -----PWKGYQPPANLPKSEHPVVVRHPETGRRSLFVNSGFTSHIV-QLSAGESRTLLNM 229

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSR---LAGRPE 286
      L D  + P +      +W      +V WDNRC  H A  WD+  P  +  R  L GRP+
Sbjct: 230 LFDLIAREPSLSCRVRWEPNTLVFWDNRCTQHHAH-WDY-FPHSRYGERVTILGGRPK 285

```

>gb|ADC34020.1| TfdA-like protein [uncultured bacterium]
Length = 196

Score = 85.5 bits (210), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 59/214 (27%), Positives = 98/214 (45%), Gaps = 26/214 (12%)

```
Query: 56 QQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW 108
          QQI FA +FGA+E      + G  +++AI++      + P + +      W
Sbjct: 1  QQIAFAAKFGALEVHPFAPHKPGHPEVLAITH-----DRERPGKEN-----TW 43

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
          H+D T+      + G++  + +P VGG T FADM AAY+ L +  +A +  R+A H  +
Sbjct: 44 HSDVTWRLEPSLGSILRSIEIPPVGGDTL FADMYAAYEGLSDTVKAKIEGRTAIH DFAFF 103

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESE 227
          + L      ++ +      Y      P+V+ HPETGR  + +      I G++A ES
Sbjct: 104 RKGLRKAGKSEAEIEAYNKKFPPAE-HPVVRTHPETGRKGIYVNA AFTQNIVGLEADESA 162

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
          L+ L  A      +W+  + WDNRC+
Sbjct: 163 SLLKHL YAQA AIP EYQCRFRWSVNALAFWDNR CV 196
```

>ref|ZP_05639075.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. tabaci ATCC

11528]
Length = 289

Score = 85.5 bits (210), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 86/298 (28%), Positives = 128/298 (42%), Gaps = 48/298 (16%)

```
Query: 4   TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
          T ++TP      +GA V GV L+ L      + A+L++ +L+F  QHL+ +Q  F +
Sbjct: 24 TVNRLTPI---IGA EVGGVDLSQPLSAEQLKEIRRAFLENHVLVFRDQHLTVEQHKAFGR 80

Query: 63 RFG-----AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV 117
          FG      +E I G D  + V+A+  R      WH D T
Sbjct: 81 LFGPLRALPVESIDGDDPELVV-VRANAQSR-----FAAGELWHTDGTADLE 126

Query: 118 MAQGAVFSAEVVPAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
          + G++  +  PA+  GG T FA+M  A + L  A +A + + +A H      G +
Sbjct: 127 PSMGSM L YKETPAIGTGGDTL FANMHLAIEMLSPAMQAFLGELTAIHD-----GEI 178

Query: 176 QQAGSAYIGYGMDDTTATPLR-PLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEG 232
          + GY      P+V  HPETGR SL +  G  +H +  + A ES  L
Sbjct: 179 -----PWKG YQPPANLPKSEHPVVVRHPETGR RSLFVNSGFTSHIV-QLSAGESRTLLNM 232

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSR---LAGRPE 286
          L D  + P +      +W  +V WDNRC  H A WD+  P  +  R  L GRP+
Sbjct: 233 LFDLIAREPSLSCRVRWEPNTLVFWDNRCTQH HAV-WDY-FPHSRYGERVTILGGRPK 288
```

>emb|CBJ20068.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 136

Score = 85.5 bits (210), Expect = 8e-15, Method: Compositional matrix adjust.
Identities = 50/141 (35%), Positives = 78/141 (55%), Gaps = 13/141 (9%)

```
Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
          A+ ++ SA  +PA GG T FADMRAAYDAL + T+  +      A HS+ +S+S++G
Sbjct: 5   ARFSMLSARAIPAEGGETEFADMRAAYDALPDETKRQIEGLIAEHSIFHSRSRIG----- 59

Query: 179 GSAYIGYGMDDTTATPLRP----LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
          +  +  D  A  L  P      +V+ HP +GR +L +  HA  + G      + +E L+
```

Sbjct: 60 ---FTDFNPD-VAQALPPVQQVMVRTHPGSGRKTLYLASHASHVIGWPIETGHKLIEDLL 115

Query: 235 DWACQAPRVHAHQWAAGDVVV 255

D+A Q V+ H+W GD+V+

Sbjct: 116 DFATQPQFVYQHRWQVGDLM 136

>gb|ACG80553.1| TfdA [uncultured bacterium]

gb|ACG80576.1| TfdA [uncultured bacterium]

Length = 119

Score = 85.5 bits (210), Expect = 8e-15, Method: Compositional matrix adjust.
Identities = 47/124 (37%), Positives = 69/124 (55%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195

T F DMRAAYDALD+ T+A V HS ++S+ +G + + + L+

Sbjct: 1 TEFQDMRAAYDALDDETKAEVENMVCEHSQMFSRQIIGF-----TDFTEERERFRPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255

+V+V+P TGR SL + HA I G E+ +L L++ A Q V+ H+W GD+V+

Sbjct: 56 CMVRVNPVTGRKSLYLSSHAGGIVGWPMPPEARGLRDLIEHATQREFVYTHKWRIGDLM 115

Query: 256 WDNR 259

WDNR

Sbjct: 116 WDNR 119

>ref|ZP_02474390.1| putative alpha-ketoglutarate-dependent taurine dioxygenase

[Burkholderia pseudomallei B7210]

Length = 380

Score = 85.5 bits (210), Expect = 8e-15, Method: Compositional matrix adjust.
Identities = 84/273 (30%), Positives = 118/273 (43%), Gaps = 35/273 (12%)

Query: 6 LQITPTGATLGATVTGVHLATL---DDAGFAALHAAWLQHALLIFPGQHLSND-QQITFA 61

L I P +GA V G+ L + +D F + A L H ++ F QH +D Q FA

Sbjct: 96 LSIRPLSGHIGAEVQGIQLGSQMAPNDIRF--ITQALLTHRVIFRRQHHLDDLAQELFA 153

Query: 62 KRFGAIER---IGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHAD--STYMP 116

+ FG I + +GG AI + + R +S WH D S+ P

Sbjct: 154 QAFGEIVKHPTMGKGTGSAILELHSHEGGRANS-----WHTDVTSSSAP 197

Query: 117 VMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVY---SQSKL 172

++ V A +P GG T +A+ AAY L + + LV + A H + S+ +L

Sbjct: 198 KLS---VLRALALPDAGDTVWANTVAAYQHLPSSLQDLVDKLWAVHGNDFDYAASRVEL 254

Query: 173 GHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG 232

H A Y T P+V++HPETG SLL+G +A D +S R E

Sbjct: 255 LHDPVAKEYRKKYAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRQFVQYDTHDSNRLEYI 313

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

L + WAAGDV +WDNR H A

Sbjct: 314 LQAHITRLENTVRWHWAAGDVVAIWDNRSTQHYA 346

>emb|CAY27213.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 119

Score = 85.5 bits (210), Expect = 8e-15, Method: Compositional matrix adjust.
Identities = 48/125 (38%), Positives = 68/125 (54%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195

T F DMRAAYDALD+AT+A V HS+V+S+ ++G A G + P++

Sbjct: 1 TEFGDMRAAYDALDDATKAEVEDLVTEHSIVFSREQIGFSDYAA-----GNEERLRPVQ 54
Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV HP +GR SL + H I G E+ F+ L++ Q V+ H+W D+V
Sbjct: 55 HRLVITHPVSGRKSLEYLSSHIGGIVGWPVEARAFIRDLMEHVTQRQFVYTHEWRVNDLV 114
Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>emb|CAY27410.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 117

Score = 85.5 bits (210), Expect = 8e-15, Method: Compositional matrix adjust.
Identities = 48/123 (39%), Positives = 67/123 (54%), Gaps = 6/123 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALD T+AL+ HS ++S+ LG ++ + A +
Sbjct: 1 TEFADMRAAYDALDGETKALIEDLVCEHSRIFSKGALGF-----SFTEEEVKAFAPVRQ 54
Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP+TGR SL + HA I G E+ L L + A Q ++H+W GD+V+
Sbjct: 55 RLVRTHPKTGRKSLEYLSSHAGRIVGWPVEAMLLRELTEHATQREFAYSHKWRVGDLMV 114
Query: 256 WDN 258
WDN
Sbjct: 115 WDN 117

>ref|YP_001714059.1| taurine dioxygenase [Acinetobacter baumannii AYE]
emb|CAM87073.1| Alpha-ketoglutarate-dependent taurine dioxygenase
(2-aminoethanesulfonate dioxygenase) (Sulfate
starvation-induced protein 3) (SSI3) [Acinetobacter
baumannii AYE]
Length = 311

Score = 85.5 bits (210), Expect = 8e-15, Method: Compositional matrix adjust.
Identities = 69/278 (24%), Positives = 110/278 (39%), Gaps = 42/278 (15%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I T+GA + + L L++ + A L + ++ F Q L+ Q A+ F
Sbjct: 25 NLNIEVIKPTIGAIHNDLNALNEQTQQIQQALLDYQVIFFRKQQLAPQAQADLARSF 84
Query: 65 G-----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
G +IE + +++ + + K D + N WH D T+
Sbjct: 85 GTLHVHPPIYPSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFS 125
Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYD----ALDEATRALVHQRSARHSLVYSQSK 171
G V A +P VGG T ++ AA+ L + R L R S + +
Sbjct: 126 KTPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQQKLRLGLTATHDIRKS--FPLER 183
Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR----HAHAIPGMDAAESE 227
H ++ + + P+V+ HP TG P L + H + +P ESE
Sbjct: 184 FAHNEEEREKLLQ-TFKRNPVVPVVRTHPVTGEPLLFVSEGFTTHINELP---EQESE 239
Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ L L + A Q +W GDV +WDNRC H+A
Sbjct: 240 QLLNFLFEHATQEQFHLRWKQDGDVAIWDNRCTQHKA 277

>emb|CAY27480.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 85.5 bits (210), Expect = 8e-15, Method: Compositional matrix adjust.
Identities = 52/125 (41%), Positives = 67/125 (53%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALDE + HS ++S+S LG + P+R
Sbjct: 1 TEFADMRAAYDALDEEIKTECENLICEHSQFLSRSILGSTDFDERRRFA-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I G E+ FL+ L + A Q V+AH+W GD+V
Sbjct: 55 QRLVRRHPVTGRKSLHLSSHAGGIVGWPVPEARAFKDLNEHATQREFVYHRWRVGDV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|YP_004006885.1| taurine dioxygenase [Rhodococcus equi 103S]
emb|CBH48201.1| putative taurine dioxygenase [Rhodococcus equi 103S]
Length = 268

Score = 85.5 bits (210), Expect = 8e-15, Method: Compositional matrix adjust.
Identities = 77/275 (28%), Positives = 115/275 (41%), Gaps = 45/275 (16%)

Query: 1 MAQTTLQITPTGATLGATVTVGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
+ T+ +TP +GA V G+H+A L A + A H +L FP Q + F
Sbjct: 4 LEAATVTVTPLAGAIGAIEVRGLHVAALSGADVELVRTALHDHGVLFPEQGVDPATHRAF 63

Query: 61 AKRFGAI-----ERIGGGDIVAISNVKAD-GTVRQHSPAEWDDMMKVIVGNMAWHADS 112
A+ FG I +G IS + D G+ Q WH D
Sbjct: 64 AQHFGDIVYPHEHLAHLGDEGYREISVISTDNGSAYQ-----TNRWHCDV 108

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+ ++ ++ +V+P VGG T +++ AA DAL R ++ +A H + L
Sbjct: 109 AWRAEPSRFSILHLQVLPEVGGDTLWSNQYAALDALSPPIREALYGLTATHRI----APL 164

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLE 231
+V +A PLV HPETGR +L + AI G+ ES R L
Sbjct: 165 PNVPEAR-----HPLVIRHPETGREALFVNDLFTSAIDGVTEDES-RALL 208

Query: 232 GLVDWACQAPRVHA-HQWAAGDVVVWDNRCLLHRA 265
GL+ P +W+ GD+ VWDN + H A
Sbjct: 209 GLLKTVSIRPEFTVRRRWSVGDIAVWDNHFVQHNA 243

>emb|CAY27505.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 85.5 bits (210), Expect = 8e-15, Method: Compositional matrix adjust.
Identities = 49/124 (39%), Positives = 67/124 (54%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALD T+AL+ HS ++S+ LG ++ + A +
Sbjct: 1 TEFADMRAAYDALDAETKALIEDLVCEHSRIFSKGALGF-----SFTEELRAFAPVRQ 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ H +T R SL + HA I G E+ L L + A Q V+AH+W GD+V+
Sbjct: 55 RLVRTHRKTSRKSLYLSSHAGRIVGWPVEAMLLRLRELTEHATQREFVYAHKWQVGDVLM 114

Query: 256 WDNR 259
WDNR
Sbjct: 115 WDNR 118

>ref|YP_001084475.1| taurine dioxygenase [Acinetobacter baumannii ATCC 17978]
Length = 278

Score = 85.5 bits (210), Expect = 8e-15, Method: Compositional matrix adjust.
Identities = 66/267 (24%), Positives = 109/267 (40%), Gaps = 38/267 (14%)

Query: 14 TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG----- 65
T+GA + + L L++ + A L H ++ F Q L+ Q A+ FG
Sbjct: 5 TIGAIIHIDIDLNALNEQTTQQIQQALLDHQVIFFRKQQLAPQAQADLARSFGTLHVHPIY 64

Query: 66 -AIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
+IE + +++ + + K D + N WH D T+ G V
Sbjct: 65 PSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFSKTPPLGCVL 105

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQQAGSAY 182
A +P VGG T ++ AA+ L + + +A H + + + H ++
Sbjct: 106 QAIKIPVGGDTLWSSNTAAFKGLPLELQQKLRGLTATHDIRKSFPLERFANNEEEREKL 165

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGR---HAAIIPGMDAAESERFLEGLVDWAC 238
+ + P+V+ HP TG P L + H + +P ESE+ L L + A
Sbjct: 166 LQ-TFKRNPVVPVVRTHPVTGEPLLFVSEGFTTHINELP---EQESEQLLNFLFEHAT 221

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
Q +W GDV +WDNRC H+A
Sbjct: 222 QEQLFHLRWKQDGDVAIWDNRCTQHKA 248

>emb|CAY27266.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 85.5 bits (210), Expect = 8e-15, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALDE + HS +YS+ KLG + P+R
Sbjct: 1 TEFADMRAAYDALDERLKHQTEDLVCLHSNMYSRGKLGADFTEEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I GM E+ L L ++A + P V++H W D V
Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMLLLDLTFATRDPFVYSHVWRNLDFV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|YP_348002.1| taurine dioxygenase [Pseudomonas fluorescens Pf0-1]
gb|ABA74013.1| putative taurine dioxygenase [Pseudomonas fluorescens Pf0-1]
Length = 289

Score = 85.5 bits (210), Expect = 9e-15, Method: Compositional matrix adjust.
Identities = 81/293 (27%), Positives = 123/293 (41%), Gaps = 49/293 (16%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T +ITP +GA + GV L+ L D + A+L++ +++F QHL+ D+ F +
Sbjct: 24 TVERITPI---IGAEIGGVDLSQPLSDEQLTEIRRAFLENHVVFVRDQHLTVDEHKAFGR 80

Query: 63 RFGA-----IERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPV 117
FG +E I G D + ++A+ R V WH D T
Sbjct: 81 LFGELRALPVEDIDGDDPELVV-IRANAQSR-----YVAGETWHTDGTADLA 126

Query: 118 MAQGAVFSAEVVPAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175

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      + G++   + PA+  GG T FA+M  A + L   + + + +A H
Sbjct: 127 PSMGSMlyVKETPAIGTGGDTLFFANMHLALEMLSPTMQQFLGELTAIHD----- 175

Query: 176 QQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEG 232
      + GY              P+V  HPETGR SL + G +H + +  ES+  L
Sbjct: 176 --GAIPWKGYEAPANLPKTEHPVVVRHPETGRKSLFVNSGFTSHIV-QLSGGESQVLLNM 232

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR 284
      L D   + P +   +W   +V WDNRC  H A WD+  P   HSR   R
Sbjct: 233 LFDLVAREPVLSCRVRWTPNSLVFWDNRCTQHHAH-WDY-FP----HSRYGER 279

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>ref|ZP_08152263.1| TauD/TfdA family dioxygenase [Rhodococcus equi ATCC 33707]
gb|EGD26110.1| TauD/TfdA family dioxygenase [Rhodococcus equi ATCC 33707]
Length = 268

Score = 85.5 bits (210), Expect = 9e-15, Method: Compositional matrix adjust.
Identities = 77/275 (28%), Positives = 116/275 (42%), Gaps = 45/275 (16%)

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Query: 1  MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
      +   T+ +TP   +GA V G+H+A L  A   +   A  H +L FP Q +   F
Sbjct: 4  LEAATVTVTPLAGAIGAIEVRGLHVAALSGADVELVRTALHDHGVLFPEQGVDPATHRAF 63

Query: 61  AKRFGAI-----ERIGGGDIVAISNVKAD-GTVRQHSPAEWDDMMKVIVGNMAWHADS 112
      A+ FG I           +G           IS +  D G+  Q +           WH D
Sbjct: 64  AQHFGDIVYPHEHLAHLGDEGYREISVISTDNGSAYQAN-----RWHCDEV 108

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
      +   ++ ++   +V+P VGG T +++  AA DAL   R  ++  +A H +   + L
Sbjct: 109 AWRAEPSRFSILHMQVLPEVGGDTLWSNQYAALDALSPPIREALYGLTATHRI----APL 164

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLE 231
      +V +A              PLV  HPETGR +L +   AI G+   ES R L
Sbjct: 165 PNVPEAR-----HPLVIRHPETGREALFVNDLFTSAIDGVTEDES-RALL 208

Query: 232 GLVDWACQAPRVHA-HQWAAGDVVVWDNRCLLHRA 265
      GL+   P           +W+ GD+ VWDN   + H A
Sbjct: 209 GLLKTVSIRPEFTVRRRWSVGDIADVNDNHFVQHNA 243

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>emb|CAY27467.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 85.5 bits (210), Expect = 9e-15, Method: Compositional matrix adjust.
Identities = 50/125 (40%), Positives = 64/125 (51%), Gaps = 7/125 (5%)

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Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
      T FADMRAAYDALD+ T+A           HSL+YS+  LG   +   +   P+R
Sbjct: 1  TEFADMRAAYDALDDETKAETEDLICEHSLMYRSGSLGFTDYSEEEKQMFK-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
      LV+ HP   R SL +  HA   + GM   E   L  L + A Q   VH H+W   D+V
Sbjct: 55  QRLVRTHPVHRRKSLYLSSHAGKVIGMTVPEGRLLLRDLNEHATQREFVHIHKWTVHDLV 114

Query: 255 VWDNR 259
      +WDNR
Sbjct: 115 MWDNR 119

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>emb|CAY27381.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 85.5 bits (210), Expect = 9e-15, Method: Compositional matrix adjust.

Identities = 49/124 (39%), Positives = 67/124 (54%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T FADMRAAYDAL T+AL+ HS ++S+ LG ++ + A +
Sbjct: 1 TEFADMRAAYDALVGETKALIEDLVCEHSRIFSKGALGF-----SFTEKEVKAFAPVRQ 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP+TGR SL + HA I G E+ L L + A Q V +H+W GD+V+
Sbjct: 55 RLVTRTHPKTGRKSLYLSSHAGRIVGWPVEAMLLRELTEHATQREFVFSHKWRVGDLMV 114

Query: 256 WDNR 259
WDNR
Sbjct: 115 WDNR 118

>ref|ZP_08152264.1| taurine dioxygenase [Rhodococcus equi ATCC 33707]
gb|EGD26111.1| taurine dioxygenase [Rhodococcus equi ATCC 33707]
Length = 321

Score = 85.1 bits (209), Expect = 9e-15, Method: Compositional matrix adjust.
Identities = 76/266 (28%), Positives = 120/266 (45%), Gaps = 27/266 (10%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFA-ALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
+ +T G +GA + GVH++ A A A+ A + +++F GQH +++D Q FA
Sbjct: 20 ITVTRLGENIGALIEGVHVSQDIPAEYAIRYALAAANKVVVFRGQHHVTDDIQYRFAGT 79

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNM-AWHADSTYMPVMAQGA 122
G+ T + D+ VI G +WH D +++ + + +
Sbjct: 80 LGS-----QTTTHPTLTSEDNRTLVIEGAANSWHTDVSFVDRIKAS 121

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ A +P GG T +A AAY+ L +ALV A HS Y + + H + G A
Sbjct: 122 ILRAVDIPPYGGATTWASTTAAYEQLPAPLKALVDSLWAVHSNEYDYAGV-HADRKGIAY 180

Query: 183 IGYGMDTTATPLR-----PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
+ T L+ P+V+VHPETG SLL+G G+ +ES + L +
Sbjct: 181 NRHETMQNFRLLKFEIEHPVVRVHPETGERSLLLGHFVKNFVGLKTSASAALFQLQERV 240

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLH 263
+ WA GD+V+WDNR H
Sbjct: 241 VRLENTLRWAWAPGDLVIWDNRATQH 266

>ref|ZP_01363100.1| hypothetical protein PaerPA_01000192 [Pseudomonas aeruginosa
PACS2]
ref|ZP_04936624.1| hypothetical protein PA2G_04110 [Pseudomonas aeruginosa 2192]
gb|EAG60743.1| hypothetical protein PA2G_04110 [Pseudomonas aeruginosa 2192]
Length = 300

Score = 85.1 bits (209), Expect = 9e-15, Method: Compositional matrix adjust.
Identities = 77/283 (27%), Positives = 120/283 (42%), Gaps = 18/283 (6%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L + P +GA + GV L+ LD A A+ AA ++H ++ F Q HL + Q FA
Sbjct: 14 LDVRPVAGRIGAEIRGVTLSGELDAATVEAIQAALVRHKVIFFRDQSHLDDQTQEAFHL 73

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
G + VA V + R + + + +WH D T++ + ++
Sbjct: 74 LG-----EPVAHPTVPSREGTRFLLELDGAEGRR-----NSWHTDVTTFVEAYPKASI 121

Query: 124 FSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL---GHVQQAGS 180
+ V P GG T +A+ +AY L R L + A HS Y + + V+Q +
Sbjct: 122 LRSVVPAPESGGDTVWANTASAYADLPAELRELADRLWAVHSNEYDYAGVKPSASVEQLEN 181

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
Y T P+V+VHP++G +LL+G + G+ +S L +
Sbjct: 182 -YRKVFTSTVYETEHPVVRVHPQSGERTLLLGHFVKRLKGLSQHDSAHLFAVLQGHVTRL 240

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+W AGDV +WDNR H A PRV+ L G
Sbjct: 241 ENTVRWRWQAGDVAIWDNRATQHYAIDDYGDQPRVVRVTLGG 283

>ref|YP_722716.1| taurine dioxygenase [Trichodesmium erythraeum IMS101]
gb|ABG52243.1| Taurine dioxygenase [Trichodesmium erythraeum IMS101]
Length = 316

Score = 85.1 bits (209), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 67/276 (24%), Positives = 106/276 (38%), Gaps = 39/276 (14%)

Query: 4 TTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
+ P +GA + G+ L TL D + +++ ++ F Q L+ Q+ FA+
Sbjct: 19 NNFNVYPLAGRIGAEIVGLDLKQTLSDETIHDRQVLIKYKVIFFRQQELTEISQVAFAR 78

Query: 63 RFGAIERI-----GGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTY 114
+FG + G +I + D Q WH D T+
Sbjct: 79 QFGILTTHAHLSSLPGHPEIFDFDYGRMDNRNTN-----WHTDVTF 120

Query: 115 MPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
+ ++ A +PAVGG T +A+ AY + R +Q A HS Y+ LG
Sbjct: 121 IDRPPFASILRAVEIPAVGGDTIWANTVTAYQDMPIPLRNFANQLWAVHSNTYN-DYLGA 179

Query: 175 V-----QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE 227
Q+ G + T L P+V+V P++G L IG + G ES
Sbjct: 180 TANISKKRQELGKIFTSIEYQT---LHPVVQVVPDSGERGLFIGAFVRQLQGFSINESM 235

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH 263
+ L+ L + + W GD+ WDNR H
Sbjct: 236 QILKILQSYIIRPENTVRWHWEQGDIADFWDNRVTQH 271

>ref|YP_558866.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia xenovorans LB400]
gb|ABE30814.1| Putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia xenovorans LB400]
Length = 315

Score = 85.1 bits (209), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 74/286 (25%), Positives = 122/286 (42%), Gaps = 16/286 (5%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++++TP A +GA + GV L L+ A + AA L+ ++ F Q L+++Q + F+ +
Sbjct: 11 SIEVTPLSAHIGAEIHGVDLTQKLEARQIAEIRAALLKWRVVFREQFLTHEQHVAFSAQ 70

Query: 64 FGAIERIG---GGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQ 120
FG + +G G + V + R+ + E + + G WH D T
Sbjct: 71 FGELT-LGHPVFGHVEGHPEVYSISKYRKATRFEGQTLQRPWTG--WHTDVTAAVNPPW 126

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
++ +P GG T + ++ AAY L R+ V H G
Sbjct: 127 ASILRGVTIPPYGGDTQWTLVAAYQKLSAPLRSFVDGLRGIHRFTPPAGASG-----TQ 181

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239
A++ PLV+VHPETG +L + +I G+ ES+ LE L + +
Sbjct: 182 AFVEAVEQRILVTEHPLVRVHPETGERALVSPSFLKSIVGVSPRESQVLELLWEHVTR 241

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA--EPWDFKLPRVMWHSRLAG 283
+W AG V WDNR H A + +D R ++ + L G
Sbjct: 242 PEFTVRFKWQAGSVAFWDNRATAHLAPTDIFDLDFDRQLYRTTLVG 287

>ref|YP_002008878.1| taurine dioxygenase [Cupriavidus taiwanensis LMG 19424]
emb|CAQ72826.1| Putative taurine dioxygenase [Cupriavidus taiwanensis LMG 19424]
Length = 282

Score = 85.1 bits (209), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 73/273 (26%), Positives = 117/273 (42%), Gaps = 26/273 (9%)

Query: 6 LQITPTGATLGATVTGVHLATLD-DAG-FAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+ P T+GA +TGV LA DAG FA + A LQ+ +L Q ++ + + FA++
Sbjct: 1 MHAELPTCTIGAELTGVSLADASRDAGLFAEIKALLLQYKVLFLRDQDITRAEHVAFARQ 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG +E V S+ + G V+ + + KV A+H D+T+ G V
Sbjct: 61 FGELE-----DHPVVGSDPEHPGLVQIYKSPD----SKVEHYENAFHCDATWRQAPPMGCV 112

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
PAVGG T + +M AY L + +A + A+HS+ ++ ++ +
Sbjct: 113 LRCVETPAVGGDTIWVNMGEAYRRLPQDIKARIEGLRAKHSIEHTFGANMAPEKRAALAA 172

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE-----GLVDW 236
+ M P+V+ HPETG L + + RF + L+ +
Sbjct: 173 QFPMVE-----HPVVRTHPETGEKILFVNAFTSHFANYHRGDVIRFGKDFMPGAGDLLHY 227

Query: 237 ACQAPRVHAHQ----WAAGDVVVWDNRCLLHRA 265
C + +Q W V +WDNRC H A
Sbjct: 228 LCAQAEIPEYQVRWRWKKHSVAIWDNRCTQHVA 260

>ref|ZP_06415883.1| Taurine dioxygenase [Frankia sp. EUN1f]
gb|EFC81286.1| Taurine dioxygenase [Frankia sp. EUN1f]
Length = 288

Score = 85.1 bits (209), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 75/285 (26%), Positives = 120/285 (42%), Gaps = 31/285 (10%)

Query: 3 QTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
Q++L+ P T+GA ++GV L L + AA L++ ++ F Q L+ Q FA
Sbjct: 10 QSSLDVQPLQPTIGAEISGVDLREPLTPEVRDQIKAALLKYKVVFFRDQELTQAQHEDFA 69

Query: 62 KRFGAI-ERIGGGD-----IVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADS 112
+ FG + G G+ I I++ + H+P DD+ + +H D+
Sbjct: 70 RHFGPLYTHPGAGNAGPDISPISIHRIASEDFKKYEKAHTPQAGDDVWE-----PYHTDT 123

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
++ V GAV A +P VGG T + D AY L + +A + H + +
Sbjct: 124 SWRLVPTWGAVLRAVNLPEVGGDTIWVDAALAYQGLPDDVKARLEGHHVTHDYRAALHQS 183

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLE 231
GH + P+V++H ETG +L + I G+D AES L
Sbjct: 184 GHDYPVVA-----HPVVRHLRETGEKTLWVNFTQRPTIVGLDRAESRELLT 229

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
++D + W G V WDNR +H A PR++
Sbjct: 230 AVIDQYRKPANQVRFSWRPGSVAFWDNRATVHYAVRNYGTFFPRL 274

>ref|ZP_04662843.1| taurine dioxygenase [Acinetobacter baumannii AB900]
Length = 293

Score = 85.1 bits (209), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 68/276 (24%), Positives = 110/276 (39%), Gaps = 38/276 (13%)

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Query: 5   TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          L I      T+GA +  + L  L++      + A L H ++ F  Q L+   Q   A+ F
Sbjct: 7   NLNIEVIKPTIGAIHIDIDLNALNEQTQQIQQALLDHQVIFFRKQQLAPQAQADLARSF 66

Query: 65  G-----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
          G      +IE +   +++ + + K D                      + N  WH D T+
Sbjct: 67  GTLHVHPIYPSIEDVP--EVMVLDSWKQD-----LRDNELWHIDVTFS 107

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLG 173
          G V  A  +P VGG T ++   AA+  L   +  +   +A H +   +  +
Sbjct: 108 KTPPLGCVLQAIKIPVGGDTLWSNTAAFKGLPLELQQKLRLGLTATHDIRKSFPLERFA 167

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR---HAAIPGMDAAESERF 229
          H ++      +      + P+V+ HP TG P L +      H + +P      ESE+
Sbjct: 168 HNEEEREKLLQ-TFKRNPPVHPVVRTHPVTGEPLLFVSEGFTTHINELP---EQESEQL 223

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          L L   A Q      +W  GDV +WDNRC  H+A
Sbjct: 224 LNFLFGHATQEQQFHLRWKWDGDVAIWDNRCTQHKA 259

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>ref|ZP_04382852.1| alpha-ketoglutarate-dependent taurine dioxygenase [Rhodococcus erythropolis SK121]
gb|EEN90245.1| alpha-ketoglutarate-dependent taurine dioxygenase [Rhodococcus erythropolis SK121]
Length = 305

Score = 85.1 bits (209), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 74/284 (26%), Positives = 113/284 (39%), Gaps = 41/284 (14%)

```

Query: 6   LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
          +TP   +GA ++ + L   +      + A L+  ++ F  Q +S+   FA +G
Sbjct: 39  FTLTPVTPFIGAEISDIDLRDPSEEQIEDVRRALLEWKVVFFRDQPISSVNHRDFAAHWG 98

Query: 66  AIE---RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
          +E   +   G++ A+   +      + SP                      WH D T+   G+
Sbjct: 99  ELEVHPLLPQGEVPAVVRFERG---EDSPG-----TENIWHVDVTWTKTPPLGS 144

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK---LGHVQQAG 179
          V  A  VP  GG T +ADM  A+D L +  + L+  + A H  V S  +      ++Q
Sbjct: 145 VLRAIDVPPAGGDTLWADMGNADFCLPDEIKDLIDGKDAIHDFVPSFGRGMSPEKLEQMK 204

Query: 180 SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAAIPGMDAAESERFLEGLV---- 234
          Y                      L P+V+ HPETGR +L +      IP MD  E   L  L
Sbjct: 205 EQYPPV-----LHPMVRKHPETGRKTLFVNSLFTTHIPMDPVEGNDLLNLLFAQVK 256

Query: 235 --DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
          D+ C+      +WA   +  WDNR  H A   F   RVM
Sbjct: 257 VPDFQCR-----FKWAPNSIAFWDNRATQHYAASDYFPHRRVM 294

```

>ref|YP_002767959.1| dioxygenase [Rhodococcus erythropolis PR4]
dbj|BAH35220.1| putative dioxygenase [Rhodococcus erythropolis PR4]
Length = 282

Score = 85.1 bits (209), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 74/284 (26%), Positives = 113/284 (39%), Gaps = 41/284 (14%)

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Query: 6   LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65

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      +TP      +GA ++ + L      +      + A L+ ++ F Q +S+      FA +G
Sbjct: 16  FTLTPVTPFFIGAEISDIDLRLDPSEEQIEDVRRALLEWKVVFFRDQPISSLNHRDFAAHWG 75

Query: 66  AIE--RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGA 122
      +E      + G++ A+      +      + SP                      WH D T+      G+
Sbjct: 76  ELEVHPLLPQGEVPAVVRFERG----EDSPG-----TENIWHVDVTWTKTPPLGS 121

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK---LGHVQQAG 179
      V A VP GG T +ADM A+D L + + L+ + A H V S +      ++Q
Sbjct: 122 VLRAIDVPPAGGDTLWADMGNADFCLPDEIKDLIDGKDAIHDFVPSFGRGMSPEKLEQMK 181

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV---- 234
      Y                      L P+V+ HPETGR +L +      IP MD E      L L
Sbjct: 182 EQYPPV-----LHPMVRKHPETGRKTLFVNSLFTTHIPDMDPVEGNDLLNLLFAQVK 233

Query: 235 --DWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVM 276
      D+ C+      +WA + WDNR H A F RVM
Sbjct: 234 VPDFQCR-----FKWAPNSIAFWDNRRATQHAAASDYFPHRRVM 271

```

>emb|CAY27496.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 85.1 bits (209), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 67/125 (53%), Gaps = 7/125 (5%)

```

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
      T FADMRAAYDALDE +      HS ++S+S LG      +      P+R
Sbjct: 1   TEFADMRAAYDALDEEIKTECENLICEHSQFLSRSILGFTDFTDDERRRFA-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
      LV+ HP TGR SL + HA AI G      E+ FL L++ + Q      V++HQW D+V
Sbjct: 55  QRLVRRHPVTGRRSLYLASHAGAILGWLVEPARAFLRDLIEHSTQPQLVYSHQWRQWDLV 114

Query: 255 VWDNR 259
      +WDNR
Sbjct: 115 MWDNR 119

```

>ref|ZP_04891715.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 1655]
gb|EDU12699.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 1655]
Length = 277

Score = 85.1 bits (209), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 80/293 (27%), Positives = 114/293 (38%), Gaps = 29/293 (9%)

```

Query: 4   TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
      T L +T      LGA V V L+ DA      + A H +L F GQ LS + FA
Sbjct: 2   TRLTLTRLTPALGAIVDDVDLSNATDALRDDIRGALAHHQVLFRRGQRLSAARHRDFAAG 61

Query: 64  FGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMP 116
      FG +      +I+ + N D      + N WH D T+
Sbjct: 62  FGDLHVHPIYSPHPDAREIMVLDAVFD-----LQDNAIWHTDVTFTE 104

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGH 174
      + ++ +A +P GG T + AAYDAL +A + +A+H      + + G
Sbjct: 105 TPPRASILAAHTLPETGGDTLWGSFGAAYDALSGRVKAQLDGLTAQHDFTKSFPLKRFG- 163

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL 233
      V A      T + P+V+ HPETGR +L +      I G+ E      L L
Sbjct: 164 VTAEDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNEGFTTEIDGLPEEEGAALLRFL 223

```

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
+ +W GDV WDNR +H A K RVM + + G RP
Sbjct: 224 FAHQSRPEFTLRWRWQPGDVAFWDNRSTIHYAVNDYGKAHRVMHRATIVGDRP 276

>ref|ZP_04520779.1| alpha-ketoglutarate-dependent taurine dioxygenase
(2-aminoethanesulfonate dioxygenase) (Sulfate
starvation-induced protein3) (SSI3) [Burkholderia
pseudomallei MSHR346]
gb|EEP49693.1| alpha-ketoglutarate-dependent taurine dioxygenase
(2-aminoethanesulfonate dioxygenase) (Sulfate
starvation-induced protein3) (SSI3) [Burkholderia
pseudomallei MSHR346]
Length = 277

Score = 85.1 bits (209), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 80/293 (27%), Positives = 114/293 (38%), Gaps = 29/293 (9%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T L +T LGA V V L+ DA + A H +L F GQ LS + FA
Sbjct: 2 TRLTLRLTPALGAIVDDVDLSNATDALRDDIRVALAHHQVLFRRGQRLSAARHRDFAAG 61

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
FG + +I+ + N D + N WH D T+
Sbjct: 62 FGD LHVHP IYPSHPDAREIMVLDNAVFD-----LQDNAIWHTDVTFTFE 104

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGH 174
+ ++ +A +P GG T + AAYDAL +A + +A+H + + G
Sbjct: 105 TPPRASILAATLPETGGDTLWGSFGAAYDALSGRVKAQLDGLTAQHDFTKSFPLKRFG- 163

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL 233
V A T + P+V+ HPETGR +L + I G+ E L L
Sbjct: 164 VTAEDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNEGFTTEIDGLPEEEGAALLRFL 223

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
+ +W GDV WDNR +H A K RVM + + G RP
Sbjct: 224 FAHQSRPEFTLRWRWQPGDVAFWDNRSTIHYAVNDYGKAHRVMHRATIVGDRP 276

>gb|ADC34028.1| TfdA-like protein [uncultured bacterium]
Length = 197

Score = 84.7 bits (208), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 64/210 (30%), Positives = 93/210 (44%), Gaps = 17/210 (8%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM 115
QQI FAK+FG + V +K +P + + G + WH+D+TY+
Sbjct: 1 QQIAFAKKFG-----EPVEYPQLKGLPESPFITPVVLEHERNNFGGI-WHSDTTYL 51

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQR---SARHSLVYSQSKL 172
PV G++ A VP GG T FA+ AY+ L R + SA ++++
Sbjct: 52 PVPPMGSM LLAAREVPPYGGDTLFANQYLAYETLSAGLRRTLDGLIGVSASSKADVTKTRE 111

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLE 231
++QAGS ++ PLV+ HPETGR +L H I G ES L+
Sbjct: 112 DALKQAGSGATPKNLEAE---HPLVRTHPETGRKALYTSVAHTAHIKGWTEKESLPLLQ 167

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
L D + W AG + WDNRC+
Sbjct: 168 FLWDHQTKPEFTCRFGWKAGSLAFWDNRCV 197

>ref|ZP_06637645.1| taurine dioxygenase [Serratia odorifera DSM 4582]
gb|EFE97368.1| taurine dioxygenase [Serratia odorifera DSM 4582]
Length = 282

Score = 84.7 bits (208), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 81/299 (27%), Positives = 126/299 (42%), Gaps = 36/299 (12%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA V V LA L D F L+ A L+H +L F Q ++ QQ A RF
Sbjct: 5 LVITPLGPHIGALVENVTLARPLGDGQFEQLYHALLKHQVLFFRNQPITPLQQRDLAGR 64

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGN-----MAWHADSTYM 115
G + I V + D+ ++IV + WH D T++
Sbjct: 65 GDLH-----IHPVYPHAS-----DVEEIIIVLDTDDNNPPDNDNWHTDVTFI 105

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
GA+ +A+ +P+ GG T +A AA+DAL + L+ A H S + H
Sbjct: 106 DNPPLGAILAAKRLPSTGGDTLWASGIAAFDALSTPFKQLLSGLRAEHDFTKSFPEYKH- 164

Query: 176 QQAGSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
+ + + + P L P+V+ HP +G+ +L + I + ES+ L G
Sbjct: 165 RGSEEQHQWRQAVQNNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDLSPKESDALL-G 223

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWVWNRCLLHRAEPWDFKLPRVMWHSRLAG-RPETEG 289
+ P +W D+ +WDNR H A R+M + + G +P +G
Sbjct: 224 FLFAHITKPEFQVRWRWQENDIAIWDNRVTQHYANADYLPQRRIMHRATVLGDKPFYKG 282

>emb|CAY27398.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 84.7 bits (208), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 50/124 (40%), Positives = 66/124 (53%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDAL E +A + A HS+ YS+ +LG + G + +
Sbjct: 1 TEFADMRAAYDALPEDMKARLEGLQAHHSIAYSRLGLF-----EFGDEAERLKGAVH 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ P TGR SL + HA+ I G + L L + A Q V+ H W AGD+V+
Sbjct: 55 PLVRTLPRTGRRSLYLASHANRILGWSVPDGRLLLLDLTEHATQRQFVYRHAWRAGDLVM 114

Query: 256 WDNR 259
WDNR
Sbjct: 115 WDNR 118

>emb|CAY27297.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 84.7 bits (208), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 50/125 (40%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DMRAAYDALDE + + HS +YS+ KLG + P+R
Sbjct: 1 TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLGLADFTEEECRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 254
LV+ HP TGR SL + HA I GM E+ L L ++A + P V++H W D V
Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMLLLLLTFATRDPFVYSHVWRLNDFV 114

Query: 255 VWDNR 259
+WDNR

```
>ref|YP_112297.1| taurine catabolism dioxygenase TauD, TfdA family protein
[Burkholderia pseudomallei K96243]
ref|YP_336597.1| taurine catabolism dioxygenase TauD, TfdA family protein
[Burkholderia pseudomallei 1710b]
ref|YP_001077129.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei 1106a]
ref|ZP_01768562.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 305]
ref|ZP_02408636.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei
DM98]
ref|ZP_02417096.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei
14]
ref|ZP_02453208.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei
91]
ref|ZP_02461344.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei 9]
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ref|ZP_02476842.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei B7210]
ref|ZP_02495489.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei NCTC 13177]
ref|ZP_02511571.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei BCC215]
ref|ZP_03455696.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 576]
ref|ZP_03794813.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pakistan 9]
ref|ZP_04521425.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei MSHR346]
ref|ZP_04812401.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1106b]
ref|ZP_04889061.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 1655]
ref|ZP_04893535.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pasteur 52237]
ref|ZP_04899052.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei S13]
ref|ZP_04954640.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1710a]
ref|ZP_04964051.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 406e]
emb|CAH39780.1| taurine catabolism dioxygenase TauD, TfdA family protein [Burkholderia pseudomallei K96243]
gb|ABA52088.1| taurine catabolism dioxygenase TauD, TfdA family protein [Burkholderia pseudomallei 1710b]
gb|ABN95296.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 1106a]
gb|EBA47004.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 305]
gb|EDO83624.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 406e]
gb|EDO90373.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pasteur 52237]
gb|EDS82064.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei S13]
gb|EDU10045.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 1655]
gb|EEC32685.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 576]
gb|EEH24687.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pakistan 9]
gb|EEP50339.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei MSHR346]
gb|EES23026.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1106b]
gb|EET04162.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei 1710a]
Length = 282

Score = 84.7 bits (208), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 79/273 (28%), Positives = 110/273 (40%), Gaps = 26/273 (9%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++I P +GA + GV LA DD FA + AA L H +L Q ++ + + FA+R
Sbjct: 1 MRIEPLTCAIGAELVGVCLADAHDDGLFAEIRAALLAHRVLFRLDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG +E VA S+ G VR + E + AWH D+T+ G V
Sbjct: 61 FGELE----DHPVAGSDPDHPGLVRIYKTPEQPNEHY----ENAWHTDATWRQAPPLGCV 112

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
P VGG T +A+M AY+ L E +A + ARHS+ ++ G
Sbjct: 113 LRCVACPEVGGDTMWANMVLAYENLPEHVKAQIADLRARHSI---EASFGAAMPIDGRLA 169

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMDAAESERFLEGL 233
A P+V+ HPETG L + A G DA L G
Sbjct: 170 LKAQFPDAE--HPVVRTHPETGEKVLVFNATFTHTNYHTPARVRVQGQDANPGAALLLG 227

Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ P +W V +WDNR H A
Sbjct: 228 LLSQAYIPEYQVRWRWRKNSVAIWDNRSTQHYA 260

>ref|YP_002780830.1| dioxygenase [Rhodococcus opacus B4]
dbj|BAH51885.1| putative dioxygenase [Rhodococcus opacus B4]
Length = 304

Score = 84.7 bits (208), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 74/278 (26%), Positives = 118/278 (42%), Gaps = 34/278 (12%)

```
Query: 5   TLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
          + ++ P   +LGA +  V+L +  DDA FA L   L++ +L F  Q +S  + +  A+
Sbjct: 22  SFRLAPMTCSLGAELFDVNLGDVSRDDALFAELRELLLEYKVLFFRDQDMSRAEHVALAE 81

Query: 63  RFGAIERIGGGDIVAISNVKADGTVRQH----SPAEWDDMMKVIVGNMAWHADSTYMPVM 118
          RFG +E          VA S+   G VR +   SPAE  +          A+H D+T+
Sbjct: 82  RFGPLE----DHPVAGSDPAHPGLVRIYKDLDSPAEHYEN-----AFHCDATWRENP 129

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
          G V  A   P VGG T + +M AY+ L + + +   ARHS+  ++  G  Q
Sbjct: 130 PMGCVLRAVETPPVGGDTIWNMALAYEKLDPGVKKQIEGLRARHSI---EASFGAAQTE 186

Query: 179 GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LE 231
          +   A   P+V+ HP+TG  L +  A          ++ R+
Sbjct: 187 EQRRALHQRFPDAE--HPVVVTHPDTGEKILFVNSFATHFVNYHTPDNIRYGDIDYAPGSS 244

Query: 232 GLVDWACQAPRVHAHQ---WAAGDVVVWDNRCLLHRA 265
          L+++   +  +Q   W   V +WDNR  H A
Sbjct: 245 NLLNYLISQASIPEYQVRWRWTPNSVAIWDNRSTQHYA 282
```

>ref|ZP_07004378.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Pseudomonas savastanoi pv. savastanoi NCPPB 3335]
gb|EFI00380.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Pseudomonas savastanoi pv. savastanoi NCPPB 3335]
Length = 286

Score = 84.7 bits (208), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 85/298 (28%), Positives = 129/298 (43%), Gaps = 48/298 (16%)

```
Query: 4   TTLQITPTGATLGATVTGVHLATLD-DAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
          T  ++TP   +GA V+GV L+   +   +  A+L++ +L+F  QHL+ +Q  F +
Sbjct: 21  TVNRLTPI---IGA EVSGVDLSQPPGEEQLTEIRRAFLENHVLVFRDQHLTVEQHKAFGR 77

Query: 63  RFG-----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV 117
          FG      +E I G D   +  V+A+   R          WH D T
Sbjct: 78  LFGPLRALPVESIDGDDPELVV-VRANAQSR-----FAAGELWHTDGTADLE 123

Query: 118 MAQGAVFSAEVPVAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
          + G++   +  PA+  GG T FA+M  A + L  A +A + + +A H          G +
Sbjct: 124 PSMGSMLYVKETPAIGTGGDTLFANMHLAIEMLSPAMQAFLEGELTAIHD-----GEI 175

Query: 176 QQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEG 232
          + GY          P+V  HPETGR SL +  G  +H +   + A ES  L
Sbjct: 176 -----PWKGYQPPANLPKSEHPVVVRHPETGRRSLVNSGFTSHIV-QLSAGESRTLLNM 229

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSR---LAGRPE 286
          L D   + P +   +W   +V WDNRC  H A WD+  P   +  R   L GRP+
Sbjct: 230 LFDLIAREPCLSCRVRWEPNTLVFWDNRCTQHHAV-WDY-FPHSRYGERVTILGGRPQ 285
```

>ref|ZP_08155875.1| taurine dioxygenase [Rhodococcus equi ATCC 33707]
gb|EGD22661.1| taurine dioxygenase [Rhodococcus equi ATCC 33707]
Length = 299

Score = 84.7 bits (208), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 78/277 (28%), Positives = 114/277 (41%), Gaps = 32/277 (11%)

```
Query: 5   TLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
          L   P   ++GA V GV L +  DD  FA L +  L+H +L F  Q +S  + +  A+
```

Sbjct: 17 NLDARPLTCSIGAEVHGVDLGEVSRDDVLF AELKSRLLEHKVLF FRDQDMSRAEHVALAQ 76

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
RFGA+E V S+ + G VR + + D + A+H D+T+ G

Sbjct: 77 RFGALE----DHPVVGSDPEHPGLVRIYK--DLDSAPEAF--ENAYHCDATWRVNPMPGC 128

Query: 123 VFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V PAVGG T + +M AY L E + + ARHS+ S ++Q

Sbjct: 129 VLRCVEGPVAVGGDTIWVNMALAYARLPERVKERIEGLRARHSIEASFGARLP IEQRLEL- 187

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA-- 240
+ P+V+VHPETG L + + AE+ R +D+A A

Sbjct: 188 ----KERFPDAEHPVVRVHPETGEKILFVNSFTTHLTNFHTAENVR---SGIDYAPGAGD 240

Query: 241 -----PRVHAH-QWAAGDVVVWDNRCLLHRA 265
P +W V +WNR H A

Sbjct: 241 LLRYLQTQATIPEYQVRWRWTKNSVAIWDNRSTQHYA 277

>ref|YP_299246.1| taurine dioxygenase [Ralstonia eutropha JMP134]
gb|AAZ64402.1| Taurine dioxygenase [Ralstonia eutropha JMP134]
Length = 280

Score = 84.7 bits (208), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 76/301 (25%), Positives = 125/301 (41%), Gaps = 43/301 (14%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHA AWLQHALLIFPGQHLSNDQQITFAKR 63
+Q+ P ++GA +TGV L + DD+ A + A L+H +L F Q ++ D + FAKR

Sbjct: 1 MQVNPLTCSIGAEELTGVLGNVARDDSLHAEIKALLKHRVLF FRDQEMTRDDHVAFKR 60

Query: 64 FGAIERIGGGDIVA-----ISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM 118
FG +E + V I VK++ R H +H+D+++

Sbjct: 61 FGDLEDHPVANTVPGYPGLIEIVKSEK--RDHF-----ENTYHSDASWRANP 105

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
+GAV P VGG T + +M AY L E + + A+H + +S + ++

Sbjct: 106 PRGAVLRCISCPEVGGDTIWVNMVDAYKNLPEEIKQKIEGLRAKHGIEHSFGAIMSTEER 165

Query: 179 GSAYIGYGMDDTTATPL--RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG---- 232
PL P+V+ HP+TG L + + E+ RF +

Sbjct: 166 EEL-----VRKHPLVDHPVVRTHPDTGEKILYVTPFSTHFINYHTPENVRFGQDKTPG 218

Query: 233 ---LVDWACQAPRVHAHQ---WAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-R 284
L+++ + +Q W V +WDN H A + PR M + + G R

Sbjct: 219 ASLLLNLYLLSQAAIPEYQVRFRWRPNNSVAIWDNMATQHYAVSDYWPAPRRMERATIMGDR 278

Query: 285 P 285
P

Sbjct: 279 P 279

>ref|YP_001206008.1| putative dioxygenase; putative taurine dioxygenase
[Bradyrhizobium
sp. ORS278]
emb|CAL77783.1| putative dioxygenase; putative taurine dioxygenase [Bradyrhizobium
sp. ORS278]
Length = 230

Score = 84.7 bits (208), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 75/275 (27%), Positives = 108/275 (39%), Gaps = 72/275 (26%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHA AWLQHALLIFPGQHLSNDQQITFAKR 63
+ +Q+ PTG LGA V V L + DD FA+ A L+H +L+ Q L++ F++R

Sbjct: 14 SLVQVLPTGKALGAEVCNVDLRSFDDWAFASFMRRALLKHQVLLVRWQRLTDRDIAAFSRR 73

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV-MAQGA 122
FG HAD Y +G

Sbjct: 74 FG-----HADLHYTSYGTTRGE 90

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
S F + AAYDAL A R+ V R + + AG

Sbjct: 91 SLS-----FCSLYAAYDALSPAMRSRVAHLKVRQRTIDTADDGRRTIFAG--- 135

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAP 241
P+ PLV +H +TGR L +G+ H+ + G++ ESE L L A +

Sbjct: 136 -----PVHPLVGLHADTGRSMLALQRRHSYVVGLEQDESEALLNDLWQLAERPE 185

Query: 242 RVHAHQWAAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
H GD++VWD RC +HR E D +PR++

Sbjct: 186 FSWTHTCRGGDLIVWDTRCTIHRHEAPD--MPRL 218

>ref|YP_583867.1| taurine catabolism dioxygenase TauD/TfdA [Cupriavidus metallidurans CH34]
gb|ABF08598.1| Taurine dioxygenase [Cupriavidus metallidurans CH34]
Length = 282

Score = 84.7 bits (208), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 73/274 (26%), Positives = 118/274 (43%), Gaps = 28/274 (10%)

Query: 6 LQITPTGATLGATVTGVHLA--TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+Q+ P +GA + GV+LA D FA + A L+H ++ Q S + + FA+R

Sbjct: 1 MQVKPLTCAIGAELVGVNLADAIKSDDLFAEIRAQLLKHVVFLRDQTF SRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E VA S+ + G VR + SP + +D + AWH+D+T+ GA

Sbjct: 61 FGELE----DHPVAGSDPEHPGLVRIYKSPDQPNDRYE----NAWHSDDTWREAPQFGA 111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V P VGG T +A+M AY+ L + ++ + ARHS+ S + +++ +

Sbjct: 112 VLRCVECPVGGDTMWANMALAYENLPDHKSQIADLRARHSIEASFGAVMPIEKRLALK 171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE-----GLVD 235
Y P+V+ HP+TG L + RF + L+

Sbjct: 172 ERY-----PDAEHPVVRTHPDTGEKILYNAFTTHTFTNYHTPARVRFQDGNPGATDLLR 226

Query: 236 WACQAPRVHAHQ---WAAGDVVVWDNRCLLHRA 265
+ + +Q W V +WDN H A

Sbjct: 227 YLISQAYIPEYQVRWRWQPNSVAIWDNTATQHYA 260

>ref|YP_788349.1| hypothetical protein PA14_02420 [Pseudomonas aeruginosa UCBPP-PA14]
ref|ZP_06876179.1| hypothetical protein PaerPab_01050 [Pseudomonas aeruginosa PAb1]
gb|ABJ15148.1| putative alkylsulfatase [Pseudomonas aeruginosa UCBPP-PA14]
Length = 300

Score = 84.7 bits (208), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 76/282 (26%), Positives = 117/282 (41%), Gaps = 16/282 (5%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
L + P +GA + GV L+ LD A A+ AA ++H ++ F Q HL + Q FA

Sbjct: 14 LDVRPVAGRIGAEIRGVTLSEGLDAATVEAIQAALVRHKVIFFRDQSHLDDQTQEAF AHL 73

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
G + VA V + R + + + +WH D T++ + ++

Sbjct: 74 LG-----EPVAHPTVPSREGTRFLELDGAEGRA----NSWHTDVTTFVEAYPKASI 121

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS--KLGHVQQAGSA 181
+ V P GG T +A+ +AY L R L + A HS Y + K +
Sbjct: 122 LRSVAPESGGDTVWANTASAYADLPaelRELADRLWAVHSNEYDYAGVKPSASLEQLEN 181

Query: 182 YIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAP 241
Y T P+V+VHP++G +LL+G + G+ +S L +
Sbjct: 182 YRKVFTSTVYETEHPVVRVHPQSGERTLLLGHFVKRLKGLSQHDSAHFLAVLQGHVTRLE 241

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+W AGDV +WDNR H A PRV+ L G
Sbjct: 242 NTVRWRWQAGDVAIWDNRATQHYAIDDYGDQPRVVRVTLGG 283

>ref|YP_003278927.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
CNB-2]
gb|ACY33631.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
CNB-2]
Length = 303

Score = 84.3 bits (207), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 68/275 (24%), Positives = 118/275 (42%), Gaps = 27/275 (9%)

Query: 5 TLQITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
+L++ P ++GA ++ VHL A D+ A + A L+H ++ F Q ++ + + FA+
Sbjct: 20 SLEVNPLTCSIGAELSNVHLGAAAEDGLMAEIRQALLKHRVIFFRDQDITRAEHVAFAR 79

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGA 122
+FG +E V S+ + G V+ + + + +WH D+T+ G
Sbjct: 80 KFGELE---DHPVVGSHPEHPGLVQIYKTPD---NPLDRNENSWHTDATWREQPPMGC 131

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V P VGG T + +M AY+ L + + + ARHS+ S + +++ +
Sbjct: 132 VLRCVECPVVGDTMWVNMVMAYENLPDDIKVKIEHLRARHSIEASFGAVMPIEKRLALK 191

Query: 183 IGYGMTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMDAAE-SERFL 230
Y P+V++HPETG L + A+ G+D + S + L
Sbjct: 192 AQY-----PDAEHPVRIHPETGEKILFVNSSFTTHFTNYNTPANVRFGLDKSPGSSQL 246

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L A +W+ V WDNR H A
Sbjct: 247 NYLTSQAMIPEYQVRFKWSKNSVAFWDNR.STQHYA 281

>ref|ZP_05127632.1| alpha-ketoglutarate-dependent taurine dioxygenase [gamma
proteobacterium NOR5-3]
gb|EED31660.1| alpha-ketoglutarate-dependent taurine dioxygenase [gamma
proteobacterium NOR5-3]
Length = 274

Score = 84.3 bits (207), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 69/262 (26%), Positives = 112/262 (42%), Gaps = 15/262 (5%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP LGA + G+ L+ L + A L ++ ++ F Q +S ++Q A F
Sbjct: 2 LAITPLAGALGAQIHGLDLSQDLSEGDAAKLRQLLNEYEVIFFRDQDISGERQRDLALAF 61

Query: 65 GAIE-RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
G ++ + I + T+ + +P ++ K+ AWH+D T+ G V
Sbjct: 62 GPLQVHPAYKTVEGIPEL----TILESTP---ENPTKI----EAWHSDMTFREHPPMGTV 110

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
+ VVP GG T +A M AYDAL A ++ + +A H + K + G +

Sbjct: 111 LKSVVPPKGGDTMWASMTTAYDALSPAMQSFLGGLTAVHDFSWG-FKESIAEPGGRERL 169

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPR 242

+ P+++VHPET R + + I G+ +ES LE L

Sbjct: 170 AAAIAANPPVRHPVIRVHPETNRKVIFVNSLFTTHIEGLAPSESRAILEFLFAHVTTVEF 229

Query: 243 VHAHQWAAGDVVVWDNRCLLHR 264

QW + +WDNR H+

Sbjct: 230 TVRFQWQPHSIAIWDNRSTQHK 251

>ref|ZP_06462103.1| taurine dioxygenase [Pseudomonas syringae pv. aesculi str. NCPPB3681]

ref|ZP_06480863.1| taurine dioxygenase [Pseudomonas syringae pv. aesculi str. 2250]
Length = 289

Score = 84.3 bits (207), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 85/298 (28%), Positives = 129/298 (43%), Gaps = 48/298 (16%)

Query: 4 TTLQITPTGATLGATVTGVHLATLD-DAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T ++TP +GA V+GV L+ + + A+L++ +L+F QHL+ +Q F +

Sbjct: 24 TVNRLTPI---IGA EVSGVDLSQPPGEEQLKEIRRAFLENHVLVFRDQHLTVEQHKAFGR 80

Query: 63 RFG-----AIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPV 117
FG +E I G D + V+A+ R V WH D T

Sbjct: 81 LFGPLRALPVESIDGDDPELVV-VRANAQSR-----FVAGELWHTDGTADLE 126

Query: 118 MAQGAVFSAEVPVAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
+ G++ + PA+ GG T FA+M A + L A +A + + +A H G +

Sbjct: 127 PSMGSMLYVKETPAIGTGGDTLFANMHLAIEMLSPAMQAFLEGELTAIHD-----GEI 178

Query: 176 QQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEG 232
+ GY P+V HPETGR SL + G +H + + ES L

Sbjct: 179 -----PWKG YQPPANLPKSEHPVVVRHPETGRRS LFN VNSGFTSHIV-QLSPGESRTVLNM 232

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSR---LAGRPE 286
L D + P + +W +V WDNRC H A WD+ P + R L GRP+

Sbjct: 233 LFDLIAREPCLSCRVRWEPNTLVFWDNRCTQHHAV-WDY-FPHSRYGERVTILGGRPQ 288

>emb|CAY27372.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 84.3 bits (207), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 53/127 (41%), Positives = 68/127 (53%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTA--TP 193
T FADMRA D+LD T+AL HS +YS+ LG + + D A P

Sbjct: 1 TEFADMRAGRDSLDPETQALCEDLICEHSQIYSRQILG-----FTDFTDDERARFAP 52

Query: 194 LRP-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
+R LV+ HP TGR SL + HA I G + FL LV+ A Q V++HQW GD

Sbjct: 53 VRQVLVRTHPVTGRKSLYLSSHAGGIEGWVPVGACAFRLDLVEHATQRQFVYSHQWRVGD 112

Query: 253 VVVWDNR 259

+V+WDNR

Sbjct: 113 LVMWDNR 119

>ref|YP_001439004.1| taurine dioxygenase [Cronobacter sakazakii ATCC BAA-894]
gb|ABU78168.1| hypothetical protein ESA_02939 [Cronobacter sakazakii ATCC BAA-894]
Length = 283

Score = 84.3 bits (207), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 75/290 (25%), Positives = 123/290 (42%), Gaps = 30/290 (10%)

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>ref|ZP_02409593.1| taurine dioxygenase [Burkholderia pseudomallei 14]
ref|ZP_02452123.1| taurine dioxygenase [Burkholderia pseudomallei 91]
ref|ZP_02460283.1| taurine dioxygenase [Burkholderia pseudomallei 9]
ref|ZP_02475779.1| taurine dioxygenase [Burkholderia pseudomallei B7210]
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ref|ZP_02494397.1| taurine dioxygenase [Burkholderia pseudomallei NCTC 13177]
ref|ZP_02502650.1| taurine dioxygenase [Burkholderia pseudomallei 112]
Length = 272

Score = 84.3 bits (207), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 80/290 (27%), Positives = 115/290 (39%), Gaps = 32/290 (11%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
++TP LGA V V L+ DA + AA H +L F GQ LS + FA FG
Sbjct: 3 RLTPA---LGAIVDDVLSNATDALRDDIRAALAHHQVLFRRGQRLSAAHRDFAAGFGD 59

Query: 67 I-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
+ +I+ + N D + N WH D T+
Sbjct: 60 LHVHPIYPSPDAREIMVLDNAVFD-----LQDNAIWHTDVTFTETPP 102

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQ 177
+ ++ +A +P GG T + AAYDAL +A + +A+H + + G V
Sbjct: 103 RASILAAHTLPETGGDTLWGSFGAAYDALSGRVKAQLDGLTAQHDFTKSFPLKRFG-VTA 161

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
A T + P+V+ HPETGR +L + I G+ E L L
Sbjct: 162 EDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNNEGFTTEIDGLPEEEGAALLRFLFAH 221

Query: 237 ACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
+ +W GDV WDNR +H A K RVM + + G RP
Sbjct: 222 QSRPEFTLRWRWQPGDVAFWDNIRSTIHYAVNDYGKAHRVMHRATIVGDRP 271

>emb|CAY27346.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 84.3 bits (207), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMR AYDALDE + + HS +YS+ KLG + I + P+R
Sbjct: 1 TEFADMRTAYDALDERLKHQIVDLVCLHSSMYSRGKLGTEFTEERIVFK-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I GM E+ L L ++A + V AH W D V
Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMLLLLTEFATREHFVCAHVVRINDFV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>emb|CAY27342.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27474.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27487.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 84.3 bits (207), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 49/125 (39%), Positives = 64/125 (51%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALD+ T+A HSL+YS+ LG + + P+R
Sbjct: 1 TEFADMRAAYDALDDETKAETEDLICEHSLMYSRSLGFTDYSEEEKQMFK-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP R SL + HA + GM E L L + A Q V+ H+W D+V
Sbjct: 55 QRLVRTHPVHRRKSLYLSSHAGKVIGMTVPEGRLLLRDLTEHATQREFVYVHRWTVHDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>gb|ACG80554.1| TfdA [uncultured bacterium]
Length = 119

Score = 84.3 bits (207), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 48/128 (37%), Positives = 65/128 (50%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T F DMRAAYDALD+ T+ V HS ++S+ +G D R
Sbjct: 1 TEFCDMRAAYDALDDETKEEVQDMVCEHSQMFSRQIIGFYDFT-----DEERERFR 51

Query: 196 P----LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251
P +V+ HP TGR SL + HA I G E+ +L L++ A Q V+ H+W G
Sbjct: 52 PVRQCMVRTHPVTGRKSLYLSSHAGGIVGWPMPEARGLRDLIEHATQREFVYTHKWQVG 111

Query: 252 DVVVWDNR 259
D+V+WDNR
Sbjct: 112 DLVMWDNR 119

>ref|ZP_06055483.1| taurine dioxygenase [alpha proteobacterium HIMB114]
gb|EEY75252.1| taurine dioxygenase [alpha proteobacterium HIMB114]
Length = 270

Score = 84.3 bits (207), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 66/278 (23%), Positives = 124/278 (44%), Gaps = 25/278 (8%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
+++TP +GA + L+ ++ + ++ ++ F Q L ++ I FAK+FG
Sbjct: 5 IKVTPNKNNVGAIIIEA-ELSKFNNDIIEVKDVLAEYGVVFFRNQRLDSEYIKFAKQFG 63

Query: 66 AIERIGGGDIVAISNVK--ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
+ + + ++ ++ TV + P E +++ G WH DSTY + +
Sbjct: 64 PL-----AEYPMLKGLEGYSEITVVEKKPNE-----EIMFGE-GWHTDSTYTKPPRFTM 112

Query: 124 FSAEVPVAVG-GRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQQAGS 180
+ P G G T FA +Y+ LDE T+ + A S S+++ V + G+
Sbjct: 113 LYSIKTPEKKGKNTMFASQYKSYETLDEKTKKKIENLKALFSADGPISKTRKNRVDEKGT 172

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
G+D + + P+V+ + + SL + HA I +D ES+ ++ L+D
Sbjct: 173 -----GIDPKSLNAIHPIVRKNERNNKKSLYLSPGHAIKICDLDENESKTLMKRLMDHQV 227

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
+ V+ +W + +W N +LH DF RVM
Sbjct: 228 KDEFVYGFWEFNPCLALWSNYSVLHNPTN-DFNAHRVM 264

>ref|ZP_08206063.1| putative dioxygenase [Gordonia neofelifaecis NRRL B-59395]
gb|EGD54173.1| putative dioxygenase [Gordonia neofelifaecis NRRL B-59395]
Length = 327

Score = 84.3 bits (207), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 71/273 (26%), Positives = 117/273 (42%), Gaps = 40/273 (14%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFA-ALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
+ + G +GA ++GV L A A A+ A + +++F Q HL +D Q FA+
Sbjct: 25 ITVDKLGEHIGARISGVRLGGDVPAEQAEAIRLALAVNKVVVFTDQQHLDDDGQYAFael 84

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
G + V + G+ ++ + +WH D +++ + + ++
Sbjct: 85 LGE-----PTLPHPTVTSRGS-----QLLTIEGAANSWHTDVSFVDRVPKASI 127

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY-----SQS 170
A +P+ GG T +A AAY+ L RALV A+HS Y ++
Sbjct: 128 LRAVTLPSWGGATTWASTVAAAEQLPAPLRALVDGLWAKHSNFYDYVTADPDAGDEETRR 187

Query: 171 KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFL 230
++ H ++ SA L P+V+VHPETG SLL+G P + AE
Sbjct: 188 RVDHYREFTSA-----EYETLHPVVRVHPETGERSLLLGHFVKEFPALKPAEFGPLF 239

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH 263
+ L + + W+ GDV +WDNR H
Sbjct: 240 QLLQNRITRLENTFRWNWSLGDVAIWDNRATQH 272

>ref|YP_298049.1| taurine dioxygenase [Ralstonia eutropha JMP134]
gb|AAZ63205.1| Taurine dioxygenase [Ralstonia eutropha JMP134]
Length = 282

Score = 84.0 bits (206), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 71/274 (25%), Positives = 114/274 (41%), Gaps = 28/274 (10%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+++ P ++GA + GV LA DD FA + A L+H +L GQ ++ + + FA+R
Sbjct: 1 MRVEPLTCSIGAEVLGVSLADAIHDDGLFAGIREALLKHRVLFVRGQDITAGEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E VA S+ + G VR + SP E + +WH D+T+ +
Sbjct: 61 FGELE----DHPVAGSDPEHPGLVRIYKSPPEPTPRYE-----NSWHTDATWREAPPLAS 111

Query: 123 VFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ P VGG T +++M AY+ L + + + ARHS+ S +++ +
Sbjct: 112 ILRCRECPVGGDTMWSNMVLAYENLPQHDKQIAGLRARHSIEASFGAAMPIEKRHALLR 171

Query: 183 IGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPR 242
+ P+V+ HP+TG L + E RF + A R
Sbjct: 172 AQF-----PDAEHPVVRTHPDTGEKVLVFNNGFTTHTFTNFHTPEHVRFGQDFNPGAADLLR 226

Query: 243 VHAHQ-----WAAGDVVVWDNRCLLHRA 265
Q W V +WDNR H A
Sbjct: 227 YLITQAYIPEYQVRWRWTPNSVAIWDNRSTQHYA 260

>emb|CAY27231.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 84.0 bits (206), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 50/128 (39%), Positives = 64/128 (50%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR 195
T FADMRAAYDALDE + + HS +YS+ KLG + D +
Sbjct: 1 TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLG-----LADFTDEERRVFK 51

Query: 196 P----LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251
P LV+ HP TGR SL + HA I GM E L L ++A + V++H W
Sbjct: 52 PVRQRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEGRMLLLDLTEFATRQQFVYSHAWRVN 111

Query: 252 DVVVWDNR 259
D V+WDNR
Sbjct: 112 DFVMWDNR 119

>ref|ZP_02503717.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei
112]
Length = 282

Score = 84.0 bits (206), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 79/273 (28%), Positives = 110/273 (40%), Gaps = 26/273 (9%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++I P +GA + GV LA DD FA + AA L H +L Q ++ + + FA+R
Sbjct: 1 MRIEPLTCAIGAELVGVCLADAAHDDDLFAEIRAALLAHRVLFRLDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQQAV 123
FG +E VA S+ G VR + E + AWH D+T+ G V
Sbjct: 61 FGELE----DHPVAGSDPDHPGLVRIYKTPEQPNEHY----ENAWHTDATWRQAPPLGCV 112

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
P VGG T +A+M AY+ L E +A + ARHS+ ++ G
Sbjct: 113 LRCVACPEVGDTMWANMVLAYENLPEHVKAQIADLRARHSI---EASFGAAMPIDGRLA 169

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMDAAESERFLEGL 233
A P+V+ HPETG L + A G DA L G
Sbjct: 170 LKAQFPDAE--HPVVRTHPETGEKVLVFNATFTTHTNYHTPARVRVGQDANPGAALLGY 227

Query: 234 VDWACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
+ P +W V +WDNR H A
Sbjct: 228 LLSQAYIPEYQVRWRWRKNSVAIWDNRSTQHYA 260

>ref|YP_004117507.1| Taurine dioxygenase [Pantoea sp. At-9b]
gb|ADU70951.1| Taurine dioxygenase [Pantoea sp. At-9b]
Length = 279

Score = 84.0 bits (206), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 72/287 (25%), Positives = 121/287 (42%), Gaps = 29/287 (10%)

Query: 8 ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
T G +GA V+ V L+ L DA F L+ L+H +L Q ++ +QQ A RFG
Sbjct: 7 FTALGPNIQAQVSDVDLSRPLSDAQFEQLYHGLLRHQVLFRLNQVITPEQQRALAVRFGD 66

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
+ G +I+ + Q +P + D+ WH D T++
Sbjct: 67 LHIHPVYPHAPGVVEIIVLD-----THQDNPPDNDN-----WHTDVTFITTPP 109

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
A+ +++++P GG T +A AAY+AL E + L+ A H S + + ++
Sbjct: 110 AIAILASKLLPESGGDTLWASGIAAYEALSEPFKTLLSGLQAEHDFKKSFEFKY-RKTE 168

Query: 180 SAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
+ + P P+++ HP +GR +L + + G+ ES+ L L
Sbjct: 169 EEHQRWQQAQVAKHPPVTHPVIRTHPVSGRKALFVNEGFTTRLIGLQEKESDALLNFLFAH 228

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W DV +WDNR H A + RVM + + G
Sbjct: 229 ITKPEFQVRWRWQENDVAIWDNRVTQHYANADYYPARRVMHRATVLG 275

>ref|YP_002240174.1| taurine dioxygenase [Klebsiella pneumoniae 342]
ref|ZP_06015536.1| taurine dioxygenase [Klebsiella pneumoniae subsp.
rhinoscleromatis
ATCC 13884]
ref|YP_003440979.1| Taurine dioxygenase [Klebsiella variicola At-22]
ref|ZP_06549393.1| taurine dioxygenase [Klebsiella sp. 1_1_55]

gb|ACI09993.1| taurine dioxygenase [Klebsiella pneumoniae 342]
gb|EEW41391.1| taurine dioxygenase [Klebsiella pneumoniae subsp. rhinoscleromatis
ATCC 13884]
gb|ADC59947.1| Taurine dioxygenase [Klebsiella variicola At-22]
gb|EFD84737.1| taurine dioxygenase [Klebsiella sp. 1_1_55]
Length = 283

Score = 84.0 bits (206), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 76/287 (26%), Positives = 117/287 (40%), Gaps = 25/287 (8%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA VTG L L D F L+ A L+H ++ Q+++ QQ A RF
Sbjct: 5 LSITPLGPYIGAQVTGADLTRPLSDNQFEQLYHAVLRHQVFLREQNITPAQQRDALALRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G + + + + D +P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPHAPGVVEIIVLDTHND-----NPPDNDN-----WHTDVTTFIDTP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P GG T+ AA++AL E R L+ A H S + + +
Sbjct: 109 PAGAILAAKELPTTGGDTLWTSGIAAWEALSEPFRQLLSGLHAEHDFRKSFEYKYNKTE 168

Query: 179 GSAYIGYGMDDTTATP-LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
P L P+V+ HP TG+ +L + I + ES L L
Sbjct: 169 AEHRRWQEAVAKHPPLLHPVVRTHPVTGKQALFVNEGFTTRIVEVSEKESAALLNLFFAH 228

Query: 237 ACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W DV +WDNR H A R+M + + G
Sbjct: 229 VTKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>emb|CAY27523.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 84.0 bits (206), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 50/125 (40%), Positives = 64/125 (51%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F+DMR AYD LD T+A V HSLVYS+ +G + + P+R
Sbjct: 1 TEFSDMRNAYDTLDAKTKAQVEGLVCEHSLVYSRSGSMGFTE-----LTEDEKAMMKPVR 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I G ES L L + A Q V+ H+W D+V
Sbjct: 55 QSLVRTHPVTGRKSLYLSSHAGTIVGWLMPESRDLLRDLNEHATQHENVYIHRWQQYDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|YP_335782.1| taurine dioxygenase [Burkholderia pseudomallei 1710b]
ref|ZP_04954436.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 1710a]
gb|ABA53326.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia
pseudomallei 1710b]
gb|EET03958.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 1710a]
Length = 277

Score = 84.0 bits (206), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 83/303 (27%), Positives = 118/303 (38%), Gaps = 49/303 (16%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 63

Sbjct: 2 T L +T LGA V V L+ DA + AA H +L F GQ LS + FA
TRLTLRLTPALGAIVDDVDLSNATDALRDDIRAALAHHQVLFRRGQRLSAAHRHDFAAAG 61

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
FG + +I+ + N D + N WH D T+

Sbjct: 62 FGD LHVHP IYPSHPDAREIMVLDNAVFD-----LQDNAIWHTDVTFTFE 104

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGH 174
+ ++ +A +P GG T + AAYDAL +A + +A+H + + G

Sbjct: 105 TPPRASILAAHTLPETGGDTLWGSFGAAYDALSGRVKAQLDGLTAQHDFTKSFPLKRFG- 163

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR---HAHAIPGMDAAESERFL 230
V A T + P+V+ HPETGR +L + +P + A RFL

Sbjct: 164 VTAEDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNEGFTTEIDELPEEEGAALLRFL 223

Query: 231 -----EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
E + W +W GDV WDNR +H A K RVM + + G

Sbjct: 224 FAHQSRPEFTLRW-----RWQPGDVAFWDNRSTIHYAVNDYGKAHRVMHRATIVG 273

Query: 284 -RP 285
RP

Sbjct: 274 DRP 276

>ref|ZP_03269249.1| Taurine dioxygenase [Burkholderia sp. H160]
gb|EDZ99180.1| Taurine dioxygenase [Burkholderia sp. H160]
Length = 282

Score = 84.0 bits (206), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 72/274 (26%), Positives = 120/274 (43%), Gaps = 28/274 (10%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+++ ++GA + GV++A DD FA + AA L+H +L Q ++ + + FA+R

Sbjct: 1 MRVEQLTYSIGAEELIGVNVARAIHDDGLFAEIRAALLKHRVLFRLDQAITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E VA S+ + G VR + +P + +D + AWHAD+T+ GA

Sbjct: 61 FGELE----DHPVAGSDPEHPGLVRIYKTPDQPNDRYE-----NAWHADATWREAPQFGA 111

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V P+VGG T +A+M AY+ L + + ARHS+ S +++ +

Sbjct: 112 VLRCVECPVSGGDTMWANMVLAYENLPAHVKTQIAGLRARHSIEASFGAAMPIEKRLALK 171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE-----GLVD 235
+ P+V+ HPET L + E RF + L+

Sbjct: 172 AQF-----PDAEHPVVRTHPETDEKVLVFVNAFTSHFTNFHTPERVRFQGDANPGAGDLLR 226

Query: 236 WACQAPRVHAHQ---WAAGDVVVWDNRCLLHRA 265
+ + +Q W + +WDNR H A

Sbjct: 227 YLISQAYIPEYQVRWRWQKNSIAIWDNRSTQHYA 260

>ref|NP_768765.1| dioxygenase [Bradyrhizobium japonicum USDA 110]
dbj|BAC47390.1| bll2125 [Bradyrhizobium japonicum USDA 110]
Length = 305

Score = 84.0 bits (206), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 66/255 (25%), Positives = 111/255 (43%), Gaps = 16/255 (6%)

Query: 15 LGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGAIE-RIG 71
+GA + V L+ L + A+++ L+H ++ F GQ HL + +Q +FA RFG +

Sbjct: 23 IGAEIRNVKLSGDLPEQTIASINGLLLEHKVIFFRGQLHLDDAEQESFAIRFGELTPHPT 82

Query: 72 GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPA 131
G I +++ + R S A+ WH D T++ + AV V+P
Sbjct: 83 LGAIKGTASIIELDSTRAGSRAD-----LWHTDGT FVDAYPKIAVLRGIVMPP 130

Query: 132 VGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTA 191
GG T +++ +AY L + L + A HS + + L V + ++ T
Sbjct: 131 FGGDTVWSNTASAYLDLAPPLQGLADRLWAVHSNAFDYAILARVSELDKKHLDEVFTKTI 190

Query: 192 TPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA 250
P+V+VHPETG +L++G G+ + ++ + W
Sbjct: 191 YRTEHPVVRVHPETGERTLVLGALVQN FVGLPKYDGGQKLFDFQSHITALENTVVRWSWRD 250

Query: 251 GDVVVWDNRCLLHRA 265
GDV +WDNR H A
Sbjct: 251 GDVAIWDNRATQHHA 265

>emb|CAY27396.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 84.0 bits (206), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 48/124 (38%), Positives = 66/124 (53%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T F DMRAAYDALD T+AL+ HS ++S+ LG ++ + A +
Sbjct: 1 TEFGDMRAAYDALDAETKALIEDLVCEHSRIFSKGALGF-----SFTEELRAFAPVRQ 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDVV 255
LV+ H +T R SL + HA I G E+ L L + A Q V+AH+W GD+V+
Sbjct: 55 RLVRTHRKTSRKSLYLSSHAGRIVGWPVEAMLLRELTEHATQREFVYAHKWQVGDLVM 114

Query: 256 WDNR 259
WDNR
Sbjct: 115 WDNR 118

>ref|ZP_02466907.1| taurine dioxygenase [Burkholderia thailandensis MSMB43]
Length = 312

Score = 84.0 bits (206), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 81/306 (26%), Positives = 124/306 (40%), Gaps = 55/306 (17%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T L++T +GA V V L+ D L AA +H +L F GQ LS Q FA
Sbjct: 37 TRLKLTRLTPAIGAIVDDVDLSNATDDLRLDRAALRHQVLFRRGQRLSAVQHRDFAAG 96

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
FG + +I+ + N D + N WH D T++
Sbjct: 97 FGD LHVHPIYPSHPDAREIMVLDAVFD-----LKD NAIWHTDVTFVE 139

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGH 174
+ ++ +A +P GG T + AAYDAL + + + +A+H + + G
Sbjct: 140 TPPRASILAARTLPETGGDTLWGSFGAAYDALSDRVKTQLDGLTAQHDFTKSFPLKRFG 199

Query: 175 VQQAGSAYIGYMDTTAT---PLRPLVKVHPETGRPSLLIGR---HAAHAIPGMDAAESE 227
+ + + +T AT P+V+ HPE GR +L + + +P ++A
Sbjct: 200 TAEDRARW---EETRATHPGVTHPVVRTHPENGRHALFVNEGFTTEINELPDEESAALL 255

Query: 228 RFL-----EGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSR 280
RFL E + W +W GDV WDNR +H A K RVM +
Sbjct: 256 RFLFAHQSRPEFTLRW-----RWQPGDVAFWDNRSTIHYAVNDYGKTHRVMHRAT 305

Query: 281 LAG-RP 285

+ G RP
Sbjct: 306 IVGDRP 311

>emb|CAY27299.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 84.0 bits (206), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 50/125 (40%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALDE + + HS +YS+ KLG + P+R
Sbjct: 1 TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLGADFTEEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I GM E+ L L ++A + P V++ W D V
Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMLLLLLDETFATRDPFVYSRVWRLNDFV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|YP_001175576.1| taurine dioxygenase [Enterobacter sp. 638]
gb|ABP59525.1| Taurine dioxygenase [Enterobacter sp. 638]
Length = 283

Score = 84.0 bits (206), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 71/288 (24%), Positives = 122/288 (42%), Gaps = 27/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G+ +A L D F L+ A L+H ++ Q ++ QQ A RF
Sbjct: 5 LTITPLGPHIGAQISGLDVARPLSDNQFELYHAVLRHQVVFLREQAVTAQQQRALALRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G + + + + D +P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPHAEGVEEIIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQ 176
GA+ +A+ +P GG T+ AA++AL E + L+ A H + + K +
Sbjct: 109 PAGAILAAKQLPETGGDTLWTSGVAAFNALSEPFKQLLSGLRAEHDFRKSQFQYKRYKTE 168

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ ++ + L P+++ HP TG+ +L + I + ESE L L
Sbjct: 169 EEHQRWLE-AVAKHPPLLHPVIRTHPVTGKQALFVNEGFTTRIVDVSEKESSETLLTFLFA 227

Query: 236 WACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W D+ +WDNR H A R+M + + G
Sbjct: 228 HITKPEFQVRWRWQQNDLAIWDNRVTQHYANADYLPQRRIMERATILG 275

>ref|YP_714255.1| putative taurine catabolism dioxygenase [Frankia alni ACN14a]
emb|CAJ62700.1| putative taurine catabolism dioxygenase [Frankia alni ACN14a]
Length = 283

Score = 84.0 bits (206), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 75/293 (25%), Positives = 118/293 (40%), Gaps = 30/293 (10%)

Query: 3 QTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
Q+ L + P T+GA + GV L+ L A + A L++ ++ F Q L+ + FA
Sbjct: 6 QSPLAVRPLPTIGAEIAGVDLSQPLSPAVRDEIRATVLKYKVFFRNQELTQEGHENFA 65

Query: 62 KRFGAIERIGGGD-----IVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADST 113


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      +FG +   G           I IS+   D   + H+P   DD+           +H D++
Sbjct: 66  GQFGPLYTHPGAADARTTAIHRISADFDKVAKVHTPQADDDIWD-----PYHTDTS 119

Query: 114  YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
      + V   GAV A +P VGG T + D   AY L + + + R   H   +   G
Sbjct: 120  WRLVPTWGAVLRAVQLPEVGGDTIWDAAALAYQGLSDEVKERLDGRHVTHDFRAALHASG 179

Query: 174  HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEG 232
      H       +           P++++H ETG       +       I G+D AES+ L
Sbjct: 180  HDYPVVA-----HPVIRIHRETGEKIAWVNFTQRPTIIGLDRAESKELLTA 225

Query: 233  LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMWHSRLAGRP 285
      ++D   +           W G V WDNR +H A           PR++   +A P
Sbjct: 226  VIDQYRKPENQVRFTWRPGSVAFWDNRAAVHYAVRNYGSAPRLLERILIADPEP 278

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>ref|ZP_04383171.1| alpha-ketoglutarate-dependent taurine dioxygenase [Rhodococcus
erythropolis SK121]
gb|EEN89557.1| alpha-ketoglutarate-dependent taurine dioxygenase [Rhodococcus
erythropolis SK121]
Length = 324

```

Score = 83.6 bits (205), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 70/266 (26%), Positives = 113/266 (42%), Gaps = 27/266 (10%)

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Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
      + +   G +GA + GVHL+ L +   A++ A   H ++ F GQH L + Q FA
Sbjct: 22  ITVHKVGELIGARIDGVHLSGDLSEETAYAINYALAAHKVVFFRQGHLLDDTSQYEFAGT 81

Query: 64  FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
      G           VK+ G           D ++ +   +WH D T++ + + ++
Sbjct: 82  LGT-----QTPHPTVKSRG-----DKLLVLDRAANSWHTDVTTFVDRIPKASI 124

Query: 124  FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG---- 179
      A +P GG T +A   AAYD L + + LV   A H+ Y   +++ V QA
Sbjct: 125  LRATTIPEYGGATTWASTTAAAYDQLPSSSLKVLVENLRAVHTNAYDYAEV--VDQANPVDA 182

Query: 180  --SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
      AY           P+V++HP TG +LL+G           G+ +ES   + L
Sbjct: 183  QRQAYYAEFTREIYETEHPVVRIPHATGEKTLGLGHFFKEFVGLKPSESVALYQILQARI 242

Query: 238  CQAPRVHAHQWAAGDVVVWDNRCLLH 263
      +           W+AGD+ +WDN+ H
Sbjct: 243  IKLENTVRWNWSAGDLAIWDNQATQH 268

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>ref|ZP_03542510.1| Taurine dioxygenase [Comamonas testosteroni KF-1]
gb|EED66796.1| Taurine dioxygenase [Comamonas testosteroni KF-1]
Length = 303

```

Score = 83.6 bits (205), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 69/279 (24%), Positives = 121/279 (43%), Gaps = 35/279 (12%)

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Query: 5   TLQITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
      ++++ P   ++GA ++ VHL A D+   A + A L+H ++ F Q ++ + + FA+
Sbjct: 20  SVEVNPLTCSIGAELSNVHLGAAAEEDEGLMAEIRQALLRHRVIFFRDQDITRAEHVAFAR 79

Query: 63  RFGAIERIGGGDIVAISNVKADGTVRQH----SPAEWDDMMKVIVGNMAWHADSTYMPVM 118
      +FG +E           V S+ + G V+ +   SP + ++           +WH D+T+
Sbjct: 80  KFGELE----DHPVVGSHPEHPGLVQIYKTPDSPLDRNEN-----SWHTDATWREQP 127

Query: 119  AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 178
      G V           P VGG T + +M AY+ L + + +   ARHS+ S   + +++

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Query: 232 GLVDWACQAPRVHAHQ----WAAGDVVVWDNRCLLHRA 265
L+++ + +Q W V +WDNR H A
Sbjct: 245 NLLNYLISQAAIPEYQVRWRWTPNSVAIWDNRSTQHYA 282

>ref|ZP_01615851.1| taurine dioxygenase [marine gamma proteobacterium HTCC2143]
gb|EAW32934.1| taurine dioxygenase [marine gamma proteobacterium HTCC2143]
Length = 275

Score = 83.6 bits (205), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 61/263 (23%), Positives = 110/263 (41%), Gaps = 15/263 (5%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T+ + +LGA ++G+ L LD++ +A + ++H ++ F Q +S Q A+
Sbjct: 2 TITVQHLSGSLGAEISGIDLTQPLDNSIYADIRQLLVEHEVIFFRDQDISLSQHKALAES 61

Query: 64 FGAIE-RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG ++ G I + T+ + +P E M++ WH+D T+ G
Sbjct: 62 FGPLQTHPAYGTIEGFPEI----TILESTP-EKPTMIE-----CWHS DMTFKKHPPMGT 110

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ + ++P GG T ++ M AAYD L + + +A H + K + G
Sbjct: 111 ILRSRIIPKGGDTLWSSMTAAYDGLSSGMQNFLSSLTAVHDFAFG-FKESLAEAGGRER 169

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAP 241
+ + P++ HPE+G+ + + I GM A ES L L +
Sbjct: 170 LAQAVADNPPVEHPVICTHPESGKKVIFVNELFTTHIVGMTAKESRALLGFLYEHIVTPE 229

Query: 242 RVHAHQWAAGDVVVWDNRCLLHR 264
W + +WDNR H+
Sbjct: 230 FTCRFSWQPN SIALWDNRSTQHK 252

>ref|ZP_06660873.1| tauD [Escherichia coli B088]
gb|EFE64381.1| tauD [Escherichia coli B088]
Length = 289

Score = 83.6 bits (205), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 73/288 (25%), Positives = 120/288 (41%), Gaps = 27/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 11 LSITPLGPYIGA QISGADLTRPLSDNQFEQLYHAVLRHQVVFRLDQTITPQQQRALAQRF 70

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 71 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 114

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++
Sbjct: 115 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHD FRKSFPEYKY-RKT 173

Query: 179 GSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ H +G+ +L + I + ESE L L
Sbjct: 174 EEEHQRWREAVAKNPPLLHPVVRTHLVSGKQALFVNEGFTTRIVDVSEKESEALLSFLFA 233

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W D+ +WDNR H A R+M + + G
Sbjct: 234 HITKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 281

>emb|CAY27288.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 83.6 bits (205), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 50/125 (40%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195

Sbjct: 1 T FADMRAAYDALDE + + HS +YS+ KLG + P+R
TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLGGLADFTEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ H TGR SL + HA I GM E+ L L ++A + P V++H W D V

Sbjct: 55 QRLVRRHSVTGRKSLFLSAHAGEIEGMSIPEARMMLLLDLTEFATRDPFVYSHVWRLNDFV 114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>ref|ZP_05068539.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase, putative [Octadecabacter antarcticus 238]
gb|EDY88076.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxxygenase, putative [Octadecabacter antarcticus 238]
Length = 286

Score = 83.2 bits (204), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 72/266 (27%), Positives = 109/266 (40%), Gaps = 26/266 (9%)

Query: 15 LGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE-RIGG 72
+GA + G+ L+ + A ++ ++ P QH+S + FA+RFG +E +

Sbjct: 1 MGARIEGLDLSPVSAEDHRVQALGENGMICIPDQHISAGELKAFARFGTLEINVAN 60

Query: 73 G-----DIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQQGAVFS 125
+++ +SN+K DG S A D WH D +Y +A V

Sbjct: 61 SFMEDDHPEVMILSNIKKDGKPIGLSDAGQD-----WHTDMSYSKDI AFANVLY 109

Query: 126 AEVVPAVGGR---TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
+P G T FA+M AYD L E + + R+A H K+ + +

Sbjct: 110 GLEIPTRDGEPLGCTEFANMHQAYDDLPEELKTKLAGRTATHDFNKFWKMRSEKGS SRP 169

Query: 182 YIGYGMDTTATP-LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
+ P L+P+ HP TGR L + I GMD ES+ L L Q

Sbjct: 170 ALTPEQRAKKPPVLQPVFLTHPITGRTVLYANPGYTMQIDGMDTQESDEILAF LFKHQLQ 229

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
H W DV++WDN LH A

Sbjct: 230 EKYRIKHMWKKFDVIMWDNIGTLHNA 255

>emb|CAY27404.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 83.2 bits (204), Expect = 4e-14, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 66/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F+DMR AYD LD+AT+ HS +YS+S LG I + P++

Sbjct: 1 TEFSDMRTAYDRLDDATKQECGLICEHSQIYSRLLGFSDFTDEDLIRF-----KPVQ 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA AI G E+ FL L + A Q V+AH W D+V

Sbjct: 55 QRLVTRHPSTGRKSLYLASHAGAIVGWPIPEARAFRLDLNEHATQRALVYAHVWKQWDLV 114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>ref|XP_003042406.1| hypothetical protein NECHADRAFT_97202 [Nectria haematococca mpVI
77-13-4]

gb|EEU36693.1| hypothetical protein NECHADRAFT_97202 [Nectria haematococca mpVI
77-13-4]
Length = 366

Score = 83.2 bits (204), Expect = 4e-14, Method: Compositional matrix adjust.
Identities = 78/268 (29%), Positives = 114/268 (42%), Gaps = 25/268 (9%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKR 63
+ITP +G V G+ L++LD L + +L+F GQ ++ D+Q F
Sbjct: 84 EITPA---VGTEVHGLQLSSLSKQKDELALLVAERGVLFVRGQDFADIGFDRQKEFGAH 140

Query: 64 FGAIE-RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG + GG + + R + D+ +K V ++ WH D +Y
Sbjct: 141 FGKLHVHQHGGHVKDYPELLP--VYRDFTAGAVDNEIKNNVSSIKWHTDMSYEINGMGT 198

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+F A P GG T + AAY+AL R +H A HS + Q++ V Y
Sbjct: 199 IFLALDAPPSGGDTLYLSTVAAYNALSPLYREKLHGLEATHS-GFEQAR---VADHKERY 254

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAP 241
I ++T + P+V+ HP T SL + R + I G+ ES L L D
Sbjct: 255 IREPIET----IHPVVRTHPVTKSKSLYVNRLYTRRIQGLKEEESANILNFLYDHIHGG 310

Query: 242 ----RVHAHQWAAGDVVVWDNRCLLHRA 265
RVH W G VVV+DNR H A
Sbjct: 311 DWHIRVH---WTPGTVVVYDNRITQHS 335

>ref|YP_003209304.1| taurine dioxygenase [Cronobacter turicensis z3032]
emb|CBA28475.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Cronobacter
turicensis z3032]
Length = 283

Score = 83.2 bits (204), Expect = 4e-14, Method: Compositional matrix adjust.
Identities = 72/287 (25%), Positives = 121/287 (42%), Gaps = 25/287 (8%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ ITP G +GA V+ ++LA L D+ F L+ A ++H +L Q ++ QQ A RF
Sbjct: 5 ITITPLGPYIGALVSDINLARPLSDSQFEQLYHALIRHQVLFVRDQPIPTPQQRALAMRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
G + G + + + + D +P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPHAEGVEEIIVLDTND-----NPPDNDN-----WHTDVTFTIDTP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ-Q 177
GA+ +A+ +P GG T + AA++AL + L+ A H S + H + +
Sbjct: 109 PAGAILAALKALPPTGGDTLWTSGIAAFEALSAPFQQLSGLRAEHDFRKSFPEWKHTKTE 168

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
++ L P+V+ HP +G+ +L + I + ES+ L L
Sbjct: 169 EEHQRWLTAVEKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSPKESDALLSFLFAH 228

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W DV +WDNR H A RVM + + G
Sbjct: 229 ITKPEFQVRWRWQENDVALWDNRVTQHYANADYLPARRVMHRATILG 275

>ref|ZP_02487377.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei
7894]
Length = 282

Score = 83.2 bits (204), Expect = 4e-14, Method: Compositional matrix adjust.
Identities = 78/273 (28%), Positives = 109/273 (39%), Gaps = 26/273 (9%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++I P +GA + GV LA DD FA + AA L H +L Q ++ + + FA+R
Sbjct: 1 MRIEPLTCAIGAELVGCLADAAHDDGLFAEIRAALLAHRVLFRLDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG +E VA S+ G VR + E + AWH D+T+ G V
Sbjct: 61 FGELE----DHPVAGSDPDHPGLVRIYKTPEQPNEHY----ENAWHTDATWRQAPPLGCV 112

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
P VGG T +A+M AY+ L E +A + RHS+ ++ G
Sbjct: 113 LRCVACPEVGGDTMWANMVLAYENLPEHVKAQIADLRTRHSI---EASFGAAMPIDGRLA 169

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMDAAESERFLEGL 233
A P+V+ HPETG L + A G DA L G
Sbjct: 170 LKAQFPDAE--HPVVRTHPETGEKVLVFNATTHFTNYHTPARVRVGQDANPGAALLGY 227

Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ P +W V +WDNR H A
Sbjct: 228 LLSQAYIPEYQVRWRWRKNSVAIWDNRSTQHYA 260

>ref|YP_003645662.1| Taurine dioxygenase [Tsukamurella paurometabola DSM 20162]
gb|ADG77323.1| Taurine dioxygenase [Tsukamurella paurometabola DSM 20162]
Length = 297

Score = 83.2 bits (204), Expect = 4e-14, Method: Compositional matrix adjust.
Identities = 78/266 (29%), Positives = 108/266 (40%), Gaps = 30/266 (11%)

Query: 12 GATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIER 69
G +G+ + G+ L L D A + A L+ ++ F QH L + F +R G +
Sbjct: 10 GEHIGSRIDGIRLGGDLADEEDIAFIRATLLERKVVFFRDQHDLDAAHQEFGRRLGDL-- 67

Query: 70 IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA--WHADSTYMPVMAQGAVFSAE 127
G V + P+ + G A WH D T+ GA+ A
Sbjct: 68 -----GAVHLNDPSAHVAAIDSEHGKANWHTDITFSEPPAGAILRAV 112

Query: 128 VVPAVGGRTCFADMRAAYDALDEATRAL-----VHQRSA-RHSLVYSQSKLGHVQQAGS 180
+P GG T +A+ AAY L R L VH SA R L Q++ +
Sbjct: 113 QLPDFGGTTIWANTAAAYAQLPAELRRLADALWAVHDNSAFRDDLSPEQARAARDHPDTA 172

Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
A+ T P+V VHPETG LL+G +A I G D +S+ L L
Sbjct: 173 AFYAKLTAQTIAAEHPVVHVHPETGERCLLLGVYARRISGYDREDSALLH-LFQRRITR 231

Query: 241 PRVHAH-QWAAGDVVVWDNRCLLHRA 265
P + W GDVV+WDNR H A
Sbjct: 232 PELTVRWDWQPGDVVIWDNRATQHYA 257

>gb|ABL97678.1| taurine dioxygenase [uncultured marine bacterium EB0_39H12]
Length = 288

Score = 83.2 bits (204), Expect = 4e-14, Method: Compositional matrix adjust.
Identities = 62/270 (22%), Positives = 109/270 (40%), Gaps = 29/270 (10%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ T+G + GV L++ LD ++ A L + ++ F Q +S ++ I F+K F
Sbjct: 16 FKNRLSPTIGGEIHGVDLSSPLDTTTEKELIYEALLVYKVIFFRDQDISTEEHINFSKSF 75

Query: 65 GAIE-----RIGGGDIVAIS-NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
G +E + +++ I+ N K+ G WH+D T+
Sbjct: 76 GELEIHPFAPKKQDFPEVLVITHNEKSKGQEN-----VWHSVDVTWRQ 117

Query: 117 VMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ G+V P GG T F+DM AAY+ L + + + A H +++L
Sbjct: 118 EPSLGSVLRMIEKQPQHGGDTLFSDMNAAYNNLSDEVKDRLEGAIAVHDFANFRNRLIKEG 177

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
++ + + P P+++ HP+T + + + I G D ES+ L L
Sbjct: 178 KSKEEITAFN-EQYPMPEHPVIRTHPDTKNKVIYVNKAFTQYIKGWDKEESDDMLNLYLS 236

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
A + WDNR H A
Sbjct: 237 RASVPEFQCRFAWQDNSIAFWDNRACQHYA 266

>ref|YP_003732553.1| taurine dioxygenase [Acinetobacter sp. DR1]
gb|ADI91180.1| taurine dioxygenase [Acinetobacter sp. DR1]
Length = 293

Score = 83.2 bits (204), Expect = 4e-14, Method: Compositional matrix adjust.
Identities = 66/266 (24%), Positives = 105/266 (39%), Gaps = 18/266 (6%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I T+GA + + L L+ + A L H ++ F Q L+ Q A+ F
Sbjct: 7 NLNIEVIKPTIGAIHDIDLNALNKQTTQQIQQALLDHQVIFFRKQQLAPQAQADLARSF 66

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G++ +I +V + D + + N WH D T+ G V
Sbjct: 67 GSLH--VHPIYPSIEDVPEVMVL-----DSWKQDLRDNELWHTDVTFSKNPPLGCVL 116

Query: 125 SAEVVPAVGGRCTCFADMRAAYD---ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
A +P VGG T ++ AA+ L + R L R S + + H ++
Sbjct: 117 QAIKIPPVGGDTLWSSNTAAFKWLPLELQQLRGLTATHDIRKS--FPLERFAHNEEERE 174

Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
+ + P+V+ HP T P L + I + ESE+ L+ L + A Q
Sbjct: 175 KLLQ-TFKRNPPVHPVVRTHPVTDEPLLFVSEGFTTRINELPEQESEQLLDFLFEHATQ 233

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
+W GD+ +WDNRC H+A
Sbjct: 234 EQFHLRWKWDGDIAIWDNRCTQHKA 259

>ref|YP_004006884.1| taurine dioxygenase [Rhodococcus equi 103S]
emb|CBH48200.1| putative taurine dioxygenase [Rhodococcus equi 103S]
Length = 321

Score = 83.2 bits (204), Expect = 4e-14, Method: Compositional matrix adjust.
Identities = 75/266 (28%), Positives = 118/266 (44%), Gaps = 27/266 (10%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFA-ALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
+ +T G +GA + GVH++ A A A+ A + +++F GQH +++D Q FA
Sbjct: 20 ITVTRLGENIGALIEGVHVSGDIPAETAYAIRYALAANKVVVFRGQHHVTDDIQYRFAGT 79

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNM-AWHADSTYMPVMAQGA 122
G+ T + D+ VI G +WH D +++ + + +
Sbjct: 80 LGS-----QTTHTPTLTSEDNRTLVIEGAANSWHTDVSFVDRIPKAS 121

Query: 123 VFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ A +P GG T +A AAY+ L +ALV A HS Y + + H + G A
Sbjct: 122 ILRAVDIPPYGGATTWASTTAAEQPLPAPLKALVDSLWAVHSNEYDYAGV-HADRKGIAGV 180

Query: 183 IGYGMDTTATPLR-----PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
+ T L+ P+V+VHPETG SLL+G G+ ES + L +

Sbjct: 181 NRHETMQNFTRLKFEIEHPVVRVHPETGERSLLLGHFVKNFVGLKTNESAAFQLLQERV 240

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLH 263

+ W GD+V+WDNR H

Sbjct: 241 VRLENTLRWAWTPGDLVIWDNRATQH 266

>ref|ZP_07043442.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni S44]

gb|EFI62925.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni S44]

Length = 303

Score = 83.2 bits (204), Expect = 4e-14, Method: Compositional matrix adjust.
Identities = 67/275 (24%), Positives = 117/275 (42%), Gaps = 27/275 (9%)

Query: 5 TLQITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62

+L++ P ++GA ++ VHL A D+ + A L+H ++ F Q ++ + + FA+

Sbjct: 20 SLEVNPLTCSIGAELSNVHLGAAAEGLEMTETIRQALLKHRVIFFRDQDITRAEHVAFAR 79

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGA 122

+FG +E V S+ + G V+ + + + +WH D+T+ G

Sbjct: 80 KFGELE---DHPVVGSHPEHPGLVQIYKTPD---NPLDRNENSWHTDATWREQPPMGC 131

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182

V P VGG T + +M AY+ L + + + ARHS+ S + +++ +

Sbjct: 132 VLRCVECPVGGDTMWVNMVMAYENLPDDIKVKIEHLRARHSIEASFGAVMPIEKRLALK 191

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMDAAE-SERFL 230

Y P+V++HPETG L + A+ G+D + S + L

Sbjct: 192 AQY-----PDAEHPVVRIPHETGEKILFVNSSFTTFTNYNTPANVRFGLDKSPGSSQLL 246

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

L A +W+ V WDNR H A

Sbjct: 247 NYLTSQAMIPEYQVRFKWSKNSVAFWDNRSTQHYA 281

>emb|CAY27518.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 119

Score = 83.2 bits (204), Expect = 4e-14, Method: Compositional matrix adjust.
Identities = 53/125 (42%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195

T F DMRAAYDALDE T+A HS ++S+S LG + P+R

Sbjct: 1 TEFWDMRAAYDALDEETKAECEENLICEHSQLFERSILGFTDFTDDERRKFA-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254

LV+ HP TGR SL + HA AI G E+ FL L + A Q V+AH W D V

Sbjct: 55 QRLVRRHPVTGRRSLYLASHAGAILGWPVEARAFRLDLTEHATQRSFVYAHVWRQWDPV 114

Query: 255 VWDNR 259

+WDNR

Sbjct: 115 MWDNR 119

>ref|ZP_08124447.1| Dioxygenase, TauD/TfdA family protein [Pseudonocardia sp. P1]

Length = 247

Score = 82.8 bits (203), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 70/255 (27%), Positives = 110/255 (43%), Gaps = 41/255 (16%)

Query: 41 QHALLIFPGQHLSNDQQ-ITFAKRFGAIERIGG-----GDIVAISNVKADGTVRQHSP 92


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      ++ ++I P Q ++D ++F + FG + G D+ +SNV R
Sbjct: 20 EYGVVILPDQADADDSAFLSFLRGFGDLTFTPGETPVPGPDLNVVSNVGRTPPRS--- 76

Query: 93 AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT 152
      ++H D++Y+ A VPA GG T F++ AYD L +
Sbjct: 77 -----SFHVDTSYIARPPAYTALRAVSVPAHGGATQFSNQYRAYDTLPDGL 122

Query: 153 RALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIG 212
      R + R+ RH + G G +T A P+ + HP +GR +L +
Sbjct: 123 RQRLAGRAIRHVVT-----GLTPGDAGGETEAE--HPVFRRHVPVSGRVALYLS 168

Query: 213 RHAH--AIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDF 270
      A ++ GM A ES + L + + +A V H W+ GDVV+WDN C+LHRA+
Sbjct: 169 TPARCVSVSGMSAQESSDVIHELFEHSTRADNVMCHAWSPGDVVIWDNACVLHRADHAGV 228

Query: 271 KLPRVMWHSRLAGRP 285
      RVM + G P
Sbjct: 229 VGDRVMHRGMITGGP 243

```

>ref|NP_746577.1| TauD/TfdA family dioxygenase [Pseudomonas putida KT2440]
gb|AAN70041.1|AE016643_2 dioxygenase, TauD/TfdA family [Pseudomonas putida KT2440]
Length = 290

Score = 82.8 bits (203), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 74/305 (24%), Positives = 127/305 (41%), Gaps = 37/305 (12%)

```

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
      + + + G+ + A + G D A + WLQ+ ++ F ++++Q I F
Sbjct: 2 LTKNKITAVSNGSGVCADIVGFDNFYDAQDVAEVRKIWLQYGVVFRDIDITDEQHIKF 61

Query: 61 AKRFGAI-----ERIGGG-----DIVAISNVKADGTVRQHSPAEDMMKVIVGNM--AW 108
      + FG +++ G +I+ I+N DG P+ +GN W
Sbjct: 62 SHHFGEAVIHPKQLQEGAHPTQKEILVIANTTKDG-----KPSG-----ALGNSEATW 109

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
      H D+ + GA+ + +P GG T + M AY+ L V R VY
Sbjct: 110 HTDTWFIYERPPAGALLRSIALPPTGGDTYVWSMYQAYETLPSYLLDAVKGRQIFFQSVYD 169

Query: 169 QSKLGHVQQAGSAYIGYMDTTATP--LRPLVKVHPETGRPSLLIG-----RHAHAIPGM 221
      + + + + D P + PLV+VH ++GR +L +G I G+
Sbjct: 170 AAGGLRLNKQ---VPSDDIREWPGIVHPLVRVHGDSEGRQALYLGAKGVREQDSWIVGL 225

Query: 222 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRL 281
      ES + L + + + QW GD+V+WDNRC +HR + + + R+M +
Sbjct: 226 PMDESNDLVAQLWEHTLKG-EIFVQQWRLGDMVMWDNRCTMHRRDSFSPEHIRIMHRTTT 284

Query: 282 AG-RP 285
      AG RP
Sbjct: 285 AGERP 289

```

>emb|CAY27560.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 82.8 bits (203), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 51/125 (40%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

```

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
      T F DMRAAYDALDE T+ HS ++S+S LG + P+R
Sbjct: 1 TEFQDMRAAYDALDEETKTECNLVCEHSQLFSSILGFTDFTEDEHRHFA-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254

```

LV+ HP TGR SL + HA AI G E+ FL L + A Q V+ H+W D+V
Sbjct: 55 QRLVRRHPVTGRRSLYLASHAGAILGWPGEARAFRLDLNEHATQPEFVYVHKWTLHDLV 114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>emb|CAY27412.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 82.8 bits (203), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 49/125 (39%), Positives = 67/125 (53%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRAAYDALD+ T+A + + HSL+YS+ LG + T P+R
Sbjct: 1 TEFGLDMRAAYDALDDETQAEIVGLISEHSLIYSRESLGFNDPTEAER-----ATMRPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
L + HP +GR S+ + H I G E+ F+ L + A Q V+AHQW D+V
Sbjct: 55 QALTRTHPVSGRKS SVYLASHIGKIIGWPVPEARAFIRDLTEHATQRRFVYAHQWRPFDLV 114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>ref|YP_001333996.1| taurine dioxygenase [Klebsiella pneumoniae subsp. pneumoniae MGH
78578]
ref|YP_002918030.1| taurine dioxygenase [Klebsiella pneumoniae NTUH-K2044]
gb|ABR75766.1| taurine dioxygenase, 2-oxoglutarate-dependent [Klebsiella
pneumoniae subsp. pneumoniae MGH 78578]
dbj|BAH61963.1| 2-oxoglutarate-dependent taurine dioxygenase [Klebsiella pneumoniae
subsp. pneumoniae NTUH-K2044]
Length = 283

Score = 82.8 bits (203), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 75/287 (26%), Positives = 117/287 (40%), Gaps = 25/287 (8%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA V+G L L D F L+ A L+H ++ Q+++ QQ A RF
Sbjct: 5 LSITPLGPYIGAQVSGADLTRPLSDNQFEQLYHAVLRHQVFLREQNITPAQQRDLALRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
G + + + + + D +P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPHAPGVVEEIIVLDTND-----NPPDNDN-----WHTDVTFTIDTP 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P GG T + AA++AL E R L+ A H S + + +
Sbjct: 109 PAGAILAAKELPTTGGDTLWTSGIAAWEALSEPFRQLLSGLHAEHDFRKSQFQYKYNKTE 168

Query: 179 GSAYIGYGMDDTTATP-LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
P L P+V+ HP TG+ +L + I + ES L L
Sbjct: 169 AEHRRWQEAVAKHPPLLHPVVRTHPVTKQALFVNEGFTTRIVEVSEKESAALLNFLFAH 228

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W DV +WDNR H A R+M + + G
Sbjct: 229 VTKPEFQVRWRWQPNDAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|YP_106556.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia
mallei ATCC 23344]
ref|ZP_00440629.1| taurine dioxygenase [Burkholderia mallei GB8 horse 4]

```
ref|YP_001025153.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia
mallei NCTC 10229]
ref|YP_001079504.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia
mallei NCTC 10247]
ref|ZP_04883134.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia
mallei ATCC 10399]
ref|ZP_04909932.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia
mallei FMH]
ref|ZP_04911795.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia
mallei JHU]
gb|AAU45462.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia
mallei ATCC 23344]
gb|ABO03239.1| taurine dioxygenase [Burkholderia mallei NCTC 10247]
gb|EDK52889.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia
mallei FMH]
gb|EDK62092.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia
mallei JHU]
gb|EDP87488.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia
mallei ATCC 10399]
gb|EEP86315.1| taurine dioxygenase [Burkholderia mallei GB8 horse 4]
gb|ABM99599.2| taurine dioxygenase [Burkholderia mallei NCTC 10229]
Length = 282
```

Score = 82.8 bits (203), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 78/273 (28%), Positives = 110/273 (40%), Gaps = 26/273 (9%)

```
Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
++I P +GA + G+ LA DD FA + AA L H +L Q ++ + + FA+R
Sbjct: 1 MRIEPLTCAIGAELVGMCLADAHDDDLFAEIRAALLAHRVLFRLDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQQAV 123
FG +E VA S+ G VR + E + AWH D+T+ G V
Sbjct: 61 FGELE----DHPVAGSDPDHPGLVRIYKTPEQPNEHY----ENAWHTDATWRQAPPLGCV 112

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
P VGG T +A+M AY+ L E +A + ARHS+ ++ G
Sbjct: 113 LRCVACPEVGGDTMWANMVLAYENLPEHVKAQIADLRARHSI---EASFGAAMPIDGRLA 169

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMDAAESERFLEGL 233
A P+V+ HPETG L + A G DA L G
Sbjct: 170 LKAQFPDAE--HPVVRTHPETGEKVLVNAFTTHTFTNYHTPARVRVGQDANPGAALLLGY 227

Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ P +W V +WDNR H A
Sbjct: 228 LLSQAYIPEYQVRWRWRKNSVAIWDNRSTQHVA 260
```

```
>ref|ZP_08022192.1| taurine dioxygenase [Dietzia cinnamea P4]
gb|EFV93249.1| taurine dioxygenase [Dietzia cinnamea P4]
Length = 299
```

Score = 82.8 bits (203), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 85/288 (29%), Positives = 116/288 (40%), Gaps = 38/288 (13%)

```
Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA 66
+ P +GA + GV LA L A L+ +L F Q HL+ Q FA +G
Sbjct: 34 VRPVTPTFIGADIEGVDLAAPTPEQIVELKTALLERKVLFFRDQQHLTAHQHRDFAAHWGE 93

Query: 67 IER---IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQQAV 123
+E + G+I + V+ D Q +P M+ I WH D T+ G+V
Sbjct: 94 LEVHPILDQGEIPEV--VRFDRG--QDNPG-----MENI-----WHVDVTWKDRPPLGSV 139

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS-----QSKLGHVQQ 177
```

```

      A VP GG T ++DM AYDAL + + + +A H S KL +Q
Sbjct: 140 LRAIEVPDAGGDTLWSDMGNAIDALPDEIKDRIDGLTATHDFTSPFGLGMPDKLAQMQA 199

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
      P+V+ HPETGR L + I G+D E L L+D
Sbjct: 200 QYPPQ-----HHPVVRTHPETGRKLLFVNSLFTTEIDGVDPVEGRELLRRLLD- 247

Query: 237 ACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
      + P +WA G V WDNR H A F RVM + G
Sbjct: 248 QVKMPDFQVRLRWAPGTVAFWDNRRATQHYACSDYFPHRRVMERVAIVG 295

```

```

>ref|YP_003364051.1| alpha-ketoglutarate-dependent taurine dioxygenase [Citrobacter
rodentium ICC168]
emb|CBG87195.1| alpha-ketoglutarate-dependent taurine dioxygenase [Citrobacter
rodentium ICC168]
Length = 283

```

Score = 82.8 bits (203), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 77/289 (26%), Positives = 121/289 (41%), Gaps = 29/289 (10%)

```

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      L ITP G +GA ++G L+ L D F L+ A L+H ++ Q ++ QQ A RF
Sbjct: 5 LSITPLGPYIGALISGADLSRPLSDNQFEQLYHAVLRHQVFLREQVITPQQQRALALRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
      G + G + + + + D +P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPHAEGVEEIIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
      GA+ +A+ +P+ GG T + AAY+AL R L+ A H + +S H +A
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSAPFRQLLSGLRAEHD--FRKSFPEHKYRA 166

Query: 179 GSAYIGYGMDTTATP---LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
      + A L P+V+ HP +GR +L + I + ES+ L L
Sbjct: 167 TEEHQWRWEAVAKHPPLLHPVVRTHPVSGRQALFVNEGFTTRIVDVTEKESDALLSFLF 226

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
      + +W DV VWDNR H A R+M + + G
Sbjct: 227 AHITRPEFQVRWRWQPNDAVVDNRVTQHYANADYLPQRRIMHRATILG 275

```

```

>ref|YP_003766141.1| taurine dioxygenase [Amycolatopsis mediterranei U32]
gb|ADJ45739.1| taurine dioxygenase [Amycolatopsis mediterranei U32]
Length = 290

```

Score = 82.4 bits (202), Expect = 7e-14, Method: Compositional matrix adjust.
Identities = 81/300 (27%), Positives = 118/300 (39%), Gaps = 45/300 (15%)

```

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
      TL + LGA VTG+ L L D L A+L H +L+F Q +S + A
Sbjct: 22 TLAVRGLTPVLGA EVTGLDLTRELTDEQLTELKTAFLDHHVLVFRDQDISVEDHKRLATS 81

Query: 64 FGAIERIGG----GDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
      FG + + GD + A + + GN WHAD T +
Sbjct: 82 FGELRPVNPPPEHGDPIYLEVATAPESAN-----VFGN-GWHADGTADEEPS 127

Query: 120 QGAVFSAEVVPA--AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 177
      G++ +P GG T FA+M AYD L + L+ + L +
Sbjct: 128 LGSMLHITRMPEPGSGGDTLFANMHLAYDMLSPKLKELL-----AGLTAIHD 174

Query: 178 AGSAYIGYGMDTTATPL---RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL 233
      A+ G+ + P P+V HPET RP L + + IP + A ES+ L+ L

```

Sbjct: 175 GAHAFRGHKIPGEYEPVSEHPVVVRHPETDRPLL FVNPA YTSRIPQLSADESQAVLDLL 234
Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL 292
P + +W +V WDNRC+ H A +D+ H+R R G L
Sbjct: 235 FSVVPNRPLACRVRWEPNTLVFWDNRCVQHAT-YDY-----YPHTRFGHRVAINGGPL 288

>emb|CAY27446.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27557.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 82.4 bits (202), Expect = 7e-14, Method: Compositional matrix adjust.
Identities = 48/125 (38%), Positives = 63/125 (50%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALD+ T+A HSL+YS+ LG + + P+R
Sbjct: 1 TEFADMRAAYDALDDETKAETEDLICEHSLMYSRGSLGFTDYSEEEKQMFK-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP R SL + HA + GM E L L + A Q + H+W D+V
Sbjct: 55 QRLVRTHPVHRRKSLYLSSHAGKVIGMTVPEGRLLLRDLTEHATQREFAYVHRWTVHDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>gb|ADC34039.1| TfdA-like protein [uncultured bacterium]
Length = 193

Score = 82.4 bits (202), Expect = 7e-14, Method: Compositional matrix adjust.
Identities = 67/219 (30%), Positives = 98/219 (44%), Gaps = 39/219 (17%)

Query: 56 QQITFAKRFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGN 105
QQI FAKR+G I + G +IV K D TV GN
Sbjct: 1 QQIAFAKRWGEIHLHPMPCLPDNPGIIEIVK---KEDDTV-----AFGGN 43

Query: 106 MAWHADSTYMPVMAQGAVFSAEVEVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSL 165
WH D A+ + A+ VPA GG T +A++ AYD+L + +A++
Sbjct: 44 --WHTDQMLTDTTPARVTMLYAKQVPAAGGDTLYANLYQAYDSLSDGMKAMIED----- 94

Query: 166 VYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGRH--AHAIPGMD 222
+ + S+ ++ + ++ A + PLV+VHPETGR +L I I GM
Sbjct: 95 LRTISQYDKKKRPAFMTPTIEVPAPEVEHPLVRVHPETGRKALYISYEGITRRIAGMT 154

Query: 223 AAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
AES L L++ A + +W G +VVWDNRC+
Sbjct: 155 EAESRPILSYLLNHAIRPEFTCRFRWQVGSLLVWDNRCV 193

>ref|YP_406805.1| taurine dioxygenase [Shigella boydii Sb227]
gb|ABB64977.1| taurine dioxygenase [Shigella boydii Sb227]
Length = 283

Score = 82.4 bits (202), Expect = 8e-14, Method: Compositional matrix adjust.
Identities = 70/271 (25%), Positives = 114/271 (42%), Gaps = 29/271 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVFLRDQAITPQQORALAQR 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++

Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GA+ +A+ +P+ GG T + AY+AL R L+ A H S + + ++

Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGITAYEALSVPFRLSGLRAEHDFRKSFPPEYKY-RKT 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ + P L P+V+ HP +G+ +L + I + ESE L G +

Sbjct: 168 EEEHQRWREAVAKNPPLLHPVVRTHPVSQKQALFVNEGFTTRIVDVSEKESEALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
P +W D+ +WDN H A

Sbjct: 227 AHITKPEFQVRWRWPNDIAIWDCVNTQHYA 257

>ref|ZP_07576923.1| Taurine dioxygenase [Sphingobium chlorophenolicum L-1]
gb|EFN08725.1| Taurine dioxygenase [Sphingobium chlorophenolicum L-1]
Length = 286

Score = 82.4 bits (202), Expect = 8e-14, Method: Compositional matrix adjust.
Identities = 78/289 (26%), Positives = 125/289 (43%), Gaps = 26/289 (8%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T L I P T+GA + G+ + + A+ AA LQ+ ++ F Q L N+ FA+

Sbjct: 12 THLDIRPLQPTIGAEIHGIDIGKPIAPEVRDAIRAALLQYKVVFVRDQQLDNESHAFAFAR 71

Query: 63 RFGAI----ERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
FG + + I N+ A + R P +K+ G A+H+D+++ V

Sbjct: 72 SFGPLYTHPSTTHDPKVTPIHNISALDSAR---PERRQAEVKIKPGE-AYHSDTSRWLVP 127

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
GAV A +P VGG T + D AY+ L +A + + A H + + L H

Sbjct: 128 TWGAVLRAVDLPPVGGDTVWDAHLAYEGLPDALKERLEGLHATHD--FRPTLLAH---- 181

Query: 179 GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWA 237
G+ A P+++ H ETG+ L + + I G++ AES +E ++

Sbjct: 182 -----GHDYPIVA--HPVIRTHRETGQKILWLNLTQNPQILGVELAESRELIEQVL-LQ 232

Query: 238 CQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
+ P W G V WDNR +H A PR++ +A P

Sbjct: 233 YKRPEFQVRFSWKPGSVAFWDNRAAVHYAVRNYGDYPRLLHRVLIADDP 281

>ref|NP_767577.1| dioxygenase [Bradyrhizobium japonicum USDA 110]
dbj|BAC46202.1| blr0937 [Bradyrhizobium japonicum USDA 110]
Length = 309

Score = 82.0 bits (201), Expect = 8e-14, Method: Compositional matrix adjust.
Identities = 75/280 (26%), Positives = 119/280 (42%), Gaps = 37/280 (13%)

Query: 5 TLQITPTGATLGATVTGVHLATL--DDA----GFAALHAAWLQHALLIFPGQHLSNDQQI 58
T+ + +GA ++GV + L DD +H A ++ ++ F QH+S Q +

Sbjct: 35 TIAVEKLTPIIGAEISGVDIGRLVSDDVRSNQMDIEIHRALAENLVIFFRDQHISPPQHL 94

Query: 59 TFAKRFGAIERIGGG----DIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTY 114
F ++FG + + A+ + AD ++SP WH+D +

Sbjct: 95 AFGRKFGEHLHFHAPAPHEDEDPALMKIYAD---KNSPR-----ANGEGWHSVDVSC 141

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
G++ + P GG T FA+M AAY+AL + +A + +A H G

Sbjct: 142 DLEPPMGSIYIKQCPPRGGDTLFANMYAAYEALSDRMKAYLDGLTALHD-----GE 193

Query: 175 VQQAGSAYIGYGM-DDTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL 230

G Y YG+ D + P P+++ HP TGR +L + R I G+ ES+ L
Sbjct: 194 PIYRG-LYANYGVADRPSPNAEHPVLRTHPVTGRKALYVNRGFTRHINGIPRDESDAML 252

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDF 270

L A +W + WDNRC HRA WD+
Sbjct: 253 AYLYQHAENPLFQCRFRWTENAIAFWDNRCTQHRAM-WDY 291

>emb|CAY27465.1| alpha-KG-dehydrogenase [uncultured bacterium]

emb|CAY27481.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 119

Score = 82.0 bits (201), Expect = 8e-14, Method: Compositional matrix adjust.

Identities = 46/128 (35%), Positives = 70/128 (54%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195

T F DMRAAYDAL + T+ + A HS+ +S+S++G + + D A L
Sbjct: 1 TEFGDMRAAYDALPDETKRQIEGLIAEHSIFHSRSRIG-----FTDFNPDV-AQALP 51

Query: 196 P----LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251

P +V+ HP +GR +L + HA + G + +E L+D+A Q V+ H+W G
Sbjct: 52 PVQQVMVRTHPGSGRKTLYLASHASHVIGWPIETGRKLIEDLLDFATQPQFVYQHRWQVG 111

Query: 252 DVVVWDNR 259

D+V+WDNR

Sbjct: 112 DLVMWDNR 119

>ref|YP_001260879.1| taurine catabolism dioxygenase TauD/TfdA [Sphingomonas wittichii
RW1]

gb|ABQ66741.1| Taurine catabolism dioxygenase TauD/TfdA [Sphingomonas wittichii
RW1]

Length = 325

Score = 82.0 bits (201), Expect = 8e-14, Method: Compositional matrix adjust.

Identities = 82/288 (28%), Positives = 119/288 (41%), Gaps = 40/288 (13%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64

L I P GA + G+ L +D A AA+ AAW++H +L+F G+ + Q+ + F
Sbjct: 11 LTIRPLAPGFGAEIVGLDLNRPIDAATEAAIRAAWIEHGILLFRGEDQDDAAQMRLSAIF 70

Query: 65 GAIERIGGGDI-----VAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY 114

G +E D+ +A +QH D G + WH D ++
Sbjct: 71 GEMEPAAATADMNDPDNRFMMTLAYDPDDKAPRFQQHYNVGGIDR----AGWLGWHWQSF 126

Query: 115 MPVMAQQGAVFSAEIVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174

MP + +GAV E+ G T F D A+D L + +A R +VY +
Sbjct: 127 MPTIVRGAVLRMEMPSPEMGETGFIDAVGAWDRLPDDLKA----RIEGLEVYVLFNP--- 179

Query: 175 VQQAGSAYIGYGMDDTTATP-----LRPLVKVHPETGRPSL-LIGRHAHA 218

S G+ D A P + P+V ETGR L L HA I
Sbjct: 180 --DFVSGQYGFPEIDRALPRERPSKEPSYDFPPVHPMVITQVETGRKVLKLSPMHARYI 237

Query: 219 PGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE 266

GMMDAAES+ L+ + + H W D+VVWDN ++H A
Sbjct: 238 LGMDAAESDALLKEVAHLVDPAHAYFHDWRKNDMVVWDNRVHIGAN 285

>emb|CAY27359.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 119

Score = 82.0 bits (201), Expect = 1e-13, Method: Compositional matrix adjust.

Identities = 52/125 (41%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALDE + HS ++S+S LG + P+R
Sbjct: 1 TEFADMRAAYDALDEEIKTECENLICEHSQFLSRSILGFTDFTDDERRRFA-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA AI G E+ FL L + A Q V+AH W D+V
Sbjct: 55 QRLVRRHPVTGRRSLYLASHAGAILGWLVPPEARAFRLDLNEHATQRQFVYAHVVRQWDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|YP_002781052.1| dioxygenase [Rhodococcus opacus B4]
dbj|BAH52107.1| putative dioxygenase [Rhodococcus opacus B4]
Length = 284

Score = 82.0 bits (201), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 69/272 (25%), Positives = 103/272 (37%), Gaps = 30/272 (11%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T + T+GA + G+ L + L A+LQH +L QHL + Q+ FAK
Sbjct: 10 TFTLERATPTIGAFIHGLDLRDEITPQCQTELRTAFLQHEVLFLRDQHLGPEDQLRFAKV 69

Query: 64 FGAIERIG-----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
FG + + G + + + G WH+D T+
Sbjct: 70 FGDPQEVSAFFPSLPGNPFIEVLESRGRA-----AGTDVWHSDLTWQA 112

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
A+ +P GG T ++ M AAYDAL E + L+ A H + + G V+
Sbjct: 113 TPNSATCLHAQDIPPCGGDTLWSSMTAAYDALPETMKNLIDGLEAVHD--WEKELTGVVR 170

Query: 177 QAGSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL 233
Q Y P P+V+ HPETGR + + I G+ S+ L
Sbjct: 171 QGDDGEARYEETRRKYPPMTHPVVRKHPEGTGRRLVYVNELFTSRISGVPPQLSDSLRNML 230

Query: 234 VDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
A +W +V+WDNR H A
Sbjct: 231 TGLAKTPEYQVRFRWEPNSLVIWDNRSTQHYA 262

>ref|ZP_04386335.1| alpha-ketoglutarate-dependent taurine dioxygenase [Rhodococcus
erythropolis SK121]
gb|EEN86336.1| alpha-ketoglutarate-dependent taurine dioxygenase [Rhodococcus
erythropolis SK121]
Length = 299

Score = 81.6 bits (200), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 72/282 (25%), Positives = 118/282 (41%), Gaps = 36/282 (12%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
++ T+++ ++GA ++GV L + DDA FA + L+H +L F Q S + +
Sbjct: 14 SRNTIRVEKLTCSIGAELSGVDLGEVARDALFAQIKGLLLEHKVLFRRDQTFSCAEHVE 73

Query: 60 FAKRFGAIERIGGGDIVAI-SNVKADGTVRQH---SPAEWDDMMKVIVGNMAWHADSTY 114
A+RFG +E D A+ S+ G VR + SP E + A+H D+T+
Sbjct: 74 LAQRFGELE-----DHPALGSDPDHPGLVRIYKDLDSPPEHFEN-----AYHCDATW 120

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
G V P VGG T + +M AY+ L + + ARHS+ +
Sbjct: 121 RVNPPMGCVLRCVETPPVGGDTIWNMALAYENLPARVKEQIKDLRARHSIESTFGARMP 180

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195

Sbjct: 1 T F DMRAAYDALD T+AL+ HS ++S+ LG ++ + A +
TEFWDMRAAYDALDGKTKALIEDIVCEHSRIFSKGALGF-----SFSEEEVKAFAPVRQ 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP+TGR SL + HA I G E+ L L + A Q V+ H+W D+V+

Sbjct: 55 RLVTRHPKTGRKSLYLSSHAGRIVGWPVPEAMLLRLDLNEHATQPEFVYVHKWTLHDLVM 114

Query: 256 WDNR 259
WDNR

Sbjct: 115 WDNR 118

>ref|YP_729190.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Ralstonia eutropha H16]
emb|CAJ95825.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Ralstonia eutropha H16]
Length = 303

Score = 81.6 bits (200), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 74/280 (26%), Positives = 117/280 (41%), Gaps = 35/280 (12%)

Query: 4 TTLQITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
++Q+ P T+GA ++ V+L A D+ A + A L+H +L F Q ++ Q + FA

Sbjct: 19 NSIQVEPVTCTIGAELSNVNLGAAAEDEQLMAEIRALLRHRVLFRRDQDITRAQHVAFA 78

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQH----SPAEWDDMMKVIVGNMAWHADSTYMPV 117
+RFG +E V S+ G V+ + SP + ++ +WH D+T+

Sbjct: 79 RRFGELE----DHPVVGSHPDYPGLVQIYKTPDSPPDRNEN-----SWHTDATWREK 126

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
G V P VGG T + +M AY+ L E + + ARH + S +++

Sbjct: 127 PPLGCVLRICIECPPVGGDTMWVNMVEAYNQLPEDIKTKIATLRARHGIEASFGAAMPIEK 186

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIP-----GMDAAE- 225
+ Y P+V+ HPETG L + + +P G+D A

Sbjct: 187 RLALKAQY-----PDAEHPVVRTHPETGEKVLVFNVSFTTHFTNYPANVRFGIDKAPG 241

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ L LV A +W V WDNR H A

Sbjct: 242 AANLLSYLVSQATIEYQVRFRWKKNVAFWDNRSTQHYA 281

>emb|CBK85931.1| Probable taurine catabolism dioxygenase [Enterobacter cloacae subsp. cloacae NCTC 9394]
Length = 283

Score = 81.6 bits (200), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 73/289 (25%), Positives = 122/289 (42%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA V+G+ + L D F L+ A L+H ++ Q ++ QQ A RF

Sbjct: 5 LTITPLGPYIGAQVSGLDVTRPLSDNQFEQLYHAVLRHQVFLREQAITPQQRALALRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM 118
G + G + + + + D +P + D+ WH D T++

Sbjct: 65 GDLHIHPVYPHAEGVEEIIVLDTND-----NPPDNDN-----WHTDVTFTIDTP 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQ 176
GA+ +A+ +P GG T +A AA++AL + L+ A H + + K +

Sbjct: 109 PAGAILAAKQLPETGGDTLWASGIAAFEALSAPLQTLLSGLRAEHDFKKSFPEYKYRKTK 168

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE-RFLEGLVD 235
+ ++ + L P+V+ HP TG+ +L + +D AE E L G +

Sbjct: 169 EEHQRWLD-AVAKHPPLLHPVVRTHPVTGKQALFVNE-GFTTRIVDVAEKESEALLGFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

P +W D+ +WDNR H A R+M + + G

Sbjct: 227 AHITKPEFQVRWRWQENDLAIWDNRVTQHYANADYLPQRRIMQRATILG 275

>ref|YP_990665.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia mallei SAVP1]

ref|ZP_02269394.1| taurine dioxygenase [Burkholderia mallei PRL-20]

gb|ABM49497.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia mallei SAVP1]

gb|EES43057.1| taurine dioxygenase [Burkholderia mallei PRL-20]

Length = 282

Score = 81.6 bits (200), Expect = 1e-13, Method: Compositional matrix adjust.

Identities = 77/273 (28%), Positives = 110/273 (40%), Gaps = 26/273 (9%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63

++I P +GA + G+ LA DD FA + AA L H +L Q ++ + + FA+R

Sbjct: 1 MRIEPLTCAIGAEVLGMCLADAAHDDDLFAEIRAALLAHRVLFRLDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAV 123

FG +E VA S+ G VR + E + AWH D+T+ G V

Sbjct: 61 FGELE----DHPVAGSDPDHPGLVRIYKTPEQPNEHY----ENAWHTDATWRQAPPLGCV 112

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183

P VGG T +A+M AY+ L E +A + ARHS+ ++ G

Sbjct: 113 LRCVACPEVGGDTMWANMVLAYENLPEHVKAQIADLRARHSI---EASFGAAMPIDGRLA 169

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMDAAESERFLEGL 233

A P+++ HPETG L + A G DA L G

Sbjct: 170 LKAQFPDAE--HPVMRTHPETGEKVLVNAFTTHTFTNYHTPARVRVQGDANPGAALLLG 227

Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

+ P +W V +WDNR H A

Sbjct: 228 LLSQAYIPEYQVRWRWRKNSVAIWDNRSTQHYA 260

>ref|ZP_02407529.1| taurine dioxygenase [Burkholderia pseudomallei DM98]

Length = 272

Score = 81.6 bits (200), Expect = 1e-13, Method: Compositional matrix adjust.

Identities = 82/300 (27%), Positives = 118/300 (39%), Gaps = 52/300 (17%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66

++TP LGA V V L+ DA + AA H +L F GQ LS + FA FG

Sbjct: 3 RLTPA---LGAIVDDVDLSNATDALRDDIRAALAHQVLFVRGQRLSARHRDFAAGFGD 59

Query: 67 I-----ERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMA 119

+ +I+ + N D + N WH D T+

Sbjct: 60 LHVHPIYPSPHDAREIMVLDNAVFD-----LQDNAIWHTDVTFETETPP 102

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQ 177

+ ++ +A +P GG T + AAYDAL +A + +A+H + + G V

Sbjct: 103 RASILAAHTLPETGGDTLWGSFGAAYDALSGRVKAQLDGLTAQHDFTKSFPLKRFVTA 161

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR----HAAIPGMDAAESERFL--- 230

A T + P+V+ HPETGR +L + +P + A RFL

Sbjct: 162 EDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNEGFTTEIDELPEEEGAALLRFLFAH 221

Query: 231 ----EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285

E + W +W GDV WDNR +H A K RVM + + G RP

Sbjct: 222 QSRPEFTLRW-----RWQPGDVAFWDNIRSTIHYAVNDYGKAHRVMHRATIVGDRP 271

>emb|CAY27203.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27205.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 81.3 bits (199), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 49/126 (38%), Positives = 66/126 (52%), Gaps = 10/126 (7%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG--HVQQAGSAYIGYGMDDTTATP 193
T FADMRAA+D LD T+ V HS +YS+ LG ++ A+ A
Sbjct: 1 TEFADMRAAWMDLARTKEQVKDLVVEHSRIYSKGVLGVPFTEEEKRAF-----APV 52

Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+PLV+ H TGR SL + HA I G +E L L++ A Q V+ H+W GD+
Sbjct: 53 TQPLVRTHQRTGRHSLFLSSHAGRIVGWPVSEGMLLLRELMEHATQREFVYRHRWRVGD 112

Query: 254 VVWDNR 259
V+WDNR
Sbjct: 113 VMWDNR 118

>ref|YP_002230865.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia
cenocepacia J2315]
emb|CAR52037.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia
cenocepacia J2315]
Length = 282

Score = 81.3 bits (199), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 74/274 (27%), Positives = 115/274 (41%), Gaps = 28/274 (10%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+++ P +GA + V LA DD FA + A L+H +L Q ++ + + FA+R
Sbjct: 1 MRVEPLTCAIGAELLDVSLADAVHDDGLFAEIRAQLLRHRVLFRLDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E VA S+ + G VR + SP + +D + AWH+D+++ G
Sbjct: 61 FGELE----DHPVAGSDPEHPGLVRIYKSPDQPNDRYE-----NAWHSASWRVAPPFGC 111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V P VGG T +A+M AY+ L + + + ARHS+ S V + +
Sbjct: 112 VLRCIEGPPVGGDTMWANMVLAYERLPDHVKQIADLRARHSIEASFGAAMPVDKRLALK 171

Query: 183 IGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LE 231
Y P+V+ HPETG L + A R+ L+
Sbjct: 172 AQY-----PDAEHPVVRTHPETGEKVLVNAFATHFTNFHTPARVRYGQDANPGAGQLLQ 226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L+ A +W V +WDNR H A
Sbjct: 227 YLISQAYIPEYQVRWRWKKNSVAIWDNRSTQHIA 260

>gb|ADC33936.1| TfdA-like protein [uncultured bacterium]
Length = 124

Score = 81.3 bits (199), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 48/128 (37%), Positives = 70/128 (54%), Gaps = 6/128 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP-- 193
T F DMR A++AL + + ARHSL S+ K G ++ D P
Sbjct: 1 TEFCDMRLAWEALPAEEQVKLEPLVARHSLWLSRRKYGD----DKSFKFNAEDAARYPPV 56

Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
RPLV VH TGR L++G + ++ +D ES FL+ L D A V++H+W+AGD+
Sbjct: 57 ERPLVDVHRPTGRRCLMLGANIASVGLDEIESVAFLELTDTRATAPAFVYSHRWSAGDL 116

Query: 254 VVWDNRCL 261
++WDNRC+
Sbjct: 117 LLWDNRCLV 124

>ref|YP_003647917.1| Taurine dioxygenase [Tsukamurella paurometabola DSM 20162]
gb|ADG79578.1| Taurine dioxygenase [Tsukamurella paurometabola DSM 20162]
Length = 305

Score = 81.3 bits (199), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 69/265 (26%), Positives = 109/265 (41%), Gaps = 23/265 (8%)

Query: 2 AQTTLQITPTGATLGVHGLA-TLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQIT 59
A + + +T +GA V GV L +DDA + ++ ++ F QH L + Q
Sbjct: 10 ATSEITVTKLSEHIGAIVHGVRLGGDIDDATAERILDLLAEYEVIFFRDQHHLDDAGQHA 69

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
FA R G TVR S D++ + +WH D +++ +
Sbjct: 70 FAGRIGV-----PTTPHPTVRSDS-----DLLPIEGAANSWHTDVSFVDRVP 111

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
+ ++ +P GG T +A AYD L E + L A H+ Y + Q
Sbjct: 112 KASILRPVTLPPHGGNTTASTTTRAYDRLEPLKVLAEENLRAIHTNDYDYAGHNSTYQRA 171

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
+ + + P+V++HPETGR SLL+G G+ + +S L L+ +
Sbjct: 172 EYHQEF-IRNIFEAEHPVVRMHPETGRRSLLLGHFVSKFAGLSSQDSAPIL-ALLQRRIE 229

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLH 263
P W GDV +WDNR H
Sbjct: 230 NPDNTVRWAWQPGDVAIWDNRSTQH 254

>ref|YP_002767506.1| dioxygenase [Rhodococcus erythropolis PR4]
dbj|BAH34767.1| putative dioxygenase [Rhodococcus erythropolis PR4]
Length = 324

Score = 81.3 bits (199), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 68/266 (25%), Positives = 112/266 (42%), Gaps = 27/266 (10%)

Query: 6 LQITPTGATLGVHGLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
+ + G +GA + GVHL+ L + A++ A H ++ F GQ HL + Q FA
Sbjct: 22 ITVHKVGELIGARIDGVHLSGDLSEETAYAINYALAANKVVFQGGQHLDDTSQYEFAGT 81

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQQAV 123
G VK+ G D ++ + +WH D T++ + + ++
Sbjct: 82 LGT-----QTPHPTVKSKEG-----DKLLVLDRAANSWHTDVTTFVDRIPKASI 124

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS--- 180
A +P GG T +A AAY+ L + + V A H+ Y +++ V QA
Sbjct: 125 LRATTIPEYGGATTWASTTAAEYQLPASLKVVENLRVHTNAYDYAEV--VNQANPVDA 182

Query: 181 ---AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
AY P+V++HP TG +LL+G G+ +ES + L
Sbjct: 183 QRLAYYAEFTREIYETEHPVRIHPATGEKTLLLGHFFKEFVGLKPSESVALYQLLQARI 242

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLH 263
+ W+AGD+ +WDN+ H
Sbjct: 243 IKLENTVRWNWSAGDLAIWDNQATQH 268

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254

LV+ HP TGR SL + HA AI G E+ FL L + A Q V+AH W D+V
Sbjct: 55 QRLVRRHPVTGRRSLYLASHAGAILGWPVPEARAFRLDLNEHATQRRFVYAHVWRQWDLV 114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>gb|ACF09927.1| probable taurine catabolism dioxygenase [uncultured marine group
III euryarchaeote KM3-28-E8]
Length = 293

Score = 80.9 bits (198), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 76/274 (27%), Positives = 117/274 (42%), Gaps = 31/274 (11%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ + P GA V GV L + A +H A ++H ++ F Q ++ +Q TFA+ F
Sbjct: 7 ITVEPASRNCGAFVDGVDLTKPVTSAICREIHTALMRHQVVFVRDQDVTPEQTTFARNF 66

Query: 65 GAIERIGGGDIVAISNVKADGTV----RQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
G + RI + + ++ +V R+H P + D +HAD +
Sbjct: 67 GPL-RIKHSASFELHDDTSEVSVIVNNREHPP--YID-----HYHADGMFRMEPEF 114

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
++ AE P +GG T F ++AA++ L +A RA + + A VY KL +
Sbjct: 115 ASMLKAEAPPKMGDDTIFVSLKAAWNGLSDALRATLDDKIA---VYDFMKLHSTPEKAR 170

Query: 181 AYIG---YGM---DTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
+ G GM D PLV HP +G L AI G++ ESE +
Sbjct: 171 NWTGSPSRQGMIKSRDENPPVQHPLVPKHPVSGERCLYFSESFTAAILGLNKYESEA-MHA 229

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
L+ C P QW G + +WDN LH A
Sbjct: 230 LLTRHCAKPEFQYRLQWRKGTIAMWDNLGSLHYA 263

>ref|ZP_04382576.1| alpha-ketoglutarate-dependent taurine dioxygenase [Rhodococcus
erythropolis SK121]
gb|EEN89969.1| alpha-ketoglutarate-dependent taurine dioxygenase [Rhodococcus
erythropolis SK121]
Length = 316

Score = 80.9 bits (198), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 80/283 (28%), Positives = 111/283 (39%), Gaps = 15/283 (5%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L + T+GA ++G+ L L DA A L A L+ +L F Q L + FA+R+
Sbjct: 41 LAVKAVAPTIGAEISGIRLGGGLSDAVIAELRRALLEWKVLFVRDQDLDRAEHRAFAERW 100

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G +E+ D T D M+ + N WH D T+ + AV
Sbjct: 101 GDLEQHPFFKYTQPGQTDVDVTTLAK-----DAMVGGVENN--WHNDVTWHEFPSFAAVL 153

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
A VP VGG T +AD AAYD L E + + A H + S + V
Sbjct: 154 RAVEVPEVGGDTLWADTAAAYDLLPEDIKKRIDPLVAEHDWINSFGRSMPVDAVEMLRPK 213

Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRV 243
+ P+V++ PE+GR L + I G+ ES L L +
Sbjct: 214 F-----PAVQHPVVRIIPESGRRVLFVNMTFTQRI LGVSEESNELLTMLYRHVNRPEFQ 268

Query: 244 HAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
+W V WDNR H A F RVM + G RP

Sbjct: 269 VRLKWEPTVAFWDNRTCQHYAASDYFPARRVMDRISIVGDRP 311

>emb|CAY27383.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 80.9 bits (198), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 51/124 (41%), Positives = 65/124 (52%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T FADMRAAYDALDE + HS ++S+S LG + + A +
Sbjct: 1 TEFADMRAAYDALDEEIKTECENLICEHSQLF SRSILG-----STDFTDDERRRFAPVTQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP TGR SL + HA AI G E+ FL L + A Q V+AH W D+V+
Sbjct: 56 RLVRHPVTGRRSLYLASHAGAILGWLVEPARAFLRDLNEHATQRQFVYAHVVRQWDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>gb|EFQ95338.1| hypothetical protein PTT_06701 [Pyrenophora teres f. teres 0-1]
Length = 386

Score = 80.9 bits (198), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 77/265 (29%), Positives = 105/265 (39%), Gaps = 27/265 (10%)

Query: 13 ATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRFGA--I 67
A +GA V GV L+ L+DAG L Q ++ F Q ++ + F FG I
Sbjct: 100 ANIGAEVHGVLQSLKNDAGKDELALFVAQKKVVAFREQDFADIPIKDALAFGGYFGRHHI 159

Query: 68 ERIGGG-----DIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
G +I + D + R D + ++ WH+D TY
Sbjct: 160 HPTSGAPEGYPEIHLVHRGTDDTSAR-----DFFEERTNSITWHS DVTYEKQPPGTT 211

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
PA GG T FA+ AAY+ L R +H HS V + G Q G
Sbjct: 212 FLYILDGPAAGGDTLFANQVAAYNRLSPEFRKRLHGLKVVSASV--EQADGSRNQGGIV- 268

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAP 241
T + PLV+ HP TG +L + + + I G ES+ L L D +
Sbjct: 269 ---RRDPVTSIHPLVRTHPATGEKALYVNPQFSRRIVGYKKEESD FLLNFLYDHIAGQ 324

Query: 242 RVHAH-QWAAGDVVVWDNRCLLHRA 265
A +WA G VVVWDNR H A
Sbjct: 325 DFQARVKWAPGTVVVWDNRVTAHSA 349

>gb|ADC33935.1| TfdA-like protein [uncultured bacterium]
gb|ADC33964.1| TfdA-like protein [uncultured bacterium]
gb|ADC33978.1| TfdA-like protein [uncultured bacterium]
Length = 121

Score = 80.9 bits (198), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 43/126 (34%), Positives = 67/126 (53%), Gaps = 5/126 (3%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T F DMR A++ L +A + + +A HS+ +S++ G + GY P R
Sbjct: 1 TEFCDMRRAWELLSPEEQAELEELTANHSIAHSRALAGFTEWPA----GYDEFLQRVP-R 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV VHP+TGR +LL H + G + E+ + L+ A +AH+W+ GD ++

Sbjct: 56 PLVGVHPDTPGRKALLTASHIETLTGKNKEETTELVAELIQRATVPENCYAHRWSKGDFLM 115

Query: 256 WDNRC 261

WDNRC+

Sbjct: 116 WDNRCV 121

>ref|NP_928338.1| hypothetical protein plu1004 [Photorhabdus luminescens subsp. laumondii TTO1]
emb|CAE13299.1| unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1]
Length = 315

Score = 80.9 bits (198), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 61/271 (22%), Positives = 109/271 (40%), Gaps = 29/271 (10%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T ++TP A + + L L+ + + +H +L+FP Q +++ + +
Sbjct: 8 TIRKLTPY---FCAEIRDIKLNQPLNKDIKTIESDLEEHEVLVFPDQDITSEDLMRIGR 64

Query: 63 RFGAI-----ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
FG + E + + + K+ P D WH+D TY
Sbjct: 65 YFQQLTVHPFAENSEKNPELIVFDYKSGN-----PPVLT-----RWHSDETYKL 109

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ + +VP +GG TCF+ M AYD L T+ + A H +S K
Sbjct: 110 CPPMATMLYSRIVPEIGGDTCFSSMTTAYDFLSIKTQDFIRGLEAIHD--FSSYKYLFPD 167

Query: 177 QAGSAYIGYGMDDTTATPL-RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLV 234
+ + P+ P+V++HP+T + +L + + I MD +S+ L L
Sbjct: 168 TEEGKLLQKKELEYPPIAHPVVRIPHKTTRKTLFVNPNYTRYIKNMDQRDS DALLAQLF 227

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ + H W +V+WDNR + H A
Sbjct: 228 NTTSVLEYQYRHHWKPMLVMWDNRSVQHAA 258

>ref|ZP_06057387.1| taurine dioxygenase [Acinetobacter calcoaceticus RUH2202]
gb|EEY78686.1| taurine dioxygenase [Acinetobacter calcoaceticus RUH2202]
Length = 282

Score = 80.9 bits (198), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 74/278 (26%), Positives = 113/278 (40%), Gaps = 36/278 (12%)

Query: 6 LQITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+QI +GA ++GV L A DD FA + L+H +L QHL+ + FA+R
Sbjct: 1 MQIEQLTCNIGAELSGVKLSDAIYDDGLFAEIRTQLLKHRVLFRLDQHLTRQDHVAFER 60

Query: 64 FGAIERIGGGDIVAI-SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E D A+ S+ G V+ + E V AWH+D+++ G
Sbjct: 61 FGQLE-----DHPAVGSDPDHPLVQIYKHPE---SPVNRYENAWHSDASWRKAPPMGC 111

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V P VGG T + +M AY++L + + + A HS+ ++ G +
Sbjct: 112 VLHCVECPVGGDTMWTNMVMAYESLPDDIKNKIADLRAYHSI---EASFG-----AAMP 163

Query: 183 IGYGMDTTAT---PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF----- 229
+ +D A P+V+ HPETG L + E RF
Sbjct: 164 LEKRLDLKAKFPDAEHPVVRTHPETGEKILYVNAFTTHFSNYHTKERVRFQGDANPGSAE 223

Query: 230 -LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L L+ A P +W + +WDNR H A
Sbjct: 224 LLRYLISQA-YIPEFQVRWRWKPNISIAIWDNRSTQHYA 260

>ref|ZP_06410835.1| Taurine dioxygenase [Frankia sp. EUN1f]
gb|EFC86427.1| Taurine dioxygenase [Frankia sp. EUN1f]
Length = 317

Score = 80.9 bits (198), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 72/291 (24%), Positives = 116/291 (39%), Gaps = 30/291 (10%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSND-QQITFAK 62
++ + A +GA + GV + LD + + A ++H ++ GQ ++D Q FA
Sbjct: 19 SITVDRVSANIGAVIGGVRIIGDDLATTVEIKRALVEHKVVFLRGQQHADDATQRAFAS 78

Query: 63 RFGAIE----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + A+G +WH D T++ +
Sbjct: 79 LLGTPTPLPHTVTGADNSVLPIDAAEGKAN-----SWHTDVTFTVDRI 120

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY-----SQSKL 172
+V A +P GG T +A+ AY L+ A +AL + A HS +Y ++ +
Sbjct: 121 PSASVLRAVTLPPYGGTTTWTANTAHAYSTLNPALQALADRLWAVHSNLYDYAAERTEKAI 180

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG 232
G + AY P+V+VHP TG +LL+G I G+ +S+
Sbjct: 181 GGIDVKEEAYRAEFGHIEYETEHPVVRVHPVTGERNLLLGHFVRRIVGLSTRDSQDIFNL 240

Query: 233 LVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + W GD+ +WDNR H A PR + LAG
Sbjct: 241 LQRHVIRLEHTVQWSWRDGDIAIWDNRATQHYAIADYDDQPRRLHRITLAG 291

>emb|CAY27389.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 80.9 bits (198), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 48/125 (38%), Positives = 64/125 (51%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMR AYD LD+ TRALV H+ +YS+ +G + P+R
Sbjct: 1 TEFADMRIAYDLLDDETRALVEDLVCEHTQLYSRSGMGFSDWTEERAMFK-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I G E+ L L + A + V+ H+W D+V
Sbjct: 55 QRLVRTHPVTGRKSLYLSSHAGTIIGWQMPPEARLRLDLNEHATRPELVYIHRWRQYDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|YP_004017671.1| taurine dioxygenase [Frankia sp. Eu11c]
gb|ADP81801.1| Taurine dioxygenase [Frankia sp. Eu11c]
Length = 321

Score = 80.9 bits (198), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 74/272 (27%), Positives = 116/272 (42%), Gaps = 25/272 (9%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
TL + P +GA + GV L+ L A A + AA L ++ F Q L+ DQ I F +
Sbjct: 20 TLDVRPMSGHIGAEIFGVLDSEPLAPAVTAEIRAALLAWKVIFFRDQRLTPDQHIAFGRL 79

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYM 115
FG + G +I+A+ + +A + D +++ WH D T++
Sbjct: 80 FGEVGPGHPTLPTLEGHPEILAL-DTRAYAGLDSSGDRRGDGGIRI---KSLWHTDVTFL 135

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
G++ +VP GG T F ++ AY+ L R LV A H ++L H+
Sbjct: 136 RTPPMGSILRGVLVPPYGGDTNFLNLVTAYETLSAPLRDLVDGLHAVHV-----NQL-HL 189

Query: 176 QQAGSAYIGYGMDTTATPLR---PLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLE 231
+ S+ + ++PL P+V+VHPETG +L + I + ES L
Sbjct: 190 DRGDSSKLSALF--ASSPLEAVHPVVRVHPETGERALFVNPTFTTRIVELTNTESAHLN 247

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH 263
L +W GD+ WDNH H
Sbjct: 248 LLYQHMTNLEFTTCRFRWQPGDLAFWDNRATAH 279

>ref|ZP_06500435.1| taurine dioxygenase [Pseudomonas syringae pv. syringae FF5]
Length = 289

Score = 80.9 bits (198), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 83/296 (28%), Positives = 125/296 (42%), Gaps = 44/296 (14%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T ++TP +GA V GV L+ L + A+L++ +L+F QHL+ +Q F +
Sbjct: 24 TVNRLTPI---IGAEVDGVDLSQPLSAEQLTEIRRAFLENHVLVFRDQHLTVEQHKAFGR 80

Query: 63 RFGAIERIG----GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM 118
FG + + GD + V+A+ R WH D T
Sbjct: 81 LFGPLRALPVD SIDGDDPELVVVRANAQSR-----FAAGELWHTDGTADLEP 127

Query: 119 AQGAVFSAEVVPAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ G++ + PA+ GG T FA+M A + L A + + +A H G +
Sbjct: 128 SMGSMlyVKETPAIGTGGDTL FANMHLAIEMLS PAMQQFLGGLTAIHD-----GEIP 179

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLV 234
G G+ + PLV HPETGR SL + G +H + + ES L L
Sbjct: 180 WKGyQPPA-GLPKSE---HPLVVRHPETGRRSLFVNSGFTSHIV-QLSPGESHA VLTMLF 234

Query: 235 DWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSR---LAGRPE 286
D + P + +W +V WDNRC H A WD+ P + R L GRP+
Sbjct: 235 DLIAREPSLSCRVRWEPNTLVFWDNRCTQHHA V-WDY-FPHSRYGERVTILGGRPQ 288

>ref|YP_586543.1| taurine dioxygenase 2-oxoglutarate-dependent [Cupriavidus metallidurans CH34]
gb|ABF11274.1| taurine dioxygenase, 2-oxoglutarate-dependent [Cupriavidus metallidurans CH34]
Length = 301

Score = 80.9 bits (198), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 77/283 (27%), Positives = 112/283 (39%), Gaps = 65/283 (22%)

Query: 14 TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE---RI 70
T+GA V+GV L LDD + AL A L H +L F QH++ Q + A+RFG +E I
Sbjct: 31 TIGAEVSGVDLGNLDDTTYRALRQALLDHKVLFFRDQHITPAQHVA AARRFGELEVHPMI 90

Query: 71 G-----GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV 117
G GGD N+ +H+D ++ +
Sbjct: 91 GHHPDHP ELVVFGRGDKRGRENL-----YHSDVSWREL 124

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHV 175
+ G++ P +GG T + +M AAY AL E + + + A H + + QS G
Sbjct: 125 PSMGSM LRCVECPEIGGDTIWNMAAAYAALPEDVKTRIAELRAVHDAMP TFGQSM DGER 184

Query: 176 QQAGSAYIGYGMDTTATPL-RPLVKVHPETGRPSLLIGR-----HAHAIP---GMDA 223

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                M      P+  P+V+ HPETG  L  +          +A  P  G  D
Sbjct: 185 YDE-----MRAKYPPMVHPVVRTHPETGEKILYVNEGFTTTHFANYARMQPYRIGSDF 236

Query: 224 AESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
      +E  L  +      AP      +W  A  V  +WDNR  H  A
Sbjct: 237 RMAEMDLMQYLFRQAAPEYQVRLRWRANTVALWDNRSTQHYA 279

```

>gb|ADC34027.1| TfdA-like protein [uncultured bacterium]
Length = 197

Score = 80.5 bits (197), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 67/213 (31%), Positives = 98/213 (46%), Gaps = 23/213 (10%)

```

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYM 115
      QQI FAK+FGA      V      +K      +P      +  +  G  + WH+D+TY+
Sbjct: 1  QQIAFAKKFGAP-----VEYPQLKGLAECPYVTPVVKLEHERNNFGGI-WHSDTTYL 51

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR----ALVHQRSARHSLVYSQSK 171
      +  G++  A  VP  GG  T  FA+  AY+AL  +  +      L+  S+  +  V  ++++
Sbjct: 52 EIPPMGSMILLAREVPPYGGDTMFANQYLA YEALSDGLKQTL DGLIGVSSSAKADV-TKTR 110

Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFL 230
      ++QAG      ++      PLV+ HPETGR +L      H  I  G      ES  L
Sbjct: 111 EDALKQAGERATPKVLEAE----HPLVRTHPETGRKALYTSVAHTARIKGWTEQESLPLL 166

Query: 231 EGLVDWACQA-PRVHAH-QWAAGDVVVWDNRCL 261
      E  L  WA  Q  P      QW  G  +  WDNRC+
Sbjct: 167 EFL--WAQQVRPEFTCRFQWLVGSLAFWDNRCV 197

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>ref|ZP_01103984.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Congregibacter
litoralis KT71]
gb|EAQ96542.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Congregibacter
litoralis KT71]
Length = 273

Score = 80.5 bits (197), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 68/268 (25%), Positives = 114/268 (42%), Gaps = 27/268 (10%)

```

Query: 6  LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      +  I  P      +GA  V+  V  L      +  D      +L      +H  L+  F  Q  ++  QQ  A  F
Sbjct: 1  MNIKPVAGAIGA EVSDVDLCNPM TDDMKRSLREL VNRHEL VFFRDQAITPAQQRDLAALF 60

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
      G  ++      D  V      +  V  +  +P  +  +      WH+D  T+      V
Sbjct: 61 GPLQSHPAYDTVPD--LPEVMVLESTPEKPSKIE-----VWHSMTFRQHPPSITVL 110

Query: 125 SAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS-KLGHVQQAGSAYI 183
      +P+VGG  T  +A  M  AAY+AL      +  +  +A  H      +SQ  K      ++  G  +
Sbjct: 111 RGVEIPSVGGDTLWASMTAA YEALSPGMQRYLQDLTAVHD--FSQGFKESLSEEGGRERL 168

Query: 184 GYGMDDTTATPLRPLVKVHPETGRPSLLIG----RHAHAIPGMDAAESERFL---EGLVDW 236
      +      P+++ HPETGR ++  +      H  I      +++AE  +FL      ++
Sbjct: 169 ADALANNPPVRHPVVIQTHPETGRKAIFVNALFTTHIEGISPLESAEVLQFLYKHSTTPEF 228

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
      C+      +WA  VV+WDNR  H+
Sbjct: 229 TCRL-----RWAKDTTVIWDNRSTQHK 250

```

>ref|YP_001808308.1| taurine dioxygenase [Burkholderia ambifaria MC40-6]
gb|ACB64092.1| Taurine dioxygenase [Burkholderia ambifaria MC40-6]

Length = 282

Score = 80.5 bits (197), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 75/274 (27%), Positives = 118/274 (43%), Gaps = 28/274 (10%)

```
Query: 6   LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
          +++ P   +GA + GV+LA   DD FA +   L+H +L   Q ++ + + FA+R
Sbjct: 1   MRVEPLTCAIGAELLGVNLADAVHDDGLFAEIRTQLLRHRVLFRLDQDITRAEHVAFARR 60

Query: 64  FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
          FG +E   VA S+ +   G VR + SP + +D +   AWH+D+++   G
Sbjct: 61  FGELE-----DHPVAGSDPEHPGLVRIYKSPDQPNDRYE-----NAWHSASWRVAPPFGC 111

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
          V   P VGG T +A+M AY+ L + + +   ARHS+ S   + + +
Sbjct: 112 VLRCIDGPPVGGDTMWANMVLAYENLPDHVKQQIADLRARHSIEASFGAAMPIDKRLALK 171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMDAAE-SERFLE 231
          Y   P+V+ HPETG L +   A   G DA + + L
Sbjct: 172 AQY-----PDAEHPVVRTHPETGEKVLVNAFTTHTFTNFHTPARVRVGDANPGAGQLLH 226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          L+ A   +W   V +WDNR H A
Sbjct: 227 YLIGQAAIPEYQVRWRWKNSVAIWDNRATQHYA 260
```

>ref|XP_388431.1| hypothetical protein FG08255.1 [Gibberella zeae PH-1]
Length = 331

Score = 80.5 bits (197), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 76/286 (26%), Positives = 121/286 (42%), Gaps = 48/286 (16%)

```
Query: 7   QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKR 63
          ITP   +G + GV ++ LD G L   + +++F Q + D+Q +
Sbjct: 51  NITPR---VGTEIRGVQISQLDQKGLDELALLAAERGVVFRDQDFKDIGFDRQKEIVRH 107

Query: 64  FGAIER-----IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY 114
          +G + +   G   V ++ K+ + P D+   WH D T+
Sbjct: 108 YGPLHQHPTMGYPKGTGPEFHVYADEKSGNLRKLLGPRTTYDL-----WHVDQTF 158

Query: 115 MPVMAQGAVFSAEVVPVAVGG-RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
          P + + F   +P+ GG T F + AAY+AL A R   Q   L ++ + G
Sbjct: 159 TPNVPSTSFVWLEIPSSGGGDTAFTSLTAAEALSPAFR----QTTLNLKLHHTSASEG 214

Query: 174 HVQQAGSAY-IGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE 231
          V++ G   + ++TT   PLV HP TG+PSL +   A + G   ES+ L
Sbjct: 215 EVKRVGQERALAEAINTT---HPLVIKHPVTGKPSLFVNPTIARQVEGFLPEESDHLLS 270

Query: 232 GL-----VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFK 271
          L   +D++C+   +W G VVWD R + H A P DF+
Sbjct: 271 FLKNHIRSLDFSCRV-----KWETGTVVVWDQRTVAHSAVP-DFQ 309
```

>ref|YP_001704349.1| taurine dioxygenase [Mycobacterium abscessus ATCC 19977]
emb|CAM63695.1| Probable taurine dioxygenase [Mycobacterium abscessus]
Length = 292

Score = 80.5 bits (197), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 71/280 (25%), Positives = 114/280 (40%), Gaps = 36/280 (12%)

```
Query: 4   TTLQITPTGATLGATVTGVHLA--TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
          + +++ P   T+GA + V LA + D F +   L+H +L   Q+++ + + A
Sbjct: 8   SKIRVQPLTCTIGAELFDVDLAEASRSEDLFGEIRTLLLEHKVLFRLDQNITRGEHVALA 67
```

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQH-----SPAEWDDMMKVIVGNMAWHADSTYMP 116
+RFG +E VA S+ G VR + +P +++ ++H D+T+
Sbjct: 68 RRFGLPE----DHPVAGSDPDHPGLVRIYKEIDSAPEHYEN-----SYHCDATWRE 114

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
GAV P VGG T + +M AY L A R + ARHS+ S ++
Sbjct: 115 SPPMGAVLRCVETPPVGGDTIWNMVEAYRRLPAAVRDRIRDLRARHSIEASFGAAMSMR 174

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF----- 229
Q + Y P+V+ HPETG L + + E+ RF
Sbjct: 175 QRHELHERY-----PDAEHPVVRTHPETGEEILFVNSFTTHLVNYHRPENVRFGIDYAPG 229

Query: 230 LEGLVDWACQAPRVHAHQ---WAAGDVVVWDNRCLLHRA 265
L+ + + V Q W V +WDNR H A
Sbjct: 230 ASELLQYLMRQATVPEFQVRWRWTPNSVAIWDNRSTQHHA 269

>ref|YP_004018099.1| taurine dioxygenase [Frankia sp. Eu1lc]
gb|ADP82229.1| Taurine dioxygenase [Frankia sp. Eu1lc]
Length = 342

Score = 80.5 bits (197), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 85/286 (29%), Positives = 120/286 (41%), Gaps = 27/286 (9%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAA-LHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
++TP +GA + G+ L TL +G A L A + H +L PGQ L D + + G
Sbjct: 59 RLTPR---IGARLDGLDLRTLPRSGRAEELRTALVAHKVLFVPGQDLDDADHVALGRALG 115

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
V S+ G +H D ++ WH D T+MP ++
Sbjct: 116 D-----VTTSHPVVPGADERHPEIYELDSHDGGTSDV-WHTDVTFMPRPPMASILR 165

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 185
A +P +GG T + D+ AY++L A RAL A H + G + G
Sbjct: 166 AVRLPDLGGATNWDLEQAYESLSPAVRALADGLEAIHD---GNREFG--EYLAHRRGGE 220

Query: 186 GMDTTATPLRPL-----VKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
G D T +R L V+VHPETGR SL + I G+ AES L+
Sbjct: 221 GNDWDGTRVRALVPVRHPVVRVHPETGRSLFVNPGFTVRIAGVSDAESRGLLDIFFAHL 280

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ + H W GDVV+WDNR H A+ R+M L G
Sbjct: 281 TRPEHLVRHHWRPGDVVLWDNRSTAHYADHDYGDFQRIIMHRITLRG 326

>emb|CAY27517.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 80.5 bits (197), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 46/124 (37%), Positives = 65/124 (52%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALD+ T+A + RHS +YS+ KLG + +
Sbjct: 1 TEFADMRAAYDALDDRTKAEIEDLVCRHSNMYSRGKLGAEFTNEERAVFKPVRQRL--- 57

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
V+ +GR SL + HA I GM ++ L L ++A + P V++H W D+V+
Sbjct: 58 --VRRQRVSGRKSLFLSAHAGEIEGMPTPQARMLLLDLTEFATREPFPVYSHVVRVNDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>ref|XP_002148602.1| alpha-ketoglutarate-dependent taurine dioxygenase [Penicillium marneffeii ATCC 18224]
gb|EEA22435.1| alpha-ketoglutarate-dependent taurine dioxygenase [Penicillium marneffeii ATCC 18224]
Length = 389

Score = 80.5 bits (197), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 68/260 (26%), Positives = 112/260 (43%), Gaps = 15/260 (5%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE-RIGGG 73
+G + G+ L L + L + +++ F Q LS QQ + FG IE G
Sbjct: 96 IGTEIVGLQLKDLTNQQRDELALLIAERSVVFVRDQDLSPQQQKALGEHFGEIEVHPQVG 155

Query: 74 DIVAISNVKADGTVRQHSPAEDWMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVG 133
+ + V Q E + + G WH+D + A + +P+VG
Sbjct: 156 QVPGVPGVTVLWPAALQ--AVEREPNFRKTGGASTWHSIDLHESQPAGITHLHNDTIPSVG 213

Query: 134 GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP 193
G T +A +AY+ L + R + ++A + +S G+ QAG ++
Sbjct: 214 GDTLWASGYSAYEKLSPSFRKFIDGKTAIYRSASHSYLDGRN-PQAGPQFVERE----- 265

Query: 194 LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAG 251
PLV+ HP TG +L + R I G+D AES+ L L D ++P + +W+
Sbjct: 266 -HPLVRTHPATGWKALWVNRSMSTVRIVGLDKAESDLILGYLYDVYERSPDIQVRFKWSPK 324

Query: 252 DVVVWDNRCLLHRAEPWDFK 271
+WDNR +H A WD++
Sbjct: 325 SSALWDNRITIHNAS-WDYE 343

>ref|XP_003042850.1| hypothetical protein NECHADRAFT_86763 [Nectria haematococca mpVI 77-13-4]
gb|EEU37137.1| hypothetical protein NECHADRAFT_86763 [Nectria haematococca mpVI 77-13-4]
Length = 363

Score = 80.5 bits (197), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 83/302 (27%), Positives = 126/302 (41%), Gaps = 36/302 (11%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQ 57
+ + ++I+ ++GA VTGV L+ LD+ L Q +++F Q + Q
Sbjct: 78 LLKEGVKISEITKSIGAEVTGVQLSLDNKAKDELALLVAQKKVVVFHDQDFNTIPIQQA 137

Query: 58 ITFAKRFGA--IERIGGGDIVAISNVKADGTV-RQHSPAEDWMMKVIVGNMAWHADSTY 114
+ FA FG + + G A+ V R D ++ +++WH+D +Y
Sbjct: 138 VDFASYFGKLHVHPVSG----AVPGFPQLHMHVHRLDDVGHDKFLETRTTSVSWHSDVSY 193

Query: 115 MPVMAQGAVFSAEV-VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
+ G F + VP GG T F + AY+ L A R + HS
Sbjct: 194 E-LQPPGTTFLYAIDVPEAGGDTLFDVNQVKAYERLSPAQRLEGLKVVHS-----A 244

Query: 174 HVQ-QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLE 231
H Q QA G T + PLV+ HP TG +L I + A +I G ES+ L
Sbjct: 245 HEQAQAALKNDGQLRRDPITSVHPLVRTHPATGEKALYIQPFARSIVGYKKEESDSLNN 304

Query: 232 GLV-----DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAGR 284
L D C+ +W+ VVVWDNR H D++ PR + +RLA +
Sbjct: 305 FLYHHIAFSQDLQCRV-----KWSPRS VVVWDNRVTAHSG-LVDWEGPRFRYIARLAAQ 357

Query: 285 PE 286
E

Sbjct: 358 AE 359

>emb|CAY27494.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 80.5 bits (197), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 48/126 (38%), Positives = 65/126 (51%), Gaps = 10/126 (7%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG--HVQQAGSAYIGYGMTTATP 193
T F DMRAA+D LD T+ V HS +YS+ LG ++ A+ A
Sbjct: 1 TEFGDMRAAWDMLDARTKEQVKDLVVEHSRIYSKGVLGVPFTEEEKRAF-----APV 52

Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+PLV+ H TGR SL + HA I G +E L L++ A Q V+ H+W GD+
Sbjct: 53 TQPLVRTHQRTGRHSLFLSSHAGRIVGWPVSEGMLLLRELMEHATQREFVYPHKWQVGD 112

Query: 254 VVWDNR 259
V+WDNR
Sbjct: 113 VMWDNR 118

>gb|ADI03640.1| taurine catabolism dioxygenase [Streptomyces bingchenggensis BCW-1]
Length = 294

Score = 80.5 bits (197), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 73/270 (27%), Positives = 105/270 (38%), Gaps = 13/270 (4%)

Query: 6 LQITP-TGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ITP +GATVT + TL + L A Q LLI QHLS Q I K
Sbjct: 1 MKITPQVDQKMGATVTEFDVETLSTSDALRLKDAIYQEKLILKQHLSPQQFIALGKAL 60

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G IE + + S E + V WHAD ++MP +
Sbjct: 61 GTIEVYIEP---MYHHPDHEEIFVSSSTPESTQQVGVPKTGAFWHADYSFMPRPFGITMT 117

Query: 125 SAEVVPVAVGGRTCTCFADMRAAYDALDEATRALVHQRSARHSLV-YSQSKLGHVQQAGSAYI 183
+VVP T + DM + L E R++ HS Y + + V + +
Sbjct: 118 YPQVVPRTNRGTHYIDMGKVFAGLPEELRSVARATKGLHSARRYFKIRPSDVYRPICELV 177

Query: 184 GYGMTTATPLRPLVKVHPETGRPSLLIGR-----HAHAIPGMDAAESERFLE--GLVD 235
T + P V VHP TG L + H ++ + LE G +D
Sbjct: 178 DEIEKKTTPVMHPTVFVHPVTGEEVLVSEALTCELHDQHGRALEDDSLHQLLEASGQLD 237

Query: 236 WACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
+H + GD+++WDNR L+HRA
Sbjct: 238 TTFSDEHIHTQTFTEGDLLIWDNRSLVHRA 267

>gb|ACG80552.1| TfdA [uncultured bacterium]
Length = 119

Score = 80.1 bits (196), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 46/128 (35%), Positives = 69/128 (53%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR 195
T F DMRAAYDAL T+ + A HS+ +S+S++G + + D A L
Sbjct: 1 TEFGDMRAAYDALPNDTKRELEGLVAEHSIFHSRSRIG-----FTDFNPDV-AQALP 51

Query: 196 PL---VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251
P+ V+ HP +GR +L + HA + G + +E L+D+A Q V+ H+W G
Sbjct: 52 PVQQVVVRTHPGSGRKTLYLASHASHVIGWPIERGRKLIEDLLDFATQPQFVYQHRWQVG 111

Query: 252 DVVVWDNR 259
D+V+WDNR
Sbjct: 112 DLVMWDNR 119

>gb|ADC33937.1| TfdA-like protein [uncultured bacterium]
Length = 124

Score = 80.1 bits (196), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 47/128 (36%), Positives = 71/128 (55%), Gaps = 6/128 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPL- 194
T F DMR A++AL +A + ARHSL S+ K G + ++ D P
Sbjct: 1 TEFCDMRLAWEALPPDEQAALPLIARHSLWLSRRKYG----SDKSFSFNEDDVRYPV 56

Query: 195 -RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
RPLV VH TGR L++G + ++ +D +S FL+ L D A +++H+W AGD+
Sbjct: 57 GRPLVDVHRPTGRRCLMLGANIASVGALDEVDSVAFDELTDRTAPDFIYSHRWTAGDL 116

Query: 254 VVWDNRCL 261
++WDNRC+
Sbjct: 117 LLWDNRCL 124

>emb|CAY27245.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 80.1 bits (196), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 49/125 (39%), Positives = 64/125 (51%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR 195
T FADMRAAYDALDE + + HS +YS+ KLG + P+R
Sbjct: 1 TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLGADTFTEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I GM + L ++A + P V++H W D V
Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPVARMLPLDLTEFATRDPFVYSHVWRLNDFV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|ZP_02894534.1| Taurine dioxygenase [Burkholderia ambifaria IOP40-10]
gb|EDS99883.1| Taurine dioxygenase [Burkholderia ambifaria IOP40-10]
Length = 282

Score = 80.1 bits (196), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 76/274 (27%), Positives = 117/274 (42%), Gaps = 28/274 (10%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+++ P +GA + V LA DD FA + A L+H +L Q ++ + + FA+R
Sbjct: 1 MRVEPLTCAIGAELLDVSLADAVHDDGLFAEIRAQLLRHVRVFLRDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E VA S+ + G VR + SP + +D + AWH+D+++ G
Sbjct: 61 FGELE----DHPVAGSDPEHPGLVRIYKSPDQPNDRYE----NAWHSASWRVAPPFGC 111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V P VGG T +A+M AY+ L E + + ARHS+ S + + +
Sbjct: 112 VLRCIDGPPVGGDTMWANMVLAYERLPEHVKKQIDGLRARHSIEASFGAAMPIDKRLALK 171

Query: 183 IGYGMTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMDAAE-SERFLE 231

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      Y          P+V+ HPETG   L +          A   G DA   + + L
Sbjct: 172 AQY-----PDAEHPVVRTHPETGEKVLVYNAFTTHTFTNFHTPARVRVGQDANPGAGQLLH 226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      L+  A          +W   V +WDNR   H A
Sbjct: 227 YLISQAAIPEYQVRWRWKNSVAIWDNRATQHYA 260

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>ref|XP_001387107.2| alpha-ketoglutarate catabolism dioxygenase [Scheffersomyces
      stipitis CBS 6054]
gb|EAZ63084.2| alpha-ketoglutarate catabolism dioxygenase [Pichia stipitis CBS
      6054]
      Length = 386

```

Score = 80.1 bits (196), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 69/264 (26%), Positives = 113/264 (42%), Gaps = 16/264 (6%)

```

Query: 7   QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQ---ITFAKR 63
      ++TP      G++VTGV L+ LD AG   L   Q  ++IF  Q  ++      + + K
Sbjct: 86  KVTPK---FGSSVTGVQLSQLDSAGKDELALLVAQRGVVIFREQDFADKGPFAVEYGLKH 142

Query: 64  FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
      FG + I          ++ +   T R+   E++ +   N+ WH+D +Y
Sbjct: 143 FGRL-HIHPTSGAPRNHPELHITYRRPDKGEFERVFSNRTNNVGWHSVSYELQPPGTTF 201

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
      FS   P  GG T FAD   AY+ L   + +   + H L  S+ +   + + G
Sbjct: 202 FSVIEGPESGGDTIFADTVEAYNRLSPEFQKRL---AGLHVLHTSKDQASNSRGQG---- 254

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPR 242
      G           + + PL++ HP TG  ++ + + A I +   ESE L+ L D   +
Sbjct: 255 GIERRKPVSNIHPLIRTHPVTGEKAIFLNKPFARKIVELKEEESYLLKFLFDHIESSHD 314

Query: 243 VHAH-QWAAGDVVVWDNRCLLHRA 265
      +   W   VV+WDNR  +H A
Sbjct: 315 LQLRANWEPNSVVLWDNRRTVHSA 338

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>gb|ADZ69844.1| Putative taurine dioxygenase protein [Polymorphum gilvum
      SL003B-26A1]
      Length = 298

```

Score = 80.1 bits (196), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 72/276 (26%), Positives = 112/276 (40%), Gaps = 47/276 (17%)

```

Query: 8   ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFG 65
      ITP      +GA + V L+ L +   A + +   +H ++ F  Q HL +  Q +FA+ G
Sbjct: 19  ITPI---IGAEIRNVRLSGNLPEGVIAEIKSRIARHKVVFFRRQDHLDDAGQESFARLLG 75

Query: 66  AIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM 118
      +           R G  I+ + +   G  Q           WH D T++P
Sbjct: 76  ELVPHPTQHIREGSAAILELDSGHG-GRADQ-----WHTDVTFVPAY 116

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY-----SQ 169
      + +V      +P  GG T +A+  AAYDAL E +   A HS  Y           ++
Sbjct: 117 PKYSVLRGITIPETGGDTIWANTAAAYDALPEPLKRFADNLRVHSNAYDYASHRPWATE 176

Query: 170 SKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF 229
      + H +   + + + D           P+V+VHPETG  +L++G           G D  S +
Sbjct: 177 VEKKHYDEVFRSKV-FQTD-----HPVVRVHPETGEHTLILGSFVQRFAGFDRFASIKL 229

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      E   +           +W AGDV +WDNR   H A

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Sbjct: 230 YELFQTYITAPENTVRWRWKAGDVAIWDNRATQHIA 265

>emb|CAY27344.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27361.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 80.1 bits (196), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 49/124 (39%), Positives = 66/124 (53%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T FADMRAA+D LD T+A HS ++S++++G G D T R
Sbjct: 1 TEFADMRAAWDTLDRETQAECLPLVCEHSQFLSRAQIGF---GDFTEQERRDFTPVQQR 56

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 255
LV+ HP TGR SL + HA I G E+ FL L + A Q V++H+W D+V+
Sbjct: 57 -LVRTHPSTGRKSLYLASHAGTIIGWPIPEARAFRLDLTEHATQRKFVYSHRWTQFDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>emb|CAY27311.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 80.1 bits (196), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 48/126 (38%), Positives = 66/126 (52%), Gaps = 10/126 (7%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG--HVQQAGSAYIGYMDTTATP 193
T FADMRAA+D LD T+ V HS +YS+ LG ++ A+ A
Sbjct: 1 TEFADMRAAWDMLDARTKEQVKDLVVEHSRIYSKGVLGVPFTEEEKRAF-----APV 52

Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+PLV+ H TGR SL + HA + G +E L L++ A Q V+ H+W GD+
Sbjct: 53 TQPLVRTHQRTGRHSLFLSSHAGRMVGWVPVSEGMLLLRELMEHATQREFVYRHRWRVGD 112

Query: 254 VVWDNR 259
V+WDNR
Sbjct: 113 VMWDNR 118

>ref|YP_002768589.1| dioxygenase [Rhodococcus erythropolis PR4]
dbj|BAH35850.1| putative dioxygenase [Rhodococcus erythropolis PR4]
Length = 316

Score = 80.1 bits (196), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 83/281 (29%), Positives = 113/281 (40%), Gaps = 18/281 (6%)

Query: 8 ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
+TPT +GA ++G+ L L DA A L A L+ +L F Q L + FA+R+G
Sbjct: 46 VTPT---IGAEISGIRLGGDLSDAVIAELRRALLEWKVLFVRVQDLGRAEHRFAERWGD 102

Query: 67 IERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
+E+ D T D M+ + N WH D T+ + AV A
Sbjct: 103 LEQHPFFKYTQPGQTDVDVTTLAK-----DAMVGGVENN--WHNDVTWHEFPSFAAVLRA 155

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 186
VP VGG T +AD AAYD L E + + A H + S G A + +
Sbjct: 156 VEVPEVGGDTLWADTAAAYDLLPEDVKKRIDPLVAEHDWINS--FGRSMPADAVEMLRP 212

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
P+V+V PE+GR L + I G+ ES L L +

Sbjct: 213 KFPVAVQ--HPVVRVIPESGRRVLFVNMTFTQRILGVSEEEESNELLTMLYRHNVRPEFQVR 270

Query: 246 HQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285

+W V WDNR H A F RVM + G RP

Sbjct: 271 LKWEPTVAFWDRNRTCQHYAASDYFPARRVMDRISIVGDRP 311

>ref|ZP_07264205.1| taurine dioxygenase [Pseudomonas syringae pv. syringae 642]
 Length = 289

Score = 80.1 bits (196), Expect = 3e-13, Method: Compositional matrix adjust.
 Identities = 83/296 (28%), Positives = 125/296 (42%), Gaps = 44/296 (14%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62

T ++TP +GA V GV L+ L + A+L++ +L+F QHL+ +Q F +

Sbjct: 24 TVNRLTPI---IGAEEVGGVDLSQPLSAEQLTEIRRAFLENHVLVFRDQHLTVEQHKAFGR 80

Query: 63 RFGAIERIG----GGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118

FG + + GD + V+A+ R WH D T

Sbjct: 81 LFGPLRALPVDSIDGDDPELVVVRANAQSR-----FAAGELWHTDGTADLEP 127

Query: 119 AQGAVFSAEVPVAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176

+ G++ + PA+ GG T FA+M A + L A + + +A H G +

Sbjct: 128 SMGSMLYVKETPAIGTGGDTLAFANMHLAIEMLSHAMQQLGGLTAIHD-----GEIP 179

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLV 234

G G+ + PLV HPETGR SL + G +H + + ES L L

Sbjct: 180 WKGYPQPA-GLPKSE---HPLVVRHPETGRSLFVNSGFTSHIV-QLSPGESHAVLNMLF 234

Query: 235 DWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSR---LAGRPE 286

D + P + +W +V WDNRC H A WD+ P + R L GRP+

Sbjct: 235 DLIAREPCLSCRVRWEPNTLVFWDNRCTQHHAH-WDY-FPHSRYGERVTILGGRPQ 288

>gb|ACG80577.1| TfdA [uncultured bacterium]
 Length = 119

Score = 80.1 bits (196), Expect = 4e-13, Method: Compositional matrix adjust.
 Identities = 46/128 (35%), Positives = 69/128 (53%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195

T F DMRAAYDAL T+ + A HS+ +S+S++G + + D A L

Sbjct: 1 TEFCDMRAAYDALPNDTKRELEGLVAEHSIFHSRSRIG-----FTDFNPDV-AQALP 51

Query: 196 PL---VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251

P+ V+ HP +GR +L + HA + G + +E L+D+A Q V+ H+W G

Sbjct: 52 PVQQVVVRTHPGSGRKTLYLASHASHVIGWPIERGRKLIEDLLDFATQPQFVYQHRWQVG 111

Query: 252 DVVVWDNR 259

D+V+WDNR

Sbjct: 112 DLVMWDNR 119

>ref|YP_001506858.1| taurine dioxygenase [Frankia sp. EAN1pec]

gb|ABW11952.1| Taurine dioxygenase [Frankia sp. EAN1pec]

Length = 288

Score = 80.1 bits (196), Expect = 4e-13, Method: Compositional matrix adjust.
 Identities = 74/294 (25%), Positives = 121/294 (41%), Gaps = 49/294 (16%)

Query: 3 QTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61

+++L + P T+GA ++GV L L + A L++ ++ F Q L+ +Q FA

Sbjct: 10 RSSLAVQPLQPTIGAEISGVDLREPLTPEVRDEIKANLLKYKVFFRDQELTQEQHEAFA 69

Query: 62 KRFGAI-----ERIGGGDIVAISNVKADGTVRQ---HSPA EWDDMMKVIVGNMAWHADS 112
 ++FG + + G AI + ++ + H+P DD +H D+
 Sbjct: 70 RQFGPLYTHPGAADSGVTPAIHRIASEDFKKYEKAHTPQAGDDTWD-----PYHTDT 123

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
 ++ V GAV A +P VGG T + D AY L + +A + H + +
 Sbjct: 124 SWRLVPTWGAVLRAVHLPEVGGDTVWVDAALAYQGLSDDVKARLEGHHVAHDYRAALHQS 183

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETG-----RPSLLIGRHAHAIPGMD 222
 GH + P+V+VH ETG RP++L G+D
 Sbjct: 184 GHDYPVVA-----HPVVRVHRETGEKIAWVNFTQRPITL-----GLD 220

Query: 223 AAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVM 276
 AES+ L ++D + W G V WDNR +H A PR++
 Sbjct: 221 RAESKELLTAVIDQYRKPANQVRFSWRPGSVAFWDNRA TVHYAVRNYGTFRLL 274

>gb|ADC33975.1| TfdA-like protein [uncultured bacterium]
 Length = 121

Score = 80.1 bits (196), Expect = 4e-13, Method: Compositional matrix adjust.
 Identities = 48/126 (38%), Positives = 71/126 (56%), Gaps = 5/126 (3%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
 T F DMRAAYDAL E TR + A HS++ S++KLG + + A P +
 Sbjct: 1 TEFCDMRAAYDALPEKTRQRIAGLVAYHSIMTSRAKLGFAFDEAEREAF---KAVP-Q 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 255
 LV+ ++GR SL + HA +I GM ++ + +E L A Q V++H+W D+V+
 Sbjct: 56 VLVRRLQDSGRMSLYLASHAGSIGGMADDARQLIEELTAHATQRFVYSHRWRVKDLVI 115

Query: 256 WDNRCL 261
 WDNRC+
 Sbjct: 116 WDNRCV 121

>emb|CAY27422.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 118

Score = 80.1 bits (196), Expect = 4e-13, Method: Compositional matrix adjust.
 Identities = 48/126 (38%), Positives = 65/126 (51%), Gaps = 10/126 (7%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG--HVQQAGSAYIGYGMDTTATP 193
 T F DMRAA+D LD T+ V HS +YS+ LG ++ A+ A
 Sbjct: 1 TEFCDMRAAWDMLDARTKEQVKDLVVEHSRIYSKGVLPFTEEEKRAF-----APV 52

Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
 +PLV+ H TGR SL + HA I G +E L L++ A Q V+ H+W GD+
 Sbjct: 53 TQPLVRTHQRTGRHSLFLSSHAGRIVGWPVSEGMLLLRELMEHATQREFVYRHRWRVGD 112

Query: 254 VVWDNR 259
 V+WDNR
 Sbjct: 113 VMWDNR 118

>emb|CAY27501.1| alpha-KG-dehydrogenase [uncultured bacterium]
 emb|CAY27558.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 80.1 bits (196), Expect = 4e-13, Method: Compositional matrix adjust.
 Identities = 51/125 (40%), Positives = 64/125 (51%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRAAYDALDE + HS ++S+S LG + P+R
Sbjct: 1 TEFGBMRAAYDALDEEIKTECENLICEHSQFLSRSILGSTDFDERRRFA-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA AI G E+ FL L + A Q V+AH W D+V
Sbjct: 55 QRLVRRHPVTGRRSLYLASHAGAILGWLVPPEARAFRLDLNEHATQRQFVYAHVWRQWDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|ZP_06411856.1| Taurine dioxygenase [Frankia sp. EUN1f]
gb|EFC85404.1| Taurine dioxygenase [Frankia sp. EUN1f]
Length = 315

Score = 80.1 bits (196), Expect = 4e-13, Method: Compositional matrix adjust.
Identities = 72/300 (24%), Positives = 120/300 (40%), Gaps = 41/300 (13%)

Query: 2 AQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
++ L + P +GA + G+ L ++ A + AA L+ ++ F QH++ QQI F
Sbjct: 19 SEVGLDVRPMSGYIGAEIFGIDLTGPIEPEVVAEVRAALLKWKVVFVRDQHITPAQQIAF 78

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMA 107
+ FG + + D A ++V ++ VR
Sbjct: 79 GRLFGQVTPGHPTLPTLEGHPEVFPPLDSRAYADVSSEYQVRS-----L 121

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH D T++ G++ V+P GG T + ++ AY+ L + R L+ A H
Sbjct: 122 WHTDVTFFVHNPPMGSILRGVVIPIYGGDTQWTNLVVAYETLSKPIRDLIDGLHAVHV--- 178

Query: 168 SQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAES 226
+++ + GS T+ + P+V+VHPETG L + I + ES
Sbjct: 179 --NQIILERGDGSKLQKMFTRTSYETVHPVVRVHPETGERVLFVSPNFTQRIVELSNTES 236

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDF--KLPRVMWHSRLAG 283
+R L+ L +W + WDNR H P D+ RVM +AG
Sbjct: 237 QRVLDLLFSLATPAFTVRFWRQPDSEAFWDNRATAHLV-PTDYGHLGFDRVMHRITIA 295

>gb|ABR27342.1| TfdA [uncultured bacterium]
Length = 118

Score = 79.7 bits (195), Expect = 4e-13, Method: Compositional matrix adjust.
Identities = 45/122 (36%), Positives = 61/122 (50%), Gaps = 5/122 (4%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPL 197
F DMRAAYDAL E ++ + HS++YS+ LG V Y + L+ L
Sbjct: 2 FCDMRAAYDALHEXXKSEIGDLICEHSVMYSRGXLFVD-----YSDEEKEMFKPVLQRL 56

Query: 198 VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWD 257
V+ HP GR L + HA + GM E L L + A Q V+ H+W D+V+WD
Sbjct: 57 VRTHPAHGRKFLYLSSHAGKVVGMSVPEGRLLLRDLTEHATQPEFVYVHRWTVHDLVMWD 116

Query: 258 NR 259
NR
Sbjct: 117 NR 118

>ref|YP_298356.1| taurine dioxygenase [Ralstonia eutropha JMP134]
gb|AAZ63512.1| Taurine dioxygenase [Ralstonia eutropha JMP134]
Length = 297

Score = 79.7 bits (195), Expect = 4e-13, Method: Compositional matrix adjust.
Identities = 75/283 (26%), Positives = 115/283 (40%), Gaps = 49/283 (17%)

```
Query: 6  LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
          + P      +GA + GV+LA LDD + AL A L++ +L F Q ++ Q + A+RFG
Sbjct: 19 FSVAPCTPAIGAEIDGVNLARLDDTTYRALRQALLKYKVLFFRDQDITPAQHVAARRFG 78

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVG-----NMAWHADSTYMPV 117
          +E                      V P + V+ G +H+D ++ V
Sbjct: 79 ELE-----VHPMIPHHPEHPELVVFGGGDKRGRENLYHSDVSWREV 120

Query: 118 MAQGA VFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHV 175
          + G++ P +GG T + +M AAY+AL E +A + + A H + + QS G
Sbjct: 121 PSMGSMRLRCLECPDMGGDTIWVNMVAAYEALPEDMKARIAELQAVHDAMPTFGQSVEGER 180

Query: 176 QQAGSAYIGYGMDDTTATPL-RPLVKVHPETGRPSLLIGR-----HAHAIP--GMDA 223
          M P+ P+V+ HPETG L + +A P G D
Sbjct: 181 YDE-----MRKQYPPMVHPVVRTHPETGEKILYVNEGFTTHFANYARLQPYRIGSDF 232

Query: 224 AESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
          +E L + AP +W A V +WDNR H A
Sbjct: 233 RMAEMDLMQYLFRQAAPEYQVRLRWRANTVALWDNRATQHHA 275
```

>ref|YP_003731487.1| taurine dioxygenase [Acinetobacter sp. DR1]
gb|ADI90114.1| taurine dioxygenase [Acinetobacter sp. DR1]
Length = 282

Score = 79.7 bits (195), Expect = 4e-13, Method: Compositional matrix adjust.
Identities = 72/277 (25%), Positives = 112/277 (40%), Gaps = 34/277 (12%)

```
Query: 6  LQITPTGATLGATVTGVHLA--TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
          +QI      +GA ++G+ LA DD FA + L+H +L QHL+ + FA++
Sbjct: 1  MQIEQLTCNIGAELSGIKLADAIYDDGLFAEIRTQLLKHRLVFLRDQHLTRQDHVAFAEK 60

Query: 64 FGAIERIGGGDIVAI-SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
          FG +E D A+ S+ G V+ + E V AWH+D+++ V G
Sbjct: 61 FGQLE-----DHPAVGSHPDHPGLVQIYKHPE---SPVDRYENAWHSDASWRKVPPMGC 111

Query: 123 VFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
          V P VGG T + +M AY++L + + A HS+ ++ G +
Sbjct: 112 VLHCVECPVGGDTMWNTNMVMAYESLPNDIKDKIADLRAYHSI---EASFG-----AAMP 163

Query: 183 IGYGMDDTTAT---PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
          + +D A P+V+ HPETG L + E RF + A +
Sbjct: 164 LEKRLDLKAKFPDAEHPVVRTHPETGEKILYVNAFTTHFSNYHTKERVRFQDANPGAAE 223

Query: 240 APRVHAHQ-----WAAGDVVVWDNRCLLHRA 265
          R Q W + +WDNR H A
Sbjct: 224 LLRYLISQAYIPEFQVRWRWKPNIAIWDNRSTQHHA 260
```

>ref|ZP_07308884.1| taurine catabolism dioxygenase [Streptomyces griseoflavus Tu4000]
gb|EFL37253.1| taurine catabolism dioxygenase [Streptomyces griseoflavus Tu4000]
Length = 229

Score = 79.7 bits (195), Expect = 4e-13, Method: Compositional matrix adjust.
Identities = 68/217 (31%), Positives = 98/217 (45%), Gaps = 21/217 (9%)

```
Query: 6  LQITPTGATLGATVTGVHLATLDDAGFAALH--AAWLQHALLIFPGQHLSNDQQITFAKR 63
          L + P + V +LAT DA A H AA QH LLI P QHL++ +T A
Sbjct: 5  LSLRPLDKSGFGAVVDTNLAT--DAEHLAPHLAAALHQHRLILIVPRQHLTHADLLTVASC 62
```

Query: 64 FGAIER-----IGG-GDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
FG ++ +GG + ISN+ DG R + D+ + WHAD+++
Sbjct: 63 FGTVDTSVDRRYAVGGFPGLTVISNIVEDG--RHIGVYDGDNEEE-----WHADNSFK 113

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
P + + + P GG T FAD AY L +A R + ARHSL +
Sbjct: 114 PQLTSATMLYSVITPQRGGETRFADATRAYSDLPDAVRQRIGPMRARHSLAQLGALQSQA 173

Query: 176 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG 212
S + + + + PLV HP TG SLL+G
Sbjct: 174 SGGQSSIVAGSLAASPEAVHPLVLPHPVTGARSLLLG 210

>ref|YP_001791206.1| taurine dioxygenase [Leptothrix cholodnii SP-6]
gb|ACB34441.1| Taurine dioxygenase [Leptothrix cholodnii SP-6]
Length = 306

Score = 79.7 bits (195), Expect = 4e-13, Method: Compositional matrix adjust.
Identities = 75/278 (26%), Positives = 118/278 (42%), Gaps = 30/278 (10%)

Query: 3 QTTLQITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
Q ++ + P ++GA ++ V+L A+ D A + A L+H +L F Q +S + + F
Sbjct: 22 QRSIHVEPLTCSIGAELSHVNLGAASRDPLVAEIRALLRHRVLFRRDQDISRAEHVAF 81

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
A+ FG +E VA S+ + G VR + +P + D + AWH D+T+
Sbjct: 82 ARHFGELE----DHPVAGSDPEHPGLVRIYKNPDQPADRYE-----NAWHTDATWREKPP 132

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
G V P VGG T +A+M AY+ L E + + ARHS+ ++ G
Sbjct: 133 FGCVLRCIECPPVGGDTMWANMVLAYERLPEHVKTQIAGLRARHSI---EASFGAAMPID 189

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER----- 228
A P+V+ HPETG L + A++ R
Sbjct: 190 KRLALKAQFPDAE--HPVVRTHPETGEKILFVNAFTTHFSNFHTADNVRVGQDYTHAGPQ 247

Query: 229 FLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
L+ L+ A Q P +W + +WDNR H A
Sbjct: 248 LLQYLIGQA-QIPEYQVRWRWRPNMAMWDNRSTQHHA 284

>ref|XP_001482071.1| hypothetical protein PGUG_05834 [Meyerozyma guilliermondii ATCC
6260]
gb|EDK41736.1| hypothetical protein PGUG_05834 [Meyerozyma guilliermondii ATCC
6260]
Length = 382

Score = 79.7 bits (195), Expect = 4e-13, Method: Compositional matrix adjust.
Identities = 77/269 (28%), Positives = 108/269 (40%), Gaps = 26/269 (9%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
++TP LG VTG+ L+ LDD G L Q ++IF Q + FA +G
Sbjct: 82 RVTPK---LGTEVTGIQLSQLDDKGKDELALYVAQRGVVIFREQDFAK-HGPQFAVEYG- 136

Query: 67 IERIGGGDIVAISNVKADG-----TVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
G I S D T R+ E+D + + WH+D +Y
Sbjct: 137 -RHFGRLHIHPTSGAPKDHPEIHVTYRRADKNEFDRLFAQRTNAVGVHSDVSYELQPPGT 195

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
FS P GG T FAD+R AY L + + H+ QA A
Sbjct: 196 TFFSVLEGPDAGGDTIFADVREAYRRLSPEFQKRLEGLHVLHT-----SADQARDA 246

Query: 182 YIGYGMDTTATP---LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
+G G P + PL++VHP TG + + R + I + ES L L D
Sbjct: 247 -VGLGGIERRKPVSSIHLPLRVHPGTGEKFIYLNRPFSRKIVELKEQESNYLLNFLYDHI 305

Query: 238 CQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
+A + +W VVVWDNR ++H A
Sbjct: 306 EKAHDLQLRAKWEPNSSVVWDNRLLVVHSA 334

>emb|CAY27408.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 121

Score = 79.7 bits (195), Expect = 4e-13, Method: Compositional matrix adjust.
Identities = 49/127 (38%), Positives = 67/127 (52%), Gaps = 9/127 (7%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDT--TATP 193
T F DMRAAYDALD+A + + HS YS+ ++G ++ + YG + P
Sbjct: 1 TEFWDMRAAYDALDDAMKTEIEDLITEHSNAYSREQIGFMK-----VDYGAENQLKLP 54

Query: 194 LR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
+R LV+ P TGR SL + H AI G E+ F+ L + A Q V AH W D
Sbjct: 55 VRHRLVRHDPRTGRKSLYLSAHIGAIVGWPVPEARMFIRDLAEHATQRRFVFAHSWRQWD 114

Query: 253 VVVWDNR 259
+V+WDNR
Sbjct: 115 LVMWDNR 121

>emb|CAY27224.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 79.7 bits (195), Expect = 4e-13, Method: Compositional matrix adjust.
Identities = 51/124 (41%), Positives = 66/124 (53%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAAYDALD+ T+A HS ++S++ LG S + A +
Sbjct: 1 TEFADMRAAYDALDDETKAECEGLICEHSQLFSRAILGF-----SDFTDEERRKFAPVKQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP TGR SL + HA AI G E+ F L + A Q V+AH W D+V+
Sbjct: 56 RLVRHPVTGRRSLYLASHAGAILGWPVPEARAFQRDLTEHATQRRFVYAHVWRQWDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>ref|ZP_08208480.1| taurine dioxygenase [Novosphingobium nitrogenifigens DSM 19370]
gb|EGD59470.1| taurine dioxygenase [Novosphingobium nitrogenifigens DSM 19370]
Length = 287

Score = 79.7 bits (195), Expect = 4e-13, Method: Compositional matrix adjust.
Identities = 76/290 (26%), Positives = 121/290 (41%), Gaps = 33/290 (11%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP ++GA V+GV L+ + A A+ AA L++ ++ F Q LSN+Q FA +F
Sbjct: 16 LHITPLQPSIGAEVSGVDLSRPITPAQREAIRAAVLRYKVIFFRDQPLSNEQHAFAAQF 75

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDD-----MMKVIVGNMAWHADSTYMPVM 118
G + + HS A DD +V+ A+H D+++ V
Sbjct: 76 GPL-----YTHPTTRHQAANTAIHSIAARDDREYGERFKRVLDSGDAYHTDTSRWLVP 128

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178

GAV +P GG T + D A+DAL + + + H+ + + +GH
Sbjct: 129 TWGAVLRDITLPENGGDTIWVDAHLAWDALSDDLKQKLEGLHVTHNFLSALKGVGH---- 184
Query: 179 GSAYIGYGMDTTATPL--RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVD 235
P+ P+V+ H ETG+ L + I G++ AES L+ ++
Sbjct: 185 -----EYPIVAHPVVRTHRETGQKILWVNFSSQQPQILGVELAESRALLDEILR 232
Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
+ W V WDNR +H A + PR + +A P
Sbjct: 233 QYKRPELQVRFTWRKNSVAFWDRSTVHYAVRNYGEFPRELHRILIADPE 282

>ref|YP_003609092.1| Taurine dioxygenase [Burkholderia sp. CCGE1002]
gb|ADG19581.1| Taurine dioxygenase [Burkholderia sp. CCGE1002]
Length = 327

Score = 79.7 bits (195), Expect = 5e-13, Method: Compositional matrix adjust.
Identities = 68/276 (24%), Positives = 113/276 (40%), Gaps = 33/276 (11%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAK 62
L+I +G V L+ LD++ LH A +++ +L F Q HL + F
Sbjct: 15 NLRIRRVAGLIGGEVQDFKLSPALDESVIDTLHRLVKYKVLFFRDQGHLLDDVSHQAFGA 74
Query: 63 RFG-----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
RFG + G + + K G +WH D T++
Sbjct: 75 RFGQTVAHPTVPSPEGTALFELDASKGGGRAD-----SWHTDVTFVD 116
Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY---SQSKLG 173
+ ++ +PA GG T +A+ AY+ L + + L A H+ Y ++ G
Sbjct: 117 AFBKISILRGVKIPAYGGDTVWANTAVAYERLPDDLKRLADSLWAVHTNDYDYGAERIAG 176
Query: 174 HVQQAGSAYIGYGMDTTATPL---RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF 229
Q+ +A + + + + + P+V VHP +G +LL+G I G+ ++ES R
Sbjct: 177 TDTQSAAARLAHHQNVFVSAVYEAHPVHVHPVSGERALLLGHFIKRIVGLSSSESARI 236
Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
E L + + QW DV +WDNR H A
Sbjct: 237 FEILQNRVIRLENTVRWQWRQNDVAIWDNRATQHYA 272

>gb|ADC34038.1| TfdA-like protein [uncultured bacterium]
Length = 200

Score = 79.7 bits (195), Expect = 5e-13, Method: Compositional matrix adjust.
Identities = 65/211 (30%), Positives = 93/211 (44%), Gaps = 16/211 (7%)

Query: 56 QQITFAKRFGAIE--RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST 113
QQI FA+R+ IE R ++ VR+ + K +G WH D +
Sbjct: 1 QQIAFARRWAPIEINRF----FTPVAGHPEIAEVRK-----EKAQKTNIGG-GWHTDHS 49
Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
Y A G++ A +P GG T FA M AAYDAL E + + A HS + G
Sbjct: 50 YDEAPAMGSILVARELPEDGGDTLFAFMYAAYDALSEGLQRTLDGLRAIHSDEHVFGAKG 109
Query: 174 HVQQAG--SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFL 230
+ ++AG S IG + P+V HPE+ R +L + G A+S+ L
Sbjct: 110 YHKKAGETSDRIGNAGAVRGEVVHPVIRHPESKRKALVYNPAFTLRFEGWSEADSKPLL 169
Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
E L A + +WA G + WDNRC+
Sbjct: 170 EHLYRHATRPEFTCRFRWAPGSIAFWDNRCV 200

>ref|ZP_03267080.1| Taurine catabolism dioxygenase TauD/TfdA [Burkholderia sp. H160]
gb|EEA01304.1| Taurine catabolism dioxygenase TauD/TfdA [Burkholderia sp. H160]
Length = 295

Score = 79.3 bits (194), Expect = 5e-13, Method: Compositional matrix adjust.
Identities = 87/303 (28%), Positives = 123/303 (40%), Gaps = 45/303 (14%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
ITP A LGA V G A AL A H +LIF Q L + A F
Sbjct: 14 FTITPLDAPLGAQVRGFDGARAASGPQILALKQALRDHHILIFKDQQLDDAAFSRLASWF 73

Query: 65 GAI-----ERIGG-----GDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW--H 109
G++ +G DIV +SNV DG ++GN+ H
Sbjct: 74 GSVYVPPADAPVLGSHDDGTVPDIVLVSNDV-DG-----VLGNIELPAH 116

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169
+D + P + G++ A VP GG T + ++ AAY+ L RA + L+
Sbjct: 117 SDHHWTPQPSSGSLLYALEVPEHGGDTTWYNLAAAYEDLSADLRAQIDDLR----LITYN 172

Query: 170 SKLGHVQQAGSAYIGYGMDDTTATPLRP-----LVKVHPETGRPSLLIG-RHAHAIPGMDA 223
L + Y PLRP LV+ HPE+GR + +G R + D
Sbjct: 173 PFLRRKHPLPEGFPLY-RHPGIEPLRPFTDHPLVRTHPESGRRLIYLGARTEVELVDYDP 231

Query: 224 AESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ R +E L + H+W+ GD+V WDN+ LH + +D RV+ LAG
Sbjct: 232 SAGARLIEALRTHILSPRYAYRHRWSVGDIVFDWNQATLHGRDDFDSGERRVLKRISLAG 291

Query: 284 -RP 285
RP
Sbjct: 292 SRP 294

>ref|XP_002179018.1| predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
gb|EEC49716.1| predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
Length = 329

Score = 79.3 bits (194), Expect = 5e-13, Method: Compositional matrix adjust.
Identities = 73/270 (27%), Positives = 115/270 (42%), Gaps = 33/270 (12%)

Query: 15 LGATVTGVH-LATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF GAI----ER 69
LGA V V L LD G + + A H +++ GQ+LS +Q+ F + G +
Sbjct: 51 LGAIVDVVDLTELDSGASKILD AVRAHGMIVIKGQNL SRAEQVEFTSKLGEVIVLPSS 110

Query: 70 IGGGD-----IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM--PVMAQ 120
G D I I+N ADGT + S WH D + P
Sbjct: 111 FEGKDPEPFHPAIQRITNFWADGTWKGPSAKL-----GAYWHQDQGQFWVPPKHNV 160

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
++ A+ P GG T FAD+R A L + + +R++R S+ S + +
Sbjct: 161 LSILHAQATPPKGGETGFADLRGARATLSQP----LLERASRASIQVSVRDIADFAKGSE 216

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER-FLEGLVDWACQ 239
+ D + +++ H G P L +G + G+++AE+ + LE L+ A
Sbjct: 217 EDLAQFPDAS---HAILQSHLLDGGPLLYVGS PHMKVQGLESAEAGKALLEMLLAHATS 272

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRAEPWD 269
+ H W GDV+VWDN LH A P++
Sbjct: 273 PAFTYFHAWDVGDVIVWDNTQTLHHAMPYN 302

>ref|YP_004016948.1| taurine dioxygenase [Frankia sp. Eu1lc]
gb|ADP81078.1| Taurine dioxygenase [Frankia sp. Eu1lc]
Length = 320

Score = 79.3 bits (194), Expect = 5e-13, Method: Compositional matrix adjust.
 Identities = 83/284 (29%), Positives = 117/284 (41%), Gaps = 17/284 (5%)

```

Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
          L I P   +GA ++GV +   LD A   AAL AA L++ ++ F   QH L+ + QI FA+
Sbjct: 16  LDIRPLTVRIGAEISGVRIGGDLDAATVAALRAAILRNRVVFVRDQHHLTPEIQIAFARL 75

Query: 64  FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
          G + +   S   DG   H   E D   G   AWH D ++   +V
Sbjct: 76  LGELTQ-----AHPSQAPLDGYPLVH---ELDASKGGRAG--AWHTDVSFTDRPPAFSV 124

Query: 124 FSAEVPVAVGGRTCFADMRAAYD----ALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
          A +P VGG T +A+ AAY   L   AL   + +H   L + +
Sbjct: 125 LRAVEIPPVGGDTIWANTVAAYGDLPAPLQH VADALRVYHTNQHDYGLRLQLDGLPEVF 184

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
          P+V+VHPETG PSL+G   + G+   +S   L   D   +
Sbjct: 185 KERFFEFRSKEFEVEHPVVRVHPETGEP SLLGGFVKQLTGVSQEQSFDLLRTFADAVAK 244

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          W   GDV +WDNR   H A   PR++   +AG
Sbjct: 245 PENTVRWHWRTGDVAIWDNRATQHYAINDYADSPRIVHRVTVAG 288
  
```

>gb|EDK37093.2| hypothetical protein PGUG_01191 [Meyerozyma guilliermondii ATCC 6260]
 Length = 430

Score = 79.3 bits (194), Expect = 5e-13, Method: Compositional matrix adjust.
 Identities = 74/276 (26%), Positives = 110/276 (39%), Gaps = 32/276 (11%)

```

Query: 5   TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          T ++P   G + G+ L+ LDDAG   L   L +F Q   D+   FA+ F
Sbjct: 92  TFDLSPN---FGTEIDGIQLSKLDDAGKNDLALYLATRGLAVFHDQDFR-DKGPEFAREF 147

Query: 65  GAIERIGGGDIVAISNVKADG-----TVRQHS-PAEWDDMMKVIVGNMAWHADSTYMPV 117
          G   R   G   +   DG   T R+   P   ++   ++ WH+D ++
Sbjct: 148 G---RYFGPLHIHPVAYSIDGYPELLVTFRKEGGPERYEGEFASRTTSGVWHS DISFEEY 204

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL----G 173
          + + F A   P   GG T +AD R AY   L   + L+   +A H+   Y Q+K   G
Sbjct: 205 PSSFSFFVALEAPESGGDTVYADTREAYRRLSPEFQKLEGLTAIHTNYY-QNKFSALTG 263

Query: 174 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESE---RF 229
          V +   Y   PLV+ HP TG   SL   +   +I G+   ES   F
Sbjct: 264 GVARVKKDYF-----TEHPLVRTHPVTGEKSLFFSKGFVKSIGLKGPESSAILNF 314

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          L+ ++   R   +   V+ WDNR +LH A
Sbjct: 315 LDAHINSTDFQVRAQHRGTSGATVIAWDNRIVLHTA 350
  
```

>ref|ZP_07572418.1| Taurine catabolism dioxygenase TauD/TfdA [Sphingobium chlorophenolicum L-1]
 gb|EFN11854.1| Taurine catabolism dioxygenase TauD/TfdA [Sphingobium chlorophenolicum L-1]
 Length = 286

Score = 79.3 bits (194), Expect = 5e-13, Method: Compositional matrix adjust.
 Identities = 70/265 (26%), Positives = 107/265 (40%), Gaps = 26/265 (9%)

```

Query: 15  LGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG----- 65
  
```

Query: 6	LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR	63
	+++ P +GA + V LA DD FA + A L+H +L Q ++ + + FA+R	
Sbjct: 1	MRVEPLTCAIGAELLDVSLADAVHDDGLFAEIRAQLLRHVRVLFRLRDQDITRAEHVAFARR	60
Query: 64	FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA	122
	FG +E VA S+ + G VR + SP + +D + AWH+D+++ G	
Sbjct: 61	FGELE----DHPVAGSDPEHPGLVRIYKSPDQPNDRYE-----NAWHSASWRVAPPPFGC	111

```

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
          V      P VGG T +A+M AY+ L      + +      ARHS+ S      + + +
Sbjct: 112 VLRCIDGPPVGGDTMWANMVLAYERLPAHVKKQIDDLRARHSIEASFGAAMPIDKRLALK 171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIP-----GMDAAE-SERFLE 231
          Y              P+V+ HPETG  L +  A              G DA  + + L+
Sbjct: 172 AQY-----PDAEHPVVRTHPETGEKVLVYNAFATHFTNFHTPARVRVGQDANPGAGQLLQ 226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          L+  A              +W      V +WDNR  H A
Sbjct: 227 YLISQAYIPEYQVRWRWKKNVSAIWDNRSTQHYA 260

```

>gb|EFV82889.1| hypothetical protein HMPREF0005_00146 [Achromobacter xylosoxidans C54]
Length = 291

Score = 79.0 bits (193), Expect = 7e-13, Method: Compositional matrix adjust.
Identities = 73/275 (26%), Positives = 113/275 (41%), Gaps = 26/275 (9%)

```

Query: 6   LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
          ++I      LGA + + LA  L DA + A+ AA  +H ++ FP Q L      FA+RF
Sbjct: 1   MKIVAGEGPLGARILDIDLARPLADADYRAIEAALGRHGVVSFPKQALEARHLKAFAERF 60

Query: 65  GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
          G +E              G  +++ +SN+  +G      S A  D              WH D +Y
Sbjct: 61  GTLEVNANMYFEPGLPEVMILSNMVENGKPVGLSDAGQD-----WHTDMSYSR 109

Query: 117 VMAQGAVFSAEVVPAVGGR----TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
          +A  V      +P  G+      T F +M AAYD L +A + + + H      +
Sbjct: 110 TIAFSNVLYGIRIPMRDGKSLGNTTEFCNMHAAAYDDLQALKDELDGMTITHDFNKFWEMM 169

Query: 173 GHVQQAGSAYIGYGMDTTATPL-RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL 230
          + + +      +      P+  P+      HP TGR  L      ++ I  + A S  L
Sbjct: 170 RREKGSTRPPLTEEQKHKRPVSHPVFLTHPITGRKVLNPNPGYSVRINELPEARSAEVL 229

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          + L      Q      + HQW  GDV++WDN  +H A
Sbjct: 230 DFLFRHQLQEKYRYRHQWQEGDVLMDWNMGTIHNA 264

```

>gb|ACG80566.1| TfdA [uncultured bacterium]
Length = 119

Score = 79.0 bits (193), Expect = 7e-13, Method: Compositional matrix adjust.
Identities = 45/126 (35%), Positives = 68/126 (53%), Gaps = 13/126 (10%)

```

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPL 197
          F DMRAAYDAL  T+  +  A HS+ +S+S++G      + +  D A  L P+
Sbjct: 3   FGDMAAYDALPNDTKRELEGLVAEHSIFHSRSRIG-----FTDFNPDV-AQALPPV 53

Query: 198 ----VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
          V+ HP +GR +L +  HA  + G      + +E L+D+A Q  V+ H+W  GD+
Sbjct: 54  QQVVVRTHPGSGRKTLYLASHASHVIGWPIERGRKLIEDLLDFATQPQFVYQHRWQVGDL 113

Query: 254 VVWDNR 259
          V+WDNR
Sbjct: 114 VMWDNR 119

```

>ref|ZP_03822519.1| alpha-ketoglutarate-dependent taurine dioxygenase
(2-aminoethanesulfonate dioxygenase) (sulfate)

starvation-induced protein 3) [Acinetobacter sp. ATCC 27244]
gb|EEH69595.1| alpha-ketoglutarate-dependent taurine dioxygenase (2-aminoethanesulfonate dioxygenase) (sulfate starvation-induced protein 3) [Acinetobacter sp. ATCC 27244]
Length = 291

Score = 79.0 bits (193), Expect = 7e-13, Method: Compositional matrix adjust.
Identities = 69/275 (25%), Positives = 114/275 (41%), Gaps = 32/275 (11%)

Query: 3 QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
+ TL I +++GA + V L T+D+ + A L H ++ F Q L+ Q A+
Sbjct: 10 EMTLNIEIIKSSIGAIHVDLNTVDENTTQQIQQALLDHHVIFFRNQQLAPQAQELAR 69

Query: 63 RFGA-----IERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADST 113
FG+ +E + +I+ + + K D + N WH D T
Sbjct: 70 GFGSLHIHPIFTVENVP--EIIVLDSWKQD-----LRDNELWHTDVT 110

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSK 171
+ G V A +P VGG T ++ AA+ LD++ + + +A H + + +
Sbjct: 111 FSKNPPLGCVLQAIKIPVGGDTLWSSGVAAAFAGLDQSLQKKLGLTATHDIRQSFPIER 170

Query: 172 LGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL 230
H + + P+V+ HP TG+P L + I ++ +ES L
Sbjct: 171 FAH-NDVERKKLEETFKNRPPVHPVVRTHPVTGQPILFVSEGFTTRINELEESAESELL 229

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
+ L A QW GDV +WDNRC H+A
Sbjct: 230 QYLFHAHATHEQFHLRWQWQEGDVAIWDNRCTQHKA 264

>gb|ADC33972.1| TfdA-like protein [uncultured bacterium]
Length = 121

Score = 79.0 bits (193), Expect = 7e-13, Method: Compositional matrix adjust.
Identities = 43/126 (34%), Positives = 67/126 (53%), Gaps = 5/126 (3%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T F DMR A++ + A +A + +A HS+ +S++ G + GY P R
Sbjct: 1 TEFCDMRQAWQVPPAEQAELEALTAHHSIAHSRALCGFTEWPE----GYDDLQKIP-R 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV VHP+TGR +LL H + G + E+ F+ L+ A ++H+W GD ++
Sbjct: 56 PLVGVHPDTGRKALLTASHIETLTGKNKDETTTEFVAELIQRATVPENCYSHRWTKGDFLM 115

Query: 256 WDNRCCL 261
WDNRC+
Sbjct: 116 WDNRCV 121

>ref|XP_001728977.1| hypothetical protein MGL_3971 [Malassezia globosa CBS 7966]
gb|EDP41763.1| hypothetical protein MGL_3971 [Malassezia globosa CBS 7966]
Length = 382

Score = 79.0 bits (193), Expect = 7e-13, Method: Compositional matrix adjust.
Identities = 67/259 (25%), Positives = 102/259 (39%), Gaps = 25/259 (9%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIE---RIGGGDIVAISN---VKADGTVRQHSPA 94
+ ++ F Q LS D+Q R G + G I + N V D V +
Sbjct: 94 RRGVVFVKQELSADEQKFVTDRLGLHTGKPATSGLHIHPVYNAERVGKQVVEKGTQN 153

Query: 95 WDDMMKVIVGNM-----AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM 141

```

      D+ + VI  N+          WH+D  + PV A          +P  GG T +A
Sbjct: 154 KDNEISVISSNLHRS�DVEPRSGADEWHS DIAFEPVPADYTS�KVHTLPQTGGDTMWASG 213

Query: 142 RAAYDALDEATRALVHQRSARH---SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLV 198
      YD L +  R +  +      + S ++ G+      G      +DT T  PL+
Sbjct: 214 YEVDLLSQPFRNMFELKGFYYPPEFINSAA RHGYALYPGPRGAAENVDTHTLAEHPLI 273

Query: 199 KVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVW 256
      + +P TG S+  IG H + I G+  ES+      + D  Q      ++W  D+ +W
Sbjct: 274 RTNPVTGWKSVFGIGHHFNRI LGVSLDESMLKRYIRD LVTQNHSTQLRYRWGKNDLAIW 333

Query: 257 DNRCLLHRAEPWDFKL-PR 274
      DNR  H A P  F L PR
Sbjct: 334 DNRSTYHAATPDYFDLGPR 352

```

>ref|YP_003932509.1| taurine dioxygenase, 2-oxoglutarate-dependent [Pantoea vagans C9-1]
gb|ADO11060.1| taurine dioxygenase, 2-oxoglutarate-dependent [Pantoea vagans C9-1]
Length = 279

Score = 79.0 bits (193), Expect = 7e-13, Method: Compositional matrix adjust.
Identities = 68/288 (23%), Positives = 121/288 (42%), Gaps = 27/288 (9%)

```

Query: 6  LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      + TP      +GA V+ + ++  L DA F  L+  L+H +L  Q ++ +Q  A RF
Sbjct: 5  ISFTPLSPYIGAQVSNLDVSRPLSDAQFEQLYHGLLRHQVLFRLDQKITPEQHRALAIRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV 117
      G +      G  +I+ +      Q +P + D+      WH D T++
Sbjct: 65 GDLHIHPVYPHAEGVEEIIIVLD-----THQDNPPDNDN-----WHTDVTTFIDT 107

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
      A+ +++V+P  GG T +  AAY+AL E  + L+  SA H  S  +  + +
Sbjct: 108 PPAIALLASKVLPEAGGDTLWTSGIAAYEALSEPFKQLLAGLSAEHDFKKS FQEYKYRKT 167

Query: 178 AGSAYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
      P++ P+++ HP +G+ +L +      I  +  ES+  L+ L
Sbjct: 168 EEEHQRWQQAVAKHPPVQHPVIRTHPVSGKKALFVNEGFTTRIVDLSEKESDALLDFLFA 227

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
      A +      +W  D+ +WDNR  H A  +  R+M  + + G
Sbjct: 228 HATKPEFQVRWRWQPDDLAIWDNRVTQHYANADYYPARRIMQRATVLG 275

```

>gb|ADC33957.1| TfdA-like protein [uncultured bacterium]
Length = 121

Score = 79.0 bits (193), Expect = 7e-13, Method: Compositional matrix adjust.
Identities = 47/126 (37%), Positives = 67/126 (53%), Gaps = 5/126 (3%)

```

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
      T F DMRAAYDAL E  +A +  A+H + +S+ ++G  +      Y      +P R
Sbjct: 1  TEFCDMRAAYDALPETMKA EIDGLVAQHDIFWSRGQIGFTEFPFGEREKY----PPSPQR 56

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
      LV++HP + R +L +  HA  I G  AE  L  L  A Q  V++H+W  GD V+
Sbjct: 57 -LVRLHPGSRRTLYLSAHASHILGWVPAEGRLLLWDLTAHATQNR FVYSHRWVRVGDAVI 115

Query: 256 WDNRC L 261
      WDNRC+
Sbjct: 116 WDNRCV 121

```


>ref|YP_773478.1| taurine dioxygenase [Burkholderia ambifaria AMMD]
 gb|ABI87144.1| Taurine dioxygenase [Burkholderia ambifaria AMMD]
 Length = 282

Score = 79.0 bits (193), Expect = 7e-13, Method: Compositional matrix adjust.
 Identities = 75/274 (27%), Positives = 117/274 (42%), Gaps = 28/274 (10%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
 +++ P +GA + V LA DD FA + A L+H +L Q ++ + + FA+R
 Sbjct: 1 MRVEPLTCAIGAELLDVSLADAVHDDGLFAEIRAQLLRHRVLFRLDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
 FG +E VA S+ + G VR + SP + +D + AWH+D+++ G
 Sbjct: 61 FGELE----DHPVAGSDPEHPGLVRIYKSPDQPNDRYE-----NAWHSASWRVAPPFGC 111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
 V P VGG T +A+M AY+ L + + + ARHS+ S + + +
 Sbjct: 112 VLRCIDGPPVGGDTMWANMVLAYENLPDHVKQIADLRARHSIEASFGAAMPIDKRLALK 171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMDAAE-SERFLE 231
 Y P+V+ HPETG L + A G DA + + L
 Sbjct: 172 AQY-----PDAEHPVVRTHPETGEKVLYVNAFTTHTFNTFHTPARVRVGDANPGAGQLLH 226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 L+ A +W V +WDNR H A
 Sbjct: 227 YLISQAAIPEYQVRWRWKKNSVAIWDNRATQHIA 260

>gb|ADY82284.1| taurine dioxygenase [Acinetobacter calcoaceticus PHEA-2]
 Length = 282

Score = 79.0 bits (193), Expect = 7e-13, Method: Compositional matrix adjust.
 Identities = 72/277 (25%), Positives = 111/277 (40%), Gaps = 34/277 (12%)

Query: 6 LQITPTGATLGATVTGVHLA--TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
 +QI +GA ++GV LA DD F + L+H +L QHL+ + FA++
 Sbjct: 1 MQIEQLTCNIGAELSGVKLADAIYDDGLFTEIRTQLLKHVRVLFRLDQHLTRQDHFVAFAEK 60

Query: 64 FGAIERIGGGDIVAI-SNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
 FG +E D A+ S+ G V+ + E V AWH+D+++ V G
 Sbjct: 61 FGQLE-----DHPAVGSHPDHPGLVQIYKHPE----SPVDRYENAWHSASWRKVPPMGC 111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
 V P VGG T + +M AY++L + + A HS+ ++ G +
 Sbjct: 112 VLHCVECPPVGGDTMWNTNMVMAYESLPNDIKDKIADLRAYHSI---EASFG-----AAMP 163

Query: 183 IGYGMDTTAT---PLRPLVKVHPETGRPSLLIGRHHAHAIPGMDAAESERFLEGLVDWACQ 239
 + +D A P+V+ HPETG L + E RF + A +
 Sbjct: 164 LEKRLDLKAKFPDAEHPVVRTHPETGEKILYVNAFTTHTFSNYHTKERVRFQDANPGAAE 223

Query: 240 APRVHAHQ-----WAAGDVVVWDNRCLLHRA 265
 R Q W + +WDNR H A
 Sbjct: 224 LLRYLISQAYIPEFQVRWRWKPNSIAIWDNRSTQHIA 260

>ref|YP_003521938.1| TauD [Pantoea ananatis LMG 20103]
 gb|ADD78810.1| TauD [Pantoea ananatis LMG 20103]
 Length = 279

Score = 79.0 bits (193), Expect = 8e-13, Method: Compositional matrix adjust.
 Identities = 73/293 (24%), Positives = 124/293 (42%), Gaps = 32/293 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I P G +GA V + ++ L DA F L+ A L+H +L Q ++ +Q A RF
Sbjct: 5 LAIKPLGPFIGAQVGNLDVSRPLSDAQFEQLYHALLRHQVLFRLREQVITPEQHRALAIRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV 117
G + G +I+ + Q +P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPHAEGVEEIIIVLD-----THQDNPPDNDN-----WHTDVTFIQT 107

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
A+ +++V+P GG T + AAY+AL + L+ + A H + + H ++
Sbjct: 108 PPAVALLASKVLPESGGDTLWTSGIAAYEALSAPFKTLAELRAEHDFTKAFPEYKH-RK 166

Query: 178 AGSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
A+ + P P+++ HP +G+ +L + I + ES+ L G +
Sbjct: 167 TEEAHRQWQQAVAKNPPVYHPVIRTHPVSGKKALFVNEGFTTRIMDISQKESDALL-GFL 225

Query: 235 DWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
P +W D+ +WDNR H A + RVM + + G RP
Sbjct: 226 FAHVTRPEFQVRWRWQPNDLAIWDNRVTQHYANADYYPARRVMQRATVLGDRP 278

>ref|ZP_06411796.1| Taurine dioxygenase [Frankia sp. EUN1f]
gb|EFC85344.1| Taurine dioxygenase [Frankia sp. EUN1f]
Length = 300

Score = 79.0 bits (193), Expect = 8e-13, Method: Compositional matrix adjust.
Identities = 75/274 (27%), Positives = 114/274 (41%), Gaps = 26/274 (9%)

Query: 5 TLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
++ +T ++LGA ++GV LA + D FA L A L+H +L Q +S + A+
Sbjct: 18 SMTVTRLTSSLGAELSGVDLADVARSDVLFAGLRALLLEHKVLFRLDQDISRADHVALAR 77

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
RFG++E VA S+ G VR + +D N ++H D ++ A GA
Sbjct: 78 RFGSLE---DHPVAPSDPDHPGLVRIYKS---EDSAPEHYEN-SYHCDGSWRREPAMGA 129

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V P+VGG T + +M AAY+ L + + + ARHS+ + V +
Sbjct: 130 VLRCVQTPSVGGDTIWNMAAAAYEGLPDHVKERIAGLRARHSIEATFGARLPVAERHRLK 189

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIP-----GMDAAESERFLEG 232
Y P+V+ HPETG L + I G D A L
Sbjct: 190 ERY-----PDAEHPVVRTHPETGEKILFVNAFTTHIVNYHTPVNVRYGADYAPGASLLLN 244

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ P +W+A +WDNR H A
Sbjct: 245 YLIGRAAIPEYQVRWRWSADSFAIWDNRATQHYA 278

>ref|XP_001883209.1| predicted protein [Laccaria bicolor S238N-H82]
gb|EDR06348.1| predicted protein [Laccaria bicolor S238N-H82]
Length = 359

Score = 79.0 bits (193), Expect = 8e-13, Method: Compositional matrix adjust.
Identities = 77/270 (28%), Positives = 111/270 (41%), Gaps = 31/270 (11%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH---LSNDQQITFAKRFGAIER-I 70
LG VTGV ++ L G L + +L+F Q LS D+QI + FG I++
Sbjct: 84 LGTEVTGVQISELSKEGLDELALFAAERKVLFLFRDQDFKDLSPDRQIEITRHFQPIQKHP 143

Query: 71 GGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGN---MAWHADSTYMPVMAQGAVFSA 126
G++ QH D + + G+ +WH+D +Y F
Sbjct: 144 TSGNVKGYPEFHVYRDAQH-----DKFQEYLGDKINQTSWHSVDVSYEQPPGATFFFI 198

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV----YSQSKLGHVQQAGSAY 182
P GG T F AY+ L + + A HS V +S+ + G V++
Sbjct: 199 LDQPETGGDTLFLSQVEAYNRLSLEFKKRLEGLRAVHSGVPQAEFSRRRDGPVRRREP--- 255

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAP 241
++T PLV+VHP TG +L + + I G ESE L+ L D +
Sbjct: 256 ----IETE----HPLVRVHPVTGEKALYVNQGFTKHIVGFKQEESEYLLKFLFDHLAKGA 307

Query: 242 RVHAH-QWAAGDVVVWDNRCLLHRAEPWDF 270
H + G VVVWDNR H A P DF
Sbjct: 308 DFHIRATYKPGTVVVWDNRVTAHSATP-DF 336

>ref|YP_234880.1| taurine dioxygenase [Pseudomonas syringae pv. syringae B728a]
gb|AA36842.1| Taurine dioxygenase [Pseudomonas syringae pv. syringae B728a]
Length = 289

Score = 79.0 bits (193), Expect = 8e-13, Method: Compositional matrix adjust.
Identities = 83/300 (27%), Positives = 127/300 (42%), Gaps = 52/300 (17%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDA-GFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T ++TP +GA V GV L+ A + A+L++ +L+F QHL+ +Q F +
Sbjct: 24 TVNRLTPI---IGA EVGGVDLSQPPSAEQLTEIRRAFLNHVLFVRDQHLTVEQHKAFGR 80

Query: 63 RFGAIERIG----GGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
FG + + GD + V+A+ R WH D T
Sbjct: 81 LFGPLRALPVDSIDGDDPELVVVRANAQSR-----FAAGELWHTDGTADLEP 127

Query: 119 AQGAVFSAEVPVAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ G++ + PA+ GG T FA+M A + L A + + +A H G +
Sbjct: 128 SMGSMLYVKETPAIGTGGDTLAFANMHLAIEMLSPAMQQFLGGLTAIHD-----GEI- 178

Query: 177 QAGSAYIGY----GMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFL 230
+ GY G+ + P+V HPETGR SL + G +H + + ES L
Sbjct: 179 ----PWKGYQPPPGLPKSE---HPVVVRHPETGRRSFLVNSGFTSHIV-QLSPGESRTVL 230

Query: 231 EGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSR---LAGRPE 286
L D + P + +W +V WDNRC H A WD+ P + R L GRP+
Sbjct: 231 SMLFDLIAREPCLSCRVRWEPNTLVFWDNRCTQHHAH-WDY-FPHSRYGERVTILGGRPQ 288

>emb|CAY27545.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 79.0 bits (193), Expect = 8e-13, Method: Compositional matrix adjust.
Identities = 46/125 (36%), Positives = 64/125 (51%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DMRAAY+ALD+ + + HS +YS+ +LG + + P+R
Sbjct: 1 TEFGDMRAAYEALDDRLLKHQIEDLVCLHSNMYSRGRGLTEFTTEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA I GM E+ L L + A + V++H W D V
Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMLLLLTELATREQFVYSHAWRVNDFV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>gb|ADC34034.1| TfdA-like protein [uncultured bacterium]
Length = 203

Score = 78.6 bits (192), Expect = 9e-13, Method: Compositional matrix adjust.
Identities = 61/219 (27%), Positives = 88/219 (40%), Gaps = 29/219 (13%)

Query: 56 QQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW 108
QOI FA+RFG I G +++ + K D KV G W
Sbjct: 1 QQIAFARRFGPISIHPPFAASVEGHPEVMRVFKEKED-----KVNFGG-GW 44

Query: 109 HADSTYMPVMAQGA VFSAE VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--- 165
H+D T+ G++ A+ VP GG T FA+ AYDAL + + +A HS
Sbjct: 45 HSDMTFQEKPLGSI LYAKEVPPYGGDTMFANQY MAYDAL SAGMKKTLESLNAVHSANAQ 104

Query: 166 --VYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMD 222
V +S+ S + A + P+V+ HPETG+ +L + G
Sbjct: 105 YGVDGRSEANKNNDKRSMPATSEEA AAEVIHPVVRTHPETGKKTLYVNVGFTTRFEGWT 164

Query: 223 AAESERFLEGLVDWACAPRVHAHQWAAGDVVWDNRCL 261
ES+ L L + + WA V WDNRC+
Sbjct: 165 KESQPLLRWLYEHCAKPEFTCRFNWATNSVAFWDNR CV 203

>gb|ADC33941.1| TfdA-like protein [uncultured bacterium]
Length = 121

Score = 78.6 bits (192), Expect = 9e-13, Method: Compositional matrix adjust.
Identities = 42/126 (33%), Positives = 64/126 (50%), Gaps = 5/126 (3%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMR A++ L + + +A HS+ +S++ G + GY P R
Sbjct: 1 TEFCDMRRAWEMLSPEEQVELEGLTANHSIAHSRALAGFTEWPA----GYEEFLQRPV-R 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACAPRVHAHQWAAGDVVV 255
PLV VHP+TGR +LL H + G E+ F+ L+ A + H+W+ GD ++
Sbjct: 56 PLVGVPDTPGRKALLTASHIETLTGKSKEETTEFVAELIQRATMPENCYVHRWSKGDFLM 115

Query: 256 WDNRC L 261
WDNRC+
Sbjct: 116 WDNRCV 121

>ref|YP_001166963.1| taurine dioxygenase [Rhodobacter sphaeroides ATCC 17025]
gb|ABP69658.1| Taurine dioxygenase [Rhodobacter sphaeroides ATCC 17025]
Length = 319

Score = 78.6 bits (192), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 72/269 (26%), Positives = 113/269 (42%), Gaps = 21/269 (7%)

Query: 8 ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFG 65
+TP +GA V+ + L+ L D+ A L H +L F Q HL + +Q F RFG
Sbjct: 16 VTPLAGRVGAIVSNIRLSGDLDPDSTIARLEQLRLHKLVLFFRDQSHLDDAEQERFGARFG 75

Query: 66 A-IERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA--WHADSTYMPVMAQGA 122
G + ++V T R P + G A WH D T++ +
Sbjct: 76 EPFAHPTQGALSGTASVLDLDTRRDREP KAGE-----AGGARADQWHTDITFVEAYPRIT 130

Query: 123 VFSAE VPAVGGRTCFADMRAAYDALDEATRAL-----VHQRSARHSLVYSQSKLGHVQ 176
+ + V PA GG T F++ AAY++L E +AL VH + ++ V + +
Sbjct: 131 ILRSVAPASGGDTVFSNTVAAYESLPEPLKALADRLWAVHSNAYDYAAVRPHATADEQK 190

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW 236
Q + +T P+V+V P +G +LL+G G+ A+ ++ D
Sbjct: 191 QFARQFTSTVFETE---HPVVRVLP-SGERTLLLGNFVQRFTGIARADFQKLFALFQDH 245

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+W AGDV +WDN H A
Sbjct: 246 IQAQENTVRWRWQAGDVALWDNTATQHYA 274

>ref|XP_001834704.1| alpha-ketoglutarate catabolism dioxygenase [Coprinopsis cinerea
okayama7#130]
gb|EAU87152.1| alpha-ketoglutarate catabolism dioxygenase [Coprinopsis cinerea
okayama7#130]
Length = 369

Score = 78.6 bits (192), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 78/268 (29%), Positives = 115/268 (42%), Gaps = 26/268 (9%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH---LSNDQQITFAKRFGAIER-I 70
LG + V ++ L G L + +LIF Q L+ ++QI A FG I+R
Sbjct: 92 LGTELNRVQISQLSPEGLNELALYTAERKVLIFRDQDFKDLTPERQIEIANHFGPIQRHP 151

Query: 71 GGGDIVAISNV----KADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
G++ + G R + +D+ + + +WH+D TY F
Sbjct: 152 TSGNVKGFPEFHVYRDPGFDRLNRYRGFDNKINL----TSWHSVDVTEYKQTPGTTFFFI 207

Query: 127 EVVPAVGGRTCFADMRAAYDAL-DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 185
P VGG T F AY+ L DE + LV R A HS V + H + G
Sbjct: 208 LDQPEVGGDTLFTSQVEAYNRLSDEFKKRLVGLR-AIHSV---PQAEHSRSIGGPVRRE 263

Query: 186 GMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAP--R 242
++T P+V+VHP TG +L + + +I G ES+ L L + + R
Sbjct: 264 PIETE----HPVVRVHPVTGEKALFVNQGFTKSIVGFKKEESDFLLNFLFEHIAKGADFR 319

Query: 243 VHAHQWAAGDVVVWDNRCLLHRAEPWDF 270
+ A + G VVVWDNR +H A P DF
Sbjct: 320 IRA-SYEPGTVVVWDNRVTVHSATP-DF 345

>gb|ACG80559.1| TfdA [uncultured bacterium]
gb|ACG80574.1| TfdA [uncultured bacterium]
Length = 118

Score = 78.6 bits (192), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 46/124 (37%), Positives = 62/124 (50%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRAAYDALD TR + A HS+ +S+ LG + + +
Sbjct: 1 TEFGDMRAAYDALDPGTREKLEGLQAHHSIAHSRQTLGF-----EFSREEEEEKLKGAH 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+++P T R SL + HA I E L L++ A Q V+ H W GD+V+
Sbjct: 55 PLVRINPRTQRRSLYLASHASRIVEWPVEGRLLLRDLIEHATQVGFVYRHWVRVGDVLM 114

Query: 256 WDNR 259
WDNR
Sbjct: 115 WDNR 118

>gb|ADC33942.1| TfdA-like protein [uncultured bacterium]
Length = 124

Score = 78.2 bits (191), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 46/128 (35%), Positives = 70/128 (54%), Gaps = 6/128 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP-- 193
T F DMR A++AL +A + ARHSL S+ K G ++ D P

Sbjct: 1 TEFCDMRLAWEALPADEQAKLEPLVARHSLWLRRKYGD---DKSFKFNEEDVRRYPPV 56

Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
RPLV H TGR +L++G + ++ +D ES FL+ L + A +++H+W AGD+

Sbjct: 57 ERPLVNTHRPTGRRALMLGANIASVGDLDEIESVAFLDELTERATAPAFIYSHRWTAGDL 116

Query: 254 VVWDNRCL 261
++WDNRC+

Sbjct: 117 LLWDNRCV 124

>ref|YP_002763816.1| dioxygenase [Rhodococcus erythropolis PR4]
dbj|BAH31077.1| putative dioxygenase [Rhodococcus erythropolis PR4]
Length = 299

Score = 78.2 bits (191), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 71/282 (25%), Positives = 117/282 (41%), Gaps = 36/282 (12%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
+ +T+++ ++GA ++GV L + D A FA + L+H +L F Q+ S + +

Sbjct: 14 STSTIRVEKLTCSIGAELSGVDLGEVARDAALFAQIKGLLLEHKVLFRRDQNFASKAEHVE 73

Query: 60 FAKRFGAIERIGGGDIVAI-SNVKADGTVRQH---SPAEWDDMMKVIVGNMAWHADSTY 114
A+RFG +E D A+ S+ G VR + SP E + A+H D+T+

Sbjct: 74 LAQRFGELE-----DHPALGSDPDHPGLVRIYKDLDSPPEHFEN-----AYHCDATW 120

Query: 115 MPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
G V P VGG T + +M AY+ L + + ARHS+ +

Sbjct: 121 RVNPPMGCVLRCVETPPVGGDTIWNMALAYENLPARVKEQIKDLRARHSIESTFGARMP 180

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF----- 229
+ Q + P+V+ HPETG L + A + E+ R+

Sbjct: 181 IDQRHQL-----KERFPDAEHPVVRTHPETGEKILFVNSFATHLVNYHTPENVRYGIDYA 235

Query: 230 --LEGLVDWACQAPRVHAHQ---WAAGDVVVWDNRCLLHRA 265
L+ + ++ +Q W V +WDNR H A

Sbjct: 236 PGAGNLLTYLASQAQIPEYQVRWRWTENSVAIWDNRSTQHYA 277

>gb|ADP10566.1| taurine dioxygenase [Erwinia sp. Ejp617]
Length = 279

Score = 78.2 bits (191), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 73/291 (25%), Positives = 122/291 (41%), Gaps = 33/291 (11%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++I G +GA V+ ++L+ L DA F L+ A ++H +L Q L+ QQ A RF

Sbjct: 5 IRIQALGPHIGALVSDINLSRPLSDAQFEQLYHALIRHQVLFRLREQPLTPPQQRQLAARF 64

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIV-----GNMAWHADSTYM 115
G + V H+P D+ ++IV N WH D T++

Sbjct: 65 GDLHI-----HPVYPHAP----DVEEIIVLDTHDENPPDNDNWHTDVTFI 105

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
A+ +A+ +PA GG T +A AA++AL + L+ A H S + +

Sbjct: 106 ETTPACAILAAKQLPASGGDTLWASGIAAWNALSAPIQELLEGLQAEHDFRKSFFQEYAY- 164

Query: 176 QQAGSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
+ + + + P P+++ HP +G+ +L + I G+ ES+ L

Sbjct: 165 RSSTEEHQRWQQAVAKNPPVQHPVIRTHPVSGKKALFVNEGFTTRIVGLHDKESDALLNF 224

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + +W DV +WDNR H A R+M + + G

Sbjct: 225 LFAHINKPDFQVRWRWQQDDVAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|YP_003658919.1| taurine dioxygenase [Segniliparus rotundus DSM 44985]
gb|ADG98088.1| Taurine dioxygenase [Segniliparus rotundus DSM 44985]
Length = 313

Score = 78.2 bits (191), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 75/264 (28%), Positives = 112/264 (42%), Gaps = 30/264 (11%)

Query: 13 ATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERI 70
A +GA V+GV L+ L A L L H +++F GQH L ++ Q FA+ G + +
Sbjct: 21 ADIGAEVSGVVLSGDLGPETVAVLRQTVDLHKVVVFRGQHSLEDQRAFAFARLLGPLT-L 79

Query: 71 GGGDIVAISNVKADGTV----RQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
G + + + DG V +H ++ +WH D T++ +V
Sbjct: 80 GHPTLAS----RVDGAVLEVNSEHGRSD-----SWHTDVTFVDRPPAFSVLRP 123

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAG 179
+P GG T +A+ AAY+ L E R L A H+ Y ++ GH G
Sbjct: 124 VALPEYGGTTAWANTTAAYNRLPEPLRLLAESLRAVHTNRYDYARTHERDAAEGHDDGKG 183

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
T P+V+ HPETG +LL+G+ I + AES+ D +
Sbjct: 184 RVQYEEFRSTQYETEHVPVRAHPETGERTLLLGQFVSHILDLKPAESDAVYRIFQDRITK 243

Query: 240 APRVHAHQWAAGDVVVWDNRCLLH 263
W+ GDV VWDNR H
Sbjct: 244 LENTLRWHWSLGDVAVWDNRATQH 267

>gb|ADC33945.1| TfdA-like protein [uncultured bacterium]
Length = 122

Score = 78.2 bits (191), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 43/127 (33%), Positives = 69/127 (54%), Gaps = 6/127 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DMR A++ + +A + +A HS+ +S++ G + GY P R
Sbjct: 1 TEFCDMRHAWEQVPAEEQAELEALTAHHSIAHSRALCGFTEWPE----GYDDLQKIP-R 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPR-VHAHQWAAGDVV 254
PLV VHP+TGR +LL H + G E+ F+ L++ A P +++H+W+ GD +
Sbjct: 56 PLVGVHPDTGRKALLTASHIETLTGKSKDETTEFVAELIERATAVPENIYSHRWSVGDFL 115

Query: 255 VWDNRCL 261
+WDNRC+
Sbjct: 116 MWDNRCV 122

>gb|ACG80571.1| TfdA [uncultured bacterium]
Length = 119

Score = 78.2 bits (191), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 48/127 (37%), Positives = 67/127 (52%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTA--TP 193
T F DMR AYD LD+ TRALV + H+ +YS+ +G + G+ + A P
Sbjct: 1 TEFGDMRIAYDLLDDDTRALVEELVCEHTQLYSRGSMG-----FSGWTEELAMFKP 52

Query: 194 LRP-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
+R LV+ HP TGR SL + HA I G E+ L + A + V+ H+W D
Sbjct: 53 VRQRLVRTHPVTGRKSLYLSSHAGTIIGWQMPEARDLPRDLNEHATRPELVYVHRWRLHD 112

Query: 253 VVVWDNR 259
+V+WDNR
Sbjct: 113 LVMWDNR 119

>emb|CAY27370.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 78.2 bits (191), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 50/124 (40%), Positives = 64/124 (51%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
T FADMRAAYDALDE + HS ++S+S LG + + A +
Sbjct: 1 TAFADMRAAYDALDEEIKTECENLICEHSQLFSRSILG-----STDFTDDERRRFAPVTQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP TGR SL + HA AI G E+ L L + A Q V+AH W D+V+
Sbjct: 56 RLVRHPVTGRRSLYLASHAGAILGWLVPPEARASLRDLNEHATQRQFVYAHVVRQWDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>ref|YP_498356.1| taurine catabolism dioxygenase TauD/TfdA [Novosphingobium
aromaticivorans DSM 12444]
gb|ABD27522.1| Taurine catabolism dioxygenase TauD/TfdA [Novosphingobium
aromaticivorans DSM 12444]
Length = 304

Score = 78.2 bits (191), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 67/243 (27%), Positives = 104/243 (42%), Gaps = 17/243 (6%)

Query: 34 ALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE-----RIGG-GDIVAISNVKADG 85
AL WL H +L+F G S + Q+ ++ FG +E R+ G +++ ++N DG
Sbjct: 32 ALKQVWLHDHGVLFVRGIGTSPEVQLELSRCFGELEPHPIEKFRLDGYPELILLTN---DG 88

Query: 86 TVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAY 145
P +D + WH D + GA+ GG+T + D AAY
Sbjct: 89 G--PVGPV-YDFAGVATTQRIPWHTDLAFTTTPNAGALLRMVRKVETGGQTGWLDTAAY 145

Query: 146 DALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATP--LRPLVKVHPE 203
D LD+AT+ + A + ++ + G + P PLV HPE
Sbjct: 146 DELDQATKDEIADLEAVYLFRAGLEEMRFNRPDGKRLSPRKDNYPDFPPVANPLVWTHPE 205

Query: 204 TGRPSL-LIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL 262
TGR L L + I G + + + L+D A Q + H+W D+V+WDNR +
Sbjct: 206 TGRKVLNLSLNLIEYIVGQRDEQGDALIRRLIDHALQPRFYVHEWENNNDMVLWDNRRTM 265

Query: 263 HRA 265
H A
Sbjct: 266 HAA 268

>ref|ZP_08156118.1| taurine dioxygenase [Rhodococcus equi ATCC 33707]
gb|EGD22302.1| taurine dioxygenase [Rhodococcus equi ATCC 33707]
Length = 320

Score = 77.8 bits (190), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 88/283 (31%), Positives = 109/283 (38%), Gaps = 34/283 (12%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64


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      +TP   T+GA V+G+ L   L D   A L   A L+   +L F   Q +       FA R+
Sbjct: 45  FSLTPKTPPTIGA EVSGIRLTGDLSDDDLAE LRALLEWKVLF FRDQDIDRADHRAFAARW 104

Query: 65  GAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
      G +E+                               AD                               D M   V NM WH D T+   +   AV
Sbjct: 105 GELEQHPFFKYTQPGQSDADVATLAK-----DAMAAGVENM-WHNDVTWHEFPSFAAVL 157

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
      VP VGG T +AD  AAYD L E   RA +   A H   + S                               G
Sbjct: 158 RGVEVPDVGGDTLWADTGAAYDLLPEDLRARIDHLEAEHDWINS-----FG 203

Query: 185 YGMDT-TATPLR-----PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
      GM   T   LR               P+V+V PETGR   L +               I G+   ES   L   L
Sbjct: 204 RGMPVETVEMLRPVFPVHPVVRVIPETGRRVLFVNSVFTQRI VGVSEESNEILRALY 263

Query: 235 DWACQAPRVHAH-QWAAGDVVWDNRCLLHRAEPWDFKLPRVM 276
      Q P               W+   +   WDNR   H A   F   RVM
Sbjct: 264 R-HVQRPEFQVRLHWSPDTIAFWDNRTCQHYASSDYFPARRVM 305

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>gb|ADC33940.1| TfdA-like protein [uncultured bacterium]
Length = 121

Score = 77.8 bits (190), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 42/126 (33%), Positives = 65/126 (51%), Gaps = 5/126 (3%)

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Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
      T F DMR A++ L   ++ +   +A HS+ +S++ G +               GY       P R
Sbjct: 1   TEFCDMRRAWEMLSPEEQSELEALTAHHSIAHSRALCGFTEWPE----GYDDL LQKIP-R 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
      PLV VHP+TGR +LL   H   + G   E+ F+ L+ A   ++H+W GD ++
Sbjct: 56  PLVGVHPDTGRKALLTASHIETLTGKSKEETTEFVAELIQRATVPENCYSHRWTGDFLL 115

Query: 256 WDNRC L 261
      WDNRC+
Sbjct: 116 WDNRCV 121

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>ref|YP_003532757.1| taurine dioxygenase, 2-oxoglutarate-dependent [Erwinia amylovora
      CFBP1430]
ref|YP_003540278.1| alpha-ketoglutarate-dependent taurine dioxygenase [Erwinia
      amylovora ATCC 49946]
emb|CBJ47890.1| alpha-ketoglutarate-dependent taurine dioxygenase [Erwinia
      amylovora ATCC 49946]
emb|CBA23625.1| taurine dioxygenase, 2-oxoglutarate-dependent [Erwinia amylovora
      CFBP1430]
emb|CBX82303.1| taurine dioxygenase, 2-oxoglutarate-dependent [Erwinia amylovora
      ATCC BAA-2158]
      Length = 279

```

Score = 77.8 bits (190), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 73/290 (25%), Positives = 120/290 (41%), Gaps = 31/290 (10%)

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Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      + I   G   +GA V+ ++L+   L DA F   L+ A ++H +L   Q L+   QQ   A RF
Sbjct: 5   ISIQALGPHIGALVSEINLSRPLSDAQFEQLYHALIRHQVLF LRDQPLTPHQQRQLAARF 64

Query: 65  GAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA-----WHADSTYM 115
      G +                               + H+P   D+ ++IV +               WH D T++
Sbjct: 65  GDLHI-----HPLYPHAP----DVEEIIIVLDTNDNPPDNDNWHTDVTFI 105

Query: 116 PVMAQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175

```

GA+ +A+ +P GG T +A AA++AL + L+ A H S + +
Sbjct: 106 ETPPAGAILTAKQLPDSGGDTLWASGIAAWNALSAPIQTLLDGLQAEHDFRKSFQEYKYR 165
Query: 176 QQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL 233
A P++ P+V+ HP +G+ +L + I G+ ES+ L L
Sbjct: 166 SSAEEHQWRQQAVAKNPPVQHPVVRTHPVSGKKALFVNEGFTTRIVGLKEKESDALLNFL 225
Query: 234 VDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W DV +WDNR H A R+M + + G
Sbjct: 226 FAHITKPDFQVRWRWRQDDVAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>gb|ADC33967.1| TfdA-like protein [uncultured bacterium]
Length = 124

Score = 77.8 bits (190), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 46/128 (35%), Positives = 70/128 (54%), Gaps = 6/128 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATP-- 193
T F DMR A++AL +A + ARH L S+ K G ++ D P
Sbjct: 1 TEFCMDRLAWEALPAEEQAKLEPLIARHPLWLSRRKYGD---DKSFSFSEEDVRRYPPV 56
Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
RPLV +H TGR +L++G + ++ +D +S FL+ L D A V++H+W AGD+
Sbjct: 57 ERPLVDIHRPTGRRALMLGANIASVGELDEIDSVAFDELTDRTAPEFVYSHRWTAGDL 116
Query: 254 VVWDNRCL 261
++WDNRC+
Sbjct: 117 LLWDNRCV 124

>gb|ADC33973.1| TfdA-like protein [uncultured bacterium]
Length = 124

Score = 77.8 bits (190), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 46/128 (35%), Positives = 70/128 (54%), Gaps = 6/128 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATP-- 193
T F DMR A++AL +A + ARHSL S+ K G ++ D P
Sbjct: 1 TEFCMDRLAWEALPADAQAELEPLVARHSLWLSRRKYGD---DKSFKFNEEDVRRYPPV 56
Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
RPLV H TGR +L++G + ++ +D ES FL+ L + A +++H+W AGD+
Sbjct: 57 ERPLVDTHRPTGRRALMLGANIASVGDLDEIESVAFDELTERATAPAFIYSHRWTAGDL 116
Query: 254 VVWDNRCL 261
++WDNRC+
Sbjct: 117 LLWDNRCV 124

>ref|YP_948716.1| taurine dioxygenase [Arthrobacter aurescens TC1]
gb|ABM08520.1| taurine dioxygenase [Arthrobacter aurescens TC1]
Length = 309

Score = 77.8 bits (190), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 77/295 (26%), Positives = 121/295 (41%), Gaps = 31/295 (10%)

Query: 1 MAQTTLQITPTGATLGATVTVGVHLA-TLDDAGFAALHAAWLQHALLIF-PGQHLSNDQQI 58
+ +T L+ G+ +GA + G+ ++ L A + AA +H L+F LS++ Q+
Sbjct: 4 ITETKLEFAKLGSRIGAEIRGLDISGDLSETVAQIRAAALNEHKALVFREANILSDEAQV 63
Query: 59 TFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMA---WHADSTYM 115
FA FG + KA TV E +++ V N + WH D T++

Sbjct: 64 KFASHFGPL-----TKAHP TVASVEGEE--NVL PV DSENGSANNWHTD VTFV 108

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
Q + + +PA GG T A AY L E R A H+ Y S ++

Sbjct: 109 VNPPQASTLRSIDLPA YGGETLIASSAGAYQDLPEELRN FADTLWAIHTNDYDYSVPKNL 168

Query: 176 QQAGS-----AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH--AIPGMDAAESER 228
+ + + + +T P+V+VHP TG L IG A I G+ ES+

Sbjct: 169 EHSNAEERRKEFTRLKFETA----HPVVRVHPLTGERGLFIGGFAQRLRIVGLSNTESKD 224

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ L + + V W VV++DNR H A PR + +AG

Sbjct: 225 IIRLLQAYVTRPENVRVNWEPNQVVLFDNRITQHYAPDNYDQGPRKLN RVTIAG 279

>ref|YP_004006193.1| taurine dioxygenase [Rhodococcus equi 103S]
emb|CBH47508.1| putative taurine dioxygenase [Rhodococcus equi 103S]
Length = 320

Score = 77.8 bits (190), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 88/283 (31%), Positives = 109/283 (38%), Gaps = 34/283 (12%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+TP T+GA V+G+ L L D A L A L+ +L F Q + FA R+

Sbjct: 45 FSLTPKTP TIGA EVSGIRLTGDLSDDLAELRRALLEWKVLF FRDQDIDRADHRAFAARW 104

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G +E+ AD D M V NM WH D T+ + AV

Sbjct: 105 GELEQHPFFKYTQPGQSDADVATLAK-----DAMAAGVENM-WHNDVTWHEFPSFAAVL 157

Query: 125 SAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
VP VGG T +AD AAYD L E RA + A H + S G

Sbjct: 158 RGVEVPDVGGDTLWADTGAAYDLLPEDLRARIDHLEAEHDWINS-----FG 203

Query: 185 YGMD-TTATPLR-----PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
GM T LR P+V+V PETGR L + I G+ ES L L

Sbjct: 204 RGMPAETVEMLRPVFPPVHPVVRVIPETGRRVLFVNSVFTQRIVGVSEESNEILRALY 263

Query: 235 DWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
Q P W+ + WDNR H A F RVM

Sbjct: 264 R-HVQRPEFQVRLHWSPDTIAFWDNRTCQHYASSDYFPARRVM 305

>gb|ADC33983.1| TfdA-like protein [uncultured bacterium]
Length = 122

Score = 77.8 bits (190), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 43/127 (33%), Positives = 68/127 (53%), Gaps = 6/127 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DMR A++ + +A + +A HS+ +S++ G + GY P R

Sbjct: 1 TEFCDMRRAWEQVPPDEQAELETTLTAHHSIAHSRALCGFTEWPE----GYDDL LQKVP-R 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPR-VHAHQWAAGDVV 254
PLV VHP+TGR +LL H + G E+ F+ L+ A P +++H+W+ GD +

Sbjct: 56 PLVGVPD TGRKALLTASHIETLTGKSKDETTEFVAELIQRATAVPENIYSHRWSVGDFL 115

Query: 255 VWDNRCL 261
+WDNRC+

Sbjct: 116 MWDNRCV 122

>gb|ADC33986.1| TfdA-like protein [uncultured bacterium]

Length = 121

Score = 77.4 bits (189), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 41/124 (33%), Positives = 64/124 (51%), Gaps = 5/124 (4%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPL 197
F DMR A++ L +A + + +A HS+ +S++ G + GY P RPL
Sbjct: 3 FCDMRRRAWELLSPEEQAELEELTANHSIAHSRALCGFTEWPE----GYDDLQKIP-RPL 57

Query: 198 VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVD 257
V VH +TGR +LL H + G E+ F+ L+ A ++H+W GD ++WD
Sbjct: 58 VGVHSDTGRKALLTASHIETLTGKSKEETTEFVAELIQRATVPENCYSHRWTKGDFLLWD 117

Query: 258 NRCL 261
NRC+
Sbjct: 118 NRCV 121

>ref|ZP_08206375.1| taurine dioxygenase [Gordonia neofelifaecis NRRL B-59395]
gb|EGD53703.1| taurine dioxygenase [Gordonia neofelifaecis NRRL B-59395]
Length = 282

Score = 77.4 bits (189), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 73/277 (26%), Positives = 112/277 (40%), Gaps = 34/277 (12%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+ + ++GA + V LA + DD FA L + L H +L F Q +S + + A+R
Sbjct: 1 MNVERLTCSIGAEHLHDVLAEVARDDDLFAELKSHLLDHKVLFRRNQTMERGEHVALAER 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH----SPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
FG +E V S+ + G VR + SP E ++H D+T+
Sbjct: 61 FGELE----DHPVLGSDPEHPGLVRIYKGLDSPRE-----AFENSYHCDATWRVNPP 108

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
G+V P VGG T + +M AY+ L E + + ARHS+ S ++Q
Sbjct: 109 MGSVLRCEGPEVGGDTMWVMGLAYERLPERVKEQIEGLRARHSIEASFGARMPIEQRL 168

Query: 180 SAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMDAAESERF 229
+ + P+V+ HPETG L + A+ G+D A
Sbjct: 169 AL-----KEKFPDAEHPVVRTHPETGEKILFVNSFTTHTLNFHTDANIRCGIDYAPGAGE 223

Query: 230 LEGLVDWACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
L + P +W V +WDNRC H A
Sbjct: 224 LLRYLQSQATIPEYQVRWRWTPNSVAIWDNRCTQHYA 260

>emb|CAY27400.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 77.4 bits (189), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 49/126 (38%), Positives = 67/126 (53%), Gaps = 10/126 (7%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH-VQQAGSAYIGYGMTTATPL 194
T F DMRAA+D LD+ T+ + HSL+YS+ LG V A P+
Sbjct: 1 TEFGLDMRAAWMLDDETKRICEPLICEHSLLYSRGLLGFDVTDEERAIF-----RPV 52

Query: 195 RPL-VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
R L V+ HP TGR SL + HA A+ G ++ FL L + A Q V++H+W D+
Sbjct: 53 RQLLVRAHPVTGRRSLYLSSHAGAVVGWVPKARAFRLDLTEHATQERFVYSHKWRRHDL 112

Query: 254 VVWDNR 259
V+WDNR
Sbjct: 113 VMWDNR 118

>ref|ZP_07300240.1| taurine dioxygenase [Streptomyces hygroscopicus ATCC 53653]
gb|EFL28609.1| taurine dioxygenase [Streptomyces hygroscopicus ATCC 53653]
Length = 204

Score = 77.4 bits (189), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 56/180 (31%), Positives = 85/180 (47%), Gaps = 17/180 (9%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGF-AALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++TP G T+GA + G L+ + G L+ A L+ +L F G HL++ QQ FA+ +
Sbjct: 13 FELTPLGRITGAIEIRGADLSRPLEPGLREELNRALLEWKVLFRRGAHLTSAQQRDFARNW 72

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G +E + + A G+ + + + + N+ WHAD T+ A GAV
Sbjct: 73 GELE-----TNPLLASGSSQDVARFDKSEGATPTFENV-WHADVTFRERPALGAVL 122

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV-----YSQSKLGHVQQA 178
VP VGG T +ADM AAYD L R + +A H + Y +L Q+A
Sbjct: 123 QLREVPPVGGDTMWADMAAAYDNLPREVRDRIDGATAVHDFIPGFSRFYGPRLAPFQEA 182

>ref|ZP_07379660.1| Taurine dioxygenase [Pantoea sp. aB]
gb|EFM18866.1| Taurine dioxygenase [Pantoea sp. aB]
Length = 279

Score = 77.4 bits (189), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 68/289 (23%), Positives = 121/289 (41%), Gaps = 29/289 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L TP G +GA V+ + + L DA F L+ L+H +L Q ++ +Q A RF
Sbjct: 5 LSFTPLGPYIGAQVSNLDSRPLSDAQFEQLYHGLLRHQVLFRLDQKITPEQHRALAIRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPV 117
G + G +I+ + Q +P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPHAEGVEEIIIVLD-----THQDNPPDNDN-----WHTDVTFIET 107

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 177
A+ +++V+P GG T + AAY+AL + L+ A H S + + ++
Sbjct: 108 PPAVALLASKVLPEAGGDTLWTSGIAAYEALSVPFKQLLEGLRAEHDFKKSQFQYKY-RK 166

Query: 178 AGSAYIGYGMDDTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAESERFLEGLV 234
++ + P P+++ HP +G+ +L + I + ES+ L L
Sbjct: 167 TEEHLRWQQAQAVAKHPPVQHPVIRTHPVSGKKALFVNEGFTTRILDLEKESDAVLGLFLF 226

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
A + +W D+ +WDNR H A + R+M + + G
Sbjct: 227 AHATKPEFQVRWRWQPDLLAIWDNRVTQHYANADYYPARRIMQRATVLG 275

>ref|YP_003101613.1| taurine dioxygenase [Actinosynnema mirum DSM 43827]
gb|ACU37767.1| Taurine dioxygenase [Actinosynnema mirum DSM 43827]
Length = 290

Score = 77.4 bits (189), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 80/302 (26%), Positives = 119/302 (39%), Gaps = 49/302 (16%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
TL + +GA V+G+ L+ L A L +L H +L+F Q L+ + A
Sbjct: 22 TLAVRGLTPVIGAEVSGDLDSRELTDGQLAELRTVFLDHHVLFVRDQDLTPEDHQRLAAH 81

Query: 64 FGAIERI-----GGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPV 117
FG + + G I+ ++ TV GN WHAD T

Sbjct: 82 FGELRPVNPPEHGNPYILEVATSPEAATV-----FGN-GWHADGTADAE 125

Query: 118 MAQGAVFSAEVVPA--VGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
+ G++ +PA GG T FA+M AYD L + L+ + L +

Sbjct: 126 PSLGSMHLHITEMPAPGSGDITLAFANMHLAYDMLSPKLKELL-----TGLTAI 172

Query: 176 QQAGSAYIGYGMDTTATPL---RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLE 231
A+ G+ + P P+V HPET RP L + + IP + A ES L+

Sbjct: 173 HDGAHAFRGHKIEPEGYEPPVSEHPVVVRHPETDRPLLYVNPAYTSRIPQLSADESRAVL 232

Query: 232 GLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGA 290
L P + +W +V WDNRC+ H A +D+ H+R R G

Sbjct: 233 LLFSVVPNRPLACRVRWEPTLVFWDNRCVQHHAH-VDY-----YPHTRFGHRVAINGG 286

Query: 291 AL 292
L

Sbjct: 287 PL 288

>ref|XP_001270812.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus clavatus NRRL 1]
gb|EAW09386.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus clavatus NRRL 1]
Length = 382

Score = 77.4 bits (189), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 74/276 (26%), Positives = 108/276 (39%), Gaps = 25/276 (9%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ---HLSNDQQ 57
+ + Q+ T+G+ + GV L+ L G L Q ++ F Q HL DQ

Sbjct: 91 LPKDKAQVDHLTPTIGSEIRGVQLSQLTKEGKDQLALYVAQRKVVAFRDQDFAHLPIDQA 150

Query: 58 ITFAKRFGA--IERIGGGDI---VAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHAD 111
+ F FG I + G + + + AD T D + + WH+D

Sbjct: 151 LDFGSYFGRHHIHQTS GAPKGYPEIHLVHRGADDT-----SGADFLATRTNTITWHS 203

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
T+ P GG T FADM AY L R +H A HS + +

Sbjct: 204 VTFEKQPPGTTFLYLDDGPTTGDDTLFADMAQAYKRLSPEFRKRLHGLKAAHSGI---EQ 260

Query: 172 LGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFL 230
+ + G G T P+V+ HP TG +L + + I G ES+ L

Sbjct: 261 INNSLNRG---GIARREGITSEHPIVRTHPVTGEKALFVNPQFTRYIVGYKKEESDMLL 316

Query: 231 EGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ L D + + A +W G VVVWDNR + H A

Sbjct: 317 KFLYDHIALSQDLQARVRWLPGTVVVWDNRVVAHSA 352

>ref|XP_001382805.1| hypothetical protein PICST_29419 [Scheffersomyces stipitis CBS 6054]
gb|ABN64776.1| predicted protein [Scheffersomyces stipitis CBS 6054]
Length = 420

Score = 77.0 bits (188), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 70/273 (25%), Positives = 112/273 (41%), Gaps = 24/273 (8%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
T+ ++P G + G+ L+ LD+AG L L +F Q ++ FAK+F

Sbjct: 90 TIDLSPN---YGTEIDGIQLSELDEAGKNDLALYLETRGLAVFRNQDFR-EKGPAFAKKF 145

Query: 65 GAIERIGGGDI---VAISNVKADGTVRQHSPA---EWDDMMKVIVGNMAWHADSTYMPV 117
G + G I V+ S ++ + + PA ++ WH+D ++

Sbjct: 146 G--QHFGPLHIHPSVSYSAEESPELLVITYRPAGGPERYNAQFAGTTTTTGWHSVDSFEEY 203

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
A + F A P GG T F D+R AY L + + H+ Y L + +

Sbjct: 204 PASFSFFVALEAPETGGDTVFLDLREAYRRLSPPIQKFFESLTIHTNYY----LNQLAK 259

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
D+ A PLV+ HP TG SL + A + G+ ES+ L L D

Sbjct: 260 LKDLDRVNADSF AE--HPLVRTHPVTGEKSLFYSGFALRVKGLKQQESDAILSFLEDH 317

Query: 237 ACQAPRVH---AHQWA-AGDVVVWDNRCLLHRA 265
P + +H+ +G ++ WDNR +H A

Sbjct: 318 INNNPEIQVRASHRGTSNGTIIAWDNRISIHTA 350

>ref|ZP_05095314.1| Taurine catabolism dioxygenase TauD, TfdA family [marine gamma
proteobacterium HTCC2148]
gb|EEB78427.1| Taurine catabolism dioxygenase TauD, TfdA family [marine gamma
proteobacterium HTCC2148]
Length = 274

Score = 77.0 bits (188), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 59/261 (22%), Positives = 106/261 (40%), Gaps = 13/261 (4%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I P LGA + G+ L+ L + FA + ++ ++ Q +S A F

Sbjct: 2 LDIKPMAGALGAEIHGLDLSGELGEGDFAPVRKLLNEYQVIFIRDQDISPANMKALALSF 61

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA VF 124
G ++ + V + T+ + +P + + WH D T+ +

Sbjct: 62 GPVQTHPAYETV---EGFPEITILESTPEKPTKIE-----TWHTDMTFNQHPPMATML 111

Query: 125 SAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
++++P GG T ++ M AAYDAL + + +A H + K + G+ +

Sbjct: 112 KSDIIPKGGDTLWSSMTAAYDALSVPMQKFLEDLNAVHDFRWG-FKESLAEPGGAERLK 170

Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRV 243
+ P+++ HPETG+ ++ + I G+ ES+ L L

Sbjct: 171 DAVAANPPVRHPVIRTHPETGKKAIFVNELEFTHIDGLRRDESDALLGFLYKHVTTTDEFT 230

Query: 244 HAHQWAAGDVVVWDNRCLLHR 264
W A +V+WDNRC H+

Sbjct: 231 CRFWHQANSLVIWDNRCTQHK 251

>ref|YP_001206266.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
(TauD-like) (2-aminoethanesulfonate dioxygenase)
(Sulfate starvation-induced protein 3) (SSI3)
[Bradyrhizobium sp. ORS278]
emb|CAL78041.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
(TauD-like) (2-aminoethanesulfonate dioxygenase)
(Sulfate starvation-induced protein 3) (SSI3)
[Bradyrhizobium sp. ORS278]
Length = 312

Score = 77.0 bits (188), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 75/284 (26%), Positives = 120/284 (42%), Gaps = 21/284 (7%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T+++ G T+GA + GV LA + +A FA +H A ++ ++F Q +S + FA+R

Sbjct: 26 TIEVRQLGPTVGAEIGGVDLAKDVSEAQFAEIHRLDENLAIVFRDQDISKEDHKRFARR 85

Query: 64 FG-AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122

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      FG ++ R      +A + + DG      + D      WH D + P      +
Sbjct: 86 FGKSLHR-----HELAATRFRRHDGPFDPFEFLSWKTDANSRFTAGDGHWPDPVSCDPSPIAVS 141

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH--SLVYSQSKLGHVQQAGS 180
      +      P +GG T FA+M AY+ L + + L+ +A H SL ++ + G      G
Sbjct: 142 LLRVTKTPPLGGDTAFANMYLAYEFLSDPIKQLLDGLTAIHGSLAWT-AGYGAKPDPGK 200

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239
      Y      P+V HP TGR L +      I + ES+ L+ L
Sbjct: 201 TY-----PQSEHPVVVTHPRTGRKFLYVNASFTSHIVQLTRRESDALLQLLFRHVES 252

Query: 240 APRVHAH-QWAAGDVVVWVWNRCLLHRAEPWDFKLPRVMWHSRLA 282
      + QW ++VWDN H A WD+ P W R++
Sbjct: 253 QLALQTRVQWRPNSSLVWVWVWNRCLLHRAEPWDFKLPRVMWHSRLA 282

```

>gb|ADD83004.1| Ptn06 [Streptomyces platensis]
Length = 280

Score = 77.0 bits (188), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 76/256 (29%), Positives = 106/256 (41%), Gaps = 24/256 (9%)

```

Query: 10 PTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE 68
      PT A GA V GV L A L AAL + LL+F GQ S ++QI F G +
Sbjct: 4 PTSAGWGARVEGVLDLGAFLGAECALVELFRARHLLVFSGQGFSLLEQIRFMGCLGPVL 63

Query: 69 RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV 128
      G I +SNVK + V +++H+D+ + V G E
Sbjct: 64 HEEGSGIGFVSNVKEGALG-----VSELSFHSDTGHCAVPLDGVSLFPED 109

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 188
      V T FA+ AAY L A R+ V +++ S + G + + GM
Sbjct: 110 VEGCVTSTRFANAAAAYGRPLAALRSRVASLVCENAMPVSLDG---RNVGLS-VAEGMP 164

Query: 189 TTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQ 247
      P+V HP +G P L++ I G++ AES LE L V+ H
Sbjct: 165 RAE---HPVWRHPVSGEPLMVNANQTTRIVGLEDAESRGLLEELFSVMAEDAVYEHS 221

Query: 248 WAAGDVVVWVWNRCLLH 263
      W GDVV+W N + H
Sbjct: 222 WQQGDVVIWHNLAVQH 237

```

>gb|EFW99864.1| alpha-ketoglutarate-dependent taurine dioxygenase [Grosmannia
clavigera kw1407]
Length = 392

Score = 77.0 bits (188), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 74/278 (26%), Positives = 114/278 (41%), Gaps = 37/278 (13%)

```

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
      ++T +G + G+ L L D L + +++ F Q+LS +Q + FG
Sbjct: 85 KVTDLTVNIGTEIEGLQLKDLTDEQRDELALLIAERSVVFRRNQLSPQEQKKLGEHFGQ 144

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQ 120
      IE ++ G V++ T R D + G WH D + A
Sbjct: 145 IEVHPQVPQVPGVPGVSVIWPALQATER-----DAHFRSPGGASRWHTDLVHEHQPAQ 197

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
      + +P VGG T +A AY+ L A RA + R+A + ++ H + G
Sbjct: 198 ITHLHNDTIPPVGGDTLWASGYGAYEKLSPAFAFIDGRTAIYRSAHTYLDLDRDH-PELGP 256

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFL-----EG 232

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      YI          P+V+VHP TG  +L + R  + I G+D AES+  L      EG
Sbjct: 257 QYIERE-----HPIVRVHPATGWKALWVNRAMTSHIVGLDRAESDVILNLYSVYEG 308

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDF 270
      VD  +          +W G  +WDNR  +H A  WD+
Sbjct: 309 NVDQQVR-----FKWTPGTSALWDNRITIHNAS-WDY 339

```

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>ref|ZP_02186847.1| Alpha-ketoglutarate-dependent taurine dioxygenase [alpha
      proteobacterium BAL199]
gb|EDP66029.1| Alpha-ketoglutarate-dependent taurine dioxygenase [alpha
      proteobacterium BAL199]
      Length = 285

```

Score = 77.0 bits (188), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 81/282 (28%), Positives = 121/282 (42%), Gaps = 11/282 (3%)

```

Query: 6   LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      + P   LGA +TG+ L   +DDA  AL AA  +  +L  PGQ L   + F
Sbjct: 5   FDLEPVTPLRGARLTGIDLKRPIDDALADALRAALAERLVLFLPGQFLDGAALKRATEVF 64

Query: 65  GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
      G + R+   +A S   D           D  ++   WH+D +++   G++
Sbjct: 65  GPLFRV---PYIAPSAEDPDVVAVLKEA---DEHRISTFGGDWHSDFSFLERPPGGSLL 117

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHS-LVYSQSKLGHVQQAGSAYI 183
      A  +P VGG T +AD  A+D L +  RAL+  R A  +  Y           V + S I
Sbjct: 118 QAVDLPPVGGDTLWADQATAWDTLPDDLRLALIAGRRAIQTGAPYGVRRHAPT VATSRSIKI 177

Query: 184 GYGMDTTATPL-RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAP 241
      G           +  P+V+ HP +GR +L +  +  + GM  AES  L  L  +
Sbjct: 178 ARGDPEADREIAHPMVRRHVPVSGRAALFLNPIYTTIRLDGMTAEASAPVLARLYAHMTRPE 237

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
      H+W  GD+V+WDNR  LH A           R++W +  AG
Sbjct: 238 FCCRRHRWQPGDLVIWDNRMTLHFAVNDYDGHRRLLWRTTFAG 279

```

```

>emb|CAY27332.1| alpha-KG-dehydrogenase [uncultured bacterium]
      Length = 119

```

Score = 77.0 bits (188), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 48/124 (38%), Positives = 62/124 (50%), Gaps = 7/124 (5%)

```

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
      T FADMRAAYDALDE  +  +          HS +YS+ KLG           +  P+R
Sbjct: 1   TEFADMRAAYDALDEWLKNQIEDLVCLHSNMYSRGKLGLADFTDEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
      LV+ HP TGR S+ +  HA  I GM   E +  L  L  ++A + P V  H   A D V
Sbjct: 55  QRLVRRHPVTGRKSMFLSAHAGKIEGMSIPEPQMLLLYLSEFATREPFVFLHACPANDFV 114

Query: 255 VWDN 258
      +WD
Sbjct: 115 IWDT 118

```

```

>emb|CAY27426.1| alpha-KG-dehydrogenase [uncultured bacterium]
      Length = 117

```

Score = 77.0 bits (188), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 44/123 (35%), Positives = 62/123 (50%), Gaps = 7/123 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRAAYD LD T+A + HSL+YS+ LG + + + TP+R
Sbjct: 1 TEFADMRAAYDGLDTKTKAEIEDLVCEHSLIYSRGTGLGFTELSDEERRMF-----TPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP GR SL + H I E+ F+ L + A Q ++H+W D+V
Sbjct: 55 QRLVRTHPVAGRKSLYLSSHIGTIVDWPMEARAFIRDLEHATQPRYTYSHKWRQFDLV 114

Query: 255 VWD 257
+WD
Sbjct: 115 MWD 117

>emb|CAY27215.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 77.0 bits (188), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 46/125 (36%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL- 194
T FADMRAAYDAL E + + A H++++S+ KLG + + T P+
Sbjct: 1 TEFADMRAAYDALPEDMKQRLRGLVAEHAIMHSRRKLGFDDFSDEE-----NQTYPPVP 54

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
+ L++ HP +GR L + HA I GM E + L+ L++ A Q V+ H+W D+V
Sbjct: 55 QTLRRHPGSGRMGLFLASHAGRIFGMPEDGKALLQRLIEHATQQQFVYTHRWRLYDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>gb|EFW71811.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli
WV_060327]
Length = 267

Score = 76.6 bits (187), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 68/267 (25%), Positives = 112/267 (41%), Gaps = 28/267 (10%)

Query: 27 LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE-----RIGGGDIVAISN 80
L D F L+ A L+H ++ Q ++ QQ A+RFG + G D + + +
Sbjct: 11 LSDNQFEQLYHAVLRHQVFLRDQAITPQQQRALAQRFGELHIHPVYPHAEGVDEIIVLD 70

Query: 81 VKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFAD 140
D +P + D+ WH D T++ GA+ +A+ +P+ GG T +A
Sbjct: 71 THND-----NPPDNDN-----WHTDVTFIQTPPAGAILAAKELPSTGGDTLWAS 114

Query: 141 MRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP--LRPLV 198
AAY+AL R L+ A H S + + ++ + + + P L P+V
Sbjct: 115 GIAAYEALSVFPRQLLSGLRAEHDFRKSFPYKY-RKTEAEHQRWREAVAKNPPLHVPV 173

Query: 199 KVPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVW 256
+ HP TG+ +L + I + ESE L G + P +W D+ +W
Sbjct: 174 RTHPVTKGQALFVNEGFTTRIVDVSEKESEALL-GFLFAHITKPEFQVRWRWQPNDAIW 232

Query: 257 DNRCLLHRAEPWDFKLPRVMWHSRLAG 283
DNR H A R+M + + G
Sbjct: 233 DNRVTQHYANADYLPQRRIMHRATILG 259

>emb|CAY27369.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 76.6 bits (187), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 42/124 (33%), Positives = 63/124 (50%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMR AYDAL R + SA ++Y+++ G+ + G + +
Sbjct: 1 TEFADMRMAYDALPSDLRDTIEDLSAEFDVLYTRALCGYTEFPPEERKGL-----PSAIH 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LVK HP +GR +L I HA I G E+ L L+++A + ++ H W D+V+
Sbjct: 56 RLVKTHPRSGRKTLFIATHACRIVGWPVPEALDLLRELLEFATKPEFIYTHSWTVRDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>gb|ACB30160.1| 2,4-D/alpha-ketoglutarate dioxygenase [Paenibacillus sp. Ao3]
Length = 121

Score = 76.6 bits (187), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 47/127 (37%), Positives = 65/127 (51%), Gaps = 7/127 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRAAYDAL ++ + A H + S+ LG + + P+
Sbjct: 1 TEFCDMRAAYDALPRDLQSELEGLRAEHYALNSRFLLGDTDYSEA-----QRNAMPPVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
PLV+ H +GR L IG HA I G+ AE L L++ A Q V+ H+W GD+V
Sbjct: 55 WPLVRTHAGSGRKFLFIGAHASHIEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGDV 114

Query: 255 VWDNRCL 261
+WDNRC+
Sbjct: 115 MWDNRCV 121

>gb|AAD50457.1|AF170704_7 similar to dioxygenase [Streptomyces spectabilis]
gb|ABW87795.1| unknown [Streptomyces spectabilis]
Length = 247

Score = 76.6 bits (187), Expect = 4e-12, Method: Compositional matrix adjust.
Identities = 75/268 (27%), Positives = 115/268 (42%), Gaps = 42/268 (15%)

Query: 27 LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIG---GGDIVAISNVKA 83
L D A + A+L+H +L+F Q + +Q FA+ FG + + G I + A
Sbjct: 2 LTDEQAAEVKRAFLRHHVLVFRDQVIDGEQHKRFARHFGELHPVALAPEGSDPHILEISA 61

Query: 84 DGTVRQHSPAEWDDMMKVI VGNMAWHADSTYMPVMAQQGAVFSAEVPVAV--GGRTCFADM 141
D R V WHAD T + G++ P + GG T F++M
Sbjct: 62 DKDSRN-----VAGHGWHADGTADLKPSLGSMLYVTRTPEIGSGGDTMFNSM 108

Query: 142 RAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVH 201
AY+ L A + L+ +A H+ + + + + Y + + P+V H
Sbjct: 109 HLAYEMLSPAMKELLDPM TAVHNGLLA-----WEGATPPPEYDVPVN---VHPVVARH 158

Query: 202 PETGRPSLLI-GRHAHAIPGMDAAESERFLEGLV---DWACQAPRVHAHQWAAGDVVVW 256
P+TGR L I G + I + ES ++ LV + A + RV +W +V W
Sbjct: 159 PDTGRKLLFINGIYVSHIEQLSKGESRAI IDMLVKQITNTALLSCRV---RWTPNTLVFW 215

Query: 257 DNRCLLHRAEPWDFKLPRVMWHSRLAGR 284
DNRC+ H A WD+ P HSR A R
Sbjct: 216 DNRCVQHAI-WDY-FP----HSRYAQR 237

>emb|CAY27229.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 76.6 bits (187), Expect = 4e-12, Method: Compositional matrix adjust.
Identities = 46/125 (36%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPL- 194
T FADMRAAYDAL E + + A H++++S+ KLG + + T P+
Sbjct: 1 TEFADMRAAYDALPEDMKQRLRGLVAEHAIMHSRRKLGFDDFSDEE-----NQTYPPVP 54

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
+ L++ HP +GR L + HA I GM E + L+ L++ A Q V+ H+W D+V
Sbjct: 55 QTLLRRHPGSGRMGLFLASHAGRIFGMPEDGKALLQRLIEHATQQQFVYTHRWRHLDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>gb|ADC33984.1| TfdA-like protein [uncultured bacterium]
Length = 124

Score = 76.6 bits (187), Expect = 4e-12, Method: Compositional matrix adjust.
Identities = 45/128 (35%), Positives = 70/128 (54%), Gaps = 6/128 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATP-- 193
T F DMR A++ L +A + ARHSL S+ K G ++ D P
Sbjct: 1 TEFCDMRLAWEELSAAEQASLEPLIARHSLWLSRRKYGD----DKSFKFNEEDVRRYPPV 56

Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
RPLV +H TGR +L++G + ++ +D +S FL+ L + A V++H+W AGD+
Sbjct: 57 ERPLVDLHRPTGRRALMLGANIASVGDLDEIDSVAFLEDELTERATAPAFVYSHRWTAGDL 116

Query: 254 VVWDNRCL 261
++WDNRC+
Sbjct: 117 LLWDNRCLV 124

>ref|YP_003072835.1| taurine dioxygenase [Teredinibacter turnerae T7901]
gb|ACR10979.1| taurine dioxygenase [Teredinibacter turnerae T7901]
Length = 266

Score = 76.6 bits (187), Expect = 4e-12, Method: Compositional matrix adjust.
Identities = 72/274 (26%), Positives = 110/274 (40%), Gaps = 28/274 (10%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
M+ T+ P +GA ++GV L L+ L A + ++ F Q L
Sbjct: 1 MSYKTIAAAPLTPHIGALISGVDLTQELNPETVEDLRQAIADYQVIFFRDQQLDPASLKR 60

Query: 60 FAKRFGAIERIGGGDIVAISNVKAD-GTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
K FG ++ I A+ + + VR+ D+ K + G WH D + V
Sbjct: 61 VGKYFGELQ-----IHALKGLSEEHPVRK---LHADENSKHVAGE-EWHTDMSCAAVP 110

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
G++ +P +GG T FA M AAYDAL + + + +A H + G
Sbjct: 111 PLGSILYLHTLPTLGGDTMFASMYAAYDALSDRMKTYLEGLTATHD---GKLAFGRFDPT 167

Query: 179 GSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
G+ + P+++ HP TG+ L + R I + ESE L L
Sbjct: 168 GNFPVA-----THPVIRTHPVTGKKLLFVNRGFTSHINEISKEESESILAYLFR-H 217

Query: 238 CQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDF 270
C+ P +W V WDNRC H A WD+

Sbjct: 218 CENPLFQLRFRWEPHSVAFWDNRCTQHILA-IWDY 250

>ref|XP_001487814.1| hypothetical protein PGUG_01191 [Meyerozyma guilliermondii ATCC 6260]
Length = 430

Score = 76.6 bits (187), Expect = 4e-12, Method: Compositional matrix adjust.
Identities = 74/276 (26%), Positives = 108/276 (39%), Gaps = 32/276 (11%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
T ++P G + G+ L+ LDDAG L L +F Q D+ FA+ F
Sbjct: 92 TFDLSPN---FGTEIDGIQLSKLDDAGKNDLALYLATRGLAVFHDQDFR-DKGPEFAREF 147

Query: 65 GAIERIGGGDIVAISNVKADG-----TVRQHS-PAEWDDMMKVIVGNMAWHADSTYMPV 117
G R G + DG T R+ P ++ + WH+D ++
Sbjct: 148 G---RYFGPLHIHPVAYSIDGYPELLVTFRKEGGPERYEGEFASRTTLVGWHSDISFEEY 204

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL----G 173
+ + F A P GG T +AD R AY L + L+ +A H+ Y Q+K G
Sbjct: 205 PSSFSFFVALEAPESGGDTVYADTREAYRRLSPEFQKLLLEGLTAHTNYY-QNKFSALTG 263

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESE---RF 229
V + Y PLV+ HP TG SL + +I G+ ES F
Sbjct: 264 GVARVKKDYF-----TEHPLVRTHPVTGEKSLFFSKGFVKSIGLKGPESSAILNF 314

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L+ ++ R V+ WDNR +LH A
Sbjct: 315 LDAHINSTDFQVRAQHRGTLGATVIAWDNRIVLHTA 350

>ref|ZP_02906590.1| Taurine dioxygenase [Burkholderia ambifaria MEX-5]
gb|EDT42255.1| Taurine dioxygenase [Burkholderia ambifaria MEX-5]
Length = 282

Score = 76.3 bits (186), Expect = 4e-12, Method: Compositional matrix adjust.
Identities = 73/274 (26%), Positives = 115/274 (41%), Gaps = 28/274 (10%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+++ P +GA + LA DD FA + L+H +L Q ++ + + FA+R
Sbjct: 1 MRVEPLTCAIGAELLDASLADAVHDDGLFAEIRTQLLRHRVLFRLDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG +E VA S+ + G VR + SP + +D + AWH+D+++ G
Sbjct: 61 FGELE----DHPVAGSDPEHPGLVRIYKSPDQPNDRYE-----NAWHSASWRVAPPFGC 111

Query: 123 VFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V P VGG T +A+M AY+ L + + + ARHS+ S + + +
Sbjct: 112 VLRCIDGPPVGGDTMWANMVLAYENLPDHVKQIADLRARHSIEASFGAAMPIDKRLALK 171

Query: 183 IGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMDAAE-SERFLE 231
Y P+V+ HPETG L + A G DA + + L
Sbjct: 172 TQY-----PDAEHPVVRTHPETGEKVLYVNAFTTHFTNFHTPARVRVGQDANPGAGQLLH 226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L+ A +W V +WDNR H A
Sbjct: 227 YLISQATIPYQVRWRWKNSVAIWDNRATQHYA 260

>ref|XP_002485629.1| alpha-ketoglutarate-dependent taurine dioxygenase [Talaromyces stipitatus ATCC 10500]
gb|EED15676.1| alpha-ketoglutarate-dependent taurine dioxygenase [Talaromyces stipitatus ATCC 10500]

Length = 388

Score = 76.3 bits (186), Expect = 4e-12, Method: Compositional matrix adjust.
Identities = 70/262 (26%), Positives = 110/262 (41%), Gaps = 19/262 (7%)

```
Query: 15  LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE-RIGGG 73
          +G + G+ L L + L + +++ F Q LS QQ + FG +E G
Sbjct: 96  IGTEIVGLQLKDLTNQQRDELALLIAERSVVFFRDQDLSPQQQKELGEHFGEVEVHPQVG 155

Query: 74  DIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVG 133
          + + V Q E + + G AWH D + A + +P+VG
Sbjct: 156 QVPGVPGVTVLWPALQA--VEREPNFRKTGGASAWHTDLVHENQAPAGITHLHNDTIPSVG 213

Query: 134 GRTCFADMRAAYDALDEATRALVHQRSA--RHSLVYSQSKLGHVQQAGSAYIGYGMTTTA 191
          G T +A +AY+ L + R + ++A R + Y K +AG YI
Sbjct: 214 GDTLWASGYSAYEKLSPSFRKFIDGKTAIYRSAHTYLDRLK---NPEAGPQYIERE----- 265

Query: 192 TPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAH-QWA 249
          PLV+ HP TG +L + R I G+D AES+ L L D + P + +W+
Sbjct: 266 ---HPLVRTHPATGWRALWVNRAMTVRIVGLDKAESDLILGYLYDVYERNPDIQVRFKWS 322

Query: 250 AGDVVVWDNRCLLHRAEPWDFK 271
          +WDNR +H A WD++
Sbjct: 323 PRTSALWDRITIHNAS-WDYE 343
```

```
>ref|YP_002007367.1| taurine dioxygenase; taud/tfda taurine catabolism dioxygenases
family [Cupriavidus taiwanensis LMG 19424]
emb|CAQ71309.1| Taurine dioxygenase; TauD/TfdA taurine catabolism dioxygenases
family [Cupriavidus taiwanensis LMG 19424]
Length = 319
```

Score = 76.3 bits (186), Expect = 4e-12, Method: Compositional matrix adjust.
Identities = 76/301 (25%), Positives = 126/301 (41%), Gaps = 33/301 (10%)

```
Query: 3  QTTLQITPTGATLGATVTGVHLA--TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
          Q ++++ +GA ++ + LA D A + A WL+H +L F Q ++ +Q F
Sbjct: 28  QHSIKVELCTPAIGAELSNISLADAAQDPDLIAEIRALWLKHKVLFVRDQDITPLEQQAF 87

Query: 61  AKRFGAIERIGGGDIVAISNVKADGTV---RQHSPAEDMMKVIVGNMAWHADSTYMPV 117
          A +FG +E +A S+ A+ + R P + + + K+ N+ WH+D TY
Sbjct: 88  AAQFGELE----AHPLAPSHPDANKLLMLYRNLDPNKQNFVEKISRENI-WHSDVTYKKA 142

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHS---LVYSQSKLGH 174
          +GAV E+ P GG T +++M AY+ L EA + + A+HS + +Q
Sbjct: 143 PPRGAVLRREMGPENGGDTIWSNMVMAYERLPEAVKQRIDGLYAKHSAEHVFLAQYPKDE 202

Query: 175 VQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIG-----RHAHAIPGMDAAESERF 229
          A + G P+V +HPET L + + D + F
Sbjct: 203 RHAAAANKPGNE-----HPVVLHPETQEKVLFVNSAFTTHFVNYFNFTDIRYGQDF 254

Query: 230 LEG---LVDWACQAPRVHAHQ---WAAGDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLA 282
          + L+ + C + +Q W V +WDN H A PR M + L
Sbjct: 255 MPESHHLMYLCSQAAIPEYQVRLKWRDNTVAMWDNLLCQHYAVADYGNAPRKMLRATLT 314

Query: 283 G 283
          G
Sbjct: 315 G 315
```

```
>ref|XP_001557971.1| hypothetical protein BC1G_03553 [Botryotinia fuckeliana B05.10]
gb|EDN20163.1| hypothetical protein BC1G_03553 [Botryotinia fuckeliana B05.10]
Length = 381
```

Score = 76.3 bits (186), Expect = 4e-12, Method: Compositional matrix adjust.
Identities = 75/273 (27%), Positives = 107/273 (39%), Gaps = 32/273 (11%)

```
Query: 6  LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH---LSNDQQITFAK 62
      +++TP      +G  + GV L+ L +AG  L      + ++ F  Q      LS      + +
Sbjct: 98  VELTPA---MGTEIKGVQLSKLSNAGKDQLARFVAERKVVAFRDQDFADLSIADAVEYGS 154

Query: 63  RFGA--IERIGGG-----DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
      FG  I  G      +I  +      D T      +  +      ++AWH+D TY
Sbjct: 155  YFGRPHIHPTSGAPLNHPEIHLVHRAAGDKTA-----ESFFEARTNSVAWHSVDVYE 206

Query: 116  PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
      VP  GG T FA+  AY+ L +A +  +H  SA HS      G
Sbjct: 207  KQPPGTTFLYVLDVPETGGDTLFGANGVEAYNRLSDAFKERLHGLSATHS-----GIE 258

Query: 176  QQAGSAY-IGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGL 233
      Q  S Y G      + P+V+ HP TG  +L + R      I G+  ES+  L  L
Sbjct: 259  QVNASRYRNGIARREPVVNVHPIVRTHPVTGEKALYVNRQFTRKIVGLKQEESDVLLNFL 318

Query: 234  VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
      D      H  +WA  VVVWDNR  H A
Sbjct: 319  YDHIALGADFHVRVKWAPKTVVVVWDNRVATHTA 351
```

>ref|XP_001937023.1| alpha-ketoglutarate-dependent taurine dioxygenase [Pyrenophora
tritici-repentis Pt-1C-BFP]
gb|EDU49610.1| alpha-ketoglutarate-dependent taurine dioxygenase [Pyrenophora
tritici-repentis Pt-1C-BFP]
Length = 382

Score = 76.3 bits (186), Expect = 5e-12, Method: Compositional matrix adjust.
Identities = 70/267 (26%), Positives = 111/267 (41%), Gaps = 25/267 (9%)

```
Query: 13  ATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE---- 68
      A +G  V G+ L  L D      L      + +++ F  Q LS  QQ      + +G IE
Sbjct: 95  AHIGTEVVGQLKDLTDQKDELGLLIAERSVVFRRDQDLSPQQKKGLEWYGEIEVHPQ 154

Query: 69  --RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
      + G  +  ++ +  D      + +P+      +  G  WH D  +  A
Sbjct: 155  VPFVPG--VPGVTVLWPDQLATEVTPS-----FRKTGGASRWHTDLVHERQPAGVTHLHN 207

Query: 127  EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG 186
      + +P +GG T ++  AAY+ L  A R ++  R A +  +      +  AG YI
Sbjct: 208  DTIPKIGDTLWSSGYAAYEKLSPAFRKIIDGREAVYRSAHPYLDNRDNT-SAGPKYIER- 265

Query: 187  MDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD-WACQAPRVH 244
      + P+V+VHP TG  SL + R      I G+D AES+  L  L D  +
Sbjct: 266  -----VHPIVRVHPATGWKSLWVNRAFTDRIVGLDKAESDVILNLYLFDVYENNVDVQV 318

Query: 245  AHQWAAGDVVVWDNRCLLHRAEPWDFK 271
      +W  G  +WDNR  +H A  WD++
Sbjct: 319  RFRWTPGTSALWDNRITIHNAS-WDYE 344
```

>ref|XP_760142.1| hypothetical protein UM03995.1 [Ustilago maydis 521]
gb|EAK85005.1| hypothetical protein UM03995.1 [Ustilago maydis 521]
Length = 413

Score = 75.9 bits (185), Expect = 6e-12, Method: Compositional matrix adjust.
Identities = 72/264 (27%), Positives = 109/264 (41%), Gaps = 24/264 (9%)

```
Query: 14  TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERIGG 72
```

```

      T+G  + G+ L  L D      L      +  ++ F GQ  + ++Q+  + +G + +
Sbjct: 103 TIGTELEGIKLGQLTDQQKDELALLVAERGVVFFRGQDDWTIEEQLALGRYWGPLHKHAT 162

Query: 73  GDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA-----WHADSTYMPVMAQGAVFSA 126
      + A  ++      V  H  +  D  K+  G  +      WH+D TY      F
Sbjct: 163 TGVPARGDLDLVHVYAHPTS--DPQEKIYRGPVKHSRSDLWHS DVTYEVNPPSYTSFKL 220

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG 186
      V P  GG T +A  AAYD L  R  +  + +A HS      V QA  A  +G
Sbjct: 221 LVSPEAGGDTLWASGYAAYDRLSYPMREYLEKLTAIHSA-----VDQADGAR-RHG 270

Query: 187 MDTTATPLR---PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPR 242
      P+      PLV+VHP T  +L      IPG+  AES+  ++ L  +  A
Sbjct: 271 NTVRRDPVETEHLVRVHPVTNHKALFFNPGFVRYIPGVPKAESDYLQFLTNHVSTASD 330

Query: 243 VHAH-QWAAGDVVVWDNRCLLHRA 265
      +W AGDV +WDNR  +H A
Sbjct: 331 FSVRFKWNAGDVVAIWDNRRTNIHSA 354

```

>ref|XP_001396406.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus niger CBS 513.88]
emb|CAK41667.1| unnamed protein product [Aspergillus niger]
Length = 385

Score = 75.9 bits (185), Expect = 6e-12, Method: Compositional matrix adjust.
Identities = 69/262 (26%), Positives = 112/262 (42%), Gaps = 19/262 (7%)

```

Query: 15  LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE---RIG 71
      +G  + G+ L  L D      L      +  +++ F  Q +S  QQ  + FG +E  ++
Sbjct: 93  IGTEIVGLQLKDLTDQQKDELGLLIAERSVVFFRDQDISPQQQKELGEWFGVEVEVHPQVP 152

Query: 72  GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VPA 131
      VA  V      SPA  +  +  G  WH D  +  A      + +P+
Sbjct: 153 QVPGVAGVTVIWPALQATESPANF---RRPGGASRWHTDLVHERQPAGVTHLHNDTIPS 208

Query: 132 VGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTA 191
      +GG T +A  AAY+ L  A R ++  ++A  +  +      H ++ G  Y+
Sbjct: 209 IGGDTLWASGYAAYEKLSPA FRKIIDGKTAIYRSAHPYLDRNHPEE-GPKYVERE----- 262

Query: 192 TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWA 249
      PLV+VHP TG  +L  + R      I G+D AES+  L  L D  +  +  +W+
Sbjct: 263 ---HPLVRVHPATGWKALWVNRAMTDRIVGLDKAESDVILGYLCDVYEKNIDIQVRFKWS 319

Query: 250 AGDVVVWDNRCLLHRAEPWDFK 271
      G  +WDNR  +H A  WD++
Sbjct: 320 PGTSALWDNRITIHNAS-WDYE 340

```

>ref|XP_001935765.1| alpha-ketoglutarate-dependent taurine dioxygenase [Pyrenophora tritici-repentis Pt-1C-BFP]
gb|EDU48352.1| alpha-ketoglutarate-dependent taurine dioxygenase [Pyrenophora tritici-repentis Pt-1C-BFP]
Length = 387

Score = 75.9 bits (185), Expect = 6e-12, Method: Compositional matrix adjust.
Identities = 78/267 (29%), Positives = 108/267 (40%), Gaps = 31/267 (11%)

```

Query: 13  ATLGATVTGVHLATLDDAGFAALHAAWLQHALLI-FPGQHLSN---DQQITFAKRFGA-- 66
      A +GA V G+ L+ L+DAG  L A ++ H  ++ F  Q  ++      + F  FG
Sbjct: 100 ANIGAEVHGIQLSKLNDAGKDEL-ALFVAHKKVVAFREQDFADIPIKDALAFGGYFGRHH 158

Query: 67  IERIGGG-----DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQG 121

```



```

      I      G      +I +      D + R      D +      ++ WH+D TY
Sbjct: 159 IHPTSGAPEGYPEIHLVHRGTDDTSAR-----DFFEERTNSITWHSVDVTEKQPPGT 210

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS- 180
      PAVGG T FA+  AAY+ L      R +H      HS V      Q GS
Sbjct: 211 TFLYILDGPAVGGDTLFANQVAAYNRLSPEFRKRLHGLKVHSAV-----EQADGSR 262

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239
      + G      T + PLV+ HP TG +L      + + I G      ES+ L L D +
Sbjct: 263 NHGGIVRRDPVTSIHPLVRTHPATGEKALYANPQFSRRIVGYKKEESDFLLNFLYDHIK 322

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
      +WA G VVVWDNR H A
Sbjct: 323 GQDFQVRIKWAPGTVVVWDNRVTAHSA 349

```

```

>ref|ZP_05006078.1| taurine dioxygenase [Streptomyces clavuligerus ATCC 27064]
ref|ZP_06774783.1| Taurine dioxygenase [Streptomyces clavuligerus ATCC 27064]
ref|ZP_08219207.1| Taurine dioxygenase [Streptomyces clavuligerus ATCC 27064]
gb|EDY50377.1| taurine dioxygenase [Streptomyces clavuligerus ATCC 27064]
gb|EFG10382.1| Taurine dioxygenase [Streptomyces clavuligerus ATCC 27064]
      Length = 324

```

Score = 75.9 bits (185), Expect = 6e-12, Method: Compositional matrix adjust.
Identities = 81/259 (31%), Positives = 113/259 (43%), Gaps = 11/259 (4%)

```

Query: 15  LGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG 73
      +GA + GV LA L A AA+ AA L+H ++ F GQ LS+ I F +R G + R G
Sbjct: 20  IGAEIPGVDLAAPLSAAVLAAIRAALLRHKVVFVRGQRLSHPAHIAFGRRLGPLTRRPGP 79

Query: 74  D-----IVAISNVKADGT-VRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
      I V D R E K + + WH D +V
Sbjct: 80  KHGVHPEGYPEILTVDPDAEDTRYGRRFEERLRPKELRPDSGWHVDLAAAVNPPAISVLR 139

Query: 126 AEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 185
      AE VP GG T + + AA+ L R L A H+L ++ +L + A I
Sbjct: 140 AETVPDHGGDTQWTSLVAAHQGLSAPLRELAAGLRAEHTL-FAGCELLSDEEDVAVIRR 198

Query: 186 GMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVH 244
      + T + P+V+VHPETG +L + + + I G+ ES LE +
Sbjct: 199 LTEDTLLSVHPVVRVHPETGERALFVPPASVSRIAGLLPWESRLLELFHGHIGRPEHTV 258

Query: 245 AHQWAAGDVVVWDNRCLLH 263
      +WAAGDV VWDNR + H
Sbjct: 259 RWRWAAGDVAVWDNRVAH 277

```

```

>gb|ADC34002.1| TfdA-like protein [uncultured bacterium]
      Length = 206

```

Score = 75.9 bits (185), Expect = 7e-12, Method: Compositional matrix adjust.
Identities = 64/230 (27%), Positives = 103/230 (44%), Gaps = 33/230 (14%)

```

Query: 38  AWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDD 97
      A+ ++ ++ F Q +S + QI A FG + R G IS + VR+ +D+
Sbjct: 4  AFARYLVIFFRDQKISFEDQIRLAGYFGPLGRHVGKS--TISKATENELVRKF--HYDE 58

Query: 98  MMKVIVGNMAWHADSTY--MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL 155
      K I G +H+D + MP + +++ V P GG T FA M AAYDAL + +
Sbjct: 59  TSKQISGE-NFHSDQSCAAMPPLG-SMLYNHTVPPDGGGDTMFASMYAAYDALSDKMKKY 116

Query: 156 VHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG--- 212
      + +A H G+ G G T + P++ HP TG+ S+ +

```

Sbjct: 117 LEGLTATHD-----GTRIFGPG--TPVSVHPVIVRHPVTGKKSIYVNTDF 159

Query: 213 -RHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

H + +P + E +R L+ LVD +A +W + WDNRC+

Sbjct: 160 TSHINELPRL---EGQRLQLVLDHCDKAEWTTFRWRPHSIAFWDNRV 206

>ref|YP_372823.1| taurine dioxygenase [Burkholderia sp. 383]

gb|ABB12179.1| Taurine dioxygenase [Burkholderia sp. 383]

Length = 315

Score = 75.9 bits (185), Expect = 7e-12, Method: Compositional matrix adjust.

Identities = 75/290 (25%), Positives = 118/290 (40%), Gaps = 18/290 (6%)

Query: 2 AQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60

A + + P A +GA + GV L L A +A+ AA L+ ++ F Q L+++Q + F

Sbjct: 8 AAQPVDDVIPLSAHIGAEIRGVDLTQPLTTAQISAIRAALLKWRVIFFREQLTHEQHVAF 67

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120

+ +FG IG + A ++ +H A + V WH D T

Sbjct: 68 SAQFGE-PTIGHPVFGHVDGHPAVYSIAKHKATRFEGEPVRRPWTGWHTDVTAAVNPPW 126

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180

++ +P GG T + ++ AY+ L R V H AG+

Sbjct: 127 ASILRGVTIPPYGGDTHWTNLVRAYETLSAPLRGFVDGLRGIHRF-----TPPAGA 177

Query: 181 AYIGYGMDDTA-TPL---RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVD 235

G D PL PLV+VHPETG +L + +I G+ ES+ LE L +

Sbjct: 178 RATGAFDDAVERRPLVTEHPLVRVHPETGERALYVSPSFLKSIIGLTPRESQALLELLWE 237

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA--EPWDFKLPRVMWHSRLAG 283

+ +W + WDNR H A + +D R ++ + L G

Sbjct: 238 HVTRPEFTIRFKWEPRSIAFWDNRATAHLAPVDIFDLDFDRQLYRTTLIG 287

>emb|CBJ20070.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase

[uncultured bacterium]

Length = 135

Score = 75.9 bits (185), Expect = 7e-12, Method: Compositional matrix adjust.

Identities = 49/141 (34%), Positives = 69/141 (48%), Gaps = 8/141 (5%)

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175

P+ A + SA VVP+ GG T F MR AY+AL E R V R HS +S+S +

Sbjct: 2 PIPAHSSALSARVVPSEGGETEFVSMRVAYEALPEDLRRQVDGRIVVHSFGFSRSLI--- 58

Query: 176 QQAGSAYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234

IG + P+R LV+ +P GR ++ IG HA I G+ ES + L+

Sbjct: 59 ----DPGIGTEVGRDYPVPRHALVRANPRNGRKNIIYIGSHAWRIEGLGIDESRILIAKLL 114

Query: 235 DWACQAPRVHAHQWAAGDVVV 255

+ + V H W GD+V+

Sbjct: 115 EVTVRPEHVFRHHWRVGDLM 135

>ref|ZP_02359146.1| taurine dioxygenase [Burkholderia oklahomensis E0147]

Length = 278

Score = 75.9 bits (185), Expect = 7e-12, Method: Compositional matrix adjust.

Identities = 71/279 (25%), Positives = 109/279 (39%), Gaps = 41/279 (14%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62

T L++T +GA V LA +DD +A+ A +H +L F Q LS Q FA

Score = 75.5 bits (184), Expect = 8e-12, Method: Compositional matrix adjust.
Identities = 51/168 (30%), Positives = 82/168 (48%), Gaps = 23/168 (13%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
L+I P +GA + GV+LAT ++ A L + ++ Q LS++Q + A+RFG
Sbjct: 2 LKIEPITPHIGARIHGVNLTATCSATELDEVYQALLTNQVIFLDDQTLSSSEQHLMIAERFG 61

Query: 66 AIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
+E R+ V++ T R ++P E WH D T+ +
Sbjct: 62 QLEPAHPFFPRVEHAPQVSVIE-----TTRGNAPME-----SYWHTDLTWRELP 105

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
++ ++ A+ VP VGG T + M A +D+LDE +A + SA HSLV
Sbjct: 106 SKASLLLAQHVPNVGGDTIWCSMTAVFDSLDEDIKAKLRSLSATHSLV 153

>ref|YP_001625716.1| alkylsulfate dioxygenase (2-oxoglutarate-dependent)
[Renibacterium
salmoninarum ATCC 33209]
gb|ABY24302.1| alkylsulfate dioxygenase (2-oxoglutarate-dependent) [Renibacterium
salmoninarum ATCC 33209]
Length = 330

Score = 75.5 bits (184), Expect = 8e-12, Method: Compositional matrix adjust.
Identities = 66/262 (25%), Positives = 108/262 (41%), Gaps = 24/262 (9%)

Query: 13 ATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHL-SNDQQITFAKRFGAIERIG 71
A +GA + G+ L ++ + + AA +H L+F ++ SN++Q+ FA FG + +
Sbjct: 23 ARIGAEIRGLDLTSVTEEQIKQIRAAALNEHKALVFREANVHSNEEQVAFASNFGLPTQAH 82

Query: 72 GGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPA 131
+ DG +P ++ V N WH D T++ Q + + +P
Sbjct: 83 P-----TTYSDVG-----APEVLPVDSEISVAN-TWHTDVTFFVNNPPQASTLRSVTLP 130

Query: 132 VGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA-----YIGYG 186
GG T A AYD L R+ A HS Y +++ S +
Sbjct: 131 YGGETLIASITVGAYDDLPELRSFAESLWAIHSNDYDYNPKNLEHKNSEEQRKIFTRIK 190

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIGRHAH--AIPGMDAAESERFLEGLVDWACQAPRVH 244
+T P+ +VHP TG+ +L IG A I G+ ES L L + + +
Sbjct: 191 FETA----HPVARVHPLTGKRNLFIFAFAQRLRILGVSNTESRDLLRLLQAYVTRPENIV 246

Query: 245 AHQWAAGDVVVDNRCLLHRAE 266
VV++DNR H A+
Sbjct: 247 RVNCEPNQVVLFDNRATQHAYQ 268

>emb|CAY27319.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 75.5 bits (184), Expect = 8e-12, Method: Compositional matrix adjust.
Identities = 45/125 (36%), Positives = 68/125 (54%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPL- 194
T F DMRAAYDAL E + + A H++++S+ KLG + + T P+
Sbjct: 1 TEFGLDMRAAYDALPEDMKQRLRGLVAEHAHMHSRRKLGFDDFSDEE-----NQTYPPVP 54

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
+ L++ HP +GR L + HA I GM E + L+ L++ A Q V+ H+W D+V
Sbjct: 55 QTLRRHPGSGRMGLFLASHAGRIFGMPEDGKALLQRLIEHATQQQFVYTHRWRLHDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

Sbjct: 4 PTSAGWGARVEGLDLRAPLGAECAALVELFRARHLLVFSQGFSLEEQIRFMGHLGPVL 63

Query: 69 RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV 128
G I +SNVK + +++H+D+ + V + AE

Sbjct: 64 HEEGSGIGFVSNVKEGAALG-----TSELSFHSDTGHCAVPLEAVSLFAED 109

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 188
V T FA++ AAY L R+ V +++ S + G + + GM

Sbjct: 110 VEGCVTSTRFANVAAAYGRLPADLRSRVASLVCENAMPVSLDG---RNVGLS-VAEGMP 164

Query: 189 TTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQ 247
P+V HP +G P L++ I G++ AES LE L V+ H

Sbjct: 165 RAE---HPVVWRHPVSGEPGLMVNANQTTRIVGLEDAESRELLEELFSVMYAEDAVYEHS 221

Query: 248 WAAGDVVVWDNRCLLH 263
W GDVV+W N + H

Sbjct: 222 WQQGDVVIWHNLAVQH 237

>ref|ZP_02384176.1| taurine dioxygenase [Burkholderia thailandensis Bt4]
ref|ZP_05590364.1| taurine dioxygenase [Burkholderia thailandensis E264]
Length = 310

Score = 75.1 bits (183), Expect = 9e-12, Method: Compositional matrix adjust.
Identities = 69/282 (24%), Positives = 109/282 (38%), Gaps = 48/282 (17%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T L++T +GA V V L+ + AA +H +L F Q LS + FA

Sbjct: 35 TRLKLTRLTPAIGAIVDNVDLSNATGDLRDGIRAALARHQVLFRRDQRLSAVRHRDFAAG 94

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
FG + +I+ + N D + N WH D T+

Sbjct: 95 FGDLHVHPPIYPSPHDAREIMVLDNAVFD-----LKDNAIWHTDVTFAE 137

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGH 174
+ ++ +A +P GG T + AAYDAL + +A + +A+H + + G

Sbjct: 138 TPTRASILAARTLPETGGDTLWGSQFAAYDALSDRVKAQLDGLTAQHDFTKSFPLKRFGL 197

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR---HAAHAIPGMDAAESERFL 230
+ + + P+V+ HPETGR +L + + +P + A RFL

Sbjct: 198 TADDRARWEDTRIKHPPV-THPVVVRTHPETGRRALFVNEGFTTEINELPEEEGAALLRFL 256

Query: 231 -----EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
E + W +W GDV WDNR +H A

Sbjct: 257 FAHQSRPEFTLRW-----RWQPGDVAFWDNRSTIHYA 288

>ref|YP_003940920.1| Taurine dioxygenase [Enterobacter cloacae SCF1]
gb|ADO47636.1| Taurine dioxygenase [Enterobacter cloacae SCF1]
Length = 282

Score = 75.1 bits (183), Expect = 1e-11, Method: Compositional matrix adjust.
Identities = 71/273 (26%), Positives = 110/273 (40%), Gaps = 26/273 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAG-FAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+++ +GA ++GV LA + DAG F + A L+H +L Q +S + + FA+

Sbjct: 1 MRVEQLTCHIGAELSGVRLADAIHDAGLFTETRAQLLKHVRVFLRQQEISRAEHVAFARL 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG +E V S+ G VR + D++ N AWH D+T+ G V

Sbjct: 61 FGELE----DHPVVGSDPDHPGLVRIYKTP---DVVNERYEN-AWHTDATWREKPPMGCV 112

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183

P VGG T +A+M AY L E + + A HSL S + ++Q +
Sbjct: 113 LRCVESPVGGDTLWANMVVAYQNLPEEVKQKIAGLRAYHSLEASFGAVKPIEQRLALKA 172
Query: 184 GYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LEG 232
+ P+V+ HP+T L + E R+ L
Sbjct: 173 QF-----PDAEHPVVRTHPDTEKILFVNAFTTHFSNYHTPEHIRYGGQDYNMGSSDLLRY 227
Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L+ A +W G + +WDNR H A
Sbjct: 228 LISQAYLPEYQVRWRWQPGSIAIWDNRSTQHYA 260

>gb|AC031282.1| Ptm06 [Streptomyces platensis]
Length = 280

Score = 75.1 bits (183), Expect = 1e-11, Method: Compositional matrix adjust.
Identities = 73/256 (28%), Positives = 106/256 (41%), Gaps = 24/256 (9%)

Query: 10 PTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE 68
PT A GA V G+ L A L AAL + LL+F GQ S ++QI F G +
Sbjct: 4 PTSAGWGARVEGLDLRAPLGAECAALVELFRARHLLVFSGQGFSLLEQIRFMGHLGPVL 63
Query: 69 RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV 128
G I +SNVK + +++H+D+ + V + AE
Sbjct: 64 HEEGSGIGFVSNVKEGAALG-----TSELSFHSDTGHCAVPLEAVSLFAED 109
Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 188
V T FA++ AAY L R+ V +++ S + G + + GM
Sbjct: 110 VEGCVTSTRFANVAAAYGRPLADLRSRVASLVCENAMPVSLDG---RNVGLS-VAEGMP 164
Query: 189 TTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQ 247
P+V HP +G P L++ I G++ AES LE L V+ H
Sbjct: 165 RAE---HPVVRHPVSGEPGLMVNANQTTRIVGLEDAESRELLEELFSVMAEDAVYEHS 221
Query: 248 WAAGDVVVWDNRCLLH 263
W GDVV+W N + H
Sbjct: 222 WQQGDVVIWHNLAVQH 237

>ref|XP_001560734.1| hypothetical protein BC1G_00762 [Botryotinia fuckeliana B05.10]
gb|EDN23289.1| hypothetical protein BC1G_00762 [Botryotinia fuckeliana B05.10]
Length = 389

Score = 75.1 bits (183), Expect = 1e-11, Method: Compositional matrix adjust.
Identities = 75/270 (27%), Positives = 111/270 (41%), Gaps = 31/270 (11%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ---HLSNDQQITFAKR 63
ITP +G ++GV + L DAG L + +++ Q H Q F
Sbjct: 87 ITPK---MGTILSGVKMEELSDAGKDELALLITERKIVVLREQSDFLHAGPQFQQDFMSY 143
Query: 64 FG--AIERIGGGDIVAISNVKADGTV----RQHSPAEWDDMMKVIVGNMAWHADSTYMPV 117
FG +I+ + G +VK R H+ E + + + + WH D +Y
Sbjct: 144 FGPLSIQPVSG-----SVKGHPFHVHRDHNEEEIANFFQKKLSTLWHHDVSYEK- 195
Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
G + P VGG T FAD AY L RA++ A HS SQ +G+ +
Sbjct: 196 QPPGYIMLG-TCPDVGGDTVFADTVEAYKRLSPTFRAMIQDLKANHS---SQKMIGYARA 251
Query: 178 AGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDW 236
A +D+ L P+V+VHP +G +L + I G+ E E ++ LVD
Sbjct: 252 ARGTVRTPIDS---LHPIVRVHPVSGEKALYLNSEFLTIDIVGLKDGEKEMLMKFLVDH 307
Query: 237 ACQAPRVHAHQ-WAAGDVVVWDNRCLLHRA 265

C A W VV++D R L H A
Sbjct: 308 VCMGHDFQARVWGWEKHSVVMFDRSTLHTA 337

>ref|YP_001584538.1| taurine dioxygenase [Burkholderia multivorans ATCC 17616]
ref|YP_001948338.1| taurine dioxygenase [Burkholderia multivorans ATCC 17616]
gb|ABX18246.1| Taurine dioxygenase [Burkholderia multivorans ATCC 17616]
dbj|BAG45802.1| taurine dioxygenase [Burkholderia multivorans ATCC 17616]
Length = 315

Score = 75.1 bits (183), Expect = 1e-11, Method: Compositional matrix adjust.
Identities = 72/286 (25%), Positives = 116/286 (40%), Gaps = 18/286 (6%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ + P A +GA + GV L L A AA+ A L+ ++ F Q L+++Q + F+ +F
Sbjct: 12 IDVIPLSAHIGAEIRGVDLTQPLTTAQAIAIRHALLKWRVIFFREQLTHEQHVAFSAQF 71

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G +G + A ++ +H A + V WH D T ++
Sbjct: 72 GE-PTVGHPVFGHVEGHPAVYSIAKHKRATREFEGEPVRRPWTGWHTDVTAAVNPPWASIL 130

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
+P GG T + ++ AY+ L R V H AG+ G
Sbjct: 131 RGVTTIPPYGGDTQWTNLVRAYETLSAPLRGFVDGLRGIHRFT-----PPAGARATG 181

Query: 185 -YGMDDTTATPL---RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239
+ PL PLV+VHPETG +L + +I G+ ES+ LE L + +
Sbjct: 182 AFDAAVERRPLVTEHPLVRVHPETGERALYVSPSFLKSIVGLTPRESQALLELLWEHVTR 241

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA--EPWDFKLPRVMWHSRLAG 283
+W + WDNR H A + +D R ++ + L G
Sbjct: 242 PEFTIRFKWEPRSIAFWDNRATAHLAPVDIFDLDFDRQLYRTTLVG 287

>ref|XP_001209049.1| conserved hypothetical protein [Aspergillus terreus NIH2624]
gb|EAU38441.1| conserved hypothetical protein [Aspergillus terreus NIH2624]
Length = 382

Score = 75.1 bits (183), Expect = 1e-11, Method: Compositional matrix adjust.
Identities = 73/270 (27%), Positives = 109/270 (40%), Gaps = 25/270 (9%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ---HLSNDQQITFAKR 63
+I T+G+ V GV L+ L D G L Q ++ F Q HL D+ + +
Sbjct: 97 EIDDLTPTIGSEVKGVSQSLSDKGDQLALFVAQRKVAFRDQDFAHLPIDKALEWGGY 156

Query: 64 FGA--IERIGGGDI----VAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPV 117
FG I + G + + + AD T Q D + ++ WH+D T+
Sbjct: 157 FGRHHIHQTS GAPKGFPEIHLVHRGADDTSGQ-----DFLATRTNSITWHS DVTFEKQ 209

Query: 118 MAQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
P+ GG T F DM AY L R +H A HS + ++ +
Sbjct: 210 PPGTTFLYLLDGPSSGGDTLFCDMAQAYRRLSPEFRRRLHGLRAVHSGI---EQINNSLN 266

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDW 236
G G+ T P+V+ HP TG +L + + I G ES+ L+ L D
Sbjct: 267 KGGIARREGIMTE----HPIVRTHPVTGEKALFVNPFQTRYIVGYKKEESDFFLLKFLYDH 322

Query: 237 ACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ + +W G VVWDNR + H A
Sbjct: 323 IALSQDIQTRVRWRPGTVVVWDNRVVAHSA 352

>gb|ABC34147.1| alpha-ketoglutarate-dependent taurine dioxygenase [Burkholderia

thailandensis E264]
Length = 335

Score = 75.1 bits (183), Expect = 1e-11, Method: Compositional matrix adjust.
Identities = 69/282 (24%), Positives = 109/282 (38%), Gaps = 48/282 (17%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T L++T +GA V V L+ + AA +H +L F Q LS + FA
Sbjct: 60 TRLKLTRLTPAIGAIVDNVDLSNATGDLRDGIRAALARHQVLFRRDQRLSAVRHRDFAAG 119

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
FG + +I+ + N D + N WH D T+
Sbjct: 120 FGDLVHVPPIYPSPHDAREIMVLDNAVFD-----LKDNAIWHTDVTFAE 162

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGH 174
+ ++ +A +P GG T + AAYDAL + +A + +A+H + + G
Sbjct: 163 TPPRASILAARTLPETGGDTLWGSFGAAYDALSDRVKAQLDGLTAQHDFTKSFPLKRFGL 222

Query: 175 VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR---HAHAIPGMDAAESERFL 230
+ + + P+V+ HPETGR +L + + +P + A RFL
Sbjct: 223 TADDRARWEDTRIKHPV-THPVVRTHPETGRRALFVNEGFTTEINELPEEEGAALLRFL 281

Query: 231 -----EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
E + W +W GDV WDNR +H A
Sbjct: 282 FAHQSRPEFTLRW-----RWQPGDVAFWDNRSTIHYA 313

>ref|ZP_03585565.1| taurine dioxygenase [Burkholderia multivorans CGD1]
gb|EEE00157.1| taurine dioxygenase [Burkholderia multivorans CGD1]
Length = 315

Score = 75.1 bits (183), Expect = 1e-11, Method: Compositional matrix adjust.
Identities = 72/286 (25%), Positives = 116/286 (40%), Gaps = 18/286 (6%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ + P A +GA + GV L L A AA+ A L+ ++ F Q L+++Q + F+ +F
Sbjct: 12 IDVIPLSAHIGAEIRGVDLTQPLTTAQIAAIRHALLKWRVIFRFREQFLTHEQHVAFSAQF 71

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G +G + A ++ +H A + V WH D T ++
Sbjct: 72 GE-PTVGHPVFGHVEGHPAVYSIAKHKATRFEGEPVRRPWTGWHTDVTAAVNPPWASIL 130

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
+P GG T + ++ AY+ L R V H AG+ G
Sbjct: 131 RGVITIPPYGGDTQWTNLVRAYETLSAPLRGFVDGLRGIHRFT-----PPAGARATG 181

Query: 185 -YGMDDTATPL--RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239
+ PL PLV+VHPETG +L + +I G+ ES+ LE L + +
Sbjct: 182 AFDEAVERRPLVTEHPLVRVHPETGERALYVSPSFLKSIVGLTPRESQALLELLWEHVTR 241

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA--EPWDFKLPRVMWHSRLAG 283
+W + WDNR H A + +D R ++ + L G
Sbjct: 242 PEFTIRFKWEPRSIAFWDNRATAHLAPVDIFDLDFDRQLYRTTLVG 287

>ref|YP_001239290.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Bradyrhizobium sp. BTAi1]
gb|ABQ35384.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Bradyrhizobium sp. BTAi1]
Length = 312

Score = 75.1 bits (183), Expect = 1e-11, Method: Compositional matrix adjust.
Identities = 75/290 (25%), Positives = 120/290 (41%), Gaps = 33/290 (11%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
 T+++ T+GA + GV L+ L D F + A ++ ++F Q LS D FA+R
 Sbjct: 26 TIEVRQLSPTVGAIEGGVDLSKDLDPDEQFTEIQRALDENLAIVFRDQDLSKDDHKRFARR 85

Query: 64 FG-AIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGA 122
 FG ++ R +A + + DG + D WH D + P + +
 Sbjct: 86 FGKSLHR-----HELAATRFRHDGPFDPFELSWKTDANSRFTAGDGHWPDVSCDPSPIRVS 141

Query: 123 VFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARH--SLVYSQSKLGHVQQAGS 180
 + P++GG T FA+M AY+ L + + L+ +A H SL ++ + G G
 Sbjct: 142 LLRVTKTPSLGGDTAFANMYLAYEFLSDPIKQLLEGLTAIHGSLAWT-AGYGAKPDPGK 200

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESE-----RFLEG 232
 Y P+V HP TGR L + I + ES+ R +EG
 Sbjct: 201 TY-----PQSEHPVVVSHPRTRGRKFLVNASFTSHIVQLTRRESALLQLFRHIEG 252

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLA 282
 + + P W ++VWDN H A WD+ P W R++
 Sbjct: 253 QLALQTRVP-----WRPNLLVWDNWNASQHHAV-WDY-YPEERWGERVS 294

>ref|ZP_07045848.1| Taurine catabolism dioxygenase TauD/TfdA family protein
 [Comamonas testosteroni S44]
 gb|EFI60508.1| Taurine catabolism dioxygenase TauD/TfdA family protein [Comamonas
 testosteroni S44]
 Length = 299

Score = 74.7 bits (182), Expect = 1e-11, Method: Compositional matrix adjust.
 Identities = 65/264 (24%), Positives = 107/264 (40%), Gaps = 17/264 (6%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 +Q P A + V L L D A L A ++ F Q ++ +Q I + F
 Sbjct: 19 IQPVPRMPNFAAWIESVDLTkPLTDEVKAE LRQALFDFEVIFFKPTITPEQHIALGQVF 78

Query: 65 GAIERIGGGDIVAIS-NVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
 G I D A + ++ + R PA + N WH D ++ G
 Sbjct: 79 GPISNGSYFDRNANAPEMEMIVSDRDRPPA-----IDN--WHTDISWKLTPPLGTA 127

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-GHVQQAGSAY 182
 V P GG TC++ A++ L + + SA H+ + QS ++ + G
 Sbjct: 128 IQITVTPPAGGNTCWSSTSKAFEWLSPGMQQYLEGLSAVHT--WEQSGFREYLGKKGDEA 185

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAP 241
 + + P+V+V+P++GR + + I G+D E+ L L+ W +
 Sbjct: 186 LIAAIKAGKPVTHPVVRVNPDSGRKCIFVNADFTRNIIGVDRHEARGVLHFLGLGWLQRPE 245

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRA 265
 + HQW AG + +WDNR H A
 Sbjct: 246 FMVHHQWEAGGIAIWDNRSTQHIA 269

>gb|ADC33980.1| TfdA-like protein [uncultured bacterium]
 Length = 122

Score = 74.7 bits (182), Expect = 1e-11, Method: Compositional matrix adjust.
 Identities = 42/127 (33%), Positives = 66/127 (51%), Gaps = 6/127 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL- 194
 T F DM AY+ L A +A + A H+L +S+++ + G + P+
 Sbjct: 1 TEFCDMYGAYERLSPAWKARIAGLRAVHNLDfsRTR-----RHGEDLMTEAQRRERPPVD 55

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
P+V+ HPETGR + +G HA +I GMD +E L A +AH+W+ G ++
Sbjct: 56 HPIVRTHPETGRKCIFLGDHAESILGMDYDAGRALIEELNALAVHPDLTYAHRWSPGQLI 115

Query: 255 VWDNRCL 261
+WDRNC+
Sbjct: 116 LWDNRCL 122

>ref|ZP_02366215.1| taurine dioxygenase [Burkholderia oklahomensis C6786]
Length = 278

Score = 74.7 bits (182), Expect = 1e-11, Method: Compositional matrix adjust.
Identities = 69/273 (25%), Positives = 107/273 (39%), Gaps = 29/273 (10%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T L++T +GA V LA +DD +A+ A +H +L F Q LS Q FA
Sbjct: 2 TRLKLTRLTPAIGAIVDNADLANAVDDVRSAIRDALRHQVLFRRDQRLSAVQHRDFAA 61

Query: 63 RFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYM 115
FG + +I+ + N D + N WH D T+
Sbjct: 62 GFGDLHVHPPIYPSHPDAREIMVLDNEVFD-----LKDNAIWHDTVTFA 104

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLG 173
++ +A +P GG T + AAYDAL + + + +A+H + + G
Sbjct: 105 ETTPCASILAACLTLPDTGGDTLWGSFGAAYDALSDRVKTQLEGLTAQHDFTKSFPLKRFG 164

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
+ + + P+V+ HPE+GR +L + I + ES L
Sbjct: 165 LTADDRARWEETRIKHPPV-THPVVRTHPESGRRALFVNDGFTTEINELPEEESAALLRF 223

Query: 233 LVDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
L + +W AGDV WDNR +H A
Sbjct: 224 LFAHQSRPEFTLRWRWQAGDVAFWDNRSTIHYA 256

>ref|XP_001598281.1| hypothetical protein SS1G_00367 [Sclerotinia sclerotiorum 1980]
gb|EDN90967.1| hypothetical protein SS1G_00367 [Sclerotinia sclerotiorum 1980
UF-70]
Length = 389

Score = 74.7 bits (182), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 76/270 (28%), Positives = 110/270 (40%), Gaps = 31/270 (11%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ---HLSNDQQITFAKR 63
ITP +G +TGV L L D G L + +++ Q H Q F
Sbjct: 87 ITPK---MGTILTVKLEELSDEGKDELALLITERKIVVLREQSDFLHSGPQFQQDFMSY 143

Query: 64 FG--AIERIGGGDIVAISNVKADGTV---RQHSPAEDDMMKVIVGNMAWHADSTYMPV 117
FG +I+ + G +VK R H+ E + + + + WH D +Y
Sbjct: 144 FGPLSIQPVSG-----SVKGHPFHVHRDHNEEEIANFFQKKLTSTLWHHDVSYEK- 195

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
G + P VGG T FAD AY L RA++ A HS SQ +G+ +
Sbjct: 196 QPPGYIMLG-TCPDVGGDTVFADTVEAYKRLSPTFRAMIQDLKATHS---SQKMIGYARA 251

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDW 236
A +D+ L P+V+VHP +G +L + I G+ E E ++ LVD
Sbjct: 252 ARGTVRTDPIDS---LHPIVRVHPVSGEKALYLNSEFLTDIVGLKDGEREMLMKFLVDH 307

Query: 237 ACQAPRVHAHQ-WAAGDVVWDNRCLLHRA 265
C A W VV++D R LH A
Sbjct: 308 VCMGHDFQARVGWEKHSVVMFDGRSTLHTA 337

>ref|NP_826592.1| taurine catabolism dioxygenase [Streptomyces avermitilis MA-4680]
dbj|BAC73127.1| putative taurine catabolism dioxygenase [Streptomyces avermitilis
MA-4680]
Length = 299

Score = 74.7 bits (182), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 75/291 (25%), Positives = 119/291 (40%), Gaps = 32/291 (10%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T ++I A +GA V+GV + LD+ AL A H L+F L + Q FA+
Sbjct: 2 TAIEIRKVTAHIGAQVSGVDIGKPLDEETVTALRDALNAHKALVFDDVDLDDAGQQAFAR 61

Query: 63 RFGAIERI-----GGGDIVAIISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTY 114
FGA+ G +++ + + + WH D T+
Sbjct: 62 HFGALTTAHTVPAVEGAPNVLPVDSERGRAN-----HWHTDVTF 101

Query: 115 MPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
+ Q + + +P GG T A+ AAY L E RAL A H+ Y +
Sbjct: 102 VLNPPQASTLRSITIPPYGGETLIANAAAAYRDLPEPLRALADTLWAEHTNDYDYAVPDE 161

Query: 175 -VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
V + + T P+V+VHP TG L IG A I G+ ES + L+
Sbjct: 162 AVDEEQARQRAQFTSITYRTAHPVVRVHPLTGERGLFIGGFAQRIVGLSTGESRKLLDLF 221

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA-EPWDFKLPRVMWHSRLAG 283
+ + + +W+ +V++DNR H A + +D + PR + +AG
Sbjct: 222 QSYVTRPENILRWRWSPNQLVLFDNRIQHYAIDNYDGR-PRRLNRVTVAG 271

>ref|XP_001836817.2| alpha-ketoglutarate-dependent taurine dioxygenase [Coprinosia
cinerea okayama7#130]
gb|EAU85034.2| alpha-ketoglutarate-dependent taurine dioxygenase [Coprinosia
cinerea okayama7#130]
Length = 385

Score = 74.7 bits (182), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 77/289 (26%), Positives = 116/289 (40%), Gaps = 27/289 (9%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRFGAIE--- 68
LG V GV L+ L + G L + +++F Q L + ++Q+ F+ FG
Sbjct: 109 LGTEVRGVQLSLSNEGLDELALFVAERKVVVFREQDLKDQPPEKQLKFSSYFGRSHVHP 168

Query: 69 -RIGGGDIVAIISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE 127
+ D ++ + D +P D+++K + + WH+D +Y F
Sbjct: 169 LSVNVKDYPELAVIYRD----PENPGFLDELVKPRINHTNWHSDVSYEQPPPGTTAFYIL 224

Query: 128 VVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 187
P VGG T F AY+ L A R + A H+ G Q G+ G+
Sbjct: 225 DGPDVGGDTLFLSQVEAYNRLSPA FRERLIGLKAVHT-----GIPQAEGAK--KRGV 274

Query: 188 DTTATPLR---PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRV 243
P+ P+V+VHP T +L + I G ES+ L L D +
Sbjct: 275 HVRREPVESEHPVVRVHPVTKEKALYVNPGFTRIVGFKKEESDALLGLFDHITKGADF 334

Query: 244 HAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAA 291
H + G VV+WDNR +H A P DF H RL + E AA
Sbjct: 335 HVRASYEPGTVVIWDNRVTVHSAIP-DFDRSLRRHHIRLTPQAEVPIAA 382

>gb|ADC33989.1| TfdA-like protein [uncultured bacterium]
Length = 187

Query: 167 YSQSKLGHVQQAGSAYIGYGMDTTATPL--RPLVKVHPETGRPSLLIGRHAAHAIPGMDAA 224
H ++ GS + + P+ +V+ H +G H +P +
Sbjct: 187 -----HSRKLGSPEFFADLVPSEPMRHKIVOTHEPSG-----HCKPLP---ES 228

Query: 225 ESERFLEGLVDWACQAPRVHAHQW-AAGDVVVWDNRCLLHRAEPWDFK 271
ES E L+ Q + + W GD+V WDN ++HRA F+
Sbjct: 229 ESAALFERLLKHVTQPKYILSVDWLNEGDMVAWDNTAVMHRATGGSFE 276

>ref|YP_001777150.1| taurine dioxygenase [Burkholderia cenocepacia MC0-3]
gb|ACA92660.1| Taurine dioxygenase [Burkholderia cenocepacia MC0-3]
Length = 315

Score = 74.3 bits (181), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 70/286 (24%), Positives = 114/286 (39%), Gaps = 10/286 (3%)

Query: 2 AQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A + + P A +GA + GV L L AA+ AA L+ ++ F Q L+++Q + F
Sbjct: 8 AAQPVDVIPLSAHIGAEIRGVDLTQPLTTPQIAAIRAALLKWRVIFFREQLTHEQHVAF 67

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
+ +FG +G + A ++ +H A + V WH D T
Sbjct: 68 SAQFGE-PTVGHPVFGHVDGHPAVYSIAKHKATRFEGEPVRRPWTGWHTDVTAAVNPPW 126

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
++ +P GG T + ++ AY+ L R V H +A
Sbjct: 127 ASILRGVTIPPYGGDTHWTNLVRAYETLSAPLRGFVDTLRGIHRFTPPPGA----RATG 181

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239
A+ PLV+VHPETG +L + +I G+ ES+ LE L + +
Sbjct: 182 AFDDAVERRPLVTEHPLVRVHPETGERALYVSPSFLKSIVGLTPRESQALLELLWEHVTR 241

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA--EPWDFKLPRVMWHSRLAG 283
+W + WDNR H A + +D R ++ + L G
Sbjct: 242 PEFTIRFKWEPRSIAFWDNRATAHLAPVDIFDLDFDRQLYRTTLIG 287

>ref|ZP_07576730.1| Taurine catabolism dioxygenase TauD/TfdA [Sphingobium
chlorophenolicum L-1]
gb|EFN08861.1| Taurine catabolism dioxygenase TauD/TfdA [Sphingobium
chlorophenolicum L-1]
Length = 308

Score = 74.3 bits (181), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 67/269 (24%), Positives = 118/269 (43%), Gaps = 22/269 (8%)

Query: 12 GATLGATVTGVHLATLD-DAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERI 70
G G V G+ ++ +A L WL L++F G ++ + QI ++ FG +E
Sbjct: 11 GLGFGREVIGLTPGDIEREAVRRELDRYWLNDGLMVFRGSEVTPEFQIALSRVFGLELVH 70

Query: 71 GGGDIVAISNVKADGTVR-QHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVP 129
++V + V QH ++ K + + WH+D + + G V +A+ +
Sbjct: 71 PVRELVTEGMPELITLVSDQHKEGLFEVDGKPSIAFLPWHSDLVFTDRINHGGVLTQRI 130

Query: 130 PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV----YSQS-----KLGHVQ 176
+ GG+T F D A+ L E +A + + L YS+ ++G +
Sbjct: 131 SSWGQTGFIDQVQAHALLPEELKARIEHLEIVYQLTINPGYSRYGTRSRVRTIRMGDFE 190

Query: 177 QAGSAYIGYGMDDTTATP-LRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLV 234
++ +G +D+ P + P+V P+TGR L I A I G D E L+ LV
Sbjct: 191 KS---VGPRLDSDFPVHPVFTQPDTRKVLNISFPGALYILGHDDDEGHALLQRLV 246

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLH 263
D P + H W +++++WDN ++H
Sbjct: 247 DHLVDCP-AYYHGWQPSEMLLWDNWRMVH 274

>ref|YP_001834136.1| taurine dioxygenase [Beijerinckia indica subsp. indica ATCC 9039]
gb|ACB96647.1| Taurine dioxygenase [Beijerinckia indica subsp. indica ATCC 9039]
Length = 290

Score = 74.3 bits (181), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 76/286 (26%), Positives = 120/286 (41%), Gaps = 31/286 (10%)

Query: 2 AQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A L I+P T+GA + GV L L A + AA L++ ++ F QH++ +QQ F
Sbjct: 11 ASFPLTISPLQPTIGAEIAGVDLREPLTPALRDEIKAAILKYKVVFRRDQHITREQQAIF 70

Query: 61 AKRFGAI-----ERIGGGDIVAISNVKA-DGTVRQHSPA--EWDDMMKVIVGNMAWHAD 111
A++FG + ++ G +I + A D + + A D++ + +H D
Sbjct: 71 ARQFGPLYTHPTTKQTDGTVDASIHRIAADVDFQLYEKEAAVRAKDEIQEF-----YHTD 124

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
+++ V GAV A +P VGG T + D AY L + R + H
Sbjct: 125 TSWRLVPTWGAVLRRAVTLDPVGGDTIWDAGLAYRNLPDDIRERLEGLHVTHDF----- 178

Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFL 230
+A + G D + +V+ H ETG L + H I G+D AES L
Sbjct: 179 -----RNALLCAGHDYPIVAHK-IVRTHRETGEKILWVNFSQLHPTIIGLDRAESRAL 230

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
E + + W G + WDNR +H A PR++
Sbjct: 231 EEVAAYVRRPEHQVRFVSWRPGSIAFWDNRASVHYAVRNYGDFPRL 276

>ref|YP_002406356.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli
IAI39]
emb|CAR16453.1| taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli
IAI39]
Length = 375

Score = 74.3 bits (181), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 62/248 (25%), Positives = 103/248 (41%), Gaps = 26/248 (10%)

Query: 27 LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE-----RIGGGDIVAISN 80
L D F L+ A L+H ++ Q ++ QQ A+RFG + G D + + +
Sbjct: 86 LSDNQFEQLYHAVLRHQVFLRDQAITPQQQRALAQRFELHIHPVYPHAEGVDEIIVLD 145

Query: 81 VKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRCTCFAD 140
D +P + D+ WH D T++ GA+ +A+ +P+ GG T +
Sbjct: 146 THND-----NPPDNDN-----WHTDVTFIETPPAGAILAAKELPSTGGDTLWTS 189

Query: 141 MRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP--LRPLV 198
AAY+AL R L+ A H S + + ++ + + P L P+V
Sbjct: 190 GIAAYEALSVFPRQLLSGLRAEHDFRKSFPYKY-RKTEEEHQWRREAVAKNPPLHPV 248

Query: 199 KVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWD 257
+ HP +G+ +L + I + ESE L L + +W D+ +WD
Sbjct: 249 RTHPVSGKQALFVNEGFTTRIVDVSEKESEALLSFLFAHITKPEFQVRWRWQPNDIAIWD 308

Query: 258 NRCLLHRA 265
NR H A
Sbjct: 309 NRVTHQHYA 316

>ref|ZP_01742153.1| taurine dioxygenase, 2-oxoglutarate-dependent [Rhodobacterales
bacterium HTCC2150]
gb|EBA03267.1| taurine dioxygenase, 2-oxoglutarate-dependent [Rhodobacterales
bacterium HTCC2150]
Length = 277

Score = 73.9 bits (180), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 66/264 (25%), Positives = 106/264 (40%), Gaps = 13/264 (4%)

```
Query: 6  LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      +QI      T+GA ++GV      L  A      ++ A L H ++      G  +S      + FA+ F
Sbjct: 1  MQIKKITPTIGAELSGVDFTKDLTTAQQDEIYQALLDHQVIFVRGCDISPANHVAFAQTF 60

Query: 65  GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
      G ++      N      G      +      ++ K      +WH D T+      + ++
Sbjct: 61  GDLDE-----PNMPYPGVDGFKNIMLLENDAKRPPDTSWHTDLTFKVEQSFASIL 111

Query: 125  SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ--AGSAY 182
      + VVP  GG T ++      AAYDAL E  +A +      SA H L      ++      + +G
Sbjct: 112  VSRVVPDCGGDTLWSSNYAAYDALSEGMDLEGLSAVHDLGDFRNNFAQPKDGLSGEER 171

Query: 183  IGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAP 241
      +      +      ++P++  HP T R L      I G      ES      L +      Q
Sbjct: 172  LNAAVGRMGHAIKPIIDEHPVTKRKFLNFNEAFITHIVGKTPNESNALRIWLANHMNQPE 231

Query: 242  RVHAHQWAAGDVVVWDNRCLLHRA 265
      +W A DV +WDNR  +H A
Sbjct: 232  FQIRRWRCANDVAMWDNRVTMHYA 255
```

>ref|NP_962663.1| hypothetical protein MAP3729 [Mycobacterium avium subsp.
paratuberculosis K-10]
gb|AAS06279.1| hypothetical protein MAP_3729 [Mycobacterium avium subsp.
paratuberculosis K-10]
Length = 258

Score = 73.9 bits (180), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 74/262 (28%), Positives = 107/262 (40%), Gaps = 40/262 (15%)

```
Query: 6  LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      L + P  A  GA + G+ L A L      L      ++ +L F GQ LS  QI FA+ F
Sbjct: 3  LSLRPAAALFGAEIGGIDLRAPLTREQRDELQRLLRQYRVLFRRGQQLSTAHQIEFAEAF 62

Query: 65  GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
      G I      ++  S V AD  QH      + V      + WH D++ +      +V
Sbjct: 63  GPI-----LIFRSVVPADP---QHP-----GVHNVGSGTVGWHLASGLIEPPVASVL 107

Query: 125  SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
      A +P  GG T +AD  AAYD + + ++ +      SA H+      + H
Sbjct: 108  RAVEIPDRGGDTVWADGMAAYDGMPDDLKSRLEGLSATHAPNQHPLVAH----- 157

Query: 185  YGMDTTATPLRPLVKVHPETGRPSLLIGRHA--HAIPGMDAAESERFLEGLVDWACQAP 241
      PLV  HP+ GR  L I      I GM  + S  +E L      ++
Sbjct: 158  -----PLVSHHPDIGRRYLNLINLAPVWDTRILGMSTSHSSALVEQLRAHHLRSD 206

Query: 242  RVHAHQWAAGDVVVWDNRCLLH 263
      +W+AG  VV+WDNR  + H
Sbjct: 207  YQLRFRWSAGAVVLWDNRGMQH 228
```

>gb|ADC33963.1| TfdA-like protein [uncultured bacterium]
Length = 121

Score = 73.9 bits (180), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 43/127 (33%), Positives = 70/127 (55%), Gaps = 7/127 (5%)

```
Query: 136  TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPL- 194
      T F DMR A++AL  A +A +      +A HS+++S++  G  + +      +      P+
```


Sbjct: 1 TEFCDMRLAFEALPAAEQARLEGLTAHHSIMHSRATYGFDEWSREEQQR-----PPVP 54

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
 R LV H E+GR +LL+ H AI G D AE+ + L+ A + H+W+ GD++

Sbjct: 55 RALVARHEESGRKALLASHIEAIDGCDDAETAAMVRDLMARATSRENCYVHRWSEGDLL 114

Query: 255 VWDNRCL 261
 +WDNRC+

Sbjct: 115 LWDNRCV 121

>ref|ZP_02370264.1| taurine dioxygenase [Burkholderia thailandensis TXDOH]
 Length = 310

Score = 73.9 bits (180), Expect = 2e-11, Method: Compositional matrix adjust.
 Identities = 67/272 (24%), Positives = 105/272 (38%), Gaps = 28/272 (10%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
 T L++T +GA V V L+ + AA +H +L F Q LS + FA

Sbjct: 35 TRLKLTRLTPAIGAIVDNVDLSNATGDLRDGIRAALARHQVLFRRDQRLSAVRHRDFAAG 94

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
 FG + +I+ + N D + N WH D T+

Sbjct: 95 FGDLVHVPPIYPSPHDAREIMVLDNAVFD-----LKDNAIWHDTVTFAE 137

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGH 174
 + ++ +A +PA GG T + AAYDAL + +A + +A+H + + G

Sbjct: 138 TPPRASILAARTLPATGGDTLWGSFGAAYDALSDRVKAQLDGLTAQHDFTKSFPLKRFG 197

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL 233
 + + + P+V+ HPETGR +L + I + E L L

Sbjct: 198 TADDRARWEDTRIKHPPV-THPVVRTHPETGRRALFVNEGFTTEINELPEEEGAALLCFL 256

Query: 234 VDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265
 + +W GDV WDNR +H A

Sbjct: 257 FAHQSRPEFTLRWRWQPGDVAFWDNRSSTIHYA 288

>ref|XP_001397270.2| 2,4-dichlorophenoxyacetate alpha-ketoglutarate dioxygenase
 [Aspergillus niger CBS 513.88]
 Length = 344

Score = 73.9 bits (180), Expect = 2e-11, Method: Compositional matrix adjust.
 Identities = 83/312 (26%), Positives = 127/312 (40%), Gaps = 59/312 (18%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
 TL P TLGA GV + + DA L AA ++ +L+F L + + FA++

Sbjct: 19 TLTFRPLHPTLGAECGVDFSKPVPDAVIEQLRAAMAKNGILVFRATGLDDARHTAFARQ 78

Query: 64 FG-----AIERIG-----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHA 110
 G A+ + G G+++ I NV DG R S W +++ G +H

Sbjct: 79 LGPEMVDSAVGKPGVPNRLDPKGELMDIGNVDGDG--RILSTTSWRS--QLLRGTRLFHV 134

Query: 111 DSTYMPVMAQGAVFSAEVV--AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
 D +Y A ++ A +P GG T FAD R AY L E T+ + HSL+ S

Sbjct: 135 DGSYFQRRAGYSLRAHQQLPPRGTTGGATAFADTRTAYADLAEETKNEIQNHVLWHSMLMQS 194

Query: 169 Q-----SKLGHVQQAG-----SAYIGYGMDTTATPLR 195
 + +L ++ G I + +R

Sbjct: 195 RYLGAPENWLIRLLVFSDDLRLRPLMAVGLIARVLEIWWQIVDISLLLVFCYALMR 254

Query: 196 PLV-KVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWA-AGDV 253
 LV ++ PE GRH I G A+S+ +E L+ A Q V W GD+

Sbjct: 255 ILVLRLLPEAATSR---GRH-QLIDGWSRADSKPVIEALMRHASQDKYVLTVDWQNNGDM 310

Query: 254 VVWDNRCLLHRA 265

++WDN C++HR+

Sbjct: 311 IMWDNTCVMHRS 322

>ref|ZP_03569866.1| taurine dioxygenase [Burkholderia multivorans CGD2M]
ref|ZP_03576507.1| taurine dioxygenase [Burkholderia multivorans CGD2]
gb|EEE09850.1| taurine dioxygenase [Burkholderia multivorans CGD2]
gb|EEE15773.1| taurine dioxygenase [Burkholderia multivorans CGD2M]
Length = 315

Score = 73.9 bits (180), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 71/286 (24%), Positives = 115/286 (40%), Gaps = 18/286 (6%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64

+ + P A +GA + GV L L AA+ A L+ ++ F Q L+++Q + F+ +F

Sbjct: 12 IDVIPLSAHIGAEIRGVDLTQPLTSGQIAAIRDALLKWRVIFRFREQFLTHEQHVAFSAQF 71

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124

G +G + A ++ +H A + V WH D T ++

Sbjct: 72 GE-PTVGHPVFGHVEGHPAVYSIAKHRKATRFEGEPVRRPWTGWHTDVTAAVNPPWASIL 130

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184

+P GG T + ++ AY+ L R V H AG+ G

Sbjct: 131 RGVTTIPPYGGDTQWTNLVRAYETLSAPLRGFVDGLRGIHRFT-----PPAGARATG 181

Query: 185 -YGMDDTATPL--RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239

+ PL PLV+VHPETG +L + +I G+ ES+ LE L + +

Sbjct: 182 AFDEAVERRPLVTEHPLVRVHPETGERALVSPSFLKSIVGLTPRESQALLELLWEHVTR 241

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA--EPWDFKLPRVMWHSRLAG 283

+W + WDNR H A + +D R ++ + L G

Sbjct: 242 PEFTIRFKWEPRSIAFWDNRATAHLAPVDIFDLDFDRQLYRTTLVG 287

>ref|ZP_01864402.1| alpha-ketoglutarate-dependent taurine dioxygenase [Erythrobacter
sp. SD-21]
gb|EDL48556.1| alpha-ketoglutarate-dependent taurine dioxygenase [Erythrobacter
sp. SD-21]
Length = 197

Score = 73.9 bits (180), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 60/190 (31%), Positives = 82/190 (43%), Gaps = 13/190 (6%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL- 165

WH D +Y + A G++ A +P GG T +A M AAYD+L + + + A H+

Sbjct: 15 GWHTDHSYDQIPAMGSILVARTLPPKGGDTLWAHMGAAYDSLDEIKQRIEGLEAYHTAD 74

Query: 166 -VYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMD 222

+Y+ + G A G T AT P+V HP TG+ L + G H GM

Sbjct: 75 HIYAPGGVYAKTDQGEALRGQERRTGAT--HPVVVRHPRTGQKLLYVNPFGFTIH-FTGMT 131

Query: 223 AAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLA 282

ES L L D A Q +WA G V +WDNR W + + H+R

Sbjct: 132 REESVPLRLRELYDHAMQPAHQCRVEWAPGTVAIWDNRRTT-----WHYAMNDYHGHAREM 185

Query: 283 GRPETEGAAL 292

R G AL

Sbjct: 186 HRITLSGEAL 195

>gb|AAS64591.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
Length = 119

Score = 73.9 bits (180), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 48/125 (38%), Positives = 61/125 (48%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR 195
T FADMRAAYD L E + + A H + S+ LG + S P+
Sbjct: 1 TEFADMRAAYDDLPEDFKKELQGLRAEHYALNSRFILGTDYSES-----QRNAMPPVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V
Sbjct: 55 WPLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>gb|EDZ70798.1| YLL057Cp-like protein [Saccharomyces cerevisiae AWRI1631]
Length = 398

Score = 73.9 bits (180), Expect = 3e-11, Method: Compositional matrix adjust.
Identities = 67/267 (25%), Positives = 108/267 (40%), Gaps = 17/267 (6%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAK 62
L++ LG + G+ L L DA L Q +++F Q+ ++ D + +
Sbjct: 99 LKVKKITPKLGLLEINGIQLTDLSDAAKDELALLVAQKGVVFRNQNFADGPDYVTEYGR 158

Query: 63 RFGA--IERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
FG I + G +N + T R+ E+ + + WH D +Y
Sbjct: 159 HFGKLHIHQTSQH---PQNNPELHITFRRPDAEEFARVFDSTSSGGWHTDVSYELQPPS 215

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
FS P GG T FAD A+D L + + + S H + S+ + + Q+ G
Sbjct: 216 YTFFSVVEGPDGGGDTLFDATIEAFDRLSKPLQDFL---STLHVHSSKEQAENSQRQG- 271

Query: 181 AYIGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
G T + PLV+VHP + L + R + I + ESE L L +
Sbjct: 272 ---GIKRRAPVTHIHPLVRVHPVLKKKCLYVNRFAFSRKIVELKRQESLNLFLYNLVES 328

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ + +W VV+WDNR + H A
Sbjct: 329 SHDLQLRAKWEPHSVVIWNNRRVQHSA 355

>ref|YP_002233738.1| putative taurine dioxygenase [Burkholderia cenocepacia J2315]
emb|CAR54978.1| putative taurine dioxygenase [Burkholderia cenocepacia J2315]
Length = 315

Score = 73.9 bits (180), Expect = 3e-11, Method: Compositional matrix adjust.
Identities = 70/286 (24%), Positives = 114/286 (39%), Gaps = 10/286 (3%)

Query: 2 AQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A + + P A +GA + GV L L AA+ AA L+ ++ F Q L+++Q + F
Sbjct: 8 AAQPVVDVIPLSAHIGAEIRGVDLTQPLTPQIAAIRAALLKWRVVFREQLTHEQHVAF 67

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
+ +FG +G + A ++ +H A + V WH D T
Sbjct: 68 SAQFGE-PTVGHPVFGHVDGHPAVYSIAKHRKATRFEGEPVRRPWTGWHTDVTAAVNPPV 126

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
++ +P GG T + ++ AY+ L R V H +A

Sbjct: 127 ASILRGVTIPPYGGDTHWTNLVRAYETLSAPLRGFVDTLRGIHRFTPPPGA-----RATG 181

Query: 181 AYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239
A+ PLV+VHPETG +L + +I G+ ES+ LE L + +

Sbjct: 182 AFDDAVERRPLVTEHPLVRVHPETGERALYVSPSFLKSIVGLTPRESQALLELLWEHVTR 241

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA--EPWDFKLPRVMWHSRLAG 283
+W + WDNR H A + +D R ++ + L G

Sbjct: 242 PEFTIRFKWEPRSIAFWDNRATAHLAPVDIFDLDFDRQLYRTTLIG 287

>ref|YP_837646.1| taurine dioxygenase [Burkholderia cenocepacia HI2424]
gb|ABK10753.1| Taurine dioxygenase [Burkholderia cenocepacia HI2424]
Length = 315

Score = 73.9 bits (180), Expect = 3e-11, Method: Compositional matrix adjust.
Identities = 70/286 (24%), Positives = 113/286 (39%), Gaps = 10/286 (3%)

Query: 2 AQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A + + P A +GA + GV L L AA+ AA L+ ++ F Q L+++Q + F
Sbjct: 8 AAQPVDVIPLSAHIGAEIRGVDLTQPLTTPQIAAIRAALLKWRVIFFREQLTHEQHVAF 67

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
+ +FG +G + A ++ +H A + V WH D T
Sbjct: 68 SAQFGE-PTVGHPVFGHVDGHPAVYSIAKHKATRFEGEPVRRPWTGWHTDVTAAVNPPW 126

Query: 121 GAVFSAEVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
++ +P GG T + ++ AY+ L R V H +A
Sbjct: 127 ASILRGVTIPPYGGDTHWTNLVRAYETLSAPLRGFVDTLRGIHRFTPPPGA-----RATG 181

Query: 181 AYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239
A+ PLV+VHPETG +L + I G+ ES+ LE L + +
Sbjct: 182 AFDDAVERRPLVTEHPLVRVHPETGERALYVSPSFLKTIVGLTPRESQALLELLWEHVTR 241

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA--EPWDFKLPRVMWHSRLAG 283
+W + WDNR H A + +D R ++ + L G
Sbjct: 242 PEFTIRFKWEPRSIAFWDNRATAHLAPVDIFDLDFDRQLYRTTLIG 287

>ref|XP_003049797.1| predicted protein [Nectria haematococca mpVI 77-13-4]
gb|EEU44084.1| predicted protein [Nectria haematococca mpVI 77-13-4]
Length = 380

Score = 73.6 bits (179), Expect = 3e-11, Method: Compositional matrix adjust.
Identities = 72/263 (27%), Positives = 105/263 (39%), Gaps = 25/263 (9%)

Query: 14 TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG 73
T+G V GV L+ L AG L + ++ F Q + D I+ A FG G
Sbjct: 103 TIGTEVEGVQLSQLSKAGKDELARYVAERKVVAFRNQDFA-DLPISALEFGGY---FGR 158

Query: 74 DIVAISNVKADGTVRQH-----SPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE 127
+ ++ +G H + K V ++AWH+D TY
Sbjct: 159 HHIHPTSGSPGHPHPEIHLVHRGAGDKSHETFFKTRVSSVAWHSIDITYEQPPGTTFLYL 218

Query: 128 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 187
P GG T FA+ AY+ L A + L+H A HS + + +A + G
Sbjct: 219 DTPDTGGDTLFANTVEAYERLSPAFQKLLHGLKATHSGI-----EQVNASVKKGS 268

Query: 188 DTTATPL---RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRV 243
P+ P+V+ HP TG SL + + I G+ ES+ L L +
Sbjct: 269 IKRREPVVNEHPIVRTHPVTGEKSLFVNPQFTRDIVGLKKEESDAILNFLYEHIAWGADF 328

Query: 244 HAH-QWAAGDVVVWDNRCLLHRA 265

HA +W VVVWDNR + H A
 Sbjct: 329 HARVKWQEKTVVVWDNRSVQHTA 351

>ref|NP_013043.1| Jlp1p [Saccharomyces cerevisiae S288c]
 sp|Q12358.1|JLP1_YEAST RecName: Full=Alpha-ketoglutarate-dependent sulfonate
 dioxygenase
 emb|CAA88000.1| ORF L0572 [Saccharomyces cerevisiae]
 emb|CAA97510.1| unnamed protein product [Saccharomyces cerevisiae]
 gb|AAT92756.1| YLL057C [Saccharomyces cerevisiae]
 gb|EDN59494.1| dnaJ-like protein [Saccharomyces cerevisiae YJM789]
 gb|EEU07677.1| Jlp1p [Saccharomyces cerevisiae JAY291]
 tpg|DAA09267.1| TPA: Fe(II)-dependent sulfonate/alpha-ketoglutarate dioxygenase,
 involved in sulfonate catabolism for use as a sulfur
 source; contains sequence that resembles a J domain
 (typified by the E. coli DnaJ protein); induced by
 sulphur starvation [Saccharomyces cerevisiae S288c]
 gb|EGA85860.1| Jlp1p [Saccharomyces cerevisiae VL3]
 Length = 412

Score = 73.6 bits (179), Expect = 3e-11, Method: Compositional matrix adjust.
 Identities = 67/267 (25%), Positives = 108/267 (40%), Gaps = 17/267 (6%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAK 62
 L++ LG + G+ L L DA L Q +++F Q+ ++ D + +
 Sbjct: 113 LKVKKITPKLGLLEINGIQLTDLSDAAKDELALLVAQKGVVFRNQNFADGPDYVTEYGR 172

Query: 63 RFGA--IERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
 FG I + G +N + T R+ E+ + + WH D +Y
 Sbjct: 173 HFGKLHIHQTSQH---PQNNPELHITFRRPDAEEFARVFDSTSSGGWHTDVSYLEQPPS 229

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
 FS P GG T FAD A+D L + + + S H + S+ + + Q+ G
 Sbjct: 230 YTFFSVVEGPDGGGDTLFDATIEAFDRLSKPLQDFL---STLHVHSSKEQAENSQRQG- 285

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
 G T + PLV+VHP + L + R + I + ESE L L +
 Sbjct: 286 ---GIKRRAPVTHIHLPLVRVHPVLKKKCLYVNRFAFSRKIVELKRQESLNLFLYNLVES 342

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
 + + +W VV+WDNR + H A
 Sbjct: 343 SHDLQLRAKWEPHSVVIWDNRVRVQHS 369

>ref|ZP_06274956.1| Taurine catabolism dioxygenase TauD/TfdA [Streptomyces sp. ACTE]
 gb|EFB64784.1| Taurine catabolism dioxygenase TauD/TfdA [Streptomyces sp. ACTE]
 Length = 293

Score = 73.6 bits (179), Expect = 3e-11, Method: Compositional matrix adjust.
 Identities = 71/269 (26%), Positives = 112/269 (41%), Gaps = 12/269 (4%)

Query: 3 QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWL-QHALLIFPGQHLSNDQQITFA 61
 +T ++I +GA +TGV L D + L + L++ ++++QQI A
 Sbjct: 7 ETEIRINDLTPFIGAEMTGVTYEDLQDPVLWDKVVSTLLHERELVVIRSLDITSEQQIELA 66

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVI--VGNMAWHADSTYMPVMA 119
 R G + ++A + S A+ +DM + VGN WH DS+Y
 Sbjct: 67 SRIGRPKPF-----LMAKYRHPEHAEIMISSNAKNDMAIGVARVGNF-WHQDSSYQKDAP 121

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
 + VP G T +A+ YD L E + + R A H++ Q
 Sbjct: 122 PYTMLHGIDVPGTSGHTLYANAADVDRLPEEWKERIEGRIAVHTVAKRQRISAEHAGLS 181

Query: 180 SAYIGYGMDDTATPLR-PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWA 237
A ++ P++ PLVK P TGR + + + G DA E+E F L++
Sbjct: 182 IAEFKALVEEQYPPVQHPLVKTDPTTGRRYVYGAPEYMERVIGFDANENEEFF-ALLNRL 240

Query: 238 CQAPR-VHAHQWAAGDVVVWVWNRCLLHRA 265
Q P V+ H+W D+VWV H A
Sbjct: 241 IQDPEHVYTHRWTPRDLVWVKELTYHAA 269

>gb|AAS64584.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
Length = 119

Score = 73.6 bits (179), Expect = 3e-11, Method: Compositional matrix adjust.
Identities = 48/125 (38%), Positives = 61/125 (48%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR 195
T FADMRAAYD L E + + A H + S+ LG + S P+
Sbjct: 1 TEFADMRAAYDDLPEDFKKELQGLRAEHYALSSRFILGDTDYSES-----QRNAMPVVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V
Sbjct: 55 WPLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>ref|ZP_04941966.1| Taurine dioxygenase [Burkholderia cenocepacia PC184]
gb|EAY65137.1| Taurine dioxygenase [Burkholderia cenocepacia PC184]
Length = 329

Score = 73.6 bits (179), Expect = 3e-11, Method: Compositional matrix adjust.
Identities = 70/286 (24%), Positives = 113/286 (39%), Gaps = 10/286 (3%)

Query: 2 AQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
A + + P A +GA + GV L L AA+ AA L+ ++ F Q L+++Q + F
Sbjct: 22 AAQPVDVIPLSAHIGAEIRGVDLTQPLTTPQIAAIRAALLKWRVIFFREQLTHEQHVAF 81

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
+ +FG +G + A ++ +H A + V WH D T
Sbjct: 82 SAQFGE-PTVGHPVFGHVDGHPAVYSIAKHKATRFEGEPVRRPWTGWHTDVTAAVNPPW 140

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
++ +P GG T + ++ AY+ L R V H +A
Sbjct: 141 ASILRGVTIPPYGGDTHWTNLVRAYETLSAPLRGFVDTLRGIHRFTPPPGA-----RATG 195

Query: 181 AYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239
A+ PLV+VHPETG +L + I G+ ES+ LE L + +
Sbjct: 196 AFDDAVERRPLVTEHPLVRVHPETGERALYVSPSFLKTIVGLTPRESQALLELLWEHVTR 255

Query: 240 APRVHAHQWAAGDVVVWVWNRCLLHRA--EPWDFKLPRVMWHSRLAG 283
+W + WDNR H A + +D R ++ + L G
Sbjct: 256 PEFTIRFKWEPRSIAFWDNRATAHLAPVDIFDLDFDRQLYRTTLIG 301

>gb|EGA57698.1| J1plp [Saccharomyces cerevisiae FostersB]
Length = 412

Score = 73.6 bits (179), Expect = 3e-11, Method: Compositional matrix adjust.
Identities = 67/267 (25%), Positives = 108/267 (40%), Gaps = 17/267 (6%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAK 62

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      L++      LG + G+ L L DA      L      Q +++F Q+ ++ D      + +
Sbjct: 113 LKVXKITPKLGLLEINGIQLTDLSDAAKDELALLVAQKGVVFRNQNFADGPDYVTEYGR 172

Query: 63 RFGA--IERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
      FG I + G      +N + T R+      E+ +      + WH D +Y
Sbjct: 173 HFGKLHIHQTSQH---PQNNPELHITFRRPDAEEFARVFDSTSSGGWHTDVSYELQPPS 229

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
      FS P GG T FAD A+D L + + + S H + S+ + + Q+ G
Sbjct: 230 YTFFSVVEGPDGGGDTLFDATIEAFDRLSKPLQDFL---STLHVHSSKEQAENSQRQG- 285

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
      G      T + PLV+VHP + L + R + I + ESE L L +
Sbjct: 286 ---GIKRRAPVTHIHPLVRVHPVLKKKCLYVNRFAFSRKIVELKRQESLNLFLYNLVS 342

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
      + + +W VV+WDNR + H A
Sbjct: 343 SHDLQLRAKWEPHSVVIWDNRVRVQHS 369

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>ref|XP_681848.1| hypothetical protein AN8579.2 [Aspergillus nidulans FGSC A4]
gb|EAA60613.1| hypothetical protein AN8579.2 [Aspergillus nidulans FGSC A4]
tpe|CBF78403.1| TPA: conserved hypothetical protein [Aspergillus nidulans FGSC A4]
Length = 429

Score = 73.6 bits (179), Expect = 3e-11, Method: Compositional matrix adjust.
Identities = 81/299 (27%), Positives = 117/299 (39%), Gaps = 39/299 (13%)

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Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITF 60
      T ++TPT G+ +TG+ L++L D L Q +L+F Q ++ DQ + F
Sbjct: 76 TVKRLTPT---TGSEITGIQLSSLTDAKQDLALFAAQRKVLVFRDQDFADLPIDQAVAF 132

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMA---WHADSTYMPV 117
      FG R + + V + D + G + WH+D TY
Sbjct: 133 GGYFG---RHHVHTTAGVPEGYPEVHVVMMDTKNGDFATFLAGKNSTVLWHSQVYDEQ 189

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
      + A +P VGG T FA+ AY L A R +H H V SQ++
Sbjct: 190 PPGMTILYALELPEVGGDTAFANQVEAYKRLSPALRERLHGLKGVHDGV-SQAE----- 242

Query: 178 AGSAYIGYGMDDTTATPL---RPLVKVHPETGRPSLLIGRHHAHAIPGMDAAESERFLEGLV 234
      Y G P+ PLV+ HP TG +L + I GM ES+ L L+
Sbjct: 243 ---PYRAGRLVRREPVIHEHPLVRTHPTVGEKALFVNALTTTRIVGMKKEESDMLLGLFLM 299

Query: 235 DWA--CQAPRVHAHQWAAGDVVVWDNRCLLHRA-----EPWDFKLPRVMWHSR 280
      + C +V +W VV+WDNR + R W LPR+ H R
Sbjct: 300 NHIGHCLEHQVRV-RWEPKTVVIWDNRVTVSLRSLRSTGELVSVGTWHASLPRLSVHLR 357

```

>gb|EAG77784.1| J1plp [Saccharomyces cerevisiae Vin13]
Length = 412

Score = 73.6 bits (179), Expect = 3e-11, Method: Compositional matrix adjust.
Identities = 67/267 (25%), Positives = 108/267 (40%), Gaps = 17/267 (6%)

```

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAK 62
      L++      LG + G+ L L DA      L      Q +++F Q+ ++ D      + +
Sbjct: 113 LKVXKITPKLGLLEINGIQLXDLSDAAKDELALLVAQKGVVFRNQNFADGPDYVTEYGR 172

Query: 63 RFGA--IERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
      FG I + G      +N + T R+      E+ +      + WH D +Y
Sbjct: 173 HFGKLHIHQTSQH---PQNNPELHITFRRPDAEEFARVFDSTSSGGWHTDVSYELQPPS 229

```

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
FS P GG T FAD A+D L + + + S H + S+ + + Q+ G
Sbjct: 230 YTFFSVVEGPDGGGDTLFDATIEAFDRLSKPLQDFL---STLHVIHSSKEQAENSQRQG- 285

Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
G T + PLV+VHP + L + R + I + ESE L L +
Sbjct: 286 ---GIKRRAPVTHIHPLVRVHPVLKKKCLYVNRASF SRKIVELKRQESLNLNLYNLVES 342

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ + +W VV+WDNR + H A
Sbjct: 343 SHDLQLRAKWEPHSVVIWDNRRVQHSA 369

>gb|EDV09264.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Saccharomyces cerevisiae RM11-1a]
Length = 412

Score = 73.6 bits (179), Expect = 3e-11, Method: Compositional matrix adjust.
Identities = 67/267 (25%), Positives = 108/267 (40%), Gaps = 17/267 (6%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAK 62
L++ LG + G+ L L DA L Q +++F Q+ ++ D + +
Sbjct: 113 LKVKKITPKLGLLEINGIQLTDLSDAAKDELALLVAQKGVVFRNQNFADGPDYVTEYGR 172

Query: 63 RFGA--IERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
FG I + G +N + T R+ E+ + + WH D +Y
Sbjct: 173 HFGKLHIHQTSQH---PQNNPELHITFRRPDAEEFARVFDSTSSGGWHTDVSVELQPPS 229

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
FS P GG T FAD A+D L + + + S H + S+ + + Q+ G
Sbjct: 230 YTFFSVVEGPDGGGDTLFDATIEAFDRLSKPLQDFL---STLHVIHSSKEQAENSQRQG- 285

Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
G T + PLV+VHP + L + R + I + ESE L L +
Sbjct: 286 ---GIKRRAPVTHIHPLVRVHPVLKKKCLYVNRASF SRKIVELKRQESLNLNLYNLVES 342

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ + +W VV+WDNR + H A
Sbjct: 343 SHDLQLRAKWEPHSVVIWDNRRVQHSA 369

>gb|ADI34062.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 1HD1]
gb|ADI34066.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 2HD1]
Length = 119

Score = 73.6 bits (179), Expect = 3e-11, Method: Compositional matrix adjust.
Identities = 45/123 (36%), Positives = 61/123 (49%), Gaps = 7/123 (5%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-P 196
F DMRAAYD L E + + A H ++S+ LG + + S P+ P
Sbjct: 2 FCDMRAAYDDLPEDFKKELQGLRAEHYALHSR FILGDTEYSES-----QRNAMPPVSWP 55

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVW 256
L++ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+W
Sbjct: 56 LIRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQPKFVYRHSWKVGDVLMW 115

Query: 257 DNR 259
DNR
Sbjct: 116 DNR 118

>ref|XP_457814.2| DEHA2C03036p [Debaryomyces hansenii CBS767]
emb|CAG85859.2| DEHA2C03036p [Debaryomyces hansenii]

Length = 385

Score = 73.6 bits (179), Expect = 3e-11, Method: Compositional matrix adjust.
Identities = 70/266 (26%), Positives = 111/266 (41%), Gaps = 20/266 (7%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
+ITP LG VTG+ L+ LDD G L Q +++F Q + + FA +G+
Sbjct: 85 RITPK---LGTEVTGIQLSQLDDKGKDELALFVAQRGVVVFREQDFAT-KGPKFATEYGS 140

Query: 67 IERIGGGDIVAISNVKADG-----TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQG 121
G I S D T R+ E+ + + ++ WH+D +Y
Sbjct: 141 --HFGRHLHIPTSGAPKDHPELHITYRRADEGEFSRVFSNRLNSIGWHS DVS YELQPPGT 198

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
F+ P GG T FAD+ AY+ L + + + H L S+ + + + G
Sbjct: 199 TFFTVLQGP D AGGDTNFADVVEAYNRLSPEFQKRL---ANLHVLHTSEDQASNSRTQG-- 253

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQA 240
G + + PL++ HP TG + + R + I + ES+ L L A
Sbjct: 254 --GIERRKPVSNIHPLIRQHPATGDKFIYLRNRPFSRRIVELKEDES DYLLNFLFQHIESA 311

Query: 241 PRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ +W VVVWDNR ++H A
Sbjct: 312 HDLQLRARWEPNSVVVWDNRVRVHSA 337

>gb|EGA61415.1| J1plp [Saccharomyces cerevisiae FostersO]
Length = 399

Score = 73.6 bits (179), Expect = 3e-11, Method: Compositional matrix adjust.
Identities = 67/267 (25%), Positives = 108/267 (40%), Gaps = 17/267 (6%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAK 62
L++ LG + G+ L L DA L Q +++F Q+ ++ D + +
Sbjct: 113 LKVXKITPKLGL EINGIQLTDLSDAAKDELALLVAQKGVVVFERNQNFADXGPDYVTEYGR 172

Query: 63 RFGA--IERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ 120
FG I + G +N + T R+ E+ + + WH D +Y
Sbjct: 173 HFGKLHIHQTS GH---PQNNPELHITFRRPDAEEFARVFDSTSSGGWHTDVSYELQPPS 229

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
FS P GG T FAD A+D L + + + S H + S+ + + Q+ G
Sbjct: 230 YTFFSVVEGPDGGGDTL FADTIEAFDRLSKPLQDFL---STLHVIHSSKEQAENSQRQG- 285

Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
G T + PLV+VHP + L + R + I + ESE L L +
Sbjct: 286 ---GIKRRAPVTHIHPLVRVHPVLKKKCLYVNRAFSRKIVELKRQES ELLNFLYNLVES 342

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ + +W VV+WDNR + H A
Sbjct: 343 SHDLQLRAKWEPHSVVIWDNRVRVHSA 369

>ref|XP_001834709.1| alpha-ketoglutarate catabolism dioxygenase [Coprinopsis cinerea
okayama7#130]
gb|EAU87157.1| alpha-ketoglutarate catabolism dioxygenase [Coprinopsis cinerea
okayama7#130]
Length = 368

Score = 73.6 bits (179), Expect = 4e-11, Method: Compositional matrix adjust.
Identities = 72/267 (26%), Positives = 108/267 (40%), Gaps = 25/267 (9%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRFGAIER-I 70

```

      +G + GV ++ L  G  L      + +L+F Q  +  ++QI A  FG I R
Sbjct: 92 IGTEIQGVQISQLSKEGLDELALLTAERKVLVFRNQDFKDLGPERQIEIASHFGPIHRHP 151

Query: 71 GGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGN-----MAWHADSTYMPVMAQGAVFS 125
      G++          V      P+   D K  +G          +WH+D +Y          F
Sbjct: 152 TSGNVKGFPEFH---VVYRDPH--DHFKEYIGGDRINLTSWHSVDVSEKQPPGTTFFF 205

Query: 126 AEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 185
      P  GG T FA      AY L + + +      HS V  Q++      ++ G
Sbjct: 206 ILDQPETGGDTLFAEQVEAYSRLSDEFKKRLEGLRVVHSAV-RQAEFS--RRIGGPVRRE 262

Query: 186 GMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVH 244
      ++T      P+V+VHP TG  +L I +  A  I G+  ES+  L+ L D  +
Sbjct: 263 PIETE----HPIVRVHPVTGEKALYINQGFARRIVGLKQEESEDFLLKFLFDHIAKGADFQ 318

Query: 245 AH-QWAAGDVVVWDNRCLLHRAEPWDF 270
      +  G VVVWDNR  +H A P DF
Sbjct: 319 IRASYEPGTVVVWDNRVTVHSATP-DF 344

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>ref|ZP_00515418.1| similar to Probable taurine catabolism dioxygenase [Crocospaera
      watsonii WH 8501]
gb|EAM51361.1| similar to Probable taurine catabolism dioxygenase [Crocospaera
      watsonii WH 8501]
      Length = 295

```

Score = 73.6 bits (179), Expect = 4e-11, Method: Compositional matrix adjust.
Identities = 69/280 (24%), Positives = 120/280 (42%), Gaps = 37/280 (13%)

```

Query: 13 ATLGATV-TGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR-FGAIERI 70
      + LG V G +L L +  + L A Q +++ QH+S +  FA++ FG +  +
Sbjct: 14 SRLGLEVLKGCNLIDLTELQRSQKQALWQQGVIVVKNQHISASELEEFARKTFGNL--M 71

Query: 71 GGGDIVAISNVKADGTVRQHS-----PAEWDDMM-KVIVGNMAWHADSTYMPVMAQGAVF 124
      G +  ++  +  Q+S      P  D  + I G  WH D  +P++ +  +
Sbjct: 72 FGSNSFSLDPEISPEIQSQYSAILGNPKGLDRKPPEKIYGARIWHQDKDGVPIIKELEMN 131

Query: 125 SAEVVPVAVGGR-----TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
      + VV  G +          T + D+  AY+ LD +      HQ++      L+Y  +
Sbjct: 132 ALYVVMLYGIVKPEEGENGQPHTTEYLDLVEAYNNLDSS-----HQKALEEILMYQMPVP 186

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIP-GMD--AAESERF 229
      Q          D  + PLV H  TG+  L +G  AIP GM+  E++++
Sbjct: 187 WFWQ-----NLDWDNVPKKVHPLVSTHKVTGKKGLYLGSWNTAIPGMEDKQEEAQY 239

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD 269
      + L +  +  V++H W  GD+V WDN  ++HR  +D
Sbjct: 240 WQDLWNMVLERTPVYSHVWEPGDIVFDWNSQVMHRGTFYD 279

```

```

>ref|ZP_06922104.1| taurine catabolism dioxygenase [Streptomyces sviveus ATCC 29083]
gb|EDY54814.1| taurine catabolism dioxygenase [Streptomyces sviveus ATCC 29083]
      Length = 297

```

Score = 73.2 bits (178), Expect = 4e-11, Method: Compositional matrix adjust.
Identities = 72/253 (28%), Positives = 103/253 (40%), Gaps = 15/253 (5%)

```

Query: 15 LGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG 73
      +GA V GV L AT D +  AL A  H ++F  L N Q  A+ FG +
Sbjct: 12 IGAVVEGVDLTATPDLSTVTALRDALNTHKAIVFDHVDLDNAGQERVARWFGEL----- 65

Query: 74 DIVAISNVKA-DGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAV 132
      A  NV A DGT  +  A  + K      WH D T++  Q  + V

```

Sbjct: 66 -TTAHPNVPATDGT--NVLAVDSETSKA----NEWHTDVTFFVINPPQLTTLRSIVTTPY 118

Query: 133 GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTAT 192
GG T A+ AAY L RAL H+ Y ++ Y + T

Sbjct: 119 GGETLIANAAAAYRDLPAPLRALADTLRVVHTNQYDYARPASTTAQRQEYDRAVFVSTPYE 178

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
P+V+VHP TG L IG A I G+ +++S L L + + + + W+

Sbjct: 179 AEHPVVRVHPLTGERGLFIGGFAKRIVGLPSSDSADLLRILQSYVTRPENILSWTWSNPQ 238

Query: 253 VVVWDNRCLLHRA 265
++++DNR H A

Sbjct: 239 LLIFDNRITQHYA 251

>gb|ABR27328.1| TfdA [uncultured bacterium]
gb|ABR27329.1| TfdA [uncultured bacterium]
gb|ABR27331.1| TfdA [uncultured bacterium]
gb|ABR27332.1| TfdA [uncultured bacterium]
gb|ABR27333.1| TfdA [uncultured bacterium]
gb|ABR27334.1| TfdA [uncultured bacterium]
gb|ABR27335.1| TfdA [uncultured bacterium]
gb|ADI34065.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 1HD6]
gb|ADI34069.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 2HD6]
gb|ADI34072.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 3HD6]
gb|ADI34075.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 10DK.1]
gb|ADI34076.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 10DK.2]
Length = 118

Score = 73.2 bits (178), Expect = 4e-11, Method: Compositional matrix adjust.
Identities = 45/123 (36%), Positives = 61/123 (49%), Gaps = 7/123 (5%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR-P 196
F DMRAAYD L E + + A H ++S+ LG + + S P+ P

Sbjct: 2 FCDMRAAYDDLPEDFKKELQGLRAEHYALHSRIFILGDTEYSES-----QRNAMPPVSWP 55

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVW 256
L++ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+W

Sbjct: 56 LIRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQPKFVYRHSWKVGDVLMW 115

Query: 257 DNR 259
DNR

Sbjct: 116 DNR 118

>gb|ADC33962.1| TfdA-like protein [uncultured bacterium]
Length = 122

Score = 73.2 bits (178), Expect = 4e-11, Method: Compositional matrix adjust.
Identities = 40/127 (31%), Positives = 65/127 (51%), Gaps = 6/127 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPL- 194
T F DM AY+ L A + + A H+L +S+++ + G + P+

Sbjct: 1 TEFCDMYGAYERLSPAWNRIATLRAMHNLDIFSRT- ----RHGEPMTEAQRDVAPPVD 55

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
P+V+ HP+TGR L +G HA + GM+ + +E L A A + H+W G+++

Sbjct: 56 HPIVRTHPDITGRKCLFLGDHAQYVVGMYEDGRALIEELNALAIHADLTYEHRWTPGELL 115

Query: 255 VWDNRCL 261
VWDNRC+

Sbjct: 116 VWDNRCV 122

>gb|ACB30159.1| 2,4-D/alpha-ketoglutarate dioxygenase [Rhodococcus sp. HDN3]
Length = 118

Score = 73.2 bits (178), Expect = 4e-11, Method: Compositional matrix adjust.
Identities = 45/123 (36%), Positives = 60/123 (48%), Gaps = 7/123 (5%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR-P 196
F DMRAAYD L E + + A H ++S+ LG + S P+ P
Sbjct: 2 FCDMRAAYDDLPEDFKKELQGLRAEHYALHSRFLGDTEYCES-----QRNAMPVSWP 55

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVW 256
L++ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+W
Sbjct: 56 LIRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQPKFVYRHSWKVGDVLMV 115

Query: 257 DNR 259
DNR
Sbjct: 116 DNR 118

>ref|XP_660564.1| hypothetical protein AN2960.2 [Aspergillus nidulans FGSC A4]
gb|EAA63531.1| hypothetical protein AN2960.2 [Aspergillus nidulans FGSC A4]
tpe|CBF83665.1| TPA: alpha-ketoglutarate-dependent taurine dioxygenase
(AFU_orthologue; AFUA_3G07960) [Aspergillus nidulans
FGSC A4]
Length = 384

Score = 73.2 bits (178), Expect = 4e-11, Method: Compositional matrix adjust.
Identities = 75/267 (28%), Positives = 110/267 (41%), Gaps = 33/267 (12%)

Query: 14 TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ---HLSNDQQITFAKRFGA--IE 68
T+G+ V+G+ L+ L G L Q ++ F Q HL D+ + F FG I
Sbjct: 107 TIGSEVSGIQLSOLSKEGKDQLALFVAQRKVVAFRDQDFAHLPIDKALEFGGYFGRHHIH 166

Query: 69 RIGGGDI-----VAISNVKADGTVRQHSPAEDWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
+ G + + + AD T D + ++ WH+D T+ V G F
Sbjct: 167 QASGAPRGYPEIHLVHRGADDT-----SGADFLAQHTNSITWHS DVTFE-VQPPGTTF 218

Query: 125 SAEVV-PAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
+ P GG T FADM AY L R +H A HS V+Q ++ +
Sbjct: 219 LYLLDGPTTGGDTLFDMAQAYKRLSPEFRKRLHGLKAVHS-----GVEQVNN-S 268

Query: 184 GYGMDTTATPL--RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239
G P+ P+V+ HP TG +L + + I G ES+ L+ L D
Sbjct: 269 NKGGIARRDPIMTEHPIVRTHPVTGEKALFVNAQFTRYIVGYKKEESDFLLKFLYDHIAL 328

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ + +W G VVVWDNR H A
Sbjct: 329 SQDIQTRVWRP GTVVVVWDNRVACHSA 355

>ref|YP_832515.1| taurine dioxygenase [Arthrobacter sp. FB24]
gb|ABK04415.1| Taurine dioxygenase [Arthrobacter sp. FB24]
Length = 306

Score = 73.2 bits (178), Expect = 5e-11, Method: Compositional matrix adjust.
Identities = 78/295 (26%), Positives = 118/295 (40%), Gaps = 31/295 (10%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIF-PGQHLSNDQQI 58
+ +T L+ G+ +GA + G+ L L A + AA +H L+F L+++ Q+
Sbjct: 4 ITETKLEFAKLGSRIGAEIRGLDLGGDLAETVAQIRAAALNEHKALVFREANILTDEAQV 63

Query: 59 TFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDWDDMMKVIVGNMA---WHADSTYM 115

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      FA  FG +          KA  TV      E  ++ V  N +  WH D T++
Sbjct: 64  KFAGHFGPL-----TKAHP TVASVEGKE--SVLPVDSSENGSANNWHTDVTVF 108

Query: 116  PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS---KL 172
           Q +  +  +PA GG T A  AY L E R      A H+ Y S  L
Sbjct: 109  VNPPQASTLRSIDLPAYGGETLIASSAGAYRDLPEELRNFAADTLWAIHTNDYDYSVPKNL 168

Query: 173  GH--VQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAH--AIPGMDAAESER 228
           H  ++  +  +T      P+V+VHP TG  L IG A  I G+ ES+
Sbjct: 169  EHENAEEERKEFTRLKFETA---HPVVRVHPLTGERGLFIGGFAQRLRIVGLSNTESKD 224

Query: 229  FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
           + L +  +  V  W  +V++DNR  H A      PR +  +AG
Sbjct: 225  IIRLLQAYVTRPENVRVNWEPNQLVLFNDRITQHYAPDNYDQPRKLN RV TIAG 279

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>ref|XP_001834272.1| alpha-ketoglutarate-dependent taurine dioxygenase [Coprinosia cinerea okayama7#130]
gb|EAU87552.1| alpha-ketoglutarate-dependent taurine dioxygenase [Coprinosia cinerea okayama7#130]
Length = 364

Score = 72.8 bits (177), Expect = 5e-11, Method: Compositional matrix adjust.
Identities = 73/270 (27%), Positives = 108/270 (40%), Gaps = 31/270 (11%)

```

Query: 15  LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRFGAIER-I 70
           LG V GV ++ L  G  L  +  ++IF Q  +  ++QI AK FG I+R
Sbjct: 88  LGTEVEGVQISQLSKEGLDELALFVAERKVVIFRNQDFKDLGFERQIEIAKHFGPIQRHP 147

Query: 71  GGGDIVAISNVKADGTVRQHSPAEDDDMMKVI---VGNMAWHADSTYMPVMAQGAVFSA 126
           G++          R +S  +D  +  +  +  AWH+D Y      F
Sbjct: 148  TSGNVKGYPEFHV--VYRDNS---YDYFKEYVTDSRINYTAWHSDVAYEKQPPGTTFFFI 202

Query: 127  EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY---SQSKLGHVQQAGSAY 182
           P+VGG T F      AY+ L +  +  +  HS V      S+ + G V++
Sbjct: 203  LDQPSVGGDTLFVSQVEAYNRLSDEFKKRLEGLKIVHSAVEQAEGSRKRNGPVRREP--- 259

Query: 183  IGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAP 241
           ++T      P+V+VHP TG  +L +      I G  ES+ L L D  +
Sbjct: 260  ----IETE----HPIVRVHPATGEKALYVNPVFGRRIVGFKKEESDALLNFLYDHIARGA 311

Query: 242  RVHAH-QWAAGDVVVWDNRCLLHRAEPWDF 270
           +  G VVVWDNR  H A P DF
Sbjct: 312  DFQIRASYEPGTVVVWDNRVTAHSAIP-DF 340

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>gb|ADC33953.1| TfdA-like protein [uncultured bacterium]
Length = 122

Score = 72.8 bits (177), Expect = 5e-11, Method: Compositional matrix adjust.
Identities = 40/127 (31%), Positives = 64/127 (50%), Gaps = 6/127 (4%)

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Query: 136  TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPL- 194
           T F DM  AY+ L  A +  +  A H+L +S+++  + G  +      P+
Sbjct: 1    TEFCDMYGAYERLSPAWNRIATLRAMHNLDLSRTR-----RHGEPMTEAQRDAVPPVD 55

Query: 195  RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
           P+V+ HP+TGR L +G HA  + GM+  +  +E L  A A  + H W  G+++
Sbjct: 56  HPIVRTHPDTGRKCLFLGDHAQYVVGMYEDGRALIEELNALAIHADLTIEHHWTPGELL 115

Query: 255  VWDNRCL 261
           VWDNRC+
Sbjct: 116  VWDNRCV 122

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>ref|YP_556155.1| putative taurine catabolism dioxygenase TauD/TfdA [Burkholderia xenovorans LB400]
gb|ABE36805.1| Putative taurine catabolism dioxygenase TauD/TfdA [Burkholderia xenovorans LB400]
Length = 321

Score = 72.8 bits (177), Expect = 5e-11, Method: Compositional matrix adjust.
Identities = 64/265 (24%), Positives = 102/265 (38%), Gaps = 18/265 (6%)

Query: 6 LQITPTGATLGATVTGVHL---ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
+ + P +GA V G+ + T+ A L+ + ++ L F +S +
Sbjct: 51 IHVEPYSPVVGARVRGLRINGKETVPAEVRAFLYDSLTRYGFLAFEPGTVSAAEFAYLVD 110

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG E G T+ D +K N WH D + P +
Sbjct: 111 LFGHSEYTGTPYTPVAEESNVNTI-----DSKVKKTRMNFIIWHIDQAFRPEPPRFT 162

Query: 123 VFSAEVVPVAVGGRTCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V + VP GG T F + AAY+ LD L Q S+ +G + A
Sbjct: 163 VLFQKVPFPFGGDTVFTNATAAYELLD----PLFAQYLETLSVAQDVETMGFLTLAYREE 218

Query: 183 IGYGMDTTATP-LR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
P +R PL++VHP+TG+ + + + I G+ S+ L L D
Sbjct: 219 EELARQKARFPWIRTPLIRVHPDTGKKQIYVNELYTQRILGLSRIASQNILGILFDLIKS 278

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHR 264
+ ++W G V++WDNR + HR
Sbjct: 279 PEVLTRYRWEEGSVLIWDNRVVQHR 303

>ref|YP_298736.1| taurine dioxygenase [Ralstonia eutropha JMP134]
gb|AAZ63892.1| Taurine dioxygenase [Ralstonia eutropha JMP134]
Length = 301

Score = 72.8 bits (177), Expect = 5e-11, Method: Compositional matrix adjust.
Identities = 70/307 (22%), Positives = 121/307 (39%), Gaps = 53/307 (17%)

Query: 3 QTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
Q+ +T LGA V + L LDD AAL A ++H +L+F Q ++ Q ++ A
Sbjct: 23 QSAFTLTRISPALGAEVGNIDLVPLDDDTIAALRRALVEHKVLVFRDQDITPSQHVSLA 82

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVG-----NMAWHADST 113
+RFG +E V P + V++G +H+D +
Sbjct: 83 RRFGLE-----VHPAFPHHEEFPELVLLGGDDKKPAMENGYHSDVS 124

Query: 114 YMPVMAQGAVFSAEVVPVAVGGRTCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
+ + + ++ P +GG T + +M AY+ L E + + A H ++ +
Sbjct: 125 WREIPSMASMLRCVQCPEIGGDTVWVNMALEYEKLPEHRKQIEGLFAAHDILPA----- 179

Query: 174 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-----RHAHAIPGMDA 223
G + P+V+ HPE+G L + R +A+ G
Sbjct: 180 ----FGDKMTPEQRKQFPFAIHPVVRTHPESGEKILYVNGAFVTHFLNFRSRNAVVGAFE 235

Query: 224 AESERFLEGLVDWACQAPRVHAHQ----WAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHS 279
+SE+ L+++ + P + +Q W + WDNR H A F R M +
Sbjct: 236 GQSEK--HDLMEYLLRQPAILEYQMLRWRPNTIAFDWNRSTQHYAIQDYFPAVRRMMRA 293

Query: 280 RLAG-RP 285
+ G RP
Sbjct: 294 TIIGDRP 300

>ref|XP_002563150.1| Pc20g06210 [Penicillium chrysogenum Wisconsin 54-1255]
emb|CAP85950.1| Pc20g06210 [Penicillium chrysogenum Wisconsin 54-1255]
Length = 380

Score = 72.8 bits (177), Expect = 5e-11, Method: Compositional matrix adjust.
Identities = 74/273 (27%), Positives = 111/273 (40%), Gaps = 34/273 (12%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKR 63
+ITP +G+ + GV L+ L D G L Q ++ F Q ++ + + +A
Sbjct: 99 EITPF---IGSEIHGVQLSQLSDKGKQDLALYVAQRRVVAFRDQDFASRPIQEVVDYAGY 155

Query: 64 FGA--IERIGGG-----DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
FG I + G +I + D T + +K + WH+D T+
Sbjct: 156 FGRHHIHQTS GAPKGFPEIHLVFRGADDRT-----GETFLKERTNTITWHS DVTFEK 207

Query: 117 VMAQGAVFSAE VVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
P+ GG T FADM AY L R +H A HS ++
Sbjct: 208 QPPGTTFLYVLDGPSTGGDTL FADMVQAYKRLSPGFRERLHGLKAVHS-----GLE 258

Query: 177 QAGSAYIGYGM--DTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGL 233
Q ++ G G+ T P+V+ HP TG +L + + I G ES+ L+ L
Sbjct: 259 QINASLNGGGIARRDPVTSEHPIVRTHPVTGEKALYVNPQFTRYIVGYKKEESDHLKFL 318

Query: 234 VDWAQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
D + + A +W AG VVVDNR H A
Sbjct: 319 YDHIALSQDLQARIRWKAGTVVVDNRNLACHSA 351

>gb|EGD74176.1| hypothetical protein PTSG_06184 [Salpingoeca sp. ATCC 50818]
Length = 285

Score = 72.8 bits (177), Expect = 6e-11, Method: Compositional matrix adjust.
Identities = 66/271 (24%), Positives = 107/271 (39%), Gaps = 47/271 (17%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG- 73
+G + G+ + TL G + A L+++++ P Q L + A+ FGA +
Sbjct: 16 IGHVLEGIDMKTLTPEGAEKVREAVLKYSVVLPKQDLEEDMARIAELFGAPVDLPSEM 75

Query: 74 -----DIVAISNVKADGTV-RQHSPA EWDDMMKVIVGNMAWHADSTY--MPVMAQ 120
+ +SN++ DGT+ + AE+ WH D + P
Sbjct: 76 AFGHQAKSQPRVTVVSNMRPDGTIIPNNKAAEY-----WHQDGNFWVAPREYV 123

Query: 121 GAVFSAE VVPVAVGGRTCFADMRAAYDALDEATR----ALVHQRSARHSLVYSQSKLGHVQ 176
+ +VP GG T FAD A +D R L + AR +S K
Sbjct: 124 MNFLYSVIVPEEGDGTGFADTVLALQQMDPELRKELEGLQIEVDARKIPDFSSLK----- 178

Query: 177 QAGSAYIGYGMTTATP--LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV 234
D P L ++ H E+G SL G I G ES + ++
Sbjct: 179 -----EDDERFPVALHSIIFNHDESGIESLYPGNGNVTIKGTKEESRDIIGRVL 228

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
+ P V+ H+W GD+V+WDN+ +HR+
Sbjct: 229 AHLDREPYVYYHKWTKGDLVLWDNKT CMHRS 259

>ref|ZP_03541596.1| Taurine dioxygenase [Comamonas testosteroni KF-1]
gb|EED65882.1| Taurine dioxygenase [Comamonas testosteroni KF-1]
Length = 280

Score = 72.8 bits (177), Expect = 6e-11, Method: Compositional matrix adjust.
Identities = 67/274 (24%), Positives = 110/274 (40%), Gaps = 30/274 (10%)

Query: 6 LQITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+++ ++GA V+ +HL A+ D + A LQH +L F Q ++ + + FA+
Sbjct: 1 MKVEQLTCSIGAEVSDIHLGDASRDKGLAEIEIRALLQHKVLFRRDQDITRAEHVGFARH 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG +E VA S+ + G V+ + + ++ +H+D + G V
Sbjct: 61 FGDLE----DHPVAGSDPEHPGLVQIYRSEKRENYENT-----YHSDGQWRENPTMGCV 110

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
PAVGG T + +M AY L E + + A+ S+ + G V
Sbjct: 111 LRCIEGPAVGGDTIWVNMAEAYRNLPEDIKQKIDGLKAKSSIEHG---FGAVMPEDKR-- 165

Query: 184 GYGMDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LE 231
+ P+ P+V+ HPETG L + E+ R+ L
Sbjct: 166 -LELGRQHPPEHPVVRTHPETGEKVLYVCSFTTHFANYHTPENVRYGQDKTPGASMLLN 224

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L+ A +W G V +WDNRC H A
Sbjct: 225 YLISQAAPPEYQVRFRWKPGSVAMWDNRCTQHYA 258

>gb|EFW97628.1| alpha-ketoglutarate catabolism dioxygenase [Pichia angusta DL-1]
Length = 398

Score = 72.4 bits (176), Expect = 7e-11, Method: Compositional matrix adjust.
Identities = 73/272 (26%), Positives = 106/272 (38%), Gaps = 19/272 (6%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK--- 62
+Q LG VTGV L+ L L Q +++F Q DQ F K
Sbjct: 82 VQTRKLSPKLGTEVTGVQLSALTTPRQKDDALLVEQRGVVFRDQDFK-DQSFDFIKDWG 140

Query: 63 -RFGAIERIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQG 121
FG + + + T R+ S E + N++WH+D TY G
Sbjct: 141 RHFGPLH-VHPTSGAPLQPEFHITFRRGSKDEARKTFANKLNNISWHSVDVY-ETQPPG 198

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
+ VGG T F D AY+ L + L+ H+ S+ + + +Q G
Sbjct: 199 ITLFGMLQTDVGGDTQFLDTVEAYERLSPTMKKLLDGLKVLHT---SKDQAFNARQQG-- 253

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW--AC 238
G T + PLV+ HP + L + R + I G+ ES+ L L C
Sbjct: 254 --GIERKTPIDSIHPLVRYHPVLKKKCLFVNRGFSRRILGLKEEESQALLNFLFRHLDT 311

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRAE-PWD 269
+ A QW + +WDNR LLH A WD
Sbjct: 312 LDAHARA-QWDERITITWDNRRLHTATLDWD 342

>ref|YP_001237505.1| putative taurine dioxygenase, 2-oxoglutarate-dependent
[Bradyrhizobium sp. BTAi1]
gb|ABQ33599.1| putative taurine dioxygenase, 2-oxoglutarate-dependent
[Bradyrhizobium sp. BTAi1]
Length = 308

Score = 72.4 bits (176), Expect = 7e-11, Method: Compositional matrix adjust.
Identities = 76/292 (26%), Positives = 113/292 (38%), Gaps = 56/292 (19%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ I P +GA + + L L D L+ A +QH ++ F Q LS Q + A+ F
Sbjct: 19 ISIRPYKPLIGAVIENIDLTRPLSDQNKQDLNRALVQHGVIFFRKQALSFAQHVDLARIF 78

Query: 65 G-----AIERIGGGDIVA-ISNVKADGTVRQHSPAEDMMKVIVGNMAWHADST 113
G ++E +++A N K GT WH D +

Query:	14	TLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGG	72
		T+GA + GV L LDD +AAL A L+ +L F Q ++ Q + AKRFG +E	
Sbjct:	31	TIGAEIRGVDLRDLDETYAALRRALLKFKVLFRRDQDITPAQHVAMAKRFGGELE----	86
Query:	73	GDIVAISNVKADGTVRQHSAPAEWDDMMKVIVG-----NMAWHADSTYMPVMAQGAVF	124
		+ P + VI+G +H+D ++ + G++	
Sbjct:	87	-----IHPAFPHHPEHPELVILGRNDTKRGRENLYHSDVSWREIPSMGSML	132
Query:	125	SAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG	184
		P VGG T + +M AAYD L + + + +A H ++ +Q +	
Sbjct:	133	RCVQCPEVGGDTMWINMVAAYDNLPPDDVKTRIAGLNAVHVDVLPFGIAPVPEQHAA----	188
Query:	185	YGMDDTTATPLR-PLVKVHPETGRPSLLIGR-----HAHAIPGMDAAESERF	229
		M P+ P+V+VHPETG L + + + G D +E	

Sbjct: 189 --MRAKFPPEHPVVRVHPETGEKILYVNEAFTTHLSNYGQLTAREYRV-GFDYKLAIED 245

Query: 230 LEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

L + QAP +W + WDNR H A F PR M + + G

Sbjct: 246 LLQYLFRQAQPEYQVRLKWRPNTIAFDNRSCQHYAVQDYFPAPRHMMRATVIG 300

>gb|ADC33960.1| TfdA-like protein [uncultured bacterium]
Length = 121

Score = 72.0 bits (175), Expect = 9e-11, Method: Compositional matrix adjust.
Identities = 44/127 (34%), Positives = 68/127 (53%), Gaps = 7/127 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPL- 194

T F DMR A++AL A +A + +A HS+++S++ G + + + P+

Sbjct: 1 TEFCDMRLAWEALPPADQARLEGLTAYHSIMHSRATYGFDEWSREEQKRF-----PIPI 54

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254

RPLV +H E+GR SLL+ H I GM ES + L A +A +W GD++

Sbjct: 55 RPLVGLHEESGRKSLLLASHVADIAGMARDESAALVRELTARATVTEHCYARRWTQGDLL 114

Query: 255 VWDNRCL 261

+WDNRC+

Sbjct: 115 LWDNRCV 121

>ref|YP_002486908.1| Taurine dioxygenase [Arthrobacter chlorophenolicus A6]

gb|ACL38819.1| Taurine dioxygenase [Arthrobacter chlorophenolicus A6]

Length = 307

Score = 72.0 bits (175), Expect = 9e-11, Method: Compositional matrix adjust.
Identities = 74/295 (25%), Positives = 118/295 (40%), Gaps = 31/295 (10%)

Query: 1 MAQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIF-PGQHLSNDQQI 58

+ +T L+ G+ +GA + G+ L A L A + A H L+F L+++ Q+

Sbjct: 4 VTETKLEFAKLGSRIGAEIRGLELSADLSPGTVAQIREALSVHKALVFREANVLTDEDQV 63

Query: 59 TFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMA---WHADSTYM 115

FA FG + +N + PA ++ V N + WH D T++

Sbjct: 64 RFASHFGPL-----TNAHPTVASVEGKPA---VLPVDSSENGSANNWHTDVTFTV 108

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175

Q + + +P GG T A AY L + R A H+ Y S+ ++

Sbjct: 109 VNPPQASTLRSITLPEYGGETLIASSAGAYRDLPELRFADTLWAIHTNDYDYSRPNL 168

Query: 176 QQAGS-----AYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAH--AIPGMDAAESER 228

+ A + + +T P+V+VHP TG L IG A I G+ ES+

Sbjct: 169 EHANAEEERRKEFTRIHFETA----HPVVRVHPLTGERGLFIGGFAQRLRIVGLSNTESKD 224

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

L L + + V W +V++DNR H A PR + +AG

Sbjct: 225 ILRILQAYITRPENVRVNWEPNQLVLFDNRITQHYAPDNYDGQPRKLN RVTIAG 279

>ref|XP_001525134.1| conserved hypothetical protein [Lodderomyces elongisporus NRRL
YB-4239]

gb|EDK44883.1| conserved hypothetical protein [Lodderomyces elongisporus NRRL
YB-4239]

Length = 388

Score = 72.0 bits (175), Expect = 9e-11, Method: Compositional matrix adjust.
Identities = 71/267 (26%), Positives = 113/267 (42%), Gaps = 20/267 (7%)

Query:	136	TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL-	194
		T F D M A Y + L A + + A H + L + S + + + + G + P +	
Sbjct:	1	TEFCDMYGAYERLSPA WKGR IAGLR A V H N L D F S R T R - - - - R H G E D P M T E A Q R R E R P P V D	55
Query:	195	RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD V V	254
		P + V + H P E T G R + + G H A + I G M D + E L A + H + W + G + +	
Sbjct:	56	HP I V R T H P E T G R K C I F L G D H A E S I O G M D Y E A G R A L I E E L N A L A V H P D L T Y R H R W S P G O L I	115

Query: 255 VWDNRCL 261
+WDNRC+
Sbjct: 116 LWDNRCV 122

>dbj|BAG68904.1| hypothetical protein [Schizosaccharomyces pombe]
Length = 391

Score = 71.6 bits (174), Expect = 1e-10, Method: Compositional matrix adjust.
Identities = 69/276 (25%), Positives = 112/276 (40%), Gaps = 16/276 (5%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGD 74
LG + G+ L+ L+DA L + ++ FP Q + ++ + +G + G
Sbjct: 111 LGTVLYGIQLSKLNDQAQKNEIARYIAERGVVYFPDQEQTLEEFQELGQYYGHSKHKGSNS 170

Query: 75 IVAISNVKADGTVRQHSPA EWDDMMKVIVGN--MAWHADSTYMPVMAQGAVFSAEVVPAV 132
V + +D K N WH+D ++ + F A VP
Sbjct: 171 RPFEDKFAEFQVVYSDFSPYDQHAK---NNSLRYWHSDFEFKQPSAQTFFFKALTVEPQ 227

Query: 133 GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT 192
GG T F AAY+AL + + ++V+S + + ++ DT A
Sbjct: 228 GGDITLFIISGYAAYEALSTPLKKYLEGL----TVVHSGKEQSEYHRRSGQHVRDLGDTNA- 282

Query: 193 PLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAA 250
P+V+ HP TG SL I IPG+ ES+ L+ L + +W +
Sbjct: 283 --HPIVRTHPVTGWKSLFISPGFTYIPGIPRGESDAILDYLYQHIANLSQSTVRIKWT 340

Query: 251 GDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPE 286
V WDNR ++HRA +D LP+ R+A + E
Sbjct: 341 NGVAAWDNRIIVHRA-TYD-HLPQTRHLVRIAAQGE 374

>ref|YP_298943.1| taurine dioxygenase [Ralstonia eutropha JMP134]
gb|AAZ64099.1| Taurine dioxygenase [Ralstonia eutropha JMP134]
Length = 304

Score = 71.6 bits (174), Expect = 1e-10, Method: Compositional matrix adjust.
Identities = 76/299 (25%), Positives = 112/299 (37%), Gaps = 44/299 (14%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
IT + T+GA V G+ LA TLDDA AAL A ++H +L F Q ++ Q + A+RF
Sbjct: 25 FTITRSTPTIGA EVGGIDLAETLDDATVAALRQALVRHKVLFVRDQDITPAQHVQLARRF 84

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVG-----NMAWHADSTYMP 116
G +E V P D V++G +H+D ++
Sbjct: 85 GELE-----VHPVFPHHEDHPELVLLGGSKDMRGRENIIYHSDVSWRE 126

Query: 117 VMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
V + ++ P GG T + DM AY AL +A + + A H ++ G
Sbjct: 127 VPSMASMLRCVECPDTGGDTIWDMDARAYALPDAVKERIDGLYAVHDIM---PGFGARM 183

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI-----GRHAHAIPGMDAAE 225
+ T P+V+ HPE+G L + G A G D
Sbjct: 184 TPEEREVNRKKFPAVT--HPVVRTHPESGEKILYVNEGFVTHLANFGEKAQFRVGFDFRY 241

Query: 226 SERFLEGLVDWACQAPRVHAH-QWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
E L + P +W + WDNR H A F R M + + G
Sbjct: 242 GELDLLQYLFRQA AVPEYQVRLKWRPNTIAFDWNRSTQHYAVQDYFPAVRRMMRATIIG 300

>gb|ADC33949.1| TfdA-like protein [uncultured bacterium]
Length = 129

Score = 71.6 bits (174), Expect = 1e-10, Method: Compositional matrix adjust.
Identities = 48/133 (36%), Positives = 69/133 (51%), Gaps = 11/133 (8%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD-----T 189
T FADM AAY AL + +A R A V++ SKL + + S G D +
Sbjct: 1 TEFADMTAAYQALPDTVKA----RIATLKGAVHASKLKNTRVTVSPRRPDGKDFYERQKS 56

Query: 190 TATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQW 248
+ PLV+ HP TG+ SL + R I G+ E++ L+GL +A V+ H+W
Sbjct: 57 LPDQVWPLVRTHPVTGKKSLLYLSRFTIGIEGLSEVEADEILDGLFAHQIRAEFVYRHRW 116

Query: 249 AAGDVVVWDNRCL 261
GD+V+WDNRC+
Sbjct: 117 QDGDLMWWDNRVCV 129

>gb|ACG80548.1| TfdA [uncultured bacterium]
Length = 117

Score = 71.6 bits (174), Expect = 1e-10, Method: Compositional matrix adjust.
Identities = 46/123 (37%), Positives = 59/123 (47%), Gaps = 7/123 (5%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-P 196
F DMRAAYD L E + + A H + S+ LG + S P+ P
Sbjct: 1 FGDMAAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWP 54

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVW 256
LV+ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+W
Sbjct: 55 LVRTHAGSGRKFLEFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDLMVM 114

Query: 257 DNR 259
DNR
Sbjct: 115 DNR 117

>gb|ADI21798.1| probable taurine catabolism dioxygenase [uncultured nuHF1 cluster
bacterium HF0130_24M16]
gb|ADI17746.1| probable taurine catabolism dioxygenase [uncultured nuHF1 cluster
bacterium HF0130_31E21]
Length = 275

Score = 71.2 bits (173), Expect = 1e-10, Method: Compositional matrix adjust.
Identities = 62/270 (22%), Positives = 107/270 (39%), Gaps = 28/270 (10%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
++I LG V V L+ + + L + +H +L+F Q LS QI FA+ FG
Sbjct: 1 MKIKCINGALGIEVCDVLSNISNQTSEDLLDLYNKHLVLMFRDQKLSPAAQIAFAELFG 60

Query: 66 AIER-----IGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMP 116
+ G ++ + N R +P ++ WH+D ++
Sbjct: 61 QVNPPLRTRPSVDGFPQVLILENQPG----RPGAPNDY-----WHS DISHSE 104

Query: 117 VMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
V + +P G T +M AY+ L R ++ A HS + + + V+
Sbjct: 105 KPPSATVLHSLTIPEGRGDTMLCNMVRAYENLSIYMREMIQGLKALHSGMATLER--SVK 162

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD 235
A A + P+V+ T + ++ + H + ++ E L L
Sbjct: 163 SASDARPIDPSEIKPPRAHPIVRKPEGTNQSAIYVNPHTIGVEHLEVEEGNWILNNLYK 222

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
A + ++ HQW GDV+VWDNR +H A
Sbjct: 223 IATRPENIYRHQWCVGDVLVWDNRRTMHYA 252

>ref|YP_004019220.1| taurine catabolism dioxygenase TauD/TfdA [Frankia sp. Eu11c]
gb|ADP83350.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. Eu11c]
Length = 278

Score = 71.2 bits (173), Expect = 1e-10, Method: Compositional matrix adjust.
Identities = 74/263 (28%), Positives = 116/263 (44%), Gaps = 15/263 (5%)

Query: 22 VHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNV 81
V A DD AAL A ++IF ++ + + + F++ G + G + V
Sbjct: 25 VDRAVADDT-LAALDAG----GVVIFREANVDDAELVAFSRLLEGEVPPKYGKVKGHPEV 79

Query: 82 KADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA-EVVPVAVGGRTCFAD 140
+A R S + +M WH D + + + + +A EV G T FA+
Sbjct: 80 QA--ITRDASKS---NMAAYREATFWWHFDGSTDTLDPDKYTLLTAREVSGDDDDGDTEFAN 134

Query: 141 MRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKV 200
AAYD+L + +A + HS SQ +V S D + PLV
Sbjct: 135 TYAAYDSLTDDEKAELAGLRVVFHSFENSQR---NVYPNPSPEEKAVWDRIPSREHPLV-W 190

Query: 201 HPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNR 260
H +GR SLL+G A + G+ E+ L+ L++ A V H+W GD+V+WDN
Sbjct: 191 HRRSGRRSLLLGGATAGEVGVGAPGEARPLLDRLRLERATAPEFVVRHKWQRGDLVIWDNTG 250

Query: 261 LLHRAEPWDFKLPRVMWHSRLAG 283
+LHRA P+ R+M + + G
Sbjct: 251 MLHRAMPYGEGSSRLMHRTSIVG 273

>ref|YP_552626.1| taurine dioxygenase [Burkholderia xenovorans LB400]
gb|ABE33276.1| Taurine dioxygenase [Burkholderia xenovorans LB400]
Length = 305

Score = 71.2 bits (173), Expect = 1e-10, Method: Compositional matrix adjust.
Identities = 77/297 (25%), Positives = 115/297 (38%), Gaps = 49/297 (16%)

Query: 14 TLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGG 72
T+GA + GV L LDD +AAL A L+ +L F Q ++ Q + AKRFG +E
Sbjct: 30 TIGAEIRGVDLRDPLDDETYAALRRALLKFKVLFRRDQDITPAQHVAVAKRFGGELE---- 85

Query: 73 GDIVAISNVKADGTVRQHSPAEWDDMMKVIVG-----NMAWHADSTYMPVMAQGAVF 124
+ P + VI+G +H+D ++ + + G++
Sbjct: 86 -----IHPAFPHHPEHPELVILGRNDTKRGRENLYHSDVSWREIPSMGSM 131

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
P VGG T + +M AAYD L +A + +A H + Q +
Sbjct: 132 RCVQCPEVGDTMWINMVAAYDNLPGDVKARIAGLNAVHDFLPLFGIAVPKQDQAT---- 187

Query: 185 YGMTTATPLR-PLVKVHPETGRPSLLIGR-----HAHAIPGMDAAESERFL 230
M P+ P+V++HPETG L + G D +E L
Sbjct: 188 --MRAKFPPEHPVVRIPHETGEKILYVNEAFTTHLSNYGQLTATEYRVGFYKLAELDL 245

Query: 231 EGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
+ QAP +W + WDNR H A F PR M + + G RP
Sbjct: 246 LQYLFRQAQPEYQVRLKWRPNTIAFDWNRSCQHYAVQDYFPAPRHMMRATVIGDRP 302

>ref|XP_001903417.1| hypothetical protein [Podospira anserina S mat+]
emb|CAP61192.1| unnamed protein product [Podospira anserina S mat+]
Length = 377

Score = 71.2 bits (173), Expect = 1e-10, Method: Compositional matrix adjust.

Identities = 75/273 (27%), Positives = 108/273 (39%), Gaps = 33/273 (12%)

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Query: 8   ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH---LSNDQQITFAKRF 64
          +T   T+G V G+ L+TL DAG L   + ++ F Q   LS +Q + F F
Sbjct: 94  VTHLTPTIGTEVKGIQLSTLSDAGKDELARFVAERKVVAFRDQDFRDLSIEQALEFGGYF 153

Query: 65  GA--IERIGGG-----DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV 117
          G I   G   +I +   D +V   D   ++AWH+D +Y
Sbjct: 154 GRHHIHPTSGAPEGYPEIHLVHRGAGDNSV-----DKFFANRTSSVAWHSVDVSYEAQ 205

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
          P GG T F +   AY+ L A + +H A HS   H Q
Sbjct: 206 PPGTTFLYIFDKPESGGDTLFFVNAAEAYNRLSPAFQERLHGLKATHS-----AHEQA 257

Query: 178 AGSAYIGYGMDTTATPL---RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGL 233
          SA G G+   P+   P+++ HP TG ++ + + I G+ ES+ L+ L
Sbjct: 258 NASALRG-GI-VRREPVIHEHPPIIRTHPVTGEKAIYVNPQFTRDIVGLKKEESDVLLKFL 315

Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
          D   A +W G VVVWDNR H A
Sbjct: 316 YDHLAYGADFQARVKWEEGTVVVVWDNRVTQHSA 348

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>emb|CBJ18784.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18799.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 71.2 bits (173), Expect = 1e-10, Method: Compositional matrix adjust.
Identities = 42/110 (38%), Positives = 59/110 (53%), Gaps = 5/110 (4%)

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Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
          AAYDALD+AT+A +   HSL+YS+++LG   S +   + L LV+ HP
Sbjct: 1   AAYDALDDATKAEIEDLVCEHSLIYSRAQLGF-----SNFTDEERHSMKPVLHKLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
          TGR SLL+ H AI G   E+ F+ L++ A Q   V+ H+W D
Sbjct: 56  VTGRKSLLSAHIGAIVGWPRPEAMAFIRDLMEHATQPQFVYVHRWTKND 105

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>ref|XP_001387108.1| Fe(II)-dependent sulfonate/alpha-ketoglutarate dioxygenase-like
protein [Scheffersomyces stipitis CBS 6054]
gb|EAZ63085.1| Fe(II)-dependent sulfonate/alpha-ketoglutarate dioxygenase-like
protein [Pichia stipitis CBS 6054]
Length = 385

Score = 71.2 bits (173), Expect = 1e-10, Method: Compositional matrix adjust.
Identities = 76/268 (28%), Positives = 115/268 (42%), Gaps = 16/268 (5%)

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Query: 3   QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQ---IT 59
          Q ++TP LG+ V GV L+ LD AG L   Q ++IF Q +   +
Sbjct: 81  QIVKKVTPK---LGSEVRGVQLSQLDSAGKDELALFVAQRGVVIFRDQDFAAKGPAFAVE 137

Query: 60  FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
          + K FG + I   ++ + T R+ P E++ +   + +H D +Y A
Sbjct: 138 YGKHFGRLH-IHPTSGAPRNHPHELHITYRRADPGEFERVFSNSTNAVQYHTDVSYELQPA 196

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
          FS   P GG T FAD AY+ L A + +   + H L S+ + + G
Sbjct: 197 GITFFSVLEGPESGGDTIFADSVEAYNRLSPAFQKRL---AGLHVLHTSEDQASNSRQGQ 253

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
          G   + + PLV++HP TG SL + R A I + ESE L+ L D
Sbjct: 254 ----GIERRKPVSNIHPLVRIHPVTGAKSLFVNRSFARRIVELKEESESLLKFLYDHF 309

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Query: 239 QAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
Q+ + W VV+WDNR + H A
Sbjct: 310 QSHDLQLRANWEPNTTVIWDNRVHSA 337

>gb|ADC33987.1| TfdA-like protein [uncultured bacterium]
Length = 121

Score = 71.2 bits (173), Expect = 1e-10, Method: Compositional matrix adjust.
Identities = 42/127 (33%), Positives = 61/127 (48%), Gaps = 7/127 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG-MDTTATPL 194
T F DMR AY+AL +A + ARH ++S+ G + A G +D
Sbjct: 1 TEFCDMRLAYEALSSEEQARLAPLKHARHTLHRSKLTGFTDWSEEALSRLGWVD----- 54

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
RPL+ H TGR +L + H + G ES L L + A ++H+W GD +
Sbjct: 55 RPLIGCHEATGRRTLALASHISELSGYSEESAPLLRALTERATAPENCYSHRWREGDFL 114

Query: 255 VWDNRCL 261
+WDNRC+
Sbjct: 115 LWDNRCV 121

>gb|EFQ31073.1| TfdA family Taurine catabolism dioxygenase TauD [Glomerella
graminicola M1.001]
Length = 395

Score = 71.2 bits (173), Expect = 1e-10, Method: Compositional matrix adjust.
Identities = 67/273 (24%), Positives = 113/273 (41%), Gaps = 25/273 (9%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
++T A +G + G+ L L L + +++ F Q LS QQ FG
Sbjct: 85 KVTDLTAHIGTEIEGLQLKDLTTEQKDELALLIAERSVVFVRDQDLSPQQKELGAYFGE 144

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ 120
+E ++ G ++ +S + D + P + G WH D + A
Sbjct: 145 VEVHPQVPQVPG--VLGVSVIWPDLMATERKPN-----FRNPGGASRWHTDLVHERQPAG 197

Query: 121 GAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
+ VP VGG T +A +AY+ L R ++ + A + ++ + + + G
Sbjct: 198 ITHLHNDTVPPVGGDTLWASGYSAYEKLSPDFRKIIDGKYAIYKSAHTYLER-NAPEDGP 256

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
+I PLV+VHP T SL + R + I G+D AES+ L L D +
Sbjct: 257 KHIERA-----HPLVRVHPATKWKSLVNRSYTTQIIGLDKAESDVILNYLFDVYER 308

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFK 271
+ + +W +WDNR +H A WD++
Sbjct: 309 SVDIQVRFKWTPNTSALWDNRITIHNAS-WDYE 340

>gb|ADC34042.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 71.2 bits (173), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 53/210 (25%), Positives = 94/210 (44%), Gaps = 19/210 (9%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM 115
QQI FA+RFG + +A +K +P + +V G + WH+D+TY+
Sbjct: 1 QQIAFAQRFG-----EPMAYPQLKGLPECPLITPVIKLEHERVNFGGV-WHSDTTYL 51

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV---YSQSKL 172
 ++ A +P+ GG T FA+ A++ L E + ++ + ++ S+++
 Sbjct: 52 ERPPTASMLYALEIPSYGGDTLFLANQYLAFETLSEGLKRVLASLAGVNTSTKAEVSKTRE 111

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLE 231
 +++AG+ + P+V+ HPETGR +L + H G ES L+
 Sbjct: 112 DRLREAGAE-----RKALAGIHPVVRTHPETGRRALYVNTGHTARFDGWTEESAPLLD 165

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
 L + +W G + WDNRC+
 Sbjct: 166 YLFRHQVRPEFTCRFRWERSLAFWDNRVCV 195

>ref|XP_003004622.1| alpha-ketoglutarate-dependent sulfonate dioxygenase
 [Verticillium
 albo-atrum VaMs.102]
 gb|EEY19626.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Verticillium
 albo-atrum VaMs.102]
 Length = 384

Score = 71.2 bits (173), Expect = 2e-10, Method: Compositional matrix adjust.
 Identities = 67/272 (24%), Positives = 112/272 (41%), Gaps = 32/272 (11%)

Query: 14 TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG 73
 ++G + GV L+TL L A + ++ F Q L+ D Q+ + +G +++
 Sbjct: 70 SIGTVLEGVQLSTLSLEQLDELAALVTERGVVFFRNQDLTDTGQVKLFEHYGVLDKHPAQ 129

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW-----HADSTYMPVMAQGAVFSAEV 128
 + +V G+ H + I+ W HAD+++ ++ E
 Sbjct: 130 K--DVKHVVIKSTEDH-----REILNYTPWPSGDFHADTSFEINPPSYSLRMEE 178

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDD 188
 PAVGG T + YDAL +A + + A H+ S+L Q S +G+
 Sbjct: 179 HPAVGGDTAWVSQYGLYDALSDAYKRFIDGLHAVHT-----SRL----QYDSIIDLWGVG 229

Query: 189 TTATPL---RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVH 244
 P+ P V+ HP TG +L I + ES++ L+ + + H
 Sbjct: 230 PNRPPIDSHHPAVRTHPVTGLKALNINPGFVTGFAELKKVESDKLLDFFA-YHIHSADDH 288

Query: 245 AH--QWAAGDVVVWDNRCLLHRAEPWDFKLPR 274
 A +W G V +WDNR +HR P + PR
 Sbjct: 289 AVRWKWEVGSVAMWDNRATIHVRVIPGTYDAPR 320

>ref|YP_587951.1| taurine dioxygenase 2-oxoglutarate-dependent [Cupriavidus
 metallidurans CH34]
 gb|ABF12682.1| taurine dioxygenase, 2-oxoglutarate-dependent [Cupriavidus
 metallidurans CH34]
 Length = 295

Score = 71.2 bits (173), Expect = 2e-10, Method: Compositional matrix adjust.
 Identities = 75/302 (24%), Positives = 113/302 (37%), Gaps = 45/302 (14%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 ITP +GA + + L TLDD + AL A ++H +L F Q ++ Q + A+RF
 Sbjct: 16 FSITPVTPVIGAEIGDIDLRETLDPTYQALRQALVRHKVLFVRDQDITPAQHVALARRF 75

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVG-----NMAWHADSTYMP 116
 G +E V P D V++G +H+D ++
 Sbjct: 76 GELE-----VHPVFPHPDPHPELVLLGGNKDTKGRENIYHSDVSWRA 117

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
 V + G++ P +GG T + +M AY L + +A + A H L+ G

Sbjct: 118 VPSMGSMRLRCVECPMGGDITWVNMAQAYAGLPDDVKARIEGLEAVHDLM---PGFGARM 174

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI-----GRHAHAIPGMDAAE 225
A + AT P+V+ HPE+G L + G H G D

Sbjct: 175 SAEERLVNREKFPPAT--HPVVRTHPESGEKILYVNEGFVTHLANYGAGHIQYRVGADFRL 232

Query: 226 SERFLEGLVDWACQAPRVHAH-QWAAGDVVWWDNRCLLHRAEPWDFKLPRVMWHSRLAG- 283
E L + P +W + WDNR H A F R M + + G

Sbjct: 233 GELDLLQYLYRQATVPEYQVRMKWRPNTIAFWDNRSTQHYAVQDYFPAVRRMMRATIIGE 292

Query: 284 RP 285
RP

Sbjct: 293 RP 294

>ref|XP_502948.1| YALI0D17622p [Yarrowia lipolytica]
emb|CAG81140.1| YALI0D17622p [Yarrowia lipolytica]
Length = 379

Score = 71.2 bits (173), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 74/296 (25%), Positives = 122/296 (41%), Gaps = 39/296 (13%)

Query: 5 TLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
+ +TP +G + L ++ DD L + ++ F Q +++DQQ +

Sbjct: 27 SFTVTPK---IGTEFPELQLTSILEDDTLIRDLAVEVSRRGVVFFRNQDITDDQQQFLGQ 83

Query: 63 RFGAI-----ERIGGGDIVAI-SNVKADGTVRQHSPAEWDDMMKVIVG 104
RFG + R G +I+ I K+ + AE D ++ +

Sbjct: 84 RFGELTGKPAESTLHVHPAKDLSPAGKEILEILPEGKSAKELVTRFDAE-DAVVPVTRA 142

Query: 105 NMAWHADSTYMPVMAQGAVFSAEVVPAVGG-RTCFADMRAAYDALDEATRALVHQRSARH 163
+ WH D T+ PV + A+ +P GG T +A AY+ L + L+ + +A H

Sbjct: 143 SRGWHTDITFEPVPSDYAILKLLTIPENGGGDTLWASGYEAYEQLSPHYKELLEKLTALH 202

Query: 164 S-----LVYSQSKLGHVQQAGS-AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HA 215
S +V + + Q G+ A +G + TT P+++ +P TG SL +

Sbjct: 203 SGQFFHQVVKRGDEVYDQPRGNPANVGKLFITT---HPVIRTNPVTGWKSLFVNPGFT 258

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVWWDNRCLLHRAEPWDF 270
I G+ ES L+ L Q H +W DV +WDNR H A +DF

Sbjct: 259 KKIIGLTPDESASLLDLLFRNLSQGHDAHVRFKWNENDVAIWDNRSTFHSAT-FDF 313

>ref|YP_003279809.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
CNB-2]
ref|ZP_07043331.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
S44]
gb|ACY34513.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
CNB-2]
gb|EFI63004.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
S44]
Length = 280

Score = 71.2 bits (173), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 67/274 (24%), Positives = 108/274 (39%), Gaps = 30/274 (10%)

Query: 6 LQITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 63
+++ ++GA V+ +HL A+ D + A LQH +L F Q ++ + + FA+

Sbjct: 1 MKVEQLTCSIGAEVSDIHLGDASRDKGLAEIEIRALLQHKVLFRRDQDITRAEHVGFARH 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG +E VA S+ G V+ + + ++ +H D + G V

Sbjct: 61 FGDLE----DHPVAGSDPDHPGLVQIYRSEKRENYENT-----YHTDGQWRENPTMGCV 110

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
PAVGG T + +M AY L E + + A+ S+ + G V
Sbjct: 111 LRCIEGPAVGGDTIWVNMAEAYRNLPEDIKKKIDGLKAKSSIEHG---FGAVMPPEEKR-- 165

Query: 184 GYGMDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LE 231
+ P+ P+V+ HPETG L + E+ R+ L
Sbjct: 166 -LELGRQHPPVEHPVVRTHPETGEKILYVCSFTTTFANYHTPENVRYGQDKTPGASMLLN 224

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L+ A +W G V +WDNRC H A
Sbjct: 225 YLISQAAIPEYQVRFRWKPGSVAMWDNRCTQHYA 258

>gb|ABR27308.1| TfdA [uncultured bacterium]
gb|ABR27309.1| TfdA [uncultured bacterium]
gb|ABR27310.1| TfdA [uncultured bacterium]
gb|ABR27311.1| TfdA [uncultured bacterium]
gb|ABR27312.1| TfdA [uncultured bacterium]
gb|ABR27313.1| TfdA [uncultured bacterium]
gb|ABR27326.1| TfdA [uncultured bacterium]
gb|ABR27327.1| TfdA [uncultured bacterium]
gb|ABR27330.1| TfdA [uncultured bacterium]
gb|ABR27337.1| TfdA [uncultured bacterium]
gb|ABR27338.1| TfdA [uncultured bacterium]
gb|ABR27339.1| TfdA [uncultured bacterium]
gb|ABR27340.1| TfdA [uncultured bacterium]
gb|ABR27341.1| TfdA [uncultured bacterium]
Length = 118

Score = 71.2 bits (173), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 44/123 (35%), Positives = 62/123 (50%), Gaps = 7/123 (5%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-P 196
F DMRAAYDAL ++ + A H + S+ LG + + P+ P
Sbjct: 2 FCDMRAAYDALPRDLQSELEGLRAEHYALNSRFLLGDTDYSEA-----QRNAMPPVSWP 55

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVW 256
LV+ H +GR L IG HA + G+ AE L L++ A Q V+ H+W GD+V+W
Sbjct: 56 LVRTHAGSGRKFLFIGAHASHVEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGDLMVW 115

Query: 257 DNR 259
DNR
Sbjct: 116 DNR 118

>emb|CBJ18839.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 70.9 bits (172), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 42/111 (37%), Positives = 55/111 (49%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
A YDALD+ TRA + HSL+YS+ LG + Y + L+ LV+ HP
Sbjct: 1 AGYDALDDETRAIEDMVCEHSLMYSRGLGFLD-----YTDEEKEMFKPVLQRLVVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E+ L L + A Q VH H+W D+
Sbjct: 56 VHGRKSLYLSSHAGAIQMSPEARLLLRDLTEHATQREFVHIHKWTVHDL 106

>gb|AAS64592.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
Length = 119

Score = 70.9 bits (172), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 46/125 (36%), Positives = 60/125 (48%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRAAYD L E + + A H + S+ LG + S P+
Sbjct: 1 TEFCDMRAAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
PLV+ H +GR L IG HA I G AE L L++ A + V+ H W GD+V
Sbjct: 55 WPLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATRRKFVYRHSWKVGDLV 114

Query: 255 VWDNR 259
+WDNR
Sbjct: 115 MWDNR 119

>gb|ADC33954.1| TfdA-like protein [uncultured bacterium]
Length = 121

Score = 70.9 bits (172), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 42/127 (33%), Positives = 63/127 (49%), Gaps = 7/127 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMR+AY AL E + L+ A HS+ +S+S + + + P+R
Sbjct: 1 TEFCDMRSAYAALPERLKMLIEDLQAEHSIAHSRSLVD-----PTVLSEAQKAESPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+++P GR +L IG HA I G + L L + + +H W GD++
Sbjct: 55 QRLVRINPINGRKALYIGAHASHIVGWPLEKGRALLAELAEGLTKPEFRLSHAWREGDLI 114

Query: 255 VWDNRCL 261
VWDNRC+
Sbjct: 115 VWDNRCV 121

>gb|ACG80567.1| TfdA [uncultured bacterium]
Length = 119

Score = 70.9 bits (172), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 44/126 (34%), Positives = 63/126 (50%), Gaps = 13/126 (10%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP- 196
FADMRAAYDAL +A V HS+V+S+++G + + + L+P
Sbjct: 3 FADMRAAYDALPPEDKAEVETLVCEHSIVFSRAQIG-----LEIKSEEHSRDLKPV 53

Query: 197 ---LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
LV P GR SL + H I E+ F+ L+ A Q V+AH+W D+
Sbjct: 54 PHRLVVSDFVNGRKSLYLSSHIGGIRDWPVEARAFIRDLIXHATQRQFVYAHEWQVNDL 113

Query: 254 VVWDNR 259
V+WDNR
Sbjct: 114 VMWDNR 119

>gb|ADC33955.1| TfdA-like protein [uncultured bacterium]
Length = 122

Score = 70.9 bits (172), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 41/127 (32%), Positives = 62/127 (48%), Gaps = 6/127 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL- 194
T F DM AY+ L +A + A H+L +S+++ + G + P+

Sbjct: 1 TEFCDMYGAYERLSPEWKARIAPLRVHNLDFSRTTR-----RHGEDPMTAQRRREVPPVD 55

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
P+V+ HPETGR + +G HA I GMD A +E L + H W AG ++

Sbjct: 56 HPIVRTHPETGRKCVFLGDHAEYIVGMDYAAGRALIEELNARIVHPDLTYEHHWCAGQLI 115

Query: 255 VWDNRCL 261
+WDNRC+

Sbjct: 116 LWDNRCV 122

>ref|XP_001263646.1| alpha-ketoglutarate-dependent taurine dioxygenase [Neosartorya
fischeri NRRL 181]
gb|EAW21749.1| alpha-ketoglutarate-dependent taurine dioxygenase [Neosartorya
fischeri NRRL 181]
Length = 383

Score = 70.9 bits (172), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 74/276 (26%), Positives = 110/276 (39%), Gaps = 25/276 (9%)

Query: 1 MAQTTLQITPTGATLGATVTVGVHLATLDDAGFAALHAAWLQHALLIFPGQ---HLSNDQQ 57
+ Q +Q+ T+G+ V GV L+ L G L Q ++ F Q HL ++

Sbjct: 91 LPQGVQVQDNLTPITIGSEVRGVQLSQLTKEGKQDLALYVAQRKVAFRDQDFAHLPIEKA 150

Query: 58 ITFAKRFGA--IERIGGGDI---VAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHAD 111
+ F FG I + G + + + AD S AE+ + + WH+D

Sbjct: 151 LEFGGYFGRHHIHQTSGAPKGYPEIHLVHRGAD----DRSGAEF---LATRTNTVTWHS 203

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
T+ P GG T FADM AY L R +H A HS + +

Sbjct: 204 VTFEKQPPGTTFLLYLLDGPTSGGDTLFDMAQAYRRLSPEFRKRLHGLKAVHSGI---EQ 260

Query: 172 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFL 230
+ + G G T P+V+ HP TG +L + + I G ES+ L

Sbjct: 261 INNSLNRG----GIARREGITSEHPIVRTHPVTGEKALFVNPQFTRYIVGYKKEESDWLL 316

Query: 231 EGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ L D + + +W G VVVWDNR + H A

Sbjct: 317 KFLYDHIALSQDLQTRVRWLPGTVVVVWDNRVVAHSA 352

>ref|XP_001816593.2| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
oryzae RIB40]
Length = 384

Score = 70.9 bits (172), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 72/267 (26%), Positives = 109/267 (40%), Gaps = 29/267 (10%)

Query: 15 LGATVTVGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
+G + G+ L L D L + +++ F Q LS QQ + FG +E

Sbjct: 93 IGTEIVGLQLKDLTDQKDELGLLIAERSVVFFRDQDLSPQQQKALGEYFGEVEVHPQVP 152

Query: 69 RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV 128
++ G V++ T R S + G WH D + A +

Sbjct: 153 QVPGLPGVSVLWLPALQATERAAS-----YRRPGGASRWHTDLVHERQPAGVTHLHND 205

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSA--RHSLVYSQSKLGHVQQAGSAYIGY 186
VP +GG T +A AAY+ L R ++ R+A R + Y K +AG YI

Sbjct: 206 VPTIGGDTLWASGYAAYEKLSPFEFRKIIDGRTAIYRSAHPYLDK---DPEAGPKYIERE 262

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
P+V+VHP TG +L + R I G+D AES+ L L D + +

Sbjct: 263 -----HPIVRVHPATGWKALWVNRAMTDRIVGLDKAESDVILGYLFDVYEKNIDIQV 314

Query: 246 H-QWAAGDVVWDNRCLLHRAEPWDFK 271
+W +WDNR +H A WD++
Sbjct: 315 RFKWTPTSALWDNRITIHNAS-WDYE 340

>ref|XP_001397508.2| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus niger CBS 513.88]
Length = 383

Score = 70.9 bits (172), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 72/276 (26%), Positives = 110/276 (39%), Gaps = 25/276 (9%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ---HLSNDQQ 57
+ + +++ T+G V GV L+ L G L Q ++ F Q HL ++
Sbjct: 93 LPKDKVEVDDITPTIGTEVRGVQLSQLSKEGKDQLALYVAQRKVAFRDQDFAHLPIEKA 152

Query: 58 ITFAKRFGA--IERIGGGDI----VAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHAD 111
+ F FG I + G + + + AD S AE+ + + WH+D
Sbjct: 153 LEFGGYFGRHHIHQTSGAPKGFPEIHLVHRGAD----DRSGAEF---LSQRTNTITWHS 205

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
T+ P+ GG T FADM AY L R +H A HS + +
Sbjct: 206 VTFEKQPPGTTFLYILDGPSSGGDTLFDMAQAYRRLSPEFRKRLHGLKAVHSGI---EQ 262

Query: 172 LGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFL 230
+ + G G T P+V+ HP TG +L + + I G ES+ L
Sbjct: 263 VNNSLNKG----GIARRDPITSEHPIVRTHPVTGEKALFVNPQFTRYIVGYKKEESDYLL 318

Query: 231 EGLVDWACQAPRVHAH-QWAAGDVVWDNRCLLHRA 265
+ L D + + +W G VVWDNR + H A
Sbjct: 319 KFLYDHIALSQDLQTRVRWRPQTVVWDNRVVTHTSA 354

>ref|XP_716238.1| potential taurine catabolic dioxygenase [Candida albicans SC5314]
gb|EAK97239.1| potential taurine catabolic dioxygenase [Candida albicans SC5314]
gb|EEQ43867.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Candida albicans WO-1]
Length = 385

Score = 70.9 bits (172), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 69/277 (24%), Positives = 115/277 (41%), Gaps = 22/277 (7%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRFGAIER-I 70
LG+ +TG+ L+ L DA L + +++F Q + + FA+ FG + +
Sbjct: 91 LGSVITGIQLSQLSDAAKNDLSRFVAERGTVVFRDQDFNQGGPQAAVEFAQYFGPLYKHA 150

Query: 71 GGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV 130
G + R S E D + +++WH+D +Y Q +FS +P
Sbjct: 151 TSGSPEGFPELHV--CFRGASQDEIDSFSDRTNSISWHSDCSYSLNALQLTLFSLQLP 208

Query: 131 AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTT 190
GG T FA+ AY+ L A + + HS V+QA + G+ T
Sbjct: 209 DSGGDTLFANSVEAYNRLSPAMKERLEGLHVLHS-----SVEQAANNKSAGGI-TR 258

Query: 191 ATP---LRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAPRVHAH 246
P + PLV+V+P T+ L + + I + ES+ L L D +A +
Sbjct: 259 REPEANIHLVRVNPVTKQKHLVYNKEFGRRIVELKEDESDYLLSFLYDHIEKAQDLQIR 318

Query: 247 -QWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLA 282
W VV+W+N +H + DF P + R++
Sbjct: 319 VTWEENTVVLWNNSTTIH-SPCVDFDEPEIRHAYRIS 354

>ref|XP_716155.1| potential taurine catabolic dioxygenase [Candida albicans SC5314]
gb|EAK97152.1| potential taurine catabolic dioxygenase [Candida albicans SC5314]
Length = 385

Score = 70.9 bits (172), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 69/277 (24%), Positives = 115/277 (41%), Gaps = 22/277 (7%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRFGAIER-I 70
LG+ +TG+ L+ L DA L + +++F Q + + FA+ FG + +
Sbjct: 91 LGSVITGIQLSQLSDAAKNDLSRFVAERGVVFRDQDFNQGGPQAAVEFAQYFGPLYKHA 150

Query: 71 GGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVP 130
G + R S E D + +++WH+D +Y Q +FS +P
Sbjct: 151 TSGSPEGFPELHV--CFRGASQDEIDSVFSDRTNSISWHSDCSYSLNALQLTLFSCQLP 208

Query: 131 AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTT 190
GG T FA+ AY+ L A + + HS V+QA + G+ T
Sbjct: 209 DSGGDTLTFANSVEAYNRLSPAMKERLEGLHVLHS-----SVEQAANNKSAGGI-TR 258

Query: 191 ATP---LRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAPRVHAH 246
P + PLV+V+P T + L + + I + ES+ L L D +A +
Sbjct: 259 REPEANIHLPLVRVNPVTKQKHYLYLNKEFGRRIVELKEDESDYLLSFLYDHIEKAQDLQIR 318

Query: 247 -QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLA 282
W VV+W+N +H + DF P + R++
Sbjct: 319 VTWEENTVVLWNNSTTIH-SPCVDFDEPEIRHAYRIS 354

>emb|CAY81185.1| J1plp [Saccharomyces cerevisiae EC1118]
Length = 412

Score = 70.5 bits (171), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 66/267 (24%), Positives = 107/267 (40%), Gaps = 17/267 (6%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAK 62
L++ LG + + L L DA L Q +++F Q+ ++ D + +
Sbjct: 113 LKVKKITPKLGLLEINRIQLTDLSDAAKDELALLVAQKGVVFRNQNFADGPDYVTEYGR 172

Query: 63 RFGA--IERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
FG I + G +N + T R+ E+ + + WH D +Y
Sbjct: 173 HFGKLHIHQTSQH---PQNNPELHITFRRPDAEEFARVFDSTSSGGWHTDVSYELQPPS 229

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
FS P GG T FAD A+D L + + + S H + S+ + + Q+ G
Sbjct: 230 YTFFSVVEGPDGGGDTLFDATIEAFDRLSKPLQDFL---STLHVIHSSKEQAENSQRQG- 285

Query: 181 AYIGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
G T + PLV+VHP + L + R + I + ESE L L +
Sbjct: 286 ---GIKRRAPVTHIHLPLRVHPVLKKKCLYVNRFAFSRKIVELKRQESLNLFLYNLVS 342

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ + +W VV+WDNR + H A
Sbjct: 343 SHDLQLRAKWEPHSVVIWDNRVQHSA 369

>ref|XP_775060.1| hypothetical protein CNBE5360 [Cryptococcus neoformans var.
neoformans B-3501A]
gb|EAL20413.1| hypothetical protein CNBE5360 [Cryptococcus neoformans var.
neoformans B-3501A]
Length = 368

Score = 70.5 bits (171), Expect = 3e-10, Method: Compositional matrix adjust.

Identities = 77/275 (28%), Positives = 111/275 (40%), Gaps = 33/275 (12%)

```
Query: 4   TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG-----QHLSND 55
          T +ITP   +G VTG+ LA+LD AG  L   + ++ F   + S +
Sbjct: 77  TVEEITPF---IGVKVTGLDLASLDKAGQDQLALLAARKGIVFFASNDKVKQTYRDTSM 133

Query: 56  QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM 115
          +++ A+ +           +I + K + TVR+H   W + +   N WH D T
Sbjct: 134 RKLEMARYYVQPRPPTSTEISVVYQDKVN-TVRKHW---WPNRLT----NAIWHIDQT-Q 184

Query: 116  PVMAQGAVFSAEV--VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
          G F +   P+ GG T   + AY+ L   + V   A HS   +K
Sbjct: 185 ERQPPGITFFCCMQHDAPS--GGDTLVGSLVEAYNRLSPKMKEFVCGLKAVHSSAVMSAKA 243

Query: 173  GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLE 231
          V           G           L PLV VHP TG  SL I           I G+   ES+ L+
Sbjct: 244 ARVG-----GASRRNEIESLHPLVTVHPATGSKSLYINPERMTYIEGLRNEESDNMLK 296

Query: 232  GLVDWACQAPRVHA-HQWAAGDVVVWDNRCLLHRA 265
          L D           HA ++W+ GDV VWD R ++H A
Sbjct: 297 FLSDHVKLGADFHARYKWSEGDVCVWDQRVIIHSA 331
```

```
>ref|YP_002007493.1| alpha-ketoglutarate-dependent taurine dioxygenase,
      2-aminoethanesulfonate dioxygenase [Cupriavidus
      taiwanensis LMG 19424]
emb|CAQ71436.1| Alpha-ketoglutarate-dependent taurine dioxygenase,
      2-aminoethanesulfonate dioxygenase [Cupriavidus
      taiwanensis LMG 19424]
Length = 280
```

Score = 70.5 bits (171), Expect = 3e-10, Method: Compositional matrix adjust.
Identities = 68/291 (23%), Positives = 114/291 (39%), Gaps = 28/291 (9%)

```
Query: 6   LQITPTGATLGATVTGVHLATLDDAGFAA--LHAAWLQHALLIFPGQHLSNDQQITFAKR 63
          +++   ++GA ++GV LA           + + L+H +L  GQ +S   + FA+R
Sbjct: 1   MRVQQLTCSIGAEISGVSLADAARDAALFAEIRSLLEHKVLFRLGQEISRADHVAFARR 60

Query: 64  FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
          FG +E           VA S+   G V+ +   + ++           ++H D ++   G V
Sbjct: 61  FGELE----DHPVAGSDPDHPGLVQIYRS DKRENYEN-----SYHTDGSWRECPMGCV 110

Query: 124  FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
          P VGG T + +M AAY+ L E   + +   A+H + +S   +
Sbjct: 111 LRCIESPPVGGDTIIVNMGAAYEHLPEEIKQRIAGLRKXGIEHSFGAAMSPENRAKLAA 170

Query: 184  GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LEG 232
          Y           P+V+ HPETG  L +   +           E+ R+           L
Sbjct: 171 QYPAVE-----HPVVRTHPETGEKVLYVCGFSTHFVNFTPENVRYGQDKTPGASHLLNY 225

Query: 233  LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
          L+ A           +W   V +WDNRC H A   + PR M   + + G
Sbjct: 226 LISQAAIPEYQVRFRWPNSVAIWDNRCTQHYAVQDYWPAPRKMERAAIIG 276
```

```
>gb|ADC33948.1| TfdA-like protein [uncultured bacterium]
Length = 123
```

Score = 70.5 bits (171), Expect = 3e-10, Method: Compositional matrix adjust.
Identities = 47/128 (36%), Positives = 61/128 (47%), Gaps = 11/128 (8%)

```
Query: 138  FADMRAAYDALDEATRALVHQRSARHSLVYSQSK---LGHVQQAGSAYIGYGMDTTATPL 194
          F DM AAYDAL +A +   +   +H   Y ++   LG           +G G   P
```


Sbjct: 3 FCDMYAAYDALPDALKKQISGATIKHDTAYDTNRKLRLG-ATAVDDPRLGSG-----PD 55

Query: 195 RPLVKVHPETGRPSLLIGRHA-HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P+V HP+TG SL +GR H I G ES L+ L A Q H W GDV

Sbjct: 56 HPIVSTHPDTGCNSLFLGRPRPHYINGCTPEESAALLDKLWAHATQPCFRITHTWRQGDV 115

Query: 254 VVWDNRCL 261
V+WDNRC+

Sbjct: 116 VMWDNRCV 123

>emb|CBJ18844.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 70.5 bits (171), Expect = 3e-10, Method: Compositional matrix adjust.
Identities = 42/110 (38%), Positives = 59/110 (53%), Gaps = 5/110 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHP 202
AAYDALD+AT+A + HSL+YS+++LG S + + L LV+ HP

Sbjct: 1 AAYDALDDATKAEIEDLVCEHSLIYSRAQLG-----FSNFTDEERHSMRPVLHKLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
TGR SLL+ H AI G E+ F+ L++ A Q V+ H+W D

Sbjct: 56 VTGRKSLLSAHIGAIVGWPCPEAMAFIRDLMEHATQPQFVYVHRWTKHD 105

>gb|ADC34021.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 70.5 bits (171), Expect = 3e-10, Method: Compositional matrix adjust.
Identities = 58/211 (27%), Positives = 92/211 (43%), Gaps = 21/211 (9%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
QQI FA++FG + + +K +P + + G + WH+D+TY+

Sbjct: 1 QQIAFARKFG-----EPIEYPQLKGLPESPLITPVVLEHERNNFGGI-WHSDTTYL 51

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATR----ALVHQRSARHSLVYSQSK 171
G++ A VP GG T FA+ AYD L + + L+ S+ + V ++++

Sbjct: 52 AEPPMGSMMLLAREVPPHGGDTMFANQYLAJDGLSDGLKKALDGLIGVSSSAKADV-TKTR 110

Query: 172 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL 230
++ AG+ T P+V+ HPETGR +L H I G ES L

Sbjct: 111 EDRMKAAGAEL-----KVLTAEHPIVRTHPETGRKALYTSDAHTAHIKGWTEKESLPL 164

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
L D + +W G + WDNRC+

Sbjct: 165 RFLWDHQTRPEFTCRFRWQVGSALAFWDNRCV 195

>emb|CBJ18740.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 70.5 bits (171), Expect = 3e-10, Method: Compositional matrix adjust.
Identities = 43/111 (38%), Positives = 54/111 (48%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHP 202
AAYDALD+ T+A + HSL+YS+ LG V Y L+ LV+ HP

Sbjct: 1 AAYDALDDETKAEIEDLVCEHSLMYSRGLGFVD-----YTDEEKQMFKPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E L L + A Q V+ HQW D+

Sbjct: 56 VHGRKSLYLSHAGAIRGMSVPEGRLLLRDLTEHATQPEFVYVHQWTVHDL 106

```
>gb|ABR27316.1| TfdA [uncultured bacterium]
gb|ABR27317.1| TfdA [uncultured bacterium]
gb|ABR27318.1| TfdA [uncultured bacterium]
gb|ABR27319.1| TfdA [uncultured bacterium]
gb|ABR27320.1| TfdA [uncultured bacterium]
gb|ABR27321.1| TfdA [uncultured bacterium]
gb|ABR27322.1| TfdA [uncultured bacterium]
Length = 118
```

Score = 70.1 bits (170), Expect = 3e-10, Method: Compositional matrix adjust.
Identities = 45/123 (36%), Positives = 61/123 (49%), Gaps = 7/123 (5%)

```
Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR-P 196
          F DMRAAYDAL ++ + A H + S+ LG + + P+ P
Sbjct: 2 FCDMRAAYDALPRDLQSELEGLRAEHYALNSRFLLGDTDYSEA-----QRNAMPPVSWP 55

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVW 256
          LV+ H +GR L IG HA I G AE L L++ A Q V+ H+W GD+V+W
Sbjct: 56 LVRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQREFVYRHRWNVGDVLMW 115

Query: 257 DNR 259
          DNR
Sbjct: 116 DNR 118
```

```
>ref|ZP_07280249.1| taurine catabolism dioxygenase [Streptomyces sp. AA4]
gb|EFL08618.1| taurine catabolism dioxygenase [Streptomyces sp. AA4]
Length = 293
```

Score = 70.1 bits (170), Expect = 3e-10, Method: Compositional matrix adjust.
Identities = 72/273 (26%), Positives = 102/273 (37%), Gaps = 34/273 (12%)

```
Query: 13 ATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERI-- 70
          A G V G T FA L ++ + + Q LS D+ + KR G
Sbjct: 9 AKFGVVVEGFDATTATSEEFALKRQVYENKIAVLKDKQLSPDEFVEMGKRMGEPSSYYE 68

Query: 71 -----GGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
          I SNV DG + V WHAD +M +
Sbjct: 69 PVYHHPDNPLIFVSSNVPKDGK-----QIGVPKTGKFWHADYQFMDKPYGLTLI 117

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVYSQSKLGHVQQAGSAY 182
          +VVP T F DM AAY+ L E+ + V A HS + + G
Sbjct: 118 YPQVVPQKNRGTYFIDMGAAYEGLPESLKQEVADAVAVHSPRRFFKIRPSDVYRPVGELL 177

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE-----RFLE--G 232
          T R +VK HP TG L + G++ A+ E R L+ G
Sbjct: 178 AEIEERTPEVRHRAVVK-HPVTGESVLYVSEGFTT--GLEDAKGEEIRGDLLSRLLDAVG 234

Query: 233 LVDWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
          +D + +H +++ GD++VWDNR L+HRA
Sbjct: 235 QLDTTFEHENIHLQRFSEGDMLVWDNRSLVHRA 267
```

```
>ref|ZP_01461615.1| putative dioxygenase [Stigmatella aurantiaca DW4/3-1]
gb|EAU67592.1| putative dioxygenase [Stigmatella aurantiaca DW4/3-1]
Length = 290
```

Score = 70.1 bits (170), Expect = 3e-10, Method: Compositional matrix adjust.
Identities = 67/278 (24%), Positives = 110/278 (39%), Gaps = 26/278 (9%)

```
Query: 1 MAQTTLQI-TPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
          M T ++I +P+ +GA ++ + L + + +H L+IF GQ S ++ I
```

Sbjct: 1 MRLTRMEIHSPSQGRIGAEISQLDLRAVTAQDATRIRQTIYEHKLVIFHGQSPSPPEEYIA 60

Query: 60 FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA--WH 109
FA++ G + ++ SNV DG KV V WH

Sbjct: 61 FARKIGRPQVYFQHNYHHPQHPELFVSSNVLEDGK-----KVG VAGTGRYWH 107

Query: 110 ADSTYMPVMAQGAVFSAE VVPVAVGGRTCFADMRAAYDALDEATRALVH-QRSARHSLVYS 168
D + + +V+P T F DM+ Y+A+ RA V R+ +

Sbjct: 108 TDYQFFQEPLPLVMVYPQVLPKAKRETYFIDMQRVYEAMPAELRAYVEGHRAIQEGKWRY 167

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESE 227
+ V +A + P V HP TGR SL + I G+ E+

Sbjct: 168 KITPEDVDKALVDILA AVEKQVPAITHPAVIEHPLTGRKSLYLSSGFTTGIEGLTHEENR 227

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ L + Q V + + GD+++W+NR LLH+A

Sbjct: 228 AAMAKLFAFIEQEAHVQTYSYQPGDILLWENRALLHKA 265

>gb|ABR27323.1| TfdA [uncultured bacterium]
gb|ABR27324.1| TfdA [uncultured bacterium]
gb|ABR27325.1| TfdA [uncultured bacterium]
Length = 118

Score = 70.1 bits (170), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 45/123 (36%), Positives = 61/123 (49%), Gaps = 7/123 (5%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-P 196
F DMRAAYDAL ++ + A H + S+ LG + + P+ P

Sbjct: 2 FCDMRAAYDALPRDLQSELEGLRAEHYALNSRFLLGDTDYSEA-----QRNAMPVSWP 55

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVW 256
LV+ H +GR L IG HA I G AE L L++ A Q V+ H+W GD+V+W

Sbjct: 56 LVRTHAGSGRKF LFIGAHASHIEGRPVAEGRMLLAELLEHATQRQFVYRHRWQVGD LVMW 115

Query: 257 DNR 259
DNR

Sbjct: 116 DNR 118

>emb|CBJ18751.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 70.1 bits (170), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 43/111 (38%), Positives = 54/111 (48%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
AAYDALD+ T+A + HSL+YS+ LG V Y L+ LV+ HP

Sbjct: 1 AAYDALDDETKAEIEDLVCEHSLMYSRGSLGFVD-----YTDEEKQMFKPV LQRLV RTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E L L + A Q V+ HQW D+

Sbjct: 56 VHGRKSLYLSSHAGAIRGMSMEGRLLLLRDLTEHATQPEFVYVHQWTVHDL 106

>gb|ADC34029.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 70.1 bits (170), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 57/211 (27%), Positives = 93/211 (44%), Gaps = 21/211 (9%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM 115
QQI FA++FG + + +K + +P + + G + WH+D+TY+

Sbjct: 1 QQIAFARKFG-----EPIEYPQLKGLPESQLITPVVKLEHERNNFGGI-WHSDTTYL 51

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR----ALVHQRSARHSLVYSQSK 171
G++ A VP GG T FA+ AY+ L + + LV S+ + V ++++

Sbjct: 52 AEPPMGSMMLLAREVPPFGGDTMFANQYLAIEGLSDGLKKTLDGLVGVSSSAKADV-TKTR 110

Query: 172 LGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL 230
++ AG+ T P+V+ HPETGR +L H I G ES L

Sbjct: 111 EDRMKAAGAE-----KMLTAEHPIVRTHPETGRKALYTSDAHTAHIKGWTEKESLPL 164

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
L + + +W G + WDNRC+

Sbjct: 165 RFLWEHQTRPEFTCRFRWQVGSALAFWDNRVCV 195

>gb|ADC33947.1| TfdA-like protein [uncultured bacterium]
Length = 121

Score = 70.1 bits (170), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 42/127 (33%), Positives = 61/127 (48%), Gaps = 7/127 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DMR+AY AL E + L+ A HS+V+S+ + + P+R

Sbjct: 1 TEFCDMRSAAYAALPERLKVLIEDLQAEHSIVHSRGLVD-----PTVLTEAQAETPPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+++P GR +L IG HA I G + L L + +H W GD++

Sbjct: 55 QRLVRINPINGRKALYIGAHASHIVGWPLEKGRALLAELTELGTGPEFCLSHAWREGDLI 114

Query: 255 VWDNRCL 261
VWDNRC+

Sbjct: 115 VWDNRVCV 121

>ref|XP_003000766.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Verticillium
albo-atrum VaMs.102]
gb|EEY23151.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Verticillium
albo-atrum VaMs.102]
Length = 378

Score = 70.1 bits (170), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 75/273 (27%), Positives = 110/273 (40%), Gaps = 25/273 (9%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T Q+ T+G+ V G+ L++L AG L Q ++ F Q + D I A

Sbjct: 91 TGTQVNHLTPTIGSEVKGIQLSSLTPAGRDELALFVAQRKVVAFRAQDFA-DLPIGEALD 149

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-----SPAEWDDMMKVIVGNMAWHADSTYMPV 117
FG G + ++ +G H + + ++AWH+D +Y

Sbjct: 150 FGGY--FGRHHIHPTSGSPEGFPEVHLVHRGANDRSAESFFATRTSSVAWHSVSYEQQ 206

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
VPAVGG T FAD AY L R +H A HS G Q

Sbjct: 207 PPGTTFLYILDVPAVGGDTLFDAGVEAYRRLSPLFRERLHGLKAVHS-----GFEQV 258

Query: 178 AGSAYIGYGMDTTATPL---RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGL 233
S + G P+ P+V+ HP TG ++ + + I G+ ES+ L+ L

Sbjct: 259 EAS--VRKGSIKRREPVA NEHPIVRTHPATGEKAIYVNPQFTRDIVGLKKEESDALLKFL 316

Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ + + A +W AG VVVWDNR H A

Sbjct: 317 YEHIAWSADIQARVKWEAGTVVVWDNRVTVQHS 349

>ref|XP_003192522.1| taurine dioxygenase [Cryptococcus gattii WM276]
gb|ADV20735.1| Taurine dioxygenase, putative [Cryptococcus gattii WM276]
Length = 372

Score = 69.7 bits (169), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 49/181 (27%), Positives = 78/181 (43%), Gaps = 9/181 (4%)

Query: 96 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL 155
D ++K +G+ WH+D T+ P + A +P GG T +A AYD L A R
Sbjct: 151 DTVLKRPLGSSSLWHS DVT FEPHPSDYATLQIRTL PESGGDTLWASAYEAYDRLSPAYRNF 210

Query: 156 VHQRSARH----SLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLI 211
+ +A H L + V++ A G +A + P+++ +P TG L +
Sbjct: 211 LENLTATHIGQNFLNIVRESNATVREPRGAPENVGQHLSA--VHPVIRTNPVTGWKGLFV 268

Query: 212 GR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWD 269
R I + ES+ LE L + + +W ++ +WDNRC H A WD
Sbjct: 269 NRVFTKKINELTQQESDSLLEFLFEHVTGNHDIQVRFRWEENNLAIWDNRCTFH-AATWD 327

Query: 270 F 270

Sbjct: 328 L 328

>ref|XP_002422326.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Candida dubliniensis CD36]
emb|CAX40332.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Candida dubliniensis CD36]
Length = 385

Score = 69.7 bits (169), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 66/274 (24%), Positives = 113/274 (41%), Gaps = 16/274 (5%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRFGAIER-I 70
LG+ +TG+ L+ L DA L + +++F Q + + FA+ FG + +
Sbjct: 91 LGSVITGIQLSQLSDAAKNDLSRFVAERG VVFRNQDFNQGGPQAAVDFARYFGPLYKHA 150

Query: 71 GGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV 130
G + R S E D + +++WH+D +Y Q +FS +P
Sbjct: 151 TSGSPEGFP E LHV--CFRGASQEEIDSVFADRTNSISWHS DCSYSLNALQLTLF SCLQLP 208

Query: 131 AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTT 190
GG T FA+ AY+ L A + + HS + + + AG G
Sbjct: 209 DAGGDTL FANTVEAYNRLSPAMKERLEGLHILHSSI---EQAANNKSAG----GIIRREP 261

Query: 191 ATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW 248
+ PLV+V+P T + L + + I + ES+ L L D +A + W
Sbjct: 262 EANIHP LVRVNPLTKQKHL YLNKEFGRRIVELKEDES DYLLAFLYDHIEKAQDLQIRVTW 321

Query: 249 AAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLA 282
VV+W+N +H + DF P + R++
Sbjct: 322 EENTVVLWNNSTTIH-SPCVDFDEPEIRHAYRIS 354

>ref|XP_571061.1| hypothetical protein [Cryptococcus neoformans var. neoformans
JEC21]
gb|AAW43754.1| conserved hypothetical protein [Cryptococcus neoformans var.
neoformans JEC21]
Length = 375

Score = 69.7 bits (169), Expect = 4e-10, Method: Compositional matrix adjust.

Identities = 77/281 (27%), Positives = 112/281 (39%), Gaps = 38/281 (13%)

```

Query: 4   TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG-----QHLSND 55
          T +ITP +G VTG+ LA+LD AG L + ++ F + S +
Sbjct: 77 TVEETPF---IGVKVTGLDLASLDKAGQDQLALLAARKGIVFFASNDKVKQTYRDTSM 133

Query: 56 QQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWH 109
          +++ A+ +G + R +++ TVR+H W + + N WH
Sbjct: 134 RKLEMARYYQQLHQHSVQPRPPTSTEISVYQDKVNTVRKHW---WPNRLT---NAIWH 186

Query: 110 ADSTYMPVMAQGAVFSAEV---VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
          D T G F + P+ GG T + AY+ L + V A HS
Sbjct: 187 IDQT-QERQPPGITTFCCMQHDAPS-GGDTLVGSLVEAYNRLSPKMKEFVCGLKAVHSSA 244

Query: 167 YSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAE 225
          +K V G L PLV VHP TG SL I I G+ E
Sbjct: 245 VMSAKAARVG-----GASRRNEIESLHPLVTVHPATGSKSLYINPERMTYIEGLRNEE 297

Query: 226 SERFLEGLVDWACQAPRVHA-HQWAAGDVVWDNRCLLHRA 265
          S+ L+ L D HA ++W+ GDV VWD R ++H A
Sbjct: 298 SDNMLKFLSDHVKLGDGFHARYKWSEGDVCVWDQRVIIHSA 338

```

```

>ref|XP_002372616.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
flavus NRRL3357]
ref|XP_003189169.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
oryzae RIB40]
gb|EED57004.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
flavus NRRL3357]
Length = 375

```

Score = 69.7 bits (169), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 71/274 (25%), Positives = 101/274 (36%), Gaps = 33/274 (12%)

```

Query: 7   QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKR 63
          ++T +G + GV L+ L DA L + ++ FP Q L + + Q F +
Sbjct: 86 KVTEIQPKIGTIEGVQLSQLSDAAKDELALLVSEKVVAFPAQDLIDAGPEAQEQFMRH 145

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-----SPAEDDDMMKVIVGNMAWHADST 113
          FG + GTVR H + E + WH D +
Sbjct: 146 FGKP-----NYQPVSGTVRGHPGFHIIHRDGNKEEISRFLSQRTTTTLWHQDVS 194

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
          Y + P VGG T FA AY L + + A HS S +
Sbjct: 195 YEIQPPSYVMLGLLEGPEVGGDTVFAATDMAYKRLSPTFCSWLDTLRAVHS---SAKMIN 251

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEG 232
          H + S +DT + PLV+VHP TG L I G I G+ E E
Sbjct: 252 HARLTNSLVRKDPVDT----VHPLVRVHPVTGEKCLFINGEFITKIQGLKEPEQRWLTEF 307

Query: 233 LVDWACQAPRVHAH-QWAAGDVVWDNRCLLHRA 265
          L++ A +W +V++DNRC LH A
Sbjct: 308 LMNHIITGHDFQARVRWQPKTIVIFDNRCTLHSA 341

```

```

>emb|CBJ18803.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

```

Score = 69.7 bits (169), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 42/110 (38%), Positives = 59/110 (53%), Gaps = 5/110 (4%)

```

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
          AAYDALD+AT+A + HSL+YS+++LG S + + L LV+ HP

```

Sbjct: 1 AAYDALDDATKAEIEDLVCEHSLIYSRAQLG-----FSNFTDEERHSMRPVLHKLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252

TGR SLL+ H AI G E+ F+ L++ A Q V+ H+W D

Sbjct: 56 VTGRKSLLSAHIGAIVGWPRLEAMAFIRDLMEHATQPQFVYVHRWTKHD 105

>ref|YP_004243121.1| taurine catabolism dioxygenase [Arthrobacter phenanthrenivorans Sphe3]

gb|ADX74987.1| putative taurine catabolism dioxygenase [Arthrobacter phenanthrenivorans Sphe3]

Length = 322

Score = 69.7 bits (169), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 77/295 (26%), Positives = 120/295 (40%), Gaps = 31/295 (10%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQ-QI 58

+ ++ LQ T A +GA + G+ L+ L A + AA H L+F ++ D+ Q+

Sbjct: 4 ITKSKLQFTKLSARIGAEIRGLDLSQDLPETVAQIRAALNTHKALVFREVNVRTDEEQV 63

Query: 59 TFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMA---WHADSTYM 115

FA FG + + VA DG PA ++ V N + WH D T++

Sbjct: 64 RFASHFGPLTK--AHPTVA----SVDG-----KPA----VLPVDSSENGSANNWHTDVTFF 108

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175

Q + + +PA GG T A AY L R A H+ Y S ++

Sbjct: 109 VNPPQASTLRSITLPAYGGETLIASSAGAYQDLPAELRNFAADTLWAIHTNDYDYSVPKNL 168

Query: 176 QQAGS-----AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH--AIPGMDAAESER 228

+ A + + ++ P+V++HP TG L IG A I G+ ES+

Sbjct: 169 EHANADERRKEFTRIHFESA---HPVVRHPLTGERGLFIGGFAQRLRIVGLSNTESKD 224

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

L L + + V W +V++DNR H A PR + +AG

Sbjct: 225 ILRLQLQAYVTRPENVRVNWEPDQLVLFNDRITQHYAPDNYDGQPRQLNRVTIAG 279

>gb|ADC34046.1| TfdA-like protein [uncultured bacterium]

Length = 187

Score = 69.7 bits (169), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 60/211 (28%), Positives = 88/211 (41%), Gaps = 29/211 (13%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYM 115

QQI FA +FG + I ++++ A + P D+ G WH+D++

Sbjct: 1 QQIAFAAQFGKLY-----IHPVADMSAKHP--EILPVYADEKSTRAFGE-EWHSASCD 51

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175

G++ +VVP VGG T + M AAYDAL E + L + H

Sbjct: 52 LEPLPLGSILQLQVVPVGGDTMLSSMYAAYDALSEPLKKLCESLTVVHD----- 100

Query: 176 QQAGSAYIGYGMDTTAT---PLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLE 231

G D T P+V HPE+GR L + ++ IP + ES+ L+

Sbjct: 101 ---GQHVFRRRFDPTKKYPANEHPIVCKHPESGRKLLFVNAQYTTTHIPQLKPRESDAVLQ 157

Query: 232 GLVDWACQAPRVHAH-QWAAGDVVVWDNRCL 261

L + P H +W VV WDNRC+

Sbjct: 158 MLYR-HIETPEFHRYFKWRPNSVVFWDNRCV 187

>gb|EFQ34669.1| TfdA family Taurine catabolism dioxygenase TauD [Glomerella graminicola M1.001]

Length = 382

Score = 69.7 bits (169), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 68/274 (24%), Positives = 107/274 (39%), Gaps = 33/274 (12%)

```
Query: 7   QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKR 63
          ++T   T+G V G+ L+ L +AG   L   +   ++ F GQ   ++   D+ + F
Sbjct: 98  EVTDLTPTIGTEVRGIQLSKLSNAGRDQLARFVAERKVVAFRGQDFADLPIDKALEFGGY 157

Query: 64  FGA--IERIGGG-----DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
          FG   I   G   +I +   D + +   ++AWH+D +Y
Sbjct: 158 FGRHHIHPTSGSPEGFPEIHLVHRAAGDRSAEK-----FFATRTSSIAWHSDVSYEQ 209

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
          P   GG T F +   AY+ L   +   +H   A HS +
Sbjct: 210 QPPGTTFLYILDKPETGGDTLFCNAVEAYNRLSPLFQERLHGLQAVHSGI----- 259

Query: 177 QAGSAYIGYGMDDTTATPL---RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEG 232
          +   +A + G   P+   P+V+ HP TG +L I +   I G+   ES+ L+
Sbjct: 260 EQINASVSKSGSIKRREPVANThPIVRTHPVTGEKALYINPQFTREIVGLKKEESDALLKF 319

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
          L +   HA   +W G VVVWDNR   H A
Sbjct: 320 LYEHIAWGADFHARIKWEEGTVVVWDNRVTQHSA 353
```

>emb|CBJ18756.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 69.7 bits (169), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 43/111 (38%), Positives = 54/111 (48%), Gaps = 5/111 (4%)

```
Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
          AAYDALD+ T+A +   HSL+YS+ LG V   Y   L+ LV+ HP
Sbjct: 1   AAYDALDDETKAEIENLICEHSLMYSRSGSLGFVD-----YTEEEKQMFKPVLRQLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
          GR SL + HA AI GM   E   L L + A Q   V+ HQW   D+
Sbjct: 56  VHGRKSLYLSSHAGAIRGMGVPEGRLLLRDLTEHATQPEFVYVHQWTVHDL 106
```

>emb|CBJ18795.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18801.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18805.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18814.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18848.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 69.7 bits (169), Expect = 5e-10, Method: Compositional matrix adjust.
Identities = 42/110 (38%), Positives = 59/110 (53%), Gaps = 5/110 (4%)

```
Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
          AAYDALD+AT+A +   HSL+YS+++LG   S +   +   L LV+ HP
Sbjct: 1   AAYDALDDATKAEIEDLVCEHSLIYSRAQLG-----FSNFTDEERHSMRPVLHKLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
          TGR SLL+ H AI G   E+ F+ L++ A Q   V+ H+W   D
Sbjct: 56  VTGRKSLLSAHIGAIVGWPRPEAMAFIRDLMEHATQPQFVYVHRWTKHD 105
```

>ref|XP_002614428.1| hypothetical protein CLUG_05914 [Clavispora lusitaniae ATCC 42720]
gb|EEQ41786.1| hypothetical protein CLUG_05914 [Clavispora lusitaniae ATCC 42720]
Length = 387

Score = 69.7 bits (169), Expect = 5e-10, Method: Compositional matrix adjust.
Identities = 72/277 (25%), Positives = 110/277 (39%), Gaps = 38/277 (13%)

```
Query: 5   TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQ---ITFA 61
          T ++TP   LG  VTGV L+ LD  G   L       Q  ++IF  Q  +       + +
Sbjct: 83  TKKVTPK---LGTEVTGVQLSQLDSKGKDELALLVAQRGVVIFRDQDFATHGPGFAVEYG 139

Query: 62  KRFGAIERIGGGDIVAISNVKADG-----TVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
          K FG +       I   S   D       T R+ +PAE++ +       + WH+D +Y
Sbjct: 140 KHFGRLH-----IHPTSGAPKDHPELHITYRRANPAEFERVFSE RTHAVGWHS DVS YEL 193

Query: 117 VMAQGAVFSAE VVPVAVGGRTCFADMR AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
          FS   P  GG T FAD   AY L   + +       H L S + + +
Sbjct: 194 QPPGITFFSVLDGPEAGGDTIFADTVEAYKRLSPEFQKRL---EGLHVLHTSGDQAANAR 250

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV- 234
          + G   G       + + PL++ HP T   + + R + I +   ES+ + L
Sbjct: 251 RQG----GVERRKPVSHIHLIRTHPVTKKKIYLNRPFSRRIVELKEQESDYLMNFLT 306

Query: 235 -----DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
          D+  +A       +W   VVVWDNR ++H A
Sbjct: 307 HIESGHDFQLRA-----KWEPRSVVVWDNR RVVHSA 337
```

>ref|XP_001215509.1| conserved hypothetical protein [Aspergillus terreus NIH2624]
gb|EAU32875.1| conserved hypothetical protein [Aspergillus terreus NIH2624]
Length = 376

Score = 69.7 bits (169), Expect = 5e-10, Method: Compositional matrix adjust.
Identities = 73/276 (26%), Positives = 108/276 (39%), Gaps = 37/276 (13%)

```
Query: 7   QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKR 63
          ++T   +G+ V GV L+ L +A   L       + ++ FP Q L +   + Q +F +
Sbjct: 87  KVTEIQPQIGSVVEGVQLSQLSNAKDELALLVAERKVVAFPNQDLIDAGPEAQESFMRY 146

Query: 64  FGAIERIGGGDIVAISNVKADGTVRQHSPA-----EWDDMMKVIVGNMAWHADS 112
          FG           +       GTVR H PA           E   ++       WH D
Sbjct: 147 FGKP-----NYQPVS GTVRNH-PAFHIIHRDGNREEISR FLEQRTTTTLWHQDV 194

Query: 113 TYMPVMAQGAVFSAE VV-PAVGGRTCFADMR AAYDALDEATRALVHQRSARHSLVYSQSK 171
          +Y +   G V   + P VGG T FA   AY L   R+ +       HS S
Sbjct: 195 SYE-IQPPGYVMLGLLEGPEVGGDTVFAATDMAYKRLSPTLR SWLDTLRVTHS---SAKM 250

Query: 172 LGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFL 230
          + H +   GS       +DT   + PLV+VHP TG   L + G   I G+   E   +
Sbjct: 251 INHARLTGSLVRKDPVDT---VHPLVRVHPVTGEKCLFVNGEFITKINGLKEPEQRWLM 306

Query: 231 EGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
          + L+       A   +W   +V++DNR LH A
Sbjct: 307 DFLMQHIVSGHDFQARVRWQPKTIVMFDNRSTLHSA 342
```

>gb|ADC33974.1| TfdA-like protein [uncultured bacterium]
Length = 123

Score = 69.7 bits (169), Expect = 5e-10, Method: Compositional matrix adjust.
Identities = 47/131 (35%), Positives = 64/131 (48%), Gaps = 13/131 (9%)

```
Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY----IGYGMDTTA 191
          T F DM AAYDAL E R +   + +H Y ++   +++ A   +G G
Sbjct: 1   TEFCDMYAAYDALPEVLRKRIRGATIKHDTAYDTNR--KLRRGAVAVDDPRLGNG----- 53
```

Query: 192 TPLRPLVKVHPETGRPSLLIGRHA-HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA 250
P P+V HP+TG SL +GR H + G ES L+ L A Q +H W
Sbjct: 54 -PGHPIVSTHPDGTGCNSLFLGRRPRHYVNGYTLSESAALLDALWAHATQLRFRISHAWRQ 112

Query: 251 GDVVVWDNRCL 261
GDVV+WDNRC+
Sbjct: 113 GDVVMWDNRCV 123

>ref|XP_505767.1| YALIOF22825p [Yarrowia lipolytica]
emb|CAG78578.1| YALIOF22825p [Yarrowia lipolytica]
Length = 385

Score = 69.3 bits (168), Expect = 5e-10, Method: Compositional matrix adjust.
Identities = 65/260 (25%), Positives = 100/260 (38%), Gaps = 21/260 (8%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFFPGQ---HLSNDQQITFAKRFGAIE-RI 70
G+ V GV L+ L D L + +++F Q L + +A+ FG
Sbjct: 106 FGSEVRGVQLSKLSDKAKDELAIFYAERGTVVFRDQDFRELPIKDALKYAEHFGRQHIHP 165

Query: 71 GGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVP 130
G A V R+ + + + ++AWH+D TY +P
Sbjct: 166 TSGSPQAYPEVHL--IFREEGDDIYKEYFSSNLSSVAWHSDDVTEYKQPPGTTFLGILEMP 223

Query: 131 AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTT 190
GG T F+D AY+ L + + A HS + A I G
Sbjct: 224 RTGGDTLFSNDTEAYNRLSPEFQKRLEGLKAVHS-----AHEQADASIRGGGVVR 273

Query: 191 ATPLR---PLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH 246
P++ P+++ HP TG+ S+ + + I G+ ES+ L L D + H
Sbjct: 274 REPVQNVHPIIRKHPATGKKSIFVNPQFTRNIVGLKQEESDLILNFLYDIIAKGSDFHVR 333

Query: 247 -QWAAGDVVWDNRCLLHRA 265
+W G VVWDNR H A
Sbjct: 334 ARWEDGSVVWDNRRTSHTA 353

>ref|XP_002502918.1| predicted protein [Micromonas sp. RCC299]
gb|AC064176.1| predicted protein [Micromonas sp. RCC299]
Length = 326

Score = 69.3 bits (168), Expect = 5e-10, Method: Compositional matrix adjust.
Identities = 62/199 (31%), Positives = 86/199 (43%), Gaps = 25/199 (12%)

Query: 108 WHADSTYMP----VMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL----DEATRALVHQ 159
WH D +++P +A A + +P GG T FA AA++AL E R L
Sbjct: 125 WHTDGSFLPNPKVAIALYAPQLDDALPPEGGETRFASCTAAFEALAREEQEKLRLGLCSVH 184

Query: 160 SARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHA-- 217
S + +S+ Q+ + I L P+V+ HP T SL I A
Sbjct: 185 SWEKFMRLLESRDPRQKVTAEQIA----EKPPQLWPVVRTHPVTKAESLYINPKNTAAV 240

Query: 218 -----IPGMDAAE-SERFLEGLV-DWACQAPRVHAHQWAAGDVVWDNRCLLHRAEP 267
IP DA +R E +V D +V+AH W GD V+WDNR LLH A P
Sbjct: 241 VNKATGEPIPEEDARRLVDRLAEEAVVGDLPGNSKVYAHTWKRGRDFVIWDNRVLLHAASP 300

Query: 268 WDF-KLPRVMWHSRLAGRP 285
+D K R+++ G P
Sbjct: 301 FDAEKYQRLLFRMEFKGEP 319

>gb|EDP53557.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus fumigatus A1163]

Length = 388

Score = 69.3 bits (168), Expect = 5e-10, Method: Compositional matrix adjust.
Identities = 66/260 (25%), Positives = 107/260 (41%), Gaps = 15/260 (5%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE-RIGGG 73
+G + G+ L L+D L + +++ F Q +S QQ + FG +E
Sbjct: 93 IGTEIVGLQLKDLNDKQKDELGLLIAERSVVFFRDQDISPQQQKELGEWFGVEVEVHPQVP 152

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVG 133
+ + V Q AE + G WH D + A + VP++G
Sbjct: 153 QVPGVPGVTVLWPALQA--AETPAAFRRPGGASRWHTDLVHERQPAGVTHLHNDTVPSIG 210

Query: 134 GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATP 193
G T +A AAY+ L + R + ++A + + H ++ G Y+
Sbjct: 211 GDTLWASGYAAEKLSPSFRQFIDGKTAIYRSAHPYLDRKHPEK-GPVYVERE----- 262

Query: 194 LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAG 251
PLV+VHP TG +L + R I G+D AES+ L L D + + +W
Sbjct: 263 -HPLVRVHPATGWKTLWVNRAMTVRIVGLDKAESDVILGYLCDVYEKNIDIQVRFKWTPR 321

Query: 252 DVVVWDNRCLLHRAEPWDFK 271
+WDNR +H A WD++
Sbjct: 322 TSALWDNRITIHNAS-WDYE 340

>gb|ADC33959.1| TfdA-like protein [uncultured bacterium]
Length = 122

Score = 69.3 bits (168), Expect = 6e-10, Method: Compositional matrix adjust.
Identities = 40/127 (31%), Positives = 63/127 (49%), Gaps = 6/127 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPL- 194
T F DM AY+ L+ +A + A H+L +S+++ + G + P+
Sbjct: 1 TEFCDMYGAYERLNPEWKARIAPLRAVHNLDFSRTTR-----RHGEDPMTEAQRREVPPVD 55

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
P+V+ HPETGR + +G HA I GM A +E L + H W+AG ++
Sbjct: 56 HPIVTRHPETGRKCVFLGDHAEDIVGMAYAAGRALIEELNALIVHPDLTYEHHWSAGQLI 115

Query: 255 VWDNRCL 261
+WDNRC+
Sbjct: 116 LWDNRCL 122

>emb|CAY27490.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 69.3 bits (168), Expect = 6e-10, Method: Compositional matrix adjust.
Identities = 52/127 (40%), Positives = 68/127 (53%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTAT--- 192
T FADMRAAYDALD+ +A + HSL+YS+ LG ++ Y + A
Sbjct: 1 TEFADMRAAYDALDDAKAEIEDMICEHSLMYRSGSLG-----FLDYTDEEKAMFKP 52

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
L+ LV+ HP R SL + HA AI GM E+ L L + A Q VH H+W D
Sbjct: 53 VLQRLVRTHPVHRRKSLYLSSHAGAIGMSVPEARLLLRDLNEHATQREFVHIHKWTVHD 112

Query: 253 VVVWDNR 259
+V+WDNR
Sbjct: 113 LVMWDNR 119

>gb|ADC34032.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 69.3 bits (168), Expect = 6e-10, Method: Compositional matrix adjust.
Identities = 59/211 (27%), Positives = 92/211 (43%), Gaps = 21/211 (9%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM 115
QQI FA+ FGA + +K +P + + G + WH+D+TY+
Sbjct: 1 QQIAFAQAFGAP-----MEYPQLKGLPECPMITPVVKLEHERDNFGGV-WHSDTTYL 51

Query: 116 PVMAQGAVFSAE VVPVAVGGRTCFADMRAAYDALDEATRA----LVHQRSARHSLVYSQSK 171
G++ A VP GG T FA+ AY++L + +A LV ++ + S+++
Sbjct: 52 ERPPMGSM LYALEVPPQGGDTMFANQY LAYESLS DGLQAVLGGLVG VNTSTKAAA-SKTR 110

Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFL 230
++ AG + P+V+ HPETGR +L + H G AES L
Sbjct: 111 EDRMRAAGEELKVLAGE-----HPVVRTHPETGRRALYVNVGHTERFKGWSEAESRPLL 164

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
E L Q +W G + WDNRC+
Sbjct: 165 EYLFAHQVQPEFTCRFRWTPGALAFWDNR CV 195

>ref|XP_002487959.1| alpha-ketoglutarate-dependent taurine dioxygenase [Talaromyces
stipitatus ATCC 10500]
gb|EED12305.1| alpha-ketoglutarate-dependent taurine dioxygenase [Talaromyces
stipitatus ATCC 10500]
Length = 384

Score = 69.3 bits (168), Expect = 6e-10, Method: Compositional matrix adjust.
Identities = 76/277 (27%), Positives = 112/277 (40%), Gaps = 38/277 (13%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKR 63
Q+T +G+ V GV L+ L DAG L Q ++ F Q + ++ + F
Sbjct: 99 QVTEITPYIGSEVRGVQLSQLTDAGK DQLALFVAQRKVVAFRDQDFAKLP IEKALEFGGY 158

Query: 64 FGA--IERIGGG-----DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
FG I G +I + D + Q + ++ WH+D +Y
Sbjct: 159 FGRHHIHPTSGAPKGFPEIHLVHRGADDNSFLQ-----TFLHEHTNSVTWHS DVSYE- 210

Query: 117 VMAQGAVFSAE VV-PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
G F + P GG T FA++ AY L R +H A HS
Sbjct: 211 AQPPGTTFLYLLDGPTSGGDTLFANLAKAYQRLSPEFRKRLHGLKAVHS-----GF 261

Query: 176 QQAGSAYIGYGMDDTTA--TPLR---PLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERF 229
+QA SA D+T P++ P+V+ HP TG +L + + I G ES+
Sbjct: 262 EQAQSAL---ARDSTVRRDPVKHEHPIVRTHPVTGEKALYVNPQFTRYIVGYKKEESDHL 318

Query: 230 LEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
L+ L D + + +WA G VVVWDNR H A
Sbjct: 319 LKFLFDHVALSQDLQTRIKWAPGTVVVWDNRVTAHSA 355

>ref|ZP_04967409.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 406e]
gb|ED087370.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 406e]
Length = 191

Score = 69.3 bits (168), Expect = 6e-10, Method: Compositional matrix adjust.
Identities = 50/148 (33%), Positives = 68/148 (45%), Gaps = 5/148 (3%)

Query: 122 AVFSAE VVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY----SQSKLGHVQQ 177
+V A +P GG T +A+ AAY L + + LV + A H + S+ +L H

Sbjct: 11 SVLRALALPDAGGDTVWANTVAAYQHLPSSLQDLVDKLWAVHGNDFDYAASRVELLHDPV 70

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA 237
A Y T P+V++HPETG SLL+G +A D +S R E L

Sbjct: 71 AKEYRKKYAAQVIKTE-HPVVQIH PETGEKSLLLGHYAQR FVQYDTHDSNRLYEILQAH I 129

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ WAAGDV +WDNR H A

Sbjct: 130 TRLENTVRWHWAAGDVVAIWDNRSTQHYA 157

>emb|CBJ18907.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 69.3 bits (168), Expect = 6e-10, Method: Compositional matrix adjust.
Identities = 42/110 (38%), Positives = 59/110 (53%), Gaps = 5/110 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
AAYDALD+AT+A + HSL+YS+++LG S + + L LV+ HP

Sbjct: 1 AAYDALDDATKAEIEDLVCEHSLIYSRAQLG-----FSNFTDEERHSMRPVLHKLVR AHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
TGR SLL+ H AI G E+ F+ L++ A Q V+ H+W D

Sbjct: 56 VTGRKSLLSAHIGAIVGWPRPEAMAFIRDLMEHATQPQFVYVHRWTKHD 105

>gb|EFY95010.1| alpha-ketoglutarate-dependent taurine dioxygenase [Metarhizium
anisopliae ARSEF 23]
Length = 378

Score = 69.3 bits (168), Expect = 6e-10, Method: Compositional matrix adjust.
Identities = 72/267 (26%), Positives = 107/267 (40%), Gaps = 22/267 (8%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
Q+TPT +G+ ++G+ L++L DAG L + ++ F Q + D I A ++G

Sbjct: 95 QLTP-----IGSEISGIQLSSLS DAGKDELAHYVAKRKVVAFRNQDFA-DLSIPDALKYG- 149

Query: 67 IERIGGGDIVAISNVKADGTVRQH--SPA EWDD----MMKVIVGNMAWHADSTYMPVMAQ 120
E G I S +G H E D + ++AWH+D +Y

Sbjct: 150 -EYFGRHHIHPTSGA-PEGYPEIHLVHRGEGDKGAAQFF EARTSSVAWHS DVSYEKQPPG 207

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
P GG T F D AY+ L + +H A HS + + A +

Sbjct: 208 TTFlyILNKPETGGDTLFDVDAQYANRLSPLFQERLHGLRATHSGIEQVN-----AAA 260

Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ 239
A P+V+ HP TG +L I + I G+ ES+ L+ L D

Sbjct: 261 ARNSIKRREP VVNDHPVIRTHPATGEKALYINPQFTREILGLKREESDAILKFLYDHLAY 320

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
A +W G VV+WDNR H A

Sbjct: 321 GADFQARVKWEEGT VVIWDNRV TQHTA 347

>emb|CAY27357.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 69.3 bits (168), Expect = 6e-10, Method: Compositional matrix adjust.
Identities = 44/124 (35%), Positives = 66/124 (53%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DM AA+DAL EA + + S+ +S++KLG Y + +

Sbjct: 1 TVFPDMPAAWDALPEAKKKKLAGLKVFPSIFHSRAKLGMTD-----YTEKERASLPGA EQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ P++GR +L + HA I GM ESE L L+++A + V+AH+W D+V+
Sbjct: 56 GLVRTIPQSGRKALYLASHAVRIQGM PDGESESLLAELMEFATERRFVYHRWRVHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>emb|CBJ18759.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 69.3 bits (168), Expect = 7e-10, Method: Compositional matrix adjust.
Identities = 39/110 (35%), Positives = 56/110 (50%), Gaps = 5/110 (4%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE 203
AYDALD T+ + HS +YS+ +LG + + L+ LV+ HP
Sbjct: 2 AYDALDSETKDEIEDLVCEHSQIYSRQQLGFTDFTEEERVRF-----KPVLQRLVTRHTPT 56

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL + HA I G E+ FL+ L ++A Q V+AH+W GD+
Sbjct: 57 TGRKSLYLSSHAGGIVGWPVPEARAFLKDLNEYATQREFVYHRWRVGD L 106

>ref|XP_001820787.2| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
oryzae RIB40]
Length = 343

Score = 68.9 bits (167), Expect = 7e-10, Method: Compositional matrix adjust.
Identities = 77/284 (27%), Positives = 110/284 (38%), Gaps = 46/284 (16%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRF 64
ITP +G + GV L+ L G L Q +L+F Q ++ +Q A +
Sbjct: 56 ITPR---IGTEIRGVQLSQLSTDGLDQLALLAAQRGVLFVRDQDFADIGTGRQRDIAAHY 112

Query: 65 GAIER-----IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA---WHADSTYM 115
G + + G V AD V ++ ++G WH D T+
Sbjct: 113 GPLHQHPTMGYPQGTSPFEFQV VYADEKVG N-----LRTL LGTRTSYDLWHIDQTFT 163

Query: 116 PVMAQGA VFSAEVVPVAVGG-RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
P F PA GG T F + AAY AL R +H R L+++ + +G
Sbjct: 164 PNTPGVTFWFVLETPASGGGDTAFTSLTAAYQALSPTFREGLH---RLKLLHTSASVGE 219

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGL 233
V + G + PLV HP T P L + A + G ESE L L
Sbjct: 220 VARIGQER---ALKDAVQTEHPLVIGHPVTHDPVLFVNPAIARQVVGYPKEESENLLSFL 276

Query: 234 -----VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFK 271
+D++C+ W G VVVWD R + H A P DF+
Sbjct: 277 HNHIRSLDFSCR V-----SWEKGTVVVWDQRAVAHSAVP-DFE 313

>emb|CAY27420.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 68.9 bits (167), Expect = 7e-10, Method: Compositional matrix adjust.
Identities = 44/124 (35%), Positives = 58/124 (46%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRAA+DALD RA + HS+ YS+ LG A +
Sbjct: 1 TEFGDMRAAHDALDAERRASLEGLCVHHSIAYSRET LGFEFSAAET-----EQLRGA AH 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ P +GR L + HA I E L L++ A Q+ V+ H W D+V+
Sbjct: 55 PLVRTIPGSGRRCLYLASHASRIIDWPVPEGRLLLRDLIEHATQSQFVYRHSWRPHDLVM 114

Query: 256 WDNR 259
WDNR
Sbjct: 115 WDNR 118

>emb|CBJ18754.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18757.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18762.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 68.9 bits (167), Expect = 7e-10, Method: Compositional matrix adjust.
Identities = 42/111 (37%), Positives = 57/111 (51%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHP 202
AAYDALD+ T+A + HSL+YS+ LG + Y + L+ LV+ HP
Sbjct: 1 AAYDALDDETKAEIEDMICEHSLMYSRGSIGFLD-----YTDEEKELFKPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E+ L L + A Q V+AH+W D+
Sbjct: 56 VHGRKSLYLSSHAGAIQGMTPEARLLLRDLNEHATQREFVYAHKWLHDL 106

>ref|XP_002836505.1| hypothetical protein [Tuber melanosporum Mel28]
emb|CAZ80696.1| unnamed protein product [Tuber melanosporum]
Length = 361

Score = 68.9 bits (167), Expect = 7e-10, Method: Compositional matrix adjust.
Identities = 67/268 (25%), Positives = 103/268 (38%), Gaps = 21/268 (7%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKR 63
Q+ +G ++GV L+++ DA L + ++ Q ++ Q FA
Sbjct: 77 QVKHISPKMGTELSGVQLSSMSDAKDELALLVSEKCVVLRDQDFADWGPSNQQDFASY 136

Query: 64 FGAIE-RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG + G I R + AE D + + + WH D +Y
Sbjct: 137 FGKPNYQPVTSIPGFPGFHI--IYRDGNQAEIDKFFEHLTSTLWHQDVSYERQPPPGYV 194

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ P VGG T FA AY+ L ++++ A H S K+ + +A
Sbjct: 195 ILCILQAPEVGGDTVFASTAEAYNRLSPGFQSMLEDLRATH---SSEKMCNFAKAN--- 247

Query: 183 IGYGMTTATPLR---PLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVDWAC 238
G P+R P+V+VHP TG SL + G I G ES+ L L+D
Sbjct: 248 ---GGLCRKDPIRTSHPIVRVHPVTGEKSLFVNGEFIRGIDGWKDPESDILLNFLIDHIT 304

Query: 239 QAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ W VV++DNR H A
Sbjct: 305 KGHDFQVRLSWKPKSVVIFDNRSTCHTA 332

>ref|YP_003951319.1| Taurine catabolism dioxygenase TauD/TfdA [Stigmatella aurantiaca
DW4/3-1]
gb|ADO69492.1| Taurine catabolism dioxygenase TauD/TfdA [Stigmatella aurantiaca
DW4/3-1]
Length = 285

Score = 68.9 bits (167), Expect = 8e-10, Method: Compositional matrix adjust.
Identities = 64/269 (23%), Positives = 105/269 (39%), Gaps = 25/269 (9%)

Query: 9 TPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE 68
+P+ +GA ++ + L + + +H L+IF GQ S ++ I FA++ G +
Sbjct: 5 SPSQGRIGAEISQLDLRAVTAQDATRIRQTIYEHKLVIHFHQSPSPPEEYIAFARKIGRPQ 64

Query: 69 RI-----GGGDIVAIISNVKADGTVRQHSPAEDDDMMKVIVGNMA--WHADSTYMPVM 118
++ SNV DG KV V WH D +
Sbjct: 65 VYFQHNHYHHPQHPELVSSNVLEDGK-----KVGVAGTGRYWHTDYQFFQEP 111

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH-QRSARHSLVYSQSKLGHVQQ 177
+ +V+P T F DM+ Y+A+ RA V R+ + + V +
Sbjct: 112 LPLVMVYPQVLPKAKRETYFIDMQRVYEAMPAELRAYVEGHRAIQEGKWRYKITPEDVDK 171

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
A + P V HP TGR SL + I G+ E+ + L +
Sbjct: 172 ALVDILAAVEKQVPAITHPAVIEHPLTGRKSLYLSSGFTTGIEGLTHEENRAAMAKLF 231

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
Q V + + GD+++W+NR LLH+A
Sbjct: 232 IEQEAHVQTYSYQPGDILLWENRALLHKA 260

>ref|ZP_08227343.1| putative taurine catabolism dioxygenase [Streptomyces cf. griseus
XylebKG-1]
Length = 299

Score = 68.9 bits (167), Expect = 8e-10, Method: Compositional matrix adjust.
Identities = 73/278 (26%), Positives = 108/278 (38%), Gaps = 32/278 (11%)

Query: 4 TTLQITPTGATLGATVTGVHLATL-DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T ++I +GA VTG L D A + L + L++ ++ +QQI A
Sbjct: 14 TGIRIGELTPFIGAEVTGATFEDLRDPALWEQLTTLHERELVVVRSIDLITPEQQIDLAG 73

Query: 63 RFG-----AIERIGGGDIVAIISNVKAD---GTVRQHSPAEDDDMMKVIVGNMAWHA 110
R G +I+ SN K + G R VGN WH
Sbjct: 74 RLGRVPVFLMAKYRHPDHEEIMISSNAKNNLAIGVAR-----VGNF-WHQ 118

Query: 111 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS 170
DS+Y + VP G T +A+ YD L + + V R+A H++ Q
Sbjct: 119 DSSYQRSAPPYTMLHGIDVPGTSGHTLYANAADVDRLPKEWKLKVEGRTAVHTVAKRQR 178

Query: 171 KLGHVQQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESER 228
A ++ P+ PL+K P TGR + + + G DA E+E
Sbjct: 179 ISPEHAGLSIAEFKALVEEQHPVEHPLIKTDPTTGRRYVYGAPEYMERVIGFDANENEE 238

Query: 229 FLEGLVDWACQAP-RVHAHQWAAGDVVVDNRCLLHRA 265
F L+D Q P RV+ H+W D+V+W H A
Sbjct: 239 FF-ALLDRLIQDPARVYEHRWTPRDLVIWKCELYHAA 275

>emb|CAY27452.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 121

Score = 68.9 bits (167), Expect = 8e-10, Method: Compositional matrix adjust.
Identities = 44/124 (35%), Positives = 61/124 (49%), Gaps = 3/124 (2%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T FADMRAA+D L + ++ A H +S+ K+G S A P +
Sbjct: 1 TEFADMRAAWDVLVPDRKRVLIGLIAEHDFHSRKKVG--LDPASITPERRASRPAPV-Q 57

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 255
L++ HP GR SL I H + GM ES + ++ L+ A Q V+ H W DVV+
Sbjct: 58 VLIRTHPVNGRKSPLYIASHITQVYGMPLIESLKLVDLMAHATQPQFVYTHHWTVDNVVM 117

Query: 256 WDNR 259
WDNR
Sbjct: 118 WDNR 121

>ref|XP_002376513.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Aspergillus flavus NRRL3357]
gb|EED53267.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Aspergillus flavus NRRL3357]
Length = 343

Score = 68.9 bits (167), Expect = 8e-10, Method: Compositional matrix adjust.
Identities = 77/284 (27%), Positives = 110/284 (38%), Gaps = 46/284 (16%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRF 64
ITP +G + GV L+ L G L Q +L+F Q ++ +Q A +
Sbjct: 56 ITPR---IGTEIRGVQLSQLSTDGLDQLALLAAQRGVLVFRDQDFADIGTGRQDIAAHY 112

Query: 65 GAIER-----IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA----WHADSTYM 115
G + + G V AD V ++ ++G WH D T+
Sbjct: 113 GPLHQHPTMGYPQGTSPFEQVVYADEKVG N-----LRTL LGTRTSYDLWHIDQTFT 163

Query: 116 PVMAQGAVFSAEVVPAVGG-RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
P F PA GG T F + AAY AL R +H R L+++ + +G
Sbjct: 164 PNTPGVTFFVWLETPASGGGDTAFTSLTAAYQALSPTFREGLH---RLKLLHTSASVGE 219

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGL 233
V + G + PLV HP T P L + A + G ESE L L
Sbjct: 220 VARIGQER---ALKDAVQTEHPLVIGHPVTHDPVLFVNPAIARQVVGYKPEESENLLSFL 276

Query: 234 -----VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFK 271
+D++C+ W G VVVWD R + H A P DF+
Sbjct: 277 HNHIRSLDFSCR V-----SWEKGTVVVWDQRAVAHSAPV-DFE 313

>ref|YP_001826806.1| putative taurine catabolism dioxygenase [Streptomyces griseus
subsp. griseus NBRC 13350]
dbj|BAG22123.1| putative taurine catabolism dioxygenase [Streptomyces griseus
subsp. griseus NBRC 13350]
Length = 299

Score = 68.9 bits (167), Expect = 8e-10, Method: Compositional matrix adjust.
Identities = 73/278 (26%), Positives = 108/278 (38%), Gaps = 32/278 (11%)

Query: 4 TTLQITPTGATLGATVTGVHLATL-DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T ++I +GA VTG L D A + L + L++ ++ +QQI A
Sbjct: 14 TGIRIGELTPFIGAEVTGATFEDLRDPALWEQLTLLHERELVVVRS LDTPEQQIDLAG 73

Query: 63 RFG-----AIERIGGGDIVAISNVKAD---GTVRQHSPA EWDDMMKVIVGNMAWHA 110
R G +I+ SN K + G R VGN WH
Sbjct: 74 RLGRVPVFLMAKYRHPDHEEIMISSNAKNNLAIGVAR-----VGNF-WHQ 118

Query: 111 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS 170
DS+Y + VP G T +A+ YD L + + V R+A H++ Q
Sbjct: 119 DSSYQRSAPPYTMLHGIDVPGTSGHTLYANAADVDRLPKEWKLKVEGR TAVHTVAKRQR 178

Query: 171 KLGHVQQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESER 228
A ++ P+ PL+K P TGR + + + G DA E+E
Sbjct: 179 ISPEHAGLSIAEFKALVEEQHPPVEHPLIKTDPTTGRRYVYGAPEYMERVIGFDANENEE 238

Query: 229 FLEGLVDWACQAP-RVHAHQWAAGDVVVWDNRCLLHRA 265
F L+D Q P RV+ H+W D+V+W H A
Sbjct: 239 FF-ALLDRLIQDPARVYEHRWTPRDLVIWKCELYHAA 275

>emb|CAY27378.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 113

Score = 68.9 bits (167), Expect = 8e-10, Method: Compositional matrix adjust.
Identities = 47/119 (39%), Positives = 59/119 (49%), Gaps = 7/119 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDALDE + HS ++S+S LG + P+R
Sbjct: 1 TEFADMRAAYDALDEEIKTECENLICEHSQLFSRSILGFTDFTDERRRFA-----PVR 54
Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
LV+ HP TGR SL + HA AI G E+ FL L + A Q V+AH W D+
Sbjct: 55 QRLVRRHPVTGRRSLYLASHAGAILGWLVEARAFRLDLNEHATQRFVYAHVVRQWDL 113

>emb|CBJ18720.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 68.9 bits (167), Expect = 9e-10, Method: Compositional matrix adjust.
Identities = 43/114 (37%), Positives = 57/114 (50%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---PLRPLVK 199
AAYDALD+ T+A + HSL+YS+ LG ++ Y D A L+ LV+
Sbjct: 1 AAYDALDDDTKAEIEDMICEHSLMYSRSLG-----FLDYTDDEKAMFKPVLQRLVR 52
Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP R SL + HA AI GM E+ L L + A Q VH H+W D+
Sbjct: 53 THPVHRRKSLYLSSHAGAIQGMSVPEARLLLRDLTEHATQREFVVIHKWTVHDL 106

>emb|CBJ18782.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 68.6 bits (166), Expect = 9e-10, Method: Compositional matrix adjust.
Identities = 41/111 (36%), Positives = 56/111 (50%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD+ T+A + HSL+YS+ LG + Y + L+ LV+ HP
Sbjct: 1 AAYDALDDETKAEIENMICEHSLMYSRSLGLLD-----YTDEEKEMFKPVLQRLVRTHP 55
Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E+ L L + A Q V+ H+W D+
Sbjct: 56 VHGRKSLYLSSHAGAIQGMSPEARLLLRDLTEHATQPEFVYVHKWTLRDL 106

>gb|AAR38315.1| alpha-ketoglutarate-dependent taurine dioxygenase [uncultured
marine bacterium 581]
Length = 275

Score = 68.6 bits (166), Expect = 9e-10, Method: Compositional matrix adjust.
Identities = 63/270 (23%), Positives = 106/270 (39%), Gaps = 29/270 (10%)

Query: 6 LQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ P +GA V G+ L A L + AL+ +++ +L F Q L+ Q + A+ F
Sbjct: 1 MYFRPLTTRIGAEEVQGIDLGAQLPNDALDALYDGLIRYQVLFREQLNPPQHLALAESF 60
Query: 65 GAIER-----IGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMP 116
G ++ G IV + N + DD WH D T+
Sbjct: 61 GEVDPGHPVYPHVDGYQSIVELRN-----EDDKAPDTDD-----WHKDLTFRA 103
Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176

```

      A  ++      VP VGG T +A M A YD+L      ++ +      A H +      +  +++
Sbjct: 104 EPAFASILRGVEVPQVGDTLWASMSAVYDSLSSGWKSDLEGLYAIHDM--GTFRNDYLR 161

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
      + G  I  +      + + P++ HP TG  L + +      I  +      S+  L+ L
Sbjct: 162 KGGVTAIDEALTEVGSGVHPVIATHPVTGLKYLNVNQSFTRNIVDLTQGASDEVLYQYLYQ 221

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      +      +W      V +WDNR      H A
Sbjct: 222 HVRPPEFQVRFRWENDSVAIWDNRITQHYA 251

```

>gb|ADC33982.1| TfdA-like protein [uncultured bacterium]
Length = 122

Score = 68.6 bits (166), Expect = 9e-10, Method: Compositional matrix adjust.
Identities = 42/132 (31%), Positives = 64/132 (48%), Gaps = 16/132 (12%)

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Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK-----LGHVQQAGSAYIGYGMDT 189
      T F DM  AY+ LD  +A +      A H+L +S+++      L  Q+      + +
Sbjct: 1   TEFCDMYGAYERLDARWKARIAGLRAVHNLDLSRTRRHAEDPLTEAQLAKPPVDH---- 56

Query: 190 TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWA 249
      P+V+ HPETGR  L +G HA  I GM  AE  +E L  A      + H+W
Sbjct: 57 -----PVVRTHPETGRKCLYLGDHAEYILGMPYAEGRALIEELNALAVHPDLTYEHRWR 110

Query: 250 AGDVVVWDNRCL 261
      ++++WDNRC+
Sbjct: 111 TRELLLWDNRCV 122

```

>gb|AAS64586.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
gb|AAS64587.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
gb|AAS64594.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
Length = 119

Score = 68.6 bits (166), Expect = 9e-10, Method: Compositional matrix adjust.
Identities = 46/126 (36%), Positives = 60/126 (47%), Gaps = 9/126 (7%)

```

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATP-- 193
      T F DMRAAYD L      ++ +      A H + S+ LG  + +      A P
Sbjct: 1   TEFGDMRAAYDELPA DLKSELEGLHAEHYALNSRFVLGDTDYSEA-----QRNAMPV 53

Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
      PLV+ H  +GR  L IG HA  I G  AE  L  L++ A Q  V+ H W  GD+
Sbjct: 54 TWPLVRTHAGSGRKFLFIGAHAGRIEGRPLAEGRMLLAEELLEHATQRRFVYRHSWKVGDL 113

Query: 254 VVWDNR 259
      V+WDNR
Sbjct: 114 VMWDNR 119

```

>emb|CBJ18765.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 68.6 bits (166), Expect = 9e-10, Method: Compositional matrix adjust.
Identities = 42/111 (37%), Positives = 54/111 (48%), Gaps = 5/111 (4%)

```

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
      AAYDALD+ T+A +      HSL+YS+ LG V      Y      L+ LV+ HP
Sbjct: 1   AAYDALDDETKAEIEDLVCEHSLMYSRGLGFVD-----YTDEEKQMFKPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

```

GR SL + HA AI GM E L L + A Q V+ H+W D+
Sbjct: 56 VHGRKSLYLSSHAGAIRGMSVPEGRLLLRDLTEHATQPQFVYVHKWTVHDL 106

>ref|XP_001794409.1| hypothetical protein SNOG_03864 [Phaeosphaeria nodorum SN15]
gb|EAT89069.2| hypothetical protein SNOG_03864 [Phaeosphaeria nodorum SN15]
Length = 348

Score = 68.6 bits (166), Expect = 9e-10, Method: Compositional matrix adjust.
Identities = 62/254 (24%), Positives = 100/254 (39%), Gaps = 34/254 (13%)

Query: 41 QHALLIFPGQH-LSNDQQITFAKRFGAI-----ERIGGGDIVAISNV 81
Q ++ F Q L+ND Q A+R G + R+GGGD IS +
Sbjct: 78 QRGVVFRAQDDLNNDLQKELAQRLGELSGKPATSKLHIHPVINSGRRLGGGD-NEISVI 136

Query: 82 KADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM 141
++ +S D K WH+D T+ P+ + A+ +P GG T +A
Sbjct: 137 SSEQAKEIYSKRLLDFAKKQSAKSGWHSIDITFEPIPSDYALLRLTELPKTGGDTLWASG 196

Query: 142 RAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI-----GYGMDTTATPL 194
YD L + +A YSQ + + + + + + T T
Sbjct: 197 YELYDRLSTPYQKFFESLTA----TYSQPEFINAAKEKNFPLYTAPRGAPENVGDTLTTT 252

Query: 195 RPLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHA-HQWA-AG 251
P+++ +P TG S+ +G H I G+ ES L+ V + H+W
Sbjct: 253 HPVIRTNPVTGWKSIFAVGHVQINGLTKEESRTALDWFVSLITDNHDLQVRHRWQNVN 312

Query: 252 DVVVWDNRCLLHRA 265
D+ +WDNR + H A
Sbjct: 313 DLAIWDNRSVYHTA 326

>ref|XP_001258733.1| alpha-ketoglutarate-dependent taurine dioxygenase [Neosartorya
fischeri NRRL 181]
gb|EAW16836.1| alpha-ketoglutarate-dependent taurine dioxygenase [Neosartorya
fischeri NRRL 181]
Length = 388

Score = 68.6 bits (166), Expect = 9e-10, Method: Compositional matrix adjust.
Identities = 68/267 (25%), Positives = 111/267 (41%), Gaps = 29/267 (10%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
+G + G+ L L+D L + +++ F Q +S QQ + FG +E
Sbjct: 93 IGTEIVGLQLKDLNDKQKDELGLLIAERSVVFVRDQDISPQQQKELGEWFGVEVEIHPQVP 152

Query: 69 RIGG--GDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
++ G G V ++A AE + G WH D + A
Sbjct: 153 QVPGVPGVTVLWPALQA-----AETPAAFRRPGGASRWHTDLVHERQPAGVTHLHN 203

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG 186
+ VP+ GG T +A AAY+ L + R + ++A + ++ H ++ G Y+
Sbjct: 204 DTVPSTGGDTLWASGYAAYEKLSPSFRQFIDGKTAIYRSAHAYLDRKHPEK-GPIYVERE 262

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
PLV+VHP TG +L + R I G+D AES+ L L D + +
Sbjct: 263 -----HPLVRVHPATGWKTLWVNRAMTDRIVGLDKAESDVILGYLCDVYEKNIDIQV 314

Query: 246 H-QWAAGDVVVWDNRCLLHRAEPWDFK 271
+W +WDNR +H A WD++
Sbjct: 315 RFKWTPRTSALWDNRITIHNAS-WDYE 340

>emb|CBJ19170.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]

Length = 106

Score = 68.6 bits (166), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 40/111 (36%), Positives = 55/111 (49%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
A YDALD+ TRA + H L+YS+ LG + Y + L+ LV+ HP
Sbjct: 1 AGYDALDDETRAIEDMVCEHPLMYSRGSLGFLD-----YTDEEKEMFKPVLQRLVTRHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA I G E+ FL L++ A Q V+ H+W GD+
Sbjct: 56 VHGRKSLYLSSHAGGIEGWVPPEARAFRLDLIEHATQREFVYTHKWRVGDL 106

>gb|ADC34014.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 68.6 bits (166), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 58/214 (27%), Positives = 92/214 (42%), Gaps = 27/214 (12%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYM 115
QQI FA++FG + +K +P + +V G + WH+D++Y+
Sbjct: 1 QQIAFAQQFG-----QPMEYPQLKGLPECPLVTPVIKLEHERVNFQGV-WHSDTSYL 51

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATR----ALVHQRSARHSLVYSQSK 171
++ A P GG T FA AY+ L E + L+ S+ + V S+S+
Sbjct: 52 ERPPMASMLYAVETPPAGGDTIFATQYLAYETLSEGLQRILAGLIGINSSTKAEV-SRSR 110

Query: 172 LGHVQQAGSAY---IGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESE 227
+++AG+ + IG P+V+ HPETGR +L + H G A ES
Sbjct: 111 EDRLREAGAEHKVLIGE-----HPVVRTHPETGRKALYVNAGHTTNFKGFTEESA 161

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
L L + + W G + WDNRC+
Sbjct: 162 PLLSYLFNHQVRPEFTCRFYWEPGSLAFWDNRV 195

>ref|XP_001387045.1| predicted protein [Scheffersomyces stipitis CBS 6054]
gb|EAZ63022.1| predicted protein [Pichia stipitis CBS 6054]
Length = 378

Score = 68.6 bits (166), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 77/273 (28%), Positives = 112/273 (41%), Gaps = 33/273 (12%)

Query: 5 TLQITPTGATLGATVTGVHLATLDAGFAALHAAWLQHALLIFPGQHLSNDQ---QITFA 61
T ITP LG V GV L+ LD AG L + L++F Q L++ Q
Sbjct: 83 TKNITPK---LGTEVFGVQLSGLDSAGKDELALFVAKRGLVVFRDQDLASKGPAFQTELG 139

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQ--HSPAEDDDMMKVIVGNMAWHADSTYMPVMA 119
+ FG + I S D + + D+ + + +H+D TY +
Sbjct: 140 RHFGPLH-----IHPTSGAPKDHPELHVYRRPDVKDLFEHRNNLVGFHSDVITYE-LQP 192

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV----YSQSKLGH 174
G F A V P GG T FAD AY+ L + + HS V +S+ G
Sbjct: 193 PGTTFLLAVVEGPESGGDTLFAADTVEAYNRLSPEFQKRLEGLHVLHSAVEQANFSRKNQGV 252

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL 233
V++ I PLV+ HP TG +L I + I + ES+ L L
Sbjct: 253 VKRDPVQNI-----HPLVRTHPTVTGEKALFINSGFSRKIVELKEEESDYLLTFL 301

Query: 234 VDWCQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
++ + + A +W A VVVWDNR ++H A
Sbjct: 302 LNHINNSHDLQARAKWEANTVVVWDNRVHSA 334

```
>ref|XP_569951.1| taurine dioxygenase [Cryptococcus neoformans var. neoformans JEC21]
ref|XP_776545.1| hypothetical protein CNBC0390 [Cryptococcus neoformans var.
neoformans B-3501A]
gb|EAL21898.1| hypothetical protein CNBC0390 [Cryptococcus neoformans var.
neoformans B-3501A]
gb|AAW42644.1| taurine dioxygenase, putative [Cryptococcus neoformans var.
neoformans JEC21]
Length = 376
```

Score = 68.6 bits (166), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 54/200 (27%), Positives = 86/200 (43%), Gaps = 11/200 (5%)

```
Query: 72 GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVPA 131
G +I ISN Q S D ++K GN WH+D T+ P + A +P
Sbjct: 130 GDEISVISNQFVFDKNFQKSD--DTVLKRPFGNTLWHSDITFEPHPSDYATLQIRTLPE 186

Query: 132 VGGRTCFADMRAAYDALDEATRALVHQRSA---RHSLVYSQSKLGHVQQAGSAYIGYGM 187
VGG T +A AYD L A R + +A +H + ++ +++ A G
Sbjct: 187 VGGDTLWASSYEAYDR LSPAYRTFLEGLTATHVGHFIDMARKTNATLREPRGAPENVGQ 246

Query: 188 DTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH 246
+A + P+++ +P TG L + R I + ES+R L L + +
Sbjct: 247 HLSA--VHPVIRTNPVTGWKGLFVN RVFTKKINELTPHESDRLLGFLYEHIDGNHDLQVR 304

Query: 247 -QWAAGDVVVWDNRCLLHRA 265
+W ++ +WDNRC H A
Sbjct: 305 FRWEENNLAIWDRCTFHSA 324
```

```
>gb|EFW99341.1| alpha-ketoglutarate-dependent taurine dioxygenase [Grosmannia
clavigera kw1407]
Length = 382
```

Score = 68.6 bits (166), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 73/277 (26%), Positives = 111/277 (40%), Gaps = 35/277 (12%)

```
Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFA 61
T Q+T T G+ V GV L+ L DAG L + ++ F Q L++ + F
Sbjct: 95 TAQVTELTPTTGSEVRGVQLSQLSDAGKNQLARFVAERKVVAFREQDLADLPIADALAFG 154

Query: 62 KRFG-----AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTY 114
FG + + G +I + D Q ++AWH+D +Y
Sbjct: 155 GYFGRHHIHPTSGQPAGYPEIHLVHRGAGDKFAEQ-----FFATR TNSVAWHS DVS Y 206

Query: 115 MPVMAQGAVFSAE VV-PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
+ G F + PA GG T F + AY+ L + +H A HS
Sbjct: 207 E-LQPPGTTFLYILDGPASGGDTL FVNAAEAYNRLSPGLQQRLHGLQATHS----- 256

Query: 174 HVQQAGSAYIGYGM DTTATPL--RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERF 229
++QA ++ G T P+ P+V+ HP TG ++ + + I G ES+
Sbjct: 257 GIEQANTSK-ARGSITRREP VFHAHPVVRTHPATGEKAIYVNPQFTREIVGFKK ESDAL 315

Query: 230 LEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
L+ L D A +W G VV+WDNR H A
Sbjct: 316 LKFLYDHLAYGADFQARVKWE PGTVVIWDRVTQHSA 352
```

```
>ref|XP_001801455.1| hypothetical protein SNOG_11212 [Phaeosphaeria nodorum SN15]
gb|EAT81711.2| hypothetical protein SNOG_11212 [Phaeosphaeria nodorum SN15]
Length = 388
```

Score = 68.6 bits (166), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 67/265 (25%), Positives = 105/265 (39%), Gaps = 16/265 (6%)

```

Query: 13  ATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE---R 69
          A +G + G+ L L          L + +++ F Q +S QQ + +G IE
Sbjct: 96  AHIGTEIVGLQLKDLTAQQKDELGLLIAERSVVFFRDQDISPQQKALGEWYGEIEVHPN 155

Query: 70  IGGGDIVAIISNVKADGTVRQHSPA-EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV 128
          I + ++ V + A E + G WH D + A +
Sbjct: 156 IEKPQVPSVPGVVGTTVIWPALQATERAASFRQTGGASRWHTDLVHERQPAGVTHLHNDT 215

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 188
          +P +GG T +A AAY+ L R ++ R A + + AG Y+
Sbjct: 216 IPKIGGDTLWASGYAAYEKLSPGFRKIIDGREAVYRSAHPYLDNRND-PNAGPKYVER--- 271

Query: 189 TTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH- 246
          + PLV+VHP TG +L + R I G+D AES+ L L D +
Sbjct: 272 -----VHPLVRVHPATGWKALWVNRAMTDRIVGLDRAESDVILNYLYDVYENNVDIQVRF 326

Query: 247 QWAAGDVVWDNRCLLHRAEPWDFK 271
          +W G +WDNR +H A WD++
Sbjct: 327 KWTPGTSALWDNRITIHNAS-WDYE 350

```

>emb|CBJ18969.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 68.2 bits (165), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 41/110 (37%), Positives = 58/110 (52%), Gaps = 5/110 (4%)

```

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
          AAYDALD+AT+A + HSL+ S+++LG S + + L LV+ HP
Sbjct: 1 AAYDALDDATKAEIEDLVCEHSLICSRAQLGF-----SNFTDEERQSMRPVLHKLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
          TGR SLL+ H AI G E+ F+ L++ A Q V+ H+W D
Sbjct: 56 VTGRKSLLSAHIGAIVGWPRPEAMAFIRDLMEHATQPEFVYVHRWTKND 105

```

>ref|XP_754818.2| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
fumigatus Af293]
gb|EAL92780.2| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
fumigatus Af293]
gb|EDP52943.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
fumigatus A1163]
Length = 383

Score = 68.2 bits (165), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 73/271 (26%), Positives = 107/271 (39%), Gaps = 25/271 (9%)

```

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ---HLSNDQQITFAK 62
          +Q+ T+G+ V GV L+ L G L Q ++ F Q HL ++ + F
Sbjct: 96 VQVDNLTPTIGSEVRGVQLSQLTKEGKDQLALYVAQRKVVAFRDQDFAHLPIEKALEFGG 155

Query: 63 RFGA--IERIGGGD---IVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMP 116
          FG I + G + + + AD S AE+ + + WH+D T+
Sbjct: 156 YFGRHHIHQTS GAPRGYPEIHLVHRGAD---DRSGAEF---LATRTNTVTWHSVDVTFEK 208

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
          P GG T FADM AY L R +H A HS + ++
Sbjct: 209 QPPGTTFLYLLDGPTSGGDTLFADMVQAYKRLSPEFRKRLHGLKAVHSGI---EQINASL 265

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVD 235

```

```

      G      G      T      P+V+ HP TG  +L +  +      I G      ES+  L+ L D
Sbjct: 266 NRG----GIARREGITSEHPIVRTHPVTGEKALFVNPQFTRYIVGYKKEESDMLLKFLYD 321

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
      +  +      +W  G VVVWDNR + H A
Sbjct: 322 HIALSQDLQTRVRWLPGTVVVWDNRVVAHSA 352

```

>gb|AAS64598.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
Length = 119

Score = 68.2 bits (165), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 46/126 (36%), Positives = 60/126 (47%), Gaps = 9/126 (7%)

```

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATP-- 193
      T F DMRAAYD L      ++ +      A H  + S+  LG      + +      A P
Sbjct: 1   TEFCDMRAAYDELPA DLKSELEGLHAEHYALNSRFVLGDTDYSEA-----QRNAMPPV 53

Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
      PLV+ H  +GR  L IG HA  I G  AE      L  L++ A Q  V+ H W  GD+
Sbjct: 54  TWPLVRTHAGSGRKFLFIGAHAGRIEGRPLAEGRMLLAELEHATQRRFVYRHSWKVGDL 113

Query: 254 VVWDNR 259
      V+WDNR
Sbjct: 114 VMWDNR 119

```

>ref|XP_001031479.1| hypothetical protein TTHERM_00823770 [Tetrahymena thermophila]
gb|EAR83816.1| hypothetical protein TTHERM_00823770 [Tetrahymena thermophila
SB210]
Length = 298

Score = 68.2 bits (165), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 62/270 (22%), Positives = 111/270 (41%), Gaps = 47/270 (17%)

```

Query: 15  LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERI---- 70
      LG T+  V +  L      F  +  A      H ++      Q L+ DQOI F +++G +  +
Sbjct: 37  LGHTINDVDVNNLTTKQFEDIKDALWTHGVICIKNQKLTMDQQIAFTQKWGKLMILPIQQ 96

Query: 71  -----GGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
      IV + N+  DG+++++ S  E+      WH D  +
Sbjct: 97  AYTKRDPNQPAIVRVGNINIDGSIKENCSDTEY-----WHKDGDFKK--PGEN 142

Query: 123 VFSAEVVP----AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
      F + ++P      VGG+T F      Y  L E  + ++      ++ SQ+ +G  Q
Sbjct: 143 FFISILIPYEIAQVGGQTGFVCSEQVYRDLPENLKEMLQDAQI---IIRSQT-IGDFQHF 198

Query: 179 GSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHA-HAIPGMD--AAESERFLEGLVD 235
      +      P+  HP TGR  I ++  + I  D      S+ F+  +
Sbjct: 199 KEN-----EHYPEAFHPVFLSHPITGRKIFNICQNVENDILFKDGTVKSSKEFISEIE- 251

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      +  ++++HQW  GDVV+WDN  ++H++
Sbjct: 252 ---KTYKIYSHQWEMGDVVIWDNIRVIHKS 278

```

>emb|CBJ18774.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 68.2 bits (165), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 41/111 (36%), Positives = 54/111 (48%), Gaps = 5/111 (4%)

```

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHP 202

```


AAYDALD+ T+A + HSL+YS+ LG V Y L+ LV+ HP
Sbjct: 1 AAYDALDDETKAEIEDMICEHSLMYSRGSLGFVD-----YTDEEKQMFKPVLRVLRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

GR SL + HA I GM E+ L L + A Q V+ H+W D+
Sbjct: 56 VHGRKSLYLSSHAGGIKMSVPEARLLLLRDLTEHATQPEFVYVHKWTLHDL 106

>ref|XP_569491.1| sulfonate dioxygenase [Cryptococcus neoformans var. neoformans JEC21]
ref|XP_776449.1| hypothetical protein CNBC5040 [Cryptococcus neoformans var. neoformans B-3501A]
gb|EAL21802.1| hypothetical protein CNBC5040 [Cryptococcus neoformans var. neoformans B-3501A]
gb|AAW42184.1| sulfonate dioxygenase, putative [Cryptococcus neoformans var. neoformans JEC21]
Length = 388

Score = 68.2 bits (165), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 63/264 (23%), Positives = 102/264 (38%), Gaps = 35/264 (13%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
LG + G+ L L D L + ++ F Q L+ Q+ K FG E
Sbjct: 90 LGTEIVGLQLNQLSDQQKDELALLIAERTVVFVRDQDLTPQTQLELGKYFGTPEIHPSAA 149

Query: 69 ---RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
+ G I+ +++ G V + K WH D T+ P
Sbjct: 150 RVPGLPGVSIITDEVLRSTGRVPDY-----KNPFATQKWHTDLTHEPQPPGVTHLH 200

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSA--RHSLVYSQSKLGHVQQAGSAYI 183
+ +P VGG T ++ AAYD L A + ++ R + Y G ++ +A+
Sbjct: 201 LDHLPVGGGDTLWSSGYAAYDKLSPAFQKVLDDGLEGLYRSAHSYPNPVTGELEPIINAH- 259

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPR 242
P+V+VHP TG +L + R+ I G + +E++ L+ L Q P
Sbjct: 260 -----PIVRVHPATGWKALFVNSRYTIGIKGFEQSEAQAAILQKLFQVYEQNPD 307

Query: 243 VHAH-QWAAGDVVVWDNRCLLHRA 265
+W +WDNR +H A
Sbjct: 308 TQVRFRWTPRSSALWDNRVSIHSA 331

>emb|CBJ18760.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 68.2 bits (165), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 41/111 (36%), Positives = 55/111 (49%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
AAYDALD+ T+A + HSL+YS+ LG + Y L+ LV+ HP
Sbjct: 1 AAYDALDDETKAEIEDMICEHSLMYSRGSLGFLD-----YTDEEKQLFKPVLRVLRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E+ L L + A Q V+ H+W D+
Sbjct: 56 VHGRKSLYLSSHAGAIKGMTVPEARLLLLRDLTEHATQPEFVYVHKWTLHDL 106

>gb|ADC33966.1| TfdA-like protein [uncultured bacterium]
Length = 123

Score = 68.2 bits (165), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 49/129 (37%), Positives = 62/129 (48%), Gaps = 9/129 (6%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVY-SQSKLGHVQQA-GSAYIGYGMDDTTATP 193
T F DM AAYDAL E R + + +H Y + KL A +G G P
Sbjct: 1 TEFCDMYAAYDALPEVLRKRIRGATIKHDTAYDTNRKLRRDAVAVDDPRLGDG-----P 54

Query: 194 LRPLVKVHPETGRPSLLIGRHA-HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
P+V HP+TG SL +GR H + G ES L+ L A Q +H W GD
Sbjct: 55 DHPIVSTHPDTGCNSLFLGRRPRHYVNGYTLLEESAALLDVLWAHATQPRFRISHAWRQGD 114

Query: 253 VVVWDNRCL 261
VV+WDNRC+
Sbjct: 115 VVMWDNRVCV 123

>ref|XP_003042297.1| predicted protein [Nectria haematococca mpVI 77-13-4]
gb|EEU36584.1| predicted protein [Nectria haematococca mpVI 77-13-4]
Length = 378

Score = 68.2 bits (165), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 76/278 (27%), Positives = 114/278 (41%), Gaps = 34/278 (12%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
++T A +G + G+ L L + L + +++ F Q LS QQ + +G
Sbjct: 85 KVTDLTAHIGTEIEGLQLKDLTNEQRDELALLIAERSVVFRRDQDLSPQQKELGEWYGE 144

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQ 120
+E ++ G V+I T R PA + G WH D + A
Sbjct: 145 VEVHPQVAQVPGLPGVSIWPDQLATER---PA---TFRQPGGASRWHTDLVHERQPAG 197

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
+ VP+VGG T +A AAY+ L R ++ RSA + + +AG
Sbjct: 198 ITHLHNDTVPSVGGDTLWASGYAAYEKLSPFRKIIDGRSAVYRSAPYLDLDRDD-PEAGP 256

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
YI + PLV+VHP TG +L + R I G+D AES+ L L D +
Sbjct: 257 KYIER-----IHPLVRVHPATGWKALWVNRAMTDRIVGLDKAESDIILGYLYDVYEK 308

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRAEPWDF--KLPR 274
+ +W V+WDNR WD+ K PR
Sbjct: 309 NIDIQLRWRWTPRTSVLWDNR-----WDYSKEPR 338

>gb|AAS64593.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
Length = 119

Score = 68.2 bits (165), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 46/126 (36%), Positives = 60/126 (47%), Gaps = 9/126 (7%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP-- 193
T F DMRAAYD L ++ + A H + S+ LG + + A P
Sbjct: 1 TEFCDMRAAYDELPA DLKSELEGLHAEHYALNSRFVLGDTDYSEA-----QRNAMPPV 53

Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 54 TWPLVRTHAGSGRKFLFIGAHAGRIEGRPLAEGRMLLAELEHATQRRFVYRHSWEVGDL 113

Query: 254 VVWDNR 259
V+WDNR
Sbjct: 114 VMWDNR 119

>ref|YP_002799362.1| TauD/TfdA family taurine catabolism dioxygenase [Azotobacter
vinelandii DJ]
gb|ACO78387.1| Taurine catabolism dioxygenase TauD/TfdA family [Azotobacter

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQ 57
+ +T +I+ +G+ V GV L L DA L + ++ FP Q L + ++Q
Sbjct: 72 LLSSTARISHIOPCIGSIVEGVOLNKLSDAAKDELALLIAERKVVAFPPDODLIDAGPEEQ 131

Query: 58 ITFAKRFGA--IERIGGG--DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST 113
+ F + FG + I G + DG V E + ++ WH D +
Sbjct: 132 YSFMRFHGKPNYQPISGSMKGYPGFHIIHRDGNV-----DEINRFLEQRTTTTLWHQDVS 186

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
Y + P VGG T FA AAY L ++ + A H+ S +
Sbjct: 187 YEIQPPAYVMLGLLQGPDVGGDTVFAATDAAYKRLSPTFQSFIDNLKAVHT---SAKMIA 243

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEG 232
H + G G + PLV+VHP TG L I G I G+ E + +
Sbjct: 244 HARLTG----GLVRKDPVESVHPLVRVHPVTGEKCLFINGEFITKIQGLKEPEFRVLQDF 299

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
L+ A +W VV++DNR +H A
Sbjct: 300 LMQHLITGHDFQARVRWQPRTVVMFDNRSTIHS 333

>emb|CBJ18836.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 68.2 bits (165), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 41/110 (37%), Positives = 58/110 (52%), Gaps = 5/110 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD+ T+A + HSL+YS+++LG S + + L LV+ HP
Sbjct: 1 AAYDALDDDTKAEIEDLVCEHSLIYSRARLG-----FSNFTDEERHSMRPVLHKLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
TGR SLL+ H AI G E+ F+ L++ A Q V+ H+W D
Sbjct: 56 VTGRKSLLSAHIGAIVGWPRPEAMAFIRDLMEHATQPQFVYVHRWTKHD 105

>emb|CBJ18778.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 68.2 bits (165), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 42/111 (37%), Positives = 54/111 (48%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALDE TR + HSL+YS+ LG + Y L+ LV+ HP
Sbjct: 1 AAYDALDEETRTEIEDMICEHSLMYRSLGFLD-----YSEEEQQLFKPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL+ HA AI GM E+ L L+ A Q V+ H+W D+
Sbjct: 56 VHGRKSLYLSSHAGAILGMSPEARLLLRDLTEHATQPQFVYVHKWKVHDL 106

>ref|XP_748422.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
fumigatus Af293]
gb|EAL86384.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
fumigatus Af293]
Length = 388

Score = 67.8 bits (164), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 65/260 (25%), Positives = 106/260 (40%), Gaps = 15/260 (5%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE-RIGGG 73
+G + G+ L L+D L + +++ F Q +S QQ + FG +E
Sbjct: 93 IGTEIVGLQLKDLNDKQKDELGLLIAERSVVFFRDQDISPQQKELGEWFGEVEVHPQVP 152

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVG 133
+ + V Q AE + G WH D + A + VP++G
Sbjct: 153 QVPGVPGVTVLWPALQA--AETPAAFRRPGGASRWHTDLVHERQPAGVTHLHNDTVPSIG 210

Query: 134 GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP 193
G T +A AAY+ L + R + ++A + + H ++ G Y+
Sbjct: 211 GDTLWASGYAAEKLSPSFRQFIDGKTAIYRSAHPYLDRKHPEK-GPVYVERE----- 262

Query: 194 LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAG 251
PLV+VHP TG +L + R I G+D AES+ L L D + + +W
Sbjct: 263 -HPLVRVHPATGWKTLWVNRAMTVRIVGLDKAESDVILGYLCDVYEKNIDIQVRFKWTPR 321

Query: 252 DVVVWDNRCLLHRAEPWDFK 271
+WDNR +H WD++
Sbjct: 322 TSALWDNRITIHNVS-WDYE 340

>emb|CBJ18775.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 67.8 bits (164), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 41/111 (36%), Positives = 55/111 (49%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD+ T+A + HSL+YS+ LG + Y + L+ LV+ HP
Sbjct: 1 AAYDALDDDTKAEIEDMICEHSLMYSRGLGFLD-----YTDEEKEMFKPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
R SL + HA AI GM E+ L L + A Q VH H+W D+
Sbjct: 56 VHRKSLYLSSHAGAIKMSMPEARLLLLRDLTEHATQPTFVHVHKWTLHDL 106

>ref|XP_659804.1| hypothetical protein AN2200.2 [Aspergillus nidulans FGSC A4]
gb|EAA63857.1| hypothetical protein AN2200.2 [Aspergillus nidulans FGSC A4]
tpe|CBF86370.1| TPA: alpha-ketoglutarate-dependent taurine dioxygenase
(AFU_orthologue; AFUA_8G02210) [Aspergillus nidulans
FGSC A4]
Length = 383

Score = 67.8 bits (164), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 77/278 (27%), Positives = 112/278 (40%), Gaps = 33/278 (11%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
++TPT +G+ VTGV L++L AG L Q ++ F Q + D I A +FG+
Sbjct: 90 KLTPT---IGSEVTGVQLSSLSAAGKDQLALLVAQRKVVAFRDQDFA-DLPIADALKFGS 145

Query: 67 IERIGGGDIVAISNVKADGTV-----RQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ 120
G + ++ + +G R S E D +AWH+D TY
Sbjct: 146 Y---FGRHHIHPTSGQPEGYPEIHLVHRHSSKGELDAFFADRNSTVAWHS DVTYEAQPPG 202

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
P VGG T F D AY L A + +H A HS + Q++ +Q G
Sbjct: 203 TTFLYILDTPEVGGDTAFVDQVEAYRRLSPAIKERLHGLKAVHS-GFEQAEFS--RQRG- 258

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHA-----HAIPGMDAAESER 228
G P+V+ HP TG +L + +I G+ ES+
Sbjct: 259 ---GVVRRDPVKNEHPIVRTHPVTGEKALFVNGGCLKKDPADGCAVTRSIVGLKKEESDA 315

Query: 229 FLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
L L++ + A +WA VVVWDNR H A
Sbjct: 316 LLGFLLNHVGRGIDYQARIKWAPRTVVVWDNRVTAHSA 353

>gb|ACG80578.1| TfdA [uncultured bacterium]
Length = 120

Score = 67.8 bits (164), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 40/122 (32%), Positives = 60/122 (49%), Gaps = 3/122 (2%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPL 197
F DMRAA++AL +A + HS++ S+ + G + A + + PL
Sbjct: 2 FGDMAAANALPPERQAQLEHLQVVHSILRSREQTGFTVEKFDAQT---LKDHPHAVHPL 58

Query: 198 VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWD 257
V+ HP GR SL + HA I G +E L+ +A Q V++H W D+V+WD
Sbjct: 59 VRTHPCNGRKSLLYLASHASHIVGWPLERGRALIEELIAFATQPRFVYSHSWQLHDLVMWD 118

Query: 258 NR 259
NR
Sbjct: 119 NR 120

>ref|XP_001273439.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
clavatus NRRL 1]
gb|EAW12013.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
clavatus NRRL 1]
Length = 376

Score = 67.8 bits (164), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 72/273 (26%), Positives = 107/273 (39%), Gaps = 29/273 (10%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
+++T +G+ V GV L+ L +A L + ++ FP Q L D +RF
Sbjct: 86 VKVTEIQPQIGSIVEGVQLSQLSNAKDELALLVSEKVVAFPAQDLI-DAGPEHLERF- 143

Query: 66 AIERIGGGDIVAISNVKADGTVRQH-----SPAEWDDMMKVIVGNMAWHADSTYM 115
+ G + +S GTVR H + E ++ WH D +Y
Sbjct: 144 -MSHFGKPNYQPVS-----GTVRNHPGFHIIHRDGNKQEIARFLEQRTTTTLWHQDVSYE 197

Query: 116 PVMAQGAVFSAEYV-PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
+ G V + P VGG T FA AY L + + A HS S + H
Sbjct: 198 -IQPPGYVMLGLLEGPEVGDTVFATDMAYKRLSPTFTSFLDGLRAVHS---SAKMINH 253

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGL 233
+ G +DT + PLV+VHP TG L I G I G+ E + L
Sbjct: 254 TRLMGLVRKDPVDT----VHPLVRVHPVTGEKCLFINGEFITRIQGLKEPEQRYLTDFL 309

Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ A +W +V++DNRC +H A
Sbjct: 310 MQHIVTGHDFQARVRWQPKTIVIFDNRCTIHS 342

>emb|CBJ19198.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 67.8 bits (164), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 42/110 (38%), Positives = 58/110 (52%), Gaps = 5/110 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD+AT+A + HSL+YS+++LG S + + L LV HP
Sbjct: 1 AAYDALDDATKAEIEDLVCEHSLIYSRAQLG-----FSNFTDEERHSMRPVLHKLVCVTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
TGR SLL+ H AI G E+ F+ L++ A Q V+ H+W D
Sbjct: 56 VTGRKSLLSAHIGAIVGWPRPEAMAFIRDLMEHATQPQFVYVHRWTKHD 105

>ref|XP_001483210.1| hypothetical protein PGUG_05165 [Meyerozyma guilliermondii ATCC
6260]

gb|EDK41067.1| hypothetical protein PGUG_05165 [Meyerozyma guilliermondii ATCC 6260]
Length = 403

Score = 67.8 bits (164), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 74/283 (26%), Positives = 107/283 (37%), Gaps = 51/283 (18%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
Q+TP +G + G+ L L++ L + +++ Q LS +Q+ K +G
Sbjct: 111 QLTPQ---VGTELVGIOLEKLNEKQLDELALLIAERVVVIRNQDLSPQKQLAIGKYYGE 167

Query: 67 IE-----RIGG--GDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
+E + G G S G + + + N WH D +
Sbjct: 168 VEVHPLVAHVPGYPGITTWSKFNRRGGPLISYQKG-----IHN-GWHQDMDHERSP 217

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
A + VP VGG T FA AAYD L + + + +R+A H +S K +V A
Sbjct: 218 AGITHLHLDVPEVGGDTGFASGYAAYDKLSKTLQEFLEKRTALHRSASHSYLKRDNVLAA 277

Query: 179 GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL---- 233
+ PLV HP TG SL + R H I G++ +ES LE L
Sbjct: 278 PEPIVRE-----HPLVITHPATGWKSLFVNRAHTFKIVGLEDSSESAVLLEYLFSVY 328

Query: 234 -----VDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEP 267
V W P G V+WDNR H A P
Sbjct: 329 ERNLDVQTRVTWQPTPEP-----GLGTSVLWDNRISQHIAIP 364

>emb|CBJ18750.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 67.8 bits (164), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 42/112 (37%), Positives = 56/112 (50%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAAGSAYIGYGMDDTTATPLRP-LVKVH 201
AAYDALD+ TRA++ HSL+YS+ +G + P+R LV+ H
Sbjct: 1 AAYDALDDKTRAMIEDVCEHSLMYSRSGSMGFTELTDE-----KAMMKPVRQRLVRRH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P TGR SL + HA I G ES FL L + A Q V+ H+W D+
Sbjct: 55 PVTGRKSLYLSSHAGNIVGWLVPESRDFLRDLNEHATQRELVIYVHRWRQYDL 106

>ref|ZP_01692308.1| putative dioxygenase [Microscilla marina ATCC 23134]
gb|EAY26667.1| putative dioxygenase [Microscilla marina ATCC 23134]
Length = 298

Score = 67.8 bits (164), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 57/258 (22%), Positives = 104/258 (40%), Gaps = 35/258 (13%)

Query: 26 TLDDAGFAALHAAWLQHALLIFPGQHLSND--QQITFAKRFGAIERI-----GGGDI 75
T D + A ++ L++ GQ++ ++ + + F ++ G + ++
Sbjct: 30 THDAPELEEIRQAIYRNKLIVIKGQNMGDNP AEYVEFTRKLGTPQVYFQENYHHPDFPEV 89

Query: 76 VAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGR 135
SN+ +G + + V WH D + + V+P
Sbjct: 90 FVSSNINKEG-----EKVGVAGTGKYWHTDCQFEQKPLSFTSITPVVIPNTVRA 138

Query: 136 TCFADMRAAYDALDEATRALV-----HQRSARHSLVYSQSKLGHVQQAAGSAYIGYGMDDT 189
T + DM Y+ L +ALV H + R+ + + + ++ I Y M+
Sbjct: 139 TYYIDMHKVENLPADLKALVEGATMIHGGNNRYKV-----QPCDIDKSIQQLIDY-MNE 192

Query: 190 TATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQ 247

P+ P V HP G L + I G+ E+E+ ++ L D+ Q +H H
Sbjct: 193 IVPPVEHPAVIEHPVNGDKILYMSSGFTMKIKGLTYEENEKAMKALFDFIEQEKHIIHHS 252
Query: 248 WAAGDVVVWDNRCLLHRA 265
W AGD+++WDNR LLH +
Sbjct: 253 WDAGDLIIWDNRYLLHMS 270

>ref|XP_001261550.1| alpha-ketoglutarate-dependent taurine dioxygenase [Neosartorya
fischeri NRRL 181]
gb|EAW19653.1| alpha-ketoglutarate-dependent taurine dioxygenase [Neosartorya
fischeri NRRL 181]
Length = 376

Score = 67.8 bits (164), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 69/267 (25%), Positives = 103/267 (38%), Gaps = 35/267 (13%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRFGAIERIG 71
+G+ V GV L+ L DA L + ++ FP Q L + ++ F + FG
Sbjct: 95 IGSVVEGVQLSLSDAAKDELALLVSRKVVAFPAQDLIDAGPEKLEQFMRHFQKP---- 150
Query: 72 GGDIVAISNVKADGTVRQH-----SPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
+ GTVR H + E ++ WH D +Y + G
Sbjct: 151 -----NYQPVSGTVRDHPGFHIIHRDGNRQEIARFLEQRTTTTLWHQDVSYE-IQPPG 202
Query: 122 AVFSAEVV-PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
V + P VGG T FA AY L + + A HS S + H + G
Sbjct: 203 YVMLGLLEGPEVGGDTVFAATDMAYKRLSPTFTSFLDGLRAVHS---SAKMINHTRLIGG 259
Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVDWACQ 239
+DT + PLV++HP TG L I G I G+ E ++ L+
Sbjct: 260 LVRKDPVDT----VHPLVRIHPVTGEKCLFINGEFITRIQGLKEPEQRYLIDFLMQHIMT 315
Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
A +W +V++DNRC +H A
Sbjct: 316 GHDFQARVRWQPKTIVIFDNRCTIHS 342

>ref|ZP_02414615.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 14]
ref|ZP_02458875.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 9]
Length = 176

Score = 67.4 bits (163), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 48/141 (34%), Positives = 65/141 (46%), Gaps = 5/141 (3%)

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY---SQSKLGHVQQAGSAYIG 184
+P GG T +A+ AAY L + + LV + A H + S+ +L H A
Sbjct: 3 LPDAGGDTVWANTVAAYQHLPSSLQDLVDKLWAVHGNDYFQYAAASRVELLHDPVAKEYRKK 62
Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH 244
Y T P+V++HPETG SLL+G +A D +S R E L +
Sbjct: 63 YAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRQVQYDTHDSNRLYEILQAHITRLENTV 121
Query: 245 AHQWAAGDVVVWDNRCLLHRA 265
WAAGDV +WDNR H A
Sbjct: 122 RWHWAAGDVAIWDNRSTQHIA 142

>ref|ZP_03545787.1| Taurine dioxygenase [Comamonas testosteroni KF-1]
gb|EED70073.1| Taurine dioxygenase [Comamonas testosteroni KF-1]
Length = 303

Score = 67.4 bits (163), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 67/302 (22%), Positives = 124/302 (41%), Gaps = 41/302 (13%)

```
Query: 2  AQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
      + T +++      +G V+G+ L  + +      L A + H +L+F Q+++ Q + F
Sbjct: 19  SSTGIELRRISPAIGVEVSGIDLRQPMSEEQTRELRQALVAHKVLFREQNITPAQHVAF 78

Query: 61  AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMM-----KVIVGNMAWHADSTYM 115
      A+RFG +E      V H P  + ++      KV      +H D ++
Sbjct: 79  ARRFGELEL-----HPVFPHPDHAELVLLGGNSKVPGTENVYHTDVSWR 123

Query: 116  PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS-QSKLGH 174
      + +V      P VGG T + +M AY+ L E  + +      A H ++ S +++
Sbjct: 124  ETPSMASVLRCEVEVGGDTVWINMEQAYEQLPETRKQQIAGLYAVHDILPSFGARMT 183

Query: 175  VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-----HAAHAIIPGMDAAESERF 229
      +QA +      + P+V+ HPE+GR L +      A+      D+ S
Sbjct: 184  AEQAQA-----RGKYPPVHPVVRTHPESGRKILYVNETFVTHFANFSSNFDSFRSANE 237

Query: 230  L----EGLVDWACQAPRVHAHQ---WAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRL 281
      +      + L+D+ + P + +Q      W      + +WDNR H A      F + R M + +
Sbjct: 238  IHAQQQDLMDYLLRQPAILEYQMRHLHWEPTNTIAMWDNRSTQHYAIQDYFPVVRMRHRTV 297

Query: 282  AG 283
      G
Sbjct: 298  KG 299
```

>ref|ZP_02484885.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 7894]
Length = 176

Score = 67.4 bits (163), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 48/141 (34%), Positives = 65/141 (46%), Gaps = 5/141 (3%)

```
Query: 129  VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY---SQSKLGHVQQAGSAYIG 184
      +P GG T +A+ AAY L + + LV + A H +      S+ +L H A
Sbjct: 3  LPDAGGDTVWANTVAAYQHLPSSLQDLVDKLWAVHGNDFDYAASRVELLHDPVAKEYRKK 62

Query: 185  YGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH 244
      Y      T      P+V++HPETG SLL+G +A      D +S R E L      +
Sbjct: 63  YAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRFVQYDTHDSNRLYEILQAHITRLENTV 121

Query: 245  AHQWAAGDVVVWDNRCLLHRA 265
      WAAGDV +WDNR H A
Sbjct: 122  RWHWAAGDVVAIWDNRSTQHAYA 142
```

>emb|CBJ18745.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 67.4 bits (163), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 40/111 (36%), Positives = 56/111 (50%), Gaps = 5/111 (4%)

```
Query: 143  AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
      AAYDALD+ T+A +      HSL+YS+ LG +      Y      +      L+ LV+ HP
Sbjct: 1  AAYDALDDETKAEIEDMICHEHSLMYSRGSLSGLFD-----YTDEEKEMFKPVLQRLVRTHP 55

Query: 203  ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
      GR SL + HA AI GM E+ L L + A +      V+ H+W D+
Sbjct: 56  VHGRKSLYLSHAGAILGMSVPEARLLLRDLTEHATKPEFVYVHKWTLHDL 106
```

>gb|ADI34074.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 4HD6]
Length = 118

Score = 67.4 bits (163), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 42/122 (34%), Positives = 59/122 (48%), Gaps = 7/122 (5%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-P 196
F DMRAAYD L E + + A H ++S+ LG + + S P+ P
Sbjct: 2 FCDMRAAYDDLPEDFKKELQGLRAEHYALHSRFLGDTEYSES-----QRNAMPPVSWP 55

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVW 256
L++ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+W
Sbjct: 56 LIRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQPKFVYRHSWKVGDVLMW 115

Query: 257 DN 258
+
Sbjct: 116 ET 117

>ref|XP_001389970.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
niger CBS 513.88]
emb|CAK38041.1| unnamed protein product [Aspergillus niger]
Length = 372

Score = 67.4 bits (163), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 64/274 (23%), Positives = 107/274 (39%), Gaps = 31/274 (11%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAK 62
+Q+T T+G + G+ L+ L AG L + ++ F Q ++ D+ + FA+
Sbjct: 86 VQVTHLPTTIGTEIRGIQLSQLSAAGKDLARYVAERKVVAFAQDFASLPIDKAVDFAR 145

Query: 63 RFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
FG + G ++ + D + + + ++ ++AWH+D +Y
Sbjct: 146 YFGPLHIHPTSGSPEGFPEVHLVHRAAGDRSAQAY-----LQTRTTSVAWHSDVSYSY 197

Query: 116 PVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
P GG T F+D AY L A + +H HS V
Sbjct: 198 AQPPGTTFLYILEKPEAGGDTLFSDTVQAYRRLSPAIQERLHGLEVVS-----GV 248

Query: 176 QQAGSAYIGYGM--DTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEG 232
+QA ++ G+ P+V+ HP TG +L + + + G+ ES L+
Sbjct: 249 EQANTSLSRGGILRRDPVVSTHPIVRTHPVTGEKALFVNPQSGREVVGLKQEESMMLKF 308

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
L D +W VVVWDNR H A
Sbjct: 309 LYDHIASGADFQVRVRWEENSVVVWDNRVTQHTA 342

>gb|ADI34073.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 4HD5]
gb|ADI34077.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 10DK.3]
Length = 118

Score = 67.4 bits (163), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 42/122 (34%), Positives = 59/122 (48%), Gaps = 7/122 (5%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-P 196
F DMRAAYD L E + + A H ++S+ LG + + S P+ P
Sbjct: 2 FCDMRAAYDDLPEDFKKELQGLRAEHYALHSRFLGDTEYSES-----QRNAMPPVSWP 55

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVW 256
L++ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+W
Sbjct: 56 LIRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQPKFVYRHSWKVGDVLMW 115

Query: 257 DN 258
+
Sbjct: 116 ET 117

>emb|CAY25791.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 67.4 bits (163), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 61/110 (55%), Gaps = 18/110 (16%)

Query: 33 AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV-----AISN 80
A + A ++A+L+FPGQ +++DQQ+ FA FG E++ GG++ +SN
Sbjct: 14 ADIEAGMDKYAVLLFPQDVTDDQQLAFALNFGEREQVHGGNVTRKEDYRLTSGLNDVSN 73

Query: 81 VKADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
+ DG + P DD + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 74 LGKDG-----KPLPRDDRTHLFNLGNSLWHSOSSFRPIPAKFSLLSARVV 118

>ref|YP_713492.1| putative taurine dioxygenase [Frankia alni ACN14a]
emb|CAJ61925.1| putative Taurine dioxygenase [Frankia alni ACN14a]
Length = 266

Score = 67.4 bits (163), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 74/262 (28%), Positives = 100/262 (38%), Gaps = 34/262 (12%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L I P GA V G+ L T L A L +H +L+F Q L + FA+ F
Sbjct: 12 LTILPLSPRFGAEVGGIDLRDLDTPERRALLRLLFEHGVLVFRDQALDTAGHVAFAEAF 71

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVF 124
G I +V S V + PA + +V G++ WH D++ +P V
Sbjct: 72 GQI-----LVFTSVVDPE-----PAR-PGVHEVHGGSVGWHFDASSLPAPPVATVL 116

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
A VPA G T +A AAY AL RAL R H G +
Sbjct: 117 RAVRVPAEGNDTLWASGVAAAYQALTPELRALATGRYVTH-----GRGVVR 161

Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIGR---HAAHAI PGMDAAESERFLEGLVDWACQAP 241
D LV+ HP TG L I + I GM +S+ + L +
Sbjct: 162 GPDDERPVVAHRLVRRHPHTGEHYLYINLPDWDSPLILGMSPPDSALVAELRAAYLRPE 221

Query: 242 RVHAHQWAAGDVVVWDNRCLLH 263
W G +V+WDN +LH
Sbjct: 222 HQIRLHWTPGTIVLWDNLAVLH 243

>emb|CBJ18744.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 67.0 bits (162), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 43/114 (37%), Positives = 57/114 (50%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---PLRPLVK 199
AAYDALDE T+A + HSL+YS+ LG ++ Y + A L+ LV+
Sbjct: 1 AAYDALDEDTKAEIDDMICEHSLMYSRGS LG-----FLDYTDEEKAMFKPVLQRLVR 52

Query: 200 VHPETGRPSLLIGRHAHAI PGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP R SL + HA AI GM E+ L L + A Q VH H+W D+
Sbjct: 53 THPVHRRKSLYLSSHAGAIQGMSIPEARLLLRDLTEHATQPEFVHVHKWTLHDL 106

Score = 67.0 bits (162), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 51/127 (40%), Positives = 68/127 (53%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTAT--- 192
 T FADMRAAYDALD+ +A + HSL+YS+ LG ++ Y + A
 Sbjct: 1 TEFADMRAAYDALDDAKAEIEDMICEHSLMYSRSLG-----FLDYTDEEKAMFKP 52

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
 L+ LV+ HP R SL + HA AI GM E+ L L + A Q V+ H+W D
 Sbjct: 53 VLQRLVRTHPVHRRKSLYLSSHAGAILGMSPEARLLLRDLTEHATQREFVYVHKWTLHD 112

Query: 253 VVVWDNR 259
 +V+WDNR
 Sbjct: 113 LVMWDNR 119

>ref|ZP_08209666.1| taurine dioxygenase [Novosphingobium nitrogenifigens DSM 19370]
 gb|EGD58043.1| taurine dioxygenase [Novosphingobium nitrogenifigens DSM 19370]
 Length = 259

Score = 67.0 bits (162), Expect = 3e-09, Method: Compositional matrix adjust.
 Identities = 73/265 (27%), Positives = 112/265 (42%), Gaps = 20/265 (7%)

Query: 27 LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA--IERIGGGDIVAISNVKAD 84
 L D A L AA ++ +L F Q L+ +Q A FG I I + NV
 Sbjct: 7 LTDEARAELKAALVERQVLFRRDQTLTEVEQRDLAAGFGPLHIHPI----YPSAPNVPEI 62

Query: 85 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAA 144
 + D + + N WH+D ++ + GAV A+ VP VGG T +A AA
 Sbjct: 63 MVL-----DTALNDLRDNATWHSVDFTKSPSFGAVLLAKQVPEVGGDTLWASAAAA 114

Query: 145 YDALDEATRALVHQRSARHSLV--YSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHP 202
 YDAL E + + A H + + + G ++ + + P+++ P
 Sbjct: 115 YDALPEGMTWLATLEATHDIAKSFPAERFGFDEET-KLKLEAAKRSNPPITHPVIRTLP 173

Query: 203 ETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
 +TGR + + I GM+ +E L L + +W AGDV +WDNR
 Sbjct: 174 DTGRKVIFVSEGFTTGIVGMEPPLAEPLLAMLFHVRPEFTVRWKWRAGDVAIWDNRST 233

Query: 262 LHRAEPWDF-KLPRVMWHSRLAGRP 285
 H A +D+ K RVM + + G P
 Sbjct: 234 QHYAT-YDYGKTRRVMNRATIVGDP 257

>gb|EFY87660.1| alpha-ketoglutarate-dependent taurine dioxygenase [Metarhizium
 acridum CQMa 102]
 Length = 382

Score = 67.0 bits (162), Expect = 3e-09, Method: Compositional matrix adjust.
 Identities = 73/271 (26%), Positives = 106/271 (39%), Gaps = 26/271 (9%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
 Q+TPT +G+ V+G+ L++L DAG L + ++ F Q + D I A ++G
 Sbjct: 95 QLTPT---IGSEVSGIQLSSLS DAGKDELAHFVAKRKVVAFRNQDFA-DLSIPDALKYG- 149

Query: 67 IERIGGGDIVAISNVKADGTVRQH--SPAEWDD---MMKVIVGNMAWHADSTYMPVMAQ 120
 E G I S +G H E D + ++AWH+D +Y
 Sbjct: 150 -EYFGRHHIHPTSGA-PEGYPEIHLVHRGEGDKGAAQFFEARTSSVAWHSVDVSYEQPPG 207

Query: 121 GAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
 P GG T F D AY+ L + +H A HS + + A +
 Sbjct: 208 TTFYLILNKPETGGDTLFDVAVQAYNRLSPLFQERLHGLRATHSGIEQVN-----AAA 260

Query: 181 AYIGYGMTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMDAAESERFLEGLVD 235
 A P+V+ HP TG +L I I G+ ES+ L+ L D
 Sbjct: 261 ARNSIKRREPVDNDHPVIRTHPATGEKALYINPQYATIVTREILGLKREESDAILKFLYD 320

Query: 236 WACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
A +W G VV+WDNR H A
Sbjct: 321 HLAYGADFQARVKWEEGTVVIWDNRVTQHTA 351

>gb|ADC34009.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 67.0 bits (162), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 57/214 (26%), Positives = 92/214 (42%), Gaps = 27/214 (12%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYM 115
QQI FA++FG + +K +P + +V G + WHD++Y+
Sbjct: 1 QQIAFAQQFG-----QPMEYPQLKGLPECPLVTPVIKLEHERVNFGGV-WHSDTSYL 51

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR----ALVHQRSARHSLVYSQSK 171
++ A P GG T FA AY+ L E + L+ S+ + V S+S+
Sbjct: 52 ERPPMASMLYAVETPPAGGDTIFATQYLAYETLSEGLQRILAGLIGINSSTKAEV-SRSR 110

Query: 172 LGHVQQAGSAY---IGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESE 227
+++AG+ + IG P+V+ HPETGR +L + H G A ES
Sbjct: 111 EDRLREAGAEHKVLIGE-----HPVVRTHPETGRKALYVNAGHTTNFKGFTAEEESA 161

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCL 261
L L + + W G + W+NRC+
Sbjct: 162 PLLSYLFNHQVRPEFTCRFYWEPGSLAFWENRCV 195

>emb|CBJ18952.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 67.0 bits (162), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 41/111 (36%), Positives = 54/111 (48%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
A YDALD TRA + HSL+YS+ LG + Y + L+ LV+ HP
Sbjct: 1 AGYDALDGETRAEIEDMVCEHSLMYSRGSGLGFLD-----YTDEEKEMFKPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E+ L L + A Q V+ H+W D+
Sbjct: 56 VHGRKSLLYLSSHAGAIQGMSPPEARLLLRDLTEHATQPEFVYVHKWTLHDL 106

>ref|XP_001483830.1| hypothetical protein PGUG_04559 [Meyerozyma guilliermondii ATCC
6260]
Length = 423

Score = 67.0 bits (162), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 69/279 (24%), Positives = 110/279 (39%), Gaps = 44/279 (15%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
+G + G+ L+ L+D L + ++ F Q LS +Q+ K FG +E
Sbjct: 128 VGTEIVGLQLSELNDKQKDELALLIAERVVVFVRDQDLSPQKQLELGKYFGQVEVHAQVP 187

Query: 69 ----RIGGGDIVAISNVKADGTVRQHS-PAEDMMKVIVGNMAWHADSTYMPVMAQGAV 123
+ G D+ IS + D + P + I GN WH D + A
Sbjct: 188 RVPNGVDGKDLNGISVIWQDYAREYYGLPLTFKSS---IGGNSQWHTDLVHEFQPA GITH 244

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA----RHSLVYSQSKLG---HVQ 176
+ +P+VGG T +A AYD L A + + ++A HS + ++ L H++
Sbjct: 245 LHNDIAIPSVGGDTLWASGYGAYDKLSPALQQFLDGKTAIYRSAHSYINRENPLNGPRHIE 304

Query: 177 QAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVD 235
+ P+++ HP TG SL + R I G++ ES LE L
Sbjct: 305 RE-----HPIIRTHPATGWKSLFVNRSMTVRIVGLNPEESRILLEYLFG 348

Query: 236 WACQAPRVHAH-QWAA----GDVVVWDNRCLLHRAEPWD 269
+ + W + G +WDNR H A WD
Sbjct: 349 VFEKNLDIQVRFNWKS KPG LGTSALWDNRISQHNA-VWD 386

>emb|CBJ18724.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 67.0 bits (162), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 42/114 (36%), Positives = 57/114 (50%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTAT---PLRPLVK 199
AAYDALD+ T+A + HSL+YS+ LG ++ Y + A L+ LV+
Sbjct: 1 AAYDALDDDTKAEIEDMICHESLMYSRGS LG-----FLDYTDEEKAMFKPVLQRLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDV 253
HP GR SL + HA AI GM E L L + A A V+ H+W D+
Sbjct: 53 THPVHGRKSLYLSSHAGAIRGMSVPEGRLLLRDLTEHATSAEFVYVHKWTVHDL 106

>gb|EDK40461.2| hypothetical protein PGUG_04559 [Meyerozyma guilliermondii ATCC
6260]
Length = 423

Score = 67.0 bits (162), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 69/279 (24%), Positives = 110/279 (39%), Gaps = 44/279 (15%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIER----- 69
+G + G+ L+ L+D L + ++ F Q LS +Q+ K FG +E
Sbjct: 128 VGTEIVGLQLSELNDKQKDELALLIAERVVFFRDQDLSPQKQLELGKYFGQVEVHAQVP 187

Query: 70 -----IGGGDIVAISNVKADGTVRQHS-PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
+ G D+ IS + D + P + I GN WH D + A
Sbjct: 188 RVPNGVDGKDLNGISVIWQDYAREYYGLPLTFKSS---IGGNSQWHTDLVHEFQIPAGITH 244

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSA----RHSLVYSQSKLG---HVQ 176
+ +P+VGG T +A AYD L A + + ++A HS + ++ L H++
Sbjct: 245 LHNDIAIPSVGGDTLWASGYGAYDKLSPALQQFLDGKTAIYRSAHSYINRENPLNGPRHIE 304

Query: 177 QAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVD 235
+ P+++ HP TG SL + R I G++ ES LE L
Sbjct: 305 RE-----HPIIRTHPATGWKSLFVNRSMTVRIVGLNPEESRILLEYLFG 348

Query: 236 WACQAPRVHAH-QWAA----GDVVVWDNRCLLHRAEPWD 269
+ + W + G +WDNR H A WD
Sbjct: 349 VFEKNLDIQVRFNWKS KPG LGTSALWDNRISQHNA-VWD 386

>ref|YP_001701411.1| putative dioxygenase [Mycobacterium abscessus ATCC 19977]
emb|CAM60757.1| Putative dioxygenase [Mycobacterium abscessus]
Length = 289

Score = 67.0 bits (162), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 68/272 (25%), Positives = 102/272 (37%), Gaps = 32/272 (11%)

Query: 12 GATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAI---- 67
G LGA VTG+ LD + +H L++ G H + +Q I + G I
Sbjct: 7 GEGLGAQVTGIDPGNLDGITTEEIRELVYRHKLVLKGVHPTPEQFIELGRLIGEIVPYY 66

Query: 68 ----ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
+I S + G R WH D +MP ++
Sbjct: 67 EPVYHHQDHPEIFVSSTEEGQGVPR-----GAFWHVDYMFMPKPFASF 111

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATR-ALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
VP T F D+ +++L T+ A + S Y + + V +
Sbjct: 112 VLPLAVPGHDRGTYFIDLSKVWESLPAKTKDAALGTFSTHTPRRYIKIRPSDVYRPIGEI 171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPG-----MDAAESERFLE--GLV 234
+ TT P V HP+TG L I DAA ++ LE G +
Sbjct: 172 LAEIERTTPPQKWPTVIKHPKTGEEILYICEAGTETIEDGAGRIQDAALLQQLLEASGQL 231

Query: 235 DWACQAPRVHAHQWAAGDVVWDNRCLLHRAE 266
D +P +HA + GD+V+WDNR L+HRA+
Sbjct: 232 DPDYASPFHAHQHYEVDIVLWDNRSLVHRAK 263

>emb|CBJ18733.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 67.0 bits (162), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 44/115 (38%), Positives = 58/115 (50%), Gaps = 13/115 (11%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRP----LV 198
AAYDALD AT+A V HS+V+S+ ++G A + A LRP LV
Sbjct: 1 AAYDALDGATKAEVEDLVTEHSIVFSREQIGFTDYA-----EGNADRLRPVQHRLV 51

Query: 199 KVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP TGR SL + H I G E+ F+ L++ A Q V+AHQW D+
Sbjct: 52 ITHPVTGRSLYLSSHIGGIVGWPPEARAFIRDLMEHATQRQFVYAHQWRVNDL 106

>ref|YP_841050.1| taurine catabolism dioxygenase [Ralstonia eutropha H16]
emb|CAJ96320.1| taurine catabolism dioxygenase [Ralstonia eutropha H16]
Length = 303

Score = 67.0 bits (162), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 64/269 (23%), Positives = 108/269 (40%), Gaps = 36/269 (13%)

Query: 14 TLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE---- 68
T+GA V G+ LDD + +L A L++ +L F Q ++ Q + A+RFG +E
Sbjct: 32 TIGADVEGIDFREPLDDDTYLSLRALLKYKVLFFRKQAITPAQHVAVARRFGELEVHPM 91

Query: 69 RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV 128
+ + DGT R N+ +H+D ++ + + G++
Sbjct: 92 FTNHPEHPELVVFGRDGTTRGRE-----NL-YHSDVSWREIPSMGSMRLRCVE 137

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD 188
P VGG T + +M AAY+ L + +A + A H + + + ++ Y
Sbjct: 138 CPEVGGDTMWINMAAAYENLPQDMKARIANLKA VHDAMPTFGSALNEEKYAEMRAKY--- 194

Query: 189 TTATPLRPLVKVHPETGRPSLLIG-----RHAHAIPGMDAAESERFLEGLVDWA 237
+ P+V+ HPETG L + + A G D +E L +
Sbjct: 195 --PPMVHPVVRTHPETGEKILFVNEAFTTHFANFVKEAPYRIGSDYRPAELDLLQYLYRQ 252

Query: 238 CQAPRVHAH-QWAAGDVVWDNRCLLHRA 265
AP +W + +WDNR H A
Sbjct: 253 AAAPYQVRLRWQPDITIALWDNRSTQHYA 281

>ref|XP_384843.1| hypothetical protein FG04667.1 [Gibberella zeae PH-1]
Length = 378

Score = 67.0 bits (162), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 70/269 (26%), Positives = 108/269 (40%), Gaps = 24/269 (8%)

```
Query: 7  QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
      ++T  A +G + G+ L L +      L      + +++  Q LS QQ      + +G
Sbjct: 85  KVTDLTAYIGTEIEGLQLKDLTNQQRDELALLIAERSVVFRLRDQDLSPQQKELGEWYGE 144

Query: 67  IE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
      +E      ++ G  V++      T R  PA      +  G  WH D +  A
Sbjct: 145  VEVHPQVPQVPLPGVSVLWPDQLQATER---PA---TFRQPGGASRWHTDLVHERQPAG 197

Query: 121  GAVFSAEVVPAVGGRTCFADMRAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
      + VP+VGG T +A  AAY+ L  R ++  RSA +  +      H +Q G
Sbjct: 198  ITHLHNDTVPSVGGDTLWASGYAAYEKLSPGFRKIIDGRSAVYKSAHPYLDRDHPEQ-GP 256

Query: 181  AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD-WAC 238
      Y+      + PLV+VHP TG  +L + R      I G+D AES+  L  L D +
Sbjct: 257  KYVER-----VHPLVRVHPATGWKALWVNRAMTDRIVGLDKAESDVILNYLYDVYET 308

Query: 239  QAPRVHAHQWAAGDVVVWDNRCLLHRAEP 267
      +W      +WDNR      EP
Sbjct: 309  NVDIQVRFKWTPRTSALWDNRWDYSGREP 337
```

>emb|CBJ18723.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 67.0 bits (162), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 42/114 (36%), Positives = 57/114 (50%), Gaps = 11/114 (9%)

```
Query: 143  AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---PLRPLVK 199
      AAYDALD+ T+A +      HSL+YS+ LG      ++ Y  +  A      L+ LV+
Sbjct: 1  AAYDALDDDTKAEIEDMICEHSLMYSRGSLG-----FLDYSDEEKAMFKPVLQRLVR 52

Query: 200  VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
      HP  R SL +  HA AI GM  E+  L  L + A Q  V+ HQW  D+
Sbjct: 53  THPVHRRKSLYLSSHAGAIQGMSVPEARLLLLRDLTEHATQREFVYVHQWTLHDL 106
```

>emb|CBJ18732.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 66.6 bits (161), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 43/114 (37%), Positives = 58/114 (50%), Gaps = 11/114 (9%)

```
Query: 143  AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---PLRPLVK 199
      AAYDALD+ T+A +      HSL+YS+ LG      ++ Y  D  A      L+ LV+
Sbjct: 1  AAYDALDDDTKAEIEDMICEHSLMYSRGSLG-----FLDYTDDEKALFKPVLQRLVR 52

Query: 200  VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
      HP  R SL +  HA AI GM  E+  L  L + A Q  V+AH+W  D+
Sbjct: 53  SHPVHRRKSLYLSSHAGAIKGMSPPEARLLLLRDLTEHATQPEFVYAHKWTLHDL 106
```

>gb|EFX01178.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Grosman
clavigera kw1407]
Length = 1222

Score = 66.6 bits (161), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 66/276 (23%), Positives = 113/276 (40%), Gaps = 40/276 (14%)

```
Query: 14  TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIER---I 70
      +LG  + GV ++ L      L      +  ++ F  Q L+ ++Q+  + +G ++R
```

Sbjct: 70 SLGTVLEGVQISQLTPQQQLDELALLVAERGTVFFRDQDLTTEKQVEVFEHYGILDRHPAQ 129

Query: 71 GGGDIVAISNVKAD-GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV 129
V I + D + +++P W G+ WHAD+++ ++ E

Sbjct: 130 RDTKHVVIRGSRDDHREISKYTP--W-----GSSEWHADTSFELNPPSYSLRMEEH 179

Query: 130 PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDT 189
P VGG T + YD L EA + V + A H+ S+L Q + +G

Sbjct: 180 PDVGGDTAWVSQYGLYDELSEALKRFVDELHAVHT-----SRL----QYDTILDLWGS GP 230

Query: 190 TATPL---RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
P+ P V+ HP TG +L I + ES++ L+ A +H+

Sbjct: 231 NRPPIDTHHPAVRTHPVTGLKALNINLGFVIGFAELKKPESDKLLDFF-----AGHIHS 284

Query: 246 H-----QWAAGDVVVWDNRCLLHRAEPWDFKLPR 274
+W G V +WDNR +HR P ++ R

Sbjct: 285 ADDHLVRWKWTVGSAWMDNRCTIHRVIPGRYEANR 320

>emb|CBJ19174.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 66.6 bits (161), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 40/111 (36%), Positives = 55/111 (49%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
AAYDALD+ T+A + HSL+YS+ LG + Y + L+ LV+ HP

Sbjct: 1 AAYDALDDDTKAEIEDMICEHSLMYSRGSLGFLD-----YTDEEKEMFKPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA I GM E+ L L + A Q V+ H+W D+

Sbjct: 56 VHGRKSLYLSSHAGGIQGMSPPEARVLLRDLTEHATQPEFVYVHKWKLHDL 106

>ref|XP_388516.1| hypothetical protein FG08340.1 [Gibberella zeae PH-1]
Length = 1284

Score = 66.6 bits (161), Expect = 3e-09, Method: Composition-based stats.
Identities = 44/173 (25%), Positives = 75/173 (43%), Gaps = 6/173 (3%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
WH+D T+ V + A+ +PA GG T +A YD L + + + +A H

Sbjct: 154 GWHS DITFEKVPSPDYAMLKIHTLPATGGDTLWASGYEVYDRLSDPMKKFLEGLTATHDAT 213

Query: 167 Y---SQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMD 222
+ +LG+ + G T + PL++ +P TG S+ + + I G+

Sbjct: 214 FFFHDEARRLGNPIRKGIRGSPLNQGEQLTSVHPLIRTNPVTGWKSVFVNKGFTKRINGLS 273

Query: 223 AAESERFLEGLVDWACQAPRVHA-HQWAAGDVVVWDNRCLLHRAEPWDFKLPR 274
ES+ L L + Q ++W+ D +WDNR H A +D++ R

Sbjct: 274 KDES DTLAYLFNLVTQNHDQVRYRWSKNDCAIWDNRSTFHCAT-YDYEAAR 325

>emb|CBJ18743.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 66.6 bits (161), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 42/114 (36%), Positives = 58/114 (50%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTAT---PLRPLVK 199
AAYDALD T+A + HSL+YS+ LG ++ Y + A L+ LV+

Sbjct: 1 AAYDALDNDTKAEIEGMICEHSLMYSRGSLG-----FLDYSDEEKAMFKPVLQRLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP R SL + HA AI GM E+ L L + A Q V++H+W GD+
Sbjct: 53 THPVHRRKSLYLSSHAGAIQGMSMPEARLLLLRELTEHATQREFVYSHKWRVGD 106

>emb|CBJ18849.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 66.6 bits (161), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 43/114 (37%), Positives = 57/114 (50%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---PLRPLVK 199
AAYDALD+ T+A + HSL+YS+ LG ++ Y D A L+ LV+
Sbjct: 1 AAYDALDDHTKAEIGDMICEHSLMYSRGSIG-----FLDYTDDEKAMFKPVLQRLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP R SL + HA AI GM E+ L L + A Q VH H+W D+
Sbjct: 53 THPVHRRKSLYLSSHAGAIQGMSVPEARLLLLRDLTEHATQREFVHIHKWTLHDL 106

>emb|CBJ19206.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 66.6 bits (161), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 43/112 (38%), Positives = 57/112 (50%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-LVKVH 201
AAYDALDE TRA V HSL+YS++ +G + P+R LV+ H
Sbjct: 1 AAYDALDERTRAEEVENLICEHSLMYSRAAVGFTDLTPEEIASF-----EPVRQRLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL + HA AI G E+ +L L + A Q V++HQW D+
Sbjct: 55 QTTGRKSLFLSAHAGAIIGWTIPEARAYLRELTEHATQREFVYSHQWRQHDL 106

>ref|YP_003060914.1| Taurine dioxygenase [Hirschia baltica ATCC 49814]
gb|ACT60217.1| Taurine dioxygenase [Hirschia baltica ATCC 49814]
Length = 278

Score = 66.6 bits (161), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 73/278 (26%), Positives = 113/278 (40%), Gaps = 40/278 (14%)

Query: 7 QITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
++TP +GA ++ + L + D L +A Q+ +L F Q +S++ T K +G
Sbjct: 17 RLTPY---MGAELSDIDLEQAIGDEAAEELRSALTQYQVLGFRNQEISHEAHKTMGKIYG 73

Query: 66 --AIERIGGG----DIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
AI G +IVAI H+ A+ K + G WHAD +
Sbjct: 74 PLAIFFAVPGIEEHPEIVAI-----HADAD----SKYVAGE-NWHADLSASDEP 117

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
G++ VP GG TCF M AYDAL + + + A H +L
Sbjct: 118 PLGSILYLHTVPETGGDTCFCSMTKAYDALSDKMKDYLDGLYAMHDSNPVYHRL----- 171

Query: 179 GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWA 237
+ Y AT + P++ HP +G+ + + + I G+ ES+ L L D
Sbjct: 172 ---FKDYDKRYPAT-IHPVIARHPRSGKKFIFVNSSNTTYIEGLPKEESDAILNFLFDHI 227

Query: 238 CQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRV 275
W +V+WDN + H A WD+ P V
Sbjct: 228 KNPNFQMRFTWEPHSIVMWDNLAVQHLA-VWDY-FPNV 263

>gb|AAS64595.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
Length = 119

Score = 66.6 bits (161), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 45/126 (35%), Positives = 59/126 (46%), Gaps = 9/126 (7%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP-- 193
T F DMRAAYD L ++ + A H + + LG + + A P
Sbjct: 1 TEFGDMRAAYDELPA DLKSELEGLHAEHYALNPRFVLGDTDYSEA-----QRNAMPV 53

Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 54 TWPLVRTHAGSGRKFLFIGAHAGRIEGRPLAEGRM LLAELLEHATQRRFVYRHSWKVGDL 113

Query: 254 VVWDNR 259
V+WDNR
Sbjct: 114 VMWDNR 119

>emb|CBJ19175.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 66.6 bits (161), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 41/111 (36%), Positives = 59/111 (53%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD AT+A + HSL+YS+++LG SA++ A + LV++HP
Sbjct: 1 AAYDALDAATKAEIEDLVCEHSLIYSRAQLGF-----SAFLPDERVAMAPVRQRLVRIHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL + H I G E+ F+ L++ A Q V+ H W D+
Sbjct: 56 VTGRKSLFLAAHIGTILGWPQPEAMAFIRDLMEHATQPQFVYVHHWTRHDL 106

>emb|CBJ18828.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 66.6 bits (161), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 43/112 (38%), Positives = 56/112 (50%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-LVKVH 201
AAYDALDE TRA V HSL+YS++ +G + P+R LV+ H
Sbjct: 1 AAYDALDERTRAEEVDLICEHSLMYSRAAVGFTDLTPEEIASF-----EPVRQRLVRRH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P +GR SL + HA I G E+ FL L + A Q V+ H W GD+
Sbjct: 55 PRSGRLSLYLSSHAGGIEGWFPPEARAFRLDLTEHATQRQFVYRHAWTPGDL 106

>emb|CBJ18763.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 66.6 bits (161), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 42/112 (37%), Positives = 55/112 (49%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-LVKVH 201
AAYDALD+ T+A + HSL+YS+ LG V + P+R LV+ H
Sbjct: 1 AAYDALDDETKAKIENLICEHSLMYSRGS LGFVDYTEEEKQMFK-----PVRQRLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P R SL + HA AI GM E+ L L + A Q VH H+W D+
Sbjct: 55 PVHRRKSLYLSSHAGAI VGMTVPEARLLLRDLTEHATQPQC VHVHKWTVHDL 106

>emb|CBJ19203.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 66.6 bits (161), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 45/111 (40%), Positives = 60/111 (54%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDAL EATR + A HSL+ S++KLG S + A + LV+
Sbjct: 1 AAYDALPEATRQKIAGLVAEHSLMTSRKLGf-----SDFNDEERKAFAPVPQVLVRRlQ 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
++GR SL + HA AI GM E+ER ++ LVD A Q VH H+W D+
Sbjct: 56 DSGRMSLYVASHAGAIRGMARPEAERLIQELVDHATQRFVHTRWRVKDL 106

>emb|CBJ18796.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 66.6 bits (161), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 41/111 (36%), Positives = 57/111 (51%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD+ T+A + + HSL+YS+ LG + Y + L LV+ HP
Sbjct: 1 AAYDALDDHTKAEIGDMTCEHSLMYSRGS LGFLD-----YSEERHSMKPVHLKLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SLL+ H AI G E+ F+ L++ A Q V+ H+W D
Sbjct: 56 VTGRKSLLSAHIGAIVGWPRPEAMAFIRDLMEHATQPQFVYVHRWTKNDF 106

>ref|XP_003006979.1| alpha-ketoglutarate-dependent sulfonate dioxygenase
[Verticillium
albo-atrum VaMs.102]
gb|EEY17009.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Verticillium
albo-atrum VaMs.102]
Length = 383

Score = 66.6 bits (161), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 68/278 (24%), Positives = 111/278 (39%), Gaps = 27/278 (9%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
++T +G + G+ L L + L + +++ F Q ++ QQ + FG
Sbjct: 85 KVTDLTTHIGTEIEGIQLKDLTNVQRDELALLIAERSVVFVRDQDITPQQQKELGEHFGQ 144

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
+E ++ G + V + T E+ + G WH+D + A
Sbjct: 145 VEVHPQVPQVPGVEGVTVIWPDLQAT-----EFPASFRPPGGASRWHSIDLVELQPAG 197

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
+ VP GG T +A +AY+ L R ++ R A + + AG
Sbjct: 198 ITHLHNDTVPTGGDTLWASGYSAYEKLSPEFRKIIDGRKAVYRSAHPYLDLDRDK-PNAGP 256

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
++ PLV+VHP TG +L + R I G+D AES+ L L D +
Sbjct: 257 KHVER-----THPLVRVHPATGWKALWVNRAMTDRIVGLDRAESDVILNLYLDVYEK 308

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRAEPWDF--KLPR 274
+ +W G +WDNR +H A WD+ K PR
Sbjct: 309 NVDIQLRFKWTPTGTSALWDNRITIHNAS-WDYAGKHPR 345

>emb|CBJ19055.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]

Length = 106

Score = 66.6 bits (161), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 40/111 (36%), Positives = 55/111 (49%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD+ +A + HSL+YS+ LG ++ Y L+ LV+ HP
Sbjct: 1 AAYDALDDEAKAEIEDMICEHSLMYSRGSLGFLE-----YTDEEKQLFKPVLQRLVLRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E+ L L + A Q+ V+ H+W D
Sbjct: 56 VHGRKSLYLSSHAGAIKGMTPEARLLLRDLNEHATQSEFVYVHKWTLHDF 106

>ref|XP_002153466.1| alpha-ketoglutarate-dependent taurine dioxygenase [Penicillium
marneffeii ATCC 18224]
gb|EEA19081.1| alpha-ketoglutarate-dependent taurine dioxygenase [Penicillium
marneffeii ATCC 18224]
Length = 384

Score = 66.6 bits (161), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 70/274 (25%), Positives = 108/274 (39%), Gaps = 32/274 (11%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKR 63
Q+T +G+ V GV L+ L + G L Q ++ F Q ++ D+ + F
Sbjct: 99 QVTEITPYIGSEVRGVQLSQTNTGKDQLALFVAQRKVVAFRDQDFASLPIDKALEFGGY 158

Query: 64 FGA--IERIGGG-----DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
FG I G +I + D + Q + ++ WH+D +Y
Sbjct: 159 FGRHHIHPTSGAPKGFPEIHLVHRGADDNSFLQ-----TFLHEHTNSVTWHSVDVSYER 211

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
P GG T FA++ AYD L + +H A HS +
Sbjct: 212 QPPGTTFLYLLDGPTSGGDTLFANLAKAYDRLSPEFKKRLHGLKAVHS-----GFE 262

Query: 177 QAGSAYIGYGMDDTTATPLR---PLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEG 232
QA SA + P++ P+V+ HP TG ++ + + I G ES+ L+
Sbjct: 263 QAQSA-LARESTVRRDPVKHEHPVVRTHPVTGEKAIYVNPQFTRYIIVGYKKEESDYLLKF 321

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
L D + + +WA G VVVWDNR H A
Sbjct: 322 LFDHIALSQDLQTRIKWAPGTVVVWDNRVTAHSA 355

>gb|ADC33969.1| TfdA-like protein [uncultured bacterium]
Length = 131

Score = 66.6 bits (161), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 44/131 (33%), Positives = 65/131 (49%), Gaps = 5/131 (3%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQS---KLGHVQQAGSAYIGYGMDDTTAT 192
T F DM AYDAL + + V R A H + +++ + + Y T
Sbjct: 1 TEFCDMYQAYDALPDDLKRAVEGR LAIHHSKTKNPRVTISPDRPGAKEYEYARAKETQE 60

Query: 193 PLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRV-HAHQWAA 250
L+PLV+ HPETGR +L I R I M AE++ L+ L + + + H+W
Sbjct: 61 ILQPLVRTHPETGRQALYISPRFTIGIADMPDAEAQSLDLRLFASFVKNRGIQYRHKWRD 120

Query: 251 GDVVVWDNRCL 261
GD+V+WDNRC+
Sbjct: 121 GDLVMWDNRVCV 131

>gb|EDP48989.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus fumigatus A1163]
Length = 396

Score = 66.6 bits (161), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 74/255 (29%), Positives = 107/255 (41%), Gaps = 25/255 (9%)

Query: 14 TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG 73
T+G+ VTGV L++L AG L Q +++F Q + D I A FG+ G
Sbjct: 94 TIGSEVTGVQLSSLSAAGKDQLALLVAQRRVVVFRDQDFA-DLPIADALEFGS--HFGRH 150

Query: 74 DIVAISNVKADGTV-----RQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE 127
I S + +G R +S E D +AWH+D TY
Sbjct: 151 HIHPTSG-QPEGYPEIHLVHRHNSQGELDAFFADRNSTVAWHSDVTYEAQPPGTTFLYL 209

Query: 128 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 187
P VGG T F D AY L A + +H A HS + Q++ +Q G
Sbjct: 210 DSPEVGGDVTFVDQVEAYRRLSPAIKERLHGLRAVHS-GFEQAEFS--RQRGGV----- 260

Query: 188 DTTATPLR---PLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVDWACQAPRV 243
P++ P+V+ HP TG +L + G +I G+ ES+ L L++ +
Sbjct: 261 -VRRDPVKHEHPIVRTHPVTGEKALFVNGGFTSRIVGLKKEESDALLGFLLNHVGRGIDY 319

Query: 244 HAH-QWAAGDVVVWD 257
A +WA VVVWD
Sbjct: 320 QARIKWAPKTVVVWD 334

>emb|CBJ18779.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 66.2 bits (160), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 42/114 (36%), Positives = 57/114 (50%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---PLRPLVK 199
AAYDALD+ T+A + HSL+YS+ LG ++ Y + A L+ LV+
Sbjct: 1 AAYDALDDDTKAEIEDMICEHSLMYSRGSLG-----FLDYTDEEKAMFKPVLQRLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP R SL + HA AI GM E+ L L + A Q VH H+W D+
Sbjct: 53 THPVHRRKSLYLSSHAGAIKGMVPEARLLLLLDLNEHATQREFVHIHKWTVHDL 106

>emb|CBJ18729.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 66.2 bits (160), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 39/111 (35%), Positives = 55/111 (49%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD+ +A + HSL+YS+ LG + Y L+ L++ HP
Sbjct: 1 AAYDALDDEKAEIEDMICEHSLMYSRGSLGFMD-----YTDEEKQMFVKPVLQRLMRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E+ L+ L + A + VH H+W D+
Sbjct: 56 VHGRKSLYLSSHAGAIKGMVPEARLLLLLDLNEHATKPEFVHVHKWTLHDL 106

>emb|CBJ18870.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18880.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 66.2 bits (160), Expect = 5e-09, Method: Compositional matrix adjust.

Identities = 43/112 (38%), Positives = 57/112 (50%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRP-LVKVH 201
AAYDALDE TRA V HSL+YS++ +G + P+R LV+ H
Sbjct: 1 AAYDALDERTRAEEVDLICEHSLMYSRAAVGFTDLTPEEIASF-----EPVRQRLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL + HA AI G E+ +L L + A Q V++HQW D+
Sbjct: 55 QATGRKSLFLSAHAGAIIGWTVPEARAYLRELTEHATQREFVYSHQWRQHDL 106

>gb|ADC33976.1| TfdA-like protein [uncultured bacterium]
Length = 122

Score = 66.2 bits (160), Expect = 5e-09, Method: Compositional matrix adjust.
Identities = 37/127 (29%), Positives = 63/127 (49%), Gaps = 6/127 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPL- 194
T F DM AY+ LD+ + + A H+L +S+++ + G + P+
Sbjct: 1 TEFCDMYGAYERLDDGWKRRIAGLRAVHNLDLSRTR-----RHGEDPMTAQKRDTPPVD 55

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 254
P+V+ H ETGR + +G HA ++ GM E +E L + H+W+ G ++
Sbjct: 56 HPIVRTHSETGRKCVFLGDHAESVVGMPYDEGRALIEELNAAIHDDLTyrHRWSPGQLI 115

Query: 255 VWDNRCL 261
+WDRNC+
Sbjct: 116 LWDNRCL 122

>emb|CBJ18739.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 66.2 bits (160), Expect = 5e-09, Method: Compositional matrix adjust.
Identities = 42/114 (36%), Positives = 56/114 (49%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTAT---PLRPLVK 199
AAYDALD T+A + HSL+YS+ LG ++ Y + A L+ LV+
Sbjct: 1 AAYDALDNDTKAEIEDMICEHSLMYSRSLG-----FLDYTDEEKAMFKPVLQRLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP R SL + HA AI GM E+ L L + A Q VH H+W D+
Sbjct: 53 THPVHRRKSLYLSSHAGAIQGMSMPEARLLLLRDLTEHATQPEFVHVHKWTVHDL 106

>ref|XP_459245.1| DEHA2D17446p [Debaryomyces hansenii CBS767]
emb|CAG87418.1| DEHA2D17446p [Debaryomyces hansenii]
Length = 380

Score = 66.2 bits (160), Expect = 5e-09, Method: Compositional matrix adjust.
Identities = 72/272 (26%), Positives = 106/272 (38%), Gaps = 33/272 (12%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHL--SNDQQIT-FAKR 63
+TP LG +TG+ L+ LDD G L + L+IF Q Q ++ + K
Sbjct: 84 NVTpk---LGTETIGIQLSQLDDRGKDELALLVAKRGLVIFRDQDFGAKGPFVSDYGY 140

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIV-----GNMAWHADSTYMPVM 118
FG + + + G H +D + + + WH+D +Y
Sbjct: 141 FGPLH-----IHPTTGSPPKHSEIHVVYRRNDYNEALTfanRTNLVQWHSdVSYELQP 193

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
FS P GG T FAD AY+ L + L+ H L S+ + ++
Sbjct: 194 PGTTFFSVIEGPESGGDTLFDADNVEAYNRLSPRLKELI---EGLHVLHSSEEQAKFSRKE 250

Query: 179 GSAYIGYGMDTTATPLR---PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
G A P+R PLV+VHP TG L + + I ES+ L L
Sbjct: 251 GGA-----ERRDPVRNIHPLVRVHPVTGDKILYVNPFGSRKIVEFKQEESDALLNFLY 303

Query: 235 DWACQAPRVHAH-QWAAGDVVWDNRCLLHRA 265
+ + + A W VVWDNR + H A
Sbjct: 304 NHIGNSHDLQARVNWEPNSVVVWDNRVSHTA 335

>gb|EFW97202.1| taurine catabolism dioxygenase [Pichia angusta DL-1]
Length = 429

Score = 66.2 bits (160), Expect = 5e-09, Method: Compositional matrix adjust.
Identities = 64/275 (23%), Positives = 109/275 (39%), Gaps = 30/275 (10%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIER----- 69
+G + G+ L L D L + ++ F Q LS +Q+ + +G +E+
Sbjct: 123 IGTEIVGLQLEDLTDQQKDELALLVAERVVFFRDQKLSPOKQLELGEYWGRVEKHPQAS 182

Query: 70 -IGGGDIVAI-----SNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQG 121
+ G + + ++ ++ T + + WD G WH D + A
Sbjct: 183 QVNLPGITVIWQDYFQKSLGSNFTYKNINLGNWDATKNSTRGAQVWHTDLVHEKRPAGI 242

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
+ +P VGG T ++ AAYD L E + + + A VY S G++ +
Sbjct: 243 THLHLDAIPDVGGDTLWSSGYAAYDKLSENFKKFLDGKQA---VYV-SAHGYLDRKNP- 296

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQA 240
+ + PLV+ HP TG +L + R I G+ + ES+ L L D +
Sbjct: 297 ---FSGPKKIERVHPLVRTHPATGWKALYVNRTMTKRIVGLSSVESDLILNYLFDVYEKN 353

Query: 241 PRVHAH-QWAA-----GDVVWDNRCLLHRAEPWD 269
+ +W G +WDNR HR+ WD
Sbjct: 354 ADIQVRFRWTPSKEGYGTSIAIWDNRVSQHRST-WD 387

>ref|YP_003344598.1| taurine dioxygenase [Streptosporangium roseum DSM 43021]
gb|ACZ91855.1| taurine dioxygenase [Streptosporangium roseum DSM 43021]
Length = 279

Score = 66.2 bits (160), Expect = 5e-09, Method: Compositional matrix adjust.
Identities = 73/278 (26%), Positives = 113/278 (40%), Gaps = 39/278 (14%)

Query: 6 LQITPTGAT--LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+ + P+ T +G T + + D LH Q L+I G L+ QQ+ A R
Sbjct: 4 IDLIPSIGTELIGVTYEDLQKDDVLDEFVDLH---QRELVIIRGIELTPGQQVGLAAR 59

Query: 64 FG-----AIERIGGGDIVAI-----SNVKADGTVRQHSPAEDDDMMKVIVGNMAWHAD 111
G +E+ ++ I N K+ G R VGN WH D
Sbjct: 60 IGKPIPFVLEQYRYPELPEIMISSNEVRNKNKSIGVAR-----VGNF-WHQD 104

Query: 112 STYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS-QS 170
S+++ A+ + VP G T FA YD L + + R A H++V +
Sbjct: 105 SSFVAKPAEYTMLHGVNVPQTSGLTLFASAVDVYDRLPGDWKKKIDRRRAWHTVVKRLRI 164

Query: 171 KLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG--RHAHAIPGMDAAESER 228
+ HV + + Y + + PLV+ P + R + L G + ++ G DA E+
Sbjct: 165 RSEHVGLSTAIEYKAWIEEKHPKVEHPLVRQDPFSKR-TYLYGAPEYLDVSVQGFANENAA 223

Query: 229 FLEGLVDWACQAPR-VHAHQWAAGDVVWDNRCLLHRA 265
F L+D Q P V+ H+W D+VWV LH A
Sbjct: 224 FF-ALLDSLIQDPEHVYTHRWTPKDLVWVKTATTLHAA 260

>emb|CBJ18776.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 66.2 bits (160), Expect = 5e-09, Method: Compositional matrix adjust.
Identities = 41/111 (36%), Positives = 58/111 (52%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD AT+A + HSL+YS+ +LG SA++ A + LV++HP
Sbjct: 1 AAYDALDAATKAEIEDLVCEHSLIYSRQLGF-----SAFLPDERVAMAPVRQRLVRIHP 55
Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL + H I G E+ F+ L++ A Q V+ H W D+
Sbjct: 56 VTGRKSLFLAAHIGTILGWPQPEAMAFIRDLMEHATQPPFVYVHHWTRHDL 106

>gb|EFQ86963.1| hypothetical protein PTT_17760 [Pyrenophora teres f. teres 0-1]
Length = 395

Score = 65.9 bits (159), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 72/268 (26%), Positives = 107/268 (39%), Gaps = 38/268 (14%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAI----- 67
+G V GV LA L DA L ++ F Q+ D+Q K FG +
Sbjct: 94 IGTEVHGVDLANLTDAQKNDLARLIATRGVVFVRDQNNFGIDEQRELKGYFGEHLKHATT 153
Query: 68 ---ERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
+R G D+ I ++SP D+ + WH+D +Y + +
Sbjct: 154 GVPKRPGLEDVHVI-----FTGENSP---DLRALFTPTFLWHSVDVSYE--LQPPSYT 200
Query: 125 SAEVVPVAV----GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
S +V+ GG T ++ AAYD L + + +A HS +Q G+
Sbjct: 201 SLKVLTPGPRGGGDTLWSSQYAAAYDMLSPHMQKYLESLTALHS-----ADLQAQGT 252
Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
+G + T PL++ +P TG SL I G+ ES+ + L +
Sbjct: 253 RDLGRTVRREPVTTEHPLIRTNPVTGWKSLYFNPGFVTKIVGVPKTESDHIISFLNEIVA 312
Query: 239 QAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
+P VHA QW GDV WDNR H A
Sbjct: 313 TSPEVHARFQWREGDVAFWDNRVTNHSA 340

>emb|CBJ18738.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.9 bits (159), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 42/112 (37%), Positives = 55/112 (49%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-LVKVH 201
AAYDALD+ T+A + HSL+YS+ LG V + P+R LV+ H
Sbjct: 1 AAYDALDDETKAEIEDLICEHSLMYSRGSLSGFVDYTEERQMFK-----PVRQRLVRTH 54
Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P R SL + HA AI GM E+ L L + A Q VH H+W D+
Sbjct: 55 PVHRRKSLYLSSHAGAIKMSVPEARLLLRDLNEHATQREFVHIHKWTVHDL 106

>emb|CBJ18721.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.9 bits (159), Expect = 6e-09, Method: Compositional matrix adjust.

Identities = 41/112 (36%), Positives = 56/112 (50%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-LVKVH 201
AAYD LD+ T+A V RHS ++S+ LG + + P+R LV+ H
Sbjct: 1 AAYDTLDDKTKAEVSDLICRHSQIFSRGILGFTDFTDDERVKWA-----PVRQVLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P GR SL + HA I G E+ FL L + A Q V++HQW GD+
Sbjct: 55 PGHGRKSLYLSSHAGGIVGWPVEARAFRLDLNEIATQRQFVYSHQWRVGD 106

>ref|XP_002486586.1| alpha-ketoglutarate-dependent taurine dioxygenase [Talaromyces
stipitatus ATCC 10500]
gb|EED14348.1| alpha-ketoglutarate-dependent taurine dioxygenase [Talaromyces
stipitatus ATCC 10500]
Length = 368

Score = 65.9 bits (159), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 67/274 (24%), Positives = 108/274 (39%), Gaps = 21/274 (7%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN--DQQ 57
+ +T +++ +G+ V GV L L DA L + ++ FP Q L + ++Q
Sbjct: 70 LLSSTAKVSHIQPCIGSIVEGVQLNKLSDAAKDELALLIAERKVVAFPDQDLIDAGPEEQ 129

Query: 58 ITFAKRFGA--IERIGGG--DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST 113
+F + FG + I G + DG V E + ++ WH D +
Sbjct: 130 YSFMRYFGKPNYQPISGSMKGYPGFHIIHRDGNV-----DEINRFLEQRTTTTLWHQDVS 184

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAYDALDEATRALVHQRSARHSLVYSQSKLG 173
Y + P VGG T FA AAY L ++ + A H+ S +
Sbjct: 185 YEIQPPAYVMLGLLQGPVEVGDDTVFAATDAAYKRLSPTFQSFIDNLKAVHT---SAKMIA 241

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEG 232
H + GS ++ + PLV+VHP TG L I G + G+ E +
Sbjct: 242 HARLTGSLVRKDPVEN---VHPLVRVHPVTGERCLFINGEFITRVEGLKEPEFRVLQDF 297

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
L+ A +W +V++DNR +H A
Sbjct: 298 LMQHLITGHDFQARVRWQPRITIVMFDNRSTIHA 331

>emb|CBJ18837.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.9 bits (159), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 43/112 (38%), Positives = 56/112 (50%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-LVKVH 201
AAYDALDE TRA V HSL+YS++ +G + P+R LV+ H
Sbjct: 1 AAYDALDERTRAEEVDLICEHSLMYSRAAVGFTDLTPEEIASF-----EPVRQRLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL + HA AI G E+ +L L + A Q V+ HQW D+
Sbjct: 55 QATGRKSLFLSAHAGAIIGWTVPEARAYLRELTEHATQREFVYTHQWRQHDL 106

>emb|CBJ19213.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.9 bits (159), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 44/111 (39%), Positives = 60/111 (54%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202

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      AAYDAL EATR  +      A HSL+ S++KLG      S +      A  + LV+
Sbjct: 1  AAYDALPEATRQKIAGLVAEHSLSMTSRAKLGF-----SDFNDEERKAFAPVPQVLVRRQLQ 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
      ++GR SL +  HA AI GM  E++R ++ LVD A Q  VH H+W  D+
Sbjct: 56 DSGRMSLYVASHAGAIRGMATPEAQRLIQELVDHATQRQFVHTRWRVKDL 106

```

>emb|CBJ18853.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.9 bits (159), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 41/111 (36%), Positives = 59/111 (53%), Gaps = 5/111 (4%)

```

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
      AAYDALD+AT+A +      HSL++S+ +G      S +      ++      L+ LV+ HP
Sbjct: 1  AAYDALDDATKAEIEDLVCEHSLIHSRGAIGF-----SEFTPEEIEGFKPVLQRLVRRHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
      TGR +L +  HA I G  E+  L LV+ A Q  VHAH+W  D+
Sbjct: 56 VTGRRNLYLSAHAGTIVGWPVPEARALLRDLVEHATQREFVHAHKWRQFDL 106

```

>ref|XP_748907.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus fumigatus Af293]
gb|EAL86869.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus fumigatus Af293]
Length = 371

Score = 65.9 bits (159), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 68/266 (25%), Positives = 102/266 (38%), Gaps = 35/266 (13%)

```

Query: 15  LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRFGAIERIG 71
      +G+ V GV L+ L DA      L      + ++ FP Q L +      ++  F + FG
Sbjct: 95  IGSIVEGVQLSQLSDAAKDELALLVAERKVVAFPAQDLIDAGPEKLEQFMRHFGKP---- 150

Query: 72  GGDIVAISNVKADGTVRQH-----SPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
      +      GTVR H      + E      ++      WH D +Y +  G
Sbjct: 151 -----NYQPVSGTVRDHPGFHIIHRDGNREEIARFLEQRTTTTLWHQDVSYE-IQPPG 202

Query: 122 AVFSAEVLV-PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
      V  +  P VGG T FA  AY L      + +  A HS  S  + H + G
Sbjct: 203 YVMLGLLEGPEVGGDTVFAATDMAYKRLSPTFTSFLDGLRAVHS---SAKMINHTRLLGG 259

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVDWACQ 239
      +DT      + PLV++HP TG  L I G      I G+  E      L+ L+
Sbjct: 260 LVRKDPIDT----VHPLVRIHPVTGEKCLFINGEFITRIQGLKEPEQRYLLDFLMQHIMT 315

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHR 264
      A  +W      +V++DNRC + +
Sbjct: 316 GHDFQARVRWQPKTIVIFDNRCTIRK 341

```

>ref|XP_001804284.1| hypothetical protein SNOG_14085 [Phaeosphaeria nodorum SN15]
gb|EAT78710.2| hypothetical protein SNOG_14085 [Phaeosphaeria nodorum SN15]
Length = 329

Score = 65.9 bits (159), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 71/255 (27%), Positives = 102/255 (40%), Gaps = 28/255 (10%)

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Query: 15  LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERIGGG 73
      +G V GV LATL +A  L      ++ F  QH  DQQ  K F  ++
Sbjct: 95  IGTEVHGVLDLATLTNAQKNDLARLIATRGGVFFRNQHNFDIDQQRELKIFWRTTQVWK- 153

```

Query: 74 DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM---PVMAQGAVFSAEVVP 130
+++S A G SP D+ + WH+D TY P V S
Sbjct: 154 --MSMSYSLAKG-----SP----DLRALFTPTFLWHS DVTYEIQPPSYTSLKVLSGPPR- 201

Query: 131 AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD-T 189
GG T ++ AAYD L + + +A HS +Q GS +G +
Sbjct: 202 GGGGDTLWSSQYAAYDMLSPHMQRYLESLTALHS-----AELQAQGS RDLGRTVRRE 253

Query: 190 TATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-Q 247
T PL++ +P TG S+ I G+ ES+ + L + +P +HA Q
Sbjct: 254 PVTTEHPLIRTNPVTGWKSIFFNPGFVTKIVGVPKTESDHIIGLLNEIVATSPEIHARFQ 313

Query: 248 WAAGDVVVWDNRCLL 262
W GDV WDNR +
Sbjct: 314 WEEGDVAFW DNRATV 328

>emb|CBJ18741.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.9 bits (159), Expect = 7e-09, Method: Compositional matrix adjust.
Identities = 42/114 (36%), Positives = 57/114 (50%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTAT---PLRPLVK 199
AAYDALD+ T+A + HSL+YS+ LG ++ Y + A L+ LV+
Sbjct: 1 AAYDALDDDTKAEIDDMICEHSLMYSRGSLG-----FLDYTDEEKAMFKPVLQRLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP R SL + HA AI GM E+ L L + A Q VH H+W D+
Sbjct: 53 THPVHRRKSLYLSSHAGAIQGMSIPEARLLLRDLTEHATQPEFVHVHKWTLHDL 106

>emb|CBJ18749.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.9 bits (159), Expect = 7e-09, Method: Compositional matrix adjust.
Identities = 42/114 (36%), Positives = 57/114 (50%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTAT---PLRPLVK 199
AAYDALD+ T+A + HSL+YS+ LG ++ Y + A L+ LV+
Sbjct: 1 AAYDALDDDTKAEIEDMICEHSLMYSRGSLG-----FLDYTDEEKAMFKPVLQRLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP R SL + HA AI GM E+ L L + A Q VH H+W D+
Sbjct: 53 THPVHRRKSLYLSSHAGAILGMSMPEARLLLRDLTEHATQPEFVHVHKWTLHDL 106

>gb|ACR50790.1| putative oxidoreductase [Streptomyces longisporoflavus]
Length = 294

Score = 65.9 bits (159), Expect = 7e-09, Method: Compositional matrix adjust.
Identities = 67/267 (25%), Positives = 97/267 (36%), Gaps = 33/267 (12%)

Query: 21 GVHLATLDD-----AGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERI----- 70
GVH+ D AL +++ QHLS + + F +R G +E
Sbjct: 12 GVHVDEFDAMTAAEDLTALKQLIYTDRIIVLRNQHLSPAEFVFEGRRLGEVETYYQPMY 71

Query: 71 ---GGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE 127
+I SNVK DG + V WH D ++MP + +
Sbjct: 72 HHPEHKEIFVSSNVKEDG-----QVGVPQTGKFVHHHDYSFMPRPFGTLTIYPQ 120

Query: 128 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV-YSQSKLGHVQQAGSAYIGYG 186

VVP T F DM AY+ L + + +S+ Y + + V + S +
Sbjct: 121 VVPQHRGTYFIDMARAYENLPAELKDEIRDTRGLNSVRRYFKIRPTDVYRPISEVLAEI 180

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIGR-----HAHAIPGMDAAESERFLE--GLVDWAC 238
T P V HP TG L I A G+ E E G D
Sbjct: 181 ESVTPAAAHPTVFTHPVTGEQVLYISEAVTYRLEDAAGNGLRQGLLEELFEACGQADTTT 240

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+H + GD+++WDNR L+HRA
Sbjct: 241 THDNIHLQTFQKGDMLLWDNRSLVHRA 267

>ref|XP_003052483.1| hypothetical protein NECHADRAFT_77499 [Nectria haematococca mpVI
77-13-4]
gb|EEU46770.1| hypothetical protein NECHADRAFT_77499 [Nectria haematococca mpVI
77-13-4]
Length = 356

Score = 65.9 bits (159), Expect = 7e-09, Method: Compositional matrix adjust.
Identities = 45/173 (26%), Positives = 75/173 (43%), Gaps = 6/173 (3%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
WH+D T+ V + A+ +PA GG T +A YD L + + +A H
Sbjct: 158 GWHSDITFEKVPSPDYAMLKIHTLPATGGDTLWASGYEIDRLSPPMKQFLEGLTATHDAS 217

Query: 167 Y---SQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMD 222
+ ++LG+ + G + + PLV+ +P TG S+ + + I G+
Sbjct: 218 FFHDEAARLGNPLRKGIRGSPLNQGENLSAVHPLVRTNPVTGWKSVYVNGFTKRINGLS 277

Query: 223 AAESERFLEGLVDWACQAPRVHA-HQWAAGDVVVWDNRCLLHRAEPWDFKLPR 274
ES+ L L + Q ++W+ D +WDNR LH A +D+ R
Sbjct: 278 KDESDTLLSYLFNLVTQNHDAQVRYRWSKNDCAIWDNRSTLHCAT-YDYDAAR 329

>emb|CBJ18777.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.9 bits (159), Expect = 7e-09, Method: Compositional matrix adjust.
Identities = 40/111 (36%), Positives = 53/111 (47%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD+ +A + HSL+YS+ LG + Y L+ LV+ HP
Sbjct: 1 AAYDALDDEEKAEIEDMICEHSLMYSRGSGLGFMD-----YTDEEKQMFKPVLRQLVLRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E L L + A Q V+ H+W D+
Sbjct: 56 VHGRKSlyLSSHAGAIRGMSVPEGRLLLRDLTEHATQPEFVYVHKWTVHDL 106

>emb|CBJ18914.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.9 bits (159), Expect = 7e-09, Method: Compositional matrix adjust.
Identities = 39/112 (34%), Positives = 58/112 (51%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-LVKVH 201
AAYDALD+AT+A + HSL+YS+ LG + + TP+R LV+ H
Sbjct: 1 AAYDALDDATKAEIEDLVCEHSLIYSGTLGFTELSDDEKKMF-----TPVRQRLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P +GR S+ + H I G E+ F+ L + A Q +AH+W D+
Sbjct: 55 PVSGRKSlyLSSHIGTIIGWPMPEARAFIRDLTEHATQPRFCYAHKWRQFDL 106

>ref|XP_001031478.1| Taurine catabolism dioxygenase TauD, TfdA family protein
[Tetrahymena thermophila]
gb|EAR83815.1| Taurine catabolism dioxygenase TauD, TfdA family protein
[Tetrahymena thermophila SB210]
Length = 268

Score = 65.5 bits (158), Expect = 8e-09, Method: Compositional matrix adjust.
Identities = 62/268 (23%), Positives = 113/268 (42%), Gaps = 39/268 (14%)

Query: 13 ATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGG 72
+ LG + GV L+ L D F + A H ++ Q+L+ QQI F +R+G + +
Sbjct: 6 SQLGFVINGVDLSNLTDQEFENIQQALWTHGVICIKNQLTAQQQIAFTERWGKLVILPS 65

Query: 73 -----GDIVAISNVKADGTVRQHSP-AEWDDMMKVIVGNMAWHADSTYMPVMAQ 120
IV + NV+ D TV+ +S AE+ WH D +
Sbjct: 66 FYAFDNREPEYPAIVRVGNVRLDDTVKPNKDAEY-----WHKDGDFRQPGEN 113

Query: 121 G--AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
++ + + + VGG+T + D + L++ L + S++ SQ+ +
Sbjct: 114 FILSILTPKEIAQVGGQTYVD---SEQILNDMPADLREKLEGAKSIIRSQN---ISDF 166

Query: 179 GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWA 237
SA + P + HP +G+ L I + + + D ++
Sbjct: 167 SSA---KPEEHYPEAHHPAIAATHPISGKKILNITYNNLNDVVLKDGITILNS--RDIPEI 221

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
Q ++++H+W GDVV+WDN ++HR+
Sbjct: 222 EQVYKIYSHRWEMGDVVIWDNIRVIHRS 249

>dbj|BAE58785.1| unnamed protein product [Aspergillus oryzae]
Length = 333

Score = 65.5 bits (158), Expect = 8e-09, Method: Compositional matrix adjust.
Identities = 73/275 (26%), Positives = 105/275 (38%), Gaps = 45/275 (16%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRF 64
ITP +G + GV L+ L G L Q +L+F Q ++ +Q A +
Sbjct: 56 ITPR---IGTEIRGVQLSQLSTDGLDQLALLAAQRGVLVFRDQDFADIGTGRQORDIAAHY 112

Query: 65 GAIER-----IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA----WHADSTYM 115
G + + G V AD V ++ ++G WH D T+
Sbjct: 113 GPLHQHPTMGYPQGTSPFEQVVYADEKVG N-----LRTL LGTRTSYDLWHIDQTFT 163

Query: 116 PVMAQGAVFSAEVVPAVGG-RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
P F PA GG T F + AAY AL R +H R L+++ + +G
Sbjct: 164 PNTPGVTFFWVLETPASGGGDTAFTSLTAAYQALSPTFREGLH---RLKLLHTSASVGE 219

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGL 233
V + G + PLV HP T P L + A + G ESE L L
Sbjct: 220 VARIGQE---RALKDAVQTEHPLVIGHPVTHDPVLFVNPAIARQVVGYPKEESENLLSFL 276

Query: 234 -----VDWACQAPRVHAHQWAAGDVVVWDNRCLL 262
+D++C+ W G VVVWD CL+
Sbjct: 277 HNHIRSLDFSCR V-----SWEKGTVVVWDQVCLV 305

>emb|CBJ18975.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.5 bits (158), Expect = 8e-09, Method: Compositional matrix adjust.
Identities = 39/111 (35%), Positives = 56/111 (50%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
AAYDALD+ T+A + HSL+YS+ LG + Y + L+ LV+ HP
Sbjct: 1 AAYDALDDDTKAEIEDMICEHSLMYSRGSLSGFTE-----YTDEEKEMFKPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL + HA +I M E+ L L + A + V+ H+W D+
Sbjct: 56 VTGRKSLYLSSHAGSIFDMPTPEARMLLRDLTEHATEPRFVYVHKWRLHDL 106

>gb|EDP48444.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
fumigatus A1163]
Length = 371

Score = 65.5 bits (158), Expect = 8e-09, Method: Compositional matrix adjust.
Identities = 68/266 (25%), Positives = 102/266 (38%), Gaps = 35/266 (13%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRFGAIERIG 71
+G+ V GV L+ L DA L + ++ FP Q L + ++ F + FG
Sbjct: 95 IGSIVEGVQLSQLSDAAKDELALLVAERKVVAFPAQDLIDAGPEKLEQFMRHFGKP---- 150

Query: 72 GGDIVAISNVKADGTVRQH-----SPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
+ GTVR H + E ++ WH D +Y + G
Sbjct: 151 -----NYQPVSGTVRDHPGFHIIHRDGNREEIARFLEQRTTTTLWHQDVSYE-IQPPG 202

Query: 122 AVFSAEVLV-PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
V + P VGG T FA AY L + + A HS S + H + G
Sbjct: 203 YVMLGLLEGFEVGGDTVFAATDMAYKRLSPTFTSFLDGLRAVHS---SAKMINHTRLLGG 259

Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVDWACQ 239
+DT + PLV++HP TG L I G I G+ E L+ L+
Sbjct: 260 LVRKDPVDT----VHPLVRIHPVTGEKCLFINGEFITRIQGLKEPEQRYLLDFLMQHIMT 315

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHR 264
A +W +V++DNRC + +
Sbjct: 316 GHDFQARVRWQPKTIVIFDNRCTIRK 341

>gb|ADC33977.1| TfdA-like protein [uncultured bacterium]
gb|ADC33979.1| TfdA-like protein [uncultured bacterium]
gb|ADC33985.1| TfdA-like protein [uncultured bacterium]
Length = 132

Score = 65.5 bits (158), Expect = 8e-09, Method: Compositional matrix adjust.
Identities = 48/137 (35%), Positives = 68/137 (49%), Gaps = 16/137 (11%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARH-----SLVYSQSKLGHVQQAGSAYIGYGM 187
T F DM AAYD L + + V R H +V S S+ G A Y G
Sbjct: 1 TEFCDMYAAYDVLDPDEVKEKVAGRYGVHVS KAINPRVISTSRPG----AKDFYEGQAQ 56

Query: 188 DTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWAC--QAPRVH 244
+ L+P+V+ H ETGR +L + R AI GM+ AE++ L+ L + P +
Sbjct: 57 KRSKV-LQPIVRTHDETGRQALYVSPRFTIAIDGMEDAEAPLLDKLFAAITDRKRPYHY 115

Query: 245 AHQWAAGDVVVWDNRCL 261
H++ GDVV+WDNRC+
Sbjct: 116 RHKYRDGDVVMWDNRCV 132

>gb|ABD39118.1| alpha-ketoglutarate dioxygenase [uncultured bacterium]
Length = 99

Score = 65.5 bits (158), Expect = 8e-09, Method: Compositional matrix adjust.

Identities = 28/65 (43%), Positives = 38/65 (58%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
P+V+ HP+TGR L +G HA + GMD E +E L A Q + H W G+++V
Sbjct: 34 PIVRTHPDTGRKCLFLGDHAEYVAGMDYDEGRALIEELNALAIQPDLYEHSWTPGELLV 93

Query: 256 WDNRC 260
WDNRC
Sbjct: 94 WDNRC 98

>gb|AAS64585.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
Length = 119

Score = 65.5 bits (158), Expect = 8e-09, Method: Compositional matrix adjust.
Identities = 50/124 (40%), Positives = 65/124 (52%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRAAYDALD+A +A + HSL+YS+ LG + Y L+
Sbjct: 1 TEFGRMRAAYDALDDAAKAEIEDMICEHSLMYSRGALGFLD-----YTEEEKQMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP GR SL + HA I GM E+ L L + A Q V+ H+W D+V+
Sbjct: 56 RLVRTHPVHGRKSLYLSSHAGGIVGMTPEARVLLRDLNEHATQPEFVYVHKWKLHDLVM 115

Query: 256 WDNR 259
WDNR
Sbjct: 116 WDNR 119

>emb|CBJ19168.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.5 bits (158), Expect = 8e-09, Method: Compositional matrix adjust.
Identities = 42/115 (36%), Positives = 56/115 (48%), Gaps = 13/115 (11%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP----LV 198
AAYDALD+ T+A + HSL+YS+ LG ++ Y D +P LV
Sbjct: 1 AAYDALDDDTKAEIEDMICEHSLMYSRGSLG-----FLDYT-DEEKAMFKPVPQRLV 51

Query: 199 KVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+ HP R SL + HA AI GM E+ L L + A Q VH H+W D+
Sbjct: 52 RTHPVHRRKSLYLSSHAGAILGMSMPPEARLLLRDLTEHATQREFVHVHKWTVHDL 106

>emb|CBJ19044.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19046.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.5 bits (158), Expect = 8e-09, Method: Compositional matrix adjust.
Identities = 40/111 (36%), Positives = 54/111 (48%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD+ +A + HSL+YS+ LG ++ Y L+ LV+ HP
Sbjct: 1 AAYDALDDEAKAEIEDMICEHSLMYSRGSLGFLE-----YTDEEKQLFKPVLQRLVTRHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E+ L L + A Q V+ H+W D
Sbjct: 56 VHGRKSLYLSSHAGAIKGMTPEARLLLRDLNEHATQPEFVYVHKWTLHDF 106

>ref|XP_001227262.1| hypothetical protein CHGG_09335 [Chaetomium globosum CBS 148.51]
gb|EAQ85321.1| hypothetical protein CHGG_09335 [Chaetomium globosum CBS 148.51]

Length = 401

Score = 65.5 bits (158), Expect = 9e-09, Method: Compositional matrix adjust.
Identities = 47/174 (27%), Positives = 73/174 (41%), Gaps = 14/174 (8%)

Query: 104 GNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARH 163
G WH+D T+ P+ + A+ +P GG T +A YD + R + +A
Sbjct: 191 GKNQWHSIDITFEPISDYALLRLTQLPKTGGDTLWASGYELYDRISPTLRHFLDTLTA-- 248

Query: 164 SLVYSQSKLGHVQQAGSAYIGYG-----MDTTATPLRPLVKVHPETG-RPSLLIGRHA 215
Y+Q + + + G T + P+V+ +P TG R +G H
Sbjct: 249 --TYAQLPFNEAARRNNFTLYSGARGAPENTGDTLDAVHPVVRTNPVTGWRSVFAVGHHV 306

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW-AAGDVVVWDNRCLLHRAEP 267
I G+ ES+ FLE V + + +W A DV +WDNR + H A P
Sbjct: 307 QRIHGLSDEESKHFLWFVRLVVENHDLQVRLRWKAVNDVAIWDNRSVYHAATP 360

>ref|XP_457378.2| DEHA2B09768p [Debaryomyces hansenii CBS767]
emb|CAG85382.2| DEHA2B09768p [Debaryomyces hansenii]
Length = 383

Score = 65.5 bits (158), Expect = 9e-09, Method: Compositional matrix adjust.
Identities = 70/267 (26%), Positives = 110/267 (41%), Gaps = 22/267 (8%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
+ITP LG VTGV L+ L+D L Q +++F Q + + FA +G
Sbjct: 83 RITPK---LGTEVTGVQLSQLNDKAKDELALYVAQRGVVVFRDQDFAT-KGPKFATDYG- 137

Query: 67 IERIGGGDIVAISNV-----KADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQG 121
G I S + T R+ E+D + + +WH+D +Y + G
Sbjct: 138 -RHFGRLHIHPTSGAPRGHPHLYTIRRADKGEFDRVFSQRSNSTSWHSDVSYE-LQPPG 195

Query: 122 AVFSAEVPV-PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
F A + P GG T FAD+ AY+ L + + H L S+ + + + G
Sbjct: 196 TTFFAVLQGPDAGGDTIFADVVEAYNRLSPEFQKRL---EGLHVLHTSEDQASNSRVQG- 251

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
G + + PL++ HP TG + + R + I + ES+ + L
Sbjct: 252 ---GIERRKPVSSIHLIRQHPATGDKFIYLRNRPFSRRIVELKQDESDYLINFLFQHIES 308

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
A + W VVVWDNR ++H A
Sbjct: 309 AHDQLRLANWEPNTVVVWDNRVRVHSA 335

>emb|CBJ18974.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.5 bits (158), Expect = 9e-09, Method: Compositional matrix adjust.
Identities = 40/112 (35%), Positives = 57/112 (50%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-LVKVH 201
AAYDALD+AT+A + HSL++S+ LG + + T P+R LV+ H
Sbjct: 1 AAYDALDDATKAEIEDLVCEHSLIFSRGSLGFTE-----LSEEERATFRPVRQRLVRAH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P TGR L + H I G E+ L L + A + RV++H W A D+
Sbjct: 55 PVTGRKPLFLSSHCGNIVGWPLPEARALLRELTEHATERERVYSHAWRADDL 106

>emb|CBJ18813.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.5 bits (158), Expect = 9e-09, Method: Compositional matrix adjust.
Identities = 40/110 (36%), Positives = 58/110 (52%), Gaps = 5/110 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD+AT+A + HSL+YS+++LG S + + L LV+ HP
Sbjct: 1 AAYDALDDATKAEIEDLVCEHSLIYSRAQLG-----FSNFTDEERHSMRPVLHKLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
T R SLL+ H AI G ++ F+ L++ A Q V+ H+W D
Sbjct: 56 VTERKSLLSAHIGAIVGWPRPKAMAFIRDLMEHATQPQFVYVHRWTKHD 105

>emb|CBJ18737.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.5 bits (158), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 42/111 (37%), Positives = 53/111 (47%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD T+A + HSL+YS+ LG V Y L+ LV+ HP
Sbjct: 1 AAYDALDGETKAEIEDLVCEHSLMYSRGLGFVD-----YTDEEKQMFKPVLRQLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E L L + A Q V+ H+W D+
Sbjct: 56 VHGRKSLYLSSHAGAIRGMSVPEGRSLRDLTEHATQPEFVYVHKWTLHDL 106

>emb|CBJ18753.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.1 bits (157), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 41/112 (36%), Positives = 58/112 (51%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPL-VKVH 201
A YDALD+ T+ V HS +YS++ LG + + + P+R + V+ H
Sbjct: 1 AGYDALDQETKDRVADLICEHSQLYSRALLGFIDFTDAERERF-----KPVRQVPVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P TGR SL + HA I G E+ FL LV+ A Q V++HQW GD+
Sbjct: 55 PVTGRKSLYLSSHAGGIEGWFPVEARAFLRDLVEHATQRQFVYSHQWRVGDL 106

>ref|XP_001482070.1| hypothetical protein PGUG_05833 [Meyerozyma guilliermondii ATCC
6260]
gb|EDK41735.1| hypothetical protein PGUG_05833 [Meyerozyma guilliermondii ATCC
6260]
Length = 384

Score = 65.1 bits (157), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 69/267 (25%), Positives = 111/267 (41%), Gaps = 22/267 (8%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLS--NDQQIT-FAKR 63
+ITP +G + GV L+ LDD L Q +++F Q + + +T + +
Sbjct: 84 KITPK---MGTEIRGVQLSQLDDKAKDELALYVAQRGVVFRDQDFAAKGPKFVTEYGRH 140

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAWEDDMMKVIVGNMAWHADSTYMPVMAQQGAV 123
FG + I + T R+ E+D + + WH+D +Y + G
Sbjct: 141 FGRLH-IHPTSGAPRGFPPELHITYRRPDEKEFDRISETTTAVQWHSDISYE-LQPSGLT 198

Query: 124 FSAEVV-PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
F A + P GG T FAD++ AY L R + HS +QA ++
Sbjct: 199 FFAVLEGPESSGDTIFADVKEAYRRLSPEFRKRLEGLHVLHS-----SNEQAQNSR 249

Query: 183 IGYGMDTTA--TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
G++ A + + PL++ HP T + + R + I + ES+ L L D +
Sbjct: 250 GGGGVERRAPVSNIHPLIRQHPATKEKYIYLNRPFSRRIVELKQEESEDYLLNFLYDHIK 309

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
A + W VVVWDNR + H A
Sbjct: 310 AHDQLRASWEPNTVVVWDNRVVEHSA 336

>gb|ADC33950.1| TfdA-like protein [uncultured bacterium]
Length = 121

Score = 65.1 bits (157), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 43/131 (32%), Positives = 63/131 (48%), Gaps = 15/131 (11%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQ-----SKLGHVQQAGSAYIGYGMDDT 190
T F DM +AY AL E + L+ A HS+V+S+ + L Q+A T
Sbjct: 1 TEFCDMGSAAYALPERLKVLIEDLQAEHSIVHSRGLVDPTVLTEAQA-----ET 50

Query: 191 ATPLRPLVKVHPETGRPSLLIGRHHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA 250
+ LV+++P GR +L IG HA I G + L L + + +H W
Sbjct: 51 PPDRQLVRINPINGRRALYIGAHASHIVGWPLEKGRALLAELTELGTRPEFRLSHAWRE 110

Query: 251 GDVVVWDNRCL 261
GD++VWDNRC+
Sbjct: 111 GDLIVWDNRCV 121

>ref|XP_001273815.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
clavatus NRRL 1]
gb|EAW12389.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
clavatus NRRL 1]
Length = 388

Score = 65.1 bits (157), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 65/268 (24%), Positives = 111/268 (41%), Gaps = 31/268 (11%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIER----- 69
+G + G+ L L+D L + +++ F Q LS QQ + +G IE
Sbjct: 93 IGTEIVGLQLKDLNDKQKDELGLLIAERSVVFRRDQDLSPQQQKELGEWYGEIEVHPQVP 152

Query: 70 ----IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
+ G ++ + A+ + P G WH+D +
Sbjct: 153 QVPGVPGVTVLWPALAAERSAAFRPPG-----GAAHWHSDLVHERQPPGVTHLH 202

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 185
+ VP++GG T +A AAY+ L A R ++ ++A + ++ H ++ G ++
Sbjct: 203 NDTVPSIGGDTLWASGYAAYEKLSPAFRQIIDGKTAIYRSAHAYLDRDHPEE-GPRHVER 261

Query: 186 GMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVH 244
PLV+VHP TG +L + R + I G D AES+ L L D + +
Sbjct: 262 E-----HPLVRVHPATGWKALWVNRGYTTQIVGFDKAESDVILGHLFDVYEKNIDIQ 313

Query: 245 AH-QWAAGDVVVWDNRCLLHRAEPWDFK 271
+W +WDNR +H A WD++
Sbjct: 314 LRFKWTPTSALWDNRITIHNAS-WDYE 340

>emb|CBJ18829.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.1 bits (157), Expect = 1e-08, Method: Compositional matrix adjust.

Identities = 39/111 (35%), Positives = 59/111 (53%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHP 202
AAYDALD+ T+A + HSL++S+ +G S + ++ + LV+ HP
Sbjct: 1 AAYDALDDDTKAEIADMICEHSLHSGAIGF-----SEFTPEEIEENFRPVRQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+TGR SL + HA AI G E+ +L L + A Q V++HQW D+
Sbjct: 56 QTGRKSLFLSSHAGAIIGWTVPEARAYLRELTEHATQREFVYSHQWRQHDL 106

>emb|CBJ18819.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.1 bits (157), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 40/111 (36%), Positives = 54/111 (48%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHP 202
AAYDALD+ T+A + HSL+YS+ LG + Y L+ LV+ HP
Sbjct: 1 AAYDALDDETKAEIEDMICEHSLMYRSGSLGFLD-----YTEEEKQMFKPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA I GM E+ L L + A Q V+ H+W D+
Sbjct: 56 VHGRKSLYLSSHAGGIVGMTVPEARLLLRDLNEHATQREFVYVHKWTLHDL 106

>gb|ACG80583.1| TfdA [uncultured bacterium]
Length = 118

Score = 65.1 bits (157), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 40/124 (32%), Positives = 58/124 (46%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR 195
T F DMRAAYDAL +A + HS+ +S+ LG + + +
Sbjct: 1 TEFGBDMRAAYDALPTDMKAQLEGLRVHHSIAHSRQILGF-----EFSQQEQENLKGAIH 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PL++ P + R SL + HA I E L L++ A Q V+ H+W D+V+
Sbjct: 55 PLIRTLPRSQRKSLYVAHASRILDWPIEGRLLLRDLMEHATQPQFVYRHEWRDHDLM 114

Query: 256 WDNR 259
WDNR
Sbjct: 115 WDNR 118

>ref|XP_002548797.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Candida
tropicalis MYA-3404]
gb|EER32669.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Candida
tropicalis MYA-3404]
Length = 386

Score = 65.1 bits (157), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 63/282 (22%), Positives = 114/282 (40%), Gaps = 19/282 (6%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQ---ITFAKR 63
+ITP LG+ + G+ L+ L D+ L + +++F Q + + FAK
Sbjct: 90 RITPK---LGSEINGIQLSQLSDSAKNDLARFVAERGTVVFKNQDFNQKGPQFAVDFAKY 146

Query: 64 FGAIER-IGGGDIVAISNVKADGTVRQHSPEWDDMMKVIIVGNMAWHADSTYMPVMAQGA 122
FG + + G + R + E + + +++WH+D +Y Q
Sbjct: 147 FGTLYKHATSGSPEGFPELHV--CFRGATQDEINSVFANRTNSISWHSDCSYALNALQLT 204

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182

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      +FS  +P  GG T FA    AY+ L  A  +  +    HS  S  +  + ++ G
Sbjct: 205 LFSC LQIPEAGGDTLFASTVEAYNRLSPAMKERLEGLHVLHS---SIEQARNNKEVG--- 258

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAP 241
      G          + PLV+++P T    L + +    I  +    ES+  L  L D    +
Sbjct: 259 -GITRREPEANIHPLVRINPLTKEKHLNKEFGRRIVELKEDESDYLLSFLFDLVETSQ 317

Query: 242 RVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLA 282
      +    +W    +V+W+N    +H +    DF  P  +    R++
Sbjct: 318 DLQLRIRWEENTIVLWNNSTTVH-SPCVDFDEPVIRHAYRIS 358

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>emb|CBJ18973.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 65.1 bits (157), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 55/110 (50%), Gaps = 5/110 (4%)

```

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPE 203
      AYDALD T+  +    HS +YS+ +LG          + +    ++ LV+ HP
Sbjct: 2   AYDALDSETKDEIEDLVCEHSQIYSRQQLGFTDFTEEEVRVF-----KPVIQRLVRTHPT 56

Query: 204 TGRPSLLIGRHAAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
      TGR SL +  HA  I G    E+  FL+ L  +  A Q    V++H+W  GD+
Sbjct: 57  TGRKSLYLSSHAGGIVGWPVPEARAFLKDLNEHATQRQFVYSHKWRVGDL 106

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>ref|XP_001939295.1| alpha-ketoglutarate-dependent taurine dioxygenase [Pyrenophora
tritici-repentis Pt-1C-BFP]
gb|EDU42014.1| alpha-ketoglutarate-dependent taurine dioxygenase [Pyrenophora
tritici-repentis Pt-1C-BFP]
Length = 395

Score = 65.1 bits (157), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 71/268 (26%), Positives = 106/268 (39%), Gaps = 38/268 (14%)

```

Query: 15  LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGAI----- 67
      +G  V GV LA L D    L          ++ F  Q  +    D+Q    K FG  +
Sbjct: 94  IGTEVHGVDLANLTDVQKNDLARLIATRGVVFVRDQKNFGIDEQRELKGYFGELHKHATT 153

Query: 68  ---ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
      +R G  D+  I          ++SP    D+  +    WH+D +Y    +  +
Sbjct: 154 GVPKRPGLEDVHVI-----FTGENSP----DLRALFTPTFLWHS DVSYE--LQPPSYT 200

Query: 125 SAEVVPVAV---GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
      S +V+          GG T ++    AAYD L    +  +    +A HS          +Q  G+
Sbjct: 201 SLKVLTPPRGGGGDTLWSSQYAA YDMLSPHMQKYLESLTALHS-----ADLQAQGT 252

Query: 181 AYIGYGMD-TTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
      +G  +    T    PL++ +P TG  SL          I G+    ES+  +  L  +
Sbjct: 253 RDLGRTVRREPVTTAHPLIRTNPVTGWKSLYFNPGFVTKIIGVPKTESDHIISFLNEIVA 312

Query: 239 QAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
      +P VHA  QW  GDV  WDNR    H A
Sbjct: 313 TSPEVHARFQWREGDVAFWDNRVTNHSA 340

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>dbj|BAB92967.1| alpha KG dependent 2,4-D dioxygenase [alpha proteobacterium BTH]
Length = 106

Score = 65.1 bits (157), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 41/111 (36%), Positives = 56/111 (50%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD+ TR + HSL+YS+ LG + Y + L+ LV+ HP
Sbjct: 1 AAYDALDDETRREIEDMVCEHSLMYSRGALGFLD-----YSEEEKEMFRPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL + HA I G+ E+ L L + A Q V+ H+WA D+
Sbjct: 56 VTGRKSLSLSSHAGGIVGLPMPEARVLLRDLNEHATQPKFVYVHKWALHDL 106

>ref|XP_001193736.1| PREDICTED: hypothetical protein [Strongylocentrotus purpuratus]
Length = 283

Score = 65.1 bits (157), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 71/288 (24%), Positives = 112/288 (38%), Gaps = 70/288 (24%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAG-FAALHAAWLQHALLIFPGQH-LSNDQQITFAK 62
T Q+ P + LG V G+ LA G + QH L+IF Q +S D+ + +
Sbjct: 6 TYQLKP--SRLGVEVFGIDLAQQQPQGVIDQIKEDVTQHRLMIFRNQSPISGDRHVEISL 63

Query: 63 RFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYM 115
FG +E + D+ +SNV+++G VG WH D ++
Sbjct: 64 WFGELSTFYKHKPSHPDVFVRVSNVESEGCRG-----VGRTGWHIDGSFQ 109

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
P +++ VVP G T FA L+E L +A+ +Y S
Sbjct: 110 PAPFNYSLYMHVVPKEGD-TVFA-----PLNEIEGLSEDQQAQWDKLYMMS----- 156

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHA-----HAIPGM---DAAE 225
D + + PLV HP TG+ +L + PG D +E
Sbjct: 157 -----DRRGSVHPLVYSHPRTGKKTLCFHLGMTDAFTWDYGTGQRMTPDSE 204

Query: 226 SERFLEGLV-----DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEP 267
+++ L + D A Q ++H+W GD ++ DN + H A P
Sbjct: 205 TQQILNEIRHEFVKDDGAIQ---YSHKWQVGDFIISDNLAVGHEATP 248

>ref|XP_002497214.1| ZYRO0F00286p [Zygosaccharomyces rouxii]
emb|CAR28281.1| ZYRO0F00286p [Zygosaccharomyces rouxii]
Length = 415

Score = 65.1 bits (157), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 70/272 (25%), Positives = 112/272 (41%), Gaps = 28/272 (10%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFA 61
T +ITP LG V G+ L+ L G L Q +++F Q + + + +
Sbjct: 119 TKRITPK---LGTEVKGIIQLSQLSPEGKDELALLVAQRGIVVFRNQDFAKHGPEFAVEYG 175

Query: 62 KRFGA--IERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMA 119
K FG I + G A + T R+ AE++ + + ++ WH D +Y
Sbjct: 176 KYFGKLHIHQTSGHPEA---PELHVITYRRPDHAEFERVFEDSHTSIGWHTDVSVELQPP 232

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
FS P GG T FAD AY+ L + + HS V+QA
Sbjct: 233 SYTFFSVLQGPPEGGDTLFAADSVEAYERLSPTLKQFLEGLHVIHS-----SVEQAQ 283

Query: 180 SAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESE---RFLEGL 233
++ + G+ + PL++ HP R SL + + + I + ES+ FL L
Sbjct: 284 NSKLQGGIQRREPTGHIHPLIRWHPVLKRKSLYVNKAFFSRRIVELKKPESDLLLNFLYSL 343

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ A ++ A+ W V +WDNR +H A
Sbjct: 344 FNNALDL-QLRAY-WEPDTVAIWDNRRTIISA 373

>gb|EFQ87965.1| hypothetical protein PTT_16348 [Pyrenophora teres f. teres 0-1]
Length = 360

Score = 64.7 bits (156), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 48/175 (27%), Positives = 80/175 (45%), Gaps = 10/175 (5%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS-- 164
 WH+D T+ PV + A+ +PA GG T +A YD L A R ++ +A H
Sbjct: 161 GWHSDITFEPVPSDYAMLKIHTLPATGGDTLWASGYEIIDRLSPAMRTMLQGLTATHDAK 220

Query: 165 -LVYSQSKLGHVQQAG--SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPG 220
 + +LG+ + + + +G TAT P+++ +P TG S+ + + I G
Sbjct: 221 FFLEEAERLGNPLRKNFRGSPLNHGDALTAT--HPVIRTNPVTGWNSVYVNGFTKTRING 278

Query: 221 MDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPR 274
 + ES+ L L + Q +W D+ +WDNR H A +D++ R
Sbjct: 279 VTKDESDLLLPYLFNLVTQNHDAQVRFKWQKNDLAIWDNRSTWHCAT-YDYEEAR 332

>ref|XP_002562688.1| Pc20g01290 [Penicillium chrysogenum Wisconsin 54-1255]
emb|CAP85458.1| Pc20g01290 [Penicillium chrysogenum Wisconsin 54-1255]
Length = 375

Score = 64.7 bits (156), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 70/271 (25%), Positives = 110/271 (40%), Gaps = 23/271 (8%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFA 61
 T +++ +LG V V L+ L AG L + ++ FP Q L + D Q +F
Sbjct: 78 TAKVSHIQPSLGTIVENVQLSDLSAAGRDELALLISERKVVAFPDQDLIDAGPDAQESFM 137

Query: 62 KRFGA--IERIGGG--DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV 117
 + FG + + G D A + DG E ++ WH D +Y +
Sbjct: 138 RHFGKPNYQPVSGSMTDHPAFHIIHRDGNR-----DEIARFLQQRTTTTLWHQDVSYE-I 191

Query: 118 MAQGAVFSAEVV-PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
 G V + P VGG T FA AY L A A + HS S + H +
Sbjct: 192 QPPGYVMLGGLLQGPEVGGDTVFAATDLAYKRLSPAVTAFLDGLKVTHS---SAKMIAHAR 248

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVD 235
 G +DT + PL++VHP TG + + G I G+ +E++ L+ L++
Sbjct: 249 MTGGLVRKDPVDT----VHPLIRVHPVTGEKCMFLNGEFITRIDGLKDSETKWVLDFLMN 304

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
 +W +V++DNR +H A
Sbjct: 305 HLVTGHDFQVRVRWQPRTIVMFDNRSTIHS 335

>emb|CBJ18735.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 64.7 bits (156), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 40/112 (35%), Positives = 59/112 (52%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVH 201
 AAYDALD+AT+A V HS+V+S+ ++G A G + P++ LV H
Sbjct: 1 AAYDALDDATKAEVGDLVTEHSIVFSREQIGFSDYAA-----GNEDGCVPVQHRLVITH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
 P +GR SL + H I G E+ F+ L++ A Q V+AH+W D+
Sbjct: 55 PVSGRKSLSLSSHVGIVGWPVPEARAFIRDLMEHATQRRFVYAHEWRVNDL 106

>gb|EFW97392.1| taurine catabolism dioxygenase [Pichia angusta DL-1]
Length = 429

Score = 64.7 bits (156), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 62/275 (22%), Positives = 109/275 (39%), Gaps = 30/275 (10%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIER----- 69
+G + G+ L L D L + ++ F Q LS +Q+ + +G +E+
Sbjct: 123 IGTEIVGLQLEDLTDQQDELALLVAERVVFFRDQKLSPOKQLELGEYWGRVEKHPQAS 182

Query: 70 -IGGGDIVAI-----SNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
+ G V++ ++ T + ++ +D + G WH D + A
Sbjct: 183 QVNLPGVSVIWQDYFQKSLGVGLTFKNNNLGNFDATKNAVRGTQVWHTDLVHEKRPAGL 242

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
+ +P GG T +A AAYD L E + + + A VY S G++ +
Sbjct: 243 THLHLDAIPEFGGDTLWASGYAAYDKLSEEFKKFLDGKQA----VYV-SAHGYLDRKNP- 296

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQA 240
+ + P+++ HP TG SL + R I G+ + ES+ L L + +
Sbjct: 297 ---FSGPKKIERVHPIIRTHPATGWKSLFVNRMGTMKRIVGLSSVESDLILNYLFEVFEKN 353

Query: 241 PRVHAH-QWAA-----GDVVWDNRCLLHRAEPWD 269
+ +W G +WDNR HR+ WD
Sbjct: 354 ADIQVRFKWTPSKPGYGTSAIWDNRVSQHRST-WD 387

>emb|CBJ19204.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 64.7 bits (156), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 39/112 (34%), Positives = 58/112 (51%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRP-LVKVH 201
AAYDALD+ T+A + HS ++S+ +LG + + + P+R LV+ H
Sbjct: 1 AAYDALDQKTKAEIEDLICEHSQIFSREQLGFTEYLPDERLKWA-----PVRQRLVRRH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAGDV 253
P +GR SL + HA I G E+ FL L + A Q V+AH+W D+
Sbjct: 55 PRSGRLSLYLSSHAGGIEGWPVEARAFRLDLTEHATQRQFVYHRWKPADL 106

>ref|XP_001391238.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus niger CBS 513.88]
emb|CAK96596.1| unnamed protein product [Aspergillus niger]
Length = 376

Score = 64.7 bits (156), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 70/268 (26%), Positives = 104/268 (38%), Gaps = 21/268 (7%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSND---QQITFAKR 63
++T +G+ V GV L L DA L + ++ FP Q L +D Q F +
Sbjct: 87 KVTEIQPRIGSIVEGVQLNQLTDAQKDELALLVAERKVVAFPDQDLIDDGPEAQEAFMRH 146

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVI---VGNMAWHADSTYMPVMAQ 120
FG V+ S G H +++ + + WH D +Y +
Sbjct: 147 FGK----PNYQPVSGSMRGHPGFHIIHRDGNREEITRFLSQRTTTTLWHQDVSYE-IQPP 201

Query: 121 GAVFSAEVV-PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
G V + P VGG T F+ AY L + + A HS S + H + G
Sbjct: 202 GYVMLGLLEGFEVGGDTVFSATDMAYKRLSPTLTSLWDLTLRATHS---SAKMIQHARLTG 258

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVDWAC 238

Sbjct: 174 EHQPPIGILITLLSVPPSGGDTIWASQTAAYARLSTPIKTLLEGLRAEHS-GYPQAEKAR 232

Query: 175 VQQAGSAYIGYGMDTTATPLR---PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL 230
 G P++ P+V++HP TG+ +L I I G+ ES+ L

Sbjct: 233 RD-----GRHVRREPVKSEHPIVRIHPATGQKALFIQPGFTKRIIGLKQEESDGLL 283

Query: 231 EGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
 + L Q A +W G V +W DNR H A

Sbjct: 284 KILFKHIAQGQDFQARVRWEEGTVALWDNRVTAHTA 319

>emb|CBJ19210.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
 Length = 106

Score = 64.7 bits (156), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 44/112 (39%), Positives = 57/112 (50%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRP-LVKVH 201
 AAYDALDEAT+ VH HS V+S+ LG + + + P+R LV+ H

Sbjct: 1 AAYDALDEATKREVHDLICAHSQVFSRGILGFDDFTEAERLKWA-----PVRQRLVRRH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
 P TGR SL + HA I G E+ FL L + A Q V+AH W D+

Sbjct: 55 PNTGRLSLYLASHAGGIEGWPVPEARAFLRDLTEHATQRQFVYAHVWKPWDL 106

>emb|CBJ18821.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
 Length = 106

Score = 64.3 bits (155), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 40/112 (35%), Positives = 57/112 (50%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRP-LVKVH 201
 AAYDALDE T+A V HSL++S++ +G + + P+R LV+ H

Sbjct: 1 AAYDALDERTKAEVQDLVCEHSLLSRAAVGFTEFTPEEVANF-----RPVRQRLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
 P +GR SL + HA I G E+ FL L + A Q V++H W D+

Sbjct: 55 PASGRKSLFLSSHAGTIVGWTVPPEARFLRDLTEHATQREFVYSHAWRQHDL 106

>emb|CBJ18746.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
 Length = 106

Score = 64.3 bits (155), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 40/112 (35%), Positives = 56/112 (50%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRP-LVKVH 201
 A +D+LD T+AL HS +YS+ LG + + P+R LV+ H

Sbjct: 1 AGWDSLDPETQALCEDLICEHSQIYSRQILGFTDFTDAERARFA-----PVRQVLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
 P TGR SL + HA I G E+ FL L++ A Q V++HQW GD+

Sbjct: 55 PVTGRKSLYLSSHAGGIIGWPVPEARAFLRDLIEHATQRQFVYSHQWRVGD 106

>emb|CBJ18722.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
 Length = 106

Score = 64.3 bits (155), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 40/111 (36%), Positives = 52/111 (46%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202

Sbjct: 1 AAYDALD+ RA + HSL+YS+ LG + Y L+ LV+ HP
AAYDALDDEIRAEIEDMICEHSLMYSRGS LGFLD-----YTEEEKQMFKPVLRQLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA I G E+ L L + A Q VH H+W D+

Sbjct: 56 VHGRKSLYLSSHAGGIVGTTVPEARLLLLRDLTEHATQPQCVMVHKWTVHDL 106

>ref|XP_746985.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
fumigatus Af293]
gb|EAL84947.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
fumigatus Af293]
Length = 396

Score = 64.3 bits (155), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 73/255 (28%), Positives = 106/255 (41%), Gaps = 25/255 (9%)

Query: 14 TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG 73
T+G+ VTGV L++L AG L Q +++F Q + I A FG+ G
Sbjct: 94 TIGSEVTGVQLSSLSAAGKDQLALLVAQRRVVVFRDQDFAG-LPIADALEFGS--HFGRH 150

Query: 74 DIVAISNVKADGTV-----RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE 127
I S + +G R +S E D +AWH+D TY
Sbjct: 151 HIHPTSG-QPEGYPEIHLVHRHNSQGELDAFFADRNSTVAWHS DVTYEAQPPGTTFLYIL 209

Query: 128 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 187
P VGG T F D AY L A + +H A HS + Q++ +Q G
Sbjct: 210 DSPEVG DTVFVDQVEAYRRLSPA IKERLHGLKAVHS-GFEQAEFS--RQRGGV----- 260

Query: 188 DTTATPLR---PLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVDWACQAPRV 243
P++ P+V+ HP TG +L + G +I G+ ES+ L L++ +
Sbjct: 261 -VRRDPVKHEHPIVRTHPVTGEKALFVNGGFTR SIVGLKKEESDALLGFLLNHVGRGIDY 319

Query: 244 HAH-QWAAGDVVVWD 257
A +WA VVVWD
Sbjct: 320 QARIKWAPKTVVVWD 334

>ref|XP_001818415.2| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
oryzae RIB40]
Length = 381

Score = 64.3 bits (155), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 70/270 (25%), Positives = 109/270 (40%), Gaps = 28/270 (10%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKR 63
++TPT +G+ V G+ L+ L D G L Q ++ F Q + ++ + F
Sbjct: 100 ELTPT---IGSEVHGIQLSQLTDKGKDQLALYVAQRKVVAFRDQDFAQLPIEKALEFGGY 156

Query: 64 FGA--IERIGGGDI---VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV 117
FG I + G + + + AD S AE+ ++ ++ WH+D T+
Sbjct: 157 FGRHHIHQSSGAPKGFPEIHLVHRGAD-----DRSGAEF---LEHTNSLTWHS DVTFEKQ 209

Query: 118 MAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
P GG T F +M AY L R +H A HS V ++ +
Sbjct: 210 PPGTTFLYLLDGPTSGGDTLFCNMAQAYRRLSPEFRKRLHGLKAVHSGV---EQVNNSLN 266

Query: 178 AGSAYIGYGM DTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDW 236
G G T P+V+ HP TG +L + + I G ES+ L+ L D
Sbjct: 267 KG---GIARRDPITTEHPVVRTHPVTGEKALYVNPQFTRYIVGYKKEESD FLLKFLYDH 322

Query: 237 ACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ + +W VVVWDNR + H A

Sbjct: 323 IALSQDIQTRVWRPNTVVVWDNRVVAHSA 352

>emb|CAY67032.1| Alpha-ketoglutarate-dependent sulfonate dioxygenase [Pichia pastoris]
Length = 419

Score = 64.3 bits (155), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 76/276 (27%), Positives = 113/276 (40%), Gaps = 35/276 (12%)

Query: 3 QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
Q +TP LG+ V GV L+ L + L Q +++F Q L D+ + K
Sbjct: 101 QEIRNLTPK---LGSEVRGVQLSQLSPSQKDDLALYVAQRGVVFRDQDL-RDKNLQEVK 156

Query: 63 RFGAIERIGGGDIVAISNVKADG-----TVRQHSPAEDDMMKVIVGNMAWHADSTYMP 116
FG + G I S +G T R+ P++ + ++AWH+D TY
Sbjct: 157 EFG--QYFGLPHIHQTSQA-PEGFPEFHITYRRAGPSK---PFINKIASIAWHSIDITYEL 210

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA-----LVHQRSARHSLVYSQS 170
A F P GG T FAD AY+ L + L+H SAR S +
Sbjct: 211 QPAGVTFFGLIEGPEAGGDTLFADAIEAYERLSPTFQKFLDGLRLIH--SARLQAADSLA 268

Query: 171 KLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFL 230
K G +Q+ T+ + PLV+ HP G+ S+ I G+ ES+ L
Sbjct: 269 K-GSIQRK-----KFTSETVHPLVRYHPVLGKKSIYAKAFGTRIIGLKQEESDLVL 318

Query: 231 EGLVDWACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
+ ++ A + + G VV WDNR + H A
Sbjct: 319 NFIQNFIATAQDLQLRASYPEGTVVAWDNRVVFHSA 354

>emb|CBJ18770.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 64.3 bits (155), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 41/114 (35%), Positives = 57/114 (50%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---PLRPLVK 199
AAYDALD+ T+A + HSL+YS+ LG ++ Y + A L+ LV+
Sbjct: 1 AAYDALDDDTKAEIEDMICEHSLMYSRGSIG-----FLDYTDDEKAMFKPVLQRLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP R SL + HA AI GM E+ L L + A Q V+ H+W D+
Sbjct: 53 THPVHRRKSLYLSSHAGAIQGMSPPEARLLLRDLTEHATQPEFVYVHKWTLHDL 106

>ref|XP_003043934.1| hypothetical protein NECHADRAFT_76975 [Nectria haematococca mpVI 77-13-4]
gb|EEU38221.1| hypothetical protein NECHADRAFT_76975 [Nectria haematococca mpVI 77-13-4]
Length = 359

Score = 64.3 bits (155), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 61/254 (24%), Positives = 100/254 (39%), Gaps = 34/254 (13%)

Query: 41 QHALLIFPGQH-LSNDQQITFAKRFQAI-----ERIGGGDIVAISNVK 82
Q ++ F Q+ L+ND Q R G + ER GGD + +S +
Sbjct: 71 QRGVVFVFRQNNLTNDLQKKLILRLGELTGRPASSTLHIHPLNLSERELGGDDLEVSTIS 130

Query: 83 ADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR 142
+ + + + + N WH+D + P A +P+ GG T +A
Sbjct: 131 SKQHAKFYRKTDQNGVVVTKRNNEMWHSIDIAFEPAPADYTSRLRLVELPSTGGDTLWASGY 190

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM-----DTTATPLR-- 195
YD L A + + +A + Q V + S + Y D LR
Sbjct: 191 DVYDHLSPAYQKFLEGLTA----TFEQPNFAKVAER-SGFELYDKPRGSPDNVNGRELRAI 245

Query: 196 -PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWA-AG 251
P+V+ +P TG S+ IG H I + A ES+ L+ D + + +W
Sbjct: 246 HPVVVRTNPVTGWKSVFPIGAHVGHINDVTAEESDNLKWFYDLVAKDHSIQVRLRWENPN 305

Query: 252 DVVVWDNRCLLHRA 265
D+ +WDNR + H A
Sbjct: 306 DIAIWDNRSVVFHSA 319

>gb|ADC33971.1| TfdA-like protein [uncultured bacterium]
Length = 131

Score = 63.9 bits (154), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 43/131 (32%), Positives = 65/131 (49%), Gaps = 5/131 (3%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQS---KLGHVQQAGSAYIGYGMDDTTAT 192
T F DM AY+AL + + V R A H + +++ + + Y T
Sbjct: 1 TEFCDMYLAYEALPDDLKRAVAGRRRAIHHSKTRNPRVTISPDRPGAKEYYEARARETRE 60

Query: 193 PLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRV-HAHQWAA 250
L+PLV+ HPETGR +L I R I M A+++ L+ L + R + H+W
Sbjct: 61 ILQPLVRTHPETGRQALYISPRFTIGIADMPDADAQALLDRLFASFVKERRFQYRHKWKD 120

Query: 251 GDVVVWDNRCL 261
GD+V+WDNRC+
Sbjct: 121 GDLVMWDNRVCV 131

>ref|XP_002617710.1| hypothetical protein CLUG_03154 [Clavispora lusitaniae ATCC 42720]
gb|EEQ39028.1| hypothetical protein CLUG_03154 [Clavispora lusitaniae ATCC 42720]
Length = 417

Score = 63.9 bits (154), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 70/279 (25%), Positives = 107/279 (38%), Gaps = 44/279 (15%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGD 74
+G + G+ L+ L+D L + ++ F Q LS +Q+ K +G +E
Sbjct: 122 IGTEIVGLQLSELNDKQKDELALLIAERVVFFRDQDLSPQKQLELGKYWGQVEV--HAQ 179

Query: 75 IVAISNVKADGTVRQHSPAEWDDMMK-----VIVGNMAWHADSTYMPVMAQGAV 123
+ + + K DG W D + I GN WH D + A
Sbjct: 180 VPRVPDTK-DGEALPGITVIWQDYAREFFGLPLTFKNSIGGNSQWHTDLVHEFQAPAGITH 238

Query: 124 FSAEVVPAVGGRTCTCFADMRAAYDALDEATRALVHQRSA----RHSLVYSQSKLG---HVQ 176
+ +P VGG T +A AAYD L A + + ++A HS + ++ L H++
Sbjct: 239 LYNDTIPEVGGDTVWASGYAAYDKLSPAFQKFLDGKTAIYRSAHSYLDRENPLNGPKHIE 298

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVD 235
+ PLV+ HP TG L + R I G+ ESE LE L
Sbjct: 299 RE-----HPLVRTHPATGWKYL FVNRSMTVRIVGLQPKESVILEYLF 342

Query: 236 WACQAPRVHAH-QWAA---GDVVVWDNRCLLHRAEPWD 269
+ + W + G +WDNR H A WD
Sbjct: 343 LFERNLDIQVRWNWWSKPGYGTSAIWDNRISQHNAV-WD 380

>ref|XP_001906307.1| hypothetical protein [Podospira anserina S mat+]
emb|CAP66973.1| unnamed protein product [Podospira anserina S mat+]

Length = 437

Score = 63.9 bits (154), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 67/295 (22%), Positives = 111/295 (37%), Gaps = 35/295 (11%)

```
Query: 5   TLQITPTGATLGATVTGVHLATL-----DDAGFAALHAAWLQHALLIFPGQH-LSNDQQI 58
          + +TP   +G   + V L L   D   L   Q   ++ F   Q   L++D Q
Sbjct: 108 SFDVTPV---IGREYSNVDLVKLLRAPNDELRLDLAITISQRGVVFFRKQEGLTDDLQK 164

Query: 59   TFAKRFG-----AIERIGGGD--IVAISNVKADGTVRQHSPAEWDDM 98
          +R G               A   GG D I   IS+ +A               + W+
Sbjct: 165 ELVQRLGQLSGKPETSGLHIHPISNAAREHGGKDDEISVISSEQAKKLYADRFASAWNGG 224

Query: 99   MKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQ 158
          G   WH+D T+ P+ +   A+   +P   GG T +A   YD +   R   +
Sbjct: 225 RHRQSGKGQWHS DITFEPIPSDYALLKLTQLPKTGGDTLWASGYELYDRISP KLRGFLDT 284

Query: 159   RSARHS---LVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL-IGRH 214
          +A ++   +   + G   +G   +   +   P+++ +P TG   S+   +G H
Sbjct: 285 LTAYYAQPLFTDAAKRNGFSIYSGERGAPENVGDVLEAIHPVIRTNPVTGWKSVFAVGHH 344

Query: 215   AHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVWDNRCLLHRAEP 267
          I G+   ES+ FL+ V   +   +   +W   DV +WDNR + H A P
Sbjct: 345 VKRIHGLSDEESKHFLDWFVQLIVENHDLQVRFKWKDVNDVAIWDNRSVYHAATP 399
```

>ref|XP_002567705.1| Pc21g06600 [Penicillium chrysogenum Wisconsin 54-1255]
emb|CAP95557.1| Pc21g06600 [Penicillium chrysogenum Wisconsin 54-1255]
Length = 367

Score = 63.9 bits (154), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 62/258 (24%), Positives = 101/258 (39%), Gaps = 37/258 (14%)

```
Query: 41   QHALLIFPGQH-LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMM 99
          Q   ++ F   Q   L ND Q   +R G +   + I V   G   R+HS   DD +
Sbjct: 79   QRGVVFFRKQDSLNDLQKELVQRLGELSGKPSTSGLHIHPVANS--REHSVK--DDEI 134

Query: 100   KVI-----VGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMR 142
          VI               WH+D T+ P+ +   +   +P   GG T +A
Sbjct: 135 SVISSASREKLYKDRNTRKQTSRREWHSDITFEPIPSDYTLRLTELPKTGGDTLWASGY 194

Query: 143   AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY-----MDTTATPLR--- 195
          YD + +   +   +A   Y+Q   V +   I G   +   LR
Sbjct: 195 EVYDRISQPYQKFLEGLTA---TYAQPGFNEVAKRNDFTIHPGPRGAPENVGEELRAEH 250

Query: 196   PLVKVHPETGRPSLL-IGRHAAIPGMDAAESERFLEGLVDWACQAPRVHA-HQWA-AGD 252
          P+++ +P TG   S+   +G H   + G+   ES R L+ V   +   +   ++W   D
Sbjct: 251 PVIRTNPVTGWKSVFAVGTHVQKVNGVSEESRRLDWFVSLIVENHDLQVRNRWQNPND 310

Query: 253   VVVWDNRCLLHRAEPWDF 270
          + +WDNR + H A   WD+
Sbjct: 311 LAIWDNRSVYH-AATWDY 327
```

>dbj|BAE54591.1| unnamed protein product [Aspergillus oryzae]
Length = 420

Score = 63.9 bits (154), Expect = 3e-08, Method: Compositional matrix adjust.
Identities = 68/257 (26%), Positives = 103/257 (40%), Gaps = 28/257 (10%)

```
Query: 15   LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
          +G   + G+ L   L D   L   +   +++ F   Q LS   QQ   + FG +E
Sbjct: 118 IGTEIVGLQLKDLTDQKDELGLLIAERSVVFFRDQDLSPQQKALGEYFGEVEVHPQVP 177
```

Query: 246 H-QWAAGDVVVWDNRCL 261
+W +WDNR +
Sbjct: 315 RFKWTPRTSALWDNRVLV 331

>ref|YP_001263745.1| taurine dioxygenase [Sphingomonas wittichii RW1]
gb|ABQ69607.1| Taurine dioxygenase [Sphingomonas wittichii RW1]
Length = 286

Score = 63.9 bits (154), Expect = 3e-08, Method: Compositional matrix adjust.
Identities = 76/302 (25%), Positives = 117/302 (38%), Gaps = 47/302 (15%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQ----- 56
+++I P T+GA V GV L+ L A A+ AA L+H ++ F Q L N+
Sbjct: 14 SIRIRPLQPTIGAEVEGVDLRPLAPQRDAIRAAVLRHKVVFVRDQALDNESQAFAAQ 73

Query: 57 -----QITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAW 108
T R I RI A+ K + + + P G+ +
Sbjct: 74 FGALYTHPSTTRDPRVAPIHRIA-----AVDAAKYEKRLHRDVPP-----GD-GY 117

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
H+D+++ V GAV A +P VGG T + D AY+ L + + H +
Sbjct: 118 HSDTSWRLVPTWGAFLRAVTLPEVGGDTIWDANLAYEGLSAELKERLEGLHVTHDFREA 177

Query: 169 QSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESE 227
+ GH Y + P+V+ H ETG+ L + I G++ AES
Sbjct: 178 LAASGH-----DYPIVA-----HPVVRHRETGQKILWVNLTQKPQILGVELAESR 223

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPET 287
L+ ++ + W G V WDNR +H A PR + +A P
Sbjct: 224 ALLDEVLRQYKRPEFQVRFSWRPGSVAFWDNRAAVHYAVRNYGDFPRHLERVLIADEPLY 283

Query: 288 EG 289
G
Sbjct: 284 AG 285

>ref|XP_002150987.1| TfdA family taurine dioxygenase, putative [Penicillium marneffei
ATCC 18224]
gb|EEA22378.1| TfdA family taurine dioxygenase, putative [Penicillium marneffei
ATCC 18224]
Length = 355

Score = 63.5 bits (153), Expect = 3e-08, Method: Compositional matrix adjust.
Identities = 44/176 (25%), Positives = 77/176 (43%), Gaps = 6/176 (3%)

Query: 105 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS 164
++ WHAD T+ V + A+ +P GG T +A YD L + + +A H
Sbjct: 153 SVGWHADITFENVPSDYAILKIHTLPETGGDTLWASGYEVYDRLSPSMAQFLEGLTATHD 212

Query: 165 LVY---SQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPG 220
+ +LG+ + G + T + P+++ +P TG S+ + + I G
Sbjct: 213 ATFFHDEARRLGNPLREGIRGSPLNSGSLTTVHPVIRTNPVTGWKSVFVNKGFTKTRING 272

Query: 221 MDAAESERFLEGLVDWACQAPRVHA-HQWAAGDVVVWDNRCLLHRAEPWDFKLPRV 275
+ ES+ L+ L + Q ++W DV +WDNR H A +D+ R+
Sbjct: 273 VTKDESDILLQYLFNLVTQNHDAQVRYKWNKNDVAIWDNRSNWHCAT-YDYDETRI 327

>emb|CBJ18752.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 63.5 bits (153), Expect = 3e-08, Method: Compositional matrix adjust.
Identities = 40/112 (35%), Positives = 53/112 (47%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRP-LVKVH 201
AAYDALDE + + HS +YS+ KLG I + P+R LV+ H
Sbjct: 1 AAYDALDERLKHQIEDLVCLHSNMYSRGKLGLTDFDTDEERIAF-----KPVRQRLVRRH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P TGR SL + HA I GM E L L ++A + V++H W D
Sbjct: 55 PVTGRKSLFLSAHAGEIEGMSIPEGRMLLLDLTEFATREQFVYSHAWRINDF 106

>ref|XP_001593138.1| hypothetical protein SS1G_06060 [Sclerotinia sclerotiorum 1980]
gb|EDO03579.1| hypothetical protein SS1G_06060 [Sclerotinia sclerotiorum 1980
UF-70]
Length = 389

Score = 63.5 bits (153), Expect = 3e-08, Method: Compositional matrix adjust.
Identities = 52/171 (30%), Positives = 78/171 (45%), Gaps = 14/171 (8%)

Query: 104 GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH 163
G WH+D + A + VP VGG T +A AAY L R ++ + A +
Sbjct: 195 GASRWHSDDLVELHPAGLTHLHNDTVPEVGGDTLWASGYAAYSKLSPEFRKFINGKQAIY 254

Query: 164 SLVYSQSKLGHVQ-QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGM 221
V + + L AG +I + P+V+VHP TG +L + R +I G+
Sbjct: 255 --VSTHTYLD RDDPSAGPKHIER-----VHPIVRVHPVTGWKTLWVNRSM TKSIVGL 304

Query: 222 DAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFK 271
D AES+ L L D + + +W AG +WDNR +H A WD++
Sbjct: 305 DKAESDLILGYLYDVFEKNVDIQVRFRTAGTSAIWDNRSTIHNAS-WDYE 354

>emb|CBJ19021.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 63.5 bits (153), Expect = 3e-08, Method: Compositional matrix adjust.
Identities = 40/111 (36%), Positives = 55/111 (49%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
AAYDALD+ T+A + HSL+ S+ LG + Y + L+ LV+ HP
Sbjct: 1 AAYDALDDDTKAEIEDMICEHSLMTSRGALGFLD-----YTDEEKEMFKPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E+ L L + A Q V+ H+W D+
Sbjct: 56 VHGRKSLYLSSHAGAIQGMSVPEARVLLRDLNEHATQPQFVYVHKWTLHDL 106

>ref|XP_001593310.1| hypothetical protein SS1G_06232 [Sclerotinia sclerotiorum 1980]
gb|EDO03751.1| hypothetical protein SS1G_06232 [Sclerotinia sclerotiorum 1980
UF-70]
Length = 393

Score = 63.5 bits (153), Expect = 3e-08, Method: Compositional matrix adjust.
Identities = 60/262 (22%), Positives = 105/262 (40%), Gaps = 30/262 (11%)

Query: 14 TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG 73
++G + G+ L +LDD L + ++ Q + +QI F FG +
Sbjct: 125 SIGTELVGIIQLTSLDDTQKNELARLVAERGVVFLRDQKMDVHEQIEFGSYFGELH----- 179

Query: 74 DIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGAVF-SAEVVP- 131
I ++ + D + P D+ K + WH+D +Y + G F + +P
Sbjct: 180 -IHQMAGIIPD--LPWVHPIHKDE TAKNGRSHQIWHSDVSYE-IQPPGLTFLRMDTL PKA 235

Query: 132 -----VGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 185
GG T +A Y++L + ++ A+HS ++QA A G
Sbjct: 236 GPDGYEAGGDTIWASGYGIYESLPTLKGILETLEAKHS-----GLEQA EKALKGN 286

Query: 186 GM--DTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAPR 242

```

      G      + P+V+ HP TG+ +L + + I G++ SE L+ L +A
Sbjct: 287 GCLRRNPIETIHPVVRTHPVTGQKTLVYVNFNFTKEIVGVEKRFSESLDLNRTVAEAYE 346

Query: 243 VHAH-QWAAGDVVVWDNRCLLH 263
      +W+ V +WDNR H
Sbjct: 347 YQVRWKWSTNAVAIWDNRATFH 368

```

>gb|ABD39120.1| alpha-ketoglutarate dioxygenase [uncultured bacterium]
Length = 98

Score = 63.5 bits (153), Expect = 3e-08, Method: Compositional matrix adjust.
Identities = 29/66 (43%), Positives = 40/66 (60%)

```

Query: 196 PLVKVHPETGRPSLLIGRHHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
      PLV+ H +GR L IG HA + G+ AE L L++ A Q V+ H+W GD+V+
Sbjct: 32 PLVRTHAGSGRKFLFIGAHASHVEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGDLM 91

Query: 256 WDNRCCL 261
      WDNRC+
Sbjct: 92 WDNRCV 97

```

>emb|CBJ18950.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 63.5 bits (153), Expect = 3e-08, Method: Compositional matrix adjust.
Identities = 40/110 (36%), Positives = 54/110 (49%), Gaps = 5/110 (4%)

```

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHP 202
      AAYDALD+ T+A + HSL+ S+ LG + Y + L+ LV+ HP
Sbjct: 1 AAYDALDDDTKAEIEDMICHSMTSRGALGFLD-----YTDEEKEMFKPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
      GR SL + HA AI GM E+ L L + A Q V+ H+W D
Sbjct: 56 VHGRKSLYLSSHAGAIQGMSVPEARVLLRDLNEHATQPEFVYVHKWTLHD 105

```

>gb|ADC33981.1| TfdA-like protein [uncultured bacterium]
Length = 123

Score = 63.5 bits (153), Expect = 3e-08, Method: Compositional matrix adjust.
Identities = 45/127 (35%), Positives = 61/127 (48%), Gaps = 5/127 (3%)

```

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR 195
      T F DM AYD L E + + A H S++ G +++ T A
Sbjct: 1 TEFCDMYDAYDRLPEELKQIRGMRAVHD--DSRTAAGGLRKGGKDVTDVRHVTGAR--H 56

Query: 196 PLVKVHPETGRPSLLIGRHHA-IPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
      PLV+ HP TGR +L +GR +A I + ESE L+ L A A +W GD+V
Sbjct: 57 PLVRTHPATGRKALYLGRRRNAYIVSLPVEESEALLDRLWSHAIAASSAWTQEWQVGDV 116

Query: 255 VWDNRCL 261
      VWDNRC+
Sbjct: 117 VWDNRCV 123

```

>emb|CBI54184.1| unnamed protein product [Sordaria macrospora]
Length = 382

Score = 63.5 bits (153), Expect = 3e-08, Method: Compositional matrix adjust.
Identities = 67/276 (24%), Positives = 105/276 (38%), Gaps = 34/276 (12%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITF 60
T +TPT +G V G+ L+ L AG L + ++ F Q ++ ++ +
Sbjct: 96 TVTHLTPT---IGTEVKGIIQLSALTSAGKDELARFIAERKVVAFRQQDFADLPIDEEALKV 152

Query: 61 AKRFGA--IERIGGG-----DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST 113
+ FG I G +I + D +V D ++AWH+D +
Sbjct: 153 GEYFGRHHIHPTSGSPEGFPEIHLVHRSAGDNSV-----DLFFANRTSSVAWHS DVS 204

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG 173
Y P GG T F D AY+ L + +H A HS
Sbjct: 205 YEQQPPGTTFLYILEKPETGGDTLFDVAEAYNRLSPLFQERLHGLKATHS----- 255

Query: 174 HVQQAGSAYIGYGMDTTATPLR--PLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFL 230
++Q SA G+ + P+++ HP TG ++ + + I G+ ES+ L
Sbjct: 256 GIEQVNSAAARGGIIKRREPVVNEHPIIRTHPATGEKAIYVNPQFTREIVGLKKEESDTLL 315

Query: 231 EGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ L D A +W VVVWDNR H A
Sbjct: 316 KFLYDHLAYGADFQARIKWEEDTVVVWDNRVTQHSA 351

>emb|CBJ18767.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 63.5 bits (153), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 41/115 (35%), Positives = 55/115 (47%), Gaps = 13/115 (11%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRP----LV 198
AAYDALD T+A + HSL+YS+ LG ++ Y D RP LV
Sbjct: 1 AAYDALDNDTKAEIDDMICEHSLMYSRGLG-----FLDYS-DEEKQMFRLVQLRV 51

Query: 199 KVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+ HP GR SL + HA AI G+ E L L + A + V+ H+W D+
Sbjct: 52 RTHPVHGRKSLYLSSHAGAIRGISVPEGRLLLRDLTEHATRPEFVYVHKWKVHDL 106

>emb|CBJ19209.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 63.5 bits (153), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 40/111 (36%), Positives = 54/111 (48%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
AAYDALD T+A + HSL+ S+ LG + Y + L+ LV+ HP
Sbjct: 1 AAYDALDNDTKAEIEDMICHSMTSRGALGFLLD-----YTDEEKEMFKPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E+ L L + A Q V+ H+W D+
Sbjct: 56 VHGRKSLYLSSHAGAIQGMSVPEARVLLRDLNEHATQPEFVYVHKWTLHDL 106

>emb|CBJ18768.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 63.5 bits (153), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 40/112 (35%), Positives = 55/112 (49%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRP-LVKVH 201
AAYDALD+AT+A V HSL+YS+ LG + + P+R LV+ H
Sbjct: 1 AAYDALDDATKAEVEDLVCEHSLLYSRGTGLFTDLSEEERAMF-----RPVRQLRVTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P TGR SL + H I G E+ F+ L + A Q ++H W D+

Sbjct: 55 PVTGRKSLFLSSHIGTIIGWPVPEARAFIRDLTEHATQKQFTYSHAWRQYDL 106

>emb|CBJ18728.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 63.5 bits (153), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 42/111 (37%), Positives = 53/111 (47%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
A YDALDE T+ALV HS +YS+ LG + P R LV+ HP
Sbjct: 1 AGYDALDEETKALVRDLVCEHSQIYSRGVLGFTEFTEEE----RRKNAPVPQR-LVRRHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL + HA I G E+ L L + A Q V+AH+W D+
Sbjct: 56 VTGRRSLFLSSHAGTIVGWVPPEARALLRDLTEHATQREFVYHRWRQYDL 106

>ref|XP_001803696.1| hypothetical protein SNOG_13485 [Phaeosphaeria nodorum SN15]
gb|EAT78932.2| hypothetical protein SNOG_13485 [Phaeosphaeria nodorum SN15]
Length = 294

Score = 63.2 bits (152), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 47/174 (27%), Positives = 75/174 (43%), Gaps = 7/174 (4%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS-- 164
WH+D T+ PV + A+ +PA GG T +A YD L A + + +A H
Sbjct: 92 GWHSDITFEPVPSDYAMLKIHTLPATGGDTLWASGYEIDRLSPAMQQFLEGLTATHDAK 151

Query: 165 -LVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE-TGRPSLLIGR-HAHAIPGM 221
+ +LG+ + G T + P+V+ +P TG S+ + + I G+
Sbjct: 152 FFLEEAEERLGNPIRKIGIRGNPLNFGEALTAVHPVVRTNPAVTGWKSVYVNGGFTKRINGV 211

Query: 222 DAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPR 274
ES+ L L + Q +W D+ +WDNR H A +D+ PR
Sbjct: 212 TKDESDVLLSYLFNLLTQNHDAQVRFKWRKNDLAIWDNRSTWHCAT-YDYNDPR 264

>ref|YP_003276123.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
CNB-2]
gb|ACY30827.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
CNB-2]
Length = 303

Score = 63.2 bits (152), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 65/305 (21%), Positives = 125/305 (40%), Gaps = 47/305 (15%)

Query: 2 AQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
++T +++ +G V+G+ L + + L A + H +L+F Q+++ Q + F
Sbjct: 19 SRTGIELRRISPAIGVEVSGIDLRQPMSEEQARELRQALVAHKVLVLFREQNITPAQHVAF 78

Query: 61 AKRFGAIE-----RIGGGDIVAI-SNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
A+RFG +E ++V + N K GT +H D
Sbjct: 79 ARRFGELELHPVFPHPDHAELVLLGGNSKIPGT-----ENVYHTDV 120

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS-QSK 171
++ + +V P VGG T + +M AY+ L E + + A H ++ S ++
Sbjct: 121 SWRETPSMASVLRCEVCEVGGDTVWINMEQAYEQLPETRKQQIAGLYAVHDILPSFGAR 180

Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-----HAHAIPGMDAAES 226
+ +QA + + P+V+ HPE+G+ L + A+ D+ S
Sbjct: 181 MTPAEQAQA-----RGKYPPVHVHPVVRTHPESGQKILYVNETFVTHFANFSSNFDSFRS 234

Query: 227 ERFL----EGLVDWACQAPRVHAHQ----WAAGDVVVWDNRCLLHRAEPWDFKLPRVMWH 278
+ + L+++ + P + +Q W + + +WDNR H A F R M
Sbjct: 235 ANEIHAAQQQDLMNYYLLRQPAILEYQMRHLWESNTIAMWDNRSTQHYAIQDYFPAVRRMRH 294

Query: 279 SRLAG 283
+ + G
Sbjct: 295 ATVVG 299

>emb|CBJ18725.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 63.2 bits (152), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 39/112 (34%), Positives = 58/112 (51%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYDALD AT+A + HSL+YS+ +LG + + P+R LV+ H
Sbjct: 1 AAYDALDAATKAEIEDLVCEHSLIYSRQQLGFTEFLPDERVA-----MKPVRHRLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P +GR SL + H I G E+ F+ L++ A Q V++H+W D+
Sbjct: 55 PGSGRKSFLPSAHIGTIIGWPQPEAMAFIRDLMEHATQPQFVYSHRWTQHDL 106

>emb|CBJ18956.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 63.2 bits (152), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 40/111 (36%), Positives = 54/111 (48%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD T+A + HSL+ S+ LG + Y + L+ LV+ HP
Sbjct: 1 AAYDALDNDTKAEIEDMICEHSLMTSRGALGFLD-----YTDEEKEMFKPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E+ L L + A Q V+ H+W D+
Sbjct: 56 VHGRKSLYLSSHAGAIQMSVPEARVLLRDLNEHATQPQFVYVHKWTLHDL 106

>ref|XP_001828620.2| alpha-ketoglutarate-dependent sulfonate dioxygenase [Coprinosia
cinerea okayama7#130]
gb|EAU93223.2| alpha-ketoglutarate-dependent sulfonate dioxygenase [Coprinosia
cinerea okayama7#130]
Length = 422

Score = 63.2 bits (152), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 73/278 (26%), Positives = 113/278 (40%), Gaps = 21/278 (7%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
A + +ITP LG V+GV+LA LD G L + L++F Q D+ F
Sbjct: 129 ATSVFEITPY---LGTEVSGVNLADLSDGRDQLALEVARRGLMVFRDQQDFIDRGPEFY 185

Query: 62 KRFGAIERIGGGDIVAISNVKADG-----TVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
++G R G V ++ +G R H ++ + + + WH+D +Y
Sbjct: 186 LQWG---RHFGRHLHVHTSGHPEGYPEFHLVYRDHK-TTFNFEIDESISSTIWHSDVSYE 241

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
F P GG T F +A L A + A HS + Q+
Sbjct: 242 LQPPGLTTFLLSAPPSGGDTLFTSQVSALRKLSPQFVAFKTLKAVHS-GFEQADFSRS 300

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLV 234
+ G+ ++ + P+V+ HP TG +L + R I G+ ESE L+ L
Sbjct: 301 GKRGA TVRREPVEH---IHPVVRKHPVTGEEALYVNRQFTRRIVGLKKEESEATLKLKY 356

Query: 235 DWACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFK 271
D ++ A +W +V+WDNR H A DFK
Sbjct: 357 DHIDKSADNQARVRWTPNTIVLWDNRITAHSAT-VDFK 393

>gb|EGB09898.1| hypothetical protein AURANDRAFT_62958 [Aureococcus anophagefferens]
Length = 1431

Score = 63.2 bits (152), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 94/323 (29%), Positives = 129/323 (39%), Gaps = 43/323 (13%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGF-AALHAAWLQHALLIFPGQHLSNDQQITF 60
A L++ P + GATV +D A+ AA+ H LL + G+ L+ D ++ F
Sbjct: 35 AACGLELLPWDGSFGATVATPMRDIVDAPCLHDAVRAAFAAHRLLRWSGEALAPDDELAF 94

Query: 61 AKRFGAIERIGGG-DIVAI SNVKADGTVRQHSPA EWDDMMK-----VIVGNMA- 107
K G ++ V A+ R PA + +++ V G+++
Sbjct: 95 MKLLPHDGSFGAAHGPQGVAGVDAEKYARWRV PARDEILLQGEGFVPAGHHGVPEGHLSS 154

Query: 108 -----WHADSTYM---PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALV-- 156
WH D Y P +A +++ V P VGG T F D R YD LD+A R +
Sbjct: 155 GKPIKEWHTDGHYEAREPSIAT-SMYCVSVKP-VGGDTLFMDARVIYDELDDAERG VFDC 212

Query: 157 ----HQRS--ARHSLVYSQSKLGH--VQQAGSAYI-GYGMDTTATPLRPLVKVHPE-TGR 206
+ RS + HS Y G GS Y G G P V V P+ GR
Sbjct: 213 ADIEYSRSPVSMHSSGYRALLEGESAASN VGS LYAEGAGRARAPGATHPAVWVLPDGDGR 272

Query: 207 PSLLIGR---HAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLH 263
SL + I G A E L A + + W GD VVVDNR LLH
Sbjct: 273 RSLPLAPMWIDKLNINGTTLAGDELQLLVAKVLARGERSLKYAWTPGDFVVDNRALLH 332

Query: 264 RAEPWDFKLP---RVMWHSRLAG 283
A P D P R++ RLAG
Sbjct: 333 SATPNDGFSPEGLRLLHRIRLAG 355

>emb|CBJ18808.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 63.2 bits (152), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 40/114 (35%), Positives = 58/114 (50%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD--TTATPLR-PLVK 199
AAYDALD+ T+A + HS ++S+ +LG + Y D T P+R LV+
Sbjct: 1 AAYDALDQKTKAEIEDLICEHSQIFSREQLG-----FTEYLPDERTMMKPVRHRLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP +GR SL + H I G E+ F+ L + A Q V++HQW D+
Sbjct: 53 THPTSGRKSLSFLSAHIGTILGWPQPEALAFIRDLTEHATQEQFVYSHQWTQHDL 106

>emb|CBJ18987.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 63.2 bits (152), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 40/111 (36%), Positives = 55/111 (49%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
AAYDALD+ T+A + HSL+ S+ LG + Y + L+ LV+ HP
Sbjct: 1 AAYDALDDDTKAEIEDMIREHSLMTSRGALGFLD-----YTDEEKEMFKPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

GR SL + HA AI GM E+ L L + A Q V+ H+W D+
Sbjct: 56 VHGRKSLYLSSHAGAIQGMSVPEARVLLRDLNEHATQPQFVYVHKWTLHDL 106

>emb|CBJ18742.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 63.2 bits (152), Expect = 5e-08, Method: Compositional matrix adjust.
Identities = 38/112 (33%), Positives = 55/112 (49%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRP-LVKVH 201
AAYD LD T+A + HSL+YS+ LG + + + TP+R LV+ H
Sbjct: 1 AAYDGLDGTKAEIEDLVCEHSLIYSRGTGLFTELSDEERRMF-----TPVRQRLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P TGR SL + H I G E+ F+ L + A Q ++H+W D+
Sbjct: 55 PVTGRKSLYLSSHIGTIVGWPMEARAFIRDLTEHATQPRYTYSHKWRQFDL 106

>emb|CBJ18726.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 63.2 bits (152), Expect = 5e-08, Method: Compositional matrix adjust.
Identities = 41/112 (36%), Positives = 56/112 (50%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR-PLVKVH 201
AAYDALD+ T+A V HSL+YS+ +G + P+R PLV+V
Sbjct: 1 AAYDALDDRTKAEVAGLVCEHSLLYSRQAVGFTDFTPEEISNF-----QPVRHPLVRVQ 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL + HA I G ES FL L++ A + V++H W D+
Sbjct: 55 KATGRKSLFLSAHAGVIVGWSVPESRAFLRDLIEHATRPEFVYSHSWWQHDL 106

>emb|CBJ18868.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 63.2 bits (152), Expect = 5e-08, Method: Compositional matrix adjust.
Identities = 41/112 (36%), Positives = 57/112 (50%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRP-LVKVH 201
AAYDALD T+A V HSL++S++ +G G+ P+R LV+ H
Sbjct: 1 AAYDALDARTKAEVEDLICEHSLIHSRAAVGFTDLTPEEIAGFA-----PVRQRLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL + HA AI G E+ +L L + A Q V++HQW D+
Sbjct: 55 QATGRKSLFLSAHAGAIIGWTIPEARAYLRELTEHATQREFVYSHQWRQYDL 106

>ref|XP_001525561.1| alpha-ketoglutarate-dependent sulfonate dioxygenase
[Lodderomyces
elongisporus NRRL YB-4239]
gb|EDK45310.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Lodderomyces
elongisporus NRRL YB-4239]
Length = 388

Score = 62.8 bits (151), Expect = 5e-08, Method: Compositional matrix adjust.
Identities = 63/235 (26%), Positives = 98/235 (41%), Gaps = 17/235 (7%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQ---ITFAKR 63
+IT G V G+ L+ L+DAG L Q +L+F Q ++ + F K
Sbjct: 81 KITRITPKFGTEVDGIQLSQLNDAGKDELALLLAQRKVLLFNDQDFASHGPGFAVEFGKY 140

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG + I + + T R+ E + + + N WH+D TY ++ V
Sbjct: 141 FGPLH-IHPSSGSPKGHPHELHITYRRPEKGELERIFRERTTNTGWHSDVTYELTPSRFTV 199

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
F + GG T FAD AY L + A+ + H L S+ Q A S +
Sbjct: 200 FQV-LESGDGGDTVFADTAEAYRRL---SPAMQQRLEGLHVLHTSED-----QAANSTFQ 250

Query: 184 GYGMD--TTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
G G++ + + PL+++ P TG S+ + R I + ESE L L D
Sbjct: 251 G-GIERRKAVSNIHPLIRLDPVTGEKSIYVNRAGRRIVELKKEESEYLLNFLYD 304

>ref|ZP_07044532.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
S44]
gb|EFI61768.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas testosteroni
S44]
Length = 303

Score = 62.8 bits (151), Expect = 5e-08, Method: Compositional matrix adjust.
Identities = 65/305 (21%), Positives = 124/305 (40%), Gaps = 47/305 (15%)

Query: 2 AQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
++T +++ +G V+G+ L + + L A + H +L+F Q+++ Q + F
Sbjct: 19 SRTGIELRRISPAIGVEVSGIDLRQPMSEEQARELRQALVAHKVLFREQNITPAQHVAF 78

Query: 61 AKRFGAIE-----RIGGGDIVAI-SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS 112
A+RFG +E ++V + N K GT +H D
Sbjct: 79 ARRFGELELHPVFPHPDHAELVLLGGNSKIPGT-----ENVYHTDV 120

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS-QSK 171
++ + +V P VGG T + +M AY+ L E + + A H ++ S ++
Sbjct: 121 SWRETPSMASVLRCEVCEVGGDTVWINMEQAYEQLPETRKQIAGLYAVHDILPSFGAR 180

Query: 172 LGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-----HAHAIPGMDAAES 226
+ +QA + + P+V+ HPE+G+ L + A+ D+ S
Sbjct: 181 MTPAEQAQA-----RGKYPPVVHPVVRTHPESGQKILYVNETFVTHFANFSSNFDSFRS 234

Query: 227 ERFL----EGLVDWACQAPRVHAHQ----WAAGDVVVWDNRCLLHRAEPWDFKLPRVMWH 278
+ + L+++ + P + +Q W + +WDNR H A F R M
Sbjct: 235 ANEIHAAQQQLMNYLLRQPAILEYQMLHWPNTIAMWDNRSTQHYAIQDYFPAVRRMHR 294

Query: 279 SRLAG 283
+ + G
Sbjct: 295 ATVVG 299

>emb|CBJ18971.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19022.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 62.8 bits (151), Expect = 5e-08, Method: Compositional matrix adjust.
Identities = 40/111 (36%), Positives = 55/111 (49%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
AAYDALD+ T+A + HSL+ S+ LG + Y + L+ LV+ HP
Sbjct: 1 AAYDALDDDTKAEIEDMICEHSLMTSRGALGFLD-----YTDEEKEMFKPVLQRLVRAHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E+ L L + A Q V+ H+W D+
Sbjct: 56 VHGRKSLYLSSHAGAIRGMSVPEARVLLRDLNEHATQPQFVYVHKWTLHDL 106

>emb|CBJ18789.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 62.8 bits (151), Expect = 5e-08, Method: Compositional matrix adjust.
Identities = 43/111 (38%), Positives = 59/111 (53%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDAL EATR + A HS + S++KLG S + A + LV+
Sbjct: 1 AAYDALPEATRQKIAGLVAEHSPMTSRAKLG-----SDFNDEERKAFAPVPQVLVRRQL 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
++GR SL + HA A+ GM E+ER ++ LVD A Q VH H+W D+
Sbjct: 56 DSGRMSLYVASHAGAVRGMARPEAERLIQELVDHATQRQFVHTRWRVKDL 106

>emb|CAY27234.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 62.8 bits (151), Expect = 5e-08, Method: Compositional matrix adjust.
Identities = 46/124 (37%), Positives = 60/124 (48%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T FADMRAAYDAL + +A + A HS+ +S+ LG + D +
Sbjct: 1 TEFADMRAAYDALSDMKAEIDGLYAHHSIAHSRQTLGF-----EFSRDEEDRLKGAHV 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ P +G SL I HA I +S L L D A Q + H W GD+V+
Sbjct: 55 PLVRTIPGSGWKSLEYIASHASRIVDQPIPDRLLLDLRDHATQPRFRYRHSWRVGDLM 114

Query: 256 WDNR 259
WDNR
Sbjct: 115 WDNR 118

>ref|XP_001836179.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Coprinosia
cinerea okayama7#130]
gb|EAU85551.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Coprinosia
cinerea okayama7#130]
Length = 405

Score = 62.8 bits (151), Expect = 5e-08, Method: Compositional matrix adjust.
Identities = 66/266 (24%), Positives = 103/266 (38%), Gaps = 29/266 (10%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIER----- 69
+G + G+ L L D L + ++ F Q + Q+ AK +G + R
Sbjct: 94 IGTEIEGIDLRQLTDEQKDELALLVAERGTVFFRDQEIDIYQLELAKHWGPLHRHATTP 153

Query: 70 IGGGDIVAIISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV 129
I + + V D + R+ P+ + + WH+D TY
Sbjct: 154 ITKNGLEHVHVYNDAS-RRPDPSAFSKLE-----LWHSVDVTYELQPPGPTSLKVITN 205

Query: 130 PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTT 189
P VGG T ++ A Y +L + + SA HS V Q G+ G+
Sbjct: 206 PEVGDDTIWSSGYALYSSLSPLGLQKYLEGLSAVHSAV-----AQADGNNR--AAGLPV 255

Query: 190 TATPLR---PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
P+ PLV+VHP TG S+ + I G+ AES+ L L + P
Sbjct: 256 RREPIETVHPLVRVHPATGWKSVFVNPGRTRRIIGIPKAESDAILTFLFRQISENPDFQV 315

Query: 246 H-QWAAGDVVVWDNRCLLHRAEPWDF 270
+W + +WDNR + H A +DF
Sbjct: 316 RFRWETNSIAIWDNRVVTHSAT-FDF 340

>emb|CBJ18785.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 62.8 bits (151), Expect = 6e-08, Method: Compositional matrix adjust.
Identities = 43/112 (38%), Positives = 55/112 (49%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-LVKVH 201
AAYDALDE T+A HS ++S+S LG + P+R LV+ H
Sbjct: 1 AAYDALDEETKAECENLICEHSQLFSSILGFTDFTDDERRKFA-----PVRQRLVRRH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P TGR SL + HA AI G E+ FL L + A Q V+AH W D+
Sbjct: 55 PVTGRRSLYLASHAGAILGWPVEARAFLRDLTEHATQRSFVYAHVWRQWDL 106

>emb|CBJ18727.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 62.4 bits (150), Expect = 7e-08, Method: Compositional matrix adjust.
Identities = 43/112 (38%), Positives = 55/112 (49%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-LVKVH 201
AAYDALDE T+A HS ++S+S LG + P+R LV+ H
Sbjct: 1 AAYDALDEETKAECENLICEHSQLFSSILGFTDFTDDERRKFA-----PVRQRLVRRH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P TGR SL + HA AI G E+ FL L + A Q V+AH W D+
Sbjct: 55 PVTGRRSLYLASHAGAILGWPGEARAFLRDLNEHATQRQSVYAHTWRQWDL 106

>ref|ZP_02189793.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
oxidoreductase protein [alpha proteobacterium BAL199]
gb|EDP63398.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
oxidoreductase protein [alpha proteobacterium BAL199]
Length = 338

Score = 62.4 bits (150), Expect = 7e-08, Method: Compositional matrix adjust.
Identities = 73/284 (25%), Positives = 111/284 (39%), Gaps = 51/284 (17%)

Query: 42 HALLIFPGQHLSDNDQQ---ITFAKRFGAIERIGGGDIVAISNVKADGTV----- 87
H LLI G H +DQ + ++ FG + + +N+ AD
Sbjct: 52 HGLLILKGMHAISDQPELLVRLSRLFGPEVEDYRQTVTSRNNIHADVPEILVVSINVPPAT 111

Query: 88 -----RQHSPAEWDDMMKV-IVGNMAWHADSTYMPVMAQGAVFSAEV-VPVAVGGRTCFAD 140
R P D + V WH D +Y ++F A++ P G+T +AD
Sbjct: 112 PRVPERDPPLTADGKLPVQFPHRRGWHTDQSYRRPPPDISLFYADLPTPKGQGQTLYAD 171

Query: 141 MRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL----- 194
AY AL A + +R A +++Q +QA A T PL
Sbjct: 172 GIGAYAALPAAMK----ERIANLEGIHAQPGRRRSEQAVRA-----GETPDPLTPREAP 221

Query: 195 --RPLVKVHPETGRPSLLI-----GRHAHAIPGMDAAESERFLEGLVDWACQAPR 242
+P+V++HP T P+L + G PG D + R L L+
Sbjct: 222 QRQPVVRIHPVTSEPALYLCESGQMDWVDGPFVGMQPGPDG-DGARLLYELMSHYTSPRF 280

Query: 243 VHAHQWAAGDVVVWDNRCLLHRAEPWDFKL-PRVMWHSRLAGRP 285
+AH W GD+V++DNR +H A +D R MW + + G P
Sbjct: 281 AYAHWDWRGDLVIYDNRSTIHSATWFDADTHRRRMWRRTTVHGNP 324

>emb|CBI56031.1| unnamed protein product [Sordaria macrospora]
Length = 380

Score = 62.4 bits (150), Expect = 7e-08, Method: Compositional matrix adjust.
Identities = 70/287 (24%), Positives = 112/287 (39%), Gaps = 36/287 (12%)

```
Query: 5   TLQITPTGATLGATVTGVHLATL-----DDAGFAALHAAWLQHALLIFPGQ-HLSNDQQI 58
          + ++TP   LG       V L+ L       D       L       Q   ++ F   Q +L++D Q
Sbjct: 62   SFEVTPA---LGREYVNVDLSELLRAPNSDELLRLDLAITISQRGVVFFRKQDNLTDQLK 118

Query: 59   TFAKRFGAI---ERIGGGDIVAISNVKADGTVRQHSPAEDW-DMMKVIVGNMA----WHA 110
          R G +       G I   ISN       R+H   + +   + V   G +   WH+
Sbjct: 119  ELVDRLGKLAGKPATSGLHIHPISNAS-----REHGGGDNEISGVGVSTGRQSAKDQWHS 173

Query: 111  DSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS 170
          D T+ P+ +   A+       +P   GG T +A       YD +   R+ +   +A       Y+Q
Sbjct: 174  DITFEPIPSDYALLRLVQLPKTGGDTLWASGYELYDRISPTLRSFLDTLTA---YYAQ 229

Query: 171  KLGHVQQAG--SAYIG-----YGMDDTTATPLRPLVKVHPETG-RPSLLIGRHAHAIPGMD 222
          +       S Y G       +   T   + P+++ +P TG R       +G H   I G+
Sbjct: 230  LFNEAAKRNGFSVYSGERGAPENVGETLEAIHPVIRTNPVTGWRSVYAVGHHHCQRINGLT 289

Query: 223  AAESERFLEGLVDWACQAPRVHAH-QWAA-GDVVVWDNRCLLHRAEP 267
          ES+ FL       +   +   +W       DV +WDNR + H A P
Sbjct: 290  EEESKYFLNWFQTLIVENHDLQVRLKWNQPNPDVAIWDNRSVYHAATP 336
```

>emb|CBJ18736.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 62.4 bits (150), Expect = 7e-08, Method: Compositional matrix adjust.
Identities = 41/112 (36%), Positives = 55/112 (49%), Gaps = 7/112 (6%)

```
Query: 143  AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-LVKVH 201
          A YDALD+ TR   V   +   HS +YS++ LG       +       P+R   LV+ H
Sbjct: 1    AGYDALDQETRDRVADQICEHSQLYSRALLGFTDFTDEERERF-----KPVRQVLVRTH 54

Query: 202  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
          P   GR SL + HA   I G       E+   FL   L + A Q       V++HQW   GD+
Sbjct: 55   PGHGRKSLYLSSHAGGIVGWPVPEARAFRLDLNEIATQRQFVYSHQWRVGD 106
```

>ref|XP_456245.1| hypothetical protein [Kluyveromyces lactis NRRL Y-1140]
emb|CAG98953.1| KLLA0F26158p [Kluyveromyces lactis]
Length = 392

Score = 62.4 bits (150), Expect = 7e-08, Method: Compositional matrix adjust.
Identities = 66/267 (24%), Positives = 111/267 (41%), Gaps = 21/267 (7%)

```
Query: 8     ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAI 67
          + P       LG   + G+ L   L DA       L       Q   ++I   Q       D+   +A+ +G
Sbjct: 84    LKPITPKLGTEIKGLQLTQLSDAAKDELALLIAQRGVILEDDQDFV-DKGPYAAEEYG-- 140

Query: 68    ERIGGGDIVAISNVKADG-----TVRQHSPAEDWDDMMKVIVGNMAWHADSTYMPVMAQG 121
          R   G   +   ++   +G       T R+       E++ + +       ++ +H D +Y   +   G
Sbjct: 141   -RHFGKLHIHQTSGAPEGHSHLHVTFRRPDRTEFNRFVFRDKTTSIGFHTDVSYE-LQPAG 198

Query: 122   AVFSAEVPV-PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
          F A++   P   GG T FAD   A++ L   +   +   S   H +   S+ +   + +   G
Sbjct: 199   YTFFAQLEGPESSGDTLFDATIEAFERLSPHFQEYL---STLHVHSSKEQAFNSKSNG- 254

Query: 181   AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ 239
          G       T +   PLV+VHP   + SL + R   +   I   +   ES+   L+ L
Sbjct: 255   ---GIQRRAPVTHIHPLVRVHPVLKKKSLFVNRSFSRRIVELKTPESDLLLDFLYSLVEN 311
```

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ + +W V VWDNR L H A
Sbjct: 312 SHDLQLRARWGPRTVAVWDNRRLQHSA 338

>gb|ABD39112.1| alpha-ketoglutarate dioxygenase [uncultured bacterium]
Length = 119

Score = 62.4 bits (150), Expect = 7e-08, Method: Compositional matrix adjust.
Identities = 30/66 (45%), Positives = 38/66 (57%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+
Sbjct: 53 PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDLVM 112

Query: 256 WDNRC 261
WDNRC+
Sbjct: 113 WDNRCV 118

>ref|ZP_06496700.1| taurine catabolism dioxygenase [Pseudomonas syringae pv. syringae
FF5]
Length = 337

Score = 62.4 bits (150), Expect = 8e-08, Method: Compositional matrix adjust.
Identities = 64/295 (21%), Positives = 107/295 (36%), Gaps = 51/295 (17%)

Query: 1 MAQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
++ +I+ + G + + L L AA+ ++F Q+L+ +QI
Sbjct: 5 LSSVPFEISYPAQSFSGVEIENLKLHKNLSFDTIAAIKKCLAYRGFVLFNRQNLTRREQIA 64

Query: 60 FAKRFG-----AIERIGGGDIVAISN-----VKADGTVRQHS 91
+ G IE GD I N D T +H+
Sbjct: 65 VTRLLGNPNLKLHSHWAPQIETATFGDDEVIPNGLPLINHGEILYFVNGPDFCDKTQDEHA 124

Query: 92 PAEWDDMMKVIVGNMAWHA-DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDE 150
+ D G WH DS + V ++ AE+ A GG T F D AAY+ L++
Sbjct: 125 IWDEKDNHTKGKGTSCWHTGDSEAINVETINCLY-AELAAQGGATLFCDTVAAYNDLED 183

Query: 151 ATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLL 210
+ + + H V Q T +PLVK +P T + L
Sbjct: 184 SLKKRIDNLRVVHYFVDPQR-----TEPVSQPLVKTNPITRQKYLY 224

Query: 211 IGRHA-HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
+ + + G+ +ES R L+ L D + V+ H W D ++W+ +H+
Sbjct: 225 LNYNTMERVEGLSKSESRYLLKFLFDHQIKDQYVYEHFWKQDDFLIWNCGTMHK 279

>gb|ABD39116.1| alpha-ketoglutarate dioxygenase [uncultured bacterium]
Length = 107

Score = 62.4 bits (150), Expect = 8e-08, Method: Compositional matrix adjust.
Identities = 30/65 (46%), Positives = 37/65 (56%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+
Sbjct: 41 PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDLVM 100

Query: 256 WDNRC 260
WDNRC
Sbjct: 101 WDNRC 105

>ref|XP_001830736.2| alpha-ketoglutarate-dependent taurine dioxygenase [Coprinosia cinerea okayama7#130]
gb|EAU91105.2| alpha-ketoglutarate-dependent taurine dioxygenase [Coprinosia cinerea okayama7#130]
Length = 366

Score = 62.4 bits (150), Expect = 8e-08, Method: Compositional matrix adjust.
Identities = 68/273 (24%), Positives = 102/273 (37%), Gaps = 28/273 (10%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRFGAIER-- 69
+G ++GV L+ L G L Q +LI Q + ++ I FG I
Sbjct: 82 IGTELSGVQLSQLSKEGLDELALLAAQRKVLILRDQDFQDLPAEKLIELTSHFGPIHSHP 141

Query: 70 -----IGGGDIVAISNVKADGTVRQ--HSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGA 122
G + V S+ + +R+ ++ + + WH+D +Y
Sbjct: 142 TAPNVKGFTEFVNRSSDDRNVPVLRPGYTSKYFASRTASSTNYVYWHSDVSYERQPPSTT 201

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
F P VGG T F AY+ L + + +A HS V + Y
Sbjct: 202 FFWLLDKPDVGGDTLFLSTVEAYNRLSPEFKKRLEGLTALHSGVAQADE-----SRKY 254

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIG---RHAHAIPGMDAAESERFLEGLVDWAC 238
G + P+V+VHP TG +L + RH I G ES+ L+ L D
Sbjct: 255 GGVVRRDPVESIHPVVRVHPVTGEKALFVNPEFTRH---IVGFKKEESDALLKFLYDHIA 311

Query: 239 QAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDF 270
+ + G VV+WDNR H A P DF
Sbjct: 312 KGADFQVRANYLPGTTVIWDNRVTNHSAPV-DF 343

>emb|CBJ19178.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19185.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 62.0 bits (149), Expect = 8e-08, Method: Compositional matrix adjust.
Identities = 38/114 (33%), Positives = 59/114 (51%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD--TTATPLR-PLVK 199
AAYDALD+ T+A + HS ++S+ +LG + Y D T P+R LV+
Sbjct: 1 AAYDALDQKTKAEIEDLICEHSQIFSREQLG-----FTEYLPDERTMMKPVHRHLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP +GR S+ + H I G E+ F+ L++ A Q V++H+W D+
Sbjct: 53 THPTSGRKSIFLSAHIGGIVGWPRPEAMSFIRDLIEQATQPQFVYSHRWTQHD 106

>ref|YP_237385.1| taurine catabolism dioxygenase [Pseudomonas syringae pv. syringae B728a]
gb|AA39347.1| similar to Probable taurine catabolism dioxygenase [Pseudomonas syringae pv. syringae B728a]
Length = 337

Score = 62.0 bits (149), Expect = 9e-08, Method: Compositional matrix adjust.
Identities = 63/295 (21%), Positives = 107/295 (36%), Gaps = 51/295 (17%)

Query: 1 MAQTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
++ +I+ + G + + L L AA+ ++F Q+L+ +Q+
Sbjct: 5 LSSVPFEISYPAQSFGVEIENLKLHKNLSFDTIAAIKKCLAYRGFVLFNRQNLTRREQVA 64

Query: 60 FAKRFG-----AIERIGGGDIVAISN-----VKADGTVRQHS 91
+ G IE GD I N D T +H+
Sbjct: 65 VTRLLGNPNLKSHSWAPQIETTTFGDDEVIPNGLPLINHGEILYFVNGPDFCDKTDQDEHA 124

Query: 92 PAEWDDMMKVIVGNMAWHA-DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDE 150
+ D G WH DS + V ++ AE+ A GG T F D AAY+ L++
Sbjct: 125 IWDEKDNHTKGKGTSCWHTGDSEAINVETINCLY-AELAAQGGATLFCDTVAAYNDLED 183

Query: 151 ATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLL 210
+ + + H V Q T +PLVK +P T + L
Sbjct: 184 SLKKRIDNLRVLHYFVDPQR-----TEPVNQPLVKTNPIRQKYLY 224

Query: 211 IGRHA-HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
+ + + G+ +ES R L+ L D + V+ H W D ++W+ +H+
Sbjct: 225 LNYNTMERVEGLSKSESYRLKFLFDHQIKDQYVYEHFWKQDDFLIWNCGTMMHK 279

>ref|XP_001409620.1| hypothetical protein MGG_12505 [Magnaporthe oryzae 70-15]
gb|EDK01381.1| hypothetical protein MGG_12505 [Magnaporthe oryzae 70-15]
Length = 371

Score = 62.0 bits (149), Expect = 9e-08, Method: Compositional matrix adjust.
Identities = 60/261 (22%), Positives = 103/261 (39%), Gaps = 45/261 (17%)

Query: 41 QHALLIFPGQ-HLSNDQQITFAKRFGAI-----ERIGGGD--IVAI 78
Q ++ F Q +L+ND Q R G + E GG D I I
Sbjct: 81 QRGVVFRAQDNLTLNDLQKKLILRLGELTGRPKTSGLHIHPLLNAERETYGDDNEISTI 140

Query: 79 SNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHAHADSTYMPVMAQGAVFSAEVVPAVGGRTCF 138
S+ + D ++ + + D++ WH+D + PV A +P GG T +
Sbjct: 141 SSAQNDKLYKK-TWTQPDELSPKKQSTAQWHSIDAFEPVPADYTSRLRTELPKTGDTLW 199

Query: 139 ADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM-----DTT 190
A YD + + + S+ ++Q + + A G+ + +
Sbjct: 200 ASGYEIYDKISAPYQKFLETL---SVTFAQKRFNEIADAN---GFSLYSQPRGAPENV 251

Query: 191 ATPLR---PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH 246
T LR PLV+ +P TG S+ +G H + G+ ES+ L+ +D + +
Sbjct: 252 GTDLRAVHPLVRTNPVTGWKSIFPVGHHVQHVNGLTDEESDGLLKWYLDLVYRNHELQTR 311

Query: 247 -QW-AAGDVVVWDNRCLLHRA 265
+W D+ +WDNR + H A
Sbjct: 312 LKWRNKNDIAIWDNRSVFHTA 332

>ref|XP_661715.1| hypothetical protein AN4111.2 [Aspergillus nidulans FGSC A4]
gb|EAA59372.1| hypothetical protein AN4111.2 [Aspergillus nidulans FGSC A4]
tpe|CBF74685.1| TPA: alpha-ketoglutarate-dependent taurine dioxygenase
(AFU_orthologue; AFUA_3G01010) [Aspergillus nidulans
FGSC A4]
Length = 381

Score = 62.0 bits (149), Expect = 9e-08, Method: Compositional matrix adjust.
Identities = 64/256 (25%), Positives = 102/256 (39%), Gaps = 14/256 (5%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE-RIGGG 73
+G + G+ L L D L + +++ F Q +S +Q + +G IE
Sbjct: 93 IGTEIVGLQLKDLTDQQKDELGLLIAERSVVFRRDQDISPQEQKKLGEWYGEIEVHPQAA 152

Query: 74 DIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHAHADSTYMPVMAQGAVFSAEVVPAVG 133
+ + V Q + E + G WH D + A + VP++G
Sbjct: 153 QVPGVPGVTVMWPALQAT--EIPASFRRPGASRWHTDLVHERQPAGVTHLHNDTVPSIG 210

Query: 134 GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATP 193
G T +A AAY+ L A R ++ R+A + + +AG Y+
Sbjct: 211 GDTLWASGYAAYEKLSPAFRKIIDGRTAVYRSAHPYLDNRD-PEAGPKYVERE----- 262

Query: 194 LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAG 251
PLV+VHP TG +L + R I G+D AES+ L L D + + +W
Sbjct: 263 -HPLVRVHPATGWKALWVNRAMTVRIVGLDKAESDLILGYLYDVFEKNVDIQVRFKWTPR 321

Query: 252 DVVVWDNRCLLHRAEP 267
+WDNR +EP
Sbjct: 322 SSALWDNRWDYEGSEP 337

>gb|ABD39117.2| alpha-ketoglutarate dioxygenase [uncultured bacterium]
Length = 105

Score = 62.0 bits (149), Expect = 9e-08, Method: Compositional matrix adjust.
Identities = 30/65 (46%), Positives = 37/65 (56%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+
Sbjct: 40 PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFFVYRHSWKVGDLMV 99

Query: 256 WDNRC 260
WDNRC
Sbjct: 100 WDNRC 104

>emb|CBJ18855.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 62.0 bits (149), Expect = 9e-08, Method: Compositional matrix adjust.
Identities = 40/111 (36%), Positives = 53/111 (47%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHP 202
AAYD LD T+A + HSL+YS+ LG + Y + L+ LV+ HP
Sbjct: 1 AAYDRLDGETKAEIEDMVCEHSLMYSRGSGLGFLD-----YSDEEKEMFKPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
R SL + HA AI GM E L L + A Q V+AH+W D+
Sbjct: 56 VHRKSLYLSSHAGAIAKMSVPEGRLLLRDLNEHATQPEFVYAHKWLHDL 106

>emb|CBJ18897.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18898.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18918.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18891.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 62.0 bits (149), Expect = 9e-08, Method: Compositional matrix adjust.
Identities = 39/111 (35%), Positives = 56/111 (50%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHP 202
AAYDAL + T+A V A H +++ LG AY + PLV+ HP
Sbjct: 1 AAYDALPDRTKAEVQDLRAEHYALHTRILLG-----DEAYTDEQKKAIPPAVWPLVQTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+ R L +G HA I G AES +L+ L++ A Q V+ H+W GD+
Sbjct: 56 GSRRKLLFVGVARQIIGWPTAESRMYLQDLLEHATQREFVYRHEWQVGD 106

>ref|XP_002615194.1| hypothetical protein CLUG_05209 [Clavispora lusitaniae ATCC 42720]
gb|EEQ41081.1| hypothetical protein CLUG_05209 [Clavispora lusitaniae ATCC 42720]
Length = 417

Score = 62.0 bits (149), Expect = 1e-07, Method: Compositional matrix adjust.

Identities = 70/279 (25%), Positives = 106/279 (37%), Gaps = 44/279 (15%)

```

Query: 15  LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGD 74
      +G + G+ LA L+D      L      + ++ F Q LS +Q+      K +G +E
Sbjct: 122 IGTEIVGLQLADLNDKQKDELALLIAERVVVFVRDQDLSPQKQLELGKYWGQVEV--HAQ 179

Query: 75  IVAISNVKADGTVRQHSPAEDDDMMK-----VIVGNMAWHADSTYMPVMAQGAV 123
      + + + K DG          W D +          I G  WH D +      A
Sbjct: 180 VPRVPDTK-DGEALPGITVIWQDYAREFYGIPLTYKNSIGGTAQWHTDLVHEFQAPAGITH 238

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSA----RHSLVYSQSKLG---HVQ 176
      + +P VGG T +A      AAYD L  A + + ++A      HS + ++ L      H++
Sbjct: 239 LHNDTIPEVGGDTVWASGYAAYDKLSPAFQKFLDGKTAIYRSAHSYLDRENPLNGPKHIE 298

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVD 235
      +                      PLV+ HP TG  L + R      I G+      ESE  LE L
Sbjct: 299 RE-----HPLVRTHPATGWKYL FVN RAMTVRIVGLQPKESLILEYLF 342

Query: 236 WACQAPRVHAH-QWAA----GDVVVDNRCLLHRAEPWD 269
      + +      W +      G +W DNR  H A  WD
Sbjct: 343 LFERNLDIQRVWNWKS KPGYGTSAIWDNRISQHNNAV-WD 380

```

>gb|ABD39115.1| alpha-ketoglutarate dioxygenase [uncultured bacterium]
Length = 91

Score = 62.0 bits (149), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 30/65 (46%), Positives = 37/65 (56%)

```

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAGDVVV 255
      PLV+ H +GR L IG HA I G  AE  L L++ A Q  V+ H W  GD+V+
Sbjct: 25  PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRK FVYRHSWKVGD LVM 84

Query: 256 WDNRC 260
      WDNRC
Sbjct: 85  WDNRC 89

```

>emb|CAK42812.1| unnamed protein product [Aspergillus niger]
Length = 376

Score = 62.0 bits (149), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 73/268 (27%), Positives = 103/268 (38%), Gaps = 33/268 (12%)

```

Query: 8   ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ---HLSNDQQITFAKRF 64
      ITPT  +G V GV L+ L  G  L      Q ++ F Q  HL  ++ + F  F
Sbjct: 103 ITPT---IGTEVRGVQLSQLSKEGKDQLALYVAQRKVVAFRDQDFAHLPIEKALEFGGYF 159

Query: 65  GA--IERIGGGDI----VAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVM 118
      G  I + G      + + + AD      S AE+  +      + WH+D T+
Sbjct: 160 GRHHIHQTS GAPKGFPEIHLVHRGAD----DRSGAEF---LSQRTNTITWHS DVT FEKQP 212

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
      P+ GG T FADM  AY  L      R  +H  A HS +      ++ +
Sbjct: 213 PGTTFLYILDGPSSGGDTLFADMAQAYRRLSPEFRKRLHGLKAVHSGI---EQVNNSLNK 269

Query: 179 GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC 238
      G  G      T  P+V+ HP      L      I G  ES+  L+ L D
Sbjct: 270 G----GIARRDPITSEHPIVRTHP-----TLTETVTRYIVGYKKEESDYLLKFLYDHIA 319

Query: 239 QAPRVHAH-QWAGDVVVVDNRCLLHRA 265
      + +      +W  G VVVVDNR + H  A
Sbjct: 320 LSQDLQTRVWRP GTVVVVDNRVVTHTSA 347

```

>gb|ABD39111.1| alpha-ketoglutarate dioxygenase [uncultured bacterium]
Length = 104

Score = 61.6 bits (148), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 30/65 (46%), Positives = 37/65 (56%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+
Sbjct: 39 PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFFVYRHSWKVGDLVM 98

Query: 256 WDNRC 260
WDNRC
Sbjct: 99 WDNRC 103

>emb|CBJ18747.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 61.6 bits (148), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 40/111 (36%), Positives = 53/111 (47%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYD LD T+A + HSL+YS+ LG + Y + L+ LV+ HP
Sbjct: 1 AAYDRLDGETKAEIEDMVCEHSLMYSRGSGLGFLD-----YSDEEKEMFKPVLQGLVTRHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
R SL + HA AI GM E L L + A Q V+AH+W D+
Sbjct: 56 VHRKSLYLSSHAGAIKMSVPEGRLLLRDLNEHATQPEFVYAHKKLHDL 106

>ref|XP_454600.1| hypothetical protein [Kluyveromyces lactis NRRL Y-1140]
emb|CAG99687.1| KLLA0E14433p [Kluyveromyces lactis]
Length = 382

Score = 61.6 bits (148), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 79/311 (25%), Positives = 126/311 (40%), Gaps = 60/311 (19%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
++I+P LG+ + G+ L+ LD+AG L + +LIF Q + + G
Sbjct: 80 VEISPITPKLGSEIRGLQLSELNAGKDELALLTAERGVLIFRDQDFVD-----RGPG 132

Query: 66 AIERIGG--GDI-----VAISNVKADGTVRQHSPAEDDMMKVIVGNMA 107
IE G G++ V NVK + ++D + + ++
Sbjct: 133 YIEEYGKYFGELHVVHASPAPGHPYIHVVYKNVKTE-----DYDKFFEQTLSVY 183

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSL-- 165
+H D T+ + F+ P GG T F D +D L + + + A H+L
Sbjct: 184 FHTDITFELQPSGYTFFAVLDAPQSGGDTLFGDAIEIFDRLSPSLQEYLSGLHAVHALPP 243

Query: 166 ---VYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGM 221
+S + S + Y + + P+V+VHP + L I + I +
Sbjct: 244 NGDAFSPDPTKRI----SRHEIYDV-----IHPVVRVHPVLKKKVLNINKVFTRKIVEL 293

Query: 222 DAAESE---RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWH 278
ES+ FL ++D A A +V A+ W G VVVWDNR L H A +DF H
Sbjct: 294 KKPESDALLAFLYQVIDNAHDA-QVRAN-WKPGTVVVWDNRRLYH-AGVYDFDASESTRH 350

Query: 279 ----SRLAGRP 285
+ LA RP
Sbjct: 351 HVRVTPLAERP 361

>emb|CBJ18874.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 61.6 bits (148), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 38/114 (33%), Positives = 59/114 (51%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD--TTATPLR-PLVK 199
AAYDALD+ T+A + HS ++S+ +LG + Y D T P+R LV+
Sbjct: 1 AAYDALDQKTKAEIEDLIREHSQIFSREQLG-----FTEYLPDERTMMKPVHRHLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP +GR S+ + H I G E+ F+ L++ A Q V++H+W D+
Sbjct: 53 THPTSGRKSIFLSAHIGGIVGWPRPEAMSFIRDLIEQATQPQFVYSHRWTQHDL 106

>gb|EFW97400.1| TfdA family taurine dioxygenase, putative [Pichia angusta DL-1]
Length = 393

Score = 61.6 bits (148), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 50/170 (29%), Positives = 74/170 (43%), Gaps = 21/170 (12%)

Query: 105 NMAWHADSTYMPVMAQGAVFSAEVVPA-----VGGRTCFADMRAAYDALDEATRALVHQ 158
+ WH+D Y A + +V+P +GG T FA+ Y++LD RA +
Sbjct: 191 SQVWHSDDVPYEINSAGISTLRFVDLPRSENGELIGGDTLFANGYLIYESLDPKFRFALET 250

Query: 159 RSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPL---RPLVKVHPETGRPSLLIGRH- 214
SA S G Q A +A GY T P+ PLV+ +P TG SL + +
Sbjct: 251 LSAESS-----GFGQAAIAAESGY--KTRRPPIATVHPLVRTNPTTGLKSLYVAENF 300

Query: 215 AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLH 263
I G++ S L+ L D ++ + QW D+ +WDNR H
Sbjct: 301 TTKIVGLEERLSNTILQYLFDHRRSLQYQCRVQWTENDIAIWDNRSHFH 350

>emb|CBJ18941.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 61.6 bits (148), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 39/110 (35%), Positives = 52/110 (47%), Gaps = 5/110 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
AAYDALD T+ + HSL+ S+ LG + Y + L+ LV+ HP
Sbjct: 1 AAYDALDNDTKVEIEDMICEHSLMTSRGALGFLD-----YTDEEKEMFKPVLQRLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
GR SL + HA AI GM E+ L L + A Q V+ H+W D
Sbjct: 56 VHGRKSLYLSSHAGAIKGMTPEARLLLRDLNEHATQPEFVYVHKWTLHD 105

>ref|XP_001584962.1| hypothetical protein SS1G_14059 [Sclerotinia sclerotiorum 1980]
gb|EDN99199.1| hypothetical protein SS1G_14059 [Sclerotinia sclerotiorum 1980
UF-70]
Length = 401

Score = 61.6 bits (148), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 69/265 (26%), Positives = 100/265 (37%), Gaps = 32/265 (12%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGAIERIGG- 72
+G V GV LA L DA L ++ F Q + + Q FG + +
Sbjct: 100 IGTEVHGVDLANLTDAAKNDLARLISIRGVVFFRNQKNFDIEAQRKLGSYFGTLHKHATT 159

Query: 73 -----GDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE 127

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          GD+  +  V  D  +          D  +          WH+D TY  +  +  S  +
Sbjct: 160 SVPKRGDLDDVHVVTYDENSK-----DQRALFTPTFLWHS DVTYE--IQPPSYTSLK 209

Query: 128 VVPAV----GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
          V+          GG T ++          AAYDAL  +  +  +A H+          H+Q GS  +
Sbjct: 210 VLTGPPRGGGGDTLWSSQYAAAYDAL SAPM QKYLESLTALHT-----SHLQAEGRAL 261

Query: 184 GYGMDTTA-TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAP 241
          G  +          T  PL++ HP TG SL          I G+  ES+  L  L  +
Sbjct: 262 GRPVRDPITTEHPLIRSHPVGTGWKSLFFNPGFVTKIVGVPKVESDTILAYLNEVVSTTQ 321

Query: 242 RVHAH-QWAAGDVVVWDNRCLLHRA 265
          +H  QW  DV  WDNR  H A
Sbjct: 322 ELHVRFQWGKDDVAFWDNRISNHTA 346

```

>emb|CBJ18783.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 101

Score = 61.6 bits (148), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 42/109 (38%), Positives = 61/109 (55%), Gaps = 11/109 (10%)

```

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTA--TPL-RPLVK 199
          AAYDAL EAT+  +  A HSL+ S++KLG          +  +  D          P+  + LV+
Sbjct: 1   AAYDALPEATKQRIAGLVAEHSLMTSRALKG-----FSDFNEDERKAFEPVPQVLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQW 248
          ++GR SL +  HA AI GM  E+ER ++ LVD A Q  V++H+W
Sbjct: 53  RLQDSGRMSLYVASHAGAIRGMAMLEAERLIQELVDHATQRQFVYSHRW 101

```

>emb|CBJ18748.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 61.2 bits (147), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 39/112 (34%), Positives = 56/112 (50%), Gaps = 7/112 (6%)

```

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRP-LVKVH 201
          A YDALD+ T+  V          HS +YS+++LG +          +          P+R  LV+ H
Sbjct: 1   AGYDALDQETKDRVADLICEHSQLYSRARLGFIDFTDEERERF-----KPVRQVLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDV 253
          P  GR SL +  HA I G  E+  FL  L + A Q  V++H+W  GD+
Sbjct: 55  PGHGRKSLYLSSHAGGIVGWPVPEARAFRLDLNEIATQRQFVYSHRWRVGD 106

```

>ref|XP_002740180.1| PREDICTED: hypothetical protein [Saccoglossus kowalevskii]
Length = 286

Score = 61.2 bits (147), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 65/289 (22%), Positives = 110/289 (38%), Gaps = 63/289 (21%)

```

Query: 1   MAQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQH-LSNDQQI 58
          MA  ++TP  LG  V G+ L  + D  A  +          +H +L+F  QH +S ++  +
Sbjct: 1   MAHGYKLTPI--KLGCEVRGIDLGKHVSDEVIAQIKKDVTEHRILVFKDQHDISPERHV 58

Query: 59  TFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHA 110
          ++ FG +E          +  DI  +SN +++G          VG  WH
Sbjct: 59  QISRWFGELESSAFYKHPKSPSQDIFRVSNDESEGCTN-----VGRTGWHI 104

Query: 111 DSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS 170
          D T+ P  +V+  VP  G T FA +          L E R          R R  +V
Sbjct: 105 DGTFFPKPYSSVYHMHVPT-NGDTVFAPLNDIVTGLSEEQR---NRWERLWMV---- 155

```

Query: 171 KLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI-----GRHAHAIPG 220
D A + PL+ HPE+G+ L++ +
Sbjct: 156 -----SDRRAGVVHPLIYSHPESGKKVLIVHMGMTDAFIWDKGTKQERM 199

Query: 221 MDAAESERFLEGLVDWACQAPRV--HAHQWAAGDVVVWDNRCLLHRAEP 267
+ E+ + L+ + + + ++H+W GD ++ DN + H A P
Sbjct: 200 TEWRETNQLLKEINHEFIKDNKAIQYSHKWNVGDFIISDNLAVGHEAAP 248

>emb|CBJ18867.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 61.2 bits (147), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 39/111 (35%), Positives = 52/111 (46%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD + + HSL+ S+ LG + Y + L+ LV+ HP
Sbjct: 1 AAYDALDSDAKTEIEDMICEHSLMTSRGALGFLD-----YTDEEKEMFKPVLQRLVLRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E+ L L + A Q VH H+W D+
Sbjct: 56 VHGRKSLYLSSHAGAIQGMSVPEARVLLRDLNEHATQPQFVHVHKWTLHDL 106

>dbj|BAD15042.1| hypothetical protein [Bradyrhizobium sp. BDV5419]
Length = 102

Score = 61.2 bits (147), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 39/111 (35%), Positives = 54/111 (48%), Gaps = 13/111 (11%)

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP----LVKVHP 202
ALD+ T+A + HSL+YS+ LG ++ Y D RP LV+ HP
Sbjct: 1 ALDDDTKAEIADMICEHSLMYRSGSLG-----FLDYS-DEEKAMFRPVLQRLVLRTHP 51

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI GM E+ L L + A Q+ V+ H+W D+
Sbjct: 52 GHGRKSLYLSSHAGAIKMSVPEARVLLRDLTEHATQSEFVYVHKWTVHDL 102

>emb|CBJ19194.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 61.2 bits (147), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 39/112 (34%), Positives = 55/112 (49%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-LVKVH 201
AAYDALD+ T+ V HS ++S+ LG + + P+R LV+ H
Sbjct: 1 AAYDALDDKTKDEVRDLICSHSQIFSRGILGFTDFTDDERLKWA-----PVRQRLVRRH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P +GR SL + HA I G E+ FL L + A Q V+AH+W D+
Sbjct: 55 PRSGRLSLYLSSHAGGIEGWPVPEARAFRLDLTEHATQRQFVYHRWKPADL 106

>ref|NP_302343.1| putative oxidoreductase [Mycobacterium leprae TN]
ref|YP_002503973.1| putative oxidoreductase [Mycobacterium leprae Br4923]
emb|CAC30947.1| putative oxidoreductase [Mycobacterium leprae]
emb|CAR72089.1| putative oxidoreductase [Mycobacterium leprae Br4923]
Length = 289

Score = 61.2 bits (147), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 67/278 (24%), Positives = 107/278 (38%), Gaps = 44/278 (15%)

Query: 12 GATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIG 71
G LGA VTGV LD A + + L++ H + ++ I + G I
Sbjct: 7 GDGLGAQVTGVDPKNLDSISTAEIRKIVYVKNLVLKDVHPTPEEFIKLGRIIGEI---- 62

Query: 72 GGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMA-----WHADSTYMPVMAQ 120
V + +H D ++ V + WH D +MP +
Sbjct: 63 -----VPYIEPIYRHK-----DYPEIFVSSTEEGQGVPTGAFWHVDYIFMP---E 105

Query: 121 GAVFSAEVPVAVGGR---TCFADMRAAYDALDEATRALVHQRSARHS-LVYSQSKLGHVQ 176
FS + A+ G T F D+ +++L A + V + HS Y + + V
Sbjct: 106 PFAFSMTPLAMPGHDRGTHFIDLQVWESLPNAMKDSVRGTYSNHSPRYIKIRPSDVY 165

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPG-----MDAAESERFL 230
+ + + T P V HP+TG+ L I A +D + L
Sbjct: 166 RPVGELVLAIEEVTPPQKWPTVIKHPKTGQEILYICEAATVSVEDKNGNLLDPMVLQELL 225

Query: 231 --EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE 266
G +D C++ +H + GDVV+WDNR L+HRA+
Sbjct: 226 TASGQLDPDCKSLLIHTQHYEVGDVVLWDNRALVHRAK 263

>emb|CBJ18811.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 60.8 bits (146), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 40/114 (35%), Positives = 54/114 (47%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTAT---PLRPLVK 199
AAYDALD+ T+A + + HSL+YS+ LG + Y D A L+ LV+
Sbjct: 1 AAYDALDDETKAEIEDLACEHSLMYSRGS LG-----FTEYTDDEKAMFKPVLQRLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP R SL + HA I M E L L + A A V+ H+W D+
Sbjct: 53 THPAHRRKSLYLSSHAGKIVSMSVPEGRLLLRDLNEHATNAEFVYVHKWKLHDL 106

>ref|ZP_06477056.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia symbiont of
Datisca glomerata]
gb|EFD26229.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia symbiont of
Datisca glomerata]
Length = 199

Score = 60.8 bits (146), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 62/218 (28%), Positives = 89/218 (40%), Gaps = 48/218 (22%)

Query: 7 QITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
++ LGA + GV LA +DDA AL + ++ +L+ QHLS D + + F
Sbjct: 10 EVRQASPVLGAEIVGVDLANGVDDATAEALRDDFWKYKVLVLRDQHLSPPDAHVEAVRIFD 69

Query: 66 A-----IERIGGGDIVAISNV-KADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPV 117
+ R +V + N+ KA G R H W + P
Sbjct: 70 EPFDHPKWLYRHEDNRLVYVFNLEKAGGAARWHIGGIWRNP-----PF 112

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
+ + +VVP +GGRT +AD++AAYD L E R L+ SA VYS
Sbjct: 113 TIESLTYY--QVVPEIGGRTLWADLQAAYDGLSEPFRRLLLESVSA----VYSD----- 158

Query: 178 AGSAYIGYGM----DTTATPLRPLVKVHPETGRPSLLI 211
Y G G T P+V+ H TGR L +
Sbjct: 159 ----YPGDGTYDRPPATGVIEHPVVRTHRHTGRKGLFL 192

>ref|XP_001394064.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus niger CBS 513.88]
emb|CAK48293.1| unnamed protein product [Aspergillus niger]
Length = 396

Score = 60.8 bits (146), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 70/260 (26%), Positives = 99/260 (38%), Gaps = 22/260 (8%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERIGGG 73
+G V GV+LA L+DA L ++ F GQ L D Q + FG + +
Sbjct: 95 IGTEVHGVNLAKLNDAQKDDLARLVAVRGVVFFRGQDDLDIDAQRELGRHFGKLHKHA-- 152

Query: 74 DIVAISNVKADGTVRQHSPAED--DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVP 130
S K +G H D D + + WH+D TY P
Sbjct: 153 ---TTSVPKREGLEDVHVVTGDNSTDQRAMFTPSFLWHS DVTYEVQPPSYTSLKVLTP 209

Query: 131 AVGG--RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 188
GG T + AAYDAL + + +A HS +Q + S +G +
Sbjct: 210 PRGGGGDTLWTSQYAAAYDALSPHMQTYLKGLTALHS-----ADMQASDSHALGRPV 261

Query: 189 -TTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH 246
T PL++ +P TG SL I G+ ES+ + L + +HA
Sbjct: 262 RDPVTTEHPLIRTNPVTGWNLSFFNPGFVTKIVGIPKTESDAIIRYLTEVIATTQEMHAR 321

Query: 247 -QWAAGDVVVDNRCLLHRA 265
QW DV +WDNR H A
Sbjct: 322 FQWNKNDVAIWDNRRTTNHSA 341

>emb|CBJ19211.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 60.8 bits (146), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 39/114 (34%), Positives = 58/114 (50%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM--TTATPLR-PLVK 199
AAYDALD+ TRA + HS ++S+ +LG + Y D T P+R LV+
Sbjct: 1 AAYDALDQKTRAIEDLICEHSQIFSREQLG-----FTEYLPDERTMMKPVRHRLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP +GR S+ + H I G E+ F+ L + A Q V++H+W D+
Sbjct: 53 THPTSGRKSIFLSAHIGGIVGWPRPEAMSFIRDLSEHATQPQFVYSHRWTQHDL 106

>emb|CBJ18766.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 60.8 bits (146), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 58/112 (51%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR-PLVKVH 201
AAYDALD+ +A + + HS+V+S+ ++G A G + P++ LV H
Sbjct: 1 AAYDALDDTAKAEIAELVTEHSIVFSREQIGFADYAA-----GNEDRLRPVQHRLVITH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P +GR SL + H I G E+ F+ L++ A Q V+AH+W D+
Sbjct: 55 PVSGRKSLYLSSHIGGIVGWVPPEARAFVRDLMEHATQRQFVYAHEWRVNDL 106

>emb|CBJ19184.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 60.8 bits (146), Expect = 2e-07, Method: Compositional matrix adjust.

Identities = 37/115 (32%), Positives = 54/115 (46%), Gaps = 13/115 (11%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRP----LV 198
 A YDALD+ T+ V + HS ++S+ +G D RP +V
 Sbjct: 1 AGYDALDDETKEEVQEMVCEHSQMFSRQIIGFYDFT-----DEERERFRPVRQCMV 51

Query: 199 KVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
 + HP TGR SL + HA I G E+ +L L++ A Q V+ H+W GD+
 Sbjct: 52 RTHPVTGRKSLYLSSHAGGIVGWPMPEARGLRDLIEHATQREFVYTHKWRVGD 106

>ref|ZP_04588005.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. oryzae str. 1_6]
 ref|ZP_04592995.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. oryzae str. 1_6]
 Length = 147

Score = 60.8 bits (146), Expect = 2e-07, Method: Compositional matrix adjust.
 Identities = 51/160 (31%), Positives = 69/160 (43%), Gaps = 21/160 (13%)

Query: 132 VGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTT 191
 GG T FA+M A + L A + + Q +A H G + G
 Sbjct: 1 TGGDTLTFANMHLAIEMLSPAMQQFLGQLTAIHD-----GEIPWKGYTPPA----NLP 48

Query: 192 TPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW 248
 P+V HPETGRP+L + G +H + + A ES L L D + P + +W
 Sbjct: 49 KSEHPVVVRHPETGRPTLFVNSGFTSHIV-QLSADESRTLLNMLYDLIAREPSLSCRVRW 107

Query: 249 AAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSR---LAGRP 285
 A +V WDNRC H A WD+ P + R L GRP
 Sbjct: 108 APNTLVFWDNRCTQHHAV-WDY-FPHSRYGERVTILGGRP 145

>ref|ZP_07308634.1| alpha-ketoglutarate-dependent taurine dioxygenase [Streptomyces viridochromogenes DSM 40736]
 gb|EFL37003.1| alpha-ketoglutarate-dependent taurine dioxygenase [Streptomyces viridochromogenes DSM 40736]
 Length = 167

Score = 60.8 bits (146), Expect = 2e-07, Method: Compositional matrix adjust.
 Identities = 49/161 (30%), Positives = 71/161 (44%), Gaps = 16/161 (9%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQ-QITFAK 62
 T L +T G GA + G+ L LDD A+ A + + +L GQH +D QI F +
 Sbjct: 2 TRLPVTTELGPFRFGAEINGIDLGRLLDDGQVLAVREALVAYKVLVFRGQHTLDDAAQIEFGR 61

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPA--EWDDMMKVIVGNMAWHADSTYMPVMAQ 120
 R G ++ V G V Q A D+ + WH D T++
 Sbjct: 62 RLG-----EVTVGHPVHDSGDVAQEYALDSQDNGFADV-----WHTDVTFVRRPPA 108

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSA 161
 +V A V+P GG T +AD + AY++L RA V +A
 Sbjct: 109 ISVLRAVVLPPSGGDTNWADSQLAYESLSPGLRAYVDTLTA 149

>emb|CBJ19014.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
 Length = 106

Score = 60.8 bits (146), Expect = 2e-07, Method: Compositional matrix adjust.
 Identities = 39/111 (35%), Positives = 54/111 (48%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHP 202
 AAYDALD+ T+A + HSL+ S+ LG + Y + L+ LV+ HP

Sbjct: 1 AAYDALDDDTKAEIEDMICEHSLMTSRGALGFLD-----YTDEEKEMFKPVLQRLVTRHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

GR SL + HA AI GM E+ L L + A Q + H+W D+
Sbjct: 56 VHGRKSLYLSSHAGAIQGMSVPEACVLLRDLNEHATQPQFAYVHKWTLHDL 106

>ref|XP_002147238.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Penicillium marneffeii ATCC 18224]
gb|EEA23727.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Penicillium marneffeii ATCC 18224]
Length = 363

Score = 60.8 bits (146), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 44/175 (25%), Positives = 75/175 (42%), Gaps = 15/175 (8%)

Query: 106 MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL 165

+ WH+D T+ P+ + V+P GG T +A YD + + + +A
Sbjct: 158 IEWHSditFEPIPSDYTSRLRLTVLPKTGGDTLWASGYEVYDRISPPYQKFLEGLTA---- 213

Query: 166 VYSQSKLGHVQQAGSAYIGY----MDTTATPLR---PLVKVHPETGRPSLL-IGRHAHA 217

Y+Q K V + + + G + LR P+++ +P TG S+ +G H
Sbjct: 214 TYAQPKFEEVARDKNFELHPGPRGAPENVGNILRAVHPVIRTNPVTGWKSVFAVGTHCQK 273

Query: 218 IPGMDAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVDNRCLLHRAEPWDF 270

+ G+ ES L+ VD + + +W D+ +WDNR + H A WD
Sbjct: 274 VNGLSQEESHLLKWFVDLIVENHDLQVRFRWQNPNDIAIWDNRSVYH-AATWDI 327

>ref|YP_003766480.1| taurine dioxygenase [Amycolatopsis mediterranei U32]

gb|ADJ46078.1| taurine dioxygenase [Amycolatopsis mediterranei U32]
Length = 298

Score = 60.8 bits (146), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 73/279 (26%), Positives = 106/279 (37%), Gaps = 30/279 (10%)

Query: 15 LGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERI--- 70

+GA + G A LD A L A +H L+F L ++ Q FA FG + +
Sbjct: 15 IGAEIVGFDPAGDLDTQVAFSLDALHEHKALVFRNARLDDEGQQRFAAHFGELTKAHT 74

Query: 71 -----GGGDIVAI SNV KADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125

G I+ + + + WH D T++ + +
Sbjct: 75 VPAVEGAPTILPVDSEGRAN-----HWHTDVTFLNPPKASTLR 114

Query: 126 AEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH-VQQAGSAYIG 184

+ VVP GG T A+ AAY L E RA A H+ Y + V + A
Sbjct: 115 SLVVPPYGGETLIANAAAAYRDLPEPLRAFADTLRAVHTNDYDYVQPPETVDEQERARRA 174

Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH 244

+ + P+V+VHP TG L IG A I G+ ES L L + + V
Sbjct: 175 QFVSRKYRTVHPVVRVHPVTGERGLFIGGFAQRIEGLSVTESRDLLRLQLSYVTRPENNV 234

Query: 245 AHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

W +V++DNR H A LPR + +AG
Sbjct: 235 RVTWEPDQLVLFNDRITQHYAIDNYDGLPRRLNRVTVAG 273

>emb|CBJ19208.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]

Length = 105

Score = 60.8 bits (146), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 40/111 (36%), Positives = 58/111 (52%), Gaps = 6/111 (5%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD+ T+A V HSL++S+ +G SA+ ++ + LV+ H
Sbjct: 1 AAYDALDDRTKAEVEDLICEHSLIHSRGAIGF-----SAFTPEEVENFRPVRQRLVTRHA 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+ GR SL + HA AI G E+ FL L + A Q V++HQW D+
Sbjct: 56 D-GRRSLFLSSHAGAIEGWTIPEARSFLRDLTEHATQREFVYSHQWRQHDL 105

>gb|ABN51234.1| 2,4-dichlorophenoxyacetate alpha-ketoglutarate dioxygenase
[Arthrobacter sp. DNB19]
Length = 118

Score = 60.5 bits (145), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 40/116 (34%), Positives = 55/116 (47%), Gaps = 7/116 (6%)

Query: 145 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVHPE 203
YD L E + + A H ++S+ LG + + S P+ PLV+ H
Sbjct: 9 YDDLPEDFKKELAGMRAEHYALHSRIFLGDEYSES-----QRNAMPVPSWPLVTRHAG 62

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNR 259
+GR L IG HA I G AE L L++ A Q V+ H W GD+V+WDNR
Sbjct: 63 SGRKFLFIGAHASHIEGRPVAEGRMLLAELEHATQPKFVYRHSWNVGDVLMWDNR 118

>ref|XP_459311.1| DEHA2D18986p [Debaryomyces hansenii CBS767]
emb|CAG87485.1| DEHA2D18986p [Debaryomyces hansenii]
Length = 393

Score = 60.5 bits (145), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 47/167 (28%), Positives = 71/167 (42%), Gaps = 12/167 (7%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
WH+D T+ PV + AV GG T +A A Y+ L R+ + + V
Sbjct: 188 GWHSDITFEPVTSYAVLKIVESTPTGGDTLWASGYALYEKLTPTFRSYLETLTG----V 243

Query: 167 YSQSKLGHVQQAG-SAYIGY----GMDTTATPLRPLVKVHPETGRPSLL-IGRHAHAIP 219
YSQ + Y G + T + PLV+ +P TG S+ IG H +I
Sbjct: 244 YSQPGFKKASEGKFEIYSGVRGAPENVGDELTAHVPLVRTNPVTGWKSIFSIGHHFTSIN 303

Query: 220 GMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
G+ +ES + L + + + +W DV +WDNR + H A
Sbjct: 304 GLSDSESALIKDYLSELLYGSHDIQVRFRWNKNDVAIWDNRSVYHTA 350

>ref|XP_001268478.1| TfdA family taurine dioxygenase, putative [Aspergillus clavatus
NRRL 1]
gb|EAW07052.1| TfdA family taurine dioxygenase, putative [Aspergillus clavatus
NRRL 1]
Length = 364

Score = 60.5 bits (145), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 62/253 (24%), Positives = 98/253 (38%), Gaps = 36/253 (14%)

Query: 41 QHALLIFPGQH-LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMM 99
Q ++ F Q L ND Q +R G + + I V G R+H DD +
Sbjct: 81 QRGVVFVRKQDDLNDNSQKELIQLRGLQAGPATSGLHIHPVTNAG--REHGGK--DDEI 136

Query: 100 KVIIVGNM-----AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR 142
VI WH+D T+ PV + AV +P GG T +A
Sbjct: 137 SVISSEQRKKLYKGRYVSGQSLKGGWHSITFEPVPSDYAVLRRLTKLPKTGGDTLWASGY 196

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY----MDTTATPLR--- 195

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      +D + E + + +A      Y+Q      + + + G      + T LR
Sbjct: 197 EVFDRISEPYQRFLESLAA-----TYAQPGFNQSAKDNNFELYSGPRGAPENVGTELRAEH 252

Query: 196 PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHA-HQW-AAGD 252
      P+++ +P TG S+ +G H I G+ ES+ L V + + H+W D
Sbjct: 253 PVIRTNPVTGWKSVFAVGAHVEKINGVAEEESKHLNWFVTLIVENHDLQVRHKWNNPNND 312

Query: 253 VVVWDNRCLLHRA 265
      + +WDNR + H A
Sbjct: 313 LAIWDNRSVYHTA 325

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>ref|NP_983695.2| ACR293Cp [Ashbya gossypii ATCC 10895]
gb|AAS51519.2| ACR293Cp [Ashbya gossypii ATCC 10895]
Length = 386

Score = 60.5 bits (145), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 63/268 (23%), Positives = 109/268 (40%), Gaps = 17/268 (6%)

```

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
      +QI+ G+ V G+ L++LD AG L Q +L+F Q ++ F +++
Sbjct: 83 NVQISKITPRFGSEVRGLQLSSLDAAGKDELALLASQRGVLVFRDQDFASKGPGYF-EQY 141

Query: 65 GAIERIGGGDIVAISNVKADG-----TVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA 119
      G+ G + S A T R+ E++ + + ++ +H+D +Y
Sbjct: 142 GS--HFGKLHVHQTSGAPAGHPYLHVTFRRPDRKEFERVFRDHHSSIRFHSVDVSYELQPP 199

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
      F+ P GG T F+D A++ L + + S H L ++ + + Q+ G
Sbjct: 200 SYTFFTVLGEPDGGGDTLFSDATEAFNRLSPPLQDFL---SKLHVLHSAKEQAQNAQEQQ 256

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
      G + PLV+VHP S + R I + ES+ L+ + +
Sbjct: 257 ----GIQRREPVAHIHPLVRVHPVLKTKSFFVNRGFTRKIVELKQTESDLLLDFIYNIIE 312

Query: 239 QAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
      + W G V VWDNR + H A
Sbjct: 313 NTHDLQLRASWEPGTVTVDNRNRVNNSA 340

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>ref|XP_001830759.2| alpha-ketoglutarate-dependent taurine dioxygenase [Coprinosia
cinerea okayama7#130]
gb|EAU91128.2| alpha-ketoglutarate-dependent taurine dioxygenase [Coprinosia
cinerea okayama7#130]
Length = 365

Score = 60.5 bits (145), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 64/274 (23%), Positives = 109/274 (39%), Gaps = 31/274 (11%)

```

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRFGAIERIG 71
      +G ++G+ L+ L G L Q L+IF Q + ++Q+ A ++ G
Sbjct: 78 IGTLSGIQLSQLTKEGLDELGLFVAQRKLVIFREQDFQDLPPEKQVAIAANGVSLTLEG 137

Query: 72 GGD-----VAISNVKAD----GTVRQHSPAEWDD--MMKVIVGNMAWHADSTYMPVM 118
      + N++ +RQ +D + + WH+D +Y P
Sbjct: 138 FTQSHFGVPHLHATLPNIEGHPAYVNLLRQPGKRNINDYFIDTFLSYAFWHSDVSYEPQP 197

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQQA 178
      F P VGG T F AY+ L + + A HS V +++ +++
Sbjct: 198 PSTTFFWPLDQPTVGGDTLFLSTTEAYNRLSPEFQKRLVGLKALHSGV---AQVEESRRS 254

Query: 179 GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG----RHAHAIPGMDAAESERFLEGLV 234
      G A ++ + P+++VHP TG S+ + RH I G+ ES+ L+ L

```

Sbjct: 255 GGAVRKEPVEA---VHPVIRVHPVTGEKSIFVNPATRH---IVGLKKEESDALLKFLY 307

Query: 235 DWACQAPRVHAH-QWAAGDVVVDNRCLLHRAEP 267

D + + G V++WDNR H A P

Sbjct: 308 DHIAKGADFQVRARHEPGSVIIWDNRVTNHSAPV 341

>ref|XP_001526244.1| hypothetical protein LELG_02802 [Lodderomyces elongisporus NRRL YB-4239]

gb|EDK44623.1| hypothetical protein LELG_02802 [Lodderomyces elongisporus NRRL YB-4239]

Length = 459

Score = 60.5 bits (145), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 72/297 (24%), Positives = 113/297 (38%), Gaps = 59/297 (19%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61

A+ + +TP +G + G+ LA LDD L + ++ F Q LS +Q+

Sbjct: 147 AKDVINLTPY---VGTEIVGLQLADLDDKQKDELALLIAERVVFFKDQDLSPKKQLELG 203

Query: 62 KRFGAIE-----RIGGGDIVAISNVKAD-GTVRQHSPAEDDMMKVIVGNMAWHADSTY 114

K +G +E R+G D I+ + D R + + K GN WH+D +

Sbjct: 204 KYWGQVEVHPQVPRVGP-DYDGITVIWQDYQNQRNGIGLSFQNSKK---GNSTWHSIDLHV 259

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174

A + +P VGG T ++ AYD L A + + ++A +Y + L

Sbjct: 260 EFQTAGITHLHIDSIPDVGGDTIWSSTYGAYDKLSPAFKEFLDGKTA---IYKSAHL-- 313

Query: 175 VQQAGSAYIGYGMDDTTATPLR-----PLVKVHPETGRPSLLIGR-HAHAIPGMDAA 224

Y+ PL+ P+V+ HP TG L + R I G+

Sbjct: 314 -----YLN-----RENPLKGPKHVEREHPIVRTHPATGWKYL FVN RAMTDRIVGLLPE 361

Query: 225 ESERFLEGL-----VDWACQAPRVH----AHQWAAGDVVVDNRCLLHR 264

ES+ L L W + P + AH+ G +WDNR H

Sbjct: 362 ESDAILNYLFSVIENNRDIQVTFKWQQLPGLKSPSDAHKTYRGTSALWDNRRIANHN 418

>ref|XP_360574.1| hypothetical protein MGG_03117 [Magnaporthe oryzae 70-15]

gb|EDK00401.1| hypothetical protein MGG_03117 [Magnaporthe oryzae 70-15]

Length = 371

Score = 60.5 bits (145), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 41/162 (25%), Positives = 68/162 (41%), Gaps = 5/162 (3%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166

AWH D ++ PV + A+ +P GG T +A YD L A + ++ +A H

Sbjct: 158 AWHTDISFEPVPSDYAMLKIHTLPPTGGDTLWASGYEIIDRLSPAMQKMLEGLTATHDAT 217

Query: 167 Y---SQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMD 222

+ +LG+ + G + P+++ +P TG S+ + R I G+

Sbjct: 218 FFLDEAERLGNPLREGIRGSPLNQGKGLKAVHPVIRTNPVTGWKSVYVNRGFTKRINGVT 277

Query: 223 AAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVDNRCLLH 263

ES+ L L + Q +W D+ +WDNR H

Sbjct: 278 RDESLLLLPYLFNLVTQNHDAQVRFKWRKNDLAIWDNRSTWH 319

>ref|XP_001821088.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Aspergillus oryzae RIB40]

dbj|BAE59086.1| unnamed protein product [Aspergillus oryzae]

Length = 360

Score = 60.5 bits (145), Expect = 3e-07, Method: Compositional matrix adjust.

Identities = 48/173 (27%), Positives = 79/173 (45%), Gaps = 22/173 (12%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
+WH D++Y P A ++ +P GG T +A YD + R + +A
Sbjct: 155 SWHTDTSYEPNPADYSILKLIKLPETGGDTIWASSCEIYDKISPVYRKFLLEGLTA---T 210

Query: 167 YSQSKLGHVQQAGSAYIGY-----GMDTTATPLRPLVKVHPETGRPSLL-IGRHAHA 217
++Q++L V A + Y + T+ + + P+V+ +P TG SL +G H
Sbjct: 211 FAQTRLRP-VTAAEKGFKLYSEPRGSPNNIGTSLSAVHPVVRTNPVTGWKSLFAVGNHVVK 269

Query: 218 IPGMDAAESER----FLEGLVDWACQAPRVHAHQWAAG-DVVVDNRCLLHRA 265
I + A ES R FL+ +V+ R H+W D+ +WDNR + H A
Sbjct: 270 INEVTADESRRLHDWFLQMIVEEHDTQLR---HRWQNPYDIAIWDNRNRTVYHSA 319

>ref|YP_003899861.1| Taurine catabolism dioxygenase TauD/TfdA [Cyanotheca sp. PCC 7822]
gb|ADN17795.1| Taurine catabolism dioxygenase TauD/TfdA [Cyanotheca sp. PCC 7822]
Length = 283

Score = 60.5 bits (145), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 47/188 (25%), Positives = 72/188 (38%), Gaps = 31/188 (16%)

Query: 98 MMKVIVGNMAW--HADSTYMP-----VMAQGAVFSAEVVPAVGGRTCFADMRA 143
+ + +VG AW H D ++P VM G AE+ T F DM
Sbjct: 95 LTQEVVGKFAWVWHDKDHLPKTEGLDMNALYVVMYGVVEIPAEGIDGEPHTTNFLDMME 154

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE 203
AY L+ R + ++S H S + L P+V H
Sbjct: 155 AYQNLERQHRQQLKQSMYHL-----SPITPPPGEDIPRKLHPIVSTHKI 199

Query: 204 TGRPSLLIGRHAHAIPGMD--AAESERFLEGLVDWACQAPRVHAHQWAAGDVVVVDNRCL 261
TGR L +G + G++ E++ + L V+AH W GD+V WDN +
Sbjct: 200 TGRKGLYLGSSTSILQGLEDKPQEAQLYWNDLFATILDCTPVYAHWQPGDIVFWDNSQV 259

Query: 262 LHRAEPWD 269
+H P++
Sbjct: 260 MHTGMPYN 267

>ref|XP_001221616.1| conserved hypothetical protein [Chaetomium globosum CBS 148.51]
gb|EAQ88902.1| conserved hypothetical protein [Chaetomium globosum CBS 148.51]
Length = 379

Score = 60.5 bits (145), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 63/265 (23%), Positives = 100/265 (37%), Gaps = 30/265 (11%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
++T +G + G+ L L L + +++ F Q ++ QQ + FG
Sbjct: 85 KVTDLTTHIGTEIEGLQLKDLTPEQRDELALLIAERSVVFRRNQDITPQQKELGEWFGE 144

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPV 117
+E + G ++ D P G +WH D +
Sbjct: 145 VEIHPQVPQVPGVAGVTVIWPDLFQAQDNAASFRKPG-----GASSWHTDLVHERQ 194

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
A + VP VGG T +A AY+ L R L+ + A + +S +
Sbjct: 195 PAGVTHLHNDTVPPVGGDTLWASGYGAYEKLSPFRKLIDGKQAVYRSAHSYLDREN-PT 253

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDW 236
AG +I PLV+VHP TG +L + R I G+D AES+ L L D
Sbjct: 254 AGPKHIER-----THPLVRVHPATGWKALWVNRAMTVRIVGLDKAESDLILNYLDV 305

Query: 237 ACQAPRVHAH-QWAAGDVVVDNRC 260
++ + +W G +WDNR
Sbjct: 306 FERSVDIQVRFKWTPGTSALWDNRS 330

>emb|CAY25737.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 60.1 bits (144), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 34/107 (31%), Positives = 54/107 (50%), Gaps = 16/107 (14%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F Q +S+DQQ+ FA+ FG E GG + +SN+
Sbjct: 16 IEAGMDKYAVLLFRDQDVSDQQLVFARNFGERENARGGTVTKKEDYRLTSGLNVDVSNLG 75

Query: 83 ADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG PA +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG NPLPRDPA----THLFNLGNCLWHSDSSFRPIPAKFSLLSARVV 118

>gb|ADI34063.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 1HD3]
Length = 95

Score = 60.1 bits (144), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 29/64 (45%), Positives = 38/64 (59%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ H +GR L IG HA I G+ AE L L++ A Q V+ H+W GD+V+
Sbjct: 32 PLVRTHAGSGRKFLFIGAHASHIEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGDLMV 91

Query: 256 WDNR 259
WDNR
Sbjct: 92 WDNR 95

>emb|CAY25758.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 60.1 bits (144), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 34/108 (31%), Positives = 57/108 (52%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A+ ++A+L+F Q +S+DQQ+ FA+ FG E GG + +SN+
Sbjct: 16 IEASMDKYAVLLFRDQDVSDQQLVFARNFGERENARGGTVTKKEDYRLTSGLNVDVSNLD 75

Query: 83 ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDPRTHLFNLGNCLWHSDSSFRPIPAKFSLLSARVV 118

>ref|NP_001191877.1| hypothetical protein LOC100163446 [Acyrtosiphon pisum]
Length = 269

Score = 60.1 bits (144), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 64/272 (23%), Positives = 105/272 (38%), Gaps = 60/272 (22%)

Query: 15 LGATVTGVHLATLDDAGF-AALHAAWLQHALLIFPGQHL-SNDQQITFAKRFGAIE---- 68
LG V GV L T + + +H +LIF Q + S D+ + ++ FG +E
Sbjct: 8 LGCEVRGVDLKTENRPEIIKQIQEDVTKHRILIFKDGIVSGDRHVEISRWFGELESTFY 67

Query: 69 ---RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
+ D+ +SN K +G VG WH D T+ P +++
Sbjct: 68 KHPKSPHPDVFRVSNKNEGCTN-----VGRSGWHIDGTFQPAPFSYSLYH 113

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 185
E VP G T F + ++LD+ T A++
Sbjct: 114 MESVVK-EGHTLFIPLTELIESLDKDT-----YDTWNKAWM-- 148

Query: 186 GMDTTATPLRPLVKVHPETGRPSLL--IGRHA-----HAIPGMDAA---ESERFLEGLVD 235
D ++P+ PL+ HP+TG+P L +G + +P A E E L+ +
Sbjct: 149 VSDRRSSPVHPLIYSHPQTGKPVLCFHLGTTGFIWNYKLPSEATASHEEYEALLKSIDS 208

Query: 236 WACQ--APRVHAHQWAAGDVVVWDNRCLLHRA 265
Q ++ H+W GD ++ DN + H A
Sbjct: 209 KINQDNGKYIYVHKWEPGDFIISDNLAUGHFA 240

>ref|ZP_06861621.1| Taurine dioxygenase [Citromicrobium bathyomarinum JL354]
Length = 282

Score = 60.1 bits (144), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 63/257 (24%), Positives = 97/257 (37%), Gaps = 28/257 (10%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSDNDQQITFAKRFGAI 67
ITP G V L D + + +H L+F Q LS D+Q R G +
Sbjct: 12 ITPFGVE-----VDLDLNDPSNDEKQVADLFKEHGFLVFREQELSQDEQKRVMARLGPL 64

Query: 68 ERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE 127
+ +SN + DG + +++H+D Y PV G
Sbjct: 65 LE-DFTTVGVVSNTRKDGLLG-----SEVSFHSDFIYTPVPLLGLISLHGI 109

Query: 128 VVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 187
VP T FA + A ++L TR + + S+ L Q+ GY
Sbjct: 110 EVPYEETWTRFASGKLALESLSPTQTRDLRLDLKGLNLFASAEGLTGRQRIE----GYPE 165

Query: 188 DTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAH 246
D ++ V P TG L + A I G+ AESE + L + ++ H
Sbjct: 166 DAPRAE-HDIIHVDPITGWEVLYATQNTALIVGLSEAESEELIGELHEHLYNDNDNIYEH 224

Query: 247 QWAAGDVVVWDNRCLLH 263
+W GD+V+W N+ H
Sbjct: 225 RWRNGDLVIWSNQAFHH 241

>emb|CBJ19164.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 60.1 bits (144), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 38/114 (33%), Positives = 58/114 (50%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM--TTATPLR-PLVK 199
AAYDALD+ T+A + HS ++S+ +LG + Y D T P+R LV+
Sbjct: 1 AAYDALDQKTKAEIEDLICEHSQIFSREQLG-----FTEYLPDERTMTKPVHRHLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP +GR S+ + H I G E+ F+ L + A Q V++H+W D+
Sbjct: 53 THPTSGRKSIFLSAHIGGIVGWPRPEAMSFIRDLSEHATQPQFVYSHRWTQHDL 106

>ref|XP_002376836.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Aspergillus flavus NRRL3357]
gb|EED53590.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Aspergillus flavus NRRL3357]
Length = 360

Score = 60.1 bits (144), Expect = 4e-07, Method: Compositional matrix adjust.

Identities = 48/173 (27%), Positives = 79/173 (45%), Gaps = 22/173 (12%)

```
Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
      +WH D++Y P A ++ +P GG T +A YD + R + +A
Sbjct: 155 SWHTDTSYEPNPADYSILKLIKLPETGGDTIWASSCEIYDKISPVYRRFLEGLTA---T 210

Query: 167 YSQSKLGHVQQAGSAYIGY-----GMDTTATPLRPLVKVHPETGRPSLL-IGRHAHA 217
      ++Q++L V A + Y + T+ + + P+V+ +P TG SL +G H
Sbjct: 211 FAQTRLP-VTAAEKGFKLYSEPRGSPNNIGTSLSAVHPVVRTNPVTGWKSLFAVGNHVVK 269

Query: 218 IPGMDAAESER----FLEGLVDWACQAPRVHAHQWAAG-DVVVWDNRCLLHRA 265
      I + A ES R FL+ +V+ R H+W D+ +WDNR + H A
Sbjct: 270 INEVTADESRRLLHDWFLQMIVEEHDQTQLR---HRWQNPYDIAIWDNRRTVYHSA 319
```

>dbj|BAD15034.1| hypothetical protein [Bradyrhizobium elkanii USDA 94]
Length = 102

Score = 60.1 bits (144), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 37/107 (34%), Positives = 51/107 (47%), Gaps = 5/107 (4%)

```
Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGR 206
      ALD+ T+A + HSL+YS+ LG + Y L+ LV+ HP GR
Sbjct: 1 ALDDETKAELEDMICEHSLMYSRGSLGFLD-----YTDEEKQMFKPVLQRLVTRTHPAHGR 55

Query: 207 PSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
      SL + HA AI GM E+ L L + A Q V+ H+W D+
Sbjct: 56 KSLYLSSHAGAIRGMSMPEARLLLLRDLTEHATQPEFVYVHKWTVHDL 102
```

>ref|ZP_07964195.1| TfdA family Taurine catabolism dioxygenase TauD [Segniliparus rugosus ATCC BAA-974]
gb|EFV14576.1| TfdA family Taurine catabolism dioxygenase TauD [Segniliparus rugosus ATCC BAA-974]
Length = 289

Score = 60.1 bits (144), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 68/275 (24%), Positives = 107/275 (38%), Gaps = 38/275 (13%)

```
Query: 12 GATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAI---- 67
      G LGA +TG+ LD + ++ L++ S +Q + + G I
Sbjct: 7 GEGLGAQITGIDPEDLDSIRADEIRDIVYENKLVVLKDVPRPSAEQFLQLGRILGEIVPY 66

Query: 68 ERI---GGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
      E I +I S + G R + WH D +MP +
Sbjct: 67 EPIYHHKDHPEIFVSSTEQQGQVPRGTGA-----FWHIDYQFMP---KPFA 108

Query: 124 FSAEVVPAVGG---TCFADMRAAYDALDEATRALVH-QRSARHSLVYSQSKLGHVQQAG 179
      FS + AV GR T F D+ +++L +A RS Y + + V +
Sbjct: 109 FSMVLPLAVPGRDRGTYFIDLNVWESLPADLQAKARGTRSIHSPRRYIKIRPSDVYRPI 168

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-----PGMDAAESERFLE-- 231
      + +TT P V HP+TG+ L I +D + + LE
Sbjct: 169 GEILAEIEETTPPQTWPTVIKPKTGQEILYICEAGTMTIEDGNGNALDPSLLQTLLEAT 228

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE 266
      G +D +P +HA + GD+V+WDNR L+HRA+
Sbjct: 229 GQLDPDYASPFIIHAQHYEVDIVLWDNRALVHRAK 263
```

>ref|XP_003009781.1| alpha-ketoglutarate-dependent taurine dioxygenase [Verticillium albo-atrum VaMs.102]
gb|EEY15355.1| alpha-ketoglutarate-dependent taurine dioxygenase [Verticillium

albo-atrum VaMs.102]
Length = 257

Score = 59.7 bits (143), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 44/173 (25%), Positives = 73/173 (42%), Gaps = 6/173 (3%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
WH+D T+ PV + A+ +PA GG T +A YD L A + + +A H
Sbjct: 59 GWHSDITFEFVPSDYAMLKIHTLPATGGDTMWASGYEIIDRLSPAMQVFLEGLTATHDAK 118

Query: 167 Y---SQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMD 222
+ +LG+ + G + P+++ +P TG S+ + R I G+
Sbjct: 119 FFLDEAERLGNPIRQGIQSPLNQAGLMAVHPVIRTNPVTGWKSVYVNRGFTKTRINGVT 178

Query: 223 AAESERFLEGLVDWACQAPRVHAH-QWAAAGDVVVDNRCLLHRAEPWDFKLPR 274
ES+ L + + Q +W D+ +WDNR H A +D+ R
Sbjct: 179 KDESDVLLAYIFNLLTQNHDQVRFKWRKNDLAIWDNRSTWHCAT-YDYDEAR 230

>ref|XP_001387469.1| taurine catabolism dioxygenase [Scheffersomyces stipitis CBS 6054]
gb|EAZ63446.1| taurine catabolism dioxygenase [Pichia stipitis CBS 6054]
Length = 424

Score = 59.7 bits (143), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 67/280 (23%), Positives = 104/280 (37%), Gaps = 37/280 (13%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSDNDQQITFAKRFGAIERIGGGD 74
LG + G+ L+ L+D L + ++ F Q LS +Q+ + +G +ER
Sbjct: 123 LGTEIVGLQLSDLNDKQKDELALLVAERVVFFRNQDLSPQKQLELGEYWGQVERHPQAP 182

Query: 75 IVAISNVKADGTVRQHSPAEE--WDDMMKVIVG-----NMAWHADSTYMPVMAQGA 122
V + + T+ + S W G WH D + A
Sbjct: 183 HVPLPIPEGTETIAKGSVSVIWRKFFSEFYGFPGGFRKKSITSGWHTDLVHEHQAPAGIT 242

Query: 123 VFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSA---RHSLVYSQSKLGHVQQA 178
+ +P GG T +A AAYD L A + + ++A H + ++ L
Sbjct: 243 HLHNDTIPKTGGDTAWASGYAAYDKLSPALQKFLDGKTAIYRSAHQYLDRENPL-----K 297

Query: 179 GSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWA 237
G YI P+V+ HP TG L + R I G++ ES+ LE L
Sbjct: 298 GPKYIERE-----HPIVRTHPATGWKYL FVNRSMTDRIVGLEPGESKVILEYLFVSVY 349

Query: 238 CQAPRVHAH-QWAA-----GDVVVDNRCLLHRA-EPWDF 270
+ + QW G +WDNR H A +DF
Sbjct: 350 EKNLDIQVRFQWQPTNEGFGTSAIWDNRVSQHNAISDYDF 389

>emb|CBJ18771.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 59.7 bits (143), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 41/111 (36%), Positives = 54/111 (48%), Gaps = 7/111 (6%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRP-LVKVHP 202
AYD LD+AT+ HS +YS+S LG I + P++ LV+ HP
Sbjct: 2 AYDRLDDATKQECGLICEHSQIYSRSLGFSDFDTEDLIRF-----KPVQQLRVTRHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDV 253
TGR SL + HA AI G E+ FL L + A Q V+AH W D+
Sbjct: 56 STGRKSLYLASHAGAIVGWPIPEARAFRLDLNEHATQRALVYAHVWKQWDL 106

```
>emb|CBJ19181.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19186.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19187.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19191.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19199.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19207.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18794.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19214.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18802.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18816.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106
```

Score = 59.7 bits (143), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 38/114 (33%), Positives = 58/114 (50%), Gaps = 11/114 (9%)

```
Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD--TTATPLR-PLVK 199
AAYDALD+ T+A + HS ++S+ +LG + Y D T P+R LV+
Sbjct: 1 AAYDALDQKTKAEIEDLICEHSQIFSREQLG-----FTEYLPDERTMMKPVRRHLVR 52
```

```
Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP +GR S+ + H I G E+ F+ L + A Q V++H+W D+
Sbjct: 53 THPTSGRKSIFLSAHIGGIVGWPRPEAMSFIRDLSEHATQPQFVYSHRWTQHDL 106
```

```
>emb|CBJ19183.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106
```

Score = 59.7 bits (143), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 38/112 (33%), Positives = 55/112 (49%), Gaps = 7/112 (6%)

```
Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRP-LVKVH 201
AAYDALD+ T+ V HS ++S+ LG + + P+R LV+ H
Sbjct: 1 AAYDALDDKTKNEVRDLICSHSQIFSRIILGFTDFTDDERLKW-----PVRQRLVRRH 54
```

```
Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P +GR SL + HA I G E+ FL L + A Q V++H+W D+
Sbjct: 55 PRSGRLSLYLSSHAGGIEGWVPPEARAFRLDLTEHATQPQFVYSHRWTQHDL 106
```

```
>ref|NP_214611.1| oxidoreductase [Mycobacterium tuberculosis H37Rv]
ref|NP_334514.1| dioxygenase, putative [Mycobacterium tuberculosis CDC1551]
ref|NP_853768.1| oxidoreductase [Mycobacterium bovis AF2122/97]
ref|YP_976233.1| putative oxidoreductase [Mycobacterium bovis BCG str. Pasteur
1173P2]
ref|YP_001281382.1| putative dioxygenase [Mycobacterium tuberculosis H37Ra]
ref|YP_001286043.1| oxidoreductase [Mycobacterium tuberculosis F11]
ref|ZP_02550532.1| hypothetical oxidoreductase [Mycobacterium tuberculosis H37Ra]
ref|ZP_03418267.1| oxidoreductase [Mycobacterium tuberculosis 02_1987]
ref|ZP_03422615.1| oxidoreductase [Mycobacterium tuberculosis 94_M4241A]
ref|ZP_03423214.1| oxidoreductase [Mycobacterium tuberculosis T92]
ref|ZP_03430933.1| oxidoreductase [Mycobacterium tuberculosis EAS054]
ref|ZP_03435126.1| oxidoreductase [Mycobacterium tuberculosis T85]
ref|ZP_03534620.1| oxidoreductase [Mycobacterium tuberculosis GM 1503]
ref|ZP_03534958.1| oxidoreductase [Mycobacterium tuberculosis T17]
ref|YP_002643170.1| putative oxidoreductase [Mycobacterium bovis BCG str. Tokyo 172]
ref|YP_003030016.1| oxidoreductase [Mycobacterium tuberculosis KZN 1435]
ref|ZP_04926818.1| hypothetical protein TBCG_00097 [Mycobacterium tuberculosis C]
ref|ZP_05139478.1| oxidoreductase [Mycobacterium tuberculosis '98-R604 INH-RIF-EM']
ref|ZP_05222739.1| putative oxidoreductase [Mycobacterium tuberculosis KZN 4207]
ref|ZP_05762427.1| oxidoreductase [Mycobacterium tuberculosis CPHL_A]
ref|ZP_05766584.1| oxidoreductase [Mycobacterium tuberculosis T46]
ref|ZP_05770731.1| oxidoreductase [Mycobacterium tuberculosis K85]
ref|ZP_06431210.1| oxidoreductase [Mycobacterium tuberculosis T46]
```

ref|ZP_06435371.1| oxidoreductase [Mycobacterium tuberculosis CPHL_A]
ref|ZP_06441558.1| oxidoreductase [Mycobacterium tuberculosis KZN 605]
ref|ZP_06448216.1| oxidoreductase [Mycobacterium tuberculosis T17]
ref|ZP_06452904.1| oxidoreductase [Mycobacterium tuberculosis K85]
ref|ZP_06507242.1| oxidoreductase [Mycobacterium tuberculosis 02_1987]
ref|ZP_06507945.1| oxidoreductase [Mycobacterium tuberculosis T92]
ref|ZP_06515537.1| oxidoreductase [Mycobacterium tuberculosis EAS054]
ref|ZP_06519574.1| conserved hypothetical protein [Mycobacterium tuberculosis T85]
ref|ZP_06523591.1| conserved hypothetical protein [Mycobacterium tuberculosis GM
1503]
ref|ZP_06798633.1| oxidoreductase [Mycobacterium tuberculosis 210]
ref|ZP_06950350.1| oxidoreductase [Mycobacterium tuberculosis KZN 4207]
ref|ZP_06958662.1| oxidoreductase [Mycobacterium tuberculosis KZN R506]
ref|ZP_07014897.1| conserved hypothetical protein [Mycobacterium tuberculosis
94_M4241A]
ref|ZP_07412516.1| oxidoreductase [Mycobacterium tuberculosis SUMu001]
ref|ZP_07417261.1| oxidoreductase [Mycobacterium tuberculosis SUMu002]
ref|ZP_07425402.1| oxidoreductase [Mycobacterium tuberculosis SUMu004]
ref|ZP_07429939.1| oxidoreductase [Mycobacterium tuberculosis SUMu005]
ref|ZP_07434001.1| oxidoreductase [Mycobacterium tuberculosis SUMu006]
ref|ZP_07438342.1| oxidoreductase [Mycobacterium tuberculosis SUMu008]
ref|ZP_07442554.1| oxidoreductase [Mycobacterium tuberculosis SUMu007]
ref|ZP_07482943.1| oxidoreductase [Mycobacterium tuberculosis SUMu009]
ref|ZP_07487176.1| oxidoreductase [Mycobacterium tuberculosis SUMu010]
ref|ZP_07491393.1| oxidoreductase [Mycobacterium tuberculosis SUMu011]
ref|ZP_07491677.1| oxidoreductase [Mycobacterium tuberculosis SUMu012]
ref|ZP_07813751.1| oxidoreductase [Mycobacterium tuberculosis KZN V2475]
sp|P67756.1|Y100_MYCBO RecName: Full=Putative dioxygenase Mb0100
sp|P67755.1|Y097_MYCTU RecName: Full=Putative dioxygenase Rv0097/MT0106
emb|CAA98933.1| POSSIBLE OXIDOREDUCTASE [Mycobacterium tuberculosis H37Rv]
gb|AAK44328.1| dioxygenase, putative [Mycobacterium tuberculosis CDC1551]
emb|CAD92962.1| POSSIBLE OXIDOREDUCTASE [Mycobacterium bovis AF2122/97]
emb|CAL70115.1| Possible oxidoreductase [Mycobacterium bovis BCG str. Pasteur
1173P2]
gb|EAY61560.1| hypothetical protein TBCG_00097 [Mycobacterium tuberculosis C]
gb|ABQ71820.1| putative dioxygenase [Mycobacterium tuberculosis H37Ra]
gb|ABR04441.1| hypothetical oxidoreductase [Mycobacterium tuberculosis F11]
dbj|BAH24402.1| putative oxidoreductase [Mycobacterium bovis BCG str. Tokyo 172]
gb|ACT23121.1| oxidoreductase [Mycobacterium tuberculosis KZN 1435]
gb|EFD11625.1| oxidoreductase [Mycobacterium tuberculosis T46]
gb|EFD15786.1| oxidoreductase [Mycobacterium tuberculosis CPHL_A]
gb|EFD19473.1| oxidoreductase [Mycobacterium tuberculosis KZN 605]
gb|EFD41686.1| oxidoreductase [Mycobacterium tuberculosis K85]
gb|EFD45391.1| oxidoreductase [Mycobacterium tuberculosis T17]
gb|EFD55880.1| oxidoreductase [Mycobacterium tuberculosis 02_1987]
gb|EFD56583.1| oxidoreductase [Mycobacterium tuberculosis T92]
gb|EFD64175.1| oxidoreductase [Mycobacterium tuberculosis EAS054]
gb|EFD75735.1| conserved hypothetical protein [Mycobacterium tuberculosis GM 1503]
gb|EFD79772.1| conserved hypothetical protein [Mycobacterium tuberculosis T85]
gb|EFI32576.1| conserved hypothetical protein [Mycobacterium tuberculosis
94_M4241A]
gb|EFO76616.1| oxidoreductase [Mycobacterium tuberculosis SUMu001]
gb|EFP16928.1| oxidoreductase [Mycobacterium tuberculosis SUMu002]
gb|EFP25065.1| oxidoreductase [Mycobacterium tuberculosis SUMu004]
gb|EFP28666.1| oxidoreductase [Mycobacterium tuberculosis SUMu005]
gb|EFP32660.1| oxidoreductase [Mycobacterium tuberculosis SUMu006]
gb|EFP36444.1| oxidoreductase [Mycobacterium tuberculosis SUMu007]
gb|EFP40386.1| oxidoreductase [Mycobacterium tuberculosis SUMu008]
gb|EFP41070.1| oxidoreductase [Mycobacterium tuberculosis SUMu009]
gb|EFP45004.1| oxidoreductase [Mycobacterium tuberculosis SUMu010]
gb|EFP48975.1| oxidoreductase [Mycobacterium tuberculosis SUMu011]
gb|EFP56553.1| oxidoreductase [Mycobacterium tuberculosis SUMu012]
gb|EGB26475.1| oxidoreductase [Mycobacterium tuberculosis CDC1551A]

Length = 289

Score = 59.7 bits (143), Expect = 5e-07, Method: Compositional matrix adjust.
Identities = 66/282 (23%), Positives = 105/282 (37%), Gaps = 52/282 (18%)

```
Query: 12  GATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIG 71
          G LGA VTGV LDD + + L++ H S + I + G I
Sbjct: 7  GEGLGAQVTGVDPKNLDDITTDIIRDIVYTNKLVVLKDVHPSREFIKLGRIIGQI---- 62

Query: 72  GGDIVAISNVKADGTVRQHSPA-EWDDMMKVIVGNMA-----WHADSTYMPVMA 119
          V + P +D ++ V + WH D +MP
Sbjct: 63  -----VPYYEPMYHHEDHPEIFVSSTEEGQGVPKTGAFWHIDYMFMPPEPF 107

Query: 120  QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ-QA 178
          ++ VP T F D+ + +L A +R V + H++ +
Sbjct: 108  AFSMVLPLAVPGHDRGTYFIDLARVWQSLPAA-----KRDPARGTVSTHDPRRHIKIRP 161

Query: 179  GSAYIGYG-----MDTTATPLR-PLVKVHPETGRPSLLI---GRHAHAIPGMDAAESERF 229
          Y G ++ T P++ P V HP+TG+ L I G + + E
Sbjct: 162  SDVYRPIGEVWDEINRTTPPIKWPTVIRHPKTGQEILYICATGTTKIEDKDGPNVDPEVL 221

Query: 230  LE-----GLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAE 266
          E G +D Q+P +H + GD+++WDNR L+HRA+
Sbjct: 222  QELMAATGQLDPEYQSPFIHTQHYQVGDIIILWDNRLVMHRAK 263
```

>emb|CBJ18780.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 59.7 bits (143), Expect = 5e-07, Method: Compositional matrix adjust.
Identities = 38/111 (34%), Positives = 51/111 (45%), Gaps = 5/111 (4%)

```
Query: 143  AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
          AAYDALD+ T+A + HSL+YS+ LG + Y L+ LV+ HP
Sbjct: 1  AAYDALDDDTKAEIEDLVCEHSLMYSRGLGFTE-----YTDDEKQMFKPVLRQLVRTHP 55

Query: 203  ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
          R SL + HA I M E L L + A Q V+ H+W D+
Sbjct: 56  VHRKSLYLSSHAGKIVSMSVPEGRLLLLRLNEHATQGEFVYVHKWKLHDL 106
```

>ref|YP_001417667.1| taurine dioxygenase [Xanthobacter autotrophicus Py2]
gb|ABS68010.1| Taurine dioxygenase [Xanthobacter autotrophicus Py2]
Length = 323

Score = 59.7 bits (143), Expect = 5e-07, Method: Compositional matrix adjust.
Identities = 56/235 (23%), Positives = 92/235 (39%), Gaps = 13/235 (5%)

```
Query: 35  LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGDIVAISNVKADGTVRQHSPA 94
          + AA L+ ++ F Q L++ Q + A+ FGA IG + ++ + A
Sbjct: 51  IRAALLKWKVFFRDQPLTHAQHVALARAFGA-PTIGHPVFGFVDGHPEVYSISRDRFAT 109

Query: 95  WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRA 154
          +I WH D T ++ +V+P GG T + ++ AY+ L R
Sbjct: 110  RHVGEPLIRPWTGWHTDVTAAVNPPAASILRGDVIPPYGGDTFTWNLAVAYEGLSAPLRG 169

Query: 155  LVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPL--RPLVKVHPETGRPSLLI 211
          V H+ + + G + + PL PLV+V PETG L +
Sbjct: 170  FVDTLRGVHAFTAPEGQ-GTTED-----FKEKNRLRPLVSEHPLVRVIPETGERVLFV 221

Query: 212  G-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
          I G+ ES++ L+ L + + +W G + WDNR H A
Sbjct: 222  SPSFLKRITGLAPRESQQILDLLFEHITRPEYTVRFRWQPGSIAFDWNRRTAHLA 276
```

>ref|XP_001558157.1| hypothetical protein BC1G_03189 [Botryotinia fuckeliana B05.10]
gb|EDN19556.1| hypothetical protein BC1G_03189 [Botryotinia fuckeliana B05.10]
Length = 394

Score = 59.7 bits (143), Expect = 5e-07, Method: Compositional matrix adjust.
Identities = 69/266 (25%), Positives = 101/266 (37%), Gaps = 34/266 (12%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGAIERIGG- 72
+G + GV LA L DA L ++ F Q + + Q FG + +
Sbjct: 93 IGTEIHGVDLANLTDAAKNDLARLISIRGVVFFRNQKNFDIEAQRKLGSYFGTLHKHATT 152

Query: 73 -----GDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE 127
GD+ + V D + D + WH+D TY + + S +
Sbjct: 153 SVPKRGDLDDVHVVTDEKSK-----DQRALFTPTFLWHS DVTYE--IQPPSYTSLK 202

Query: 128 VVPAV----GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
V+ GG T ++ AAYDAL + + +A H+ H+Q GS +
Sbjct: 203 VLTGPPRGGGGDTLWSSQYAAAYDAL SAPM QKYLESLTALHT-----SHLQAEGRSAL 254

Query: 184 GYGM--DTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQA 240
G + D T PL++ HP TG SL I G+ ES+ L L +
Sbjct: 255 GRPVRDPDIITE-HPLIRSHPVGTGWSLFFNPGFVTKIVGIPKVESDVILAYLNEVVATT 313

Query: 241 PRVHAH-QWAAGDVVVWDNRCLLHRA 265
+H QW DV WDNR H A
Sbjct: 314 QELHVRFQWGKDDVAFWDNRISNHTA 339

>ref|XP_002376025.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Aspergillus flavus NRRL3357]
gb|EED54753.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Aspergillus flavus NRRL3357]
Length = 296

Score = 59.7 bits (143), Expect = 5e-07, Method: Compositional matrix adjust.
Identities = 51/196 (26%), Positives = 87/196 (44%), Gaps = 16/196 (8%)

Query: 78 ISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVPAVGGRTC 137
IS + ++G + +++ M V WH+D ++ A + +P GG T
Sbjct: 63 ISTINSEGRKTLTKGSDYTKMAAV-----WHS DISFEKAPADFSSRLVLQPKTGGDTL 116

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLV---YSQSKLGHV-QQAGSAYIGYGMDDTTAT 192
+A YD + + RA + SA H+ V +Q+ H+ ++ A + G D TA
Sbjct: 117 WASGYEIIYDRISKPYRAFLETLSATHAGVGFMRLAQTGKFHLYEKERGAPVNVGGDLTA- 175

Query: 193 PLRPLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW-A 249
+ P+V+ +P TG S+ IG I G+ ES L+ D + +W +
Sbjct: 176 -VHPVVRTNPITGWKSIFPIGSFPTQIDGLTRRESASMLQWFHDMITHGHDLQVRFKWNS 234

Query: 250 AGDVVVWDNRCLLHRA 265
D+ +WDNR + H A
Sbjct: 235 PNDIAIWDNRSVFHTA 250

>ref|XP_003030923.1| hypothetical protein SCHCODRAFT_56708 [Schizophyllum commune H4-8]
gb|EFI96020.1| hypothetical protein SCHCODRAFT_56708 [Schizophyllum commune H4-8]
Length = 347

Score = 59.3 bits (142), Expect = 5e-07, Method: Compositional matrix adjust.
Identities = 44/164 (26%), Positives = 70/164 (42%), Gaps = 8/164 (4%)

Query: 108 WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-V 166
WHAD T+ + + A+ +P VGG T +A AYD L A R + +A H+
Sbjct: 147 WHADITFENIPSDYAILKMHTLPKVGDTLWASAYEAYDRLSPAYRKFLGLELTAIHNAF 206

Query: 167 YSQSKLGH---VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMD 222
+++ H + + A G D TA + P+++ +P TG L + I +
Sbjct: 207 FNEYARVHGLPINELRGAPDNKGSDLTA--IHPVIRTNPVTGFKGLFVNPFTKRIVELS 264

Query: 223 AAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
ES L L + + W+ D+ +WDNR H A
Sbjct: 265 LDESNDVLAFLARHVSSENHDLQVRFTWSLNDLAIWDNRSTFHTA 308

>emb|CBJ18858.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 59.3 bits (142), Expect = 5e-07, Method: Compositional matrix adjust.
Identities = 38/114 (33%), Positives = 57/114 (50%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVK 199
AAYDALD+ T+A + HS ++S+ +LG + Y D T P+R LV+
Sbjct: 1 AAYDALDQKTKAEIEDLICEHSQIFSREQLG-----FTEYLPDERTMMKPVHRHLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP +GR S+ + H I G E+ F+ L++ A Q V+ H+W D
Sbjct: 53 THPTSGRKSIFLSAHIGGIVGWPRPEAMAFIRDLMEHATQPQFVNVHRWTKHDF 106

>ref|XP_002836921.1| hypothetical protein [Tuber melanosporum Mel28]
emb|CAZ81112.1| unnamed protein product [Tuber melanosporum]
Length = 381

Score = 59.3 bits (142), Expect = 5e-07, Method: Compositional matrix adjust.
Identities = 53/214 (24%), Positives = 90/214 (42%), Gaps = 20/214 (9%)

Query: 72 GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVA 131
G ++ IS G R+ P+ D+ + + + WH + T+ + + +V +P
Sbjct: 132 GDEVTVISTEGKKGLNRRRLRPSYKDE--RSGLASSGWHMEITFEEIPSDYSVLKMTTLPE 189

Query: 132 VGGRTCFADMRAAYDALDEATRALVH-----QRSARHSLVYSQSKLGHVQQAGSAYIGY 186
GG T +A AYD L + R ++ S R + V ++ GS + G
Sbjct: 190 TGGDTLWASAYEAYDRLSPSFRQILEGLTATHDSRFAEVAARDGFQLRTDRGSPH-NAG 248

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV-----DWAC 238
+D A + P+++ +P TG L + R I + ES+ L+ L D C
Sbjct: 249 LDLVA--VHPVIRTNPVTGWKGLFVNRGFTRRINELTKDESDYMLDFLKHVSENHDLQC 306

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA--EPWDF 270
+ + A DV +WDNR H A + +DF
Sbjct: 307 RLKWMAYENKNAHDVAIWDNRSAFHTATDDYFDF 340

>ref|XP_664343.1| hypothetical protein AN6739.2 [Aspergillus nidulans FGSC A4]
gb|EAA58557.1| hypothetical protein AN6739.2 [Aspergillus nidulans FGSC A4]
tpe|CBF71363.1| TPA: alpha-ketoglutarate-dependent taurine dioxygenase
(AFU_orthologue; AFUA_7G06030) [Aspergillus nidulans
FGSC A4]
Length = 376

Score = 59.3 bits (142), Expect = 6e-07, Method: Compositional matrix adjust.
Identities = 69/277 (24%), Positives = 105/277 (37%), Gaps = 35/277 (12%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSND---QQITFA 61
+++T +G+ + GV L+ L A L + ++ FP Q L + Q F
Sbjct: 85 NVKVTDIQPRIGSVLEGVQLSQLSAAAKDELALLVSEKVVAFPNQDLIDAGPAAQAAM 144

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQ-----HSPAEDDDMMKVI---VGNMAWHAD 111
FG + GTVR H +++ + + WH D
Sbjct: 145 SHFGKP-----NYQPVSGTVRGYPGFHIIHRDGNREEICRFLEQRTTTTLWHQD 193

Query: 112 STYMPVMAQGAVFSAEVV-PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS 170
+Y + G V + P VGG T FA AY L + + SA HS S
Sbjct: 194 VSYE-IQPPGYVMLGLLEGPEVGGDTVFAATDLAYKRLSATLCSWLDTL SAVHS---SAK 249

Query: 171 KLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL-LIGRHAHAIPGMDAAESERF 229
+ H + G +DT + PLV++HP TG L G IPG+ E
Sbjct: 250 MINHARLTGGLVRKDPVDT----VHPLVRIHPVTGEKCLWFNGEFITKIPGLKEPEQRWL 305

Query: 230 LEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
L+ L+ A +W +V++DNR +H A
Sbjct: 306 LDFLMQHIVSGHDFQARVRWQPKTIVIFDNRSTIHS 342

>emb|CBJ18772.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 59.3 bits (142), Expect = 6e-07, Method: Compositional matrix adjust.
Identities = 38/111 (34%), Positives = 51/111 (45%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
AAYDALD+ T+A + HSL+YS+ LG + Y L+ LV+ HP
Sbjct: 1 AAYDALDDDTKAEIEDLVCEHSLMYSRSGSLGFTE-----YTDEKQMFKPVLRQLVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
R SL + HA I M E L L + A A V+ H+W D+
Sbjct: 56 VHRKSLYLSSHAGKIVSMSVPEGRLLLRDLNEHATNAEFVYVHKWKLHDL 106

>ref|XP_002376500.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
flavus NRRL3357]
gb|EED53254.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
flavus NRRL3357]
Length = 396

Score = 59.3 bits (142), Expect = 6e-07, Method: Compositional matrix adjust.
Identities = 65/257 (25%), Positives = 100/257 (38%), Gaps = 16/257 (6%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERIGGG 73
+G + GV+LA LD+A L ++ F Q L D Q + FG + +
Sbjct: 95 IGTEIHGVNLAKLDEAQKDDLARLVAVRGVVFVRDQKDLIDAQRELGRHFGRLLHKHATT 154

Query: 74 DIVAISNVKADGTVRQHSPAEDDDMMKVIIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVG 133
+ ++ V +S D + + WH+D TY + P G
Sbjct: 155 SVPRKQGLEDVHVV--YSGDNSGDQRALFTPSFLWHSVTVYEVQPPSYTMLKVLTGPPRG 212

Query: 134 G--RTCFAADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD-TT 190
G T + AAYDAL + + +A HS +Q + S +G +
Sbjct: 213 GGGDTLWTSQYAAAYDALSSHMOTYKGLTAIHS-----ADMQASDSRALGRPVRRREP 264

Query: 191 ATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW 248
T PL++ +P TG SL I G+ ES+ ++ L D +HA QW
Sbjct: 265 VTTEHPLIRTNPVTGWNSLFFNPGFVTKIVGIPKTESDAIKYLTVDVIATTQEMHARFQW 324

Query: 249 AAGDVVVWDNRCLLHRA 265
D+ +WDNR H A

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDD--TTATPLR-PLVK 199

Sbjct: 1 AAYDALD+ T+A + HS ++S+ +LG + Y D T P+R LV+
AAYDALDQKTKAEIEDLICEHSQIFSREQLG-----FTEYLPDERMTMMKPVHRHLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

HP +GR S+ + H I G E+ F+ L + A Q +++H+W D+
Sbjct: 53 THPTSGRKSIFLSAHIGGIVGWPRPEAMSFIRDLSEHATQPQFIYSHRWTQHDL 106

>ref|XP_001820775.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
oryzae RIB40]
dbj|BAE58773.1| unnamed protein product [Aspergillus oryzae]
Length = 396

Score = 59.3 bits (142), Expect = 6e-07, Method: Compositional matrix adjust.
Identities = 65/257 (25%), Positives = 100/257 (38%), Gaps = 16/257 (6%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERIGGG 73
+G + GV+LA LD+A L ++ F Q L D Q + FG + +
Sbjct: 95 IGTEIHGVNLAKLDEAQKDDLARLVAVRGVVFFRDQKDLIDAQRELGRHFGRLHKHATT 154

Query: 74 DIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVG 133
+ ++ V +S D + + WH+D TY + P G
Sbjct: 155 SVPRKQGLEDVHV--YSGDNSGDQRALFTPSFLWHS DVTYEVQPPSYTMLKVLTPGPRG 212

Query: 134 G--RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM-DT 190
G T + AAYDAL + + +A HS +Q + S +G +
Sbjct: 213 GGGDTLWTSQYAAAYDALSSHMTYKGLTAIHS-----ADMQASDSRALGRPVRRP 264

Query: 191 ATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW 248
T PL++ +P TG SL I G+ ES+ ++ L D +HA QW
Sbjct: 265 VTTEHPLIRTNPVTGWNSLFFNPGFVTKIVGIPKTESDAIKYLTVDVIATTQEMHARFQW 324

Query: 249 AAGDVVVWDNRCLLHRA 265
D+ +WDNR H A
Sbjct: 325 NKDDLAIWDNRRTTNHTA 341

>ref|XP_962940.1| hypothetical protein NCU07819 [Neurospora crassa OR74A]
gb|EAA33704.1| hypothetical protein NCU07819 [Neurospora crassa OR74A]
Length = 333

Score = 59.3 bits (142), Expect = 6e-07, Method: Compositional matrix adjust.
Identities = 64/256 (25%), Positives = 106/256 (41%), Gaps = 24/256 (9%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
+G + G+ L L L + +++ F Q L+ QQ + FG +E
Sbjct: 93 IGTEIEGLQLKDLTPQQRDELALLIAERSVVFFRNQDLTPQQQKELGEWFGVEVHPQTP 152

Query: 69 RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV 128
++ G + ++ + D + PA + + G WH+D + A +
Sbjct: 153 QVPG--VPGVTVIWPDFTLER-PANF----RRPGGASNWHS DLVHERQPAGITHLHNDT 205

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM-D 188
VP GG T +A +AY+ L R ++ + A VY + +Q +A Y
Sbjct: 206 VPPTGGDTLWASGYSAYEKLSPFEFRKIIDGKYA----VYRSHAPYLD RQDPNAGPKYIER 261

Query: 189 TTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAH- 246
T PLV+VHP TG +L + R I G+D AES+ L L D + +
Sbjct: 262 T-----HPLVRVHPATGWKALWVNRSM TVRIVGLDKAESDVILNYLYDVYEKNVDIQVRF 316

Query: 247 QWAAGDVVVWDNRCLL 262
+W G +WDNR ++
Sbjct: 317 KWTPGTSALWDNRSVI 332

>emb|CBJ18919.1| alpha-ketoglutarate dioxxygenase-like protein [uncultured bacterium]
Length = 106

Score = 59.3 bits (142), Expect = 6e-07, Method: Compositional matrix adjust.
Identities = 38/111 (34%), Positives = 55/111 (49%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHP 202
AAYDAL + T+A V A H +++ LG AY + PLV+ HP
Sbjct: 1 AAYDALPDRTKAEVQDLRAEHYALHTRILLG-----DEAYTDEQKKAIPPAVWPLVQTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+ R L +G A I G AES +L+ L++ A Q V+ H+W GD+
Sbjct: 56 GSRRKLLFVGVRARQIIGWPTAESRMYLQDLLEHATQREFVYRHEWQVGDL 106

>emb|CAY27326.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 59.3 bits (142), Expect = 6e-07, Method: Compositional matrix adjust.
Identities = 45/122 (36%), Positives = 56/122 (45%), Gaps = 15/122 (12%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR 195
T FADMRAAYDALDE + HS ++S+S LG + P+R
Sbjct: 1 TEFADMRAAYDALDEEIKTECENLICEHSQFLSRSILGFTDFTDDERRRFA-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
LV+ HP TGR SL + HA AI G ++ FL L D HA V+
Sbjct: 55 QRLVRRHPVTGRRSLYLASHAGAILGCLEPKARAFLSYLND-----HATHRQFFFI 106

Query: 255 VW 256
VW
Sbjct: 107 VW 108

>ref|XP_001805839.1| hypothetical protein SNOG_15699 [Phaeosphaeria nodorum SN15]
gb|EAT77074.1| hypothetical protein SNOG_15699 [Phaeosphaeria nodorum SN15]
Length = 368

Score = 59.3 bits (142), Expect = 6e-07, Method: Compositional matrix adjust.
Identities = 70/254 (27%), Positives = 99/254 (38%), Gaps = 27/254 (10%)

Query: 13 ATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGG 72
A +GA V GV L+ L AG L Q ++ F Q + D I A +G G
Sbjct: 99 ANIGAEVHGVQLSKLTAAGKDELALFVAQKKVVAFRDQDFA-DLPIQDALNYGGY--FGR 155

Query: 73 GDIVAIISNVKADGTVRQH-----SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
I S +G + H D + ++ WH+D TY
Sbjct: 156 HHIHPTSGA-PEGYPQVHLVHRGTDDTSARDFFEERTNSITWHS DVTYEKQPPGTTFLYL 214

Query: 127 EVVPAVGGRTCTCFADMRAAYDALDEATRALVHQRSARHSLV----YSQSKLGHVQQAGSAY 182
PA GG T FA+ AAY+ L R +H HS V S+++ G V++
Sbjct: 215 LDGPAAGGDTLFANQAAAYNRLSPEFRKRLHGLKVVHSAVEQADNSKNRGGIVRR----- 269

Query: 183 IGYGMTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAP 241
T + PLV+ HP TG +L + + + I G ES+ L L D +
Sbjct: 270 -----DPVTSIHPLVRTHPATGEKALFVNPQFSRRIVGYKKEESDFLLNFLYDHIAGQ 323

Query: 242 RVHAH-QWAAGDVV 254
A +WA G VV
Sbjct: 324 DFQARVKWAPGTVV 337

>ref|XP_001727715.2| tfdA family taurine dioxygenase [Aspergillus oryzae RIB40]
 Length = 354

Score = 59.3 bits (142), Expect = 7e-07, Method: Compositional matrix adjust.
 Identities = 51/196 (26%), Positives = 87/196 (44%), Gaps = 16/196 (8%)

Query: 78 ISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTC 137
 IS + ++G + +++ M V WH+D ++ A + +P GG T
 Sbjct: 121 ISTINSEGRKTLTKGSDYTKMAAV-----WHSDISFEKAPADFSSLRLVQLPKTGGDTL 174

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLV----YSQSKLGHV-QQAGSAYIGYGMDTTAT 192
 +A YD + + RA + SA H+ V +Q+ H+ ++ A + G D TA
 Sbjct: 175 WASGYEYDRISKPYRAFLETLSATHAGVGMRLAQTKGFHLYEKERGAPVNVGGDLTA- 233

Query: 193 PLRPLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW-A 249
 + P+V+ +P TG S+ IG I G+ ES L+ D + +W +
 Sbjct: 234 -VHPVVRTNPITGWKSIFPIGSFPTQIDGLTRRESASMLQWFHDMITHGHDLQVRFKWN 292

Query: 250 AGDVVVWDNRCLLHRA 265
 D+ +WDNR + H A
 Sbjct: 293 PNDIAIWDNRSVFHTA 308

>emb|CAY25785.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 59.3 bits (142), Expect = 7e-07, Method: Compositional matrix adjust.
 Identities = 34/108 (31%), Positives = 56/108 (51%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
 + A ++A+L+F Q +S+DQQ+ FA+ FG E GG + +SN+
 Sbjct: 16 IEAGMDKYAVLLFRDQDVSDQQLVFARNFGERENARGGTVTKKEDYRLTSGLNVDVSNLD 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
 DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
 Sbjct: 76 KDG-----NPLPRDHRTHLFLNGLNCLWHSDDSSFRPIPAKFSLLSARVV 118

>emb|CBJ19188.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
 Length = 106

Score = 59.3 bits (142), Expect = 7e-07, Method: Compositional matrix adjust.
 Identities = 38/114 (33%), Positives = 58/114 (50%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD--TTATPLR-PLVK 199
 AAYDALD+ T+A + HS ++S+ +LG + Y D T P+R LV+
 Sbjct: 1 AAYDALDQKTKAEIEDLIYEHSQIFSREQLG-----FTEYLPDERTMMKPVHRHLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
 HP +GR S+ + H I G E+ F+ L + A Q V++H+W D+
 Sbjct: 53 THPTSGRKSIFLSAHIGGIVGWPRPEAMSFIRDLSEHATQPQFVYSHRWTQHDL 106

>ref|XP_962844.2| hypothetical protein NCU07610 [Neurospora crassa OR74A]
 gb|EAA33608.2| hypothetical protein NCU07610 [Neurospora crassa OR74A]
 Length = 376

Score = 58.9 bits (141), Expect = 7e-07, Method: Compositional matrix adjust.
 Identities = 58/253 (22%), Positives = 101/253 (39%), Gaps = 30/253 (11%)

Query: 41 QHALLIFPGQH-LSNDQQITFAKRFGAI-----ERIGGGDIVAISNVK 82
 + ++ F QH L+ND Q R GA+ ER GG+ IS +

Sbjct: 84 RRGVVFRAQHSLTNDLQKQLILRLGALTGRPPTSGLHIHPILNSERELGGNDPEISTIS 143

Query: 83 A--DGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFAD 140
+ H+ + D + WH+D + PV A +P GG T +A

Sbjct: 144 SIQHRKFYNHTSEDDQLSPKKQYTAQWHSIDIAFEPVPADYTSRLVQLPKTGGDTLWAS 203

Query: 141 MRAAYDALDEATRALVHQRSA--RHSLVYSQSKLGH--VQQAGSAYIGYGMTTATPLR 195
YD + E + + + + + ++G ++ A G + A +

Sbjct: 204 GYEIYDRISEPYQKFLEGLTVTFQQPGFNRTAERIGFKIYEKPRGAPENVGSELKA--VH 261

Query: 196 PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAA-GD 252
P+V+ +P TG S+ +G H + G+ ES+R LE ++ + + +W D

Sbjct: 262 PVVRTNPVTGWKSVFPVGGHVQVNGVTKEESDRLEWFLLELLQKNHDLQVRFRWTGEND 321

Query: 253 VVWVDNRCLLHRA 265
+ +WDNR + H A

Sbjct: 322 IAIWDNRSVFHTA 334

>ref|XP_500006.1| YALI0A12177p [Yarrowia lipolytica]
emb|CAG83935.1| YALI0A12177p [Yarrowia lipolytica]
Length = 382

Score = 58.9 bits (141), Expect = 8e-07, Method: Compositional matrix adjust.
Identities = 50/170 (29%), Positives = 69/170 (40%), Gaps = 29/170 (17%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WHAD TY P GG T + A YD+L E + + +A HS

Sbjct: 176 WHADVTYEKQPPSYTSLKVLNPPTGGDTLWTSNYAVYDSLSEPMQKYLESLTAIHS--- 232

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLR-----PLVKVHPETGRPSLLIGR-HAHAI 218
G Q A SA +G PLR P+++ HP TG S+ + A+

Sbjct: 233 -----GVAQAADSARVG-----QPLRRDPIETHEPVRTHPVTGWKSVFLNPGFVTAL 280

Query: 219 PGMDAAESE---RFLEGLVDWACQAPRVHAHQWAAAGDVVWVDNRCLLHRA 265
G+ +ES+ ++ LV A Q +W + DV WDNR H A

Sbjct: 281 RGIPTSESQAIMTYINSLV--ATQQEDTVRFKWNQDVAFWDNRRTTSHSA 328

>gb|EFQ34526.1| TfdA family Taurine catabolism dioxygenase TauD [Glomerella
graminicola M1.001]
Length = 210

Score = 58.9 bits (141), Expect = 8e-07, Method: Compositional matrix adjust.
Identities = 52/192 (27%), Positives = 90/192 (46%), Gaps = 17/192 (8%)

Query: 52 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHAD 111
+S + + +K GA +G ++ N+ ++ V SP+ D ++ GNM +H D

Sbjct: 29 VSKEIRDAISKDTGAPSLMGRPELTDQGNIDSNRNVI--SPS--DPRAQISKGNMLFHVD 84

Query: 112 STYMPVMAQGAVFSAEVVPAVGG--RTCFADMRAAYDALDEATRALVHQRS--ARHSLVY 167
S++ A ++ A +P GG T FAD RAA+D L E + + ++ A HS +

Sbjct: 85 SSFNSRRASYSILLAHEIPPSGGGGNTEFADTRAADWDELPECWKQGLMEKDYVAGHSFWH 144

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPL--RPLVKVHPETGRPSLLIGRHAHAIPGMDAAE 225
S+ K A + ++ P+ + ++H +GR +L + H H I G+ A E

Sbjct: 145 SRKK-----ACPEFFA-KLEPEKHPMSKHKVAQLHQASGRMNLFPVSHCHHIEGLQAEE 197

Query: 226 SERFLEGLVDWA 237
LE L +A

Sbjct: 198 GREKLEYLCRYA 209

>ref|XP_001383149.1| taurine catabolism dioxygenase [Scheffersomyces stipitis CBS 6054]
gb|ABN65120.1| taurine catabolism dioxygenase [Scheffersomyces stipitis CBS 6054]
Length = 414

Score = 58.9 bits (141), Expect = 8e-07, Method: Compositional matrix adjust.
Identities = 70/275 (25%), Positives = 108/275 (39%), Gaps = 40/275 (14%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
LG + G+ L+ L+D L + ++ F Q LS +Q+ +G +E
Sbjct: 123 LGTEIVGLQLSDLNDQQDELALLVAERVVVFRRDQDLSPQKQLELGHYWGQVEVHPQVP 182

Query: 69 RIGGGDIVAISNVKADGTVRQHSAPWD---DMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
RI + +S + D + A++ K I GN WH D + A
Sbjct: 183 RISE-EFNGVSVIWD-----YYRAKYGLHLSFKKAIGNAQWHTDLVHELQAPAGITHLH 236

Query: 126 AEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSA---RHSLVYSQSKLGHVQQAGSA 181
+ +P+VGG T +A AAYD L A + + ++A H V ++ L G
Sbjct: 237 NDAIPSVGGDTLWASGYAAYDKLSPAFQKFLDGKTAIYRSAHQYVDPENPL-----KGPK 291

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQA 240
Y+ P+V+ HP TG L + R I G++ ES+ LE L +
Sbjct: 292 YV-----EREHPIVRTHPATGWKFLFVNRSMTVRIVGLEPEESKTILEYLFVSVEYKN 343

Query: 241 PRVHAH-QW-----AAGDVVVDNRCLLHRAEPWD 269
+ W G +WNR H A WD
Sbjct: 344 LDIQVRFNWRPTKEGLGTSAIWDNRASQHFHFA-VWD 377

>ref|XP_001905437.1| hypothetical protein [Podospira anserina S mat+]
emb|CAP65678.1| unnamed protein product [Podospira anserina S mat+]
Length = 375

Score = 58.9 bits (141), Expect = 8e-07, Method: Compositional matrix adjust.
Identities = 67/278 (24%), Positives = 110/278 (39%), Gaps = 34/278 (12%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN--DQOI 58
A + +TP +G + G+ L+ L+D L + +++F Q + ++Q
Sbjct: 80 ALKVINLTPG---IGTEIRGLQLSQLNDIQKDELALLIAERGVVVFRRDQDFKDIEKQK 136

Query: 59 TFAKRFGA--IERIGGGDIVAISNVKADGTVRQHSAPWDDMMKVIVGN---MAWHADS 112
F + FG I +G + + + S E+ + + GN +H+D
Sbjct: 137 EFGRYFGPLHIHPVGA---HVKESQELHNIYLGSDNEYRNR--GNRLTTTGYHSDV 189

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+Y + + VP GG T + AAY L +AL+ A HS
Sbjct: 190 SYERQPPGITILTLLSVPTGGDTAWESQTAAYARLSPPIQALLENLRAEHS----- 241

Query: 173 GHVQQAGSAYIGYGMDTTATPLR---PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESER 228
G Q G+ G+ P++ P+V+VHP TG+ +L + I G+ ESE
Sbjct: 242 GFPQAEGARRD--GLFVRREPVKTEHPVIRVHPATGQKALFVNPGFTKRIVGLKDEESEA 299

Query: 229 FLEGLVDWACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
L+ L +W G V +WNR H A
Sbjct: 300 LLKLLFHHITFGQDFQVRVKWEEGTVALWDNRVTSHTA 337

>emb|CAY25764.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 58.9 bits (141), Expect = 8e-07, Method: Compositional matrix adjust.
Identities = 34/102 (33%), Positives = 55/102 (53%), Gaps = 18/102 (17%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167

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      WH D + + VVP GG T FA YD L + + + V
Sbjct: 181 WHHDIGFENNTSDYTSIMRVVPEYGGDTVFASAYEVYDRLSAPYQKFLEGLTCTFRPVG 240

Query: 168 SQSK-----LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETG-RPSLLIGRHAHAIPGM 221
      + L V + IG + T + P+++ +P TG R +G HA + +
Sbjct: 241 FEEDPEVAHLYAVPRGSPVNIGPSL----TAIHPMLRSNPVTGWRSVFGVGHHAQRVNEL 296

Query: 222 DAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPR 274
      AES++ L+ L D + + +W D+ VWDNR + H A +D+ PR
Sbjct: 297 TEAESQKLLKWLSDLITENHDLQLRMKWGVNDLAVWDNRVAVYHTAT-YDYDGPR 349

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>ref|XP_001258197.1| alpha-ketoglutarate-dependent taurine dioxygenase [Neosartorya fischeri NRRL 181]
gb|EAW16300.1| alpha-ketoglutarate-dependent taurine dioxygenase [Neosartorya fischeri NRRL 181]
Length = 396

Score = 58.5 bits (140), Expect = 9e-07, Method: Compositional matrix adjust.
Identities = 64/257 (24%), Positives = 98/257 (38%), Gaps = 16/257 (6%)

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Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERIGGG 73
      +G + GV+LA L+DA L ++ F Q D Q K FG + R
Sbjct: 95 IGTEIHGVNLARLNDARDDLARLIAVRGVVFFRNQKDFDIDAQRELKGYFGTLHRHATT 154

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVG 133
      + ++ V ++ D + + WH+D TY P G
Sbjct: 155 AVPKKKGLEDVHV--YTGDNSSDQRALFSPSFLWHS DVTYEVQPPSYTSLKVLGTGPPRG 212

Query: 134 G--RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTA 191
      G T ++ AAYDAL + + +A H+ ++Q + S +G +
Sbjct: 213 GGGDTLWSSQYAAAYDALSSHMQNYLKGLTALHT-----ANMQASDSRALGRTIRREP 264

Query: 192 -TPLRPLVKVHPETGRPSLLIGR-HAHAIPGM DAAESERFLEGLVDWACQAPRVHAH-QW 248
      T PL++ +P TG SL I G+ ES+ + L + HA QW
Sbjct: 265 ITTEHPLIRTNPVTGWNSLFFNPGFVTKIVGIPKTESDAIIRYLTEVVATTQEAHARFQW 324

Query: 249 AAGDVVVWDNRCLLHRA 265
      DV +WDNR H A
Sbjct: 325 GENDVALWDNRRTTNHSA 341

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>tpe|CBF78371.1| TPA: TfdA family taurine dioxygenase, putative (AFU_orthologue; AFUA_1G17170) [Aspergillus nidulans FGSC A4]
Length = 372

Score = 58.5 bits (140), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 42/166 (25%), Positives = 75/166 (45%), Gaps = 9/166 (5%)

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Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
      WH+D ++ V + A+ +P GG T +A YD L A + + +A H
Sbjct: 172 GWHSDISFERVPSDYAMLKIHTLPETGGDTLWASGYEVYDRLSPEMAAFLERLTATHDAT 231

Query: 167 Y---SQSKLGHVQQAG--SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPG 220
      + +LG+ + G + + +G + TA + P+++ +P TG S+ + + I G
Sbjct: 232 FFHDEARRLGNPLRKGIKIRGSPNLHGEELTA--VHPVIRTNPVTGWKSVYVKNKGFTKIRING 289

Query: 221 MDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
      + ES+ L+ L + Q +W D+ +WDNR H A
Sbjct: 290 VTKDESDVLLQYLFNLVTQNHDAQVRFKWRKNDMAIWDNRSTWHCA 335

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>emb|CAY25795.1| alpha-KG-dehydrogenase [uncultured bacterium]

emb|CAY25800.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 58.5 bits (140), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 34/108 (31%), Positives = 57/108 (52%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ + ++A+LIF GQ ++++QQ+ FA FG E GG +V +SN+
Sbjct: 16 IESGMDKYAVLIFHGQDITDEQQALAFALNFGERENPRGGSVVKPEDSRLQTGLNDVSNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG P D + + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 RDG-----KPLPRDSRINLFNLGNCLWHSDSSFRPIPAKFSLLSARVV 118

>ref|XP_002490893.1| Fe(II)-dependent sulfonate/alpha-ketoglutarate dioxygenase,
involved in sulfonate catabolism for use [Pichia
pastoris GS115]
emb|CAY68613.1| Fe(II)-dependent sulfonate/alpha-ketoglutarate dioxygenase,
involved in sulfonate catabolism for use [Pichia
pastoris GS115]
Length = 417

Score = 58.5 bits (140), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 74/282 (26%), Positives = 109/282 (38%), Gaps = 45/282 (15%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
A ITP LG+ V GV L+ L D AL A Q +++F Q L D+ +
Sbjct: 98 AHKISNITPK---LGSKEGVQLSQLTPDQKDDLALFVA--QRGVVVFRDQDL-RDKDLG 151

Query: 60 FAKRFGAIERIGGGDIVAISNVKADG-----TVRQHSPAEWDDMMKVI-VGNMAWHADST 113
K+FG + G I S +G T ++ P + + + WH+D T
Sbjct: 152 EVKKFG--QHFGPLHIHQTSQA-PEGYPEFHITFKRAGPP---NTFRNKISAPGWHSDVT 205

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQS 170
Y A F P GG T FAD AY+ L + + + HS
Sbjct: 206 YELQPAGITFFGLIEGPEAGGDTLFAAIEAYERLSPSFQKFLDGLRLIHSARAQAEDSL 265

Query: 171 KLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAES---- 226
K G +Q+ T+ + PL++ HP + S+ I G+ ES
Sbjct: 266 KKGSIQRK-----KFTSETVHPLIRYHPVLNKRISIFAKAFGTKIVGLKQEEEDLIL 316

Query: 227 ---ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+RF+ +D +A + G VV WDNR + H A
Sbjct: 317 NFIQRFIATALDLQLRA-----SYEPGTVVAVDNRVVFHSA 352

>emb|CBJ20076.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 140

Score = 58.5 bits (140), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 42/143 (29%), Positives = 66/143 (46%), Gaps = 9/143 (6%)

Query: 117 VMAQGAVFSAEVVPAVG----GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
+ A+ ++ SA +P+ G T AD+R A+DAL + + H + S+S++
Sbjct: 3 IPAKCSLLSARELPSPSPMGDGETELADLRATAWDALPATRKGELEGLVVEHGIFRSRSRI 62

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG 232
G Y A LV+ HP +GR SL + HA I G +E
Sbjct: 63 GFADFNDIYRRLPPVPQA-----LVRHHPGSGRTSLYLASHASHIVGWPVERGRARIEE 117

Query: 233 LVDWACQAPRVHAHQWAAGDVVV 255

L+ +A Q V+ H+WA GD+V+
Sbjct: 118 LIAFAAQPQFVYRHRWAVGDLVI 140

>emb|CBJ18797.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 58.5 bits (140), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 53/112 (47%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRP-LVKVH 201
AAYDALD T+ + HS ++S+ +G + P+R +V+ H
Sbjct: 1 AAYDALDAETKVEIEGMVCEHSQMFSRQLIGFTDFTDEERERFK-----PVRQCMVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P TGR SL + HA I G E+ FL LV+ A Q V+ H+W D+
Sbjct: 55 PVTGRKSLYLSSHAGTIIGWPQPEARAFRLDLVEHATQREFVYTHKWRVDDL 106

>emb|CAY27301.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 106

Score = 58.5 bits (140), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 44/124 (35%), Positives = 56/124 (45%), Gaps = 18/124 (14%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR 195
T FADMRAAYDALDE + + HS +YS+ KL + + R
Sbjct: 1 TEFADMRAAYDALDEQLKHQIEDLVCLHSNMYSRGKL-----ELADFTEEERRVFKPVRR 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
LV+ HP T R SL + HA I GM E+ L L ++A P V+
Sbjct: 56 RLVRHPVTRRKSLFLSAHAGEIEGMSIPEARMLLLLDLTEFA-DMP-----VM 102

Query: 256 WDNR 259
WDNR
Sbjct: 103 WDNR 106

>dbj|BAF81037.1| 2,4-D dioxygenase [Bradyrhizobium sp. M75-VN10-2W]
Length = 104

Score = 58.5 bits (140), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 36/104 (34%), Positives = 49/104 (47%), Gaps = 5/104 (4%)

Query: 153 RALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIG 212
RA + HSL+YS+ LG + Y L+ LV+ HP GR SL +
Sbjct: 6 RAEIDDMICEHSLMYSRGSLSGLFD-----YTEEEKQMFKPVLRVLRTHPVHGRKSLYLS 60

Query: 213 RHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVW 256
HA AI GM E+ L L + A Q V+ H+W D+V+W
Sbjct: 61 SHAGAIRGMSMPEARLLLLRDLTEHATQPEFVYVHKWTVHDLVMW 104

>ref|ZP_04982597.1| hypothetical oxidoreductase [Mycobacterium tuberculosis str.
Haarlem]
gb|EBA44110.1| hypothetical oxidoreductase [Mycobacterium tuberculosis str.
Haarlem]
Length = 289

Score = 58.5 bits (140), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 66/282 (23%), Positives = 104/282 (36%), Gaps = 52/282 (18%)

Query: 12 GATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIG 71

```

      G  LGA VTGV   LDD      +      + L++   H S  + I   +  G I
Sbjct: 7  GEGLGAQVTGVDPKNLDDITTEIRDIVYTNKLVVLKDVHPSREFIKLGRIIGQI----- 62

Query: 72  GGDIVAISNVKADGTVRQHSPA-EWDDMMKVIVGNMA-----WHADSTYMPVMA 119
              V  + P      +D  ++ V  +              WH D  +MP
Sbjct: 63  -----VPYYEPMYHHEDHPEIFVSSTEEGQGVPKTGAFWHIDYMFMPPEF 107

Query: 120  QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ-QA 178
              ++      VP      T F D+  + +L  A      +R      V  +      H++  +
Sbjct: 108  AFSMVLPLAVPGHDRGTYFIDLARVWQSLPAA-----KRDPAAGTVSTHDPRRHIKIRP 161

Query: 179  GSAYIGYG-----MDTTATPLR-PLVKVHPETGRPSLLI---GRHAHAIPGMDAAESERF 229
              Y  G      ++ T  P++ P V  HP+TG+  L I  G      +  + E
Sbjct: 162  SDVYRPIGEVWDEINRTTPPIKWPTVIRHPKTGQEILYICATGTTKIEDKDGPNVDPEVL 221

Query: 230  LE-----GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE 266
              E      G +D  Q+P +H  +  GD+ +WDNR L+HRA+
Sbjct: 222  QELMAATGQLDPEYQSPFIHTQHYQVGDITLWDNRVLMHRAK 263

```

>ref|XP_681863.1| hypothetical protein AN8594.2 [Aspergillus nidulans FGSC A4]
gb|EAA60628.1| hypothetical protein AN8594.2 [Aspergillus nidulans FGSC A4]
Length = 774

Score = 58.5 bits (140), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 42/165 (25%), Positives = 75/165 (45%), Gaps = 9/165 (5%)

```

Query: 108  WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
              WH+D ++  V  +  A+      +P  GG T +A      YD L      A  +  + +A H  +
Sbjct: 173  WHSDISFERVPSDYAMLKIHTLPETGGDTLWASGYEVYDRLSPEMAAFLERLTATHDATF 232

Query: 168  ---SQSKLGHVQQAG--SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGM 221
              +LG+  + G  +  + +G + TA  + P+++ +P TG  S+  +  +      I G+
Sbjct: 233  FHDEARRLGNPLRKGIRGSPLNHGEELTA--VHPVIRTNPVTGWKSVYVNGGFTKRINGV 290

Query: 222  DAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
              ES+  L+ L +  Q      +W  D+ +WDNR  H A
Sbjct: 291  TKDESDVLLQYLFNLVTQNHDAQVRFKWRKNDMAIWDNRSTWHCA 335

```

>emb|CAY25719.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY25734.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY25773.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 58.2 bits (139), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 34/108 (31%), Positives = 56/108 (51%), Gaps = 18/108 (16%)

```

Query: 35  LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
              + A  ++A+L+F  Q  +S+DQQ+ FA+ FG  E  GG  +              +SN+
Sbjct: 16  IEAGMDKYAVLLFRDQDVSDQQLVFARNFGERENARGGTVTKKEDYRLTSGLNDVSNLG 75

Query: 83  ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
              DG      +P  D      +  +GN  WH+DS++ P+ A+ ++ SA VV
Sbjct: 76  KDG-----NPLPRDHRTHLFLNLGNCLWHSDDSSFRPIPAKFSLLSARVV 118

```

>ref|XP_002486237.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Talaromyces stipitatus ATCC 10500]
gb|EED13999.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Talaromyces stipitatus ATCC 10500]
Length = 349

Score = 58.2 bits (139), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 63/274 (22%), Positives = 102/274 (37%), Gaps = 52/274 (18%)

```
Query: 15  LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERI---- 70
      +G + GV L+ LD+      L      + ++ F Q L+ + Q F K FG ++ I
Sbjct: 56  IGTELQGVQLSQLDEKQKNELALLVAERGTVFFRDQDLTLEGQHEFTKHFQIVDLIHLSF 115

Query: 71  -GGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV 129
      G DI I      GT+ +      ++      +H+D ++      +
Sbjct: 116 YGRLDI-DIPLFSKTGTLTKSIH-----VIAFAEFHSDHSFEINPPSYTLRMVKT 165

Query: 130 PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT 189
      P GG T +      A +D L      +      HS      + + + + G+ +
Sbjct: 166 PEYGGDTIWTSQTALFDKLSPTFQKTFEGLHGVHS--SEHTYINTINRGGTTTF----- 216

Query: 190 TATPLR---PLVKVHPETGRPSLLIGR----HAAHAI PGMDAAESERFLEGLVDWACQAPR 242
      P+R PLV+ HP T + +L      H + G +A + FL      R
Sbjct: 217 -RLPVRREHPLVRTHPVTKQKALFYNPAPFVIHIAELKGFALHTLNFL-----R 264

Query: 243 VHAH-----QWAAGDVVWVDNRCLLHRAEP 267
      H H      QW AG + +WDNR +HRA P
Sbjct: 265 EHLHSADDLTVRWQWEAGSIALWDNRVAVHRAVP 298
```

>gb|AA039411.1| TfdA alpha-like protein [uncultured bacterium]
Length = 119

Score = 58.2 bits (139), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 35/108 (32%), Positives = 55/108 (50%), Gaps = 18/108 (16%)

```
Query: 35  LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
      + A ++A+L+F GQ +S+DQQ+ FA FG E GG +      +SN+
Sbjct: 16  IEAGMDKYAVLVFHGQDISDDQMAFAPNFGKRENARGGTVTKKEDYRLSSGLNDVSNLG 75

Query: 83  ADGTVRQHSPAEDDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
      DG      P D      + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76  KDG-----KPLPKDHRTHLNLGNCLWHSDDSSFRPIPAKFSLLSARVV 118
```

>gb|ABR27336.1| TfdA [uncultured bacterium]
Length = 99

Score = 58.2 bits (139), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 28/64 (43%), Positives = 36/64 (56%)

```
Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
      PL++ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+
Sbjct: 36  PLIRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQPKFVYRHSWKVGDLVM 95

Query: 256 WDNR 259
      WDNR
Sbjct: 96  WDNR 99
```

>gb|ADC33958.1| TfdA-like protein [uncultured bacterium]
>gb|ADC33961.1| TfdA-like protein [uncultured bacterium]
Length = 131

Score = 58.2 bits (139), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 40/131 (30%), Positives = 60/131 (45%), Gaps = 5/131 (3%)

```
Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK---LGHVQQAGSAYIGYGMTTAT 192
      T F DM YDAL      +      R A H + +++++ + + Y      T
```

Sbjct: 1 TEFCDMSMVYDALPAELKRAAEGRYAIHHVSKTRNRRVTISPDRPGAKDYERRATETHE 60
Query: 193 PLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRV-HAHQWAA 250
+PLV+ HPETGR +L I R I M E++ L+ L + + + H W
Sbjct: 61 VRQPLVRTHPETGRQALYISPRFTIGIADMPDEEAQALLDKLFATFVVRERKFQYRHTWRD 120
Query: 251 GDVVVWDNRCL 261
GD+V+WDNRC+
Sbjct: 121 GDLVMWDNRCV 131

>ref|XP_001880709.1| predicted protein [Laccaria bicolor S238N-H82]
gb|EDR08484.1| predicted protein [Laccaria bicolor S238N-H82]
Length = 359

Score = 58.2 bits (139), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 67/278 (24%), Positives = 116/278 (41%), Gaps = 30/278 (10%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
A+ +TP +G + GV L L D L + ++ F Q + QQ+ A
Sbjct: 41 AKNVNHLTPA---IGTEIEGVDLRQLTDVQKDELALLVAERGVVFFRDQEIDIHQQLDLA 97
Query: 62 KRFGAIER-----IGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMP 116
+ FG + + I + + V D + R+ P+ + + WH+D +Y
Sbjct: 98 RYFGPLHKHATTPIPRNGLEEVHVYNDAS-RRDPSPAFSKL-----ELWHSVSYE- 148
Query: 117 VMAQGAVFSAEVV--PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
+ ++ S +++ P VGG T ++ A Y +L + + +A HS V ++
Sbjct: 149 -LQPPSITSLKLITGPEVGGDTLWSSGYALYSSLSPLGLQTYLEGLTAVHSV--AQADG 204
Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL 233
+ AG ++T + PLV+VHP T S+ + I G+ AES+ L L
Sbjct: 205 NRAAGLPVRRQEIET----IHPLVRVHPATQWKSVMYVNPFGFTRRIVGVPKAESDAVLTF 260
Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDF 270
+ P +W + WDNR + H A +DF
Sbjct: 261 FRQINENPDHQVRFWRPNSIAFWDNRIVTHSAT-FDF 297

>emb|CBJ19162.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19172.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19173.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19177.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19179.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19190.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19193.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 104

Score = 58.2 bits (139), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 56/110 (50%), Gaps = 7/110 (6%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE 203
AYDA+DE +A + A H +S+ LG + ++ + P+V+ P
Sbjct: 2 AYDAMDEDMKAFLDPLEAEHFHAFHSRELLGAMPTQEER-----NSIPPAVWPIVR-KPA 54
Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL IG HAH + GM A+ L L++ A Q V+ H+W+ GD+
Sbjct: 55 TGRRSLFIGAHAKVIGMPLAQGRMLLLDLLEHATQRQFVYRHEWSPGDL 104

>emb|CAY25745.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 58.2 bits (139), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 32/108 (29%), Positives = 57/108 (52%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F Q +S+DQQ+ FA+ FG E GG + ++N+
Sbjct: 16 IEAGMDKYAVLLFRDQDVSDQQLVFARNFGERENARGGTVTKKEDYRLTSGLNVDVTNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG +P D ++ +GN WH+D+++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPPRPDPHTRLFNLGNCLWHSNDSFRPIPAKFSLLSARVV 118

>emb|CAY25747.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 58.2 bits (139), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 34/108 (31%), Positives = 56/108 (51%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F Q +S+DQQ+ FA+ FG E GG + ++SN+
Sbjct: 16 IEAGMGKYAVLLFRDQDVSDQQLVFARNFGERENARGGTVTKKEDYRLTSGLNVDVSNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTLFLNLGNCLWHSNDSFRPIPAKFSLLSARVV 118

>ref|XP_001909009.1| hypothetical protein [Podospira anserina S mat+]
emb|CAP70141.1| unnamed protein product [Podospira anserina S mat+]
Length = 372

Score = 58.2 bits (139), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 59/254 (23%), Positives = 96/254 (37%), Gaps = 33/254 (12%)

Query: 41 QHALLIFPGQ-HLSNDQQITFAKRFGAI-----ERIGGGDIVAISNVK 82
Q ++ F Q L+N+ Q R G + ER GGD IS +
Sbjct: 79 QRGVVFRAQDELTLNELQKKLILRLGELTGRPATSGLHIHPLLNSERELGGDDPEISTIS 138

Query: 83 ADGTVRQHSP-AEWDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRCTCFADM 141
+ + ++ A D++ WH+D + PV A +P GG T +A
Sbjct: 139 SIQNKKFYARGAIADELSPKKQSTGQWHSIDAFEPVPADYTSRLVELPTTGGDTLWASG 198

Query: 142 RAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI-----GYGMDTTATPL 194
YD L E + + ++ + Q V +A + + T +
Sbjct: 199 YELYDRLSEPYQKFLESL----TVTFQQPGFNKVAEAGFKLYDKPRGAPENIGTELKAV 254

Query: 195 RPLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWA-AG 251
P+++ +P TG SL +G H I G+ ES+ L +D + + QW
Sbjct: 255 HPVIRTNPTVGWKSFLFPVGGHVKHINGVTEEESKALLTWFLDLVYKNHDLTVRLQWKNKN 314

Query: 252 DVVVWDNRCLLHRA 265
D+ +WDNR H A
Sbjct: 315 DIAIWDNRSTFHTA 328

>emb|CAY25751.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 58.2 bits (139), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 33/108 (30%), Positives = 58/108 (53%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F GQ ++++QQ+ FA FG E GG + ++SN+

Sbjct: 16 IEAGMDKYAVLLFRGQDITDEQQALAFALNFGEREHARGGTVTKKEDYRLTSGLNDVSNLG 75

Query: 83 ADGTVRQHSPAEDDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

DG +P D +++ +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 76 KDG-----NPLPRDHRTRLNLGNCLWHSDDSSFRPIPAKFSLLSARVV 118

>ref|YP_003467274.1| Pyoverdine biosynthesis protein [Xenorhabdus bovienii SS-2004]

emb|CBJ80487.1| Pyoverdine biosynthesis protein [Xenorhabdus bovienii SS-2004]

Length = 299

Score = 58.2 bits (139), Expect = 2e-06, Method: Compositional matrix adjust.

Identities = 49/199 (24%), Positives = 79/199 (39%), Gaps = 34/199 (17%)

Query: 109 HADSTYMPVMAQGAVFSAEVVP--AVGGRTCFADMRAAY-DALDEATRALVHQRSARHSL 165

H D Y P + + +F P + GGRT F D DA D+ + ++

Sbjct: 102 HWDGMYKPTIPEFQIFHCVSAPEASQGGRTTFVDTEQLIADASDDERHEWKNT-----TI 156

Query: 166 VYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPE-----TGRPSLLIGR 213

Y S++ H YG + + PL+ +HP+ TG+

Sbjct: 157 TYRTSRVTH-----YGGEVVS---PLICLHPDGKKWVMRYNEPMTGKDDKYADH 202

Query: 214 HAHAI PGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLP 273

H I G+ + + F + L + + +AHQW +GD+V+ DN LLH E + P

Sbjct: 203 HLLTIHGLSIEQQKEFEKNLNFRLYDSRYFYAHQWQSGDLVISDNFTLLHGREAFITHSP 262

Query: 274 RVMWHSRLAGRPETEGAAL 292

R + + G P E +

Sbjct: 263 RHLQRVHVHGTVPVCENLSF 281

>gb|AAO39410.1| TfdA alpha-like protein [uncultured bacterium]

Length = 119

Score = 58.2 bits (139), Expect = 2e-06, Method: Compositional matrix adjust.

Identities = 34/110 (30%), Positives = 56/110 (50%), Gaps = 18/110 (16%)

Query: 33 AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISN 80

A + A ++A+L+F Q +++DQQ+ FA+ FG E GG + +SN

Sbjct: 14 ADIEAGMDKYAVLLFRDQDITDDQQLIFARNFGERENARGGTVTKKEDYRLTSGLNDVSN 73

Query: 81 VKADGTVRQHSPAEDDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

+ DG P D + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 74 LGKDG-----KPLPRDHRTHLNFNLGNCLWHSDDSSFRPIPAKFSLLSARVV 118

>emb|CBJ18761.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]

Length = 106

Score = 57.8 bits (138), Expect = 2e-06, Method: Compositional matrix adjust.

Identities = 39/115 (33%), Positives = 54/115 (46%), Gaps = 13/115 (11%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKV-- 200

A YDALD+ T+ V + HS +YS++ LG D +P+ +V

Sbjct: 1 AGYDALDQETKDRVADQICEHSQLYSRALLGFTD-----FTDEERERFKPVRQVPV 51

Query: 201 --HPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

HP GR SL + HA I G E+ FL L + A Q V++HQW GD+

Sbjct: 52 CTHPGHGRKSLYLSSHAGGIVGWPVPEARAFRLDLNEIATQRQFVYSHQWRVGD 106

>emb|CBJ19182.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]

Length = 104

Score = 57.8 bits (138), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 56/110 (50%), Gaps = 7/110 (6%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE 203
AYDA+DE +A + A H +S+ LG + ++ + P+V+ P
Sbjct: 2 AYDAMDEDMKAFLDPLEAEHLAFHSRELLGAMPTQEER-----NSIPPAVWPIVR-KPA 54

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL IG HAH + GM A+ L L++ A Q V+ H+W+ GD+
Sbjct: 55 TGRRSLFIGAHAKVIGMPLAQGRMLLLDLLEHATQRQFVYRHEWSPGDL 104

>ref|ZP_03790613.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pakistan 9]
gb|EEH28823.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei Pakistan 9]
Length = 147

Score = 57.8 bits (138), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 29/70 (41%), Positives = 37/70 (52%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
P+V++HPETG SLL+G +A D +S R E L + WAAGDV +
Sbjct: 44 PVVQIHPETGEKSLLLGHYAQRFFVQYDTHDSNRLYEILQAHITRLENTVRWHWAAGDVAI 103

Query: 256 WDNRCLLHRA 265
WDNR H A
Sbjct: 104 WDNIRSTQHYA 113

>gb|ADC33943.1| TfdA-like protein [uncultured bacterium]
Length = 131

Score = 57.8 bits (138), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 40/131 (30%), Positives = 60/131 (45%), Gaps = 5/131 (3%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK---LGHVQQAGSAYIGYGMDDTTAT 192
T F DM YDAL + R A H + +++ + + Y T
Sbjct: 1 TEFCDMSMVYDALPAELKRAAEGRYAIHVSKTRNRRVTISPDRPDAKDYYERRATETHE 60

Query: 193 PLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRV-HAHQWAA 250
+PLV+ HPETGR +L I R I M E++ L+ L + + + H W
Sbjct: 61 VRQPLVRTHPETGRQALYISPRFTIGIADMPDEEAQALLDKLFATFVREKRFQYRHTWRD 120

Query: 251 GDVVVWDNRCL 261
GD+V+WDNRC+
Sbjct: 121 GDLVMWDNRCV 131

>ref|XP_001522837.1| hypothetical protein MGCH7_ch7g935 [Magnaporthe oryzae 70-15]
gb|EAQ71528.1| hypothetical protein MGCH7_ch7g935 [Magnaporthe oryzae 70-15]
Length = 437

Score = 57.8 bits (138), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 60/261 (22%), Positives = 103/261 (39%), Gaps = 47/261 (18%)

Query: 41 QHALLIFPGQ-HLSNDQQITFAKRFGAI-----ERIGGGD--IVAI 78
Q ++ F Q +L+ND Q R G + E GG D I I
Sbjct: 81 QRGVVFRAQDNLTNDLQKKLILRLGELTGRPKTSGLHIHPLNAERETYGDDNEISTI 140

Query: 79 SNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCF 138
S+ + D ++ + + D++ WH+D + PV A +P GG T +
Sbjct: 141 SSAQNDKLYKK-TWTQPDELSPKKQSTAQWHSIDAFEPVPADYTSRLRLTELPKTGGDTLW 199

Query: 139 ADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM-----DTT 190
A YD + + + S+ ++Q + + A G+ + +
Sbjct: 200 ASGYEIYDKISAPYQKFLETL----SVTFAQKRFNEIADAN----GFSLYSQPRGAPENV 251

Query: 191 ATPLR---PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH 246
T LR PLV+ +P TG S+ +G H + G+ ES+ L+ +D + +
Sbjct: 252 GTDLRAVHPLVRTNPVTGWKSIFPVG--GHHVNGLTDEESDGLLKWYLDLVYRNHELQTR 309

Query: 247 -QW-AAGDVVVWDNRCLLHRA 265
+W D+ +WDNR + H A
Sbjct: 310 LKWRNKNDIAIWDNRSVFHTA 330

>emb|CAY25729.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 57.8 bits (138), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 34/108 (31%), Positives = 56/108 (51%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F Q +S+DQQ+ FA+ FG E GG + +SN+
Sbjct: 16 IEAGMDKYAVLLFRDQDVSDQQLVFARNFGEREDARGGTVTKKEDYRLTSGLNVDVSNL 75

Query: 83 ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLFLNCLWHS DSSFRPIPAKFSLLSARVV 118

>gb|AAO39412.1| TfdA alpha-like protein [uncultured bacterium]
emb|CAY25728.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY25733.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY25774.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 57.8 bits (138), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 34/110 (30%), Positives = 56/110 (50%), Gaps = 18/110 (16%)

Query: 33 AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISN 80
A + A ++A+L+F Q +++DQQ+ FA+ FG E GG + +SN
Sbjct: 14 ADIEAGMDKYAVLLFRDQDITDDQQLIFARNFGERENARGGTVTKKEDYRLTSGLNVDVN 73

Query: 81 VKADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
+ DG P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 74 LGKDG-----KLPKDHRTHLFLNCLWHS DSSFRPIPAKFSLLSARVV 118

>gb|EFQ35578.1| TfdA family Taurine catabolism dioxygenase TauD [Glomerella
graminicola M1.001]
Length = 395

Score = 57.8 bits (138), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 41/168 (24%), Positives = 76/168 (45%), Gaps = 10/168 (5%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARH---- 163
WH+D T+ PV + ++ +P GG T +A YD + + + + +A +
Sbjct: 182 WHSDITFEPVPSDYSLLRLTELPKTGGDTLWASGYELYDRVSKPLQGFLETLTATYAQP 241

Query: 164 -SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL-IGRHAHAIPGM 221
+ ++ ++A A G A + P+++ +P TG S+ +G+H I G+
Sbjct: 242 FNATAKKNFSLFREARGAPENVGELLEA--VHPVIRTNPVTGWKSIFAVGQHVSRINGL 299

Query: 222 DAAESERFLEGLVDWACQAPRVHA-HQWA-AGDVVVWDNRCLLHRAEP 267

ES FL+ V + + ++W D+ +WDNR + H A P
Sbjct: 300 SEDESRHFLDWFVQLIVENHDLQVRNRWQNVNDIAIWDNRSVYHAATP 347

>ref|XP_956199.1| hypothetical protein NCU01562 [Neurospora crassa OR74A]
emb|CAC18150.2| related to 2, 4-dichlorophenoxyacetate dioxygenase [Neurospora crassa]
gb|EAA26963.1| predicted protein [Neurospora crassa OR74A]
Length = 356

Score = 57.8 bits (138), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 68/300 (22%), Positives = 122/300 (40%), Gaps = 56/300 (18%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
T+ + T GA V G+ L + +I L++ ++F++ F
Sbjct: 17 TITVKELHPTFGAEVLGIQWGDNGVISDEQLQELRDYGFILRATPLTDSTHVSFSRLF 76

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSP-----AEWDDMMKVIV-----GN 105
+ G + IS G V ++ P + D + I+ N
Sbjct: 77 AS-----GPLDDISRLPPGRVPRYPHLELFDASNLSDGAILDPSSSPRAMLLRAN 130

Query: 106 MAWHADSTYMPVMAQGAVFSAEVPVPA-----VGGRTCFADMRAAYDALD-EATRALV 156
+WH+D Y P + ++ A +P+ + G T FAD R A++ L E R L+
Sbjct: 131 SSWHSDLAYNPRRSSYSLRAVELPSREPGEMGEIEGNTFADSRTAWEELAAEKKRELL 190

Query: 157 HQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPL--RPLVKVHPETGRPSLLIGRH 214
+ + VY+ + H ++ G+ ++ P+ +V+ H E+GR +L +G +
Sbjct: 191 ---TKDWTGVYNAA---HSRKLGAPEYFKDVNPEEGPIARHKVVQEHVESGRMNLVCGAY 244

Query: 215 -----AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWA-AGDVVVDNRCLLHRA 265
+PG SE ++ L + V + +W GD+V+WDNR +LHRA
Sbjct: 245 LWRLEDGEGKTVPG-----SEGIKFLNEHVANKSFVASVRWERPGDLVIWDNRVLHRA 299

>gb|AA039408.1| TfdA alpha-like protein [uncultured bacterium]
Length = 119

Score = 57.8 bits (138), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 35/108 (32%), Positives = 55/108 (50%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F GQ +S+DQQ+ FA FG E GG + +SN+
Sbjct: 16 IEAGMDKYAVLVFHGQDISDDQQMAFALNFGKRENARGGTVTKKEDHRLSSGLSDVSNLG 75

Query: 83 ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVPV 129
DG P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----KPLPKDHRTHLFNLGNCLWHS DSSFRPIPAKFSLLSARVV 118

>ref|YP_001265314.1| taurine catabolism dioxygenase TauD/TfdA [Sphingomonas wittichii RW1]
gb|ABQ71176.1| Taurine catabolism dioxygenase TauD/TfdA [Sphingomonas wittichii RW1]
Length = 308

Score = 57.8 bits (138), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 68/280 (24%), Positives = 118/280 (42%), Gaps = 30/280 (10%)

Query: 5 TLQITPTGATLGATVTGVHLATLD-DAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+++ G G V G+ +D +A A L W++ L++F G ++ + QI ++
Sbjct: 4 SVETLREGLGFGKQVVGRLARQDIDREAVRAELRDHWIRGLVVFVRGSEVTPEFQIALSRV 63

Query: 64 FGAIE-----RIGGGD----IVAISNVKADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTY 114

FG +E + D I +S+ +G E D + V + WH+D +
Sbjct: 64 FGELEVHPIPELRSADHPELITLVSDKDEGLF-----EVDGVESVAF--LPWHSDLIF 115

Query: 115 MPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ--SKL 172
+ + G + +A+ + + GG+T F D AY+ L E +A + + L + S+
Sbjct: 116 VDSINHGGLLTAKTIASWGGQTGFIDQVQAYELLPETLKAIEGLEIVYQLCVNPGGSRV 175

Query: 173 GHVQQAGSAYIGYGMDTTATPL-----RPLVKVHPETGRPSLLIGRH-AHAIPGMDA 223
G + + G + L P+V V P+TGR L + A I G D
Sbjct: 176 GTRSRVRTILTGFDEKSVGPRLDADYPPVHPVVFVQPDTRKVLNVSPFGALHILGHDD 235

Query: 224 AESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH 263
L LVD P + HQW +++++WDN + H
Sbjct: 236 EAGHALLGRLVDHLTACP-AYFHQWQPSEMLLDWNWRMAH 274

>emb|CAY25765.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 57.8 bits (138), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 34/108 (31%), Positives = 55/108 (50%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F Q +S DQQ+ FA+ FG E GG + +SN+
Sbjct: 16 IEAGMDKYAVLLFRDQDVSGDQQLVFARNFGKRENARGGTVTKKEDYRLASGLNDVSNLG 75

Query: 83 ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAE V 129
DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDPRTHLFNLGNCLWHS DSSFRPIPAKFSLLSARV 118

>ref|XP_001555605.1| hypothetical protein BC1G_05880 [Botryotinia fuckeliana B05.10]
gb|EDN25174.1| hypothetical protein BC1G_05880 [Botryotinia fuckeliana B05.10]
Length = 363

Score = 57.8 bits (138), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 70/272 (25%), Positives = 107/272 (39%), Gaps = 30/272 (11%)

Query: 29 DAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGAIER---IGGGDIVAISNVK-A 83
DA L Q + +FPGQ +L+ Q R G + G +I ++ +
Sbjct: 70 DAIIRDLAITISQRGVCVFPQGKNLTVADQKLLCHRLGQLTTRPYTSGLNHPLNQTELP 129

Query: 84 DGTVRQHSPA EWDDMMKVI-VGNMA-----WHADSTYMPVMAQGAVFSAE V 130
DGT+ D K +V WH D +Y + A + +V P
Sbjct: 130 DGTIDAELTTLARDPKKKLVQQAGFGKKEKKQSHSDGWHTDCSYENIPADYTMLHMKVTP 189

Query: 131 AVGGRTCFADMRAAYDALDEATRALVHQRSAR----HSLVYSQSKLGHVQQAGSAYIGY 185
A GG T FA AYD L + ++ + A H ++ + +G
Sbjct: 190 ASGGDTLFA SAYEAYDLLSPMAKMLERCQATFMPPGHRPENIVDRMWKGPRGAPENVGP 249

Query: 186 GMDTTATPLRPLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH 244
+ T P V+ +P TG SL +G H AI G+ E+ LE L ++
Sbjct: 250 ELRAT----HPAVRTNPVTGWKSLYAMGHHLAIEGLGDLENRMVLELLERLLVDNHQLQ 305

Query: 245 AH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRV 275
+W A D+V+WDNR + H A +D+ RV
Sbjct: 306 LRVKWEADDLVIWDNRVYHCAT-FDYTAKRV 336

>gb|ADI34068.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 2HD5]
Length = 98

Score = 57.8 bits (138), Expect = 2e-06, Method: Compositional matrix adjust.

Identities = 29/64 (45%), Positives = 37/64 (57%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H+W GD+V+
Sbjct: 35 PLVRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQREFVYRHRWNVGDLM 94

Query: 256 WDNR 259
WDNR
Sbjct: 95 WDNR 98

>gb|ADI34071.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 3HD5]
Length = 82

Score = 57.8 bits (138), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 29/64 (45%), Positives = 36/64 (56%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+
Sbjct: 19 PLVRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQREFVYRHSWNVGDLM 78

Query: 256 WDNR 259
WDNR
Sbjct: 79 WDNR 82

>gb|AAO39409.1| TfdA alpha-like protein [uncultured bacterium]
Length = 119

Score = 57.8 bits (138), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 35/108 (32%), Positives = 55/108 (50%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F GQ +S+DQQ+ FA FG E GG + +SN+
Sbjct: 16 IEAGMDKYAVLVFHGQDISDDQQMAFALNFGKRENARGGTVTKKEDYRLSSGLNDVSNLG 75

Query: 83 ADGTVRQHSAPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----KPLPKDHRTHLFNLGNCLWHSDSSFRPIPAKFSLLSARVV 118

>gb|ADC34030.1| TfdA-like protein [uncultured bacterium]
Length = 204

Score = 57.4 bits (137), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 58/221 (26%), Positives = 87/221 (39%), Gaps = 32/221 (14%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQH----SPAEWDDMMKVIVGNMAWHAD 111
QQI FA RFG +E VA S+ G V + SP ++ + AWH D
Sbjct: 1 QQIAFAHRFGQLE----DHPVAGSDPDHPGLVCIYKDLDSPPDFYEN-----AWHCD 48

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
+T+ GAV P VGG T +A+M AY L + + + ARHS+ S
Sbjct: 49 ATWRDCPPMGAVLRYIEGPEVGDTMWANMAKAYADLPDHIKVAIDGLHARHSIEASFGA 108

Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-- 229
+++ + + P+V+ HPETG L + ++ R+
Sbjct: 109 RMPIEKRHALKAQF-----PDAEHPVVRTHPETGEKILFVNAFTTHFTDYHTPDNVRYGQ 163

Query: 230 -----LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
L L+ A +W V +WDNRC+
Sbjct: 164 DYAPGGANLLHYLIGRAAIPEYQVRWRWEFNSVAIWDNRCV 204

>gb|ADC34022.1| TfdA-like protein [uncultured bacterium]
Length = 204

Score = 57.4 bits (137), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 58/217 (26%), Positives = 84/217 (38%), Gaps = 24/217 (11%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYM 115
QQI FA RFG +E VA S+ G V + D N AWH D+T+
Sbjct: 1 QQIAFAHRFGQLE----DHPVAGSDPDHPLVCIYKDL---DSPPDFYEN-AWHCDATWR 52

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
GAV P VGG T +A+M AY L + + + ARHS+ S +
Sbjct: 53 DCPPMGAVLRYIEGPEVGGDTMWANMAKAYADLPDHIKEAIDGLHARHSIEASFGARMPI 112

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF----- 229
++ + + P+V+ HPETG L + ++ R+
Sbjct: 113 EKRHALKAQF-----PDAEHPVVRTHPETGEKILFVNFTTHFTDYHTPDNVRYGQDYAP 167

Query: 230 -----LEGLVDWACQAPRVHAHQWAAGDVVVWVWNRCL 261
L L+ A +W V +WVNRCL+
Sbjct: 168 GGANLLHYLIGRAAIPEYQVRWRWEPNSVAIWDNRCLV 204

>ref|XP_001908518.1| hypothetical protein [Podospira anserina S mat+]
emb|CAP69191.1| unnamed protein product [Podospira anserina S mat+]
Length = 388

Score = 57.4 bits (137), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 70/280 (25%), Positives = 112/280 (40%), Gaps = 44/280 (15%)

Query: 7 QITPTGATLGATVTGVHLATLDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
++T A +G + G+ L L L + +++ Q +S QQ + FG
Sbjct: 85 KVTDLTAHIGTEIEGLQKDLTPEQRDELALLIAERSVVFRLRDQDISPQQRELGEWFG 144

Query: 67 IE-----RIGG--GDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
+E ++ G G V +++A Q PA + + G WH D +
Sbjct: 145 VEVHPQVPQVPGVPGVTVIWPDQLA-----QDLPANFRNPG---GASRWHTDLVHERQP 195

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
A + VP VGG T +A AY+ L R + + A V ++
Sbjct: 196 AGITHLHNDTVPPVGGDTLWASGYGAYEKLSPFRKFIDGKQA-----VYRS 242

Query: 179 GSAYIGYGMDDTTATP-----LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
AY+ + +A P + PLV+VHP TG +L + R I G+D AES+ L
Sbjct: 243 AHAYLDR-ENPSAGPKFVERVHPLVRVHPATGWKALWVNRAMTTRIVGLDKAESDLILNY 301

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWVWNRCLLHRAEPWDFK 271
L D + + +W AG +WVNRCLLHRAEPWDFK
Sbjct: 302 LHDVYEKNADIQVRFRWTAGTSALWDNSA-----SWDYE 335

>gb|EFQ35233.1| TfdA family Taurine catabolism dioxygenase TauD [Glomerella
graminicola M1.001]
Length = 387

Score = 57.4 bits (137), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 40/164 (24%), Positives = 68/164 (41%), Gaps = 5/164 (3%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
WH D ++ V + A+ +P GG T +A YD L A + + +A H
Sbjct: 189 GWHTDISFEQVPSDYAMLKIHTLPPTGGDTLWASGYEYIDRLSPAMQKFLGLTATHDAT 248

Query: 167 Y---SQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMD 222
+ +LG+ + G T + P+++ +P TG S+ + + I G+
Sbjct: 249 FFFHEARRLGNPLRDGLRGSPLNKGTELKAVHPVIRTNPVTGWKSVYVKNKGFTKRINGVT 308

Query: 223 AAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
ES+ L L + Q +W D+ +WDNR + H A
Sbjct: 309 KDES DVLLNYLFNLVTQNHDQVRFKWRQNDLAIWDNRSMWHCA 352

>ref|XP_002483625.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Talaromyces stipitatus ATCC 10500]
gb|EED16391.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Talaromyces stipitatus ATCC 10500]
Length = 359

Score = 57.4 bits (137), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 65/262 (24%), Positives = 93/262 (35%), Gaps = 40/262 (15%)

Query: 16 GATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDI 75
G + G+ L L L + ++ F Q LS QQ FG I G
Sbjct: 98 GTEIVGLQLKDLTPTQLDELALLVAERNVVFRRDQDLSPQQQRDVTGHFGPIFCQGP--- 154

Query: 76 VAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGR 135
+ V + A WH D ++ + VP GG
Sbjct: 155 -HVPGVPEASVIWSQFFASHIRKPTFRTPFQGWHTDIVHLKQNFGITHLHYDTVPPYGGD 213

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP-- 193
+A AAY+ L + R + + A V ++G YI D A P
Sbjct: 214 ILWASGYAAYNKLSPSFRDFIDGKMA-----VMRSGDPYIDEN-DPGAGPKY 259

Query: 194 ---LRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWA 249
+ P+V+VHP TG L + G I G++ AES+ + W W
Sbjct: 260 VEKIHPIVRVHPATGWKCLYVNGPWVLRILGLEKAESD-----MCRW-----HWT 304

Query: 250 AGDVVVWDNRCLLHRAEPWDFK 271
G +WDNRC LH A WD++
Sbjct: 305 PGTSALWDNRCTLHNAS-WDYE 325

>ref|XP_002339994.1| TfdA family taurine dioxygenase, putative [Talaromyces
stipitatus
ATCC 10500]
gb|EED22607.1| TfdA family taurine dioxygenase, putative [Talaromyces stipitatus
ATCC 10500]
Length = 374

Score = 57.4 bits (137), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 73/305 (23%), Positives = 116/305 (38%), Gaps = 44/305 (14%)

Query: 5 TLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
+ +TPT +G V L L +D L + ++ F Q +++DQQ +
Sbjct: 47 SFDVTPT---IGREFPDVQLTDLNNDQTLRDLAITVSRRGVVFFRNQDINSDDQKVLGQ 103

Query: 63 RFGAIERIGGGDIV---AISNVKADGTVRQHSPAEWDDMMKVIVGNM----- 106
+ G + + A++N K + TV + + DD + VI +
Sbjct: 104 KLGELTGKPATSKLHRHAVNNSKRNITVNE---GKLDDEISVISSEINRKLYGDRFKSSS 160

Query: 107 -----AWHADSTYMPVMAQGAVFSAEVPVA--VGGRTCFADMRAAYDALDEATRALVHQ 158
WHAD T+ V + A+ P GG T +A YD L + L
Sbjct: 161 HHLASEGWHADITFENVPSDYAILKITDSPEDNPGGDTLWASGYEVYDRLLSSPIQQQLADT 220

Query: 159 RSA-----RHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR 213
A R + + + + ++ A G + AT PLV+ +P TG SL

Sbjct: 221 LKAVHYQPRFNQIAKEHGIDLIEGDRGAPENTGYEFKAT--HPLVRTNPVTGWKSLFGAA 278

Query: 214 H--AHA-IPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWD 269
H H I G+ ESE + + +W DV +WDNR + H A D

Sbjct: 279 HQVEHGWIEGVTPRESEILKQYFNQLIAENHDLQVRFKWNTNDVAIWDNRSVFHTATN-D 337

Query: 270 FKLPR 274
+K R

Sbjct: 338 YKGKR 342

>dbj|BAD15040.1| hypothetical protein [Bradyrhizobium sp. BDV5111]
Length = 102

Score = 57.4 bits (137), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 36/107 (33%), Positives = 50/107 (46%), Gaps = 5/107 (4%)

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGR 206
ALD+ T+A + HSL+YS+ LG + Y + L+ LV+ HP GR
Sbjct: 1 ALDDETKAEIEDMICEHSLMYSRGSLGFLD-----YSDEEKEMFKPVLQRLVTRHPVHGR 55

Query: 207 PSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
SL + HA AI M E L L + A Q V+ H+W D+
Sbjct: 56 KSLYLSSHAGAIRDMSMPEGRVLLRDLTEHATQGEFVYVHKWTLHDL 102

>emb|CBJ18731.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 57.4 bits (137), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 36/115 (31%), Positives = 58/115 (50%), Gaps = 13/115 (11%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP----LV 198
AAYDAL T+ + A HS+ +S+S++G + + D A L P +V
Sbjct: 1 AAYDALPNDTKRELEGLVAEHSIFHSRSRIG-----FTDFNPDV-AQALPPVQQVMV 51

Query: 199 KVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+ HP +GR +L + HA + G + +E L+D+A Q V+ H+W GD+
Sbjct: 52 RTHPGSGRKTYLASHASHVIGWPIETGRKLIEDLLDFATQPQFVYQHRWQVGDL 106

>ref|XP_960110.1| hypothetical protein NCU09800 [Neurospora crassa OR74A]
gb|EAA30874.1| hypothetical protein NCU09800 [Neurospora crassa OR74A]
Length = 398

Score = 57.4 bits (137), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 42/170 (24%), Positives = 71/170 (41%), Gaps = 14/170 (8%)

Query: 108 WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+D T+ P+ + A+ +P GG T +A YD + R+ + +A Y
Sbjct: 189 WHSDITFEPIPSDYALLRLVQLPKTGGDTLWASGYELYDRISPTLRSFLDTLTA----YY 244

Query: 168 SQSKLGHVQQAGSAYIGY-----MDTTATPLRPLVKVHPETG-RPSLLIGRHAHAIP 219
+Q + + I G + + P+++ +P TG R + H I
Sbjct: 245 AQPLFNEAAKRNNFSIYSGERGAPENVGEILEAIHPVIRTNPVTGWRSVYAVDHHQCRIH 304

Query: 220 GMDAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVWDNRCLLHRAEP 267
G+ ES+ FL+ V + + +W DV +WDNR + H A P
Sbjct: 305 GLTDEESKHFLDWFVRLIVENHDLQVRLKWQNPNDVAIWDNRSVYHAATP 354

>emb|CAY25732.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 57.4 bits (137), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 33/111 (29%), Positives = 57/111 (51%), Gaps = 20/111 (18%)

Query: 33 AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISN 80
A + A ++A+L+F Q +++DQQ+ FA+ FG E GG + +SN
Sbjct: 14 ADIEAGMDKYAVLLFRDQDITDDQQLIFARNFGERENARGGTVTKKEDYRLTSGLNDSVN 73

Query: 81 VKADGT--VRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV 129
+ DG + H ++ +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 74 LGKDGKPLPKDHRTHPFN-----LGNCLWHSDDSSFRPIPAKFSLLSARVV 118

>ref|YP_001869152.1| taurine catabolism dioxygenase TauD/TfdA [Nostoc punctiforme PCC 73102]
gb|ACC84209.1| Taurine catabolism dioxygenase TauD/TfdA [Nostoc punctiforme PCC 73102]
Length = 287

Score = 57.4 bits (137), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 63/267 (23%), Positives = 101/267 (37%), Gaps = 38/267 (14%)

Query: 23 HLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA-KRFGAI---ERIGGGDIVAI 78
+LA++ D L + +H +++ Q L+ Q FA K FG R D
Sbjct: 22 NLASITDQQVEELKQSLWEHGVIVVRKQKLTASQLKDFAIKTFGDSTIGRRPKPLDPEIA 81

Query: 79 SNVKADGTVRQHSPAEDDDMMKVIVGNMAW--HADSTYMP-----VMAQGAVF 124
++++ G +P + + G +AW H D ++P VM G
Sbjct: 82 PDLQSPGVSIILGNPK---GLSGEVAGKIAWQWHHDKDHLPKTEGLDMNALYVVMYLGVSI 138

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
E T F DM AY LD R + S H L + I
Sbjct: 139 PEEGTGQPHTEFLDMVEAYHNLDPPQHRQQLLELLSMYH-----LSPISPQPGVEI- 189

Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAE--SERFLEGLVDWACQAPR 242
L P+V H TGR L +G + G++ +++ + L +
Sbjct: 190 -----PRKLHPIVSTHKVTGRYCLYLGSDTSILKGLNQPEVAKQYWQELFEDILDCTP 243

Query: 243 VHAHQWAAGDVVVDNRCLLHRAEPWD 269
V+AH W GD+V WDN ++H P++
Sbjct: 244 VYAHIWQPGDIVFWDNSQVMHTGMPYN 270

>emb|CAY25797.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 57.4 bits (137), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 33/109 (30%), Positives = 57/109 (52%), Gaps = 20/109 (18%)

Query: 35 LHAOWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F GQ ++++QQ+ FA FG E GG + +SN+
Sbjct: 16 IEAGMDKYAVLLFRGQDITDEQQLAFALNFGEREHARGGTVTKKEDYRLTSGLNDSVNLG 75

Query: 83 ADGT--VRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG R H +++ +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDGNNPLPRDHRTHQFN-----LGNCLWHSDDSSFRPIPAKFSLLSARVV 118

>emb|CBJ19195.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 42/111 (37%), Positives = 57/111 (51%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
AAYDAL EATR + A HSL+ S+SKLG S + A + LV+
Sbjct: 1 AAYDALPEATRQKIAGLVAEHSLMTSRSKLGF-----SDFDENERKAFAPVPQVLVRLQ 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
++GR SL HA +I GM E+ LE L+ A Q V++H+W D+
Sbjct: 56 DSGRLSLYTASHAGSIRGMADGEARALLEELIAHATQRQFVYSHRWRVKDL 106

>dbj|BAD15036.1| hypothetical protein [Bradyrhizobium sp. th-b2]
dbj|BAD15038.1| hypothetical protein [Bradyrhizobium sp. DesB1]
Length = 102

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 36/107 (33%), Positives = 50/107 (46%), Gaps = 5/107 (4%)

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGR 206
ALD+ T+A + HSL+YS+ LG + Y L+ LV+ HP GR
Sbjct: 1 ALDDETAEIADMICEHSLMYRSGSLGFLD-----YTDEEKQMFKPVLRVLRTHPVHGR 55

Query: 207 PSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
SL + HA AI GM E+ L L + A V+ H+W D+
Sbjct: 56 KSLYLSSHAGAIRGMSMPPEARLLLRDLTEHATSPEFVYVHKWTVHDL 102

>ref|XP_002502407.1| predicted protein [Micromonas sp. RCC299]
gb|ACO63665.1| predicted protein [Micromonas sp. RCC299]
Length = 380

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 54/207 (26%), Positives = 82/207 (39%), Gaps = 23/207 (11%)

Query: 108 WHADSTYM-PVMAQGAVFSAEVPVA-VGGRTCFADMRAAYDALDEATRALVHQRSARHSL 165
WH D + P ++ + PA GG T FADM AA +ALD R + + A S
Sbjct: 171 WHTDQAFRDPPPFASLLYCVKSPAGAGGDTAFADMTAACNALDNRREELRKLRAVCSY 230

Query: 166 VYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL-----LIGRHAH 216
+ +K+ + +++ P+T SL +I
Sbjct: 231 AHHNAKVNRRTPPTYLLTPTQRAAHPPVAQRRIIRADPDNTESLYGFSSAVCAVIDEKDE 290

Query: 217 AIPG-----MDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAE 266
P DA+ + L+ +A A + H W GD+VVVDN +H A
Sbjct: 291 VTPEDLDRLDYLGEEDASVRALMYDELLPFATGAFTYRHSWTEGDLVVVDNLRRTIHTAT 350

Query: 267 PWDFKLPRVMWHSRLAGRPETEGAALV 293
P+D + R MW + +A ET G A +
Sbjct: 351 PFDERYDREMWRTTVAH--ETGGEAYL 375

>emb|CAY25723.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY25724.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY25742.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY25767.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY25770.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 33/102 (32%), Positives = 54/102 (52%), Gaps = 18/102 (17%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVKADGTVR 88
++A+LIF GQ ++++QQ+ FA FG E+ GG + +SN+ DG
Sbjct: 22 KYAVLIFHGQDITDEQQLAFAFNFGEREKARGGTVTKKEDYRLTTGLNDVSNLKGKD--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 79 --KPLSRDHRTHLFNLGNCLWHSDSSFRPIPAKFSLLSARVV 118

>dbj|BAD15035.1| hypothetical protein [Bradyrhizobium sp. jwc91-2]
Length = 102

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 53/110 (48%), Gaps = 11/110 (10%)

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTAT---PLRPLVKVHPE 203
ALD+ +A + HSL+YS+ LG ++ Y + A L+ LV+ HP
Sbjct: 1 ALDDEKAEIEDMICEHSLMYSRGSLG-----FLDYTNEEKAMFKPVLQRLVRTHPV 52

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI M E+ L L + A Q V+ H+W A D+
Sbjct: 53 HGRKSLYLSSHAGAIRDMSPEARLLLRDLTEHATQGEFVYXHKWTAHDL 102

>gb|EGD92386.1| taurine dioxygenase [Trichophyton rubrum CBS 118892]
Length = 358

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 44/168 (26%), Positives = 68/168 (40%), Gaps = 14/168 (8%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD-----EATRALVHQRS 160
WH+D + P+ A+ VP GG T +A YD + E A Q
Sbjct: 153 WHSDVAFEPAPAEYTTTLRLTQVPKTTGGDTLWASGYELYDRISKPYQRFLETLTATCAQPG 212

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLL-IGRHAHAIP 219
+ KL Q+ IG + + P+V+ +P TG S+ G H I
Sbjct: 213 YNKVAASGKFKLFDGQRGAPENIGSNFSS----VHPVVRTNPVTGWKSIYSAGFHVQKIN 268

Query: 220 GMDAAESERFLEGLVDWACQAPRVHAHQWA-AGDVVVWDNRCLLHRA 265
+ AES+ L+ + + +W A D+ +WDNRC+ H A
Sbjct: 269 DVTEAESKALLDWFLRLINENNDLQVRFKWKNANDMAIWDNRCVFHTA 316

>dbj|BAD15037.1| hypothetical protein [Bradyrhizobium sp. DesT1]
Length = 102

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 53/110 (48%), Gaps = 11/110 (10%)

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTAT---PLRPLVKVHPE 203
ALD+ T+A + HSL+YS+ LG ++ Y + A L+ LV+ HP
Sbjct: 1 ALDDETKAEIEDMICEHSLMYSRGSLG-----FLDYTDEEKAMFKPVLQRLVRTHPV 52

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA AI M E+ L L + A Q V+ H+W D+
Sbjct: 53 HGRKSLSLSSHAGAIRDMSPEARLLLRDLTEHATQGEVYVHKWTVHDL 102

>emb|CBJ18790.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 35/111 (31%), Positives = 53/111 (47%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHP 202
AAYDALD+ T+A + RHS +YS+ KLG + + +
Sbjct: 53 HGRKSLSLSSHAGAIRDMSPEARLLLRDLTEHATQGEVYVHKWTVHDL 102

Sbjct: 1 AAYDALDDRTKAEIEDLVCRHSNIYSRGKLGAEFTNEERAVFKPVRQRL-----VRRQR 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

+GR SL + HA I GM ++ L L ++A + P V++H W D+

Sbjct: 56 VSGRKSFLSAHAGEIEGMPTPQARMLLLDLTEFATREPFVYSHVWRVNDL 106

>emb|CBJ18862.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 104

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 38/110 (34%), Positives = 53/110 (48%), Gaps = 7/110 (6%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE 203

AYDA+DE RA + A H +S LG + ++ + P+V+ P

Sbjct: 2 AYDAMDEDMRAFLDPLEAEHFHAFHSHELLGAMPTQEER-----NSIPPAVWPIVR-KPA 54

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

TGR SL IG HAH + GM A+ L L++ A Q V+ H W GD+

Sbjct: 55 TGRRSFIGAHAKVIGMPLAQGRMLLLDLLEHATQRQFVYRHAWTPGDL 104

>ref|XP_003015010.1| alpha-ketoglutarate-dependent taurine dioxygenase [Arthroderma
benhamiae CBS 112371]
gb|EFE34370.1| alpha-ketoglutarate-dependent taurine dioxygenase [Arthroderma
benhamiae CBS 112371]
Length = 358

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 44/168 (26%), Positives = 68/168 (40%), Gaps = 14/168 (8%)

Query: 108 WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALD-----EATRALVHQRS 160

WH+D + P+ A+ VP GG T +A YD + E A Q

Sbjct: 153 WHSDVAFEPPIAEYTTTLRLTQVPKTTGGDTLWASGYELYDRISKPYQRFLETLTATCAQPG 212

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL-IGRHAHAIP 219

+ KL Q+ IG + + P+V+ +P TG S+ G H I

Sbjct: 213 YNKVAATGKFKLFDGQRGAPENIGSNFSS----VHPVVRTNPVTGWKSIYSAGFHVQKIN 268

Query: 220 GMDAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVWDNRCLLHRA 265

+ AES+ L+ + + +W A D+ +WDNRC+ H A

Sbjct: 269 DVTEAESKALLDWFLRLINENNDLQVRFKWKNANDMAIWDNRCVFHTA 316

>emb|CAY25752.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 33/108 (30%), Positives = 56/108 (51%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82

+ A ++A+L+F Q ++++QQ+ FA FG E GG +V +SN+

Sbjct: 16 IEAGMDKYAVLLFRNQDITDEQQALAFALNFGGERENPRGGSVVKPEDSRLQTGLNDVSNLG 75

Query: 83 ADGTVRQHSAPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVS 129

DG P D + + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 76 RDG-----KPLPRDSRVNLFNLGNCLWHSDDSSFRPIPAKFSLLSARV 118

>ref|XP_003025681.1| alpha-ketoglutarate-dependent taurine dioxygenase [Trichophyton
verrucosum HKI 0517]
gb|EFE45070.1| alpha-ketoglutarate-dependent taurine dioxygenase [Trichophyton
verrucosum HKI 0517]

Length = 358

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 44/168 (26%), Positives = 68/168 (40%), Gaps = 14/168 (8%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD-----EATRALVHQRS 160
WH+D + P+ A+ VP GG T +A YD + E A Q
Sbjct: 153 WHSDVAFEPPIPAEYTTTLRLTQVPKTGGDTLWASGYELYDRISKPYQRFLETLTATCAQPG 212

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLL-IGRHAHAIP 219
+ KL Q+ IG + + P+V+ +P TG S+ G H I
Sbjct: 213 YNKVAASGKFKLFDGQRGAPENIGSNFSS----VHPVVRTNPVTGWKSIYSAGFHVQKIN 268

Query: 220 GMDAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVWDNRCLLHRA 265
+ AES+ L+ + + + +W A D+ +WDNRC+ H A
Sbjct: 269 DVTEAESKALLDWFLRLINENNDLQVRFKWKNANDMAIWDNRCVFHTA 316

>ref|XP_001264040.1| TfdA family taurine dioxygenase, putative [Neosartorya fischeri
NRRL 181]
gb|EAW22143.1| TfdA family taurine dioxygenase, putative [Neosartorya fischeri
NRRL 181]
Length = 350

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 40/166 (24%), Positives = 70/166 (42%), Gaps = 5/166 (3%)

Query: 105 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS 164
++ WH+D ++ V + A+ +P GG T +A YD L A + +A H
Sbjct: 149 SVGWHSDFSERVPSDYAMLKIHTLPPTGGDTLWASAYEVYDRLSPAMATFLEGLTATHD 208

Query: 165 LVY---SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPG 220
+ +LG+ + G + + P+++ +P TG S+ + R I G
Sbjct: 209 ASFFHDEARRLGNPLRKGVRSPLNVGEELQAVHPVIRTNPVTGWKSVYVNRGFTKRIK 268

Query: 221 MDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ ES+ L+ L + Q +W D+ +WDNR H A
Sbjct: 269 VTKDESDVLLQYLFNLVTQNHDAQVRFKWNKNDLAIWDNRSTWHCA 314

>emb|CAY25784.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 32/102 (31%), Positives = 54/102 (52%), Gaps = 18/102 (17%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVKADGTVR 88
++A+LIF GQ ++++QQ+ FA FG E+ GG + +SN+ DG
Sbjct: 22 KYAVLIFHGQDITDEQQLAFLNFGEREKARGGTVTKEDYRLTTGLNDVSNLKGKD--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
P D ++ +GN WH+D ++ P+ A+ ++ SA VV
Sbjct: 79 --KPLSRDHRTFLNLGNCLWSDGSFRPIPAKFSLLSARVV 118

>emb|CAY25778.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 33/108 (30%), Positives = 56/108 (51%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F Q +S+D+Q+ FA+ FG E GG + +SN+

Sbjct: 16 IEAGMDKYAVLLFRDQDVSDDRQLVFARNFGERENARGGTVTKKEDYRLTSGLNDVSNLG 75

Query: 83 ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

DG +P D + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 76 KDG-----NPLPRDHRTHLFLNGLNCLWHS DSSFRPIPAKFSLLSARVV 118

>emb|CAY25736.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 34/110 (30%), Positives = 56/110 (50%), Gaps = 18/110 (16%)

Query: 33 AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISN 80

A + A ++A+L+F Q +++DQQ+ FA+ FG E GG + +SN

Sbjct: 14 ADIEAGMDKYAVLLFRDQDIADDQQLIFARNFGERENAHGGTVTKKGDYRLTSGLNDVSN 73

Query: 81 VKADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

+ DG P D + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 74 LGKDG-----KPLPKDHRTHLFLNGLNCLWHS DSSFRPIPAKFSLLSARVV 118

>ref|XP_753085.1| TfdA family taurine dioxygenase [Aspergillus fumigatus Af293]
gb|EAL91047.1| TfdA family taurine dioxygenase, putative [Aspergillus fumigatus Af293]
gb|EDP56934.1| TfdA family taurine dioxygenase, putative [Aspergillus fumigatus A1163]
Length = 349

Score = 57.0 bits (136), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 40/166 (24%), Positives = 70/166 (42%), Gaps = 5/166 (3%)

Query: 105 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS 164

++ WH+D ++ V + A+ +P GG T +A YD L A + +A H

Sbjct: 149 SVGWHS DISFERVPSDYAMLKIHTLPPTGGDTLWASAYEVDRLSPAMATFLEGLTATHD 208

Query: 165 LVY---SQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPG 220

+ +LG+ + G + + P+++ +P TG S+ + R I G

Sbjct: 209 ASFFHDEARRLGNPLRKGVRGSPLNVGEELQAVHPVIRTNPVTGWKSVYVNRGFTKRING 268

Query: 221 MDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

+ ES+ L+ L + Q +W D+ +WDNR H A

Sbjct: 269 VTKDESDVLLQYLFNLVLTQNHD AQVRFRWNKNDLAIWDNRSTWHCA 314

>ref|YP_857772.1| pyoverdine chromophore biosynthetic protein PvcB [Aeromonas hydrophila subsp. hydrophila ATCC 7966]
gb|ABK38504.1| pyoverdine chromophore biosynthetic protein PvcB [Aeromonas hydrophila subsp. hydrophila ATCC 7966]
Length = 291

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 51/171 (29%), Positives = 70/171 (40%), Gaps = 31/171 (18%)

Query: 109 HADSTYMPVMAQGAVFSAEVVPAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166

H D Y P + + +F PAV GGRT F + R LD +R AR V

Sbjct: 107 HWDGMYKPTLPEFQLFHCVHAPAVDEGGRTTFINTRQLLELDG-----ERLARWERV 159

Query: 167 YSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSL-----LIGRHA 215

+ ++ V + YG + PL+ HP +G L + HA

Sbjct: 160 HITYRIKQV-----VHYGGQVRS----PLLVPHPVSGETVLRVNEPPREGVRFNLQHA 208

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE 266

I G+ AE F++ L +AHQW GDVV+ DN LLH E
Sbjct: 209 LEIEGVAPAEQAQAFVQDLHQRLYDPRYFYAHQWQGGDVVIADNLGLLHGRE 259

>ref|XP_661174.1| hypothetical protein AN3570.2 [Aspergillus nidulans FGSC A4]
gb|EAA59778.1| hypothetical protein AN3570.2 [Aspergillus nidulans FGSC A4]
tpe|CBF75866.1| TPA: conserved hypothetical protein [Aspergillus nidulans FGSC A4]
Length = 368

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 45/190 (23%), Positives = 77/190 (40%), Gaps = 20/190 (10%)

Query: 94 EWDDMMKVIVGNMA--WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA 151
E + K GN+A WH+D ++ + + ++P GG T +A YD + +
Sbjct: 135 ERKKLYKGAYGNLAAIWHSDISFEKAPSDFSALRLTLLPPTGGDTLWASGYELYDRISKP 194

Query: 152 TRALVHQRSARHS-----LVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGR 206
RA + +ARHS G ++ + + G + T+ P+V+ +P TG
Sbjct: 195 YRAFLETLTARHSGDGFHRAAQAGGFGLYEKPRGSPLNVGSELTSD--HPVVRTNPITGW 252

Query: 207 PSLL-----IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW-AAGDVVV 255
S+ G + G+ ESE L+ D + +W D+ +
Sbjct: 253 KSIFPVGTIELIAATGTFFPKVNLSTRESENLLKYFHDLITYGHDLQVRFKWNEPNIDIAI 312

Query: 256 WDNRCLLHRA 265
WDNR + H A
Sbjct: 313 WDNRSVFHTA 322

>ref|XP_003195287.1| hypothetical protein CGB_G4140W [Cryptococcus gattii WM276]
gb|ADV23500.1| Conserved hypothetical protein [Cryptococcus gattii WM276]
Length = 433

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 72/268 (26%), Positives = 107/268 (39%), Gaps = 39/268 (14%)

Query: 15 LGATVTG-VHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFG----- 65
+G + G V LA L +A L Q +++ F Q ++ +QQ K FG
Sbjct: 123 IGTVIEGDVKLADLGEAEKDDLALLVAQRSVVFRRNQSMTIEQQRELKHFGLHPLHAT 182

Query: 66 -AIERIGGGD--IVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
A R G D +V S+ + + S AE +H+D TY
Sbjct: 183 YATPRRGDLDDVVVYSRDRSRPDLYAFSRAEL-----FHSDVTYEVQPPGTT 230

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
+ P VG T ++ A Y +L + + + SA HS G Q S+
Sbjct: 231 MLRLTTPEVGNDTLWSSGYAVYSSLSKPFQYLESLSAIHS-----GFDQ--ASSR 280

Query: 183 IGYGMDDTTATPLR---PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD-WA 237
G+ P+ P+V+VHP TG S+ + + G+ AES+ L L D +A
Sbjct: 281 TGFSKIPRREPIETIHPVVRVHPVTGMKSVFVNPGFVTRLVGVPKAESDMVLSFLKDCFA 340

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
Q WA DV +WDNR +H A
Sbjct: 341 QQTDATVRWSWAPHDVAIWDNRVCVHTA 368

>ref|XP_001217728.1| hypothetical protein ATEG_09106 [Aspergillus terreus NIH2624]
gb|EAU30243.1| hypothetical protein ATEG_09106 [Aspergillus terreus NIH2624]
Length = 380

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 67/267 (25%), Positives = 103/267 (38%), Gaps = 36/267 (13%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE----- 68
+G + G+ L L L + +++ F Q +S QQ + +G IE
Sbjct: 93 IGTELVGIIQLKDLTAQQRDELGLLIAERSVVFRRDQDISPQQQKELGEWYGEIEVHPQVP 152

Query: 69 RIGG--GDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
++ G G V ++A T + G WH D + A
Sbjct: 153 QVPGVPGVTVMWPALQATETAAG-----FRKPGGASHWHTDLVHERQPAGVTHLHN 203

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA----RHSLVYSQSKLGHVQQAGSAY 182
+ VP VGG T +A AAY+ L R + ++A RH + + G Y
Sbjct: 204 DTVPTVGGDTLWASGYAAYEKLSPMLREFIDGKTAIYRSRHPYLDNRNP-----EDGLKY 258

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAP 241
+ PLV+VHP TG +L + R I G+D AES+ L L D + P
Sbjct: 259 VERE-----HPLVRVHPATGWKALWVNRAMTVRIVGLDKAESDVILGLLCDVYEKNP 310

Query: 242 RVHAH-QWAAGDVVVWDNRCLLHRAEP 267
+ +W+ +WDNR +EP
Sbjct: 311 DIQVRFKWSPRSSALWNRWDYEGSEP 337

>emb|CAY25776.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 33/102 (32%), Positives = 54/102 (52%), Gaps = 18/102 (17%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVKADGTVR 88
++A+LIF GQ ++++QQ+ FA FG E+ GG + +SN+ DG
Sbjct: 22 KYAVLIFHGQDITDEQQLAFALNFGEREKARGGTVTKKEDYRLTTGLNDVSNLKGKD--- 78

Query: 89 QHSPAEDDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 79 --KPLSRDHRTHLFLNLGNCLWHSDDSSFRPIPAKFSLMSARVV 118

>emb|CAY25720.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 34/110 (30%), Positives = 55/110 (50%), Gaps = 18/110 (16%)

Query: 33 AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISN 80
A + A ++A+L+F Q +++DQQ+ FA+ FG E GG + +SN
Sbjct: 14 ADIEAGMDKYAVLLFRDQDITDDQQLIFARNFGERENAHGGTVTKKEDYRLTSGLNDVSN 73

Query: 81 VKADGTVRQHSPAEDDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
+ DG P D + +GN WH+DS++ P+ A+ + SA VV
Sbjct: 74 LGKD-----KPLPKDHRTHLFLNLGNCLWHSDDSSFRPIPAKFPLLSARVV 118

>gb|ADC33956.1| TfdA-like protein [uncultured bacterium]
Length = 128

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 39/128 (30%), Positives = 57/128 (44%), Gaps = 2/128 (1%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSAHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR 195
T F DMRAAYDAL EA + + + H + + + + P+
Sbjct: 1 TEFCDMRAAYDALPEALKRRLEGMTVLHDFNKFWEEMMRREKSGKRPLTEAQRKAKPPVS 60

Query: 196 -PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

P+ HP TGR SL +A I + ES+ L+ L + A +W GDV
Sbjct: 61 HPIFLTHPVTGRRSLYANPGYAVRINELPEKESDEMLQLLFAHQTRPEFKFAARWQVGDV 120

Query: 254 VVWDNRCL 261
++WDNRC+

Sbjct: 121 LMWDNRCV 128

>emb|CAY25799.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 34/108 (31%), Positives = 54/108 (50%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F Q +S+DQQ+ FA+ FG E GG + +SN+

Sbjct: 16 IEAGMDKYAVLLFRDQDVSDQQLVFARNFGERENARGGTVTKKEDYRLTSGLNDVSNLG 75

Query: 83 ADGTVRQHSPA EWDDMMKVIV-GNMAWHADSTYMPVMAQGAVFSAEVV 129
DG P D + GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 76 KDG-----RPLARDGRTHLFNPGNCLWHSDSSFRPIPAKFSLLSARVV 118

>emb|CBJ18922.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 36/111 (32%), Positives = 54/111 (48%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDAL + T+A V A H ++++ LG AY + PLV+ HP

Sbjct: 1 AAYDALPDRTKAEVQDLRAEHYALHTRILLG-----DEAYTDEQKKAIPPAVWPLVQTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+ R L +G HA I G +S +L+ ++ A Q V+ H+W GD+

Sbjct: 56 GSRKLLFVGVARQIIGWPTTKSGMYLQDFMEHATQRELVYHHEWQVGD 106

>emb|CBJ18981.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18854.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 104

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 54/110 (49%), Gaps = 7/110 (6%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE 203
AYDA+DE +A + A H +S+ LG + ++ + P+V+ P

Sbjct: 2 AYDAMDEDMKAFLDPLEAEHFHAFHSRELLGTMPQTQEER-----NSIPPAVWPPIVR-KPA 54

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL IG HAH + GM A+ L L++ A Q V+ H W GD+

Sbjct: 55 TGRSLFIGAHAKVIGMPLAQGRMLLLDLLEHATQRQFVYRHAWTPGDL 104

>emb|CBJ18872.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 104

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 54/110 (49%), Gaps = 7/110 (6%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE 203
AYDA+DE +A + A H +S+ LG + ++ + P+V+ P

Sbjct: 2 AYDAMDEDMKAFLDPLEAEHFHAFHSRELLGAMPTQEER-----NSIPPAVWPPIVR-EPA 54

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL IG HAH + GM A+ L L++ A Q V+ H W GD+
Sbjct: 55 TGRSLFIGAHAKVIGMPLAQGRMLLLDLEHATQRFVYRHAWTPGDL 104

>emb|CAY25786.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 33/102 (32%), Positives = 54/102 (52%), Gaps = 18/102 (17%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVKADGTVR 88
++A+LIF GQ ++++QQ+ FA FG E+ GG + +SN+ DG
Sbjct: 22 KYAVLIFHGQDITDEQQLAFALNFGEKEKARGGTVTKKEDYRLTTGLNDVSNLKGKDG--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 79 --KPLSRDHRTHLFLNLGNCLWHSDDSSFRPIPAKFSLLSARVV 118

>emb|CBJ19197.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 39/114 (34%), Positives = 53/114 (46%), Gaps = 11/114 (9%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---PLRPLVK 199
AAYDALD+ T+A + HSL+ S+ LG ++ Y D A L+ LV+
Sbjct: 1 AAYDALDDDTKAEIADMICEHSLMTRGALG-----FLDYTDDEKAMFKPVLQRLVR 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
HP R SL + HA I M E L L + A A V+ H+W D+
Sbjct: 53 THPAHRRKSLYLSSHAGKIVSMSVPEGRLLLRDLNEHATNAEFVYVHKWKLHDL 106

>emb|CBJ18902.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18916.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18921.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18983.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18988.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18994.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18998.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19007.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19020.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19192.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18831.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18833.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18834.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18840.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18841.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18842.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18843.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18845.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18846.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18847.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18851.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18852.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18857.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18860.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18861.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18863.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18864.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]


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emb|CBJ18866.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18871.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18873.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18875.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18876.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18877.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18878.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18879.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18881.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18882.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18884.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18886.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18893.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 104
```

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 54/110 (49%), Gaps = 7/110 (6%)

```
Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPE 203
      AYDA+DE +A + A H +S+ LG + ++ + P+V+ P
Sbjct: 2 AYDAMDEDMKAFLDPLEAEHFAPHSRELLGAMPTQEER-----NSIPPAVWPPIVR-KPA 54

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
      TGR SL IG HAH + GM A+ L L++ A Q V+ H W GD+
Sbjct: 55 TGRSLFIGAHAAHKVIGMPLAQGRMLLLDLLEHATQRQFVYRHAWTPGDL 104
```

```
>gb|AAQ21538.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 13]
gb|AAQ21539.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 14]
gb|AAQ21540.1| 2,4-D/alpha-ketoglutarate dioxygenase [Variovorax sp. 55]
gb|AAQ21541.1| 2,4-D/alpha-ketoglutarate dioxygenase [Alcaligenes sp. 92]
Length = 111
```

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 41/117 (35%), Positives = 52/117 (44%), Gaps = 7/117 (5%)

```
Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR 195
      T F DMRAAYD L E + + A H + S+ LG + S P+
Sbjct: 1 TEFCDMRAAYDDLPEDFKKEQLGLRAEHYALNSRFILGDTDYSES-----QRNAMPVVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251
      PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W G
Sbjct: 55 WPLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVG 111
```

```
>emb|CBJ18832.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 104
```

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 54/110 (49%), Gaps = 7/110 (6%)

```
Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPE 203
      AYDA+DE +A + A H +S+ LG + ++ + P+V+ P
Sbjct: 2 AYDAMDEDMKAFLDPLEAEHFAPHSRELLGAMPTQEER-----NSIPPAVWPPIVR-KPA 54

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
      TGR SL IG HAH + GM A+ L L++ A Q V+ H W GD+
Sbjct: 55 TGRSLFIGAHAAHKVIGMPPAQGRMLLLDLLEHATQRQFVYRHAWTPGDL 104
```

```
>emb|CAY25771.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119
```

Score = 56.6 bits (135), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 33/102 (32%), Positives = 54/102 (52%), Gaps = 18/102 (17%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVKADGTVR 88
++A+LIF GQ ++++QQ+ FA FG E+ GG + +SN+ DG
Sbjct: 22 KYAVLIFHGQDIADQQALAFALNFGEREKARGGTVTKKEDYRLTTGLNDVSNLGKDG--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 79 --KPLSRDHRTHLFLNLGNCLWHSDDSSFRPIPAKLSLLSARVV 118

>emb|CAY25740.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 56.2 bits (134), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 32/102 (31%), Positives = 54/102 (52%), Gaps = 18/102 (17%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVKADGTVR 88
++A+L+F GQ ++++QQ+ FA FG E+ GG + +SN+ DG
Sbjct: 22 KYAVLVFHGQDITDEQQALAFALNFGEREKARGGTVTKKEDYRLTTGLNDVSNLGKDG--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 79 --KPLSRDHRTHLFLNLGNCLWHSDDSSFRPIPAKFSLLSARVV 118

>ref|ZP_07778867.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli
2362-75]
gb|EFR18515.1| alpha-ketoglutarate-dependent taurine dioxygenase [Escherichia coli
2362-75]
Length = 182

Score = 56.2 bits (134), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 43/157 (27%), Positives = 70/157 (44%), Gaps = 6/157 (3%)

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172
T++ GA+ +A+ +P+ GG T +A AAY+AL R L+ A H S +
Sbjct: 2 TFIQTTPAGAILAAKELPSTGGDTLWASGIAAYEALSVPFRQLLSGLRAEHDFRKSFPY 61

Query: 173 GHVQQAGSAYIGYGMDDTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERF 229
+ ++ + + + P L P+V+ HP TG+ +L + I + ESE
Sbjct: 62 KY-RKTEAEHQRWREAVAKNPPLLHPVVRTHPVTGKQALFVNEGFTTRIVDVSEKESEAL 120

Query: 230 LEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
L G + P +W D+ +WDNR H A
Sbjct: 121 L-GFLFAHITKPEFQVRWRWQPNDAIWDNRVTQHYA 156

>emb|CAY25757.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 56.2 bits (134), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 33/108 (30%), Positives = 57/108 (52%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F GQ ++++QQ+ FA FG E GG + +SN+
Sbjct: 16 IEAGMDKYAVLLFRGQDITDEQQALAFALNFGEREHARGGTVTKKEDYRLTSGLNDVSNLG 75

Query: 83 ADGTVRQHSPEAWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG +P D ++ +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLLNLGNCLWHSDDSSFRPIPAKFSLLSARVV 118

>ref|XP_001526245.1| hypothetical protein LELG_02803 [Lodderomyces elongisporus NRRL YB-4239]
gb|EDK44624.1| hypothetical protein LELG_02803 [Lodderomyces elongisporus NRRL YB-4239]
Length = 437

Score = 56.2 bits (134), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 67/296 (22%), Positives = 110/296 (37%), Gaps = 57/296 (19%)

Query: 2 AQTTLQITPTGATLGATVTVGHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
A+ + +TP +G + G+ LA LDD L + ++ F Q LS +Q+
Sbjct: 125 AKDVINLTPY---VGTEIVGLQLADLDDKQKDELALLIAERVVFFKQDLSPKKQLELG 181

Query: 62 KRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM 115
K +G +E RIG D I+ + D + + G WH D ++
Sbjct: 182 KYWGQVEVHPQANRIGP-DYDGITVIWQDYFNEKGGLGL--SFQSRQGTSRWHGDLSE 238

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
A + +P GG T ++ AYD L A + + ++A +
Sbjct: 239 FQTAGITHLHQDSIPDAGGETIWSSTYGAYDKLSPAFKEFLDGKTA-----I 285

Query: 176 QQAGSAYIGYGMDDTTATPLR-----PLVKVHPETGRPSLLIGR-HAHAIPGMDAAE 225
++ Y+ + PL+ P+V+ HP TG L + R + I G+ E
Sbjct: 286 FKSAHVYL-----SRENPLKGPKHVEREHPIVRTHPATGWKYL FVNRSYTTRIVGLLPEE 340

Query: 226 SERFLEGL-----VDWACQAPRVH---AHQWAAGDVVVDNRCLLHR 264
S+ L L W + P + AH+ G +WDNR H
Sbjct: 341 SDAILNLYLFSVIENNRDIQVTFSWQQLPGLKSPSDAHKTYRGTSALWDNRNRIANHN 396

>gb|AAQ21542.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 54]
gb|AAQ21543.1| 2,4-D/alpha-ketoglutarate dioxygenase [Ralstonia sp. 80]
Length = 111

Score = 56.2 bits (134), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 39/117 (33%), Positives = 55/117 (47%), Gaps = 7/117 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRAAYDAL ++ + A H + S+ LG + + P+
Sbjct: 1 TEFCDMRAAYDALPRDLQSELEGLRAEHYALNSRFLLGDTDYSEA-----QRNAMPPVN 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251
PLV+ H +GR L IG HA + G+ AE L L++ A Q V+ H+W G
Sbjct: 55 WPLVRTHAGSGRKFLFIGAHAGHVEGLPVAEGRMLLAELLEHATQREFVYRHRWNVG 111

>ref|XP_001821071.1| tfdA family taurine dioxygenase [Aspergillus oryzae RIB40]
dbj|BAE59069.1| unnamed protein product [Aspergillus oryzae]
Length = 355

Score = 56.2 bits (134), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 42/168 (25%), Positives = 74/168 (44%), Gaps = 9/168 (5%)

Query: 105 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS 164
++ WH D ++ V + A+ +P GG T +A YD L + +A H
Sbjct: 154 SVGWHTDISFERVPSDYAMLKIHTLPETGGDTLWASGYEIIDRLSPQMAEFLEGLTATHD 213

Query: 165 LVY---SQSKLGHVQQAG--SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI 218
+ +LG+ + G + + +G + TA + P+V+ +P TG S+ + + I
Sbjct: 214 ATFFHDEARRLGNPLRKGVRSPLNHGEELTA--VHPVVRTNPVTGWKSVYVKNKGFTTRI 271

Query: 219 PGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
G+ ES+ L+ L + Q +W D+ +WDNR H A
Sbjct: 272 NGVTKDESDMLLQYLFNLVTQNHDAQVRFKWNKNDMAIWDNRSTWHCA 319

>ref|XP_002376815.1| TfdA family taurine dioxygenase, putative [Aspergillus flavus
NRRL3357]
gb|EED53569.1| TfdA family taurine dioxygenase, putative [Aspergillus flavus
NRRL3357]
Length = 355

Score = 56.2 bits (134), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 42/168 (25%), Positives = 74/168 (44%), Gaps = 9/168 (5%)

Query: 105 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS 164
++ WH D ++ V + A+ +P GG T +A YD L + +A H
Sbjct: 154 SVGWHTDISFERVPSDYAMLKIHTLPETGGDTLWASGYEIDRLSPQMAEFLEGLTATHD 213

Query: 165 LVY---SQSKLGHVQQAG--SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI 218
+ +LG+ + G + + +G + TA + P+V+ +P TG S+ + + I
Sbjct: 214 ATFFHDEARRLGNPLRKGVRSPLNHGEELTA--VHPVVRTNPVTGWKSVYVNGKFTRRI 271

Query: 219 PGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
G+ ES+ L+ L + Q +W D+ +WDNR H A
Sbjct: 272 NGVTKDESDMLLQYLFNLVTQNHDAQVRFKWNKNDMAIWDNRSTWHCA 319

>emb|CBJ18896.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 104

Score = 56.2 bits (134), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 54/110 (49%), Gaps = 7/110 (6%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPE 203
AYDA+DE +A + A H +S+ LG + ++ + P+V+ P
Sbjct: 2 AYDAMDEDMKAFLDPLEAEHFHAFHSRELLGAMPTREER-----NSIPPAVWPIVR-KPA 54

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL IG HAH + GM A+ L L++ A Q V+ H W GD+
Sbjct: 55 TGRRSFIGAHAKVIGMPLAQGRMLLLDLEHATQRQFVYRHAWTPGDL 104

>ref|XP_002736248.1| PREDICTED: hypothetical protein [Saccoglossus kowalevskii]
Length = 306

Score = 56.2 bits (134), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 57/283 (20%), Positives = 108/283 (38%), Gaps = 64/283 (22%)

Query: 7 QITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRF 64
Q+TP A +G V G+ + + + A + +H +L+F QH + ++ + + F
Sbjct: 26 QLTP--AKIGCEVHGIDIGLPVSEKVIAQIKKDVTEHRILVFRNQHNIPPERHVEIGRWF 83

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMP 116
G +E + +I ISNVK++G++ + G WH D ++
Sbjct: 84 GELESSMFYKHPKSPSPEIFRISNVKSEGSINR-----GRFGWHIDGSHFM 129

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
++ VP G Y+ L+E + L +R R ++ +S
Sbjct: 130 KPVSHTLYQIVHVPNEGD-----TVYNPLNEIVQGLSTERLDRWERLWVRS----- 175

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI-----GRHAHAIPGMDAA 224
+ + PL+ HP+TG+ + I G + G D
Sbjct: 176 -----NPPPQVIHPLIYSHPDGKKVICIHLGTTASFIWDRGTNNERETGFDET 224

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEP 267
 + E E ++ ++H+W GD ++ DN + H + P
 Sbjct: 225 K-ELLAEIKHEFTKNQTLQYSHKWEVGDYIITDNLVAHESAP 266

>ref|XP_002373641.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
 flavus NRRL3357]
 dbj|BAE56413.1| unnamed protein product [Aspergillus oryzae]
 gb|EED58029.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
 flavus NRRL3357]
 Length = 393

Score = 56.2 bits (134), Expect = 5e-06, Method: Compositional matrix adjust.
 Identities = 66/262 (25%), Positives = 104/262 (39%), Gaps = 28/262 (10%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKR 63
 ++TPT +G+ V G+ L+ L D G L Q ++ F Q + ++ + F
 Sbjct: 100 ELTPT---IGSEVHGIQLSQLTDKGKDQLALYVAQRKVVAFRDQDFAQLPIEKALEFGGY 156

Query: 64 FGA--IERIGGGDI---VAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV 117
 FG I + G + + + AD S AE+ ++ ++ WH+D T+
 Sbjct: 157 FGRHHIHQSSGAPKGFPEIHLVHRGAD----DRSGAEF---LEHTNSLTWHSDDVTFEKQ 209

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
 P GG T F +M AY L R +H A HS V ++ +
 Sbjct: 210 PPGTTFLYLLDGPSTSGGDTLFCNMAQAYRRLSPEFRKRLHGLKAVHSGV---EQVNNSLN 266

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDW 236
 G G T P+V+ HP TG +L + + I G ES+ L+ L D
 Sbjct: 267 KG---GIARRDPITTEHPVVRTHPVTGEKALYVNPQFTRYIVGYKKEESDFLLKFLYDH 322

Query: 237 ACQAPRVHAH-QWAAGDVVVD 257
 + + +W VVVD
 Sbjct: 323 IALSQDIQTRVRWRPNTVVVD 344

>emb|CBJ19033.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
 emb|CBJ18769.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
 emb|CBJ18804.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
 emb|CBJ18822.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
 Length = 106

Score = 56.2 bits (134), Expect = 6e-06, Method: Compositional matrix adjust.
 Identities = 35/111 (31%), Positives = 53/111 (47%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
 AAYDALD+ T+A + RHS +YS+ KLG + + V+
 Sbjct: 1 AAYDALDDRTKAEIEDLVCRHSNMYSRGKLGAEFTNEERAVFKPVRQRL-----VRRQR 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
 +GR SL + HA I GM ++ L L ++A + P V++H W D+
 Sbjct: 56 VSGRKSFLSAHAGEIEGMPTPQARMLLLDLTEFATREPFVYSHVVRVNDL 106

>ref|XP_500332.2| YALI0A21439p [Yarrowia lipolytica]
 emb|CAG84270.2| YALI0A21439p [Yarrowia lipolytica]
 Length = 372

Score = 56.2 bits (134), Expect = 6e-06, Method: Compositional matrix adjust.
 Identities = 51/183 (27%), Positives = 78/183 (42%), Gaps = 11/183 (6%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGG-RTCFADMRAAYDALDEATRALVHQRSARHS-- 164

```

      WH D T+ V + A+      P+ GG T +A  AAY+ L  + ++  +A HS
Sbjct: 155 WHTDITFEKVPSDYAILKIIKKPSSGGGDTLWASGYAAYEKLSPYQKILESLTAHHSQG 214

Query: 165 ---LVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPG 220
      V QS G V      + G D A  P+++ +P TG SL +      +I G
Sbjct: 215 HFHAVAKQSGHGIVTTPRGHPLNSGDDLYAD--HPIIRTNPVTGWKSLYVNPIFTESING 272

Query: 221 MDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHS 279
      + ES L+ L      + +H +W DV +WDNR H A +D+      + H
Sbjct: 273 LGWDESRISILDFLNQNLKENHDIHVRFRWVNDNDVAIWDNRSTYHTA-TYDYSTTDLRGHR 331

Query: 280 RLA 282
      L+
Sbjct: 332 VLS 334

```

>emb|CAY25796.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 56.2 bits (134), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 33/108 (30%), Positives = 56/108 (51%), Gaps = 18/108 (16%)

```

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
      + A ++A+L+F GQ ++++QQ+ FA FG E GG +      +SN+
Sbjct: 16 IEAGMDKYAVLLFRGQDITDEQQLAFAFNFGERENARGGTVTKKEDYRFTSGLNDVSNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
      DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLFNLGNCLWHSDDSFRPIPAKFSLLSARVV 118

```

>ref|YP_001870085.1| taurine catabolism dioxygenase TauD/TfdA [Nostoc punctiforme PCC
73102]
gb|ACC85044.1| Taurine catabolism dioxygenase TauD/TfdA [Nostoc punctiforme PCC
73102]
Length = 287

Score = 56.2 bits (134), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 64/267 (23%), Positives = 104/267 (38%), Gaps = 38/267 (14%)

```

Query: 23 HLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA-KRFGAI---ERIGGGDIVAI 78
      + A++ D L + +H +++ Q L+ Q FA + FG R D
Sbjct: 22 NFASITDQQVEELKQSLWEHGVIVVRKQKLTASQLKDFAIQTFGDSTLGRRPKPLDPEIA 81

Query: 79 SNVKADGTVRQHSPAEWDDMMKVIVGNMAW--HADSTYMP-----VMAQGAVF 124
      ++++ G +P + +VG +AW H D ++P VM G
Sbjct: 82 PDLQSPGVSI LGNPK---GLSGEVVGKVAWQWHHDKDHLPKTQGLDMNALYVVMYLGVSI 138

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
      E T F DM AY L A HQ+ + +Y S + Q G
Sbjct: 139 PDEGTDGHPHTTLFLDMVEAYHNL-----APQHQQQLKLLSMYHLSPIS--PQPGVE--- 188

Query: 185 YGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAE--SERFLEGLVDWACQAPR 242
      L P+V H TGR L +G + G++ +++++ L
Sbjct: 189 -----IPRKLHPIVSTHKVTGRYCLYLGSDTSILKGLLENKPEAAKQYWQELFQEILSCTP 243

Query: 243 VHAHQWAAGDVVVDNRCLLHRAEPWD 269
      V+AH W AGD+V WDN ++H P++
Sbjct: 244 VYAHIQAGDIVFWDNSQVMHTGMPYN 270

```

>ref|YP_001508997.1| taurine dioxygenase [Frankia sp. EAN1pec]
gb|ABW14091.1| Taurine dioxygenase [Frankia sp. EAN1pec]

Length = 276

Score = 56.2 bits (134), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 75/290 (25%), Positives = 116/290 (40%), Gaps = 38/290 (13%)

```

Query: 5   TLQITPTGATLGATVTGV--HLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFA 61
      +++      +GA V GV  H+A  D+   + L  +  +H +L F      +S++Q  F+
Sbjct: 16  SIRFEKVTGNIGAIVHGVDVHVAHGDEVA-SVLLRSLHEHGVLFHSDTAISSEQFSGFS 74

Query: 62  KRFGA--IERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMA 119
      FG   +   G G   ++   AD                      V +   WH D +
Sbjct: 75  SVFGEQYVYPYKGPQGQFVTEEGADA-----VRLRTSYWHTDGGSPQEKPP 119

Query: 120  QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
      Q A+  A  VPA GG T +A M AA+DAL   + L   A   V+S + +   A
Sbjct: 120  QAALLCAVEVPAFGGDTMWASMTAAFDALSSRYQRLFEGMEA----VHSTATVARYHDA- 174

Query: 180  SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
      G G   +   P+V   P T R +L +   +   + GM   E+E  L  L +
Sbjct: 175  ---FGQG----ESHAHPVITDPVTRRKALYVNSVYTERLVGM SERENETLLRMLYE-HV 226

Query: 239  QAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RPE 286
      P  H   +W   + VW+ R  HRA  D+   RV+   + G RP+
Sbjct: 227  NTFEFHVRLRWQPNMIAVWEERV TQHRAVA-DYAERRVLRITITGDRPK 275

```

>emb|CAY25759.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 56.2 bits (134), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 34/108 (31%), Positives = 55/108 (50%), Gaps = 18/108 (16%)

```

Query: 35  LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
      + A   ++A+L+F GQ +++ QQ+ FA  FG  E   GG+IV          +S +
Sbjct: 16  IEAGMDKYAVLLFRGQDITDAQQMAFALNFGERENPRGGNIVKPEDSRLQTGLVDVSTLD 75

Query: 83  ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
      DG   P + D   +GN  WH+DS++ P+ A+ ++ SA VV
Sbjct: 76  KDG-----KPMQRDSRANSFN LGNCLWHS DSSFRPIPAKFSLLSARVV 118

```

>ref|XP_002384446.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Aspergillus flavus NRRL3357]
gb|EED45510.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Aspergillus flavus NRRL3357]
Length = 341

Score = 56.2 bits (134), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 43/164 (26%), Positives = 66/164 (40%), Gaps = 7/164 (4%)

```

Query: 106  MAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL 165
      + +H+D +Y      +   +P  GG T +A   YD L   +   +A+H
Sbjct: 137  LEYHSDGSYEVCPDFTMLRMTEIPPTGGDTLWASGYELYDRLSTPYQKFFESLTAQHE- 195

Query: 166  VYSQSKLGHVQQA--GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGM 221
      V S  KL   +   G   D   P+V+ HP TG  +L  G  H   +   +
Sbjct: 196  VPSLRKLAETEPGIYDGPRGAPANTDMQFKQSHPMVVRTHPVTGWKTLFAGGLHCRRVNDV 255

Query: 222  DAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVWDNRCLLH 263
      ESE+ L  ++      +   +W   GDV +WDNRC+LH
Sbjct: 256  TDFESEQLLSKIISLVGDNHD LQVRFRWNNPGDVAIWDNRCVLH 299

```

>ref|XP_001827203.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Aspergillus oryzae RIB40]
 dbj|BAE66070.1| unnamed protein product [Aspergillus oryzae]
 Length = 341

Score = 56.2 bits (134), Expect = 6e-06, Method: Compositional matrix adjust.
 Identities = 43/164 (26%), Positives = 66/164 (40%), Gaps = 7/164 (4%)

Query: 106 MAWHADSTYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSL 165
 + +H+D +Y + +P GG T +A YD L + +A+H
 Sbjct: 137 LEYHSDGSYEVCPDFTMLRMTEIPPTGGDTLWASGYELYDRLSTPYQKFFESLTAQHE- 195

Query: 166 VYSQSKLGHVQQA--GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGM 221
 V S KL + G D P+V+ HP TG +L G H + +
 Sbjct: 196 VPSLRKLAETEPGIYDGPRGAPANTDMQFKQSHPMVVRTHPVTGWKTLFAGGLHCRRVNDV 255

Query: 222 DAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVWDNRCLLH 263
 ESE+ L ++ + +W GDV +WDRNC+LH
 Sbjct: 256 TDFESEQLLSKIISLVGDNHDLQVRFRWNNPGDVAIWDNRCLVH 299

>ref|ZP_05095406.1| hypothetical protein GPB2148_781 [marine gamma proteobacterium HTCC2148]
 gb|EEB78156.1| hypothetical protein GPB2148_781 [marine gamma proteobacterium HTCC2148]
 Length = 182

Score = 55.8 bits (133), Expect = 6e-06, Method: Compositional matrix adjust.
 Identities = 50/172 (29%), Positives = 71/172 (41%), Gaps = 18/172 (10%)

Query: 128 VVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA----- 179
 VV G T F D+ AYDALD T+ L+ + +S + + +V G
 Sbjct: 2 VVAEEDGLTGFGDLAKAYDALDSETQDLLEKLEVAYSFSMQRRHMRVYNLEGYEPGPSP 61

Query: 180 --SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMDAAESERFLE 231
 A +GY A + P V HP +GR L I G+ ES LE
 Sbjct: 62 KKPADVGYP--DFADAVYPAVVTHPVSGRKVLEIVEQFLDRVITPQQFGLSNDESIELLE 119

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
 LV + + HQW GD+V+WDN +H A + RV+ + + G
 Sbjct: 120 RLVAHTKKPEFTYFQWRDGMVLWDNWRAMHCATGTRPGIKRVINRTTIEG 171

>ref|XP_002392556.1| hypothetical protein MPER_07845 [Moniliophthora perniciosa FA553]
 gb|EEB93486.1| hypothetical protein MPER_07845 [Moniliophthora perniciosa FA553]
 Length = 321

Score = 55.8 bits (133), Expect = 6e-06, Method: Compositional matrix adjust.
 Identities = 46/160 (28%), Positives = 64/160 (40%), Gaps = 7/160 (4%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
 WH+D +Y F P GG T F + L A + A HS V
 Sbjct: 133 WHSDVSYELQPPGLTTFFLLAQPKTGGDTLFTSQVSTLKRSLSPQFVAFRLTLKAVHSGV- 191

Query: 168 SQSKLGHVQQAAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAES 226
 Q++ + G G + PLV+ HP TG +L + R I G+ ES
 Sbjct: 192 EQAEFSRSGKRG---GIVRREPVEHVHPLVRRHPVTGEEALYVNRQFTRRIVGLKREES 247

Query: 227 ERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
 E L+ L D ++ + A +W VV+WDNR H A
 Sbjct: 248 ENILKFLFDHVDKSVDLQARVKWTPNTVVLWDNRITAHSA 287

>ref|ZP_04996765.1| taurine catabolism dioxygenase TauD/TfdA [Streptomyces sp. Mgl]
gb|EDX21276.1| taurine catabolism dioxygenase TauD/TfdA [Streptomyces sp. Mgl]
Length = 275

Score = 55.8 bits (133), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 57/219 (26%), Positives = 89/219 (40%), Gaps = 26/219 (11%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERI-----GGGDIVAISNVKADGTVRQHSP 92
+H +L+ PGQHL++ + A G ++ G + +SN+ GT
Sbjct: 68 RHRVLVLPQHLNHADLLAVASLVGTVDATDRRYTVPGFPGTLTVVSNHQGGTP----- 122

Query: 93 AEWDDMMKVIVGNMA--WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDE 150
+ + G+ WHAD+++ P + + + GG T AD AYD L
Sbjct: 123 -----IGIYDGDQEEWHADNSFKPELTAATLLYSVITAGEGGGETRSADATRAYDDLPS 176

Query: 151 ATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATP--LRPLVKVH-PETGRP 207
A V SA HS+ + ++ G + G T P PL VH P TG
Sbjct: 177 GLPARVDDL SAVHSVQHLATRQADAAD-GRSSTQAGTPRTLWPEVTHPLAPVHPPPTGAR 235

Query: 208 SLLIGRHA-HAIPGMDAAESERFLEGLVDWACQAPRVHA 245
SLL+G I + ES L+ L+ P V++
Sbjct: 236 SLLLGPMVIRGITTLESESRALLKKLLAHTTSVPYVYS 274

>ref|YP_001565905.1| taurine dioxygenase [Delftia acidovorans SPH-1]
gb|ABX37520.1| Taurine dioxygenase [Delftia acidovorans SPH-1]
Length = 273

Score = 55.8 bits (133), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 67/269 (24%), Positives = 104/269 (38%), Gaps = 24/269 (8%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL-----LIFPGQHLSNDQQITF 60
+Q+ +G+ + G+ L+ D HA L+ L + F Q L QQ+
Sbjct: 1 MQVEHITPCIGSEIYGIDLS---DPAQVHDHADALRLLAERQVIFFRDQTLDPAQQVRV 57

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ 120
A+ FG +E + + + + Q + G WHAD T+
Sbjct: 58 AQVFGKVEPVSSSTFPSPHDDPHVELLISQGT-----RTGTDIWHADLTWQTKPPA 107

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS--QSKLGHVQQA 178
GA A VP GG T +A M A+ +L +A + + A H+ + L +
Sbjct: 108 GACLYAVDVPTGGDTMWASMTTAFASLAPQLAYLRKLRATHNWEAPALRQSLMRRDPS 167

Query: 179 GSAYIGYGMTTATPL-RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
G AY + PL +P+V HP TG P + + I G+ + ES + L
Sbjct: 168 GEAYRATRLK--HPPLEQPVVLEHPVTGLPVAFVNSLYTTHIEGVTSDESAALIAML SGL 225

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
A +W G V +WDN H A
Sbjct: 226 AKVPEWQVRFRWRKGSVAIWDNLATQHYA 254

>emb|CBJ18869.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 104

Score = 55.8 bits (133), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 54/110 (49%), Gaps = 7/110 (6%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPE 203
AYDA+DE +A + A H +S+ LG + ++ + P+V+ P
Sbjct: 2 AYDAMDEDMKAFLDPLEAEHF AFHSRELLGAMPTQEER-----NSIPPAVWPVVR-KPA 54

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

TGR SL IG HAH + GM A+ L L++ A Q V+ H W GD+
Sbjct: 55 TGRSLFIGAHAKVIGMPLAQGRMLLLDLLEHATQRQFVYRHAWTPGDL 104

>emb|CBJ18815.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 55.8 bits (133), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 38/112 (33%), Positives = 54/112 (48%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYDAL E T+ + H ++S+ LG + + P+R PLV+ H
Sbjct: 1 AAYDALPERTKQDLGGLFTEHWALHSRFLMGDEEDYTEAKAAF-----PPVRWPLVRAH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P +GR +L IG HA + GM E L L++ A Q V+ H W GD+
Sbjct: 55 PGSGRKALFIGAHAREVVGMTVPEGRLLSSELLEHATQPEFVYRHHWRLGDL 106

>emb|CAY25753.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 55.8 bits (133), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 33/108 (30%), Positives = 56/108 (51%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F GQ ++++QQ+ FA FG E GG + +SN+
Sbjct: 16 IEAGMDKYAVLLFRGQDITDEQQALAFALNFGGREHARGGTVTKKEDYRLTSGLNNVSNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLFNLGNCLWHSDFSFRPIPAKFSLLSARVV 118

>ref|YP_002007989.1| taurine dioxygenase, 2-oxoglutarate-dependent [Cupriavidus
taiwanensis LMG 19424]
emb|CAQ71933.1| taurine dioxygenase, 2-oxoglutarate-dependent [Cupriavidus
taiwanensis LMG 19424]
Length = 303

Score = 55.8 bits (133), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 65/289 (22%), Positives = 107/289 (37%), Gaps = 59/289 (20%)

Query: 4 TTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T + TPT +GA V G+ D + +L A L++ +L F Q ++ Q + A+
Sbjct: 25 TVRRCTPT---IGAEVEGIDFREAFDHDYLSLRRALLKYKVLFFRKQAITPAQHVAVAR 81

Query: 63 RFGAIE-----RIGGGDIVAI-SNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY 114
RFG +E ++V N K G +H+D ++
Sbjct: 82 RFGELEVHPMFTNHPEHPVLVFGGRNDKTRGR-----ENLYHSDVSW 123

Query: 115 MPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLV-----YS 168
+ + G++ P VGG T + +M AAY+ L + + + A H + S
Sbjct: 124 REIPSMGSMRLRCLECPEVGGDTIWINMAAAYENLPQEMKDRIASLKAVHDAMPAGGAALS 183

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-----HAAHAIP- 219
+ K ++ + P+V+ HPETG L + A P
Sbjct: 184 EEKYAEMRAKYPPMV-----HPVVRTHPETGEKILFVNEAFTTHFANFAKEQPY 232

Query: 220 --GMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
G D +E L + AP +W + +WDNR H A
Sbjct: 233 RFGSDFRPAELDLMQYLYRQAAPEYQVRLRWQPDITIALWDNRSTQHYA 281

>ref|XP_002484418.1| alpha-ketoglutarate-dependent taurine dioxygenase [Talaromyces stipitatus ATCC 10500]
gb|EED17184.1| alpha-ketoglutarate-dependent taurine dioxygenase [Talaromyces stipitatus ATCC 10500]
Length = 374

Score = 55.8 bits (133), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 72/268 (26%), Positives = 109/268 (40%), Gaps = 24/268 (8%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKR 63
++TPT G+ V GV L+ L AG L Q ++ F Q L++ ++ + F
Sbjct: 93 KLTPT---TGSEVRGVQLSKLSAAGKQQLALLVAQRKVVAFRDQDLADLPIDEEALEFGGY 149

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
FG I + + R S E + ++ WH+D +Y
Sbjct: 150 FGR-HHIHPTSGAPEGHPELHIVYRNGSDGEVEAYFANRNSSVQWHSVSYEQPPGTTTF 208

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV----YSQSKLGHVQQAG 179
P VGG T F + AY+ L A + +H +A HS V +S+ + G V++
Sbjct: 209 LYILDSPEVGGDTAFVNQVEAYNRLSPA IQERLHGLTAIHSGVEQAEFSRGRGGVVVRE- 267

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVDWAC 238
T P+V+ HP TG +L + G +I G+ ESE L L+
Sbjct: 268 -----PVTNEHPIVRTHPATGEKALYVNGGFTRSI VGLKKEESESLLSFLLSHIS 317

Query: 239 QAPRVHAH-QWAAGDVVVDNRCLLHRA 265
+ A +W VVVVDNR H A
Sbjct: 318 RGIDYQARVRWEPKTVVVVDNRVTAHSA 345

>ref|YP_003468246.1| hypothetical protein XBJ1_2349 [Xenorhabdus bovienii SS-2004]
emb|CBJ81475.1| hypothetical protein XBJ1_2349 [Xenorhabdus bovienii SS-2004]
Length = 250

Score = 55.8 bits (133), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 60/262 (22%), Positives = 109/262 (41%), Gaps = 35/262 (13%)

Query: 42 HALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKV 101
+ LL+F Q + +D + FA R G +++++ + + E + +
Sbjct: 8 YGLLVFNQKMDDDALVNFALRVGDGRLEEPARKISLTDNRKHIAYLTNLCDEKGEKLG 67

Query: 102 IVGNMA-WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAY--DALDEATRALVHQ 158
N WH+D + A ++ E V GG T FA AA+ ++DE + L
Sbjct: 68 SGNNTDFWHS DQEFRINPASVSILYGESVKCQGNTSFASTSAAHLGYSIDEIS-TLNTL 126

Query: 159 RSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAI 218
S R V S + H+ T P++ + +T + + I +A I
Sbjct: 127 WSTRQPAV-SHDNVPHI-----TV AHPV I IENKQTKKQYVYISENA--I 167

Query: 219 PGMDAAE-----SERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWD----- 269
+D + SE + +++ + +++HQW GD++++DN LLHR E +
Sbjct: 168 KFLDNDQPLPHSEALKQAILEKILSSDNIYSHQWVDGDL LLYDNSQLLHRRRECFTGDRFI 227

Query: 270 --FKL-PRVMWHSRLAGRPETE 288
K+ P V + S + GR E
Sbjct: 228 KALKIYPDVHYQSEIPGREIKE 249

>emb|CBJ18835.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 104

Score = 55.8 bits (133), Expect = 7e-06, Method: Compositional matrix adjust.

Identities = 37/110 (33%), Positives = 53/110 (48%), Gaps = 7/110 (6%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPE 203
AYDA+DE +A + A H +S LG + ++ + P+V+ P
Sbjct: 2 AYDAMDEDMKAFLDPLEAEHFHAFHSHELLGAMPTQEER-----NSIPPAVWPIVR-KPA 54

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL IG HAH + GM A+ L L++ A Q V+ H W GD+
Sbjct: 55 TGRRSLFIGAHAKVIGMPLAQGRMLLLDLEHATQRQFVYRHAWTPGDL 104

>ref|ZP_03525650.1| putative taurine dioxygenase protein [Rhizobium etli CIAT 894]
Length = 169

Score = 55.8 bits (133), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 43/162 (26%), Positives = 70/162 (43%), Gaps = 27/162 (16%)

Query: 15 LGATVTGVHLA-TLDDAGFAALHAAWLQHALLIIFPGQ-HLSNDQQITFAKRFGAI----- 67
+GA + G+ L L D AA++ L+H ++ F Q HL + +Q FA+R G +
Sbjct: 23 VGAEIKGIRLGGELSDTTVAAINQLLLKHKVIFFRDQGHLDSEQEAFARRLGDLVPHPHT 82

Query: 68 --ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
G I+ + + + G Q WH D T++ + +V
Sbjct: 83 QGPVDGTASILNLDSSRGGGRADQ-----WHTDVTFVDAYPKFVSCLR 124

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
V+PA GG T +++ AAY++L + L A HS Y
Sbjct: 125 GVVIPAAGGDTIWSNTHAAYESLPAPLKLAEICGAIHSNAY 166

>emb|CAY25768.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 55.8 bits (133), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 33/108 (30%), Positives = 56/108 (51%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F GQ ++++QQ+ FA FG E GG + +SN+
Sbjct: 16 IEAGMDKYAVLLFRGQDITDEQQALAFALNFGEREHARGGTVTKKEDYRLTSGINDVSNLG 75

Query: 83 ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLFSLGNCLWHS DSSFRPIPAKFSLLSARVV 118

>emb|CAY25746.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY25762.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY25782.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 55.8 bits (133), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 33/108 (30%), Positives = 56/108 (51%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F GQ ++++QQ+ FA FG E GG + +SN+
Sbjct: 16 IEAGMDKYAVLLFRGQDITDEQQALAFALNFGEREHARGGTVTKKEDYRLTSGINDVSNLG 75

Query: 83 ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLFLNCLWHS DSSFRPIPAKFSLLSARVV 118

>emb|CAY25725.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 119

Score = 55.8 bits (133), Expect = 8e-06, Method: Compositional matrix adjust.
Identities = 33/102 (32%), Positives = 53/102 (51%), Gaps = 18/102 (17%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVKADGTVR 88
++A+LIF GQ ++++QQ+ FA FG E+ GG + +SN+ DG
Sbjct: 22 KYAVLIFHGQDITDEQQLAFALNFGEREKARGGTVTKKEDYRLTAGLNDVSNLGKDG--- 78

Query: 89 QHSPAEWDDMMKVIV-GNMAWHADSTYMPVMAQGAVFSAEVV 129
P D + GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 79 --KPLSRDHRTHLFNPGNCLWHS DSSFRPIP AKFSLLSARVV 118

>ref|XP_001267511.1| taurine dioxygenase family protein [Neosartorya fischeri NRRL 181]
gb|EAW25614.1| taurine dioxygenase family protein [Neosartorya fischeri NRRL 181]
Length = 357

Score = 55.8 bits (133), Expect = 8e-06, Method: Compositional matrix adjust.
Identities = 48/173 (27%), Positives = 76/173 (43%), Gaps = 22/173 (12%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
AWH D+ Y A ++ +P GG T + YD + A R+ + +A
Sbjct: 151 AWH TDTGYERNPADYSILKLVKLPETGGDTIWGSSCEIYDKISPAYRSFLEGLTA---T 206

Query: 167 YSQSKLGHVQQAGSAYIGYGM----DTTATPLR---PLVKVHPETGRPSLL-IGRHAHA 217
++Q++L + A + Y + T LR P+V+ +P TG SL +G H
Sbjct: 207 FAQTRL P-ISA AEKGFEL YAE PRGSPNNVGTSLRAVHPVVRTNPVTGWKSLFAVG NHVER 265

Query: 218 IPGMDAAESER----FLEGLVDWACQAPRVHAHQWAAG-DVVVWDNRCLLHRA 265
I + ES R FL+ +V+ R H+W D+ +WDNR + H A
Sbjct: 266 INELTPDESRLHDWFLQMIVEEHDTQLR---HRWENQYDIAIWDNR TVYHSA 315

>ref|XP_001389376.2| tfdA family taurine dioxygenase [Aspergillus niger CBS 513.88]
Length = 357

Score = 55.5 bits (132), Expect = 8e-06, Method: Compositional matrix adjust.
Identities = 43/168 (25%), Positives = 73/168 (43%), Gaps = 9/168 (5%)

Query: 105 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS 164
++ WH D ++ V + A+ +P GG T +A YD L A + +A H
Sbjct: 154 SVGWHTDISFERVPSDYAMLKIHTLPETGGDTLWASGYEIDRLSPEMA AFLEGLTATHD 213

Query: 165 LVY---SQSKLGHVQQAG--SAYIGYGM DTTATPLRPLVKVHPETGRPSLLIGR-HAHAI 218
+ +LG+ + G + + G D A + P+V+ +P TG S+ + + I
Sbjct: 214 ASFFHDEARRLGNPLRK GIRGSPLNQGEDLKA--VHPVVRTNPVTGWKSVYV NKGFTKRI 271

Query: 219 PGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
G+ ES+ L+ L + Q +W D+ +WDNR H A
Sbjct: 272 NGVTKDESDMLLQYLFNLVTQNHDAQVRFRWNKNDMAIWDNRSTWHCA 319

>emb|CBJ19084.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19112.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 105

Score = 55.5 bits (132), Expect = 8e-06, Method: Compositional matrix adjust.
Identities = 38/110 (34%), Positives = 53/110 (48%), Gaps = 6/110 (5%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM DTTATPLRPLVKVHPE 203
A+D LDE TR LV HS ++S+++LG S + A L+ LV+ HP

Sbjct: 2 AWDNLDEPTRELVLPLIGEHSRLFSRAELG-----SDFTDEERLKFAPVLQRLVRRHPS 55

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
T R SL + H I G E+ L L + A Q RV++H W D+

Sbjct: 56 TRRLSLYLSSHCGNIVGWPLPEARALLRELTEHATQREERVYSHAWRTDDL 105

>ref|YP_003270385.1| taurine catabolism dioxygenase TauD/TfdA [Haliangium ochraceum DSM

14365]
gb|ACY18492.1| Taurine catabolism dioxygenase TauD/TfdA [Haliangium ochraceum DSM
14365]
Length = 301

Score = 55.5 bits (132), Expect = 8e-06, Method: Compositional matrix adjust.
Identities = 67/266 (25%), Positives = 100/266 (37%), Gaps = 17/266 (6%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
+ P+G G V V TL A+ + L++ P Q L + F+ R
Sbjct: 3 FESLPSG--FGVRVYDVPRTLTPEDAKAIRMMTYRERLVLPDQDLDAAYVAFSYRLA 60

Query: 66 AIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQ 120
+ D I V A+G V + M V WH+D +
Sbjct: 61 RPQVYLQPNYHHPDHAEIF-VSANGPVHGR-----MGVARTGYVWHSDFEAFNPLA 112

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS-LVYSQSKLGHVQQAG 179
++ +V+P T F DM A+ L A R V A H + + G V +
Sbjct: 113 FSMLYPQVLPKGERSTHFLDMAKAWRRPLSALRERVGLGLHAMHCGRAKYKIQAGDVGRPL 172

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC 238
+ ++ + T + PLV HP TG L I G+ ES L + A
Sbjct: 173 HELLDIVIEHSLTGIHPLVIQHPGTGEELLYASSGFTSRILGLSVYESWSVLREIFRHA 232

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHR 264
+V ++W GD+ +WDNR LLHR
Sbjct: 233 DPAQVVGVEWEDGDIALWDNRALLHR 258

>emb|CAK44006.1| unnamed protein product [Aspergillus niger]
Length = 366

Score = 55.5 bits (132), Expect = 8e-06, Method: Compositional matrix adjust.
Identities = 43/168 (25%), Positives = 73/168 (43%), Gaps = 9/168 (5%)

Query: 105 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS 164
++ WH D ++ V + A+ +P GG T +A YD L A + +A H
Sbjct: 163 SVGWHTDISFERVPSDYAMLKIHTLPETGGDTLWASGYEIDRLSPEMAFLGLTATHD 222

Query: 165 LVY---SQSKLGHVQQAG--SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI 218
+ +LG+ + G + + G D A + P+V+ +P TG S+ + + I
Sbjct: 223 ASFFHDEARRLGNPLRKIRGSPNLNQGEDLKA--VHPVVRTNPVTGWKSVYVNGFTKRI 280

Query: 219 PGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
G+ ES+ L+ L + Q +W D+ +WDNR H A
Sbjct: 281 NGVTKDESDMLLQYLFNLVTQNHDAQVRFWRNKNDMAIWDNRSTWHCA 328

>ref|XP_001031480.1| hypothetical protein THERM_00823780 [Tetrahymena thermophila]
gb|EAR83817.1| hypothetical protein THERM_00823780 [Tetrahymena thermophila
SB210]
Length = 250

Score = 55.5 bits (132), Expect = 8e-06, Method: Compositional matrix adjust.

Identities = 59/266 (22%), Positives = 109/266 (40%), Gaps = 44/266 (16%)

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Query: 8   ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQH----ALLIFPGQHLSNDQQITFAKR 63
++   + LG T+TGV L L + F + A H L+I P + +++ +
Sbjct: 1   MSEVKSQQLGYTITGVDLNNTLTEEQFKNIQEALWTHEKWGKLVILPPYYAFDNRD----PQ 56

Query: 64   FGAIERIGGGDIVAISNVKADGTVRQHSP-AEWDDMMKVIVGNMAWHADSTYMPVMAQG- 121
+ AI R+G NV+ DG+V+ +S AE+ WH D +
Sbjct: 57   YPAIVRVG-----NVRLDGSVKPNSKDAEY-----WHKDG NFRQPGENFI 96

Query: 122  -AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
++   + + VGG+T +A + L + + + +V +Q+ + + A
Sbjct: 97   ISILVPKEIAQVGGQTGYA---CSEQVLKDLPENIKEKLEGAQIIIVRTQT-ISDFKDAKP 152

Query: 181   AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ- 239
+ P+ HP TGR I + + + R ++ +
Sbjct: 153   E-----EHLPEAHHPVFAPHPITGRKVFNITQKNQN--DVILKDG NRIDSKDINPEIEN 204

Query: 240   APRVHAHQWAAGDVVVWDNRCLLHRA 265
+ ++H HQW GDVV+WDN ++HR+
Sbjct: 205   SYKIHGHQWEMGDVVIWDNIRVIHRS 230

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>emb|CAY25783.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 55.5 bits (132), Expect = 8e-06, Method: Compositional matrix adjust.
Identities = 32/102 (31%), Positives = 54/102 (52%), Gaps = 18/102 (17%)

```

Query: 41   QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVKADGTVR 88
++A+LIF GQ ++++Q++ FA FG E+ GG + +SN+ DG
Sbjct: 22   KYAVLIFHGGQDITDEQRLAFALNFGEREKARGGTVTKKEDYRLTTGPN DVS NLGKDG--- 78

Query: 89   QHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAE VV 129
P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 79   --KPLSRDHRTHLFNLGNCLWHSDSSFRPIPAKFSLLSARVV 118

```

>emb|CBI55832.1| unnamed protein product [Sordaria macrospora]
Length = 381

Score = 55.5 bits (132), Expect = 8e-06, Method: Compositional matrix adjust.
Identities = 59/254 (23%), Positives = 101/254 (39%), Gaps = 31/254 (12%)

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Query: 41   QHALLIFPGQH-L SNDQQITFAKRFGAI-----ERIGGGD--IVAIS 79
+ ++ F Q+ L+ND Q R G + +GG D I IS
Sbjct: 88   RRGVVFRAQN NLTNDLQQLILRLGELTGRPSTSGLHIHPILNSDRELGGNDPEISTIS 147

Query: 80   NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVPAVGGRTCF 139
+V+ R S + +++ WH+D + PV A +P GG T +
Sbjct: 148   SVQNRKLYRDWSGEKAEELSTKKQYTSQWHS D IAFEPVPADYTS LRLVQLPKTGGDTLWG 207

Query: 140   DMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQ---QAGSAYIGYGMDTTATPL 194
YD + E + + +A ++L Q +A A G D A +
Sbjct: 208   SGYEIYDRISEPYQKFLEGLTATFEQPGFNKAAELNGFQIYAEARGAPENVGTDLKA--V 265

Query: 195   RPLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWA-AG 251
P+V+ +P TG S+ +G H + G+ ES++ L V+ + + +W+
Sbjct: 266   HPVVRTNPVTGWKSVYPVGGHVKHVNGVTKEESQKLLGW FVELLERNHDLQVRFKWSNEN 325

Query: 252   DVVVWDNRCLLHRA 265
D+ +WDNR + H A
Sbjct: 326   DIAIWDNRSVFHTA 339

```

>emb|CAY25781.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 55.5 bits (132), Expect = 8e-06, Method: Compositional matrix adjust.
Identities = 33/108 (30%), Positives = 56/108 (51%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F Q +S+DQQ+ FA+ FG E GG + +SN+
Sbjct: 16 IEAGVDKYAVLLFRDQDVSDQQLVFARNFGERENARGGTVTKKEDYRLTSGLNDSVNLG 75
Query: 83 ADGTVRQHSPAEDDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG +P D + +G+ WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLFNLGSCLWHSDFSFRPIPAKFSLLSARVV 118

>emb|CAY25749.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 55.5 bits (132), Expect = 8e-06, Method: Compositional matrix adjust.
Identities = 33/108 (30%), Positives = 56/108 (51%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F GQ ++++QQ+ FA FG E GG + +SN+
Sbjct: 16 IEAGMDKYAVLLFRGQDITDEQQLAFALNFGEREHARGGTVTRKEDYRLTSGLNDSVNLG 75
Query: 83 ADGTVRQHSPAEDDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLFNLGNCLWHSDFSFRPIPAKFSLLSARVV 118

>ref|XP_750960.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
fumigatus Af293]
gb|EAL88922.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
fumigatus Af293]
gb|EDP49646.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
fumigatus A1163]
Length = 396

Score = 55.5 bits (132), Expect = 8e-06, Method: Compositional matrix adjust.
Identities = 63/259 (24%), Positives = 102/259 (39%), Gaps = 20/259 (7%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERIGGG 73
+G + GV+LA L+DA L ++ F Q D Q K FG + +
Sbjct: 95 IGTEIHGVNLARLNDLQRRDLARLIAVRGVVFRNQKDFDIDAQRELKGYFGLHKHATT 154
Query: 74 DIVAISNVKADGTVRQHSPAEDDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVVPAV- 132
+ ++ V ++ D + + WH+D TY + + S +V+
Sbjct: 155 AVPKKKGLEDVHV--YTGDNSSDQRALFSPSFLWHSFVTE--IQPPSYTSLKVLGTGPP 210
Query: 133 ---GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT 189
GG T ++ AAYDAL + + +A H+ ++Q + S +G +
Sbjct: 211 RGGGGDTLWSSQYAAAYDALSSHMQNYLKGLTALHT-----ANMQASDSRALGRTVRR 262
Query: 190 TA-TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH- 246
T PL++ +P TG SL I G+ ES+ + L + H
Sbjct: 263 EPITTEHPLIRTNPVTGWNSLFFNPGFVTKIVGIPKTESDAIIRYLTEVVATTQEAHVRF 322
Query: 247 QWAAGDVVVWDNRCLLHRA 265
QW DV +WDNR H A
Sbjct: 323 QWGENDVALWDNRRTTNHSA 341

>gb|ACB30158.1| 2,4-D/alpha-ketoglutarate dioxygenase [Terrabacter sp. DMA]
Length = 111

Score = 55.5 bits (132), Expect = 9e-06, Method: Compositional matrix adjust.
Identities = 40/117 (34%), Positives = 54/117 (46%), Gaps = 7/117 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRAAYDAL ++ + A H + S+ LG + + P+
Sbjct: 1 TEFCDMRAAYDALPRDLQSELEGLRAEHYALNSRFLLGDTDYSEA-----QRNAMPPVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H+W G
Sbjct: 55 WPLVRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQREFVYRHRWNVG 111

>ref|XP_001265562.1| taurine catabolism dioxygenase TauD, TfdA family protein
[Neosartorya fischeri NRRL 181]
gb|EAW23665.1| taurine catabolism dioxygenase TauD, TfdA family protein
[Neosartorya fischeri NRRL 181]
Length = 366

Score = 55.5 bits (132), Expect = 9e-06, Method: Compositional matrix adjust.
Identities = 72/296 (24%), Positives = 114/296 (38%), Gaps = 37/296 (12%)

Query: 13 ATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE-- 68
A +G + + L+ + DDA L Q ++ Q+LS Q A + G +
Sbjct: 47 AAIGREFSTLQLSEILHDDAKIRDLGIIVSQRGVFLRNQNLSIADQKNLAIKIGQLTGR 106

Query: 69 -----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVG-----NMAWHA 110
G + + K D V S + M + G + WH+
Sbjct: 107 PEASYLHKHPLSNGKRGLAVDKDGKLDDEVTIMSSEQNKKMYRGRCGPGTKRLASEGWH 166

Query: 111 DSTYMPVMAQGAVFSAEVVPA-VGGRTCFADMRAAYDALDEATRAL-----VHQRSARH 163
D T+ PV + A+ P VGG T +A AYD L A + H + A +
Sbjct: 167 DITFEPVPSDYAILKIVTPPEDVGGDTLWASGYEAYDRLSPAWKKFAEGLTATHYQPAFN 226

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI-GRHAHA--IPG 220
V +Q + G+ G++ A+ P+V+ +P TG SL G A I
Sbjct: 227 DAVRNQDMELITENRGNPE-NSGVEFKAS--HPVVRTNPVTGWKSLFAAGFQIRAGWIDN 283

Query: 221 MDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRV 275
+ ESE + + + +W+ DV +WDNR+ H A +D+ RV
Sbjct: 284 VTDYESEMLKSYFLKLISENHDLQVRFRWSENDVAIWDNRCVFHTAT-YDYNGARV 338

>ref|XP_501183.1| YALI0B21472p [Yarrowia lipolytica]
emb|CAG83436.1| YALI0B21472p [Yarrowia lipolytica]
Length = 345

Score = 55.5 bits (132), Expect = 9e-06, Method: Compositional matrix adjust.
Identities = 50/167 (29%), Positives = 71/167 (42%), Gaps = 10/167 (5%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGG-RTCFADMRAAYDALDEATRALVHQRSARHSL 165
WH D T+ V + AV P GG T +A AY+ L A RA + +A HS
Sbjct: 138 GWHTDITFEKVPSPDYAVLKILSPPTGGGGDTLWASGYHAYEKLTPAYRAFLTLTAHHS 197

Query: 166 VYSQ-----SKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIP 219
Y + S G V++ + G A PL++ +P TG S+ + +I
Sbjct: 198 EYFKTVAAASGHGIVERPRGHPLNQGDYLAQAD--HPLIRTNPVTGWKSVYVNPIFTKSIN 255

Query: 220 GMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
G+ ES+ LE L + H +W DV +WDNR H A

Sbjct: 256 GLSWDESKSILEFLNQNLVENHDTTHRFRWNPNDVAIWDNRSTYHTA 302

>emb|CBJ18986.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 55.5 bits (132), Expect = 9e-06, Method: Compositional matrix adjust.
Identities = 38/112 (33%), Positives = 53/112 (47%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-LVKVH 201
AAYDALD+ T+ V HS +YS+ +G + + P+R LV+ H
Sbjct: 1 AAYDALDDETKEEVQDMVCEHSQMYSRQIIGFYDFTDDERVKWA-----PVRQRLVRRH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P +GR SL + HA I G E+ L L + A Q V+AH W D+
Sbjct: 55 PRSGRLSLYLSSHAGEIEGWPVPEARASLRDLNEHATQRQFVYAHVWRPHDI 106

>emb|CAY25726.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 55.5 bits (132), Expect = 9e-06, Method: Compositional matrix adjust.
Identities = 33/108 (30%), Positives = 55/108 (50%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F Q +S+DQQ+ FA+ FG GG + +SN+
Sbjct: 16 IEAGMDKYAVLLFRDQDVSDQQLVFARNFGERGNARGGTVTKKEDYRLTSGLDVSNL 75

Query: 83 ADGTVRQHSPAEDDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLFLNGLNCLWHSDDSSFRPIPAKFSLLSARVV 118

>emb|CBJ19176.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 104

Score = 55.5 bits (132), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 36/110 (32%), Positives = 55/110 (50%), Gaps = 7/110 (6%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE 203
AYDA+D +A + A H +S+ LG + ++ + P+V+ P
Sbjct: 2 AYDAMDVDMKAFLDPLEAEHFHAFHSRELLGAMPTQEER-----NSIPPAVWPIVR-KPA 54

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
TGR SL IG HAH + GM A+ L L++ A Q V+ H+W+ GD+
Sbjct: 55 TGRSLFIGAHAKVIGMPLAQGRMLLLDLLEHATQRQFVYRHEWSPGDL 104

>emb|CAY25722.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 55.5 bits (132), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 32/102 (31%), Positives = 53/102 (51%), Gaps = 18/102 (17%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVKADGTVR 88
++A+LIF GQ ++++QQ+ FA FG E+ GG + +SN+ DG
Sbjct: 22 KYAVLIFHGQDITDEQQLAFALNFGEREKARGGTVTKKEDYRLTTGLNDVSNLGKDG--- 78

Query: 89 QHSPAEDDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
P D + +GN WH+DS++ P+ + ++ SA VV
Sbjct: 79 --KPLSRDHRTHLFLNGLNRLWHSDDSSFRPIPVKFSLLSARVV 118

>emb|CAY25787.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 55.5 bits (132), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 32/103 (31%), Positives = 54/103 (52%), Gaps = 20/103 (19%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVKADGT-- 86
++A+LIF GQ ++++QQ+ FA FG E+ GG + + N+ DG
Sbjct: 22 KYAVLIFHGQDITDEQQLAFAFNFGEREKARGGTVTKKEDYRLTTGLNDVFNLGKDGKPL 81

Query: 87 VRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV 129
R H ++ +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 82 FRDHRTHLFN-----LGNCWLHSDSSFRPIPAKFSLLSARVV 118

>dbj|BAE92218.1| 2,4-D/alpha-ketoglutarate dioxygenase [Ralstonia sp. Y103]
dbj|BAE92219.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. Y212]
dbj|BAE92220.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. C308]
dbj|BAE92221.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. T201]
dbj|BAE92222.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. T301]
dbj|BAE92223.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. M701]
dbj|BAE92224.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. H801]
dbj|BAE92225.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. Ff54]
Length = 109

Score = 55.5 bits (132), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 38/115 (33%), Positives = 54/115 (46%), Gaps = 7/115 (6%)

Query: 142 RAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR-PLVKV 200
RAAYD L E + + A H ++S+ LG + + S P+ PL++
Sbjct: 1 RAAYDDLPEDFKKELQGLRAEHYALHSRFLGDTEYSES-----QRNAMPPVSWPLIRT 54

Query: 201 HPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+
Sbjct: 55 HAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQPKFVYRHSWKVGDLMV 109

>ref|XP_001387032.1| predicted protein [Scheffersomyces stipitis CBS 6054]
gb|EAZ63009.1| predicted protein [Pichia stipitis CBS 6054]
Length = 412

Score = 55.1 bits (131), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 61/264 (23%), Positives = 104/264 (39%), Gaps = 27/264 (10%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE---RI 70
+G + G+ L+ L D L + ++ F Q LS +Q + FG +E ++
Sbjct: 123 IGTEIVGLQLSELTDQQRDELALLIAERVVVFVRDQDLSPQKQFELGEYFGKVEVHPQQV 182

Query: 71 GGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVP 130
I I+ + + ++ P + + WH D + + +P
Sbjct: 183 HVPGIRGITVIWPE-LFKKFGPITFRKTLNHFTSR--WHTDLVHELQPPGITHLHNDTIP 239

Query: 131 AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ--AGSAYIGYGM 188
VGG T +A AAYD L A + + + A + +S +K + G+ +I
Sbjct: 240 EVGGDTVWASGYAAYDKLSPALQEFLDGKKA---VYFSANKYVDRENPLKGTVHIERE-- 294

Query: 189 TTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAH- 246
P+++ HP TG SL + R + I G++ ES+ LE L D + +
Sbjct: 295 -----HPIIRTHPVTGWKSLYVNRAMTSRIVGLEPGESKVILEYLFDFVEKNLDIQVRF 348

Query: 247 -----QWAAGDVVVVDNRCLLHRA 265
Q G +WDNR H A
Sbjct: 349 NWKPSQPLGTSALWDNRISQHFA 372

>ref|ZP_06475349.1| dioxygenase, TauD/TfdA [Frankia symbiont of Datisca glomerata]
gb|EFD27965.1| dioxygenase, TauD/TfdA [Frankia symbiont of Datisca glomerata]
Length = 126

Score = 55.1 bits (131), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 35/86 (40%), Positives = 47/86 (54%), Gaps = 8/86 (9%)

Query: 196 PLVKVHPETGRPSL---LIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG 251
P+V VHPETGR L L+ RH I G++ ES L L D + V ++W G
Sbjct: 26 PVVAVHPETGRKDLFVNPLLRH---IKGLEPVESAALLALLYDRGARLENNVIQYRWRRG 82

Query: 252 DVVVWDNRCLLH-RAEPWDFKLPRVM 276
D+V+WDNR + H R E D PR++
Sbjct: 83 DLVLWDNRRAVRHRRVEDNDPAAPRIV 108

>ref|XP_002165715.1| PREDICTED: similar to Taurine catabolism dioxygenase TauD, TfdA
family protein [Hydra magnipapillata]
Length = 325

Score = 55.1 bits (131), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 52/245 (21%), Positives = 98/245 (40%), Gaps = 39/245 (15%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAI-----ERIGGGDIVAISNVKADGTVR- 88
+H +++ Q+L+ +QQ F R G +G I +SN +G+ +
Sbjct: 83 KHGVVVIKNQNLTRNQEVFTARLGKTIILPSSFQGNNSYLGHPAIAVVSNYWLNKSWKG 142

Query: 89 -QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS---AEVVPVAV--GGRTCFADMR 142
QHS ++ WH D Y P +FS + + A GG T F D
Sbjct: 143 PQHSFGQY-----WHKGDGYFPY-PNNFIFSILYGDEISAFLEGGDTGFID-- 187

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
A + A +++ ++ +V K+ + + + ++ AT + HP
Sbjct: 188 -GCLAAENAPQSILDVLNSTKIIV---KVSFIDDFRNLKDH-LELYATVKHNFISKHP 241

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL 262
R + + + A + E R + + + Q + H+W+ D+++WDN +
Sbjct: 242 LNKRDVCFMFKVAKQELLYTQEELRAFDEMWKYMLQDKFFYFHKWSQSDILIWDNMAVF 301

Query: 263 HRAEP 267
HRA P
Sbjct: 302 HRAMP 306

>ref|YP_003040556.1| pyoverdine biosynthesis protein PvcB-like protein [Phototaxillum
asymbiotica subsp. asymbiotica ATCC 43949]
emb|CAQ83812.1| similar to pyoverdine biosynthesis protein pvcB of pseudomonas
aeruginosa [Phototaxillum asymbiotica]
Length = 281

Score = 55.1 bits (131), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 72/306 (23%), Positives = 118/306 (38%), Gaps = 53/306 (17%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG--QHLSNDQQIT-FA 61
T +I P G + + H+ TL L +H LLI G +LS+ ++ +A
Sbjct: 9 TEEIFPFGKITPQYSDQHIDTSLVEQLKELTK--KHNLLILRGFKSNLSDHEKYEYEA 65

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGN--MAWHADSTYMPVMA 119
+ +G I G I+ VR+H D + N M H D Y P +
Sbjct: 66 RNWGEIMMWPFGAIL-----DVREHQ-----DATDHVFDNSYMPHWDGMYKPTIP 111

Query: 120 QGAVFSAEVVPAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
+ +F P GGRT F + R + AT+ + Q S+ Y +K+ H
Sbjct: 112 EFIMFHCAHAPESDQGGRTTFVNTRRV---IANATQQQLSQWKNI-SVTYRINKITH--- 164

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPE-----TGRPSL----LIGRHAHAIPGMDAAES 226
YG + + PL++ HP+ P++ + +HA + +
Sbjct: 165 -----YGGEVHS---PLLEEHPDGNGYVIRYNEPAIDGEKFLNKHAIEYHNISPDQV 213

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPE 286
F + ++ ++AH W GD+V+ DN LLH E + K R + + P
Sbjct: 214 AEFQQDFINILYDKRHLYAHSWQKGDLVVDNFSLLHGREGFTSKSERHLQRIHIQSNPV 273

Query: 287 TEGAAL 292
AL
Sbjct: 274 FNNQAL 279

>ref|XP_001903801.1| hypothetical protein [Podospora anserina S mat+]
emb|CAP61577.1| unnamed protein product [Podospora anserina S mat+]
Length = 377

Score = 55.1 bits (131), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 46/194 (23%), Positives = 76/194 (39%), Gaps = 27/194 (13%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
AWH+D T+ PV + A+ +P GG T +A YD L E R ++ + +A H
Sbjct: 157 AWHSDITFEPVPSDYAMLKIHTLPVTGGDTLWASGYEVYDRLSEPMREMLKLTATHTDAK 216

Query: 167 Y---SQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPE----- 203
+ LG+ + + P+++ + E
Sbjct: 217 FFLDEARNLGNPLRECERGSPLNKGAEELAAVHPVIRTNREFPHLCLCTSLRVKLTTFMVIA 276

Query: 204 -TGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVDNR 260
TG S+ + + I G+ ES+ L+ L + Q +W+ DV +WDNR
Sbjct: 277 VTGWNSVYVNGFTKRINGVTKDESILLKYL FNMVTQNHDAQVRFVRSKNDVAIWDNRS 336

Query: 261 LLHRAEPWDFKLPR 274
H A +D+ PR
Sbjct: 337 TWHCAT-YDYNDPR 349

>ref|ZP_07151278.1| taurine dioxygenase domain protein [Escherichia coli MS 21-1]
gb|EFK21949.1| taurine dioxygenase domain protein [Escherichia coli MS 21-1]
Length = 127

Score = 55.1 bits (131), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 39/139 (28%), Positives = 63/139 (45%), Gaps = 23/139 (16%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFRLDQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTC 137
GA+ +A+ +P+ GG T
Sbjct: 109 PAGAILAAKELPSTGGDTL 127

>ref|XP_002900145.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Phytophthora infestans T30-4]

gb|EEY60349.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Phytophthora infestans T30-4]
Length = 355

Score = 55.1 bits (131), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 62/274 (22%), Positives = 103/274 (37%), Gaps = 30/274 (10%)

```
Query: 4   TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
          T   +T   +G  ++G+ L  L  +   L   ++ F  Q  ++ +QQ+  +
Sbjct: 70  TDATVTHLAPKIGTELSGIQLHELNSVQRDELALLIAHRGVVFFRDQEVNIEQQLELGRY 129

Query: 64  FGAI---ERIG-----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY 114
          +G +   + +G           +V  S   ++G +++   ++           AWH+D +
Sbjct: 130 YGPLHAHQNLGHPKDHHEVVVENSSETSEGFLKRQMYDPFN-----AWHSDVSN 179

Query: 115 MPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
          F   P  VGG T +A   AYD L   R  +   +A H+   G
Sbjct: 180 ERQPPSYTSFKVLTNPPVGGDTLWASASEAYDRLTPPMREFISGLTAIHT-----GI 231

Query: 175 VQQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
          Q   +A  G  +   P+V+ HP  TGR  L  +   I  +  AES+  L+
Sbjct: 232 PQATAAAARQQTIRPPVEFEHPVVRTHPVTGRQGLYVNPFAFTTRIVQLSKAESDAVLKL 291

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
          L   A  +   H   W   V  +WDNR  H  A
Sbjct: 292 LYQHATEGHEFHVRFSWTKNAVAIWDNRSTFHYA 325
```

```
>ref|XP_571891.1| hypothetical protein [Cryptococcus neoformans var. neoformans
JEC21]
ref|XP_774302.1| hypothetical protein CNBG2830 [Cryptococcus neoformans var.
neoformans B-3501A]
gb|EAL19655.1| hypothetical protein CNBG2830 [Cryptococcus neoformans var.
neoformans B-3501A]
gb|AAW44584.1| conserved hypothetical protein [Cryptococcus neoformans var.
neoformans JEC21]
Length = 432
```

Score = 55.1 bits (131), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 69/264 (26%), Positives = 106/264 (40%), Gaps = 31/264 (11%)

```
Query: 15  LGATVTG-VHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERIGG 72
          +G  V G V L  L +A   L   Q  ++ F  Q  ++ +QQ   K FG + +
Sbjct: 122 IGTVEGDVKLEDLGEAEKDDLALLVAQRGVVFFRNQQSMTIEQQRELKHFGLPKHAT 181

Query: 73  -----GDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
          GD+  +  V +D   R  P   D+   +  +H+D TY   +
Sbjct: 182 YATPRRGDLDDVVVVYSD---RDSRP----DLYAFSRAEL-FHSDVTYEVQPPGTTMLRL 233

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG 186
          P  VG  T ++   + Y +L +   +   SA HS   G  Q  S+   +
Sbjct: 234 LTTPEVGNDTLWSSGYSVYSSLSKPFQQYLESLSAIHS-----GFDQ--ASSRTNFS 283

Query: 187 MDTTATPLR---PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD-WACQAP 241
          P+   P+V+VHP TG  S+ +   + G+  AES+  L  L D +A  Q
Sbjct: 284 KIPRREPIETIHPVVRVHPVTGMKSVFVNPGFVTRLVGVPKAESDMVLSFLKDCFAQQTD 343

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRA 265
          WA GDV +WDNR + H  A
Sbjct: 344 ATVRWSWAPGDVAIWDNRNVNHS 367
```

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>dbj|BAD15043.1| hypothetical protein [Bradyrhizobium sp. BDV5680]
```

Length = 102

Score = 55.1 bits (131), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 35/107 (32%), Positives = 50/107 (46%), Gaps = 5/107 (4%)

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGR 206
ALD+ T+A + HSL+YS+ LG + Y + L+ LV+ HP R
Sbjct: 1 ALDDETKAEIEDFVCEHSLMYRSGSLGFAE-----YTDDEKEMFKPVLQRLVVRTHPVHRR 55

Query: 207 PSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
SL + HA + GM E L L + A QA V+ H+W D+
Sbjct: 56 KSLYLSSHAGKVVGMSVPEGRVLLRDLNEHATQAEFVYVHKWRLHDL 102

>ref|XP_002149540.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Penicillium marneffeii ATCC 18224]
gb|EEA23373.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Penicillium marneffeii ATCC 18224]
Length = 419

Score = 55.1 bits (131), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 64/271 (23%), Positives = 107/271 (39%), Gaps = 35/271 (12%)

Query: 16 GATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRFGAIERIG- 71
G + GV ++ L G + + L+F Q N ++Q A+ FG + + G
Sbjct: 128 GTEIQGVQISELTPEGLDEMLLCAERGCIVFRDQEFGNIGFEKQKEIARHFGPLHKHGW 187

Query: 72 -GGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA--EV 128
A+ + + + V + E + +H D + V G F E
Sbjct: 188 MPHPRAAVHSSSETEEFVIVYDSKEKSPIQ-----FHVDQS-PEVQPPGMTFFCMLES 238

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 188
P GG T + M A++ L + R + A H+ S+ ++ G +
Sbjct: 239 PPGAGGDTLISSMTRAFLRSPSFRKRLEGLQALHTTAGPVSR--ELRDNGKGAVLRRPI 296

Query: 189 TTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLV-----DWACQA 240
+A + P+V VHP TG+ +L + + I G D ESE L L D+ C+
Sbjct: 297 NSA--IHPVTVHPVTGQKALFVNSSYTERIIGWDDEESEYLLRFLFDHVNRRGQDFCCRV 354

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFK 271
++ G VVVWD R H ++ D+K
Sbjct: 355 -----RYEPGTVVVWDQRTVQH-SQTLQYK 378

>emb|CAY25721.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 55.1 bits (131), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 34/110 (30%), Positives = 55/110 (50%), Gaps = 18/110 (16%)

Query: 33 AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISN 80
A + A + A+L+F Q +++DQQ+ FA+ FG E GG + +SN
Sbjct: 14 ADIEAGMDKCAVLLFRDQDITDDQQLIFARNFGERENARGGTVTKKEDYRLTSGLNVDVN 73

Query: 81 VKADGTVRQHSPAEDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVS 129
+ DG P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 74 LGKDG-----KPLPKDHRTHLFLNGLNCLWHSDDSSFWPIPAKFSLLSARVV 118

>ref|XP_002549195.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Candida
tropicalis MYA-3404]
gb|EER33067.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Candida
tropicalis MYA-3404]

Length = 388

Score = 55.1 bits (131), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 64/236 (27%), Positives = 98/236 (41%), Gaps = 20/236 (8%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQ---ITF 60
+T +ITP G V G+ L+ LDD G L Q +L+F Q ++ + F
Sbjct: 82 STKRITPN---FGTEVDGIQLSQLDDKGKDELALFLAQRKVLFFNDQDFADKGPFGFAVEF 138

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ 120
K FG + I + T R+ E + ++ +H+D +Y ++
Sbjct: 139 GKYFGR LH-IHPSSGAPRGYPELHITYRRPEKGELQRVFANRTTSIGFHS DVS YELTPSR 197

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
VFS + GG T F D AY L + AL + H L S+ Q A S
Sbjct: 198 FTVFSV-LESGDGGDTVFVDAGEAYRRL---SPALQQRLEGLHVLHTSED-----QAANS 248

Query: 181 AYIGYGMD--TTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL 233
Y G G++ + + PLV++ P TG SL + R I + ES+ L+ L
Sbjct: 249 TYQG-GVERRKPVSNIHPLVRLDPVTGEKSLYVNRAFGRRIVELKKEESDALLDLDFL 303

>ref|XP_003028210.1| hypothetical protein SCHCODRAFT_70480 [Schizophyllum commune H4-8]
gb|EFI93307.1| hypothetical protein SCHCODRAFT_70480 [Schizophyllum commune H4-8]
Length = 401

Score = 55.1 bits (131), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 62/266 (23%), Positives = 102/266 (38%), Gaps = 29/266 (10%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA----- 66
+G + G+ L L D L + ++ F Q + Q+ A+ +G
Sbjct: 98 IGTVLKGIDLRQLSDTQKDELALLVAERG VVFFRDQEIDVHGQLDLARYWGKLHKHATTP 157

Query: 67 IERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA 126
I R G ++ + N + R+ P + + WH+D +Y
Sbjct: 158 IPRNGLEE VHVYNDHS----RRPDPQAFSKLQ-----LWHS DVS YERQPPSTTSLKV 206

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG 186
P GG T ++ A Y +L + + +A HS V A +A +
Sbjct: 207 ISGPEYGGDTHWSSGYAVYSSLSPGFQKYLEGLTALHS AV-----AQADGARAAGLPVR 260

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
D T + P+V+VHP TG S+ + I G+ AES+ L+ L + P A
Sbjct: 261 RDPIET-IHPVVRVHPVTGWKSVYVNHGFTTRRIIGVPKAESDAILQFLFHQFAENPDFQA 319

Query: 246 H-QWAAGDVVVWDNRCLLHRAEPWDF 270
W + +WDNR + H A +DF
Sbjct: 320 RFHWKPN SIAIWDNRV VNH SAT-FDF 344

>emb|CAY25754.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 55.1 bits (131), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 33/102 (32%), Positives = 53/102 (51%), Gaps = 18/102 (17%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVKADGTVR 88
++A+LIF GQ ++++QQ+ FA FG E+ G I +SN+ DG
Sbjct: 22 KYAVLIFHGQDITDEQQLAFALNFGEREKARGSTITKKEDYRLTTGLNDVSNLKGKD--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAE VV 129
P D + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 79 --KPLSRDHRTHLFNLGNCPWHS DSSFPPIPAKFSLLSARVV 118

>ref|XP_459377.1| DEHA2E01188p [Debaryomyces hansenii CBS767]
emb|CAG87583.1| DEHA2E01188p [Debaryomyces hansenii]
Length = 413

Score = 55.1 bits (131), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 63/282 (22%), Positives = 104/282 (36%), Gaps = 55/282 (19%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGD 74
+G + G+ L L+D L + ++ F Q LS +Q+ +G +E+
Sbjct: 125 IGTEIIGLQLKDLNDQQKDELALLIAERVVFFRDQDLSPQKQLELGSYWGTVEK--HAQ 182

Query: 75 IVAISNVKADGTVRQHSPA EWDDMMK-----VIVGNMAWHADSTYMPVMAQGAV 123
V + + + W D+ + + G WH D T+
Sbjct: 183 QVHVPGLHGITVI-----WQDLFRRNGLDINFKNAIGQGTISIWHTDLTHELQPPGITH 235

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
+ +P VGG T ++ AAYD L A + + ++A V + + Y+
Sbjct: 236 LHNDAIPGVGGDTVWSSGYAAYDKLSPAFQKFLGKNA-----VYISANKYV 282

Query: 184 GYGMDTTATPLR-----PLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGL 233
PLR P+++ HP TG SL + R I G++ ES+ LE L
Sbjct: 283 -----DRENPLRGSANIEREHPIIRTHPATGWKSLFVNRSMTTRIVGLEPEESKVILEYL 337

Query: 234 VDWACQAPRVHAH-QWAA-----GDVVVDNRCLLHRAEPWD 269
+ + + W G +W DNR H A WD
Sbjct: 338 FEVFENLDIQVRFNWKPTIDGLGTSALW DNRVSQHFA-IWD 378

>ref|NP_930051.1| hypothetical protein plu2817 [Photorhabdus luminescens subsp.
laumondii T101]
emb|CAE15191.1| unnamed protein product [Photorhabdus luminescens subsp. laumondii
T101]
Length = 281

Score = 54.7 bits (130), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 73/306 (23%), Positives = 118/306 (38%), Gaps = 53/306 (17%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG--QHLSNDQQI-TFA 61
T +ITP G + + H+ TL L +H LLI G LS+ ++ +A
Sbjct: 9 TEEITPFGKLTIPQYSDQHIDTL--PVEQLKELARKHLLILRGFKSDLSDEKYEKYA 65

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGN--MAWHADSTYMPVMA 119
+ +G I G I+ VR+H D + N M H D Y P +
Sbjct: 66 RNWGEIMMWPF GAIL-----DVREHQ----DATDHVFDNSYMPLHWDGMYKPTIP 111

Query: 120 QGAVFSAEVPVAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
+ +F P GGRT F + R + AT+ + Q S+ Y +K+ H
Sbjct: 112 EFIMFHCAHAPESDQGGRITFVNTRRV---VANATQQQLEQWKNI-SITYRINKVTH--- 164

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETG-----RPSL----LIGRHAHAIPGMDAAES 226
YG + + PLV+ HP+ P++ + +HA ++ +
Sbjct: 165 -----YGGEVHS---PLVEEHPDRNGFVIRYNEPAVDGEKFLNKHAIEYHNINPDQV 213

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAAGDVVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPE 286
F + ++ ++AH W D+V+ DN LLH E + K R + + P
Sbjct: 214 AEFQQDFINILYDKRHLYAHAWKKS D LVVDNFSLHGREGFTSKSERHLQRIHIQSNPA 273

Query: 287 TEGAAL 292
AL
Sbjct: 274 FNNQAL 279

>emb|CAY25738.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 54.7 bits (130), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 32/102 (31%), Positives = 52/102 (50%), Gaps = 18/102 (17%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVKADGTVR 88
++ +LIF GQ ++++QQ+ FA FG E+ GG + +SN+ DG
Sbjct: 22 KYTVLIFHGQDITDEQQLAFLNFGEREKARGGTVTKKEDYRLTTGLNDVSNLGKDG--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
P D + +GN WH+DS++ P A+ ++ SA VV
Sbjct: 79 --KPLSRDHRTHLFLNGLNCLWHS DSSFRPTAEFSLLSARVV 118

>ref|XP_001268176.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
clavatus NRRL 1]
gb|EAW06750.1| alpha-ketoglutarate-dependent taurine dioxygenase [Aspergillus
clavatus NRRL 1]
Length = 397

Score = 54.7 bits (130), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 62/257 (24%), Positives = 98/257 (38%), Gaps = 16/257 (6%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQ-QITFAKRFGAIERIGGG 73
+G + GV+L L+DA L ++ F Q + Q Q K FG + +
Sbjct: 96 IGTEIRGVNLGKLNDQAQRDDLARLIAVRGVVFFRNQKDFDIQAQRELKGYFGTLHKHATT 155

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVVPAVG 133
+ ++ V ++ D + + WH+D TY P G
Sbjct: 156 AVPKKKGLEDDVHV--YTKENAGDQRALFPFSLWHS DVTYEVQPPSYTSLKVLTPGPRG 213

Query: 134 G--RTC FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD-TT 190
G T ++ AAYDAL + + +A HS ++Q + S +G +
Sbjct: 214 GGGDTLWSSQYAAAYDALSSHMQNYLKGLTALHS-----ANMQASDSRALGRTVRRDP 265

Query: 191 ATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW 248
T PL++ +P TG SL I G+ ES+ ++ L + H QW
Sbjct: 266 VTTEHPLIRTNPVGTGWSLFFNPGFVTKIVGIPKTESDAI IKYLTEIIATTQEAHVRFQW 325

Query: 249 AAGDVVVWDNRCLLHRA 265
DV +WDNR H A
Sbjct: 326 GEDDVALWDNRRTTNHSA 342

>ref|XP_003051284.1| hypothetical protein NECHADRAFT_41873 [Nectria haematococca mpVI
77-13-4]
gb|EEU45571.1| hypothetical protein NECHADRAFT_41873 [Nectria haematococca mpVI
77-13-4]
Length = 379

Score = 54.7 bits (130), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 67/289 (23%), Positives = 110/289 (38%), Gaps = 42/289 (14%)

Query: 13 ATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERI 70
A +G + L+ + DD L Q ++ F Q ++ + Q +R G E
Sbjct: 60 AVIGREFPKLQLSEILKDDTKLRDLAVLISQRGVVFFRNQDINIEDQKYLQRLG--ELT 117

Query: 71 GGGDIV-----AISNVKADGTVRQHSPAEWDDMMKVI-----VGNM 106
G + A+SN K V ++ + DD + VI +
Sbjct: 118 GKPETSKLHRHALSNSKRGIAVDEN--GKLDDEVSVISSEQNRKFYSDFSSLSRSLAGE 175

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPA-VGGRTCFADMRAAYDALDEATRALVHQRSARH-- 163
WHAD T+ + + A+ P VGG T +A YD L + L +A H
Sbjct: 176 GWHADITFENIPSDYAILKIIQPPEDVGGDTLWASGYELYDRLSPPIQKLAESLTATHHQ 235

Query: 164 -SLVYSQSKLGH--VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH---AHA 217
+ V +++ G + + + G+D A P+++ +P TG SL H A
Sbjct: 236 PNFVRVKNEFGQELIDENRGSPENGLDFKAE--HPVIRTNPVTGWKSLFAAGHQLTAGH 293

Query: 218 IPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
I G+ ESE + + +W D+ +WDNR + H A
Sbjct: 294 INGVTESEILKNYFRQLITENHDLQVRFWGNLAIWDNRSVFHTA 342

>emb|CAY25743.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 54.7 bits (130), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 33/110 (30%), Positives = 55/110 (50%), Gaps = 18/110 (16%)

Query: 33 AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISN 80
A + A ++A+L+F Q +++QQ+ FA FG E GG + +SN
Sbjct: 14 ADIEAGMDKYAVLLFRNQDITDEQQALAFALNFGERESARGGTVTKKEDYRLTSGLNVDVN 73

Query: 81 VKADGTVRQHSPAEDDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
+ DG P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 74 LGKDG-----RPLARDSRTHLFNLGNCLWHSDDSSFRPIPAKFSLLSARVV 118

>emb|CAY25730.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 54.7 bits (130), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 33/110 (30%), Positives = 55/110 (50%), Gaps = 18/110 (16%)

Query: 33 AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISN 80
A + A ++A+L+F Q +++ QQ+ FA+ FG E GG + +SN
Sbjct: 14 ADIEAGMDKYAVLLFRDQDITDGQQILIFARNFGERENARGGTVTKKEDYRLTSGLNVDVN 73

Query: 81 VKADGTVRQHSPAEDDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
+ DG P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 74 LGKDG-----KPLPKDHRTHLFNLGNCLWHSDDSSFRPIPAKFSLLSARVV 118

>ref|XP_746445.1| TfdA family taurine dioxygenase [Aspergillus fumigatus Af293]
gb|EAL84407.1| TfdA family taurine dioxygenase, putative [Aspergillus fumigatus Af293]
gb|EDP47069.1| TfdA family taurine dioxygenase, putative [Aspergillus fumigatus A1163]
Length = 350

Score = 54.3 bits (129), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 67/281 (23%), Positives = 107/281 (38%), Gaps = 47/281 (16%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
A + +TP +G + G+ L L A L + ++ F Q + +QI FA
Sbjct: 81 ATEIIHLTPD---IGTEIAGLQLTALTPAQKDDLALLVAERGVVFFRDQMDVHEQIAFA 137

Query: 62 KRFGA--IERIGG--GDIVAINVKADGTV---RQHSPAEDDDMMKVIVGNMAWHADSTY 114
FG I ++ G D+ + + D T R H WH+D +Y
Sbjct: 138 AYFGELHIHQMAGIIPDLPVWHPIYKDRITAVNGRSHQ-----IWHSDVSY 182

Query: 115 MPVMAQGAVFSAEVVPA-----VGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167

```

      +   + +PA      GG T +A   A Y++L   RA +   A+HS
Sbjct: 183 ELQPPGLTMLRMDTLPAAGPGGSLAGGDTVWASGYALYESLSPKLRAFLETLEAKHS--- 239

Query: 168 SQSKLGHVQQAGSAYIGYGM---DTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDA 223
      ++QA A   G   D   T + P+V+ HP T   +L +   +   I G++
Sbjct: 240 -----GLEQAEKALKTNGCLRRDPIET-IHPVVRTHPVTKWKTLYVNFNFTKEIIGIEK 292

Query: 224 AESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLH 263
      S+ L+ L   +A   +W   V +WDNR   H
Sbjct: 293 RVSDALLDTLYRTIAEAYEQVRWKWTPNAVAIWDNRVTFH 333

```

>gb|EFY94168.1| hypothetical protein MAA_10359 [Metarhizium anisopliae ARSEF 23]
Length = 359

Score = 54.3 bits (129), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 58/255 (22%), Positives = 96/255 (37%), Gaps = 36/255 (14%)

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Query: 41 QHALLIFPGQH-LSNDQQITFAKRFGAI-----ERIGGGDIVAISNVK 82
      + ++ F Q L+ND Q   R G +   ER GG   IS +
Sbjct: 74 ERGVVFFRAQDDLNDLQKELILRLGKLTGRPETSGLHIHPLLNSERELGGS DPEISTIS 133

Query: 83 ADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR 142
      +   + + E + +   WH+D + PV A   +P GG T +A
Sbjct: 134 SVQHQQYYKNTAEALSPKKQTTAQWHS DIAFEPVPADYTSRLVQLPKTGGDTLWASGY 193

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQS KLGHV--QQAGSAY-----IGYGM DTTATP 193
      YD + E + +   ++ + Q G V +Q Y   G + A
Sbjct: 194 EIYDKISEPYQKFLETL----TVTFEQPGFGAVAERQGFQLYDKPRGAPENVGRELKA-- 247

Query: 194 LRPLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWA-A 250
      + P+V+ +P TG S+ +G H I G+ ES+ L+ +D   +   +W
Sbjct: 248 VHPVVRTNPVTGWKSIFPVGGHVSHINGVTKEESQNLQWFLDLVYHNHDLQVRFKWQNP 307

Query: 251 GDVVVWDNRCLLHRA 265
      D+ +WDNR + H A
Sbjct: 308 NDIAIWDNRSVFHTA 322

```

>emb|CBJ18856.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 104

Score = 54.3 bits (129), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 36/110 (32%), Positives = 53/110 (48%), Gaps = 7/110 (6%)

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Query: 144 AYDALDEATRALVHQRSARHSLVYSQS KLGHVQQAGSAYIGYGM DTTATPLRPLVKVHPE 203
      AYDA+DE +A +   A H +S+ LG +   ++   + P+V+ P
Sbjct: 2 AYDAMDEDMKAFLDPLKAEHF AFHSRELLGAMPTQEER-----NSIPPAVWPPIVR-KPA 54

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
      TGR SL G HAH + GM A+ L L++ A Q V+ H W GD+
Sbjct: 55 TGRSLFTGAHAHKVIGMPLAQGRMLLLDLLEHATQRQFVYRHAWTPGDL 104

```

>emb|CAY25761.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 54.3 bits (129), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 33/110 (30%), Positives = 55/110 (50%), Gaps = 18/110 (16%)

```

Query: 33 AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISN 80
      A + A ++A+L+F Q +++++QQ+ FA FG E GG +   +SN
Sbjct: 14 ADIEAGMDKYAVLLFRNQDITDEQQALAFALNFGERESARGGTVTKKEDYRLTSGLNDVSN 73

```

Query: 81 VKADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
+ DG P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 74 LGKDG-----RPLARDSRAHLFNLGNCLWHS DSSFRPIPAKFSLLSARVV 118

>emb|CAY25748.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 54.3 bits (129), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 32/108 (29%), Positives = 54/108 (50%), Gaps = 18/108 (16%)

Query: 35 LHA A WLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F Q + +DQQ+ FA+ FG E G + +SN+
Sbjct: 16 IEAGMDKYAVLLFRDQEV PDDQQLVFARNFGERENARGCTVTKKEDYRLTSG LNDVSNLG 75

Query: 83 ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHL FNLGNCLWHS DSSFRPIPAKFSLLSARVV 118

>gb|EFX06123.1| taurine catabolism dioxygenase [Grosman nia clavigera kw1407]
Length = 349

Score = 54.3 bits (129), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 64/283 (22%), Positives = 110/283 (38%), Gaps = 32/283 (11%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF--- 64
+TP + V L D+ F L A + ++ Q L+ +Q F R
Sbjct: 38 LTPCIGREFNDLQAVDLLDADEQVFTDLAATISERGVVFLRDQQLTPEQMKQFCLRITRA 97

Query: 65 -GAIERIG-----GGDIVAISNVK-ADGTVRQHSPA EWDDMMKVIVGNMAWH 109
G E G G I IS+ K G H + +D+ + + WH
Sbjct: 98 AGCPSSGLHIHPLTEPSSSELGDQISVISSEKQKKGGGLTH---QLNDVSRF--ASTGWH 152

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY-- 167
+D ++ V + A+ +P GG T +A YD L + + +A H ++
Sbjct: 153 SDISFETVPSDYAMLKIHTLPPTGGDTLWASGYE IYDR LSPNMQDFLEGLTATHDAMFFH 212

Query: 168 -SQSKLGH--VQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDA 223
+LG+ + + G + AT P+++ +P TG S+ + + I G+
Sbjct: 213 EEAERLGNPIRKDIRGSPLNQGGNLKAT--HPVIRTNPVTGWKSVYV NKGFTKRINGVTK 270

Query: 224 AESERFLEGLVDWACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
ES+ L L++ Q +W D+ +WDNR H A
Sbjct: 271 DESDMLLSYLLNLVTQNHD AQVRFRWRKNDMAIWDNRSTWHCA 313

>emb|CAY25755.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 54.3 bits (129), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 31/105 (29%), Positives = 53/105 (50%), Gaps = 8/105 (7%)

Query: 33 AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVK-----ADG 85
A + A ++A+L+F Q +S++QQ+ FA FG E GG + + + A
Sbjct: 14 ADIEAGMDKYAVLLFRNQDISDEQQLAFALNFGERESARGGT VTKKEDYRLTSG LNDASN 73

Query: 86 TVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
+ P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 74 LGKDGRPLARDSRTHL FNLGNCLWHS DSSFRPIPAKFSLLSARVV 118

>gb|AAL65149.1| 2,4-dichlorophenoxyacetate monooxygenase [Burkholderia sp. JRB1]
Length = 115

Score = 53.9 bits (128), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 24/64 (37%), Positives = 34/64 (53%)

Query: 213 RHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKL 272
R+A + G+ AE L L + A Q V+ H+W GD V+WDNRC+ HR +D
Sbjct: 41 RNASHVEGLPVAEGRMLLAELXEHAHQREXVYRHRWNVGDVVMWDNRCVFHRGRYDISA 100

Query: 273 PRVM 276
R +
Sbjct: 101 RREL 104

>ref|XP_002896478.1| poly [ADP-ribose] polymerase, putative [Phytophthora infestans
T30-4]
gb|EEY67505.1| poly [ADP-ribose] polymerase, putative [Phytophthora infestans
T30-4]
Length = 1353

Score = 53.9 bits (128), Expect = 2e-05, Method: Composition-based stats.
Identities = 59/269 (21%), Positives = 103/269 (38%), Gaps = 28/269 (10%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAI 67
+T +G ++G+ L L +A L ++ F Q ++ +QQ+ + +G +
Sbjct: 88 VTQLSPRIGTELSGIQLHQLTNAQRDELALLVSHRGVIFFRDQEIINIEQQLDLGRYYGPL 147

Query: 68 ---ERIG---GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG 121
+ +G G +V + + R ++D + WH+D +
Sbjct: 148 HVHQNLGHPEGHPVVLVVEDSVGSDRIIQRQQYDP-----DNVWHSVSNRQPPSY 200

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
F P +GG T +A AY+ L + + +A HS SK ++AG
Sbjct: 201 TSFKVLTNPLGGGTLWASAYEAYERLTTPPKTFIEGLTAIHS-----SK-AQAERAGR 254

Query: 182 YIGYGMDTTATPLR---PLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWA 237
G P+ P+V+ HP TGR +L + IP + + ES+ L+ L
Sbjct: 255 ----GHTIRRAPVEFEHPVVRTHPVTGRKALFVNPAFTRRIPQLSSRESDAVLKVLYKHI 310

Query: 238 CQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ +W VWDN H A
Sbjct: 311 TEGHEFQVRFRWTKNAAAVWDNHITTHFA 339

>ref|XP_002587293.1| hypothetical protein BRAFLDRAFT_129135 [Branchiostoma floridae]
gb|EEN43304.1| hypothetical protein BRAFLDRAFT_129135 [Branchiostoma floridae]
Length = 257

Score = 53.9 bits (128), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 57/247 (23%), Positives = 96/247 (38%), Gaps = 59/247 (23%)

Query: 41 QHALLIFPGQ-HLSNDQQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSP 92
+H +L+F Q +S + + ++ FG +E + D+ +SN +A+G
Sbjct: 39 KHRILVFKNQGTISGSRHVEISRWFGELESTFYKHPKSPHPDVFVRSNDEAEGCTG---- 94

Query: 93 AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEAT 152
VG WH D ++ P +++ VVP G T FA L+E
Sbjct: 95 -----VGRGTGWHIDGSFQPAPFGYSLYHVVVPKEGN-TVFA-----PLNELI 136

Query: 153 RALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLL-- 210
L ++ R ++ S D P+ PL+ HP TG +L
Sbjct: 137 SGLTEEQRRRWEQLWMVS-----DRRGVPVHPLIYSHPLTGAKTLCFH 179

Query: 211 IGRHAHAIPGMDAAESER-----FLEGLVDWACQAPRV--HAHQWAAGDVVVWDNRC 260
+G + G+ +AE R L + + R ++H+W AGD ++ DN
Sbjct: 180 LGMTEFFLVGLPSAEKRRTDWKETNQLLREIHQEFVKNNRAIQYSHKWEAGDFIISDNLA 239

Query: 261 LLHRAEP 267
+ H A P
Sbjct: 240 VGHEASP 246

>ref|ZP_06458186.1| taurine catabolism dioxygenase TauD/TfdA [Pseudomonas syringae pv.
aesculi str. NCPPB3681]
Length = 285

Score = 53.9 bits (128), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 55/182 (30%), Positives = 72/182 (39%), Gaps = 25/182 (13%)

Query: 104 GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAY-----DA 147
G WH D +Y + VP G T F D A
Sbjct: 90 GGGYWHTDMSYKSANTVFTSLLSVQVPDQHGGETQFIDCVAGLHQVRQWLSPGCPQHLKG 149

Query: 148 LDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRP 207
LD + H+ R +L + + VQQ S G DT + PLV HP +
Sbjct: 150 LDLENLRIHHRFGNRDALRNADAA--VQQLNSQEAGALEDTV--VHPLVLKHPLSCTT 203

Query: 208 SLLI-GRHAHAIPGMDAAESERFLEGLVDWACQ-APRVHAHQWAAGDVVVWDNRCLLHRA 265
SL A I G+ A S R L+ LVD+ Q APR + H + GD+V+WDN LH+
Sbjct: 204 SLYAPAATAMQIEGVTPALSHRILDSLVDFLVQQAPR-YRHAYRPGDIVIWDNLSTLHKG 262

Query: 266 EP 267
P
Sbjct: 263 PP 264

>emb|CBJ18885.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 105

Score = 53.9 bits (128), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 52/110 (47%), Gaps = 6/110 (5%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPE 203
A+D LDE TR LV HS ++S+++LG + A L+ LV+ HP
Sbjct: 2 AWDNLDEPTRGLVLPLIGEHSRLFSRAELGF-----DFTDEERLKFAPVLQRLVRRHPS 55

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
T R SL + H I G E+ L L + A Q RV++H W D+
Sbjct: 56 TRRLSLYLSSHCGNIVGWPLPEARALLRELTEHATQRErvYSHAWRTDDL 105

>emb|CBJ19165.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 105

Score = 53.9 bits (128), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 52/110 (47%), Gaps = 6/110 (5%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPE 203
A+D LDE TR LV HS ++S+++LG + A L+ LV+ HP
Sbjct: 2 AWDNLDEPTRGLVLPLIGEHSRLFSRAELGF-----DFTDEERLKFAPALQRLVRRHPS 55

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
T R SL + H I G E+ L L + A Q RV++H W D+
Sbjct: 56 TRRLSLYLSSHCGNIVGWPLPEARALLRELTEHATQRErvYSHAWRTDDL 105

>emb|CBJ18957.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 105

Score = 53.9 bits (128), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 52/110 (47%), Gaps = 6/110 (5%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPE 203
A+D LDE TR LV HS ++S+++LG + A L+ LV+ HP
Sbjct: 2 AWDNLDEPTRELVLPLIGEHSRLFSRAELGF-----DFTDKERLKFAPVLQRLVRRHPS 55

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
T R SL + H I G E+ L L + A Q RV++H W D+
Sbjct: 56 TRRLSLYLSSHCGNIVGWPLPEARALLRELTEHATQRErvYSHAWRTDDL 105

>ref|ZP_07276031.1| hypothetical protein SSMG_00071 [Streptomyces sp. AA4]
gb|EFL04400.1| hypothetical protein SSMG_00071 [Streptomyces sp. AA4]
Length = 283

Score = 53.9 bits (128), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 67/272 (24%), Positives = 105/272 (38%), Gaps = 35/272 (12%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
+++ +LG V+G L A + L++F Q L + A+R G
Sbjct: 1 MKVASLSRSLGLQVSGGALQDCSSGELAEALRLVERAGLVVFRRQCLDDGDLHALARRIG 60

Query: 66 AIERIGGG-----DIVAISNVK-ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP 116
+E +I +SN++ DG A+ D WH+D +
Sbjct: 61 PLEESSRKVCLSPHEPEISYLSNLRDEDGQFIGFPGADTD-----YWHSDQQHRE 110

Query: 117 VMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
A AV V A GG T F LDEAT A + R A + ++ V+
Sbjct: 111 RPATLAVLYCVVPAASGGATSFVSADVESAGLDEATVADLAGRRVYEPAFNHDNAPVR 170

Query: 177 QAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW 236
+ A + T+ T R V T +G G+ A ES + ++
Sbjct: 171 VSHPLL-----TSRTGDRHYAYVSDNT-----LG-----FTGLADESAALKQRVLSR 214

Query: 237 ACQAPRVHAHQWAAGDVVWDNRCLLHRAEPW 268
+ R++AH+W AGD ++DN LLHR E +
Sbjct: 215 LLEPSRIYAHRWQAGDFALYDNTQLLHRRERF 246

>emb|CAY25741.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 53.9 bits (128), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 33/110 (30%), Positives = 55/110 (50%), Gaps = 18/110 (16%)

Query: 33 AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISN 80
A + A ++A+L+F Q ++++QQ+ FA FG E GG + +SN
Sbjct: 14 ADIEAGMDKYAVLLFRDQDITDEQQALAFALNFGERESARGGTVTKKEDYRLTSGLNVDVN 73

Query: 81 VKADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
+ DG P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 74 LGKDG-----RPLARDSRTHLFLNGLNCLWHSDDSSFRPIPAKFSLLSARVV 118

>ref|ZP_06478274.1| taurine catabolism dioxygenase TauD/TfdA [Pseudomonas syringae pv.
aesculi str. 2250]
Length = 281

Score = 53.9 bits (128), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 55/182 (30%), Positives = 72/182 (39%), Gaps = 25/182 (13%)

Query: 104 GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAY-----DA 147
G WH D +Y + VP G T F D A
Sbjct: 86 GGGYWHTDMSYKSANTVFTSLLSVQVPDQHGETQFIDCVAGLHQVRQWLVSFGCPQHLLKG 145

Query: 148 LDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRP 207
LD + H+ R +L + + VQQ S G DT + PLV HP +
Sbjct: 146 LDLENLRIHHRFGNRDALRNADAA--VQQLNSQEAGALEDTV--VHPLVLKHPLSCTT 199

Query: 208 SLLI-GRHAHAIPGMDAAESERFLEGLVDWACQ-APRVHAHQWAAGDVVWDNRCLLHRA 265
SL A I G+ A S R L+ LVD+ Q APR + H + GD+V+WDN LH+
Sbjct: 200 SLYAPAATAMQIEGVTPALSHRILDSLVDLVLVQQAPR-YRHAYRPGDIVIWDNLSTLHKG 258

Query: 266 EP 267
P
Sbjct: 259 PP 260

>gb|ABD39119.1| alpha-ketoglutarate dioxygenase [uncultured bacterium]
Length = 95

Score = 53.9 bits (128), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 25/63 (39%), Positives = 34/63 (53%)

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV 254
+P+V+ HPETGR L +G HA I GM E +E L A + H W AG+++
Sbjct: 33 QPIVRTHPETGRKCLYLGDHAEYIVGMPYDEGREMIEELNALAVHPDLTYEHCWTAGELI 92

Query: 255 VWD 257
WD
Sbjct: 93 AWD 95

>gb|EFY85365.1| hypothetical protein MAC_08614 [Metarhizium acridum CQMa 102]
Length = 359

Score = 53.9 bits (128), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 53/253 (20%), Positives = 95/253 (37%), Gaps = 32/253 (12%)

Query: 41 QHALLIFPGQ-HLSNDQQITFAKRFAGI-----ERIGGGDIVAISNVK 82
+ ++ F Q +L+ND Q R G + ER GG IS +
Sbjct: 74 ERGVVFFRAQDNLNDLQKELILRLGKLTGRPETSGLHIHPILNSERELGGSDEISTIS 133

Query: 83 ADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRCTCFADMR 142
+ + + +++ WH+D + PV A +P GG T +A
Sbjct: 134 SVQHKQYYKTGAEELSPKKQTTAQWHSIDAFEPVPADYTSRLVLQPKTGGDTLWASGY 193

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI-----GYGMDTTATPLR 195
YD + E + + ++ + Q G + ++ I + +
Sbjct: 194 EIYDKISEPYQKFLETL----TVTFEQPGFGAIAESQGFQIYDKPRGAPENVGRVLKAIH 249

Query: 196 PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWA-AGD 252
P+V+ +P TG S+ +G H I G+ ES+ L+ +D + +W D
Sbjct: 250 PVVRTNPVTGWKSIFPVGGHVSHINGVTDEESQHLLKWFLLDLYHNHDLQVRFKWQNPND 309

Query: 253 VVVDNRCLLHRA 265
+ +WDNR + H A
Sbjct: 310 IAIWDNRSVFHTA 322

>ref|NP_968348.1| pyoverdine biosynthesis protein PvcB [Bdellovibrio bacteriovorus]

HD100]
emb|CAE79341.1| pyoverdine biosynthesis protein PvcB [Bdellovibrio bacteriovorus
HD100]
Length = 278

Score = 53.9 bits (128), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 65/292 (22%), Positives = 109/292 (37%), Gaps = 32/292 (10%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG-QHLSNDQQI-TFAKRFG 65
+ P GA + G A++ D ALH +LQ +++ G N ++ ++ + +G
Sbjct: 8 LKPFGAIVEPKAQG--ASVKDLDLKALHQLFLQEQIVVLRGFTTFKNSEEFASYCETWG 64

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
I G ++ + V Q +P D + M W D Y P + + +F
Sbjct: 65 EISIWPFKGVLLEL-----VEQENPQ--DHIFDHSYVPMHW--DGMYPQVPEYQIFH 112

Query: 126 AEVVPVAVG--GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
P G GRT F++ A +A + + +Y + + + S I
Sbjct: 113 CVKAPLSGHGGRRTTFSNTVLALKNASPELKAFWGKVTG----IYQREMEFYKSKTVSPII 168

Query: 184 GYGMDTTATPLRPLVKV---HPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA 240
T P R + P + + G+ E E F +GL
Sbjct: 169 -----TKHPKRDFSVIRYNEPPSADKGHFVNPPDLEFAGVPVGELEAFHQGLKSALYAP 222

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL 292
+AH+W GDVV+ DN LLH E + K PR + ++ P + L
Sbjct: 223 ENFYAHEWQGDVVITDNFTLLHGREAFTSKSPRHLQRVQVQSSPPFDNPGL 274

>emb|CBJ18895.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18920.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18951.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18972.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19000.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19016.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19085.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19087.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19089.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19090.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19091.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19092.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19093.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19099.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19100.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19102.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19103.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19104.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19105.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19106.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19113.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19114.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19115.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19116.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19118.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19119.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19120.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19121.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19122.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19123.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19124.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19125.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19166.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18889.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]

Length = 105

Score = 53.9 bits (128), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 52/110 (47%), Gaps = 6/110 (5%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPE 203
A+D LDE TR LV HS ++S+++LG + A L+ LV+ HP
Sbjct: 2 AWDNLDEPTRELVLPLIGEHSRLFSRAELGF-----DFTDEERLKFAPVLQRLVRRHPS 55

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
T R SL + H I G E+ L L + A Q RV++H W D+
Sbjct: 56 TRRLSLYLSSHCGNIVGWPLPEARALLRELTEHATQRErvYSHAWRTDDL 105

>emb|CBJ18888.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 104

Score = 53.9 bits (128), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 36/110 (32%), Positives = 53/110 (48%), Gaps = 7/110 (6%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPE 203
AYDA+DE +A + A H +S+ LG + ++ + P+V+ P
Sbjct: 2 AYDAMDEDMKAFLDPLEAEHF AFHSRELLGAMPTQEER-----NSIPPAVWPIVR-KPA 54

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
T R SL IG HAH + GM A+ L L++ A Q V+ H W GD+
Sbjct: 55 TDRSLFIGAHAKVIGMPLAQGRMLLLDLLEHATQRQFVYRHAWTPGDL 104

>ref|XP_661712.1| hypothetical protein AN4108.2 [Aspergillus nidulans FGSC A4]
gb|EAA59369.1| hypothetical protein AN4108.2 [Aspergillus nidulans FGSC A4]
tpe|CBF74691.1| TPA: conserved hypothetical protein [Aspergillus nidulans FGSC A4]
Length = 363

Score = 53.9 bits (128), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 63/275 (22%), Positives = 109/275 (39%), Gaps = 31/275 (11%)

Query: 5 TLQITPTGATLGATVTGVHLATLD DAGFAALHAAWLQHALLIFPGQHLSN---DQQITFA 61
++ IT +G+ V G+ L+ L D L + +++F Q + +Q FA
Sbjct: 72 SVSITKLTPRVGSEVRGLQLSQLSDVQKDELALLIAERGVVFRDQDFKDIGPGKQKEFA 131

Query: 62 KRFGA--IERIGG--GDIVAINVK--ADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM 115
FG + +G D + N+ AD R + + + +H+D +Y
Sbjct: 132 GYFGRHLVHPVGAHVKDHI EFHNIYLGADNLYRLQTRS-----TKLTTGYHSDVSYE 184

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175
+ + VP+ GG T + AAY+ L + + L+ A HS + Q++
Sbjct: 185 HQPPGVTLTLLSVPSSGGDTAWVSQVAAYERLSDPIKKLLEGLRAEHS-GFPQAERARA 243

Query: 176 QQAGSAYIGYMDTTATPLR---PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLE 231
G P++ P+V+VHP TG +L + I G+ ES+ L+
Sbjct: 244 D-----GKFVRREPVKSEHPVVRVHPVTGEKALFVNSGFTKRIIGLKDEESDAILQ 294

Query: 232 GLVDWACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
L + + +W V +WDNR H A
Sbjct: 295 LLFKHISLSQDIQVRVKWDDRTVSLWDNRVTAHTA 329

>ref|ZP_03831920.1| pyoverdine biosynthesis protein PvcB [Pectobacterium carotovorum
subsp. carotovorum WPP14]
Length = 292

Score = 53.9 bits (128), Expect = 3e-05, Method: Compositional matrix adjust.

Identities = 54/193 (27%), Positives = 80/193 (41%), Gaps = 43/193 (22%)

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Query: 109 HADSTYMPVMAQGAVFSAEVPVAVG----GRTCFADMRAAYDALDEATRALVHQRSARHS 164
          H D Y+ + + VF + V AVG GRT F+ AA T+AL
Sbjct: 110 HWDGMYLKTVPQLQVF--QCVSAVGEGQGGRITFSSTTAALRLASPETKALW----- 159

Query: 165 LVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----LIG 212
          Q G Q+A Y ++T P+++ HP P + +
Sbjct: 160 ----QRATGQYQRAVELY-----SSTAQAPIIEQHPYRTHPVIRFCEPPIAGDKEFLN 208

Query: 213 RHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDFK 271
          + G++ E E+ L L D A PRV+ AHQW +GD+ + DN LLH E + +
Sbjct: 209 PSTYHFSGIEPEEQQLSSSLQD-ALYDPRVYAHQWQSGDIAIADNYSLHGRESYTSQ 267

Query: 272 ----LPRVMWHSR 280
          L RV H++
Sbjct: 268 SGRHLRRVHIHAK 280

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>ref|XP_001595570.1| hypothetical protein SS1G_03659 [Sclerotinia sclerotiorum 1980]
gb|ED001185.1| hypothetical protein SS1G_03659 [Sclerotinia sclerotiorum 1980
UF-70]
Length = 331

Score = 53.5 bits (127), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 57/238 (23%), Positives = 93/238 (39%), Gaps = 31/238 (13%)

```

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFA 61
          T+ +TP +G + GV L+ L +AG L + ++ F Q ++ + + +
Sbjct: 97 TVDLTPA---MGTEIKGVQLSKLSNAGKDQLARFVAERKVVAFRDQDFADLPAAEAVEYG 153

Query: 62 KRFGA--IERIGGG-----DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY 114
          + FG I G ++ + D T + + ++AWH+D TY
Sbjct: 154 RYFGRPHIHPTSGAPAGHPEVHLVHRSAGDKTA-----ESFFETRNSVAWHSVDVY 205

Query: 115 MPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH 174
          VP GG T FA+ AY+ L ++ + +H SA HS G
Sbjct: 206 EKQPPGTTFLYVLDPESGGDTLFGANGVEAYNRLSDSFKERLHGLSATHS-----GI 257

Query: 175 VQQAGSAY-IGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL 230
          Q S Y G + P+V+ HP TG +L + R + G ES+ L
Sbjct: 258 EQVNASRYRNGIARREPVVNVHPIVRTHPVTGEKALYVNRQFTRKVVGFKEESDMLL 315

```

>dbj|BAE92213.1| 2,4-D/alpha-ketoglutarate dioxygenase [Ralstonia sp. K101]
dbj|BAE92214.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. K301]
dbj|BAE92215.1| 2,4-D/alpha-ketoglutarate dioxygenase [Ralstonia sp. K401]
Length = 109

Score = 53.5 bits (127), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 37/115 (32%), Positives = 55/115 (47%), Gaps = 7/115 (6%)

```

Query: 142 RAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKV 200
          RAAYDAL ++ + A H + S+ LG + + P+ PLV+
Sbjct: 1 RAAYDALPRDLQSELEGLRAEHYALNSRFLGDTDYSEA-----QRNAMPVNVWPLVRT 54

Query: 201 HPETGRPSLLIGRHHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
          H +GR L IG HA + G+ AE L L++ A Q V+ H+W GD+V+
Sbjct: 55 HAGSGRKFLFIGAHASHVEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGDVLM 109

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>emb|CAY25735.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 53.5 bits (127), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 31/108 (28%), Positives = 55/108 (50%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F Q ++++QQ+ F+ FG E+ GG + +SN+
Sbjct: 16 IEAGMDKYAVLLFRNQDITDEQQALFSLNFGEREKSRGGTVTKKEDYRLTSGLNDVSNLG 75

Query: 83 ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----KPLPKDHRTHLFLNGLNCLWHS DSSFRPIPAKFSLLSARVV 118

>emb|CAY25779.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 53.5 bits (127), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 32/109 (29%), Positives = 56/109 (51%), Gaps = 17/109 (15%)

Query: 33 AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG-----DIVAISNV 81
AA+HA + +L+F Q + +DQQ+ F++ G +E+ G D+ ISN+
Sbjct: 14 AAVHAGMDEFGVLVFDQKIDDDQQLVFSRSLGPLEQATGDIAAPQDWRMSMDLNDISNL 73

Query: 82 KADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
+ + DD ++ +GN WH+DS++ V A+ ++ SA VV
Sbjct: 74 DKNNKILAR-----DDRRRLFLGLGNQLWHS DSSF KDVPKYSLLSARVV 117

>emb|CAY25789.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY25790.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 53.5 bits (127), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 33/108 (30%), Positives = 54/108 (50%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F Q +S+DQQ+ FA FG E GG + +S++
Sbjct: 16 VEAGMDKYAVLLFRNQDISDDQQLAFALNFGEREHARGGT VTKKEDYRLTSGLNDVSSLG 75

Query: 83 ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----KPLPRDHRTHLFLNGLNCLWHS DSSFRPIPAKFSLLSARVV 118

>ref|YP_908226.1| oxidoreductase [Mycobacterium ulcerans Agy99]
gb|ABL06755.1| oxidoreductase [Mycobacterium ulcerans Agy99]
Length = 289

Score = 53.5 bits (127), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 64/280 (22%), Positives = 102/280 (36%), Gaps = 48/280 (17%)

Query: 12 GATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAI---- 67
G LGA +TGV LDD + + L+I + S ++ + K G I
Sbjct: 7 GEGLGAQITGVDPKILDDITDEIRDIVYANKLVILKDVNPSP EEF LKLGKIVGQIVPYY 66

Query: 68 ----ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV 123
+I S V+ G + + WH D +MP ++
Sbjct: 67 EPMYHHEDHPEIFVSSTVEGQGVPKTGA-----FWHIDYMFMEPEFAFSM 111

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
VP T F D+ + +L A +A AR +L + + Y
Sbjct: 112 VLPLAVPGHDRGTYFIDLAKVWQSLPSAQQ A-----PARGTLSTHDP RRHIKIRPSDVYR 166

Query: 219 PGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWVWNRCLLHRAEPWDFKLPRVMW 277

Sbjct: 225 AELKKVESDKLLDFFSYHLHSADDHYVRWKWTVGAVAMWDNRCVLHRVIPGTYDTPRRGI 284

Query: 278 HSRLAGR-----PETEGAA 291

+ + G P +EG A

Sbjct: 285 RTTVFGEKPYYPDPNSEGRA 303

>emb|CAY25766.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 53.5 bits (127), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 32/102 (31%), Positives = 54/102 (52%), Gaps = 18/102 (17%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGD-----IVAISNVKADGTVR 88

++A+LIF GQ ++++QQ+ FA FG E+ GG + +SN+ DG

Sbjct: 22 KYAVLIFHGQDITDEQQLAFAFNFGEREKARGGTATKKEDYRPTTGLNDVSNLKGKDG--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

P D + +GN W++DS++ P+ A+ ++ SA VV

Sbjct: 79 --KPLSRDHRTHLFNLGNCLWYSDSSFRPIPAKFSLLSARVV 118

>gb|EFX01815.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Grosmannia
clavigera kw1407]
Length = 375

Score = 53.5 bits (127), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 65/270 (24%), Positives = 102/270 (37%), Gaps = 36/270 (13%)

Query: 28 DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV---AISNVKAD 84

DDA L Q ++ F Q + D Q +R G + + A+SN K

Sbjct: 73 DDAKIRDLAVLVSQRGVVFRRQDIGIDDQKRLGQRLGELTGKPATSRHLRHALSNSKRG 132

Query: 85 GTVRQHSPAEWDDMMKVI-----VGNMAWHADSTYMPVMAQGAVFS 125

V ++ DD + +I + + WHAD T+ + + A+

Sbjct: 133 IAVDEN--GRLDDEISIISEQNRLIYDRDFGSSSRRLAGVGWHADITFENIPSDYAILK 190

Query: 126 AEVVPVPA-VGGRTCFADMRAAYDALDEATRALVHQRSARH---SLVYSQSKLG--HVQQAG 179

P VGG T +A YD L + L +A H + V ++ G + +

Sbjct: 191 IVQPPEDVGGDTLWASGYELYDRLSPPIQKLTEGLTATHHQPAPVAKDFTGIELISED 250

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH---AHAIPGMDAAESERFLEGLVDW 236

A G+D A PL++ +P TG SL H A I G+ ES+ +

Sbjct: 251 GAPENNGLDFAE--HPLIRTNPVTGWKSLFGAGHQVDAGWINGVSERESDILKAYFLQL 308

Query: 237 ACQAPRVHAH-QWAAGDVVWDNRCLLHRA 265

+ + +W DV +WDNR + H A

Sbjct: 309 ITENHDLQVRFRWNKNDVAIWDNRSVFHTA 338

>ref|XP_001547565.1| hypothetical protein BC1G_13809 [Botryotinia fuckeliana B05.10]

gb|EDN20012.1| hypothetical protein BC1G_13809 [Botryotinia fuckeliana B05.10]
Length = 344

Score = 53.5 bits (127), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 46/171 (26%), Positives = 77/171 (45%), Gaps = 21/171 (12%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGRTCFADMRAAYDALDEATRALVHQRSARH--SL 165

WHAD T+ V + A+ +P GG T +A Y+ L + ++ +A H S

Sbjct: 160 WHADITFERVPSDYAMLKIHTLPETGGDTLWASGNEIYERLSPKMKEMLEGLTATHDASF 219

Query: 166 VYSQS-KLGH--VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG----RHAHAI 218

+ ++ +LG + + + G + +A + P+V+ +P TG+ SL I R H +

Sbjct: 220 FHDEARRLGQDIREDMRGSPLNIGKELSA--VHPVVRTNPVTGKKSLFINQGFTRRLLHPL 277

Query: 219 PGMDAAESERFLEGLVDWACQAPRVHAHQ----WAAGDVVVWDNRCLLHRA 265

++ +L+ LV P H Q W+ DV +WDNR H A

Sbjct: 278 TKDESDLLLPLWLSLV-----PLNHDAQVRWKWSKNDVAIWDNRSNWHCA 322

>emb|CAY25750.1| alpha-KG-dehydrogenase [uncultured bacterium]

emb|CAY25756.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 119

Score = 53.5 bits (127), Expect = 4e-05, Method: Compositional matrix adjust.

Identities = 31/108 (28%), Positives = 56/108 (51%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82

+ A ++A+L++ GQ ++++QQ+ +A FG E GG + +SN+

Sbjct: 16 IEAGMDKYAVLLYRGQDITDEQQLAYALNFGEREHARGGTVTKKEDYRLTPGLNDVSNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

DG +P D + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 76 KDG-----NPLPRDHRTHLFNLGNCLWHSDSSFRPIPAKFSLLSARVV 118

>ref|XP_659802.1| hypothetical protein AN2198.2 [Aspergillus nidulans FGSC A4]

gb|EAA63855.1| hypothetical protein AN2198.2 [Aspergillus nidulans FGSC A4]

tpe|CBF86366.1| TPA: conserved hypothetical protein [Aspergillus nidulans FGSC A4]

Length = 372

Score = 53.5 bits (127), Expect = 4e-05, Method: Compositional matrix adjust.

Identities = 66/296 (22%), Positives = 115/296 (38%), Gaps = 42/296 (14%)

Query: 5 TLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62

+ +TP +G + + L + DD L + ++ F Q +++D+Q +

Sbjct: 47 SFDVTPI---IGREFSDLQLTDILHDDQKLRDLAITVSRRGVVFFRNQSINSDEQKVLGQ 103

Query: 63 RFGAIERIGGGDIV---AISNVKADGTVRQHSPAEWDDMMKVI----- 102

+ G + + A++N TV +H + DD + VI

Sbjct: 104 KLGELTGKPATSKLHRHAVNNAGRKLTVNEH--GKLDDEVSVISSETNRKYYGDRFANNT 161

Query: 103 --VGNMAWHADSTYMPVMAQGAVFSAEVVPA--VGGRTCFADMRAAYDALDEATRALVHQ 158

+ + WHAD T+ V + A+ P GG T +A YD L +AL

Sbjct: 162 RHLASEGWHADITFERVPSDYAILKITHSPEDQTGGDTLWASGYEVYDRLSPPIQALTDT 221

Query: 159 RSARH-----SLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLL--I 211

+A H + + + + +Q A G D A+ PL++ +P TG SL

Sbjct: 222 LTAVHHQPSFNNAIKEHGIELIQGDRGAPENTGYDFRAS--HPLIRTNPVTGWKSLFGAA 279

Query: 212 GRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAHQ--QWAAGDVVVWDNRCLLHRA 265

G+ + I G+ ESE + + + +W D+ +WDNR + H A

Sbjct: 280 GQVDNGWIEGVTKRESEILKKYFRQLIAENHDLQVRFKWGTNDLAIWDNRSVFHTA 335

>ref|NP_925626.1| taurine dioxygenase [Gloeobacter violaceus PCC 7421]

dbj|BAC90621.1| gll2680 [Gloeobacter violaceus PCC 7421]

Length = 256

Score = 53.5 bits (127), Expect = 4e-05, Method: Compositional matrix adjust.

Identities = 71/279 (25%), Positives = 104/279 (37%), Gaps = 59/279 (21%)

Query: 1 MAQTTL-QITPTGATLGATVTGVHLATLD-DAGFAALHAAWLQHALLIFPGQHLSNDQQI 58

M+ T L +T LGA +TG+ L+ A + A ++H LL+FPQQ L+ QQI

Sbjct: 1 MSTTALFSVTRLAPHLGAEITGLDLSRPTVPKTLALIRYALVEHQLLVFPQTLTPIIQI 60

Query: 59 TFAKRFGAIERIG----GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTY 114
++ FG +E D I V D R+ P VG WH D ++
Sbjct: 61 ALSRAFGEVEIFSPHPATADFP EIFPVSNP--RRGHPD-----VGRY-WHHDGSF 108

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA-----LVHQRSARHSLVYS 168
+ + F G F++ AY++LD + VH RH+
Sbjct: 109 RKQATRLSFFYFREASEWVGDFLFSNSYLAYESLDRDVQSF EPLITVHSNGVRHA---- 164

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESE 227
LV HP TGR L I A + GM A +
Sbjct: 165 -----LVPTHPLTGRKLLYINLGLTAGVVGM-AKQDY 195

Query: 228 RFLEGLVDWACQAPRVHA-HQWAAGDVVWDNRCLLHRA 265
L G ++ P H+ GD+++ DN + H A
Sbjct: 196 IKLAGFINRHL SRPEFTLRHKPRPGDLILCDNHSVAHNA 234

>gb|AAD55077.1|AF176240_1 2,4-D-alpha ketoglutarate dioxygenase [Rhodoferax sp. P230]
dbj|BAE92216.1| 2,4-D/alpha-ketoglutarate dioxygenase [Ralstonia sp. T101]
dbj|BAE92217.1| 2,4-D/alpha-ketoglutarate dioxygenase [Ralstonia sp. I502]
Length = 109

Score = 53.1 bits (126), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 39/115 (33%), Positives = 52/115 (45%), Gaps = 7/115 (6%)

Query: 142 RAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKV 200
RAAYD L E + + A H + S+ LG + S P+ PLV+
Sbjct: 1 RAAYDDLPEDFKKELQGLRAEHYALNSR FILGDTDYSES-----QRNAMPVPSWPLVRT 54

Query: 201 HPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+
Sbjct: 55 HAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGD LVM 109

>ref|YP_001140900.1| pyoverdine biosynthesis protein [Aeromonas salmonicida subsp.
salmonicida A449]
gb|ABO89152.1| pyoverdine biosynthesis protein [Aeromonas salmonicida subsp.
salmonicida A449]
Length = 291

Score = 53.1 bits (126), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 49/171 (28%), Positives = 69/171 (40%), Gaps = 31/171 (18%)

Query: 109 HADSTYMPVMAQGAVFSAEVVPAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
H D Y P + + +F PA GGRT F + R LD A R R +
Sbjct: 107 HWDGMYKPTVPEFQLFHCVHAPAADEGGRTIFINTRQLLDLDGERLA----RWERV RIT 162

Query: 167 YSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL-----LIGRHA 215
Y ++ H YG + ++ PL+ HP +G + + +HA
Sbjct: 163 YRIKQVVH-----YGGEVSS---PLLVPHPVSGETVMRYNEPPREGGRFLNQHA 208

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAE 266
I G+ E FL+ L + +AHQW GDVV+ DN LLH E
Sbjct: 209 LQIEGIPPEEQGAFLQDLHERLYDPRYFYAHQWQPGDVVIADNFGLLHGRE 259

>emb|CBJ18887.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 105

Score = 53.1 bits (126), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 52/110 (47%), Gaps = 6/110 (5%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPE 203

```

      A+D LDE TR LV      HS ++S+++LG      +      A L+ LV+ HP
Sbjct: 2  AWDNLDEPTRELVLPLIGEHSRLFSRAELGF-----DFTDEERLKFAPVLQRLVRRHPS 55

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
      T R SL + H I G E+ L L + A Q RV++H W D+
Sbjct: 56 TRRLSLYLSPHCGNIVGWPLPEARALLRELTEHATQRRERVYSHAWRTDDL 105

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>emb|CAY25727.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 53.1 bits (126), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 31/102 (30%), Positives = 52/102 (50%), Gaps = 18/102 (17%)

```

Query: 41  QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVKADGTVR 88
      ++A+L F G ++++QQ+ FA FG E+ GG + +SN+ DG
Sbjct: 22  KYAVLTFHGHGHDITDEQQLAFAFNFGEREKARGGTVTKKEDYRLTTGLNDVSNLKGKD--- 78

Query: 89  QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
      P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 79  --KPLSRDHRTHLFNLGNCLWHS DSSFRPIPAKFSLLSARVV 118

```

>emb|CBJ18788.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 53.1 bits (126), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 53/112 (47%), Gaps = 7/112 (6%)

```

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
      AAYDAL E T+ + H ++S+ LG + + P+R PLV+ H
Sbjct: 1  AAYDALPERTKQDLGGLFTEHWALHSRFLMGDEDYTEAQKAAF-----PPVRWPLVRAH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
      P +GR +L IG HA + GM E L L++ A Q V+ W GD+
Sbjct: 55  PGSGRKALFIGAHAREVVGMTVPEGRLLLSELLEHATQPEFVYRRHWRLGDL 106

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>ref|XP_002419144.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative;
dnaJ-like protein, putative [Candida dubliniensis CD36]
emb|CAX42733.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Candida dubliniensis CD36]
Length = 388

Score = 53.1 bits (126), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 66/278 (23%), Positives = 113/278 (40%), Gaps = 41/278 (14%)

```

Query: 4  TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
      TT I+P LG + G+ L+ L+DA + Q +L+F Q D+ F +
Sbjct: 83  TTSNISPK---LGTEIKGIQLSQLNDAAKDEVALLAQRGVLVFRDQDFI-DKGPEFVTK 138

Query: 64  FGAIERIGGGDIVAIS-----NVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY 114
      + + G I S +V G +++ P E + V+ ++++ + T
Sbjct: 139 Y--VSHYGPLHIHPTSGAPKGHPDIHVLSGDTKEY-PFEKKTNLVVLHSDVSYELNPTA 195

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV----YSQS 170
      + +A + + + GG T F + AYD L + + A HS V ++
Sbjct: 196 LSFLA-----ATNIPQSGGGDTVFVNTVEAYDRLSPLFKEKLEGLKAVHSAVEQANFAIF 250

Query: 171 KLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERF 229
      K GHV++ + P+V+ P G+ L + I G+ ES
Sbjct: 251 KKGHVKRH-----PVENVHPIVRTTP-LGQKVLYVNNGFTRKIEGLKEEESSYL 298

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Query: 230 LEGLVD--WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L L+D W ++ AH W VV++DNR + H A
Sbjct: 299 LNFLLDHIWKGHDFQIRAH-WEPNTVVIFDNRVVGHSA 335

>ref|XP_503099.1| YALI0D21098p [Yarrowia lipolytica]
emb|CAG81291.1| YALI0D21098p [Yarrowia lipolytica]
Length = 399

Score = 53.1 bits (126), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 69/281 (24%), Positives = 113/281 (40%), Gaps = 42/281 (14%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSDQQTITFAKRFGA-IER---- 69
+G + GV LA L++ L + ++ F Q L +Q+ + +G+ IE+
Sbjct: 111 IGTEIVGVQLADLNEQQQLDELALLIAERTVVFVRDQDLPPAKQLEIGQFWGSQIEKHPQV 170

Query: 70 --IGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE 127
+ G I+ + D + + A + K G WH D + A +
Sbjct: 171 PHVPG--YPGITVLWPDHQILEGRKANF----KQPGGASGWHTDLVHEAQPAGLTHLHND 224

Query: 128 VVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 187
+P+VGG T ++ AYD L A + ++ ++A + ++ YI
Sbjct: 225 QIPSVGGDTAWSSGYGAYDKLSPAFQEFNLNGKTA-----IYRSAHTYIDRN- 270

Query: 188 DTTATPL-----RPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAP 241
D A P PLV+ HP TG +L + R I G++ ES+ L L D +
Sbjct: 271 DPLAGPKHIEREHLVRTHPVTGWKTLWVNRAMTVRIVGLEPKESDAILSYLYDVYEKNQ 330

Query: 242 RVHAH-QWAA-----GDVVVWDNRCLLHRAEPWDF--KLPR 274
+ +W G +WDNR H A WD+ K PR
Sbjct: 331 DIQVRFRWQPTKEGLGTSAINWNRISQHNAI-WDYEGKEPR 370

>emb|CBJ18962.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 105

Score = 53.1 bits (126), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 52/110 (47%), Gaps = 6/110 (5%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE 203
A+D LDE TR LV HS ++S+++LG + A L+ LV+ HP
Sbjct: 2 AWDNLDEPTRELVLPLIGEHSRLFSRAELGF-----DFTDEERLKFAPVLQRLVRRHPS 55

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
T R SL + H I G E+ L L + A Q RV++H W D+
Sbjct: 56 TRRLSLYLSSHCGNIVGWPLPEARALLRELTEHATQRRERVYSHAWHTDDL 105

>gb|ACG80575.1| TfdA [uncultured bacterium]
Length = 118

Score = 53.1 bits (126), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 45/129 (34%), Positives = 58/129 (44%), Gaps = 20/129 (15%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDD---TTATP 193
FADMRAAYDAL E +A + A HS+ YS+ +LG A G T A
Sbjct: 3 FADMRAAYDALPEDMKARLEGLQAHHSIAYSRLGFEFSGDEAXAPEGRRASAGTHAAA 62

Query: 194 LRPLVKVHPETGRPS---LLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA 250
RP + + R S L+ R A P A ++R V+ H W A
Sbjct: 63 HRPQISL-SRLARESHTRLVRPRRQAAAPRSHRAPTRQRF-----VYRHAWRA 109

Query: 251 GDVVVWDNR 259

GD+V+WDNR
Sbjct: 110 GDLVMWDNR 118

>ref|XP_003174143.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Arthroderma gypseum CBS 118893]
gb|EFR01313.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Arthroderma gypseum CBS 118893]
Length = 359

Score = 53.1 bits (126), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 44/169 (26%), Positives = 68/169 (40%), Gaps = 15/169 (8%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGG-RTCFADMRAAYDALD-----EATRALVHQR 159
WH+D + PV A+ VP GG T +A YD + E A Q
Sbjct: 153 WHSDVAFEPVPAEYTTTLRLTEVPKTTGGADTLWASGYELYDRISKPYQRFLETLTATCAQP 212

Query: 160 SARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLL-IGRHAHAI 218
+ KL Q+ +G + + P+V+ +P TG S+ G H I
Sbjct: 213 GYNKVAATGKFKLFDGQRGAPENVGSNFSS---VHPVVRTNPVTGWKSIYSAGFHVQKI 268

Query: 219 PGMDAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVWDNRCLLHRA 265
+ AES+ L+ + + + +W A D+ +WDNRC+ H A
Sbjct: 269 NDLTEAESKSLLDWFLRLINENNDLQVRFKWKNANDMAIWDNRCVFHTA 317

>emb|CAY25718.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 53.1 bits (126), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 32/108 (29%), Positives = 55/108 (50%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F GQ ++++Q++ FA FG E GG + +SN+
Sbjct: 16 IEAGMDKYAVLLFRGQDITDEQRLAFALNFGEREHARGGTVTKKEDYRLTSGLNVDVSNLG 75

Query: 83 ADGTVRQHSAPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG +P D + +GN WH DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLFNLGNCLWHFDSSFRPIPAKFSLLSARVV 118

>gb|ADI34070.1| 2,4-D/alpha-ketoglutarate dioxygenase [Burkholderia sp. 3HD3]
Length = 100

Score = 53.1 bits (126), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 26/62 (41%), Positives = 35/62 (56%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H+W GD+V+
Sbjct: 37 PLVRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQREFVYRHRWNVGDLVM 96

Query: 256 WD 257
W+
Sbjct: 97 WE 98

>ref|XP_001826717.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Aspergillus oryzae RIB40]
dbj|BAE65584.1| unnamed protein product [Aspergillus oryzae]
Length = 372

Score = 53.1 bits (126), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 40/174 (22%), Positives = 72/174 (41%), Gaps = 15/174 (8%)

Query: 108 WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+D T+ P+ + V +P GG T +A YD + + + + +A Y
Sbjct: 165 WHSDITFEPIPSDYTVLRLTELPKTGGDTLWASGYELYDRISKPYQQFLEGLTA----TY 220

Query: 168 SQSKLGHVQQAGSAYIGYG-----MDTTATPLRPLVKVHPETGRPSLL-IGRHAHAIP 219
+Q V + I G + + P+++ +P TG S+ +G H +
Sbjct: 221 AQPGFNRVAKENDFEIFTGPRGAPENVGDKLEAIHPVIRTNPVTGWKSVFAVG VHVAKVN 280

Query: 220 GMDAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVWDNRCLLHRAEPWDFK 271
+ ES+ L V + + +W D+ +WDNR + H A +D+K
Sbjct: 281 DLSEESDHLRLWFVSLIVENHDLQVRLRWENPNDLAIWDNRSVYH-AATYDYK 333

>emb|CBX93828.1| hypothetical protein [Leptosphaeria maculans]
Length = 465

Score = 53.1 bits (126), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 63/262 (24%), Positives = 96/262 (36%), Gaps = 50/262 (19%)

Query: 12 GATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGAIERI 70
+ +G + GV LA L D L ++ F Q +L+ D+Q + FG+
Sbjct: 191 NSKIGTEIHGVDLANLTDLQKNDLARLISTRGVVFFRNQKNLTIDKQRELGCFCFS---- 246

Query: 71 GGGDIVAISNVKADGTVRQHSPAEWDDMMK-VIVGNMAWHADSTYM---PVMAQGAVFSA 126
R H A + + WH+D TY P + +A
Sbjct: 247 -----PAHARHHRGATTRFRPLFTQTFHWHSDVTYETQPPSYTSLKLLTA 293

Query: 127 EVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG 186
P GG T ++ AAYD L A + + +A HS +Q G+ +G
Sbjct: 294 PP-PGAGDTIWSSQYAYDMLSPALQTYLESALTALHS-----ADLQTQGTALGRA 344

Query: 187 MDTTA-TPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC-QAPRVH 244
+ T PL++ +P TG A + F+ L++ +P V
Sbjct: 345 VRRDPITTEHPLIRTNPVTG-----SAEDESDFVIALLNQVVATSPEVQ 388

Query: 245 AH-QWAAGDVVVWDNRCLLHRA 265
+W GDV WDNRC H A
Sbjct: 389 VRFRWGEQDVAFWDNRC'TNHSA 410

>ref|XP_002841597.1| hypothetical protein [Tuber melanosporum Mel28]
emb|CAZ85788.1| unnamed protein product [Tuber melanosporum]
Length = 393

Score = 53.1 bits (126), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 68/272 (25%), Positives = 97/272 (35%), Gaps = 46/272 (16%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFG----- 65
+G + GV L TL DA L ++ F Q Q+ + +G
Sbjct: 92 IGTEIHGVKLKTLTDAQKNDLARLVAYRGVVFFRDQGDQDFEVDQDLGQRYWGPHLKHATT 151

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
++ R G D + + A+G D + WHAD TY +
Sbjct: 152 SVPRKEGLDEIHVVYHDANGL-----DQRALFTPTHLWHADVTYELQPPSYTLLK 201

Query: 126 AEVVPVAVGG--RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
P GG T ++ AAYD L + + +A HS Q GS
Sbjct: 202 VLHGPPRGGGDTLWSSQYAYDVLSAPMQKYLEGLTALHS-----AEEQAIGSR-- 251

Query: 184 GYGMDTTATPLR-----PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
T P+R PLV+ HP TG SL + I G+ ES+ L+ L
Sbjct: 252 -----ATGRPVRREPVITEHPLVRTHPVTGWKSLFVNPGFVKQIVGVPKMESDAILKYLN 306

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>ref|XP_721596.1| potential taurine catabolic dioxygenase Tcd3 [Candida albicans  
SC5314]
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gb|EAL02800.1| potential taurine catabolic dioxygenase Tcd3 [Candida albicans SC5314]
gb|EEQ44269.1| hypothetical protein CAWG_02534 [Candida albicans WO-1]
Length = 388

Score = 52.8 bits (125), Expect = 6e-05, Method: Compositional matrix adjust.
Identities = 69/282 (24%), Positives = 112/282 (39%), Gaps = 49/282 (17%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
TT I+P LG + G+ L+ L+DA + Q +L+F Q D+ F +
Sbjct: 83 TTSNISPK---LGTEIKGIQLSQLNDAKDEVALLAQRGVLFVRDQDFI-DKGPEFVTK 138

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGN-----MAWHAD 111
+ + G I S +P + D+ V+ G+ +A H+D
Sbjct: 139 Y--VSHYGLPHIHPTSG-----APKDHPDIHVLSGDTKEYPFEEKTNLVALHSD 186

Query: 112 STYMPVMAQGAVFSAEVVP-AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV---- 166
+Y + +A +P + GG T F D AY+ L + + A HS V
Sbjct: 187 VSYELNPTALSFLAATNIPQSGGGDTVFVDTEAYNRLSPLFKEKLEGLKAVHSAVEQAN 246

Query: 167 YSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAE 225
++ K GHV++ + P+V+ P G+ L + I G+ E
Sbjct: 247 FAIFKKGHVVRHPVENV-----HPIVRTTP-LGQKVLVYVNNGFTRRIEGLKEEE 294

Query: 226 SERFLEGLVD--WACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
S L L+D W ++ AH W VV++DNR + H A
Sbjct: 295 SSYLLNFLLDHIWKGHDFQIRAH-WEPNTVVIFDNRVVGHTA 335

>ref|ZP_03517935.1| putative taurine dioxygenase protein [Rhizobium etli IE4771]
Length = 156

Score = 52.8 bits (125), Expect = 6e-05, Method: Compositional matrix adjust.
Identities = 39/150 (26%), Positives = 64/150 (42%), Gaps = 26/150 (17%)

Query: 26 TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGAI-----ERIGGGDIVA 77
+ DA AA++ L+H ++ F Q HL + +Q FA+R G + G I+
Sbjct: 14 SFSDATVAAINQLLLKHKVIFFRDQDHLDDSEAEAFARRLGDLVPHPTQGPVTGTASILN 73

Query: 78 ISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTC 137
+ + + G Q WH D T++ + +V V+PA GG T
Sbjct: 74 LDSSRGGGRADQ-----WHTDVTFVDAYPKFSVLRGVVIPAAGGDTI 115

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVY 167
+++ AAY++L + L A HS Y
Sbjct: 116 WSNTHAAYESLPAPLKLLADNLWAIHSNAY 145

>ref|XP_002385365.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative [Aspergillus flavus NRRL3357]
gb|EED45236.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative [Aspergillus flavus NRRL3357]
Length = 372

Score = 52.8 bits (125), Expect = 6e-05, Method: Compositional matrix adjust.
Identities = 40/174 (22%), Positives = 72/174 (41%), Gaps = 15/174 (8%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+D T+ P+ + V +P GG T +A YD + + + + +A Y
Sbjct: 165 WHSDITFEPIPSDYTVLRLTELPKTTGGDTLWASGYELYDRISKPYQQFLEGLTA----TY 220

Query: 168 SQSKLGHVQQAGSAYIGY-----MDTTATPLRPLVKVHPETGRPSLL-IGRHAHAIP 219
+Q V + I G + + P+++ +P TG S+ +G H +

Sbjct: 221 AQPGFNRVAKENDFEIFTGPRGAPENVGDKLEAIHPVIRTNPVTGWKSVFAVGVHVAKVN 280

Query: 220 GMDAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVWDNRCLLHRAEPWDFK 271

+ ES+ L V + + +W D+ +WDNR + H A +D+K

Sbjct: 281 DLSEEDSDHLLRWVSLIVENHDLQVRLRWENPNDLAIWDNRSVYH-AATYDYK 333

>emb|CAY25760.1| alpha-KG-dehydrogenase [uncultured bacterium]

emb|CAY25763.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 119

Score = 52.8 bits (125), Expect = 6e-05, Method: Compositional matrix adjust.

Identities = 33/110 (30%), Positives = 54/110 (49%), Gaps = 18/110 (16%)

Query: 33 AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISN 80

A + A ++A+L F Q ++++QQ+ FA FG E GG + +SN

Sbjct: 14 ADIEAGMDKYAVLPFRNQDITDEQQALAFALNFGERESARGGTVTKEEDYRLTSGLNDSVN 73

Query: 81 VKADGTVRQHSPAEDDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

+ DG P D + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 74 LGKDG-----RPLARDSRTHLFNLGNCLWHSDDSSFRPIPAKFSLLSARVV 118

>ref|XP_002419281.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Candida dubliniensis CD36]

emb|CAX42871.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Candida dubliniensis CD36]

Length = 423

Score = 52.8 bits (125), Expect = 6e-05, Method: Compositional matrix adjust.

Identities = 66/294 (22%), Positives = 108/294 (36%), Gaps = 54/294 (18%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61

A+ + +TP +G + G+ L+ L D L + ++ F Q LS +Q+

Sbjct: 110 AEDVIHLTPY---IGTEIVGLQLSELTDKQKDELALLIAERVVVFFKDQDLSPQKQLELG 166

Query: 62 KRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADS 112

+G +E RIG + IS + ++ WD + GN WH+D

Sbjct: 167 HYWGQVEVHPQASRIGE-EFDGISVI-----WQEQQRDRWDLNLTfKQSKKGNSQWHS DL 220

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA----RHSLVYS 168

+ A + +P +GG T ++ AYD L A + + ++A H +

Sbjct: 221 VHEKQTAGITHLHLDAIPGIGGETLWSSTYGAYDKLSPALQKFLDGKTAIYRSAHQYQLDR 280

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESE 227

+ L G Y+ P+V+ HP TG L + R I G+ ES+

Sbjct: 281 KDPL-----KGPKYVERE-----HPIVRTHPVTGWKYLfVNRSM TVRIVGLLPEESD 327

Query: 228 RFLEGL-----VDWACQAP-----RVHAHQWAAGDVVVWDNRCLLH 263

L L V W+ Q + + G +WDNR H

Sbjct: 328 LILNLYSVIETNRDIQVRWSWQKELGSVKNNKKEPKQYRGVSALWDNRISNH 381

>ref|XP_002569045.1| Pc21g20580 [Penicillium chrysogenum Wisconsin 54-1255]

emb|CAP96955.1| Pc21g20580 [Penicillium chrysogenum Wisconsin 54-1255]

Length = 400

Score = 52.4 bits (124), Expect = 7e-05, Method: Compositional matrix adjust.

Identities = 62/257 (24%), Positives = 97/257 (37%), Gaps = 16/257 (6%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGAIERIGGG 73

+G + GV L+ LDDA L ++ F Q + + Q + +G + R

Sbjct: 99 IGTEIHGVDLSKLDDAQRDDLARLIAYRGVVFRRSQKNFDIESQRQLGQYWGKLHRHATT 158

Query: 74 DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTY--MPVMAQGAVFSAEVVPA 131
+ ++ V ++ D + + WH+D TY P +
Sbjct: 159 SVPRKPGLEDVHV--YTGDNSGDNRALFTPSFLWHS DVTYEIQPPSYTSLKLLSGPPRG 216

Query: 132 VGGRTCFADMR AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM D-TT 190
GG T ++ AAYD L + + +A HS +Q S +G +
Sbjct: 217 GGGDTLWSSQY AAYDILSSHMQNYLKGLTALHS-----ADMQANDSRALGRPVRRDP 268

Query: 191 ATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW 248
T PL++ +P TG L I G+ AAES+ + L D +HA W
Sbjct: 269 VTTEHPLIRTNPVTGWNGLFFNPGFVKKIVGIPAAESDAIRFLTDVIATTQEMHARFSW 328

Query: 249 AAGDVVVWDNRCLLHRA 265
DV +WDNR H A
Sbjct: 329 GEEDVAIWDNRSTNHSA 345

>gb|EFQ27447.1| TfdA family Taurine catabolism dioxygenase TauD [Glomerella
graminicola M1.001]
Length = 390

Score = 52.4 bits (124), Expect = 7e-05, Method: Compositional matrix adjust.
Identities = 61/274 (22%), Positives = 105/274 (38%), Gaps = 31/274 (11%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAK 62
++ T +G + G+ L+ L+ L + ++ F Q N ++Q F +
Sbjct: 98 IKATKLTPVIGTEIRGLQLSRLNSRQKDELALLIAERG VVAFRDQDFKNIGA EKQKEFGR 157

Query: 63 RFGA--IERIGG--GDIV AISNVK--ADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP 116
FG I +G D + N+ D R S + + +H+D +Y
Sbjct: 158 SFGPLHIHPVGAHV RDNLEFHNIYLGPDNEYRNRSKSNK-----LSTIGYHSDVSYEH 210

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMR AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ + VP GG T + AAY L + L+ A HS G+ Q
Sbjct: 211 QPPGV TILTL LSV PETGGDTAWVSQTAAYARLSRPIQTLLLEGLRAEHS-----GYPQ 262

Query: 177 QAGSAYIGYGM DTTATPLR---PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG 232
+ G + P++ P+V++H TG+ +L + I G+ ES+ L+
Sbjct: 263 ADNARRDGRFV--RREP VKSDHPVVRIHRATGQKALFVNPGFTKKIIGLRDEESDALLKL 320

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
L + +W G V +WDNR H A
Sbjct: 321 LFNHINH GQDFQVRVKWEEGTVALWDNRVTAHTA 354

>dbj|BAF81030.1| 2,4-D dioxygenase [Burkholderia sp. M3-VN6-5W]
dbj|BAF81031.1| 2,4-D dioxygenase [Burkholderia sp. 51-VN6-1W]
dbj|BAF81032.1| 2,4-D dioxygenase [Burkholderia sp. 27-VN4-2W]
dbj|BAF81033.1| 2,4-D dioxygenase [Burkholderia sp. 59-VN4-1W]
dbj|BAF81034.1| 2,4-D dioxygenase [Burkholderia sp. 70-VN5-1W]
dbj|BAF81038.1| 2,4-D dioxygenase [Ralstonia sp. 3-VN9-1W]
dbj|BAF81039.1| 2,4-D dioxygenase [Burkholderia sp. 62-VN9-1W]
dbj|BAF81040.1| 2,4-D dioxygenase [Burkholderia sp. 64-VN9-2W]
dbj|BAF81041.1| 2,4-D dioxygenase [Burkholderia sp. M10-VN8-1W]
dbj|BAF81042.1| 2,4-D dioxygenase [Burkholderia sp. M26-VN8-1W]
dbj|BAF81043.1| 2,4-D dioxygenase [Burkholderia sp. M27-VN8-1W]
dbj|BAF81048.1| 2,4-D dioxygenase [Burkholderia sp. M1-VN7-4W]
dbj|BAF81049.1| 2,4-D dioxygenase [Burkholderia sp. 77-VN7-2W]
dbj|BAF81050.1| 2,4-D dioxygenase [Burkholderia sp. 58-VN7-1W]
dbj|BAF81051.1| 2,4-D dioxygenase [Ralstonia sp. M1-VN1-7W]
dbj|BAF81052.1| 2,4-D dioxygenase [Ralstonia sp. 10-VN1-1W]
Length = 104

Score = 52.4 bits (124), Expect = 7e-05, Method: Compositional matrix adjust.
Identities = 25/61 (40%), Positives = 35/61 (57%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ H +GR L IG HA + G+ AE L L++ A Q V+ H+W GD+V+
Sbjct: 44 PLVRTHAGSGRKFLFIGAHASHVEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGDLM 103

Query: 256 W 256
W
Sbjct: 104 W 104

>dbj|BAF81045.1| 2,4-D dioxygenase [Burkholderia sp. 51-VN3-2W]
Length = 104

Score = 52.4 bits (124), Expect = 8e-05, Method: Compositional matrix adjust.
Identities = 25/61 (40%), Positives = 35/61 (57%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ H +GR L IG HA + G+ AE L L++ A Q V+ H+W GD+V+
Sbjct: 44 PLVRTHAGSGRKFLFIGAHASHVEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGDLM 103

Query: 256 W 256
W
Sbjct: 104 W 104

>emb|CBJ18798.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 52.4 bits (124), Expect = 8e-05, Method: Compositional matrix adjust.
Identities = 32/92 (34%), Positives = 46/92 (50%), Gaps = 5/92 (5%)

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPG 220
HSL+YS+++LG S + + L LV+ HP TGR SLL+ H AI G
Sbjct: 19 CEHSLIYSRAQLG----FSNFTDEERHSMRPVLHKLVRTHPVTGRKSLLLSAHIGAIVG 73

Query: 221 MDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
E+ F+ L++ A Q V+ H+W D
Sbjct: 74 WPRPEAMAFIRDLMEHATQPQFVYVHRWTKHD 105

>dbj|BAF81035.1| 2,4-D dioxygenase [Nocardioides sp. 116-VN10-1W]
Length = 104

Score = 52.4 bits (124), Expect = 8e-05, Method: Compositional matrix adjust.
Identities = 25/61 (40%), Positives = 35/61 (57%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ H +GR L IG HA + G+ AE L L++ A Q V+ H+W GD+V+
Sbjct: 44 PLVRTHAGSGRKFLFIGAHASHVEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGDLM 103

Query: 256 W 256
W
Sbjct: 104 W 104

>dbj|BAF81044.1| 2,4-D dioxygenase [Burkholderia sp. M38-VN3-2W]
dbj|BAF81046.1| 2,4-D dioxygenase [Burkholderia sp. 47-VN3-1W]
dbj|BAF81047.1| 2,4-D dioxygenase [Burkholderia sp. 124-VN3-1W]
dbj|BAF81053.1| 2,4-D dioxygenase [Ralstonia sp. M10-VN2-1W]
Length = 104

Score = 52.4 bits (124), Expect = 8e-05, Method: Compositional matrix adjust.
Identities = 25/61 (40%), Positives = 35/61 (57%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDVVW 255
PLV+ H +GR L IG HA + G+ AE L L++ A Q V+ H+W GD+V+
Sbjct: 44 PLVRTHAGSGRKFLFIGAHASHVEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGDLVM 103

Query: 256 W 256
W
Sbjct: 104 W 104

>dbj|BAD15039.1| hypothetical protein [Bradyrhizobium sp. ApB16]
Length = 102

Score = 52.0 bits (123), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 34/107 (31%), Positives = 47/107 (43%), Gaps = 5/107 (4%)

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGR 206
ALD+ T+A + HSL+YS+ LG + Y L+ LV+ HP R
Sbjct: 1 ALDDETAEIEDLVCEHSLMYSRGSLGFTE-----YTDDEKQMFKPVLQRLVRTHPVHRR 55

Query: 207 PSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDV 253
SL + HA I M E L L + A Q V+ H+W D+
Sbjct: 56 KSLYLSSHAGKIVMSVPEGRLLLRDLNEHATQGEFVYVHKWKLHDL 102

>ref|XP_001526184.1| hypothetical protein LELG_02742 [Lodderomyces elongisporus NRRL
YB-4239]
gb|EDK44563.1| hypothetical protein LELG_02742 [Lodderomyces elongisporus NRRL
YB-4239]
Length = 384

Score = 52.0 bits (123), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 67/280 (23%), Positives = 109/280 (38%), Gaps = 47/280 (16%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
T ++P LG + G+ L+ L+DAG + Q +L+F Q L
Sbjct: 83 TTNLSPK---LGTEIRGIQLSELNDAGRDQVALLASQRGVLVFRDQDL----- 127

Query: 65 GAIERIGGGDIVAISNVKADGTVRQH----SPAEWDDMMKVIVGN-----MAW 108
I G + V GT H +P D+ V+ G+ + W
Sbjct: 128 -----IDKGPENLVEYVSHYGTPHIHPTSGAPKGHPDIHSLVTGDTKEDAFSTRNNLVW 182

Query: 109 HADSTYMPVMAQGAVFSAEVVP-AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
H+D +Y + + +P A GG T FAD R AY+ L + + A HS V
Sbjct: 183 HSDVSYELNPTAVSFLAVTNIPKAGGGDTVFADNREAYNRLSPLFKEKIDNLKAVHSV- 241

Query: 168 SQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAES 226
Q+ L V+ G + ++ + P+V+ P +G+ L + I + ES
Sbjct: 242 DQANLAVVK--GGVVKRHPVEN----IHPVVRTTP-SGQKVLYVNSGFTRRIVDLKGEES 294

Query: 227 ERFLEGLVDWACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
+ L+ L+ + W G V ++DNR + H A
Sbjct: 295 DFLKFLQLQHIASSQDFQVRVNWQPGTVAIFDNRIVSHSA 334

>ref|XP_001201468.1| PREDICTED: hypothetical protein, partial [Strongylocentrotus
purpuratus]
Length = 176

Score = 52.0 bits (123), Expect = 9e-05, Method: Compositional matrix adjust.

Identities = 50/186 (26%), Positives = 77/186 (41%), Gaps = 34/186 (18%)

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Query: 5   TLQITPTGATLGATVTGVHLATLDDAG-FAALHAAWLQHALLIFPGQH-LSNDQQITFAK 62
          T Q+ P+  LG V G+ LA      G   +   QH L+IF Q  +S D+ + +
Sbjct: 6   TYQLKPS--RLGVEVFGIDLAQQQPQGVIDQIKEDVTQHRMIFRNQSPISGDRHVEISL 63

Query: 63  RFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM 115
          FG +E      +   D+  +SNV+++G      VG   WH D ++
Sbjct: 64  WFGELESTFYKHKPSHPDPVFRVSNVESEGCRG-----VGRTGWHIDGSFQ 109

Query: 116  PVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRA---LVHQRSAR-----HSLVY 167
          P      +++   VVP G T FA +   + L E  +A   ++ S R      H LVY
Sbjct: 110  PAPFNYSLYMHVVPKEGD-TVFAPLNEIIEGLSEDQQA KWDKLYMMSDRRGS LVHPLVY 168

Query: 168  SQSKLG 173
          S   + G
Sbjct: 169  SHPRTG 174

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>ref|XP_001211559.1| conserved hypothetical protein [Aspergillus terreus NIH2624]
gb|EAU37343.1| conserved hypothetical protein [Aspergillus terreus NIH2624]
Length = 398

Score = 52.0 bits (123), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 61/257 (23%), Positives = 94/257 (36%), Gaps = 16/257 (6%)

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Query: 15   LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERIGGG 73
          +G V G++LA L+D      L      ++ F Q      D Q      + G + +
Sbjct: 97   IGTEVHGINLAKLNDQQKDDLARLVAVRGVVFVRNQEDFDIDAQRELGRHLGKLHKHATT 156

Query: 74   DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVPAVG 133
          +      ++   V ++      D   +   + WH+D TY      P G
Sbjct: 157  AVPRKQGLEDVHV--YTGDNSSDQRALFTPSFLWHS DVTYEQPPSYTSLKLLTGPPRG 214

Query: 134  G--RTC FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD-TT 190
          G T +A   AAYDAL   +   +   +A HS      +Q + S +G +
Sbjct: 215  GGGDTLWASQYAAAYDALSSHMQTYLKGLTALHS-----ADMQASDSRALGRPVRRREP 266

Query: 191  ATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW 248
          T PL++ +P TG SL      I G+   ES+   + L +      H QW
Sbjct: 267  VTTEHPLIRTNPVTGWNSLFFNPFGFVTKIVGIPKTESDAIIRYLTEVVATTQEAHVRFQW 326

Query: 249  AAGDVVVWDNRCLLHRA 265
          DV +WDNR   H A
Sbjct: 327  GKNDVAIWDNRRTTNHSA 343

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>ref|XP_002472100.1| predicted protein [Postia placenta Mad-698-R]
gb|EED82716.1| predicted protein [Postia placenta Mad-698-R]
Length = 365

Score = 52.0 bits (123), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 42/164 (25%), Positives = 68/164 (41%), Gaps = 11/164 (6%)

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Query: 108  WHADSTYMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEAT-----RALVHQRSA 161
          WH+D T+ PV + A+      +P GG T +A   AYD L A      +H+ S
Sbjct: 157  WHSDITFEPVPSDFAILKIH TL PETGGDTVWASGYEAYDRLSPALAKHLEGLTAIHEASK 216

Query: 162  RHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPG 220
          V S K   +   +G+      G D A   + P+++ +P TG   +L + ++   I
Sbjct: 217  FKRYVESHGKTL YDGERGNPE-NVGADLRA--VHPVIRTNPITGWKALFVNKNFTTRILE 273

Query: 221  MDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLH 263

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+ ES+ L+ L + +W DV +W N H
Sbjct: 274 LTKDESDATLDYLFKLVNDNHDQLQVRFKWNKNDVAIWANSATFH 317

>gb|EGD74167.1| taurine catabolism dioxygenase TauD [Salpingoeca sp. ATCC 50818]
Length = 162

Score = 52.0 bits (123), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 44/164 (26%), Positives = 66/164 (40%), Gaps = 21/164 (12%)

Query: 128 VVPAVGGRCTCFADMRAAYDALDEATR----ALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
+VP GG T FAD A +D R L + AR +S K
Sbjct: 8 IVPEEGDGTGFADTVLALQQMDPELRKELEGLQIEVDARKIPDFSSLK----- 55

Query: 184 GYGMDTTATP--LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAP 241
D P L ++ H E+G SL G I G ES + ++ + P
Sbjct: 56 ---EDDERFPVALHSIIFNHDESGIESLYPGNGNVTIKGKTKEESRDIIGRVLAHLDREP 112

Query: 242 RVHAHQWAAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
V+ H+W GD+V+WDN+ +HR+ PR ++ ++ P
Sbjct: 113 YVYYHKWTKGDLVLWDNKTCMHRSMGGYGNHPRKLFRTQCFHHP 156

>ref|XP_001391155.2| tfdA family taurine dioxygenase [Aspergillus niger CBS 513.88]
Length = 342

Score = 52.0 bits (123), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 44/191 (23%), Positives = 77/191 (40%), Gaps = 10/191 (5%)

Query: 78 ISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTC 137
IS + ++G + + +++ M V WH+D + A + +P GG T
Sbjct: 113 ISTINSEGRKKLYQGSYTRMAAV-----WHS DIAFEKAPADFSSLRLTQLPVTGGDTL 166

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPL 197
+A YD + + R + SA H + ++G G + + P+
Sbjct: 167 WASGYEVYDRISKPYRGFLEGLSATH-VGAGFKRMGVKVTYGERGAPVNVGDELEAVHPV 225

Query: 198 VKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVV 254
V+ +P TG S+ IG I G++ ES L+ D + +W D+
Sbjct: 226 VRTNPITGWKSIFPIGAFPSKINGLNRRSANMLQYFHDLLITYGHDLQVRFKWNPNDIA 285

Query: 255 VWDNRCLLHRA 265
+WDNR + H A
Sbjct: 286 IWDNRSVFHTA 296

>ref|ZP_06192176.1| hypothetical protein SOD_f01220 [Serratia odorifera 4Rx13]
gb|EFA15197.1| hypothetical protein SOD_f01220 [Serratia odorifera 4Rx13]
Length = 287

Score = 52.0 bits (123), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 77/300 (25%), Positives = 114/300 (38%), Gaps = 49/300 (16%)

Query: 9 TPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG--QHLSNDQQIT-FAKRFG 65
TP GA L G ++ L AAL A +H LL+ G ++ Q +T +A +G
Sbjct: 14 TPFGAULTPKYPGQPISELP---VAALRALAQRHLLVLRGFDSGFTDPQLVTRYAGGWG 70

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
I G ++ V++H A+ D + + W D Y P + + +F
Sbjct: 71 EIMMWPFGAUL-----DVKEHPDAK-DHIFDSSYVPLHW--DGMYPKTIPEFQLFH 118

Query: 126 AEVVPVAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
P+ GGRT F D DE+ A + + S+ Y ++ H

Sbjct: 119 CVAAPSQDEGGRTTFVDTRLLLANADESLLA----QWLKVSISYRIKQVVH----- 165
Query: 184 GYGMDTTATPLRPLVKVHP-----ETGRP----SLLIGRHAHAIPGMDAAESERFLEG 232
YG + + PLV HP P + +HA G+ E E F +
Sbjct: 166 -YGGEVCS----PLVVTHPSGSGVIMRYNEPPTGKKFLNQHALEYHGVQPQEEQETFHQ 220
Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL 292
L +AHQW GDVVV DN LLH E + + R + + P AL
Sbjct: 221 LQQHLYDPRHYAHQWQQGDVVVADNFSLLHGREGFTARSARHLQRVHIQSNPVCANLAL 280

>dbj|BAD15041.1| hypothetical protein [Bradyrhizobium sp. BDV5329]
Length = 102

Score = 52.0 bits (123), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 34/107 (31%), Positives = 47/107 (43%), Gaps = 5/107 (4%)

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGR 206
ALD+ T+A + HSL+YS+ LG + Y L+ LV+ HP R
Sbjct: 1 ALDDDTKAEIEDLVCEHSLMYSRGS LGFTE----YTDDEKQMFKPVLRVLRTHPVHRR 55
Query: 207 PSLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
SL + HA I M E L L + A Q V+ H+W D+
Sbjct: 56 KSLYLSSHAGKIVSMSVPEGRLLLRDLNEHATQGEFVYVHKWKLHDL 102

>ref|YP_003711498.1| Pyoverdine biosynthesis protein [Xenorhabdus nematophila ATCC
19061]
emb|CBJ89293.1| Pyoverdine biosynthesis protein [Xenorhabdus nematophila ATCC
19061]
Length = 296

Score = 52.0 bits (123), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 48/197 (24%), Positives = 78/197 (39%), Gaps = 31/197 (15%)

Query: 109 HADSTYMPVMAQGAVFSAEVP--AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
H D Y + + +F P A GGRT F + LD + ++ ++
Sbjct: 102 HWDGMYREAIPEFQIFHCVSAPEAAQGGRITFVNTEQL--ILDASEDEFNTWKNT--TIT 157
Query: 167 YSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-----HA 215
Y K+ H YG + + PLV +HP+ + + H+
Sbjct: 158 YRTKKVTH-----YGGEVVS----PLVCLHPKGNKVVIRYNEPMHQEDKYADHHS 203
Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRV 275
I G+ + E + F E L + +AHQW +GD+V+ DN LLH E + + PR
Sbjct: 204 VTIQGLLSEEQKA FEETLYNRLYDPRYFYAHQWQSGDMVISDNFSLLHGREAFISRSPRH 263
Query: 276 MWSRLAGRPETEGAAL 292
+ + G P E +
Sbjct: 264 LQRVHVHGMPCVNNNSF 280

>emb|CBJ18982.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 105

Score = 51.6 bits (122), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 36/111 (32%), Positives = 54/111 (48%), Gaps = 8/111 (7%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRP-LVKVHP 202
A+D LDE TR LV HS ++S+++LG + + P+R +V+ HP
Sbjct: 2 AWDTLDEPTRELVLPLIGEHSRLFSRAELG-FDFTDEERLKFA-----PVRQRMVRRHP 54
Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

T R S L + H I G E + L L + A + R V + + H W A D +
Sbjct: 55 STRRLSLYLSSHCGNIVGWPLPEARALLRELTEHATERERVYSHAWRADDL 105

>ref|XP_382474.1| hypothetical protein FG02298.1 [Gibberella zeae PH-1]
Length = 346

Score = 51.6 bits (122), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 57/218 (26%), Positives = 90/218 (41%), Gaps = 45/218 (20%)

Query: 50 QHLSNDQQITFAKRFGAIERIGGGD-----IVAISNVKAD-----GTVRQHSPAE- 94
+ L+N+ Q+ A R G R+ G + + N D T + +PAE
Sbjct: 87 KDLTNELQMEADRLG---RLTGKPESSTLHVHPLQNFNPDEEKHVNTITDKAANPAED 143

Query: 95 -WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR 153
W + I +WH D+ Y P ++ +P GG T +A YD + + R
Sbjct: 144 LWKNRPSDIRN--SWHTDAGYEPNPPDYSILKVVKMPPTGGDTMWASSCEIYDKISPSYR 201

Query: 154 ALVHQRSARHSLVYSQSKLGHV-----QQAGSA-YIGYGMDTTATPLRPLVKVHP 202
+ +A+ +SQ +L V Q GS +G + TT P+V+ +P
Sbjct: 202 KFLEGLTAQ----FSQRLPKVAAEKGFEYLTQPRGSPNNVGDSLTTT----HPVVRTNP 253

Query: 203 ETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQ 239
TG SL +G H +I + ES+R L+DW Q
Sbjct: 254 VTGWKSLFAVGNHCESINDLTPDESKR----LLDWFLQ 287

>emb|CBJ18755.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 51.6 bits (122), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 35/112 (31%), Positives = 53/112 (47%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRP-LVKVH 201
AAYDAL +A +A + H + +S+ ++G + G P R LV+ H
Sbjct: 1 AAYDALTDQAIDDLVVEHDVFWSRGQIGFTE-----FPPGEREQFPSPRQRLVRRH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P +GR +L + HA I G E L L + A Q V++H+W GD+
Sbjct: 55 PGSGRKTLYLSHASHIVGWPVPEGRLLLADLTEHATQRQFVYSHEWRVGDL 106

>ref|YP_003531145.1| pyoverdine biosynthesis protein PvcB [Erwinia amylovora CFBP1430]
ref|YP_003538829.1| siderophore biosynthesis protein [Erwinia amylovora ATCC 49946]
emb|CBJ46425.1| putative siderophore biosynthesis protein [Erwinia amylovora ATCC 49946]
emb|CBA20737.1| pyoverdine biosynthesis protein PvcB [Erwinia amylovora CFBP1430]
Length = 292

Score = 51.6 bits (122), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 78/308 (25%), Positives = 115/308 (37%), Gaps = 46/308 (14%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAG--FAALHAAWLQ-----HALLIFPG-QHLSNDQ 56
TL + P G + L AG L WL+ H L++ G H ++
Sbjct: 9 TLDVAPLTGETGEPSCSFILIKPCRAGRHHIGELSVTWLRALVYSHQLVVLRGFDHFASD 68

Query: 57 QIT-FAKRFGAIERIGGG---DIVAISNVKADGTVRQHSPAEDWDDMMKVIVGNMAWHADS 112
+T + FG I G ++V +N + P WD M V
Sbjct: 69 SLTRYCATFGEIMMWPYGAVLELVEHANPDDHIFANSYVPLHWDGMYLDTVPEF-----Q 123

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL---VHQRSARHSLVYSQ 169
+ V A G + GGRT F+ AA A R L H R R +YS
Sbjct: 124 LFQCVHAAGDM-----QGGRTTFSSTNAALRIATPAVRELWARAHGRYQRSVELYSN 175

Query: 170 SKLGHVQQAGSAYIGYGMDDTATPLR--PLVK-VHPETGRPSLLIGRHAHAIPGMDAAES 226
+ + IG PLR P+++ P + + +++ G++ E
Sbjct: 176 T-----VEAPIIG-----IHPLREFPVIRFCEPPDENDATFLNPSSYSFGGINKDEE 222

Query: 227 ERFLEGLVDWACQAPRVH-AHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
E L L+ + PRV+ AHQW GD V+ DN LLH E + R + + GRP
Sbjct: 223 EMLLVSLMK-TLRDPRVYAHQWQTGDFVLSNLSLLHGREQYTHHSGRHLRRVHIHGRP 281

Query: 286 ETEGAALV 293
+ LV
Sbjct: 282 QIANHHLV 289

>emb|CBJ19101.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19117.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 105

Score = 51.6 bits (122), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 51/110 (46%), Gaps = 6/110 (5%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPE 203
A+D LDE TR LV HS + S+++LG + A L+ LV+ HP
Sbjct: 2 AWDNLDEPTRELVLPLIGEHSRLSSRAELGF-----DFTDEERLKFAPVLQRLVRRHPS 55

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
T R SL + H I G E+ L L + A Q RV++H W D+
Sbjct: 56 TRRLSLYLSSHCGNIVGWPLPEARALLRELTEHATQRErvYSHAWRTDDL 105

>gb|ABI95434.1| 2,4-D/alpha-ketoglutarate dioxygenase [uncultured bacterium]
Length = 109

Score = 51.6 bits (122), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 39/112 (34%), Positives = 51/112 (45%), Gaps = 7/112 (6%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR 195
T F DMRAAYD L E + + A H + S+ LG + + S P+
Sbjct: 2 TEFCDMRAAYDDLPEDFKKELEGLRAEHYALNSRFILGDTEYSES-----QRNAMPPVS 55

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH 246
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H
Sbjct: 56 WPLVRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQRFVYRH 107

>ref|XP_001598964.1| hypothetical protein SS1G_01054 [Sclerotinia sclerotiorum 1980]
gb|EDN91650.1| hypothetical protein SS1G_01054 [Sclerotinia sclerotiorum 1980
UF-70]
Length = 344

Score = 51.6 bits (122), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 42/168 (25%), Positives = 73/168 (43%), Gaps = 15/168 (8%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WHAD T+ V + A+ +P GG T+A Y+ L + ++ +A H +
Sbjct: 160 WHADITFERVPSDYAMLKIHTLPETGGDTLWASGNEIYERLSPKMKEVLEGLTATHDANF 219

Query: 168 ---SQSKLGH--VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGM 221
+LG + + + G + +A + P+V+ +P TG+ +L + + + +
Sbjct: 220 FHDEARRLQDIREDMRGSPLNIGKELSA--IHPVVRTNPVTGKKTLFVNQGFTKRLHPL 277

Query: 222 DAAESERFLEGLVDWACQAPRVHAHQ---WAAGDVVWDNRCLLHRA 265
ES+ L L + P H Q W+ DV +WDNR H A

Sbjct: 278 TKDESDLLLPLWLNK---VPLNHDAQVRWKWSKNDVAIWDNRSNWHCA 322

>ref|XP_001216869.1| hypothetical protein ATEG_08248 [Aspergillus terreus NIH2624]
gb|EAU31421.1| hypothetical protein ATEG_08248 [Aspergillus terreus NIH2624]
Length = 331

Score = 51.6 bits (122), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 40/176 (22%), Positives = 68/176 (38%), Gaps = 28/176 (15%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVH----- 157
WH+D + PV A +P GG T +A YD + +
Sbjct: 129 WHSDIQFEPVPADYTSRLTLQPKTGDTLWASGYELYDRFSKPYQKFFEGLTATFIGSG 188

Query: 158 -----QRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL-I 211
+R + +Y++ + GS + G D + P+V+ +P TG S+ +
Sbjct: 189 FLQAAERDPDNVRIYTEPR-----GSP-LNVGKDLAT--VHPVVRTNPVTGWKSIFAV 238

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW-AAGDVVVWDNRCLLHRA 265
G H I + ES+ L+ + + + +W D+ +WDNRC H A
Sbjct: 239 GPFPHKINELTQTESDELLKKFYNTILENHDIQVRFKWRNKNDIAIWDNRCFAHTA 294

>ref|ZP_03827804.1| pyoverdine biosynthesis protein PvcB [Pectobacterium carotovorum
subsp. brasiliensis PBR1692]
Length = 292

Score = 51.2 bits (121), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 49/177 (27%), Positives = 72/177 (40%), Gaps = 39/177 (22%)

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVG----GRTCFADMRAAYDALDEATRALVHQRSARHS 164
H D Y+ + + VF + V AVG GRT F+ A T+AL
Sbjct: 110 HWDGMYLKTVPQLQVF--QCVSAVGEQGGRITFSSTTTALRLASPETKALW----- 159

Query: 165 LVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----LIG 212
Q G Q+A Y ++T P+++ HP P + +
Sbjct: 160 ----QRATGQYQRAVELY-----SSTAQAPIIEQHPYRTHPVIRFCEPPIAGDKEFLN 208

Query: 213 RHAHAIPGMDAAESERFLEGLVDWACQAPRV-HAHQWAAGDVVVWDNRCLLHRAEPW 268
+ G++ E E+ L L A PRV +AHQW +GD+V+ DN LLH E +
Sbjct: 209 PSTYHFGIEPEEQEQLLSSL-QHALYDPRVQYAHQWQSGDIVIADNYSLHGRESY 264

>ref|ZP_02383058.1| pyoverdine biosynthesis protein PvcB [Burkholderia ubonensis Bu]
Length = 280

Score = 51.2 bits (121), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 52/199 (26%), Positives = 73/199 (36%), Gaps = 33/199 (16%)

Query: 109 HADSTYMPVMAQGAVFSAEVVPAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLV 166
H D Y + + +F P V GGRT F++ +A + + RAL
Sbjct: 98 HWDGMYRKQVPEFQIFHCVSAPEVEQGGRITFSNTKALLERAEPQARAL----- 146

Query: 167 YSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----LIGRH 214
K+ V + Y T A P+V HP G P + + R
Sbjct: 147 --WDKVTGVYHRKMEF--YDSKTIA----PIVTTHPTQGFVVRVYNEPSIEGDDSFVNRP 198

Query: 215 AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQAAGDVVVWDNRCLLHRAEPWDFKLPR 274
A G+D A+ F L +AH W GDVV+ DN LLH E + PR
Sbjct: 199 TLAFTGVDEADIGDFHRSRLRAALYAPENFYAHAWQTGDVVISDNYTLLHGREGFTSGAPR 258

Query: 275 VMWHSRLAGRPETEGAALV 293
+ + G P + LV

Sbjct: 259 HLRRVHVLGNPPLDNPHLV 277

>emb|CBJ19133.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 51.2 bits (121), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 50/112 (44%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPFVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
E+GR L IG HA + G AE L L++ A Q V+ H W GD+
Sbjct: 55 AESGRKFLFIGAHAGHVEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>emb|CAY25731.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 51.2 bits (121), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 31/108 (28%), Positives = 54/108 (50%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F G+ ++++QQ+ FA FG E GG + + N+
Sbjct: 16 IEAGMDKYAVLVFHGRDITDEQQMAFALNFGERESSRGGTVTKKEDYRLSSGLNDVGNLG 75

Query: 83 ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----KPLPKDHRTHLFLNCLGNCLWHS DSSFRPIPAKFSLLSARVV 118

>gb|EEQ91806.1| alpha-ketoglutarate-dependent taurine dioxygenase [Ajellomyces dermatitidis ER-3]
Length = 391

Score = 51.2 bits (121), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 68/260 (26%), Positives = 93/260 (35%), Gaps = 22/260 (8%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERIGGG 73
+G V GV+LA L D AL ++ F Q + Q + FG + R
Sbjct: 90 IGTEVHGVNLAKLTDNQNALARLIAIRGVVFFRAQDDFDIEAQRDLGRYFGTLHRHATT 149

Query: 74 DIVAISNVKADGTVRQHSPA EW--DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVP 130
+ K G H D D + + WH+D TY P
Sbjct: 150 AVP-----KKAGLEDVHVVTG DYSDVQRALFSPSFLWHS DVTYEVQPPSYTSLKVLTP 204

Query: 131 AVGG--RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 188
GG T ++ AAYDAL + + +A HS +Q GS G +
Sbjct: 205 PRGGGGDTLWSSQYAAYDALSPHMQTYLKGLTALHS-----ADMQADGSRAAGRPVR 256

Query: 189 TTA-TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH 246
T PL++ +P TG SL I G+ ES+ + L +HA
Sbjct: 257 REPITTKHPLIRTNPVTGWNSLFFNPGFITKIVGVPKLES DAIINYLSVVVTTQELHAR 316

Query: 247 -QWAAGDVVVWDNRCLLHRA 265
QW DV WDNR H A
Sbjct: 317 FQWGKNDVAFW DNRSTNHTA 336

>emb|CBJ19006.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 51.2 bits (121), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 38/112 (33%), Positives = 50/112 (44%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+S LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRSILGDTDYSES-----QRNAMPPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFFVYRHSWKVGDL 106

>ref|XP_001217671.1| hypothetical protein ATEG_09049 [Aspergillus terreus NIH2624]
gb|EAU30186.1| hypothetical protein ATEG_09049 [Aspergillus terreus NIH2624]
Length = 380

Score = 51.2 bits (121), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 58/277 (20%), Positives = 100/277 (36%), Gaps = 56/277 (20%)

Query: 41 QHALLIFPGQH-LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMM 99
Q ++ F Q L++D Q +R G + + + V G R+HS DD +
Sbjct: 78 QRGVVFVRKQDGLNDDLQKELVQRLGQLSGKPATSGLVHVPVANS--REHSVK--DDEI 133

Query: 100 KVIVGNM-----AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR 142
VI WH+D T+ P+ + + +P GG T +A
Sbjct: 134 SVISSEQRKTLYDRNNRKQSSRREWHSDITFEPIPSDYTLRLTLQLPRTGGDTLWASGY 193

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY-----MDTTATPLR 195
YD + E + + +A Y+Q V + +I G + +
Sbjct: 194 EVYDRISEPYQKFLESFTA----TYAQPGFNRVAKENDFHIHTGPRGAPENVGDELKAIH 249

Query: 196 PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDV 253
P+++ +P TG S+ +G H I G+ ES L+ V + + +W +
Sbjct: 250 PVIRTNPVTGWKSVFAVGTHVEKINGLTEESRHLLDWFVTLIVENHDLQVRLRWQNPND 309

Query: 254 V-----VWDNRCLLHRAEPWDF 270
+ +WDNR + H A WD+
Sbjct: 310 LGELYRKILRTLLELISHASAIWDNRSVYH-AATWDY 345

>gb|ABD39113.1| alpha-ketoglutarate dioxygenase [uncultured bacterium]
Length = 91

Score = 51.2 bits (121), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 26/61 (42%), Positives = 33/61 (54%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+
Sbjct: 31 PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFFVYRHSWKVGDLVM 90

Query: 256 W 256
W
Sbjct: 91 W 91

>ref|YP_001848583.1| oxidoreductase [Mycobacterium marinum M]
gb|ACC38728.1| oxidoreductase [Mycobacterium marinum M]
Length = 289

Score = 51.2 bits (121), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 64/284 (22%), Positives = 103/284 (36%), Gaps = 56/284 (19%)

Query: 12 GATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSDNDQQITFAKRFGAIERIG 71
G LGA +TGV LDD + + L+I + S ++ + K G I
Sbjct: 7 GEGLGAQITGVDPKNLDDITTDIEIRDIVYANKLVILKDVNPSPEEFLKLGKIVGQI---- 62

Query: 72 GGDIVAISNVKADGTVRQHSPA-EWDDMMKVIVGNMA-----WHADSTYMPVMA 119
V + P +D ++ V + WH D +MP
Sbjct: 63 -----VPYYEPMYHHEDHPEIFVSSTEEGQGVPKTGAFWHIDYMFMPPEPF 107

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
++ VP T F D+ + +L A +A AR +L + +
Sbjct: 108 AFSMVLPLAVPGHDRGTYFIDLAKVWQSLPAAQQA-----PARGTLSTHDPRRHIKIRPS 162

Query: 180 SAYIGYG-----MDTTATPLR-PLVKVHPETGRPSLLI-----GRHAHAIPGMDAA 224
Y G + P++ P V HP+TG L I + + + D A
Sbjct: 163 DVYRPIGEVWDEISRATPPIKWPTVIRHPKTGEEILYICATGTTKIEDKGNLV--DPA 219

Query: 225 ESERFL--EGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAE 266
L G +D +P +H + GD+++WDNR L+HRA+
Sbjct: 220 VLAELLAATGQLDPEYNSPFIHTQHYEVGDIILWDNRVLMHRAK 263

>emb|CBJ18942.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 51.2 bits (121), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 39/113 (34%), Positives = 49/113 (43%), Gaps = 9/113 (7%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATP--LRPLVKV 200
AAYD L E + + A H + S+ LG + S A P RPLV+
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFVLGDTDYSES-----QRNAMPPVSRPLVRT 53

Query: 201 HPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
H +GR L IG HA I G AE L L+ A Q V+ H W GD+
Sbjct: 54 HAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLKHATQRKFVYRHSWKVGDL 106

>gb|ABD39121.1| alpha-ketoglutarate dioxygenase [uncultured bacterium]
Length = 95

Score = 51.2 bits (121), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 25/61 (40%), Positives = 34/61 (55%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ H +GR L IG HA + G+ AE L L+ A Q V+ H+W GD+V+
Sbjct: 35 PLVIRTHAGSGRKFLFIGAHASHVEGLPVAEGRMLLAELLGHATQREFVYRHRWNVGDVLM 94

Query: 256 W 256
W
Sbjct: 95 W 95

>emb|CBJ19136.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 50.8 bits (120), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 38/112 (33%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q VH H W GD+

Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVHRHSWKVGDL 106

>emb|CBJ18830.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 105

Score = 50.8 bits (120), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 36/110 (32%), Positives = 48/110 (43%), Gaps = 6/110 (5%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDALD TRA + HS+VYS+ L G + D + PLV+ P
Sbjct: 1 AAYDALDAETRASIEGLRVHHSIVYSRHVL-----GFDFSEDEQDKLKGAVHPLVRTIP 54

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
+GR +L + HA + E L L D A Q ++ H W D
Sbjct: 55 GSGRRALYLASHAAHVVDWQVPEGRLLLRDLSDHATQPQFIYCHVWRPHD 104

>dbj|BAF81036.1| 2,4-D dioxygenase [Burkholderia sp. M36-VN10-2W]
Length = 103

Score = 50.4 bits (119), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 26/61 (42%), Positives = 34/61 (55%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H+W GD+V+
Sbjct: 43 PLVRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQRQFVYRHRWQVGDLVM 102

Query: 256 W 256
W
Sbjct: 103 W 103

>ref|ZP_06474867.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia symbiont of
Datisca glomerata]
gb|EFD28431.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia symbiont of
Datisca glomerata]
Length = 214

Score = 50.4 bits (119), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 46/153 (30%), Positives = 65/153 (42%), Gaps = 20/153 (13%)

Query: 1 MAQTTLQITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQI 58
+ T L I +GA + G+ L A DD A++ AA ++H L F GQ L + Q
Sbjct: 3 VVSTNLDIRRVGTGRIGAEIVGLDLRDALGDDTVIASIRAAALVEHKALFFRGQELDDAGQQ 62

Query: 59 TFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGN---MAWHADSTYM 115
FA RFGA+ A TV S A ++++V WH D T++
Sbjct: 63 RFAARFGAL-----TTAHP TV--PSLAGSPNVLRVDSTEGRANNWHTDVT FV 107

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL 148
+ A V+P GG T A+ AY L
Sbjct: 108 VSPPAASTLRAVVIPPAGGDTLIANSVTAYQDL 140

>ref|YP_001476938.1| taurine catabolism dioxygenase TauD/TfdA [Serratia
proteamaculans
568]
gb|ABV39810.1| Taurine catabolism dioxygenase TauD/TfdA [Serratia proteamaculans
568]
Length = 287

Score = 50.4 bits (119), Expect = 3e-04, Method: Compositional matrix adjust.

Identities = 75/300 (25%), Positives = 114/300 (38%), Gaps = 49/300 (16%)

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Query: 9   TPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG--QHLSNDQQIT-FAKRFG 65
          TP GA L   G   ++ +   AAL +   QH LL+   G   ++ Q +T +A+ +G
Sbjct: 14  TPFGAVLTPQYPG---QSIRELPVAALRSLAQQHLLVLRGFDSGFTDPQLLTRYAEGWG 70

Query: 66  AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
          I   G ++          V++H A+ D +          + W D Y P + + +F
Sbjct: 71  EIMMWPFGAVL-----DVKEHPDAK-DHIFDSSYVPLHW--DGMYPKTIPEFQLFH 118

Query: 126  AEVVPVAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
          P+   GGRT F D          DE+   L   R   S+ Y   ++ H
Sbjct: 119  CVAAPSQDEGGRTTFVDTTCLLANADESL--LAQWREV--SISYRIKQVVH----- 165

Query: 184  GYGMDTTATPLRPLVKVHPE-----TGRP----SLLIGRHAHAIPGMDAAESERFLEG 232
          YG + +   PLV HP          P          + +HA   G+   + E F +
Sbjct: 166  -YGGEVRS---PLVVDHPNGNGQIMRYNEPPTGKKFLNQHALEYHGVQPQEAFHQ 220

Query: 233  LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL 292
          L          +AHQW GDVV+ DN LLH E + + R + + P   AL
Sbjct: 221  LQQHLYDPRHYAHQWQQGDVVIADNFSLLHGREGFTARSARHLQRVHIQSNPVCANQAL 280

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>emb|CBJ18781.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 50.4 bits (119), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 34/111 (30%), Positives = 56/111 (50%), Gaps = 5/111 (4%)

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Query: 143  AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
          AAYDAL +AT+ +   +H + +S+++G +   Y   +P R LV++HP
Sbjct: 1   AAYDALPDATKVAIDGLIVQHDFWWSRAQIGFTEFPFGEREQY---PPSPQR-LVRLHP 55

Query: 203  ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
          + R +L + HA I G A+   L L A Q V++H+W GD+
Sbjct: 56  GSKRKTLYLSAHASHIVGWPIADGRLLLLDLNTHATQPDFVYSHKWRVGD 106

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>ref|XP_001224283.1| hypothetical protein CHGG_05069 [Chaetomium globosum CBS 148.51]
gb|EAQ88450.1| hypothetical protein CHGG_05069 [Chaetomium globosum CBS 148.51]
Length = 375

Score = 50.1 bits (118), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 55/269 (20%), Positives = 97/269 (36%), Gaps = 48/269 (17%)

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Query: 41   QHALLIFPGQH-LSNDQQITFAKRFGAI-----ERIGGGDIVAISNVK 82
          Q ++ F Q L+N+ Q   R G +          ER GG+ IS +
Sbjct: 71  QRGVVFFRAQDGLTNELQKQLILRLGELVGRPATSGLHIHPILNSERELGCNDPEISTIS 130

Query: 83   ADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPVAVGGRTCFADMR 142
          +   + +S   D +   + WH+D + PV A   +P+ GG T +A
Sbjct: 131  SIQNKKFYSKTVSDSLSPKKQSSAQWHS DIAFEPVPADYTSRLRLVELPSTGGDTLWASGY 190

Query: 143  AAYDALDEATRALVHQRSARHSLVYSQS-----KLGHVQQAGSAYIGYGMDTTATPLR 195
          YD + E + + +A   Y +          +L +   +G +   +
Sbjct: 191  EIYDRISEPYQKFLEGLTATFEQPYFRKVAEDAGFQLYDKPRGAPENVGGELKA----IH 246

Query: 196  PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDV 253
          P+V+ +P TG S+ +G H I G+ ES + L +D + + +W +
Sbjct: 247  PVVRTNPVTGWKSIFPVGGHVKHINGLTEEESKLLSWFLDLVYKNHDLQVRLKWKPNPD 306

Query: 254  V-----VWDNRCLLHRA 265
          +          +WDNR + H A

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Sbjct: 307 IGESPWIGYRWQLLTCEAIWDNRSVFHTA 335

>emb|CBJ19135.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 50.1 bits (118), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 50/112 (44%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYD L E + + A+H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAKHIALNSRFILGDTDYSES-----QRNAMPFVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>ref|XP_003057027.1| predicted protein [Micromonas pusilla CCMP1545]
gb|EEH58672.1| predicted protein [Micromonas pusilla CCMP1545]
Length = 315

Score = 50.1 bits (118), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 51/199 (25%), Positives = 76/199 (38%), Gaps = 23/199 (11%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVP--AVGGRTCFADMRAAYDALDEATRALVHQRSARHSL 165
WH D + +V + P GG T FAD+ AAY AL E R + + A S
Sbjct: 117 WHTDQAFRDPPPYASVLYCKTAPPPGAGGATIFADVTAAYAALPEDKRLELERYRAVCSY 176

Query: 166 VYSQSKLGHVQQAGSAYIGYGMDDTTATPL-RPLVKVHPETGRPSLL----- 210
+ +K+ + P+ +PLV + TG S+
Sbjct: 177 AHHNAKVRKRGTPSYPLLTPEQRAEHPPVYQPLVLTNAATGEKSVYGFNSSVCAVVAEGE 236

Query: 211 -IGRHAHAIPGMDAAESERFLEGLVDWA---CQAPR-VHAHQWAAGDVVWDNRCLLHRA 265
+ + A I + E E + D C P V+ H+W GD ++WDN +H A
Sbjct: 237 TLSQEALDIYDLQGEEHESVSRIMYDDLPHCTRPEFVYEHEWMEGDALIWDNMRTIHAA 296

Query: 266 EPW-DFKLPRVMWHSRLAG 283
P D R MW + +A
Sbjct: 297 TPLEDGSHAREMWRTTVAS 315

>gb|ACB21020.1| TfdA [uncultured bacterium]
Length = 64

Score = 50.1 bits (118), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 26/59 (44%), Positives = 35/59 (59%)

Query: 105 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH 163
N WH+DS++ A+ ++ SA VVP GG T F DMRAAYDAL ++ + A H
Sbjct: 1 NQFWHSDSSFQQPAARYSMLSAVVVPPSGGDTFCDMRAAYDALPRDLQSELEGLRAEH 59

>emb|CBJ19127.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 50.1 bits (118), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 50/112 (44%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYD L E ++ + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDSKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPFVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>emb|CBJ19060.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 50.1 bits (118), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDGLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVPSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>gb|EGD93099.1| hypothetical protein TSEG_00655 [Trichophyton tonsurans CBS 112818]
Length = 339

Score = 49.7 bits (117), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 42/162 (25%), Positives = 64/162 (39%), Gaps = 14/162 (8%)

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD-----EATRALVHQRSARHSLV 166
Y P+ A+ VP GG T +A YD + E A Q
Sbjct: 140 YSPIPAEYTTLRRLTQVPKTGGDTLWASGYELYDRISKPYQRFLTLTATCAQPGYNKVS 199

Query: 167 YSOSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL-IGRHAHAIPGMDAAE 225
+ KL Q+ IG + + P+V+ +P TG S+ G H I + AE
Sbjct: 200 TGKFKLFDGQRGAPENIGSNFSS----VHPVVRTNPVTGWKSIYSAGFHVQKINDVTEAE 255

Query: 226 SERFLEGLVDWACQAPRVHAH-QWA-AGDVVVDNRCLLHRA 265
S+ L+ + + +W A D+ +WDNRC+ H A
Sbjct: 256 SKALLDWFRLINENNDLQVRFKWKNANDMAIWDNRCVFHTA 297

>emb|CBJ18908.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 105

Score = 49.7 bits (117), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 35/111 (31%), Positives = 53/111 (47%), Gaps = 8/111 (7%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-LVKVHP 202
A+D LDE TR LV HS ++S+++LG + + P+R +V+ HP
Sbjct: 2 AWDYLDEPTRELVLPLIGEHSRLFSRAELG-FDFTDEERLKFA-----PVRQRMVRRHP 54

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
T R SL + H I G E+ L L + A + RV++H W D+
Sbjct: 55 STRRLSLYLSSHCGNIVGWPLPEARALLRELTEHATERERVYSHAWRTDDL 105

>gb|EGE04589.1| taurine dioxygenase [Trichophyton equinum CBS 127.97]
Length = 339

Score = 49.7 bits (117), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 42/162 (25%), Positives = 64/162 (39%), Gaps = 14/162 (8%)

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD-----EATRALVHQRSARHSLV 166
Y P+ A+ VP GG T +A YD + E A Q
Sbjct: 140 YSPIPAEYTTLRRLTQVPKTGGDTLWASGYELYDRISKPYQRFLTLTATCAQPGYNKVS 199

Query: 167 YSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL-IGRHAHAIPGMDAAE 225
+ KL Q+ IG + + P+V+ +P TG S+ G H I + AE
Sbjct: 200 TGKFKLFDGQRGAPENIGSNFSS----VHPVVRTNPVTGWKSIYSAGFHVQKINDVTEAE 255

Query: 226 SERFLEGLVDWACQAPRVHAH-QWA-AGDVVVDNRCLLHRA 265
S+ L+ + + + +W A D+ +WDNRC+ H A
Sbjct: 256 SKALLDWFLRLINENNDLQVRFKWKNANDMAIWDNRCVFHTA 297

>gb|EFW98179.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Pichia angusta DL-1]
Length = 666

Score = 49.7 bits (117), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 72/313 (23%), Positives = 121/313 (38%), Gaps = 61/313 (19%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITF 60
T + ++P+ +G + G L+ L AG L Q +++F Q ++ ++Q+
Sbjct: 366 TIMDLSPS---IGTEIRGTQLSQTLSAGLDELALLAAQRGVVVFRDQDYADIGFERQLEI 422

Query: 61 AKRFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS 112
A+ FG + G + + I + K D VR+ W + +H+D
Sbjct: 423 ARHFGPLHIHGWAHPANGSPEFMIIYDDKDDLVRVRR----SWKGRSPI-----QFHSQ 473

Query: 113 TYMPVMAQGAVFSA-EVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
+ P + E P GG T F+ AY+ L R + A H
Sbjct: 474 SAEPQTPGTTILCMLECPPTAGGDTIFSSGYGAYERLSPKFRKRLEGLRAVHC----- 526

Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVH-----PETGRPSLLIGR-HAHAIPGMDA 223
+V A + GM +A R + + P T R +L + + +I GM
Sbjct: 527 --NVGVANA-EVTNNGM--SAIQRRNICRTEHPVVVVHPVTKRKALYVTPVYTESIVGMQK 582

Query: 224 AESERFLEGLV-----DWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVM 276
ES+ L L D+AC+ ++ G VVVD R H ++ D+ + +
Sbjct: 583 EESDALLNLFNHIIRGQDFACRV-----RYDKGTVVVDQIRITCH-SQTLDPVDQYR 635

Query: 277 WH----SRLAGRP 285
H + LA RP
Sbjct: 636 RHGFRLTPLANRP 648

>ref|XP_002476351.1| predicted protein [Postia placenta Mad-698-R]
gb|EED78451.1| predicted protein [Postia placenta Mad-698-R]
Length = 363

Score = 49.7 bits (117), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 46/188 (24%), Positives = 76/188 (40%), Gaps = 21/188 (11%)

Query: 90 HSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVVPVAVGGRTCFADMRAAYDAL 148
H E ++ + V WH+D T+ PV + A+ +P GG T +A + Y+A
Sbjct: 135 HKQIELEEDLNVSQFATKEWHSDFEVPVPSDFAILKIHTLPETGGDTLWA---SGYEAY 191

Query: 149 DEATRAL-----VHQRSARHSLVYSQSKLGHVQQAGS-AYIGYGMDDTTATPLRPLV 198
D +RAL VH+ + S V Q K H G+ +G + T + P++
Sbjct: 192 DRLSRALAKHLEGLTAVHEATFFKSYVERQKTLHEGPRGNPENVTDLRT---VHPVI 247

Query: 199 KVHPETGR--PSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVV 255
+ +P TG + I + ES+ L+ L + +W+ DV +
Sbjct: 248 RTNPVTGMIATESCLYSFTRRILELTKDESDATLDYLFRLVSDNHDQLQVRFKWSKNDVAI 307

Query: 256 WDNRCLLH 263
W N H

Sbjct: 308 WANSASFH 315

>ref|XP_001947612.1| PREDICTED: hypothetical protein, partial [Acyrtosiphon pisum]
Length = 222

Score = 49.7 bits (117), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 46/176 (26%), Positives = 71/176 (40%), Gaps = 32/176 (18%)

Query: 15 LGATVTGVHLATLDDAGF-AALHAAWLQHALLIFPGQHL-SNDQQITFAKRFGAIE---- 68
LG V GV L T + + +H +LIF Q + S D+ + ++ FG +E
Sbjct: 8 LGCEVRGVDLKTENRPEIIKQIQEDVTKHRILIFKDGQGVSGDRHVEISRWFGELESTFY 67

Query: 69 ---RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
+ D+ +SN K +G VG WH D T+ P +++
Sbjct: 68 KHPKSPHPDVFRVSNKNEGCTN-----VGRSGWHIDGTFQPAPFSYSLYH 113

Query: 126 AEVVPAVGGRTCFADMRAAYDALDEATRA-----LVHQR--SARHSLVYSQSKLG 173
E VP G T F + ++LD+ T +V R S H L+YS + G
Sbjct: 114 MESVVK-EGHTLFIPLTELIESLDKDYDTWNAWMSDRSSLVHPLIYSHPQTG 168

>emb|CBX80659.1| pyoverdine biosynthesis protein PvcB [Erwinia amylovora ATCC
BAA-2158]
Length = 179

Score = 49.7 bits (117), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 49/168 (29%), Positives = 71/168 (42%), Gaps = 21/168 (12%)

Query: 133 GGRTCFADMRAAYDALDEATRAL--VHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT 189
GGRT F+ AA A R L H R R +YS + + IG
Sbjct: 23 GGRTTFSSTNAALRIATPAVRELWARAHGRYQRSVELYSNT-----VEAPIIG----- 70

Query: 190 TATPLR--PLVK-VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-A 245
PLR P+++ P + + +++ G++ E E L L+ + PRV+ A
Sbjct: 71 -IHPLREFPVIRFCEPPDENDATFLNPSSYSFGINKDEEEMLLVSLMK-TLRDPRVYYA 128

Query: 246 HQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAALV 293
HQW GD V+ DN LLH E + R + + GRP+ LV
Sbjct: 129 HQWQTGDFVLSNLSLLHGREQYTDHSGRHLRRVHIHGRPQIANHHLV 176

>emb|CBJ18943.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 49.7 bits (117), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 37/111 (33%), Positives = 48/111 (43%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHP 202
AAYD L E + + A H + S+ LG + S D PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSESQ-----RDAMPPVSWPLVRTHA 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 56 GSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQKRFVYRHSWKVGDL 106

>emb|CAY25780.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 49.7 bits (117), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 31/109 (28%), Positives = 54/109 (49%), Gaps = 17/109 (15%)

Query: 33 AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG-----DIVAISNV 81
AA+HA +L+F Q + +D Q+ F++ G +E+ G D+ ISN+
Sbjct: 14 AAVHAGMDGFGVLVFDQKIDDDHQLVFSRSLGPLEQATGDIAAPQDRRMSMDLNDISNL 73

Query: 82 KADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
+ + DD ++ +GN WH+DS++ V A+ ++ SA VV
Sbjct: 74 DKNSKI-----LARDRRRLFLGLGNQLWHSDDSSFKDVPKYSLLSARVV 117

>ref|XP_001594485.1| hypothetical protein SS1G_04292 [Sclerotinia sclerotiorum 1980]
gb|ED01817.1| hypothetical protein SS1G_04292 [Sclerotinia sclerotiorum 1980
UF-70]
Length = 368

Score = 49.7 bits (117), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 42/181 (23%), Positives = 70/181 (38%), Gaps = 18/181 (9%)

Query: 97 DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV 156
D + + WHAD ++ P A + EV+P GG T +A YD + E + +
Sbjct: 157 DRANGLSNSKWHADISFEPKPADYSSSLKLEVLPKTGGDTLWASGYEYDRISEPYQKFL 216

Query: 157 HQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP-----LRPLVKVHPETGRP 207
+L + + G ++ A + P + P+V+ +P TG
Sbjct: 217 -----ETLTVTFQQPGFIEAAANGGFELYDKPRGAPENIGKELKAVHPVVRTNPVTGWK 270

Query: 208 SLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVWDNRCLLHR 264
S+ +G H I + ES+ LE + +W D+ +WDNR H
Sbjct: 271 SVFPVGGHVSINDVTRWESQALLEWFKRLLDVNDLQVRFKWKNNQNDLAIWDNRSTFHT 330

Query: 265 A 265
A
Sbjct: 331 A 331

>emb|CBJ19142.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 49.7 bits (117), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGRIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>emb|CBJ18944.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 49.7 bits (117), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMLVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGRIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>ref|YP_003262840.1| Taurine catabolism dioxygenase TauD/TfdA [Halothiobacillus neapolitanus c2]
gb|ACX95793.1| Taurine catabolism dioxygenase TauD/TfdA [Halothiobacillus neapolitanus c2]
Length = 303

Score = 49.3 bits (116), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 58/268 (21%), Positives = 99/268 (36%), Gaps = 28/268 (10%)

Query: 19 VTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERI----- 70
V + + D L +++ Q+ + + F +R G +
Sbjct: 12 VISRQVTEMTDDEIHNLKKIVFDSGIVVLKAQNATASDFVDFGRRIGELSPYYEEMYYHHP 71

Query: 71 GGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVP 130
++ SNV+ DG V + V WHAD +M + +VV
Sbjct: 72 NHKELFVSSNVQTDGKV-----IGVPRTGKFWHADYAFMAKPFAFTITYPQVVS 120

Query: 131 AVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-VYSQSKLGHVQQAGSAYIGYGMDT 189
+ T F DM +AY+ L + + HS+ Y + + V + S +
Sbjct: 121 SQERGTYFIDMASAYERLSPENMKRKEGGVGTHSVRRYFKIRPTDVYRPISEILHEIDAK 180

Query: 190 TATPLRPLVKVHPETGRPSLLIGRHAHAIPGM--DAAESERFLEGLVDWACQA-----P 241
T T PLV HP TG L + R + D +++ L+ L+ + Q+ P
Sbjct: 181 TPTVTHPLVNHVPVTGAKILYVSRGFTETISLKDDDLDADEVLDLLVESGQSDDTFTHP 240

Query: 242 RVHAHQWAAGDVVVVDNRCLLHRAEPWD 269
+ GD+ +WDNR +H A+ D
Sbjct: 241 DIRQININEGDIFLWDNRRYVHHAKHND 268

>emb|CBJ18984.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 49.3 bits (116), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHAHQVYRHSWKVGDL 106

>emb|CBJ18927.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 49.3 bits (116), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGETDYSES-----QRNAMPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHAHQVYRHSWKVGDL 106

>ref|XP_001548982.1| hypothetical protein BC1G_12213 [Botryotinia fuckeliana B05.10]
gb|EDN18235.1| hypothetical protein BC1G_12213 [Botryotinia fuckeliana B05.10]

Length = 368

Score = 49.3 bits (116), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 44/172 (25%), Positives = 69/172 (40%), Gaps = 22/172 (12%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WHAD ++ P A + EV+P GG T +A YD + + + + SL
Sbjct: 168 WHADISFEPKPADYSSLKLEVLPKTGGDTLWASGYEIIDRISKPYQKFL-----ESLTV 221

Query: 168 SQSKLGHVQQAGSAYIGYGMDTTATP-----LRPLVKVHPETGRPSLL-IGRHAHA 217
+ + G ++ A + P + P+V+ +P TG S+ +G H
Sbjct: 222 TFQQPGFIEAAANGGFELYDKPRGAPENVGKELKAVHPVVRTNPVTGWKSVFPVGGHVSH 281

Query: 218 IPGMDAAESER----FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
I + ESE F LVD +V D+ +WDNR + H A
Sbjct: 282 INDVTQLESEALLGWFKRLLDV--NHDLQVRFKWKNQNDLAIWDNRSVFHTA 331

>emb|CBJ19138.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 49.3 bits (116), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVH 201
AAYD L E + + A H + S LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSHFILGDTDYSES-----QRNAMPVPSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLEFIGAHAGHIEGRSVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>ref|XP_001552854.1| hypothetical protein BC1G_09036 [Botryotinia fuckeliana B05.10]
gb|EDN29090.1| hypothetical protein BC1G_09036 [Botryotinia fuckeliana B05.10]
Length = 341

Score = 49.3 bits (116), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 44/172 (25%), Positives = 71/172 (41%), Gaps = 22/172 (12%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+D T+ P+ + A+ +P GG T +A YD + + + + +A Y
Sbjct: 134 WHSDITFEPIPSDYALLRLTELPKTGGDTLWASGYEVYDRISKPVQKFLETLTA----TY 189

Query: 168 SQSKLGHVQQAGSAYIGYGMDTTATP-----LRPLVKVHPETGRPSLL-IGRHAHA 218
+Q + I Y + A + P+V+ +P TG S+ +G H I
Sbjct: 190 AQPEFNKAADKNGFKI-YSEERGAPENVGEKLEAVHPVVRTNPVTGWKSIFALGHVSHI 248

Query: 219 PGMDAAESER----FLEGLVDWACQAPRVHAHQWA-AGDVVVWDNRCLLHRA 265
+ ES+ FL +VD R H+W D+ +WDNR H A
Sbjct: 249 NDLTTIESDALLAWFLRLVVDNHDLQVR---HRWENVNDLAIWDNRSNYHVA 297

>emb|CBJ20077.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 147

Score = 49.3 bits (116), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 39/140 (27%), Positives = 58/140 (41%), Gaps = 6/140 (4%)

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVYSQSKLGHVQQAG 179
+ A VP GG T F +M AY+ L R ++ SA HS +Y + Q+
Sbjct: 8 VIMRAVTVPEFGGDTGFLNMVRAYETLSPTLRKVLVDGLSAVHSATRIYGSAYQAQQRFS 67

Query: 180 SAYIGYGMDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
+ MD A + PLV HP +GR L + + + I M ES L+ L D
Sbjct: 68 GTSVKTEMDVAAGDRET VHPVCTHPTSGRRFLYVNKVYVQRIDSMTDDESRLQLFLYD 127

Query: 236 WACQAPRVHAHQWAGDVVV 255
+ +W A V++
Sbjct: 128 HCSKFELTCRVRWTADQVLI 147

>ref|XP_002621709.1| alpha-ketoglutarate-dependent taurine dioxygenase [Ajellomyces dermatitidis SLH14081]
gb|EEQ73713.1| alpha-ketoglutarate-dependent taurine dioxygenase [Ajellomyces dermatitidis SLH14081]
Length = 373

Score = 49.3 bits (116), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 66/255 (25%), Positives = 91/255 (35%), Gaps = 22/255 (8%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERIGGG 73
+G V GV+LA L D AL ++ F Q + Q + FG + R
Sbjct: 90 IGTEVHGVNLAKLTDNQRNALARLIAIRGVVFFRAQDDFDIEAQRDLGRYFGTLHRHATT 149

Query: 74 DIVAISNVKADGTVRQHSPAEDW---DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVP 130
+ K G H D D + + WH+D TY P
Sbjct: 150 AVP-----KKAGLEDVHVVTGDYSVDQRALFSPSFLWHSVDVTEVQPPSYTSLKVLTP 204

Query: 131 AVGG--RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD 188
GG T ++ AAYDAL + + +A HS +Q GS G +
Sbjct: 205 PRGGGGDTLWSSQYAAAYDALSPHMQTYLKGLTALHS-----ADMQADGSRAAGRPVR 256

Query: 189 TTA-TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH 246
T PL++ +P TG SL I G+ ES+ + L +HA
Sbjct: 257 REPITTKHPLIRTNPVTGWNLSLFFNPGFITKIVGVPKLESDAIINYLSVVVTTQELHAR 316

Query: 247 -QWAGDVVVWDNRC 260
QW DV WDNR
Sbjct: 317 FQWGKNDVAFWDNRS 331

>ref|XP_003038633.1| hypothetical protein SCHCODRAFT_28913 [Schizophyllum commune H4-8]
gb|EFJ03731.1| hypothetical protein SCHCODRAFT_28913 [Schizophyllum commune H4-8]
Length = 340

Score = 49.3 bits (116), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 71/285 (24%), Positives = 106/285 (37%), Gaps = 29/285 (10%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T +ITP LG V+GV L+ +DDA L + L+IF Q D K
Sbjct: 45 TLSEITPN---LGVEVSGVSLSQIDDAARDDLALLVARRGLVIFRNQQEFIDSSPEAYKE 101

Query: 64 FGAIERIGGGDIVAISNVKADG-----TVRQHSPAEDWDDMMKVIVGNMAWHADSTYMPVM 118
+G R G + ++ +G V + + ++ + + ++WH+D +Y
Sbjct: 102 WG---RYFGRHLIHPTSGHPEGHPEIHLVYRDENSTFNFEREDSISTLSWHSVDVSYELQP 158

Query: 119 AQGAVFSAEVPVAV-----GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS 168
F P GG T F AA L + A HS +
Sbjct: 159 PGLTTFFLIAQPHARGEGLSEFSGGDTLFTSQVAALKRLSPEFVEFLRGLKAVHS-GFE 217

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESE 227
Q+ G G + PL++ HP TG +L + R I + ESE
Sbjct: 218 QADYSRAGNRG---GIVRRDPVEHVHPLIRRHVPVTGEEALYVNRQFTRRIVNLKREESE 273

[illegible]


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emb|CBJ19126.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19128.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19129.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19130.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19131.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19132.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19134.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19137.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19139.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19140.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19141.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19144.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19145.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19146.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19148.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19149.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19150.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19151.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19152.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19154.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19155.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19156.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19157.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19161.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19167.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19171.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19180.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19196.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19200.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19202.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19205.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18787.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18791.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18793.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18800.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18806.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18809.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18812.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18817.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18818.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18820.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18827.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

```

Score = 49.3 bits (116), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

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Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
          AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVPSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
          +GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQQRKFVYRHSWKVGDL 106

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>emb|CBJ18939.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

```

Score = 49.3 bits (116), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

```

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201

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      AAYD L E + +      A H + S+ LG      + S      P+ PLV+ H
Sbjct: 1  AAYDDLPEDFKKELQGLRAEHYAMNSRFLGDTDYSES-----QRNAMPPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
      +GR L IG HA I G AE      L L++ A Q      V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

```

>dbj|BAE60876.1| unnamed protein product [Aspergillus oryzae]
Length = 349

Score = 48.9 bits (115), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 49/201 (24%), Positives = 86/201 (42%), Gaps = 21/201 (10%)

```

Query: 78 ISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTC 137
      IS + ++G      + +++ M V      WH+D ++      A +      +P GG T
Sbjct: 111 ISTINSEGRKTLYKGS DYTKMAAV-----WHSDISFEKAPADFSSRLVLQPKTGGDTL 164

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLV----YSQSKLGHV-QQAGSAYIGYGMDTTAT 192
      +A      YD + + RA +      SA H+ V      +Q+      H+ ++      A + G D TA
Sbjct: 165 WASGYEIIDRISKPYRAFLETLSATHAGVGFMRLAQTGKFHLYEKERGAPVNVGGDLTA- 223

Query: 193 PLRPLVKVHPETGRPSLL-IGR--HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH--- 246
      + P+V+ +P TG S+ IG+      I G+      ES      L+ + +      V +
Sbjct: 224 -VHPVVRTNPITGWKSIPIGKAQSPCCIDGLTRRESASMLQSVSNGTALMTLVGVVVPY 282

Query: 247 --QWAAGDVVVDNRCLLHRA 265
      + +WDNR + H A
Sbjct: 283 ILHCELTGLAIWDNRSVFHTA 303

```

>emb|CBJ18892.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 48.9 bits (115), Expect = 8e-04, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

```

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVH 201
      AAYD L E + +      A H + S+ LG      + S      P+ PLV+ H
Sbjct: 1  AAYDDLPEDFKKELQGLRAEHYALNSRFLGDTDYSES-----QRNAMPPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
      +GR L IG HA I G AE      L L++ A Q      V+ H W GD+
Sbjct: 55 AGSGRKFLFIGGHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

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>ref|XP_002904406.1| taurine dioxygenase, putative [Phytophthora infestans T30-4]
gb|EEY53775.1| taurine dioxygenase, putative [Phytophthora infestans T30-4]
Length = 335

Score = 48.9 bits (115), Expect = 8e-04, Method: Compositional matrix adjust.
Identities = 59/269 (21%), Positives = 101/269 (37%), Gaps = 56/269 (20%)

```

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERI---- 70
      +G + + L L D+      L      Q ++ F Q +S + Q+      + +G +
Sbjct: 85 IGTEILNLQLHELTD SQKDELALLVAQRGVVFFRDQKISIEDQLALGRYYGPLHVYQTVA 144

Query: 71 ---GGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE 127
      G      + + N+ D R + A      +      WH+D +Y      F
Sbjct: 145 HAKGTPQVHVVENLLEDSEKRIKTQA-----LEPVNLWHSVDVSYERQPPSYTSFKVL 196

Query: 128 VVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 187
      P GG T +A      +AY+A      A+ + ++ R +V      + H

```

Sbjct: 197 TTPPTGGDTLWA---SAYEA-----AIANGKTLRRPIV---EFEH----- 230

Query: 188 DTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ-APRVHA 245

P+V+ HP TGR +L + + I + AAES F ++ + Q + H

Sbjct: 231 -----PVVRTHPVTGRKALYVNAQFTTRINNLSAAESGAFFSSILRFLHQHIAQGH 282

Query: 246 HQ---WAAGDVVVWDNRCLLHRAEPWDF 270

Q W V +WDNR +H A +D+

Sbjct: 283 FQVRYRWTKDAVAIWDNRATVHYAT-YDY 310

>emb|CBJ18980.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]

emb|CBJ19040.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]

Length = 106

Score = 48.9 bits (115), Expect = 8e-04, Method: Compositional matrix adjust.

Identities = 37/112 (33%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201

AAAYD L E + + A H + S+ LG + S P+ PLV+ H

Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALSSRFILGDTDYSES-----QRNAMPVPSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

+GR L IG HA I G AE L L++ A Q V+ H W GD+

Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>gb|EFY94724.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative

[Metarhizium anisopliae ARSEF 23]

Length = 374

Score = 48.9 bits (115), Expect = 8e-04, Method: Compositional matrix adjust.

Identities = 49/192 (25%), Positives = 77/192 (40%), Gaps = 38/192 (19%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRT-----CFADMRAA---- 144

+WH D+ Y P ++ +P GG C M A+

Sbjct: 150 SWHTDAGYEPNPPDYSILKLIKLPKTGGGMPCLAPFHAPFYIVLTVPCIDTMWASSCEI 209

Query: 145 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM-----DTTATPLR---P 196

YD + A R + +A +SQS+L +V A + Y + T LR P

Sbjct: 210 YDKVSPAYRKFLGLELTAD----FSQSRLPNVA-AAKGFEYLSKPRGSPNNIGTSLRAVHP 264

Query: 197 LVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAG-DV 253

+V+ +P TG SL +G H I + + ES+R L+ + + H+W D+

Sbjct: 265 VVRTNPVTGWKSLFAVGNHVERINDVTSDESKRLLDWFLQLLIVEEHDCQLRHRWENPYDI 324

Query: 254 VVWDNRCLLHRA 265

+WDNR + H A

Sbjct: 325 AIWDNRSVYHTA 336

>emb|CAY25739.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 119

Score = 48.9 bits (115), Expect = 9e-04, Method: Compositional matrix adjust.

Identities = 31/108 (28%), Positives = 54/108 (50%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82

+ A ++A+L+F GQ ++++QQ+ FA G E GG + +SN+

Sbjct: 16 IEAGMDKYAVLLFRGQDITDEQQLAFALNSGEREHARGGTVTKKEDYRLTSGLNVDVSNL 75

Query: 83 ADGTVRQHSAPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

DG +P D + +G WH+DS++ P+ A+ ++ SA VV

Sbjct: 76 KDG-----NPLPRDHRTHLFNLGYCLWHSDSSFRPIPAKFSLLSARVV 118

>emb|CBJ18993.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 48.9 bits (115), Expect = 9e-04, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFLGDTDYSESP-----RNAMPPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>emb|CBJ18823.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 48.9 bits (115), Expect = 9e-04, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRLILGDTDYSES-----QRNAMPPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>gb|EFQ93253.1| hypothetical protein PTT_09428 [Pyrenophora teres f. teres 0-1]
Length = 354

Score = 48.5 bits (114), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 43/179 (24%), Positives = 73/179 (40%), Gaps = 27/179 (15%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRS----- 160
WH+D + V +VF VP GG T FA YD L + + V +
Sbjct: 154 WHSDVGFEAVPGDYVFIVPEVPETGGDTMFASGCELYDRLSKPMQQFVENLTIINGSPS 213

Query: 161 -----ARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL-IGR 213
A + +Y++ + G Q +G + +P V+ +P TG S+ +G+
Sbjct: 214 LEDAVRAENPNLYAKER-GCPQNSGLHF-----RHEQPFVVRTNPVTGWKSIYALGQ 263

Query: 214 HAHAI PGMDAAESERFLEGLVD--WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDF 270
+ +I + ES+ L+ ++ + V D+V+WDNR H WD+
Sbjct: 264 NTISIKDLAPEESQMLLDWIIGILYKNHDTTVRIKYLNRNDLVIWDNRSTFH-CVTWDY 321

>gb|AAB08969.1| alpha ketoglutarate dioxygenase [Variovorax paradoxus]
Length = 106

Score = 48.5 bits (114), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 36/112 (32%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

Query: 145 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVHPE 203
YD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 YDDLPEDFKKELQGLRAEHYALNSRFLGDTDYSESP-----QRNAMPPVSWPLVRTHAG 54

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255

+GR L IG HA I G AE L L++ A Q V+ H W GD+V+
Sbjct: 55 SGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDLVM 106

>emb|CBJ19160.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 48.5 bits (114), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 38/113 (33%), Positives = 49/113 (43%), Gaps = 9/113 (7%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR--PLVKV 200
AAYD L E + + A H + S+ LG + S A P PLV+
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVGWPLVRT 53

Query: 201 HPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
H +GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 54 HAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>emb|CBJ19070.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 48.5 bits (114), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWRVGDL 106

>emb|CBJ19042.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19078.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ18786.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 48.5 bits (114), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRRFVYRHSWKVGDL 106

>gb|AA51275.1| TdfA [uncultured bacterium]
Length = 105

Score = 48.5 bits (114), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 38/110 (34%), Positives = 49/110 (44%), Gaps = 7/110 (6%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR 195
T F DMRAAYD L E + + A H + S+ LG + S P+
Sbjct: 2 TEFCDMRAAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVS 55

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH 244
PLV+ H +GR L IG HA I G AE L L++ A Q V+

Sbjct: 56 WPLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKIFY 105

>gb|ACB21019.1| TfdA [uncultured bacterium]
Length = 63

Score = 48.5 bits (114), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 25/56 (44%), Positives = 34/56 (60%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH 163

WH+DS++ A+ ++ SA VVP GG T F DMRAAYDAL ++ + A H

Sbjct: 3 WHSDSSFQQPAARYSMLSAVVVPPSGDTEFCDMRAAYDALPRDLQSELEGLRAEH 58

>emb|CBJ18792.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 48.5 bits (114), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR-PLVKVH 201

AAYD L E + + A H + S+ LG + S P+ PLV+ H

Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVPSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

GR L IG HA I G AE L L++ A Q V+ H W GD+

Sbjct: 55 AGFGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKIFYRHSWKVGDL 106

>emb|CBJ18773.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 48.5 bits (114), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 31/93 (33%), Positives = 42/93 (45%), Gaps = 5/93 (5%)

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPG 220

HSL+YS+ LG + A L+ LV+ HP GR SL + HA I G

Sbjct: 19 CEHSLMYSRGSLGFLDYAEEE-----KQMFKPVQLRLVRTHPVHGRKSLYLSSHAGGIVG 73

Query: 221 MDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

M E+ L L + A Q V+ H+W D+

Sbjct: 74 MTMPPEARVLLRDLSEHATQPEFVYVHKWKLHDL 106

>emb|CBJ19037.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 48.5 bits (114), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 37/111 (33%), Positives = 48/111 (43%), Gaps = 7/111 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR-PLVKVH 201

AAYD L E + + A H + S+ LG + S P+ PLV+ H

Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVPSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252

+GR L IG HA I G AE L L++ A Q V+ H W GD

Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKIFYRHSWKVGDL 105

>gb|ACB21025.1| TfdA [uncultured bacterium]
Length = 64

Score = 48.1 bits (113), Expect = 0.001, Method: Compositional matrix adjust.

Identities = 25/56 (44%), Positives = 34/56 (60%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH 163
WH+DS++ A+ ++ SA VVP GG T F DMRAAYDAL ++ + A H
Sbjct: 4 WHSDSSFQQPAARYSMLSAVVVPPSGGDTFCDMRAAYDALPRDLQSELEGLRAEH 59

>sp|P83309.1|SDPA_DELAC RecName: Full=(S)-2-(2,4-dichlorophenoxy)propionate,
2-oxoglutarate dioxygenase
Length = 45

Score = 48.1 bits (113), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 26/33 (78%), Positives = 27/33 (81%)

Query: 3 QTTLQITPTGATLGATVTGVHLATLDDAGFAAL 35
QTTLQITPTGATLGATVTGVHLAT+ A L
Sbjct: 2 QTTLQITPTGATLGATVTGVHLATVIVGNTAGL 34

>emb|CBJ19008.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 48.1 bits (113), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 36/111 (32%), Positives = 48/111 (43%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYD L E + + A H + S+ LG + Y + PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILG-----DTDYFESQRNAMPPVSWPLVRTHA 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 56 GSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWRVGD L 106

>ref|ZP_01630848.1| taurine dioxygenase [Nodularia spumigena CCY9414]
gb|EAW44516.1| taurine dioxygenase [Nodularia spumigena CCY9414]
Length = 124

Score = 48.1 bits (113), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 24/76 (31%), Positives = 40/76 (52%), Gaps = 2/76 (2%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAE--SERFLEGLVDWACQAPRVHAHQWAAGDV 253
P+V +H TG+ L +G GM+ +++F + L + + V+ H W GD+
Sbjct: 32 PIVSIHQVTGKKGLYLGS DTSIPVGMEDKLDLAKQFWQDLFETVLERTPVYTHIWQPGDL 91

Query: 254 VVWDNRCLLHRAEPWD 269
VVWDN ++H P+D
Sbjct: 92 VVWDNSQVMHAGIPYD 107

>gb|ACB21023.1| TfdA [uncultured bacterium]
Length = 61

Score = 48.1 bits (113), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 25/56 (44%), Positives = 34/56 (60%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH 163
WH+DS++ A+ ++ SA VVP GG T F DMRAAYDAL ++ + A H
Sbjct: 3 WHSDSSFQQPAARYSMLSAVVVPPSGGDTFCDMRAAYDALPRDLQSELEGLRAEH 58

>ref|ZP_04588004.1| taurine dioxygenase [Pseudomonas syringae pv. oryzae str. 1_6]
Length = 149

Score = 48.1 bits (113), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 38/138 (27%), Positives = 66/138 (47%), Gaps = 15/138 (10%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
T ++TP +GA V+GV L+ L +A A + A+L++ +L+F QH++ +Q F +
Sbjct: 24 TVERLTPI---IGA EVSGVDLSQPLQEAQLAEIRRAFLENHVLVFRDQHMTVEQHKAFGR 80

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA 122
FG + + DI DG + + + G + WH D T + G+
Sbjct: 81 LFGPLRALPVEDI-----DGDDAELVVVRANAQSRFVAGEL-WHTDGTADAEPMSG 131

Query: 123 VFSAEVVPVAV--GGRTCF 138
+ + PA+ GG T F
Sbjct: 132 MLYVKETPAIGTGGDTLF 149

>emb|CBJ19082.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19110.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
emb|CBJ19147.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 48.1 bits (113), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVPSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L+ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLGHATQRKFVYRHSWKVGDL 106

>gb|ACB21028.1| TfdA [uncultured bacterium]
Length = 62

Score = 48.1 bits (113), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 23/41 (56%), Positives = 29/41 (70%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPVAVGGRTCFADMRAAYDAL 148
WH+DS++ A+ ++ SA VVP GG T F DMRAAYDAL
Sbjct: 3 WHSDSSFQQPAARYSMLSAVVVPPSGDTEFCDMRAAYDAL 43

>emb|CBJ18890.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 48.1 bits (113), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 36/112 (32%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVPSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q ++ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFMYRHSWKVGDL 106

>gb|AAB18140.1| 2,4-dichlorophenoxyacetate dioxygenase [Halomonadaceae gen. sp.
strain I-18]
Length = 105

Score = 48.1 bits (113), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 25/60 (41%), Positives = 32/60 (53%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+
Sbjct: 46 PLVRTHAGSGRKFLFIGAHAXHIEGRPVAEGRMLLAELLEHATQRFVYRHSWKVGDLVM 105

>gb|EFQ92006.1| hypothetical protein PTT_10996 [Pyrenophora teres f. teres 0-1]
Length = 354

Score = 48.1 bits (113), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 42/174 (24%), Positives = 70/174 (40%), Gaps = 16/174 (9%)

Query: 104 GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH 163
G WH+D + PV A +P GG T +A YD A + +A
Sbjct: 146 GAAQWHSDIQFEPVPADYTSRLTLQLPETGGDTLWASGYEMYDRFSTAYQRFEGLTATF 205

Query: 164 S---LVYSQS-----KLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL-IGR 213
S LV + K+ ++ +G + T + P+V+ +P TG S+ +G
Sbjct: 206 SGDGLVKAEEANPEVVKIYEKERGSPKNVGRSL----TAVHPVVRTNPVTGWKSIFALGP 261

Query: 214 HAAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW-AAGDVVVWDNRCLLHRA 265
I ++ ES+ L+ + + +W A D+ +WDNR + H A
Sbjct: 262 FPKYINELNVEESDELLKRFRSVIIENHDLQVRFKWRNANDLAIWDNRSVFHTA 315

>gb|AA51279.1| TdA [uncultured bacterium]
Length = 102

Score = 47.8 bits (112), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 37/105 (35%), Positives = 47/105 (44%), Gaps = 7/105 (6%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRAAYD L E + + A H + S+ LG + S P+
Sbjct: 1 TEFCDMRAAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
PLV+ H +GR L IG HA I G AE L L++ A Q
Sbjct: 55 WPLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQ 99

>gb|ABE68889.1| TfdA [Burkholderia glathei]
Length = 103

Score = 47.8 bits (112), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 37/105 (35%), Positives = 47/105 (44%), Gaps = 7/105 (6%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRAAYD L E + + A H + S+ LG + S P+
Sbjct: 1 TEFCDMRAAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
PLV+ H +GR L IG HA I G AE L L++ A Q
Sbjct: 55 WPLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQ 99

>emb|CBJ19079.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 47.8 bits (112), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 36/112 (32%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKEQLGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG H I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHVGHIEGRPVAEGRMLLAELLEHATQQRKFVYRHSWKVGDL 106

>gb|ACB21024.1| TfdA [uncultured bacterium]
Length = 61

Score = 47.8 bits (112), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 23/41 (56%), Positives = 29/41 (70%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL 148
WH+DS++ A+ ++ SA VVP GG T F DMRAAYDAL
Sbjct: 2 WHSDSSFQQPAARYSMLSAVVVPPSGDTEFCDMRAAYDAL 42

>emb|CBJ18764.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 104

Score = 47.8 bits (112), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 34/111 (30%), Positives = 51/111 (45%), Gaps = 7/111 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP 202
+AYDAL + +A + HS+ YS++ LG + M T + PLV+ P
Sbjct: 1 SAYDALSDMKAKLEGLRVEHSIAYSRAMLGF-----EFNEREMQTLKGAVHPLVRTLP 54

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
GR SL + HA +I ++ L L + A Q V+ H W GD+
Sbjct: 55 -YGRKSLYLASHAASIIDWPLPKARLLLRDLTEHATQPQFVYRHSWRVGDL 104

>ref|ZP_05883092.1| PvcB protein [Vibrio metschnikovii CIP 69.14]
gb|EEX36342.1| PvcB protein [Vibrio metschnikovii CIP 69.14]
Length = 282

Score = 47.8 bits (112), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 64/309 (20%), Positives = 113/309 (36%), Gaps = 52/309 (16%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQ--I 58
M + P G + A + H+ LD ++L + +H L++ G + +
Sbjct: 1 MPYKITSLDPFQVMVEAQHSSTHVVELD---ISSLRHLFERHQLVLLRGFTVFEQAEDFA 57

Query: 59 TFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
+ +++G + G ++ + +++ P D + M W D Y P +
Sbjct: 58 DYCEQWGEVSIWPFGRVLEL-----IQKEQPE--DHIFDSSYMPMHW--DGMYPQV 105

Query: 119 AQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ +F +P GGRT F A D E R+L + + GH Q
Sbjct: 106 PEYQIFQCVEAPLPGNGGRTTFCHTMLALDNASEQERSLWRKVT-----GHYQ 153

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF----LEG 232
+ Y + + P+V HP G ++ H + D + G
Sbjct: 154 RKMEFY-----HSKTVSPIVMPHPYKGY-DVIRYNEPHVVDNGDLLNPPDVTLSGISG 205

Query: 233 LVDWACQA-----PR-VHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
AC PR +AH+W +GD+V+ DN LLH E + PR + ++
Sbjct: 206 SEAMACHQSLRRALYDPRNFYAHEWQSGDIVITDNFSLHGREAFSHTPRHIRRVQVLS 265

Query: 284 RPETEGAAL 292
 P +L
 Sbjct: 266 NPPYHNPSL 274

>emb|CBJ19143.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
 Length = 106

Score = 47.8 bits (112), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 37/112 (33%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
 AAYD L E + + A H + S+ LG + S P+ PLV+ H
 Sbjct: 1 AAYDDLPEDFKKELRGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
 GR L IG HA I G AE L L++ A Q V+ H W GD+
 Sbjct: 55 AGPGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHAHQVYRHTWKVGDL 106

>ref|ZP_06188335.1| PvcB [Legionella longbeachae D-4968]
 ref|YP_003455680.1| pyoverdine biosynthesis protein PvcB [Legionella longbeachae
 NSW150]
 gb|EEZ94273.1| PvcB [Legionella longbeachae D-4968]
 emb|CBJ12617.1| putative pyoverdine biosynthesis protein PvcB [Legionella
 longbeachae NSW150]
 Length = 278

Score = 47.8 bits (112), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 45/201 (22%), Positives = 71/201 (35%), Gaps = 33/201 (16%)

Query: 106 MAWHADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH 163
 M H D Y P + + +F +P GGRT F++ + L H+ +
 Sbjct: 93 MPLHWDGMYRPQVPEYQIFHCVKAPLPQGGRRTTFSNTLLVLKNTSSEIKELWHKVT--- 149

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGR-----PSLLIGRHA 215
 G Q+ Y + + P++ HP+ G PS G
 Sbjct: 150 -----GTYQRKMKFY-----NSKTISPIITDHPQKGYSVIRYNEPPSQDKGHFV 193

Query: 216 H---AIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFK 271
 + G+ E + F L +AH+W GD+V+ DN LLH E + K
 Sbjct: 194 NPPELEFTGISHEELDVFHTSLAKALYSPDNFYAHEWQTGDIVDIADNFSLLHGREEFTSK 253

Query: 272 LPRVMWHSRLAGRPETEGAAL 292
 PR + + P + L
 Sbjct: 254 SPRHIQRVHVLSPNPPFDNPGL 274

>gb|AA51272.1| TfdA [uncultured bacterium]
 gb|AA51286.1| TdfA [uncultured bacterium]
 Length = 101

Score = 47.8 bits (112), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 37/105 (35%), Positives = 47/105 (44%), Gaps = 7/105 (6%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
 T F DMRAAYD L E + + A H + S+ LG + S P+
 Sbjct: 1 TEFCDMRAAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
 PLV+ H +GR L IG HA I G AE L L++ A Q
 Sbjct: 55 WPLVRTHAGSGRKFIFIGAHAGHIEGRPVAEGRMLLAELLEHAHQ 99

>emb|CBJ19153.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 47.8 bits (112), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 37/112 (33%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L + A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELPEHATQQRKFVYRHSWKVGDL 106

>ref|XP_001559770.1| hypothetical protein BC1G_01926 [Botryotinia fuckeliana B05.10]
gb|EDN28807.1| hypothetical protein BC1G_01926 [Botryotinia fuckeliana B05.10]
Length = 401

Score = 47.8 bits (112), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 52/238 (21%), Positives = 95/238 (39%), Gaps = 29/238 (12%)

Query: 14 TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG 73
++G + G+ L +LDD L + ++ Q + +QI F FG +
Sbjct: 106 SIGTELVGIQLTSLDDTQKNELARLVAERGVVFLRDQEMDVHEQIEFGSYFGELH----- 160

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF-SAEVVP- 131
I ++ + D + P D+ K + WH+D +Y + G F + +P
Sbjct: 161 -IHQMAGIIPD--LPWVHPHDKDETAKNRSHQIWHSDVSYE-LQPPGLTFLRMDTLPKA 216

Query: 132 -----VGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY 185
GG T +A Y++L + ++ A+HS ++QA A G
Sbjct: 217 GPDGYEAGGDTIWASGYIYESLSPTLKGILENLEAKHS-----GLEQA EKALKGN 267

Query: 186 GM--DTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQA 240
G + P+V+ HP T + +L + + I G++ SE L+ L + +A
Sbjct: 268 GCLRRNPIETIHPVVRTHPVTQOKTLYVNENFTKEIVGVEKRFSESLDLNRYVAEA 325

>emb|CBJ18734.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 47.4 bits (111), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 31/111 (27%), Positives = 54/111 (48%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202
AAYDAL + T+ + A+H + +S+ ++G + ++ + + LV+ HP
Sbjct: 1 AAYDALPDDTKGAIDGLVAQHDFVWSRGQIGFTE-----FLPGEREKYPPSQQLVRRHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+ R +L + HA I G E L L + A Q V++H+W GD+
Sbjct: 56 GSKRKALYLSAHASHIVGWVPPEGRLLLLADLNEHATQQQFVYSHKWRIGDL 106

>gb|ADP12603.1| putative siderophore biosynthesis protein [Erwinia sp. Ejp617]
Length = 292

Score = 47.4 bits (111), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 78/307 (25%), Positives = 115/307 (37%), Gaps = 40/307 (13%)

Query: 3 QTTLQITPTGATLGATVTGVHLATLDDAGF--AALHAAWLQ-----HALLIFPG--QHLS 53
Q TL P G + L AG + L AWL+ H L++ G S

Sbjct: 7 QDTLDAEPLIGETGEPSCSFGVLIKPRHAGLHISELPVAWLRLSVHTHQLVVLRGFDPFDS 66

Query: 54 NDQQITFAKRFGAIERIGGGDIVA-ISNVKADGTVRQHS--PAEWDDMMKVIVGNMAWHA 110
+D + FG I G ++ I + D + HS P WD M V

Sbjct: 67 SDSLTRYCATFGEIMMWPFAGVLELIEHENPDDHIFAHSYVPLHWDGMYLDTVPEF---- 122

Query: 111 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS 170
+ V A G + GGRT F+ A + RAL + R Y +S

Sbjct: 123 -QLFQCVHAGGDM-----QGGRTTFSCCTGALRIATPSVRALWRRARGR----YQRS 169

Query: 171 KLGHVQQAGSAYIGYMDTTATPLR--PLVK-VHPETGRPSLLIGRHAHAIPGMDAAESE 227
+ + + IG P R P+++ P + I +++ G++ E E

Sbjct: 170 VELYSNRVEAPVIG-----IHPQREFPVIRFCEPPVENDATFINPSSYSFVGINEDEKE 223

Query: 228 RFLEGLVDWACQAPRVH-AHQWAAGDVVWVWNRCLLHRAEPWDFKLPRVMWHSRLAGRPE 286
L L + P+V+ AHQW GDVV+ DN LLH E + + R + + G P

Sbjct: 224 MLLASL-KRTL RDPQVYYAHQWQTGDVVLSDNLSLLHGREQYTHRSGRHLRRVHIHGNPH 282

Query: 287 TEGAALV 293
LV

Sbjct: 283 IANHHLV 289

>gb|AAF02720.2| alpha ketoglutarate dependent dioxygenase [Ralstonia sp. CS2]
gb|AAF62390.2| alpha ketoglutarate dependent dioxygenase [Alcaligenes sp. CS1]
Length = 104

Score = 47.4 bits (111), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 25/60 (41%), Positives = 32/60 (53%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+

Sbjct: 45 PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDLVM 104

>gb|EFY88508.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Metarhizium acridum CQMa 102]
Length = 374

Score = 47.4 bits (111), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 47/192 (24%), Positives = 73/192 (38%), Gaps = 38/192 (19%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR-----AA 144
+WH D+ Y P ++ +P GG F R

Sbjct: 150 SWHTDAGYEPNPPDYSILKLIKLPKTGGGNQFYITRFQAHLYIILTPTYIDTMWASSCEI 209

Query: 145 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM-----DTTATPLR---P 196
YD + A R + +A +SQS+L +V A + Y + + LR P

Sbjct: 210 YDKISPAYRKFLGLELTAD----FSQSRLPNVA-AAKGFEYSEPRGSPNNIGSSLRAVHP 264

Query: 197 LVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAG-DV 253
+V+ +P TG SL +G H I + ES R L+ + + H+W D+

Sbjct: 265 VVRTNPVTGWKSLFAVGNHVERINDVTPDESRRLLDWFLQLIVEEHDCQLRHRWENPYDI 324

Query: 254 VVWVWNRCLLHRA 265
+WDNR + H A

Sbjct: 325 AIWDNRSVYHTA 336

>emb|CBJ19158.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 47.4 bits (111), Expect = 0.002, Method: Compositional matrix adjust.

Identities = 36/112 (32%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVPSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G E L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVPEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>emb|CBJ18931.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 47.4 bits (111), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 36/112 (32%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVPSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q + H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFAYRHSWKVGDL 106

>emb|CBJ18906.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 47.4 bits (111), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 36/112 (32%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVPSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG +A I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGVYAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>ref|XP_002736252.1| PREDICTED: hypothetical protein [Saccoglossus kowalevskii]
Length = 307

Score = 47.4 bits (111), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 61/278 (21%), Positives = 105/278 (37%), Gaps = 66/278 (23%)

Query: 15 LGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGAIERIG- 71
LG V + L L + + +H +LIF Q ++S D+ + + FG +E
Sbjct: 31 LGCEVHSIDLGNPLPENVIETIKKDVTEHRILIFKNQRNISPDKHVEIGRWFGLESTSF 90

Query: 72 -----GGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
+I +SN ++G +V VGN WH D Y+ +++
Sbjct: 91 YKHPKSPSLNIFRVSNDASEG-----QVGVGNTGWHIDGQYLQKPCSYSIY 136

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184
V + G T FA L++ L H++ R +L V+
Sbjct: 137 HM-VNISRGAETLFA-----PLNDIIEGLSHRQRHR-----WERLWVVRNP----- 176

Query: 185 YGMDDTTATPLRPLVKVHPETGRPSLLI-----GRHAHAIPGMDAAESERFLEG 232
+G D + PL+ HPE+G+ L + G + M ++ L+
Sbjct: 177 HGTDV----IHPLIYSHPESGKKVCLHTGLTGAFYWDGNNVQRLTNMKETQA---LKK 229

Query: 233 LVDWACQAPR---VHAHQWAAGDVVVWDNRCLLHRAEP 267
+D + ++H+W GD ++ DN L H A P
Sbjct: 230 EIDHVFTKDKHTVQYSHKWEFGDFIISDNLALAHVAPP 267

>emb|CAK48940.1| unnamed protein product [Aspergillus niger]
Length = 300

Score = 47.4 bits (111), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 52/202 (25%), Positives = 78/202 (38%), Gaps = 29/202 (14%)

Query: 73 GDIVAISNVKADGTVRQHSPAEDMMKVIIVGNMA---WHADSTYMPVMAQGAVFSAEVV 129
GD + + + +H+ ++DD + A WHAD++Y + +
Sbjct: 110 GDDEVLDRPEIYAVSSEHNDRDKFDDYLNTHKHKQFASRGWHADTSYENIPSDYIAIKMVKA 169

Query: 130 PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSAYIG 184
P GG T FA AYD L E + + S L L GH Q G ++
Sbjct: 170 PMTGGDTLFAFCYDAYDLSEPWQRMADSLSYIMPLADKGINLWLGPRGHPQNFSGSF-- 227

Query: 185 YGMDTTATPLRPLVKVHPETGRPSL-----LIGRHAHAIPGMDAAESE-----RFLEGLVD 235
AT PLV +P TG +L + R I G+ E E FL+ + D
Sbjct: 228 -----EAT--HPLVVTNPVTGWKALWGFSPISMRANGRINGVTDHEQELMKAYFLKLITD 280

Query: 236 WACQAPRVHAHQWAAGDVVVWD 257
+ H+W D+V+WD
Sbjct: 281 ---NHDLQYRHRWKPDDIVIWD 299

>emb|CBJ19057.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 47.0 bits (110), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 36/112 (32%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVH 201
AAYD L E + + A H + + LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKEQLGLRAEHYALNPRFILGDTDYSES-----QRNAMPVPSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLEFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>ref|YP_125606.1| hypothetical protein lp10237 [Legionella pneumophila str. Lens]
emb|CAH14466.1| hypothetical protein lp10237 [Legionella pneumophila str. Lens]
Length = 278

Score = 47.0 bits (110), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 46/201 (22%), Positives = 74/201 (36%), Gaps = 33/201 (16%)

Query: 106 MAWHADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH 163
M H D Y P + + +F +P GGRT F++ A + L ++ S
Sbjct: 93 MPLHWDGMYRPQVPEYQIFHCVKAPLPGQGGRTTFSNTILALQFASSEIKELWNKVS--- 149

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPE-----TGRPSLLIGRHA 215
G Q+ Y + + P++ HP+ PS+ G
Sbjct: 150 -----GTYQRKMEFY-----NSKTVSPIITKHPQKDFSVIRYNEPPSVDKGHFV 193

Query: 216 H----AIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFK 271
+ G+D E + F L A +AH+W GD+V+ DN LLH E + +
Sbjct: 194 NPPDIEFTGIDQEELDSFHRSLNKALYSADNFYAHEWQNGDIVIADNFSLLHGREGFVSR 253

Query: 272 LPRVMWHSRLAGRPETEGAAL 292

PR + + P + L
Sbjct: 254 SPRHIQRVHVLSPNPPFDNPGL 274

>emb|CBJ19054.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 47.0 bits (110), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 36/112 (32%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L G HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFTGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>emb|CBJ19163.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 47.0 bits (110), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 31/93 (33%), Positives = 42/93 (45%), Gaps = 5/93 (5%)

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPG 220
HSL+YS+ LG + Y L+ LV+ HP GR SL + HA I G
Sbjct: 19 CEHSLMYSRGALGFLD-----YSEEEKQMFKPVLRTHPVHGRKSLYLSSHAGGIVG 73

Query: 221 MDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
M E+ L L + A Q V+ H+W D+
Sbjct: 74 MTVPEARVLLRDLNEHATQPEFVYVHRWKLHDL 106

>gb|ABI94568.1| TfdA [Burkholderia hospital]
Length = 99

Score = 47.0 bits (110), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 36/103 (34%), Positives = 46/103 (44%), Gaps = 7/103 (6%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR-P 196
F DMRAAYD L E + + A H + S+ LG + S P+ P
Sbjct: 1 FCDMRAAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVSWP 54

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
LV+ H +GR L IG HA I G AE L L++ A Q
Sbjct: 55 LVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQ 97

>emb|CBJ19169.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 47.0 bits (110), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 31/93 (33%), Positives = 42/93 (45%), Gaps = 5/93 (5%)

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPG 220
HSL+YS+ LG + Y L+ LV+ HP GR SL + HA I G
Sbjct: 19 CEHSLMYSRGALGFLD-----YSEEEKQMFKPVLRTHPVHGRKSLYLSTHAGGIVG 73

Query: 221 MDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
M E+ L L + A Q V+ H+W D+
Sbjct: 74 MTVPEARVLLRDLNEHATQPEFVYVHRWKLHDL 106

>gb|AD034958.1| putative (R)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 95

Score = 47.0 bits (110), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 30/100 (30%), Positives = 51/100 (51%), Gaps = 8/100 (8%)

Query: 42 HALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKV 101
+ ++ FPGQ ++N+Q I F++RFG ++ + + +I +R+ E ++ +V
Sbjct: 2 YQVIYFPGQAITNEQHIAFSRRFGPVPDVPVL--LKSIEGYPEVQMIRR----EANESGRV 55

Query: 102 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM 141
I + WH DST++ V A VP GG T F M
Sbjct: 56 IGDD--WHTDSTFLDAPPAAVVMRAVDVPEHGGDTGFLSM 93

>gb|AAX51288.1| TdfA [uncultured bacterium]
Length = 105

Score = 47.0 bits (110), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 49/110 (44%), Gaps = 7/110 (6%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR 195
T F DMRAAYD L E + + A H + S+ LG + S P+
Sbjct: 1 TEFCDMRAAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH 244
PLV+ H +GR L IG HA + G AE L L++ A Q V+
Sbjct: 55 WPLVRTHAGSGRKFLFIGAHAGHMEGRPVAEGRMLLAELLEHATQRFVY 104

>gb|AAX51276.1| TdfA [uncultured bacterium]
Length = 99

Score = 47.0 bits (110), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 36/103 (34%), Positives = 46/103 (44%), Gaps = 7/103 (6%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR-P 196
F DMRAAYD L E + + A H + S+ LG + S P+ P
Sbjct: 2 FCDMRAAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWP 55

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
LV+ H +GR L IG HA I G AE L L++ A Q
Sbjct: 56 LVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQ 98

>gb|EEQ42086.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Candida
albicans WO-1]
Length = 386

Score = 47.0 bits (110), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 66/275 (24%), Positives = 113/275 (41%), Gaps = 36/275 (13%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQ---ITFAKR 63
+ITP G+ + GV L+ L+D G L Q +L+F Q ++ + F K
Sbjct: 83 RITPK---FGSEIDGVQLSQLNDKGKDELALFLAQRKVLLFNEQDFADKGPFGFAVEFGKY 139

Query: 64 FGAIERIGGGDIVAISNVKADG-----TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV 117
FG + V S+ G T R+ E + ++ +H+D +Y
Sbjct: 140 FGRLH-----VHPSSGSPRGHQELHITYRRPEKGELQRVFAHRTTSVGFHSDVSYEIT 192

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177

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      ++ +F + GG T F D AY+ L + A + H L S+ Q
Sbjct: 193 PSRFTLFQV-LESGDGGDTVFVD TVEAYNRL---SPAFQKRLEGLHVLHTSED-----QA 243

Query: 178 AGSAYIGYGMD--TTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
      A SA+ G G++ + + PLV++ P TG SL + + I + ES+ L+ L
Sbjct: 244 ANSAHQG-GVERRKAVSNIHPLVRLDPVTGEKSLYVNKAFGRRIVELKKEESDYLLDFLH 302

Query: 235 DWACQAPRVHAH-QWAAGD---VVVWDNRCLLHRA 265
      + ++ + W G+ V ++ N + H A
Sbjct: 303 NHIEKSSDLQLRVNWERGERRKVALFHNSGVSHTA 337

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>ref|XP_002419465.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Candida dubliniensis CD36]
emb|CAX43059.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Candida dubliniensis CD36]
Length = 426

Score = 47.0 bits (110), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 64/297 (21%), Positives = 105/297 (35%), Gaps = 58/297 (19%)

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Query: 2 AQTTLQITPTGATLGATVTVGHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
      A+ + +TP +G + G+ L+ L + L + ++ F Q LS +Q+
Sbjct: 111 AEDIIHLTPY---IGTEIVGLQLSELTKQKDELALLIAERVVFFKDQDLSPQKQLELG 167

Query: 62 KRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDM----MKVIVGNMAWHAD 111
      +G +E RIG S + QH E + + GN WH+D
Sbjct: 168 HYWGQVEIHPQAARIG-----SEFDGVTVIWQHYAKERRSINLTFKQSKKGNSTWHSD 220

Query: 112 STYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSA---RHSLVY 167
      + A + +P +GG T ++ AYD L + + + ++A H +
Sbjct: 221 LVHEKQTAGITHLHLDAIPNIGGETLWSSTYGAYDKLSPSLQQFLDGKTAIYRSAHQYLD 280

Query: 168 SQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAES 226
      L G YI P+++ HP TG L + R I G+ ES
Sbjct: 281 RNDPL-----KGPKYIERE-----HPIIRTHPVTGWKYL FVNVRGMTVRIVGLLPEES 327

Query: 227 ERFLEGL-----VDWACQAP-----RVHAHQWAAGDVVVWDNRCLLH 263
      + L L V W+ Q + + G +WDNR H
Sbjct: 328 DLILNLYLSVIENNRDIQVRWSWQKELGSIKKNKSKEEDSKQYRGVSALWDNRISNH 384

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>ref|XP_657819.1| hypothetical protein AN0215.2 [Aspergillus nidulans FGSC A4]
gb|EAA66088.1| hypothetical protein AN0215.2 [Aspergillus nidulans FGSC A4]
tpe|CBF89959.1| TPA: conserved hypothetical protein [Aspergillus nidulans FGSC A4]
Length = 352

Score = 47.0 bits (110), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 45/158 (28%), Positives = 68/158 (43%), Gaps = 17/158 (10%)

```

Query: 122 AVFSAEVPVAVGGRTCF---DMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
      ++ E P VGG T +A YDAL +A + + A H+ S+L Q
Sbjct: 149 SLLRMEEHPEVGGDTAWARKVSQYGLYDALSDAYKKFLDGLHAVHT-----SRL----QY 199

Query: 179 GSAYIGYGMDTTATPL---RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
      + +G P+ P V+ HP TG +L + + AES++ L+ L
Sbjct: 200 DTILDWGTGPNRPPIDTHHPAVRTHPVTGLKALNVNPGFVTGF AELKKAESDKVLDFLA 259

Query: 235 DWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFK 271
      A + +WA G V +WDNRC LHR P ++
Sbjct: 260 YHIHSADDDHYVRWKWAVGSVAMWDNRCTLHRVIPGTYE 297

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>ref|XP_713065.1| potential taurine catabolic dioxygenase [Candida albicans SC5314]
ref|XP_713033.1| potential taurine catabolic dioxygenase [Candida albicans SC5314]
gb|EAK93908.1| potential taurine catabolic dioxygenase [Candida albicans SC5314]
gb|EAK93946.1| potential taurine catabolic dioxygenase [Candida albicans SC5314]
Length = 386

Score = 47.0 bits (110), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 66/275 (24%), Positives = 113/275 (41%), Gaps = 36/275 (13%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQ---ITFAKR 63
+ITP G+ + GV L+ L+D G L Q +L+F Q ++ + F K
Sbjct: 83 RITPK---FGSEIDGVQLSQLNDKGKDELALFLAQRKVLLFNEQDFADKGPFGFAVEFGKY 139

Query: 64 FGAIERIGGGDIVAISNVKADG-----TVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV 117
FG + V S+ G T R+ E + ++ +H+D +Y
Sbjct: 140 FGRLH-----VHPSSGSPRGHQELHITYRRPEKGELQRFVFAHRTTSVGFHSDVSYEIT 192

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ 177
++ +F + GG T F D AY+ L A + + H L S+ Q
Sbjct: 193 PSRFTLFQV-LESGDGGDTVFVDVTVEAYNRLSPAFAQKRL---EGLHVLHTSED-----QA 243

Query: 178 AGSAYIGYGMD--TTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
A SA+ G G++ + + PLV++ P TG SL + + I + ES+ L+ L
Sbjct: 244 ANSAHQG-GVERRKAVSNIHPLVRLDPVTGEKSLYVNKAFGRRIVELKKEESDYLLDFLH 302

Query: 235 DWACQAPRVHAH-QWAAGD---VVVWDNRCLLHRA 265
+ ++ + W G+ V ++ N + H A
Sbjct: 303 NHIEKSSDLQLRVNWERGERRKVALFHNSGVSHTA 337

>emb|CBJ19159.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 46.6 bits (109), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 31/93 (33%), Positives = 42/93 (45%), Gaps = 5/93 (5%)

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPG 220
HSL+YS+ LG + Y L+ LV+ HP GR SL + HA I G
Sbjct: 19 CEHSLMYSRGALGFLD-----YSEEEKQMFKPVLQHLVLRTHPVHGRKSLYLSSHAGGIVG 73

Query: 221 MDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
M E+ L L + A Q V+ H+W D+
Sbjct: 74 MTVPEARVLLRDLNEHATQPEFVYVHRWKLHDL 106

>gb|AA51287.1| TdfA [uncultured bacterium]
Length = 100

Score = 46.6 bits (109), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 36/103 (34%), Positives = 46/103 (44%), Gaps = 7/103 (6%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-P 196
F DMRAAYD L E + + A H + S+ LG + S P+ P
Sbjct: 2 FCDMRAAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVSWP 55

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
LV+ H +GR L IG HA I G AE L L++ A Q
Sbjct: 56 LVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQ 98

>gb|EEQ44600.1| hypothetical protein CAWG_02874 [Candida albicans WO-1]
Length = 425

Score = 46.6 bits (109), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 56/249 (22%), Positives = 94/249 (37%), Gaps = 42/249 (16%)

```
Query: 2  AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
      A+  + +TP  +G  + G+ L+ L D      L      +  ++ F  Q LS  +Q+
Sbjct: 110 AEDIIHLTPY---IGTEIVGLQLSELTDKQKDELALLIAERVVVFQDLSPQKQLELG 166

Query: 62  KRFGAIE-----RIGGGDIVAISNVKADGT--VRQHSPAEWDDM----MKVIVGNMAWH 109
      +G +E      R+G      + DG  + QH  E  +      +  GN WH
Sbjct: 167 HYWGQVEVHPQAARVGP-----EFDGVTVIWQHYAKERRSINLTFKQSKKGNSVWH 217

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSA---RHSL 165
      +D  +      A      + +P +GG+T ++      AYD L  +  +  ++A      H
Sbjct: 218 SDLVHEKQTAGITHLHLDAIPGIGGKTLWSSTYGAYDKLSPGLQRFLDGKTAIYRSAHQY 277

Query: 166 VYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAA 224
      +      L      G Y+      P+V+ HP TG  L + R      I G+
Sbjct: 278 LDRNDPL-----KGPKYVERE-----HPIVRTHPVTGWKYL FVN RGMTVRIVGLLPE 324

Query: 225 ESERFLEGL 233
      ES+  L  L
Sbjct: 325 ESDLILNYL 333
```

```
>ref|XP_001937063.1| taurine dioxygenase family protein[Pyrenophora tritici-repentis
      Pt-1C-BFP]
gb|EDU49650.1| taurine dioxygenase family protein [Pyrenophora tritici-repentis
      Pt-1C-BFP]
      Length = 354
```

Score = 46.6 bits (109), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 40/174 (22%), Positives = 70/174 (40%), Gaps = 16/174 (9%)

```
Query: 104 GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARH 163
      G  WH+D  + PV A      +P GG T +A      YD  A  +      +A
Sbjct: 146 GAAQWHSDIQFEPVPADYTSRLRLTQLPKTGGDTLWASGYEMYDRFSTAYQKFFEGLTATF 205

Query: 164 S---LVYSQS-----KLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLL-IGR 213
      +  L+ +      K+  ++      +G  +      T  + P+V+ +P TG  S+  +G
Sbjct: 206 AGDGLIRAAEANPDVVKIYEKERGSPKNVGRSL----TAVHPVVRTNPVTGWKSIFALGP 261

Query: 214 HAAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW-AAGDVVVWDNRCLLHRA 265
      I  ++  ES+  L+      +  +      +W  A D+ +WDNR  + H A
Sbjct: 262 FPKYINELNVEESDELLKRFRSVITENHDLQVRFKWRNANDLAIWDNRSVFHSA 315
```

```
>gb|ADO34952.1| putative (R)-2,4-dichlorophenoxypropionate dioxygenase-like protein
      [uncultured bacterium]
gb|ADO34953.1| putative (R)-2,4-dichlorophenoxypropionate dioxygenase-like protein
      [uncultured bacterium]
gb|ADO34954.1| putative (R)-2,4-dichlorophenoxypropionate dioxygenase-like protein
      [uncultured bacterium]
gb|ADO34955.1| putative (R)-2,4-dichlorophenoxypropionate dioxygenase-like protein
      [uncultured bacterium]
gb|ADO34956.1| putative (R)-2,4-dichlorophenoxypropionate dioxygenase-like protein
      [uncultured bacterium]
gb|ADO34957.1| putative (R)-2,4-dichlorophenoxypropionate dioxygenase-like protein
      [uncultured bacterium]
gb|ADO34959.1| putative (R)-2,4-dichlorophenoxypropionate dioxygenase-like protein
      [uncultured bacterium]
gb|ADO34960.1| putative (R)-2,4-dichlorophenoxypropionate dioxygenase-like protein
      [uncultured bacterium]
gb|ADO34961.1| putative (R)-2,4-dichlorophenoxypropionate dioxygenase-like protein
```

[uncultured bacterium]
gb|ADO34962.1| putative (R)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
gb|ADO34963.1| putative (R)-2,4-dichlorophenoxypropionate dioxygenase-like protein
[uncultured bacterium]
Length = 95

Score = 46.6 bits (109), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 30/100 (30%), Positives = 51/100 (51%), Gaps = 8/100 (8%)

Query: 42 HALLIFPGQHLSDNQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKV 101
+ ++ FPGQ ++N+Q I F++RFG ++ + + +I +R+ E ++ +V
Sbjct: 2 YQVIYFPGQAITNEQHIAFSRRFGPVDVPL--LKSIEGYPEVQMIRR----EANESGRV 55

Query: 102 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM 141
I + WH DST++ V A VP GG T F M
Sbjct: 56 IGDD--WHTDSTFLDAPPAAVVMRAIDVPEHGGDTGFLSM 93

>ref|ZP_02357712.1| pyoverdine biosynthesis protein PvcB [Burkholderia oklahomensis
E0147]
Length = 303

Score = 46.6 bits (109), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 52/186 (27%), Positives = 74/186 (39%), Gaps = 23/186 (12%)

Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRAL---VHQRSARH 163
H D Y+ + + VF + A GGRT F+ A TRAL H R R
Sbjct: 110 HWDGMYLDTVPEFQVQVQQAIGEADGGRTTFSSTTEALRIATPQTRALWRRAHGRYQRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR--PLVK-VHPETGRPSLLIGRHAHAIPG 220
+YS + + + P R P+++ P S I ++A G
Sbjct: 170 VELYSNTVEAPIIEKH-----PRREFPILRFCEPPIANDSTFINPSSYAFGG 216

Query: 221 MDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHS 279
+ E E L G + A PR H AH+W GDV + DN LLH E + + R +
Sbjct: 217 IADDEKEALL-GSLKRALYDPRAHYHRWQTGDVALTDNFTLLHGRERFTSRTGRHLRRV 275

Query: 280 RLAGRP 285
+ G P
Sbjct: 276 HIHGEP 281

>emb|CBW98417.1| hypothetical protein LPW_02691 [Legionella pneumophila 130b]
Length = 278

Score = 46.6 bits (109), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 46/201 (22%), Positives = 74/201 (36%), Gaps = 33/201 (16%)

Query: 106 MAWHADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH 163
M H D Y P + + +F +P GGRT F++ A + L ++ S
Sbjct: 93 MPLHWDGMYRPQVPEYQIFHCVKAPLPGQGGRRTTFSNTILALQFASSEIKELWNKVS--- 149

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPE-----TGRPSLLIGRHA 215
G Q+ Y + + P++ HP+ PS+ G
Sbjct: 150 -----GTYQRKMEFY-----NSKTVSPIITKHPQKDFSVIRYNEPPSVDKGHFV 193

Query: 216 H----AIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFK 271
+ G+D E + F L A +AH+W GD+V+ DN LLH E + +
Sbjct: 194 NPPDIEFTGIDQEELDFHRSNLKALYSADNFYAHQWQNGDIVIADNFSLLHGREGFVSR 253

Query: 272 LPRVMWHSRLAGRPETEGAAL 292
PR + + P + L

Sbjct: 254 SPRHIQVRVHVLNPPFDNPGL 274

>ref|ZP_02364837.1| pyoverdine biosynthesis protein PvcB [Burkholderia oklahomensis
C6786]
Length = 303

Score = 46.6 bits (109), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 52/186 (27%), Positives = 74/186 (39%), Gaps = 23/186 (12%)

Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRAL---VHQRSARH 163
H D Y+ + + VF + A GGRT F+ A TRAL H R R
Sbjct: 110 HWDGMYLDTVPEFQVFQCVQAIGEADGGRTTFSSTTEALRIATPQTRALWRRAHGRYQRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR--PLVK-VHPETGRPSLLIGRHAHAIPG 220
+YS + + + P R P+++ P S I ++A G
Sbjct: 170 VELYSNTVEAPIIEKH-----PRREFPILRFCEPPIANDSTFINPSSYAFGG 216

Query: 221 MDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHS 279
+ E E L G + A PR H AH+W GDV + DN LLH E + + R +
Sbjct: 217 IADDEKEALL-GSLKHALYDPAHYAHRWQTGDVALTDNFTLLHGRERFTSRTGRHLRRV 275

Query: 280 RLAGRP 285
+ G P
Sbjct: 276 HIHGEP 281

>emb|CBJ18810.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 46.6 bits (109), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 35/112 (31%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYD L E + ++ +H + S+ LG + P+R P V H
Sbjct: 1 AAYDDLPEDFKKVLRGLGGQHYALNSRFILGDTDYSER-----QRNAMAPVRWPPVPTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>emb|CBJ19063.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 46.6 bits (109), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 36/112 (32%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEDRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>ref|XP_002383259.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Aspergillus flavus NRRL3357]
gb|EED47079.1| alpha-ketoglutarate-dependent sulfonate dioxygenase, putative
[Aspergillus flavus NRRL3357]
Length = 366

Score = 46.6 bits (109), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 62/294 (21%), Positives = 109/294 (37%), Gaps = 54/294 (18%)

```
Query: 14  TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGG 73
          ++G + V L+ L++ L + ++ F Q L+ ++Q+ + +G +++
Sbjct: 70  SIGTLLEDVQLSQLNEQQQLDELALLVTERGVVFFRDQDLTTEKQVELFQHYGVLDKHPAQ 129

Query: 74  DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW-----HADSTYMPVMAQGAVF---- 124
          N+ G+ H + I W HAD+++ + F
Sbjct: 130 KDQKFVNIH--GSREDH-----REIANYTPWPSGEFHADTSFE-INRMSCTFNEYN 177

Query: 125  -----SAEVVPAVGGRTCF-----ADMRAAYDALDEATRALVHQRSARHSL 165
          SA + P GR YDAL +A + + A H+
Sbjct: 178 IGYLLTSTSAIIFPPENGRASSRRRRYS LGNQVVSQYGVYDALSDAYKKFLDGLHAVHT- 236

Query: 166  VYSQSKLGHVQQAGSAYIGYGMDDTTATPL---RPLVKVHPETGRPSLLIGR-HAHAIPGM 221
          S+L Q + +G+ P+ P V+ HP TG +L + +
Sbjct: 237 ----SRL----QYDTILDWGVGPNRPPIDTHHPAVRTHPVTGLRALNVNNGFVTGFAEL 288

Query: 222  DAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLP 274
          ES++ L+ L A + +WA G V +WDNRC +HR P +K R
Sbjct: 289 KKLESDKLLDFLSHHIHAADDHYVRWKWAVGVSAMWDNRCTVHRVIPGRYKENR 342
```

>gb|EFN53016.1| hypothetical protein CHLNCDRAFT_137505 [Chlorella variabilis]
Length = 291

Score = 46.2 bits (108), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 68/306 (22%), Positives = 120/306 (39%), Gaps = 73/306 (23%)

```
Query: 9  TPTGATLGATVTGVHLATLD-DAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGA 66
          T T +GA V G+ L D + + +H LL+F Q +S ++Q+ + FG
Sbjct: 8  TLTPLPVGAEVHGIQLQQPQPDEVVQQIKSDVTKHRLLVFRDQGIMSGERQVEISSWFGE 67

Query: 67  IERIGGG-----DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMA 119
          +E D+ +SN +A+G VG WH D ++
Sbjct: 68  LESTFYKHPSSPHDPVFRVSNERAEGCTD-----VGRTGWHIDGSF----- 108

Query: 120  QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG 179
          Q A FS + V +C + L E +L ++ AR ++ S H Q
Sbjct: 109 QTAPFSSHLYHIV---SCPTQGD TVFAPLHEIVGSLPAEQRARWDRWLWMLSDRRHRQ--- 162

Query: 180  SAYIGYGMDDTTATPLRPLVKVHPETGRPSLL-----IGRHAHAIPGM DAAESE 227
          +PL+ HP +G+ ++ +G + AE+
Sbjct: 163 -----AKPLLYEHPLSGQDAMCFHLGMTDGFVWDVGTQQQRV--ASGAETR 206

Query: 228  RFLE---GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLP-----RVMWH 278
          L+ G++ +C+ +++H+W GD ++ DN L H A P + +LP R+M
Sbjct: 207 ALLDEIHGVITSSCRH-LLYSHKWRPGDFIISDNLALGHEAAP-ETQLPLEQVGLRIMHR 264

Query: 279  SRLAGR 284
          + + G+
Sbjct: 265 TTVKGQ 270
```

>emb|CBJ19019.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 46.2 bits (108), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 36/112 (32%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

```
Query: 143  AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
          AAYD L E + + A H + S+ LG + S P+ PLV+ H
```

Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A V+ H W GD+

Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATLRKFVYRHSWKVGDL 106

>emb|CBJ19189.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 46.2 bits (108), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 31/93 (33%), Positives = 41/93 (44%), Gaps = 5/93 (5%)

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPG 220
HSL+YS+ LG + Y L+ LV+ HP GR SL + HA I G

Sbjct: 19 CEHSLMYSRGALGFLD-----YSEEEKQMFKPVLRQLVRTHPVHGRKSLYLSSHAGGIVG 73

Query: 221 MDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

M E+ L L A Q V+ H+W D+

Sbjct: 74 MTVPEARVLLRDLNKHATQPEFVYVHRWKLHDL 106

>ref|YP_001629703.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Bordetella
petrii DSM 12804]
emb|CAP41433.1| Alpha-ketoglutarate-dependent taurine dioxygenase [Bordetella
petrii]
Length = 97

Score = 46.2 bits (108), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 22/70 (31%), Positives = 38/70 (54%), Gaps = 1/70 (1%)

Query: 217 AIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRA-EPWDFKLPRV 275
+I GM AE++ L L + + Q + H GD+++WDNRC +H A + +D R

Sbjct: 16 SIVGMTLAEAQPIRLFLFEHSTQPEFTYRHSCQPGDLMIWDNRCAIHLALDDYDHGYARR 75

Query: 276 MWHSRLAGRP 285

++ + + G P

Sbjct: 76 LYRTTILGTP 85

>gb|EEQ44372.1| hypothetical protein CAWG_02639 [Candida albicans WO-1]
Length = 423

Score = 46.2 bits (108), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 64/297 (21%), Positives = 105/297 (35%), Gaps = 60/297 (20%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
A+ + +TP +G + G+ L+ L + L + ++ F Q LS +Q+

Sbjct: 110 AEDVIHLTPY---IGTEIVGLQLSELTEQQRDELALLIAERVVFFKDQDLSPQKQLELG 166

Query: 62 KRFGAIE-----RIGGGDIVAISNVKADGTV---RQHSPAEDW---DMMKVIVGNMAWH 109
+G +E RIG + DG ++ W + GN WH

Sbjct: 167 HYWGQVEVHPQATRIGE-----EYDGISVIWQEQQQRDRWGLNLTFKQSKKGNSQWH 217

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSA---RHSL 165
+D + A + +P +GG T ++ AYD L A + + ++A H

Sbjct: 218 SDLVHEKQTAGITHLHLDAIPGIGGETLWSSTYGAYDKLSPALQKFLDGKTAIYRSAHQY 277

Query: 166 VYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAA 224
+ L G Y+ P+V+ HP TG L + R I G+

Sbjct: 278 LDRNDPL-----KGPKYV-----EREHPIVRTHPVTGWKYL FVNRSMTVRIVGLLPE 324

Query: 225 ESERFLEGL-----VDWACQAP-----RVHAHQWAAGDVVVDNRCLLH 263

ES+ L L V W+ Q + + G +WDNR H
Sbjct: 325 ESDLILNLYSVIETNRDIQVRWSWQKELGSKNNKKDEPKQYRGVSALWDNRISNH 381

>emb|CBJ18912.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 46.2 bits (108), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 36/112 (32%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVPSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+ R L IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSERKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>emb|CBJ19023.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 46.2 bits (108), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 36/112 (32%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVPSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L ++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAEPLEHATQRKFVYRHSWKVGDL 106

>ref|YP_003018467.1| Taurine catabolism dioxygenase TauD/TfdA [Pectobacterium
carotovorum subsp. carotovorum PC1]
gb|ACT13931.1| Taurine catabolism dioxygenase TauD/TfdA [Pectobacterium
carotovorum subsp. carotovorum PC1]
Length = 292

Score = 46.2 bits (108), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 68/283 (24%), Positives = 103/283 (36%), Gaps = 60/283 (21%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG--QHLSNDQQITFAKRF 64
+I P G + +GVH+ L L L+I G S + T+
Sbjct: 21 EIYPFGVRIEKPQSGVHIGELSPNWLRTLVE---NQQLVILRGFDSFTSAENLTTYCAAM 77

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGN--MAWHADSTYMPVMAQGA 122
G I + G ++ + E D I N + H D Y+ + +
Sbjct: 78 GDIMQWPFAGVLEL-----VEQPDATDHIFANNYVPLHWDGMYLKTVPELQ 123

Query: 123 VFSAEVVPAVG----GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA 178
VF + V A+G GRT F+ A T+AL Q G Q+A
Sbjct: 124 VF--QCVSAIGEGQGGRTTFSSTTTALRLASPETKALW-----QRATGQYQRA 169

Query: 179 GSAYIGYGMTTATPLRPLVKVHPETGRPSL-----LIGRHAHAIPGMDAAES 226
Y ++T L P+++ HP P + + + G++ E
Sbjct: 170 VELY-----SSTALAPIIEQHYPRTYPVIRFCEPPIAGDKEFLNPSTYHFSGIEPEEQ 222

Query: 227 ERFLEGLVDWACQAPRV-HAHQWAAGDVVWDNRCLLHRAEPW 268
E L L PRV +AHQW +GD+V+ DN LLH E +
Sbjct: 223 ELLSSSLQQALYD-PRVQYAHQWQSGDIVIADNYSLLHGRESY 264

>ref|XP_720183.1| potential taurine catabolic dioxygenase [Candida albicans SC5314]
ref|XP_720050.1| potential taurine catabolic dioxygenase [Candida albicans SC5314]
gb|EAL01194.1| potential taurine catabolic dioxygenase [Candida albicans SC5314]
gb|EAL01331.1| potential taurine catabolic dioxygenase [Candida albicans SC5314]
Length = 423

Score = 46.2 bits (108), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 64/297 (21%), Positives = 105/297 (35%), Gaps = 60/297 (20%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
A+ + +TP +G + G+ L+ L + L + ++ F Q LS +Q+
Sbjct: 110 AEDVIHLTPY---IGTEIVGLQLSELTEQQRDELALLIAERVVFFKDQDLSPQKQLELG 166

Query: 62 KRFGAIE-----RIGGGDIVAISNVKADGTV---RQHSPAEDW---DMMKVIVGNMAWH 109
+G +E RIG + DG ++ W + GN WH
Sbjct: 167 HYWGQVEVHPQATRIGE-----EYDGISVIWQEQQRDWRGLNLTQKSKKGNQSWH 217

Query: 110 ADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSA----RHSL 165
+D + A + +P +GG T ++ AYD L A + + ++A H
Sbjct: 218 SDLVHEKQTAGITHLHLDAIPGIGGETLWSSTYGAYDKLSPALQKFLDGKTAIYRSAHQY 277

Query: 166 VYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAA 224
+ L G Y+ P+V+ HP TG L + R I G+
Sbjct: 278 LDRNDPL-----KGPKYVERE-----HPIVRTHPVTGWKYL FVNRSMTVRIVGLLPE 324

Query: 225 ESERFLEGL-----VDWACQAP-----RVHAHQWAAGDVVWDNRCLLH 263
ES+ L L V W+ Q + + G +WDNR H
Sbjct: 325 ESDLILNLYSVIETNRDIQVRWSQKELGSKNNKKDEPKQYRGVSALWDNRISNH 381

>emb|CBJ18997.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 46.2 bits (108), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 36/112 (32%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYES-----QRNAMPVSVWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR IG HA I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFHFFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDL 106

>ref|YP_094229.1| pyoverdine biosynthesis protein PvcB [Legionella pneumophila subsp.
pneumophila str. Philadelphia 1]
gb|AAU26282.1| pyoverdine biosynthesis protein PvcB [Legionella pneumophila subsp.
pneumophila str. Philadelphia 1]
Length = 278

Score = 46.2 bits (108), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 45/201 (22%), Positives = 74/201 (36%), Gaps = 33/201 (16%)

Query: 106 MAWHADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH 163
M H D Y P + + +F +P GGRT F++ A + L ++ S
Sbjct: 93 MPLHWDGMYRPQVPEYQIFHCVKAPLPGQGRTTFSNTILALQFASSEIKELWNKVS--- 149

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPE-----TGRPSLLIGRHA 215
G Q+ Y + + P++ HP+ PS+ G
Sbjct: 150 -----GTYQRKMEFY-----NSKTVSPIITKHPKQKDFSVIRYNEPPSVDKGHFV 193

Query: 216 H----AIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFK 271
 + G+D E + F L + +AH+W GD+V+ DN LLH E + +
 Sbjct: 194 NPPDIEFTGIDQEELDFHRSLENALYSPDNFYAHEWQNGDIVIADNFSLLHGREGFVSR 253

Query: 272 LPRVMWHSRLAGRPETEGAAL 292
 PR + + P + L
 Sbjct: 254 SPRHIQRVHVLSPNPPFDNPGL 274

>emb|CBJ19026.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
 Length = 106

Score = 45.8 bits (107), Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 36/112 (32%), Positives = 48/112 (42%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR-PLVKVH 201
 AAYD L E + + A H + S+ LG + S P+ PLV+ H
 Sbjct: 1 AAYDDLPEDFKELQGLRAEHYALNSRFILEGTDYSES-----QRNAMPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
 +GR L I HA I G AE L L++ A Q V+ H W GD+
 Sbjct: 55 AGSGRKFLFIRAHAGHIEGRPVAEGRMLLAELLEHATQRKFFVYRHSWKVGDL 106

>ref|XP_714705.1| potential taurine catabolic dioxygenase [Candida albicans SC5314]
 gb|EAK95658.1| potential taurine catabolic dioxygenase [Candida albicans SC5314]
 Length = 425

Score = 45.8 bits (107), Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 56/249 (22%), Positives = 93/249 (37%), Gaps = 42/249 (16%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSDNDQQITFA 61
 A+ + +TP +G + G+ L+ L D L + ++ F Q LS +Q+
 Sbjct: 110 AEDIIHLTPY---IGTEIVGLQLSELTDKQKDELALLIAERVVVFFKDQDLSPQKQLELG 166

Query: 62 KRFGAIE-----RIGGGDIVAISNVKADGT--VRQHSPAEDDM----MKVIVGNMAWH 109
 +G +E R+G + DG + QH E + + GN WH
 Sbjct: 167 HYWGQVEVHPQAARVGP-----EFDGVTVIWQHYAKERRSINLTFKQSKKGNVSWH 217

Query: 110 ADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSA---RHSL 165
 +D + A + +P +GG T ++ AYD L + + ++A H
 Sbjct: 218 SDLVHEKQTAGITHLHLDAIPGIGGETLWSSTYGAYDKLSPGLQRFGLDGTATYRSAHQY 277

Query: 166 VYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAA 224
 + L G Y+ P+V+ HP TG L + R I G+
 Sbjct: 278 LDRNDPL----KGPKYVERE-----HPIVRTHPVTGWKYL FVNRGMTVRIVGLLPE 324

Query: 225 ESERFLEGL 233
 ES+ L L
 Sbjct: 325 ESDLILNYL 333

>gb|ACG80556.1| TfdA [uncultured bacterium]
 Length = 115

Score = 45.8 bits (107), Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 39/128 (30%), Positives = 52/128 (40%), Gaps = 20/128 (15%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATP-- 193
 T F DMRAAYDAL E +A + A HS+ YS+ +LG + D P
 Sbjct: 1 TEFMDMRAAYDALPEDMKARLEGLQAHSIAYSQRGL-----FEFSGDEAEAEPEG 51

Query: 194 LRPLVKVHPETGRPSLLIGR-----HAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQW 248

R H RP + + R H + A + R Q V+ H W
Sbjct: 52 RRASAGTHAAHRPQISLSRLARESHTRLVRPRRQAAAPRSHRA----PTQRQFVYRHAW 107

Query: 249 AAGDVVVW 256
AGD+V+W

Sbjct: 108 RAGDLVMW 115

>ref|XP_003002132.1| alpha-ketoglutarate-dependent sulfonate dioxygenase
[Verticillium
albo-atrum VaMs.102]
gb|EEY21481.1| alpha-ketoglutarate-dependent sulfonate dioxygenase [Verticillium
albo-atrum VaMs.102]
Length = 386

Score = 45.4 bits (106), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 35/163 (21%), Positives = 66/163 (40%), Gaps = 7/163 (4%)

Query: 108 WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 167
WH+D T+ P+ + G + + A ++ A Q +
Sbjct: 178 WHSDITFEPIPSDYPCSDLPLNTLWASGYEVDYDRISATLQGFSLDTATYAQPGFNEAADK 237

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLL-IGRHAHAIPGMDAAES 226
+ K+ ++ +G ++ + P+++ +P TG S+ +G H I G+ ES
Sbjct: 238 NGFKIYSAERGAPENVGELLEA---IHPVIRTNPVTGWKSVFAVGHHVQKINGLSDEES 293

Query: 227 ERFLEGLVDWACQAPRVHA-HQWA-AGDVVVWDNRCLLHRAEP 267
+ FL V + + ++W DV +WDNR + H A P
Sbjct: 294 KHFLAWFVQLIVENHDLQVRYKWKDVNDVAIWDNRSVYHAATP 336

>ref|YP_122580.1| hypothetical protein lpp0237 [Legionella pneumophila str. Paris]
emb|CAH11384.1| hypothetical protein lpp0237 [Legionella pneumophila str. Paris]
Length = 278

Score = 45.4 bits (106), Expect = 0.009, Method: Compositional matrix adjust.
Identities = 46/201 (22%), Positives = 73/201 (36%), Gaps = 33/201 (16%)

Query: 106 MAWHADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH 163
M H D Y P + + +F +P GGRT F++ A + L ++ S
Sbjct: 93 MPLHWDGMYRPQVPEYQIFHCVKAPLPGQGGRTTFSNTILALQFASSEIKELWNKVS--- 149

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPE-----TGRPSLLIGRHA 215
G Q+ Y + + P++ HP+ PS G
Sbjct: 150 -----GTYQRKMEFY-----NSKTVSPIITKHPKQDFSVIRYNEPPSADKGHFV 193

Query: 216 H---AIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFK 271
+ G+D E + F L A +AH+W GD+V+ DN LLH E + +
Sbjct: 194 NPPDIEFTGIDQEELDFHRSNLKALYSADNFYAHEWQNGDIVIADNFSLLHGREGFVSR 253

Query: 272 LPRVMWHSRLAGRPETEGAAL 292
PR + + P + L
Sbjct: 254 SPRHIQRVHVLNPPFDNPGL 274

>gb|ADC33970.1| TfdA-like protein [uncultured bacterium]
Length = 128

Score = 45.4 bits (106), Expect = 0.009, Method: Compositional matrix adjust.
Identities = 34/128 (26%), Positives = 53/128 (41%), Gaps = 2/128 (1%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPL- 194
T F DM AAYD L + + + ++A H + + + P+

Sbjct: 1 TEFCDMCAAYDDLDPDLKLELEGKTALHDFNRFWEMMRSPGSTRPPLSEAQRNAKPPVS 60

Query: 195 RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
P+V HP + R L + I + A+S+R L L D + + W GD

Sbjct: 61 HPVVLTHTPISKRRVLYANPGYTVRINELPEADSDRTLALLFDHQTRDKYRYVFHWQVGDA 120

Query: 254 VVWDNRCL 261
+VWDNRC+

Sbjct: 121 LVWDNRCV 128

>ref|XP_387766.1| hypothetical protein FG07590.1 [Gibberella zeae PH-1]
Length = 364

Score = 45.4 bits (106), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 44/180 (24%), Positives = 70/180 (38%), Gaps = 28/180 (15%)

Query: 104 GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR----- 153
G +WH+D + A +P+ GG T +A YD + +

Sbjct: 156 GAASWHSDIQFEEYPADYTSRLRLTKLPSGGGDTLWASGYELYDRYSDPYQKFFEGLTATF 215

Query: 154 ---ALVHQRSAR--HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPS 208
+ R AR H +Y + + GH + G A + T+ P+V+ +P TG S

Sbjct: 216 SGDGLFKARDARPDHFKIYEEPR-GHPENIGDA-----LKTS---HPVVRTNPVTGWKS 265

Query: 209 LL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW-AAGDVVVWDNRCLLHRA 265
L +G I + A ES+ LE + + +W + D+ WDNR H A

Sbjct: 266 LFAVGNFPRRINELSARESKELLESFYKRIEENHDLQVRFRWRSPNDIAFWDNRSFAHSA 325

>ref|ZP_02484143.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
7894]
ref|ZP_02508453.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
BCC215]
Length = 304

Score = 45.4 bits (106), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 54/202 (26%), Positives = 76/202 (37%), Gaps = 41/202 (20%)

Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQ--RSARH 163
H D Y+ + + VF + A GGRT F+ A TRAL H+ R R

Sbjct: 110 HWDGMYLETVPFQVQVQQAIGDAHGGRTTFSSTTEALRVATPETRALWHRAHGRYRRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL-----LI 211
+YS + P+V+ HP P L I

Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPTFI 207

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDF 270
++A G+ +E + L G + A PR H AH+W GDVV+ DN LLH E +

Sbjct: 208 NPSSYAFSGIADSERDALL-GSLTRALYDPRAHYAHRWRTGDVVLTDNFTLLHGRERFTS 266

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292
+ R + + G P L

Sbjct: 267 RSGRHLRRVHIHGDPPLRNPHL 288

>gb|AA51278.1| TdfA [uncultured bacterium]
Length = 105

Score = 45.4 bits (106), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 37/110 (33%), Positives = 48/110 (43%), Gaps = 7/110 (6%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR 195

T F DMRAAYD L E + + A H + S+ LG + S P+
Sbjct: 1 TEFCDMRAAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH 244

PLV+ +GR L IG HA I G AE L L++ A Q V+
Sbjct: 55 WPLVRTRAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVY 104

>gb|AA51283.1| TdFA [uncultured bacterium]
gb|AA51284.1| TdFA [uncultured bacterium]
gb|AA51285.1| TdFA [uncultured bacterium]
Length = 96

Score = 45.4 bits (106), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 35/101 (34%), Positives = 45/101 (44%), Gaps = 7/101 (6%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195

T F DMRAAYD L E + + A H + S+ LG + S P+
Sbjct: 1 TEFCDMRAAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD 235

PLV+ H +GR L IG HA I G AE L L++
Sbjct: 55 WPLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLE 95

>emb|CBJ18883.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 45.1 bits (105), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 31/111 (27%), Positives = 53/111 (47%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202

AA+DAL + + HSL++S+++G A+ + LV+ H
Sbjct: 1 AAWDALPQKLKDECFDLVTDHSLIFSRAQMGF-----EAFSAEELARCEPVPQRLVRRHA 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

+GR SL + H I G E+ + L ++A Q V+AH W+ GD+
Sbjct: 56 GSGRLSLYLSAHIGEIHGWARPEALALIRELTFATQPQFVYAHHWSVGDL 106

>gb|ADC33968.1| TfdA-like protein [uncultured bacterium]
Length = 128

Score = 45.1 bits (105), Expect = 0.011, Method: Compositional matrix adjust.
Identities = 36/128 (28%), Positives = 52/128 (40%), Gaps = 2/128 (1%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL- 194

T F DM AYD L A + + ++A H + + + P+
Sbjct: 1 TEFCDMCTAYDDLPGALKLELAGKTALHDFNRFWEMMRARPGSTRPPLSEAQRNAKPPVS 60

Query: 195 RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

P+V HP + R L + I + AES R L L D + + W GDV
Sbjct: 61 HPVVLTHPISKRKVLYANPGYTVRINELPEAESARTLALLFDHQTRNKYRYVFHWQVGDV 120

Query: 254 VVWDNRCL 261

+VWDNRC+
Sbjct: 121 LVWDNRCV 128

>emb|CBJ18865.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 104

Score = 45.1 bits (105), Expect = 0.011, Method: Compositional matrix adjust.

Identities = 32/96 (33%), Positives = 47/96 (48%), Gaps = 7/96 (7%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPE 203
AYDA+DE +A + A H +S+ LG + ++ + P+V+ P
Sbjct: 2 AYDAMEDMKAFLDPLEAEHFHAFHSRELLGAMPTQEER-----NSIPPAVWPIVR-KPA 54

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
TGR SL IG HAH + GM A+ L L++ A Q
Sbjct: 55 TGRRSFIGAHAKVIGMPLAQGRMLLLDLEHATQ 90

>ref|ZP_04522600.1| PvcB [Burkholderia pseudomallei MSHR346]
gb|EEP51514.1| PvcB [Burkholderia pseudomallei MSHR346]
Length = 304

Score = 45.1 bits (105), Expect = 0.012, Method: Compositional matrix adjust.
Identities = 54/202 (26%), Positives = 75/202 (37%), Gaps = 41/202 (20%)

Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRAL---VHQRSARH 163
H D Y+ + + VF + A GGRT F+ A TRAL H R R
Sbjct: 110 HWDGMYLETVPFQVQVCQAIGDAHGGRTTFSSTTEALRVATPETRALWQRAHGRYRRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL-----LI 211
+YS + P+V+ HP P L I
Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPTFI 207

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDF 270
++A G+ +E + L G + A PR H AH+W GDVV+ DN LLH E +
Sbjct: 208 NPSSYAFSGIADSERDALL-GSLTRALYDPRAHYAHRWRTGDDVLTDFNFTLLHGRERFTS 266

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292
+ R + + G P L
Sbjct: 267 RSGRHLRRVHIHGDPPLRNPHL 288

>emb|CBJ18758.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 45.1 bits (105), Expect = 0.013, Method: Compositional matrix adjust.
Identities = 30/111 (27%), Positives = 49/111 (44%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHP 202
AAYDAL ++T+ + H + +S+ ++G + Y LV+ HP
Sbjct: 1 AAYDALPDSTKQAIIDPLVIEHDVFWSRGQIGVTEFPFGEREQYPPSKQR-----LVRTHP 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+ R +L + HA I G E L + A Q V++H+W GD+
Sbjct: 56 GSKRKTYLSAHASHIVGWPVPEGRLLFADLNEHATQRQFVYSHKWRVGDL 106

>emb|CBJ20073.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 139

Score = 45.1 bits (105), Expect = 0.013, Method: Compositional matrix adjust.
Identities = 39/144 (27%), Positives = 63/144 (43%), Gaps = 12/144 (8%)

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA----LVHQRSARHSLVYSQS 170
+ + G++ A VP GG T FA+ AY+AL + +A L+ S+ + V S++
Sbjct: 1 LEIPPMGSMMLLAREVPPYGGDTVFANQYMAEALSDGLKATLDGLIGVSSSTKAEV-SKT 59

Query: 171 KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERF 229
+ ++ AG + P+V+ HPETGR +L H I G ES

Sbjct: 60 REDRLKAAGKETKPLAAE-----HPIVTRHPETGRKALYTSSAHTSHIKGWTERESLAL 113

Query: 230 LEGLVDWACQAPRVHAHQWAAGDV 253

LE L + + +W G +

Sbjct: 114 LEFLWEHQVRPEFTTCRFRWETGSL 137

>ref|XP_003039403.1| hypothetical protein NECHADRAFT_98371 [Nectria haematococca mpVI
77-13-4]

gb|EEU33690.1| hypothetical protein NECHADRAFT_98371 [Nectria haematococca mpVI
77-13-4]

Length = 327

Score = 45.1 bits (105), Expect = 0.013, Method: Compositional matrix adjust.
Identities = 36/160 (22%), Positives = 64/160 (40%), Gaps = 23/160 (14%)

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV 175

P+ + A+ +P GG T +A YD + + + +A+ Y+Q +

Sbjct: 133 PIPSDYALLRLTQLPETGGDTLWASGYELYDRISPTLQRFLDTLTAK----YAQPQFNQA 188

Query: 176 QQAGSAYI-----GYGMDTTATPLRPLVKVHPETGRPSLL-IGRHAHAIPGMDAAESE 227

+ + I + + P+V+ +P TG S+ +G+H I G+ E+

Sbjct: 189 AKENNFSIYSAQRGAPENVGEVLEAVHPVVRTNPVTGWKSIFAVGQHVRIHGLSETENR 248

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEP 267

FL+ +D A DV +WDN + H A P

Sbjct: 249 HFLDWFIDLIN-----ANDVAIWDNGSVYHAATP 277

>gb|AAZ39276.1| oxygenase [uncultured organism]

Length = 271

Score = 44.7 bits (104), Expect = 0.014, Method: Compositional matrix adjust.
Identities = 52/201 (25%), Positives = 73/201 (36%), Gaps = 40/201 (19%)

Query: 74 DIVAISNVKADGTVRQHSAPAEWDDMMKVIIVGNMA--WHADSTYMPVMAQGAVFSAEVVPA 131

D AI+N++A + + + N A +H D ++ + F P

Sbjct: 81 DFGAINNLQAQSEAKNY-----LFTNRAVPFHWGAFVGRIPHWIFFHCASAPE 129

Query: 132 --VGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDT 189

GG T F +A+ A RA S R YS KL H YG

Sbjct: 130 ENTGGETLFCHTPLLLLEAVSAAGRAQWENISIR----YSTEKLAH-----YGGSF 175

Query: 190 TATPLRPLVKVHPETGRPSLLIGRHAH-----AIPGMDAAESERFLEGLVDWACQAPR 242

T+ PL+ HP G+ L + I G+ FLEG+

Sbjct: 176 TS---PLLAHPHIGQTILRYAEPVNDLNPVHLEIQGLPEESHTAFLEGMHTRLYDPAV 231

Query: 243 VHAHQWAAGDVVVWDNRCLLH 263

+AH W GD+V+ DN LLH

Sbjct: 232 CYAHAWQTGDIVDIADNFTLLH 252

>ref|ZP_04896071.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
Pasteur 52237]

gb|EDO92909.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
Pasteur 52237]

Length = 304

Score = 44.7 bits (104), Expect = 0.014, Method: Compositional matrix adjust.
Identities = 54/202 (26%), Positives = 76/202 (37%), Gaps = 41/202 (20%)

Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQ--RSARH 163

H D Y+ + + VF + A GGRT F+ A TRAL H+ R R

Sbjct: 110 HWDGMYLETVPFQVFCVQAIGDAHGGRTTFSSTTEALRVATPETRALWHAHGRYRRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL-----LI 211
+YS + P+V+ HP P L I

Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPTFI 207

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDF 270
++A G+ +E + L G + A PR H AH+W GDVV+ DN LLH E +

Sbjct: 208 NPSSYAFGGIADSERDALL-GSLTRALYDPAHYAHRWRTGDVVLTDNFTLLHGRERFTS 266

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292
+ R + + G P L

Sbjct: 267 RSGRHLRRVHIHGDPPLRNPHL 288

>ref|ZP_03454489.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
576]
gb|EEC33915.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
576]
Length = 304

Score = 44.7 bits (104), Expect = 0.015, Method: Compositional matrix adjust.
Identities = 53/195 (27%), Positives = 74/195 (37%), Gaps = 41/195 (21%)

Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRAL---VHQRSARH 163
H D Y+ + + VF + A GGRT F+ A TRAL H R R

Sbjct: 110 HWDGMYLETVPFQVFCVQAIGDAHGGRTTFSSTTEALRVATPETRALWQRAHGRYRRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL-----LI 211
+YS + P+V+ HP P L I

Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPTFI 207

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDF 270
++A G+ +E + L G + A PR H AH+W GDVV+ DN LLH E +

Sbjct: 208 NPSSYAFGGIADSERDALL-GSLTRALYDPAHYAHRWRTGDVVLTDNFTLLHGRERFTS 266

Query: 271 KLPRVMWHSRLAGRP 285
+ R + + G P

Sbjct: 267 RSGRHLRRVHIHGDP 281

>gb|EFQ32023.1| TfdA family Taurine catabolism dioxygenase TauD [Glomerella
graminicola M1.001]
Length = 367

Score = 44.7 bits (104), Expect = 0.016, Method: Compositional matrix adjust.
Identities = 41/169 (24%), Positives = 69/169 (40%), Gaps = 15/169 (8%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGG-RTCFADMRAAYDALDEATRALVHQRSARHSLV 166
WH+D + PV A + +P GG T +A YD L + + +A

Sbjct: 160 WHSDIAFEPVPADYSSLRLVQLPKTGGGDTLWASGYEIDRLSTPYQKFLESLTA----T 215

Query: 167 YSQSKLGHV-QQAGSAYIGY-----GMDTTATPLRPLVKVHPETGRPSLL-IGRHAHAI 218
+ Q V ++AG + + + P+V+ +P TG S+ +G H I

Sbjct: 216 FEQPGFAAAVEEAGFTLYDKPRGNPKNVGSILKAVHPVVRTNPVTGWKSVYPVGGHVKHI 275

Query: 219 PGMDAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVWDNRCLLHRA 265
+ A ES+ L+ +D + + +W D+ +WDNR H A

Sbjct: 276 NDVTAESKHLLDWFLDLLQKNHEIQVRFRWQNPNDIAIWDNRSTFHTA 324

>emb|CBJ18960.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 44.7 bits (104), Expect = 0.016, Method: Compositional matrix adjust.
Identities = 35/112 (31%), Positives = 47/112 (41%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR-PLVKVH 201
AAYD L E + + A H + S+ LG + S P+ PL + H
Sbjct: 1 AAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWPLARTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDV 253
+GR L IG A I G AE L L++ A Q V+ H W GD+
Sbjct: 55 AGSGRKFLFIGAQAGHIEGRPVAEGRMLLAELLEHAHQVYRHSWKVGDL 106

>ref|ZP_02405336.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
DM98]
Length = 304

Score = 44.7 bits (104), Expect = 0.016, Method: Compositional matrix adjust.
Identities = 54/202 (26%), Positives = 75/202 (37%), Gaps = 41/202 (20%)

Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRAL---VHQRSARH 163
H D Y+ + + VF + A GGRT F+ A TRAL H R R
Sbjct: 110 HWDGMYLETVPEFQVFQCVQAIGDAHGGRTTFSSTTEALRVATPETRALWQRAHGRYRRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSL-----LI 211
+YS + P+V+ HP P L I
Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPTFI 207

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAGDVVVWDNRCLLHRAEPWDF 270
++A G+ +E + L G + A PR H AH+W GDVV+ DN LLH E +
Sbjct: 208 NPSSYAFGGIADSERDALL-GSLTRALYDPRAHYHRWRTGDVVLTDNFTLLHGRERFTS 266

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292
+ R + + G P L
Sbjct: 267 RSGRHLRRVHIHGDPPLRNPHL 288

>ref|ZP_02449958.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
91]
Length = 290

Score = 44.7 bits (104), Expect = 0.017, Method: Compositional matrix adjust.
Identities = 54/202 (26%), Positives = 76/202 (37%), Gaps = 41/202 (20%)

Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQ---RSARH 163
H D Y+ + + VF + A GGRT F+ A TRAL H+ R R
Sbjct: 96 HWDGMYLETVPEFQVFQCVQAIGDAHGGRTTFSSTTEALRVATPETRALWHRAGRYRRT 155

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSL-----LI 211
+YS + P+V+ HP P L I
Sbjct: 156 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPTFI 193

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAGDVVVWDNRCLLHRAEPWDF 270
++A G+ +E + L G + A PR H AH+W GDVV+ DN LLH E +
Sbjct: 194 NPSSYAFGGIADSERDALL-GSLTRALYDPRAHYHRWRTGDVVLTDNFTLLHGRERFTS 252

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292
+ R + + G P L
Sbjct: 253 RSGRHLRRVHIHGDPPLRNPHL 274

>ref|YP_106451.1| pyoverdine chromophore biosynthetic protein PvcB [Burkholderia
mallei ATCC 23344]

ref|ZP_00441307.1| PvcB [Burkholderia mallei GB8 horse 4]
 ref|YP_990537.1| pyoverdine chromophore biosynthetic protein PvcB [Burkholderia mallei SAVP1]
 ref|YP_001025026.1| pyoverdine chromophore biosynthetic protein PvcB [Burkholderia mallei NCTC 10229]
 ref|YP_001079371.1| pyoverdine chromophore biosynthetic protein PvcB [Burkholderia mallei NCTC 10247]
 ref|ZP_02264991.1| pyoverdine biosynthesis protein PvcB [Burkholderia mallei PRL-20]
 ref|ZP_04883179.1| pyoverdine chromophore biosynthetic protein PvcB [Burkholderia mallei ATCC 10399]
 ref|ZP_04909818.1| pyoverdine biosynthesis protein PvcB [Burkholderia mallei FMH]
 ref|ZP_04911688.1| pyoverdine biosynthesis protein PvcB [Burkholderia mallei JHU]
 ref|ZP_04972418.1| pyoverdine biosynthesis protein PvcB [Burkholderia mallei 2002721280]
 gb|AAU45504.1| pyoverdine chromophore biosynthetic protein PvcB [Burkholderia mallei ATCC 23344]
 gb|ABM47797.1| pyoverdine chromophore biosynthetic protein PvcB [Burkholderia mallei SAVP1]
 gb|ABO03616.1| pyoverdine chromophore biosynthetic protein PvcB [Burkholderia mallei NCTC 10247]
 gb|EDK52775.1| pyoverdine biosynthesis protein PvcB [Burkholderia mallei FMH]
 gb|EDK61985.1| pyoverdine biosynthesis protein PvcB [Burkholderia mallei JHU]
 gb|EDK83293.1| pyoverdine biosynthesis protein PvcB [Burkholderia mallei 2002721280]
 gb|EDP87533.1| pyoverdine chromophore biosynthetic protein PvcB [Burkholderia mallei ATCC 10399]
 gb|EEP87158.1| PvcB [Burkholderia mallei GB8 horse 4]
 gb|EES46890.1| pyoverdine biosynthesis protein PvcB [Burkholderia mallei PRL-20]
 gb|ABM98824.2| pyoverdine chromophore biosynthetic protein PvcB [Burkholderia mallei NCTC 10229]
 Length = 299

Score = 44.7 bits (104), Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 56/196 (28%), Positives = 77/196 (39%), Gaps = 43/196 (21%)

Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQ---RSARH 163
 H D Y+ + + VF + A GGRT F+ A TRAL H+ R R
 Sbjct: 110 HWDGMYLETVPFQVFCVQAIGDAHGGRTTFSSTTEALRVATPETRALWHRAGHGRYRRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL-----LI 211
 +YS + P+V+ HP P L I
 Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPTFI 207

Query: 212 GRHAHAIPGMDAAESER-FLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWD 269
 ++A G+ A+SER L G + A PR H AH+W GDVV+ DN LLH E +
 Sbjct: 208 NPSSYAFGGI--ADSERDALFGSLTRALYDPRAHYAHRWRTGDVVLTDNFTLLHGRERFT 265

Query: 270 FKLPRVMWHSRLAGRP 285
 + R + + G P
 Sbjct: 266 SRSGRHLRRVHIHGDP 281

>ref|ZP_02495768.1| pyoverdine chromophore biosynthetic protein PvcB [Burkholderia pseudomallei NCTC 13177]
 Length = 304

Score = 44.3 bits (103), Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 53/195 (27%), Positives = 74/195 (37%), Gaps = 41/195 (21%)

Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRAL---VHQRSARH 163
 H D Y+ + + VF + A GGRT F+ A TRAL H R R
 Sbjct: 110 HWDGMYLETVPFQVFCVQAIGDAHGGRTTFSSTTEALRVATPETRALWQRAHGRYRRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----LI 211
+YS + P+V+ HP P L I
Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPTEFI 207

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDF 270
++A G+ +E + L G + A PR H AH+W GDVV+ DN LLH E +
Sbjct: 208 NPSSYAFGGIADSERDALL-GSLTRALYDPAHYAHRWRTGDVVLTDNFTLLHGRERFETS 266

Query: 271 KLPRVMWHSRLAGRP 285
+ R + + G P
Sbjct: 267 RSGRHLRRVHIHGDP 281

>ref|XP_001903241.1| hypothetical protein [Podospora anserina S mat+]
emb|CAP61013.1| unnamed protein product [Podospora anserina S mat+]
Length = 355

Score = 44.3 bits (103), Expect = 0.019, Method: Compositional matrix adjust.
Identities = 63/237 (26%), Positives = 93/237 (39%), Gaps = 45/237 (18%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV-----AISNVKADGTVRQHSPAEW 95
Q ++ F Q LS D Q +R G E G + A++N K V ++ +
Sbjct: 112 QRGVVFVRNQLDLSIDDQKLLGQRLG--ELTGKPETSKLHKHALANSKRGIAVDEN--GKL 167

Query: 96 DDMMKVI-----VGNMAWHADSTYMPVMAQGAVFSAEVPVA-VGGR 135
DD + VI + + WHAD T+ + + A+ P VGG
Sbjct: 168 DDEVSVISSEQNRKYYADRYGYTAKRLASEGWHADITFEHIPSDYAILKIVQPPEDVGGD 227

Query: 136 TCFADMRAAYDALDEATRALVHQRSARH---SLVYSQSKLGH--VQQAGSAYIGYGMDDTT 190
T +A YD L A + L +A H + V + G + Q A G+D
Sbjct: 228 TLWASGYEVYDRLSPALQKLAESLTATHHQPNFVRVKEAFGAELIDQFRGAPENNGLDFK 287

Query: 191 ATPLRPLVKVHPETGRPSLL-IGRHAHA--IPGMDAAESE-----RFLEGLVDWAC 238
A P+V+ +P TG SL G HA I G+ ESE RF + + +C
Sbjct: 288 AE--HPVVRTNPVTGWKSLFGAGHQVHAGWINGVTERESEILKAYCRFFQNMKVSSC 342

>gb|AA51281.1| TdfA [uncultured bacterium]
Length = 100

Score = 44.3 bits (103), Expect = 0.019, Method: Compositional matrix adjust.
Identities = 37/105 (35%), Positives = 48/105 (45%), Gaps = 8/105 (7%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
T F DMRAAYD ++ + L R A H + S+ LG + S P+
Sbjct: 1 TEFCDMRAAYDLPEDFKKELQGLR-AEHYALNSRFILGDTDYSES-----QRNAMPVVS 53

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
PLV+ H +GR L IG HA I G AE L L++ A Q
Sbjct: 54 WPLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQ 98

>gb|EFX05042.1| taurine catabolism dioxygenase [Grosmanina clavigera kw1407]
Length = 550

Score = 44.3 bits (103), Expect = 0.020, Method: Compositional matrix adjust.
Identities = 61/266 (22%), Positives = 102/266 (38%), Gaps = 21/266 (7%)

Query: 5 TLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
+ +TPT +G + + L +L DDA L Q ++ F Q L Q +
Sbjct: 20 SFDVTPT---IGREFSHLQLCSLLSDDAKIRDLAVLVSQRGVVFVRNQLDKPFDQREVQ 76

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW-HADS-TYMPVMAQ 120

```

      + G +   G           +A G           + D+++ +   +A + DS T+ V +
Sbjct: 77 KLGQLS--GKPQTSKGKAAEAAGKTLPDGEPKPDDEVLVITSEVLALVNKDSITFENVPSD 134

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARH-SLVYSQSKLGHVQQAG 179
      A+   + P   GG T +A   AYD L   A + L   +A H +   ++   ++ +
Sbjct: 135 YAILKMNIAPETGGDTIWASGYEAYDRLSPAWKKLAEGLTATHRNRAAAEVDAQYIGENR 194

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
      +   G+D AT L +   H   L G   P D   FL+ +V+
Sbjct: 195 GSPENAGLDFEATHL--MAAGH-----QLHDGEFIGLTPREDEILKAYFLQIVVENHDL 246

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
      R   +W   D+ +WDNR   H A
Sbjct: 247 QVRF--KWNTNDIAIWDNRSCFHTA 269

```

>gb|ABD39114.1| alpha-ketoglutarate dioxygenase [uncultured bacterium]
Length = 107

Score = 44.3 bits (103), Expect = 0.020, Method: Compositional matrix adjust.
Identities = 28/96 (29%), Positives = 47/96 (48%), Gaps = 6/96 (6%)

```

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIP 219
      A H+L +S+++   + G   +   A P+ P+V++HPETGR + +G HA I
Sbjct: 10 AVHNLDLSRTR----RHGIDLMTTEEQKREAPPVEHPVVRHHPETGRCCIYLGDAEWIV 64

Query: 220 GMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
      GM E   +E L   A   + H+W   +++V
Sbjct: 65 GMPYEEGRALIEELNALAVHPDLSYEHWRPNELIV 100

```

>ref|XP_002484628.1| conserved hypothetical protein [Talaromyces stipitatus ATCC 10500]
gb|EED14675.1| conserved hypothetical protein [Talaromyces stipitatus ATCC 10500]
Length = 376

Score = 44.3 bits (103), Expect = 0.021, Method: Compositional matrix adjust.
Identities = 41/166 (24%), Positives = 63/166 (37%), Gaps = 9/166 (5%)

```

Query: 107 AWHADSTYMPVMAQGAVFSAEVPV--AVGGRTCFADMRAAYDALDEATRALVHQRSARHS 164
      WH D ++ V   +   VP   GG T FA   AYD L   + +   SA
Sbjct: 170 GWHTDGSFENVPPDYTLHMKVVPVEGSGDTMFASAYEAYDLLSPPMKKFLEGISATF- 228

Query: 165 LVYSQSKLGHVQQAGSAYIGYGMDTTATPLR---PLVKVHPETGRPSLL-IGRHAHAIPG 220
      + +   +   G   +   LR   P ++ +P TG   SL   G H   G
Sbjct: 229 MPWDHKPENIIDHMKGTRG-APENQGPELRASHPCIRTNPVTGWKSLFAFGHHLEEFEG 287

```

```

Query: 221 MDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
      + E+   E +   + ++ A +W   D+V+WDNR + H A
Sbjct: 288 LGDVENRMMKEFVQRLITENHQLQARVRWEQDDLVIWDNRVYHSA 333

```

>gb|AA51277.1| TdfA [uncultured bacterium]
Length = 97

Score = 44.3 bits (103), Expect = 0.022, Method: Compositional matrix adjust.
Identities = 35/101 (34%), Positives = 45/101 (44%), Gaps = 7/101 (6%)

```

Query: 140 DMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLV 198
      DMRAAYD L E + +   A H + S+ LG   + S   P+ PLV
Sbjct: 1 DMRAAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWPLV 54

Query: 199 KVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239

```

+ H +GR L IG HA I G AE L L++ A Q
Sbjct: 55 RTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQ 95

>gb|ACB21022.1| TfdA [uncultured bacterium]
Length = 63

Score = 44.3 bits (103), Expect = 0.022, Method: Compositional matrix adjust.
Identities = 24/56 (42%), Positives = 31/56 (55%)

Query: 108 WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARH 163
WH+D A+ ++ SA VVP GG T F DMRAAYDAL ++ + A H
Sbjct: 3 WHSDXXXXXAARYSMLSAVVVPPSGGDETFCDMRAAYDALPRDLQSELEGLRAEH 58

>ref|ZP_06035601.1| PvcB protein [Vibrio cholerae RC27]
gb|EEY42329.1| PvcB protein [Vibrio cholerae RC27]
Length = 282

Score = 44.3 bits (103), Expect = 0.023, Method: Compositional matrix adjust.
Identities = 61/308 (19%), Positives = 109/308 (35%), Gaps = 50/308 (16%)

Query: 1 MAQTTLQITPTGATLGATVTVGVHLATLDDAGFAALHAAWLQHALLIFPG-QHLSNDQQIT 59
M + P G + +H+ LD L +L+ L++ G + + +Q
Sbjct: 1 MPYKITALQPFVIVEPKHAPIHVNELD---IDELRELFLREQLVLLRGFETFEHSEQFA 57

Query: 60 -FAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
+ +R+G + G ++ + + G D + M W D Y P +
Sbjct: 58 DYCERWGEVSVWPFGRVLDLVQKEDPG-----DHIFDSSYMPMHW--DGMYPQV 105

Query: 119 AQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ +F +P GGRT F+ A Q + + L Q GH Q
Sbjct: 106 PEYQIFQCVCAPLPGHGGRTTFSHTMLAL-----QHAPQPDLELWQQVGTGHYQ 153

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDAA 224
+ Y + + P+V HP P L+ ++ G+
Sbjct: 154 RKMEFY-----HSKTVSPIVMQHPYRDYQVIRYNEPHFEENGDLLNPPDVSLSGITPE 206

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR 284
++ F + L +AH+W GD+V+ DN LLH E ++ PR + ++
Sbjct: 207 QAIEFHKSLRRALYDPRNFYAHEWQTGDIVITDNFSLHGREAFNSHTPRHIRRVQVLSN 266

Query: 285 PETEGAAL 292
P +L
Sbjct: 267 PPYNNPSL 274

>emb|CBJ18923.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 43.9 bits (102), Expect = 0.024, Method: Compositional matrix adjust.
Identities = 34/116 (29%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 143 AAYDALDEATR---ALVHQRSARHS-LVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPL 197
AAYD L E + L ++S R+S + ++ Q+ + + PL
Sbjct: 1 AAYDDLPEDFKKEWQGLCSEQSGRNSRFILGDTEYFESQRNAMPVSW-----PL 50

Query: 198 VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
V+ H +GR L IG HA + G AE L L++ A Q V+ H W GD+
Sbjct: 51 VRTHAGSGRKFLFIGVHAGHMEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGD 106

>ref|XP_003041645.1| hypothetical protein NECHADRAFT_49706 [Nectria haematococca mpVI]

77-13-4]
gb|EEU35932.1| hypothetical protein NECHADRAFT_49706 [Nectria haematococca mpVI
77-13-4]
Length = 361

Score = 43.9 bits (102), Expect = 0.024, Method: Compositional matrix adjust.
Identities = 40/174 (22%), Positives = 69/174 (39%), Gaps = 16/174 (9%)

Query: 104 GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH 163
G +WH+D + A +P+ GG T +A YD + + + +A
Sbjct: 154 GAASWHSDIQFEEFPADYTSRLTLQLPSTGGDTLWASGYEYDRFSDPWQKFLEGLTATF 213

Query: 164 S----LVYSQSKLGHVQ-----QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLL-IGR 213
+ + ++ Q + A +G G+ T + P+V+ +P TG S+ IG
Sbjct: 214 KGEFGIKAADARPDKFQIYEPRGNPANVGRGL----TAVHPVVRTNPVTGWKSVFAIGN 269

Query: 214 HAAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW-AAGDVVVWDNRCLLHRA 265
I + ES+ LE L + + +W D+ +WDNR H A
Sbjct: 270 FPQRINELSVRESKELLELLYKRIEENHDLQVRFKWRNKNDIAIWDNRSAFHSA 323

>ref|ZP_01680907.1| PvcB protein [Vibrio cholerae V52]
ref|YP_001217475.1| PvcB protein [Vibrio cholerae O395]
gb|EAX62290.1| PvcB protein [Vibrio cholerae V52]
gb|ABQ20398.1| PvcB protein [Vibrio cholerae O395]
gb|ACP10052.1| PvcB protein [Vibrio cholerae O395]
Length = 287

Score = 43.9 bits (102), Expect = 0.025, Method: Compositional matrix adjust.
Identities = 61/308 (19%), Positives = 109/308 (35%), Gaps = 50/308 (16%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG-QHLSNDQQIT 59
M + P G + +H+ LD L +L+ L++ G + + +Q
Sbjct: 6 MPYKITALQPFQVIVEPKHAPIHVNELD---IDELRELFLREQLVLLRGFETFEHSEQFA 62

Query: 60 -FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVM 118
+ +R+G + G ++ + + G D + M W D Y P +
Sbjct: 63 DYCERWGEVSVWPFGRVLDLVQKEDPG-----DHIFDSSYMPMHW--DGMYPQV 110

Query: 119 AQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ +F +P GGRT F+ A Q + + L Q GH Q
Sbjct: 111 PEYQIFQCCKAPLPGHGGRTTFSHTMLAL-----QHAPQPDLELWQVVTGHHYQ 158

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDAA 224
+ Y + + P+V HP P L+ ++ G+
Sbjct: 159 RKMEFY-----HSKTVSPIVMQHPYRDYQVIRYNPHFEENGDLLNPPDVSLSGITPE 211

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR 284
++ F + L +AH+W GD+V+ DN LLH E ++ PR + ++
Sbjct: 212 QAIEFHKSLRRALYDPRNFYAEHWQTGDIVITDNFSLHGREAFNSHTPRHRRVQVLSN 271

Query: 285 PETEGAAL 292
P +L
Sbjct: 272 PPYNNPSL 279

>dbj|BAD15044.1| hypothetical protein [Sphingomonas sp. B6-5]
Length = 106

Score = 43.9 bits (102), Expect = 0.025, Method: Compositional matrix adjust.
Identities = 32/114 (28%), Positives = 49/114 (42%), Gaps = 13/114 (11%)

Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRP----LVK 199

Sbjct: 2 A++ LD+ + A HS +S+SK+ G L P +V
AFERLDKDVAKRLENTFAWHSYAHRSKVA-----TGLATTEEVDALPPVCWRMVW 52

Query: 200 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

+P GR +L + HA+ + GMDA + +E L + A + HQW GDV
Sbjct: 53 RNPVNGRGALYLASHAYGVEGMDADAGKALIEQLTEAATALGVTYLHQWKQGDV 106

>emb|CBJ20460.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 43.9 bits (102), Expect = 0.028, Method: Compositional matrix adjust.
Identities = 37/132 (28%), Positives = 56/132 (42%), Gaps = 5/132 (3%)

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG-M 187

VP GG T F M +A++ L +A + + HS L Q + M
Sbjct: 15 VPEHGGDTGFLSMYSAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRRFSNTSVKVM 74

Query: 188 DTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRV 243

D A + PLV HP +GR L + + + I GM AES+ L+ L + A +
Sbjct: 75 DVEAGDRETVHPLVVTHTPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLFEHATRFDF 134

Query: 244 HAHQWAAGDVVV 255

+ +W V+V
Sbjct: 135 YRVRWKKDQVLV 146

>ref|XP_002395867.1| hypothetical protein MPER_04001 [Moniliophthora perniciosa FA553]
gb|EEB96797.1| hypothetical protein MPER_04001 [Moniliophthora perniciosa FA553]
Length = 171

Score = 43.9 bits (102), Expect = 0.030, Method: Compositional matrix adjust.
Identities = 34/128 (26%), Positives = 57/128 (44%), Gaps = 8/128 (6%)

Query: 144 AYDALDEATRALVHQRSARHSL---VYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVK 199

AYD L A + + +A H+ VY+Q+ +Q + G + TA + P+++
Sbjct: 7 AYDRLSPAFQRFLEGLTAVHNADFFNVYAQTHGLKIQDPRGSPENTGSNLTA--VHPVIR 64

Query: 200 VHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWD 257

+P TG SL + + I + ES+ L+ L + + +W DV +WD
Sbjct: 65 TNPVTGFKSLFVNKTFTKRILELTPDESDDVLDYLAKHISENHDLQVRFKWQKNDVAIWD 124

Query: 258 NRCLLHRA 265

NR H A
Sbjct: 125 NRVTFHTA 132

>ref|ZP_01767510.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
305]
gb|EBA47906.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
305]
Length = 304

Score = 43.9 bits (102), Expect = 0.030, Method: Compositional matrix adjust.
Identities = 51/186 (27%), Positives = 75/186 (40%), Gaps = 23/186 (12%)

Query: 109 HADSTYMPVMAQGAVFSAE--VPAVGGRTCFADMRAAYDALDEATRAL---VHQRSARH 163

H D Y+ + + VF + A GGRT F+ A TRAL H R R
Sbjct: 110 HWDGMYLETVPEFQVFQCAQAIGDAHGGRTTFSSTTEALRVATPETRALWQRAHGRYRRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR--PLVK-VHPETGRPSLLIGRHAHAIPG 220

+YS + + + P R P+++ P I ++A G

Sbjct: 170 VELYSNTVEASIVERH-----PRREFPILRFCEPPIADDP TFINPSSYAFGG 216

Query: 221 MDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHS 279

+ +E + L G + A PR H AH+W GDVV+ DN LLH E + + R +

Sbjct: 217 IADSERDALL-GSLTRALYDPRAHYHRWRTGDVVLTDNFTLLHGRERFTSRSGRHLRRV 275

Query: 280 RLAGRP 285

+ G P

Sbjct: 276 HIHGDP 281

>ref|XP_001214255.1| hypothetical protein ATEG_05077 [Aspergillus terreus NIH2624]

gb|EAU34146.1| hypothetical protein ATEG_05077 [Aspergillus terreus NIH2624]

Length = 371

Score = 43.5 bits (101), Expect = 0.032, Method: Compositional matrix adjust.

Identities = 41/185 (22%), Positives = 73/185 (39%), Gaps = 26/185 (14%)

Query: 105 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS 164

++ WH D ++ V + A+ +P GG T +A YD L + +A H

Sbjct: 154 SVGWHTDISFERVPSDYAMLKIHTLPETGGDTLWASGYEIDRLSPQMAEFLEGLTATHD 213

Query: 165 LVY---SQSKLGHVQQAG--SAYIGYGMDDTATPLRPLVKVHPE----- 203

+ +LG+ + G + + +G D A + P+++ + E

Sbjct: 214 ASFFHDEARRLGNPLRKGVRSPLNHGEDLKA--VHPVIRTNREFSGLLSRAVSIDKISA 271

Query: 204 -TGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNR 260

TG S+ + + I G+ ES+ L+ L + Q +W D+ +WDNR

Sbjct: 272 VTGWKSVYVNGFTKRINGVTKDESDMLLQYLFNLVTQNHDAQVRFKWNKNDMAIWDNRS 331

Query: 261 LLHRA 265

H A

Sbjct: 332 TWHCA 336

>emb|CBJ20476.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase

[uncultured bacterium]

Length = 141

Score = 43.5 bits (101), Expect = 0.034, Method: Compositional matrix adjust.

Identities = 35/121 (28%), Positives = 57/121 (47%), Gaps = 12/121 (9%)

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH-----QRSARHSLVYSQSKLGHV 175

G++ ++ +P GG T FA+ AY+ L + + L+ SA+ + S+++ +

Sbjct: 7 GSMLLSQEIPPYGGDTLAFANQYLAYETLSDTMKKLLDGLVGISTSAKADV--SRTREDRM 64

Query: 176 QQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLV 234

+ G + D A P+V+ HPETGR SL + H I GM ES L L

Sbjct: 65 KSDGKSEA--PKDYVAE--HPIVRTHPETGRKSLYVNVVAHTSGIKGMSDHESAALLSFLF 120

Query: 235 D 235

+

Sbjct: 121 E 121

>ref|YP_001249599.1| pyoverdine biosynthesis protein PvcB [Legionella pneumophila str. Corby]

ref|YP_003617441.1| pyoverdine biosynthesis protein PvcB [Legionella pneumophila 2300/99 Alcoy]

gb|ABQ54253.1| pyoverdine biosynthesis protein PvcB [Legionella pneumophila str. Corby]

gb|ADG23489.1| pyoverdine biosynthesis protein PvcB [Legionella pneumophila 2300/99 Alcoy]

Length = 278

Score = 43.5 bits (101), Expect = 0.036, Method: Compositional matrix adjust.
Identities = 46/197 (23%), Positives = 70/197 (35%), Gaps = 25/197 (12%)

Query: 106 MAWHADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRAL-----VH 157
M H D Y P + + +F +P GGRT F++ A + L +
Sbjct: 93 MPLHWDGMYRPPQVPEYQIFHCVKAPLPGQGRTTFSNTILALQFASSEIKELWNKVCPTY 152

Query: 158 QRSAR--HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHA 215
QR +S S + H Q+ S I Y P + +
Sbjct: 153 QRKMEFYNSKTVPSPIMKHPKQDFSV-IRYN-----EPPSADKGHFVNPPD 197

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRV 275
G+D E + F L A +AH+W GD+V+ DN LLH E + + PR
Sbjct: 198 IEFTGIDQEELDFHRSNLKALYSADNFYAHEWQNGDIVIADNFSLLHGREGFVSRSPRH 257

Query: 276 MWHSRLAGRPETEGAAL 292
+ + P + L
Sbjct: 258 IQRVHVLSNPPFDNPGL 274

>ref|YP_001061325.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
668]
gb|ABN85844.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
668]
Length = 304

Score = 43.1 bits (100), Expect = 0.040, Method: Compositional matrix adjust.
Identities = 53/202 (26%), Positives = 75/202 (37%), Gaps = 41/202 (20%)

Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQ---RSARH 163
H D Y+ + + VF + A GGRT F+ A TRAL H+ R R
Sbjct: 110 HWDGMYLETVPFQVQVQCAIGDAHGGRTTFSSTTEALRVATPETRALWHRAHGRYRRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----LI 211
+YS + P+V+ HP P L I
Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPTFI 207

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVWDNRCLLHRAEPWDF 270
++ G+ +E + L G + A PR H AH+W GDVV+ DN LLH E +
Sbjct: 208 NPSSYTFGGIADSERDALL-GSLTRALYDPAHYAHRWRTGDVVLTDNFTLLHGRERFTS 266

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292
+ R + + G P L
Sbjct: 267 RSGRHLRRVHIHGDPPPLRNPHL 288

>emb|CBJ20449.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20472.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 43.1 bits (100), Expect = 0.041, Method: Compositional matrix adjust.
Identities = 40/138 (28%), Positives = 57/138 (41%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L T+A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTTQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A

Sbjct: 69 TSVKVMVDVDAGDRETVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255

+ +W V+V

Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>emb|CAY25794.1| alpha-KG-dehydrogenase [uncultured bacterium]

emb|CAY25798.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 118

Score = 43.1 bits (100), Expect = 0.042, Method: Compositional matrix adjust.

Identities = 30/107 (28%), Positives = 53/107 (49%), Gaps = 7/107 (6%)

Query: 30 AGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE-----RIGGGDIVAISNVKA 83

A AA+ A ++A+L+F Q ++++QQI F++ G +E R G + +

Sbjct: 11 ATMAAIGEAAADRYAVLVFHDQRITDEQQIAFSRGLGPLETTIKAYRPGHKPRLDLHISDV 70

Query: 84 DGTVRQHSAPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

Q DD ++ +GN WH DS++ + A+ ++ SA VV

Sbjct: 71 SNLDEQSRVLAADDRRRMNLGNRLWHTDSSFKAIPARYSLLSARVV 117

>ref|ZP_04967066.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
406e]

gb|ED086844.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
406e]

Length = 304

Score = 43.1 bits (100), Expect = 0.043, Method: Compositional matrix adjust.

Identities = 53/202 (26%), Positives = 74/202 (36%), Gaps = 41/202 (20%)

Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRAL---VHQRSARH 163

H D Y+ + + VF + A GGRT F+ A TRAL H R R

Sbjct: 110 HWDGMYLETVPFQVQVQCVQAIGDAHGGRTTFSSTTEALRVATPETRALWQRAHGRYRRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL-----LI 211

+YS + P+V+ HP P L I

Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPFTFI 207

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDF 270

++ G+ +E + L G + A PR H AH+W GDVV+ DN LLH E +

Sbjct: 208 NPSSYTFGGIADSERDALL-GSLTRALYDPAHYAHRWRTGDVVLTDNFTLLHGRERFTS 266

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292

+ R + + G P L

Sbjct: 267 RSGRHLRRVHIHGDPPLRNPHL 288

>emb|CBJ20434.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]

Length = 146

Score = 43.1 bits (100), Expect = 0.047, Method: Compositional matrix adjust.

Identities = 41/141 (29%), Positives = 60/141 (42%), Gaps = 11/141 (7%)

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182

V A VP GG T F M A++ L +A + + HS + G + QA +

Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHS---ATRVFGSLYQAQNR 65

Query: 183 IGYG----MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234

G MD A + PLV HP +GR L + + + I GM AES+ L+ L

Sbjct: 66 FGNTSVKVMVDVDAGDRETVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLY 125

Query: 235 DWACQAPRVHAHQWAAGDVVV 255
+ A + +W V+V
Sbjct: 126 EHATRFDFTCRVRWKKDQVLV 146

>ref|ZP_01981895.1| PvcB protein [Vibrio cholerae 623-39]
gb|EDL73401.1| PvcB protein [Vibrio cholerae 623-39]
Length = 287

Score = 43.1 bits (100), Expect = 0.048, Method: Compositional matrix adjust.
Identities = 60/301 (19%), Positives = 107/301 (35%), Gaps = 50/301 (16%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG-QHLSNDQQIT-FAKRFG 65
+ P G + +H+ LD L +L+ L++ G + + +Q + +R+G
Sbjct: 13 LQPFQVIVEPKHAPIHVNELD---IDELRELFLREQLVLLRGFETFEHSEQFADYCERWG 69

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS 125
+ G ++ + + G D + M W D Y P + + +F
Sbjct: 70 EVSVWPFGRVLDLVQKEDPG-----DHIFDSSYMPMHW--DGMYPQVPEYQIFQ 117

Query: 126 A--EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI 183
+P GGRT F+ A Q + + L Q GH Q+ Y
Sbjct: 118 CVKAPLPGHGGRTTFSHTMLAL-----QNAPQPDLELWQQVTGHHYQKMEFY- 164

Query: 184 GYGMDTTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDAAESERFLE 231
+ + P+V HP P L+ ++ G+ ++ F +
Sbjct: 165 -----HSKTVSPIVMQHPYRDYQVIRYNEPHFEENGDLLNPPDVSLSGITPEQAIEFHK 218

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAA 291
L +AH+W GD+V+ DN LLH E + PR + ++ P +
Sbjct: 219 SLRRALYDPRNFYAHEWQTGDIVITDNFSLHGREAFSTHTPRHRRVQVLSNPPYNNPS 278

Query: 292 L 292
L
Sbjct: 279 L 279

>ref|ZP_06050330.1| PvcB protein [Vibrio cholerae CT 5369-93]
gb|EEY50537.1| PvcB protein [Vibrio cholerae CT 5369-93]
Length = 282

Score = 43.1 bits (100), Expect = 0.049, Method: Compositional matrix adjust.
Identities = 61/308 (19%), Positives = 109/308 (35%), Gaps = 50/308 (16%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG-QHLSNDQQIT 59
M + P G + +H+ LD L +L+ L++ G + + +Q
Sbjct: 1 MPYKITALQPFQVIVEPKHAPIHVNELD---IDELRELFLREQLVLLRGFETFEHSEQFA 57

Query: 60 -FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM 118
+ +R+G + G ++ + + G D + M W D Y P +
Sbjct: 58 DYCERWGEVSVWPFGRVLDLVQKEDPG-----DHIFDSSYMPMHW--DGMYPQV 105

Query: 119 AQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ +F +P GGRT F+ A Q + + L Q GH Q
Sbjct: 106 PEYQIFQCCKAPLPGHGGRTTFSHTMLAL-----QHAPQPDLELWQQVTGHHYQ 153

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDAA 224
+ Y + + P+V HP P L+ ++ G+
Sbjct: 154 RKMEFY-----HSKTVSPIVMQHPYRDYQVIRYNEPHFEENGDLLNPPDVSLSGITPE 206

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR 284
++ F + L +AH+W GD+V+ DN LLH E + PR + ++

Sbjct: 207 QAIEFHKSLRRALYDPRNLYAHEWQTGDIVITDNFSLHGGREGFTSHTPRHRRVQVLSN 266

Query: 285 PETEGAAL 292

P +L

Sbjct: 267 PPYNNPSL 274

>emb|CBJ18838.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 43.1 bits (100), Expect = 0.050, Method: Compositional matrix adjust.
Identities = 30/111 (27%), Positives = 52/111 (46%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP 202

AA+DAL + + H L++S++++G A+ + + LV+ H

Sbjct: 1 AAWDALPQKLKDECFDLVTDHLLIFSRAQMGF-----EAFSAEELARCEPVPQRLVRRHA 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

+GR SL + H I G E+ + L ++A Q V+AH W+ GD+

Sbjct: 56 GSGRLSLYLSAHIGEIHGWARPEALALIRELTEFATQPQFVYAHHWSVGDL 106

>emb|CBJ20482.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 43.1 bits (100), Expect = 0.050, Method: Compositional matrix adjust.
Identities = 40/138 (28%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182

V A VP GG T F M A++ L +A + + HS L Q +

Sbjct: 9 VMRAIDVPGHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237

MD A + PLV HP +GR L + + + I GM AES+ L+ L + A

Sbjct: 69 TSVKVMDDVAGDRETVDHPLVTHPGSGRKGGLVYNQVYQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255

Q +W V+V

Sbjct: 129 TQFDFTCRVRWKKDQVLV 146

>emb|CBJ20170.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 42.7 bits (99), Expect = 0.052, Method: Compositional matrix adjust.
Identities = 40/138 (28%), Positives = 57/138 (41%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182

V A VP GG T F M A++ L +A + + HS S L Q +

Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFSSLYQAQNRFRSN 68

Query: 183 IGYG-MDDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237

MD A + PLV HP +GR L + + + I GM AES+ L+ L + A

Sbjct: 69 TSVKVMDDVAGDRETVDHPLVTHPGSGRKGGLVYNQVYQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255

+ +W V+V

Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>ref|ZP_07276033.1| hypothetical protein SSMG_00073 [Streptomyces sp. AA4]

gb|EFL04402.1| hypothetical protein SSMG_00073 [Streptomyces sp. AA4]
Length = 285

Score = 42.7 bits (99), Expect = 0.052, Method: Compositional matrix adjust.
Identities = 44/147 (29%), Positives = 62/147 (42%), Gaps = 16/147 (10%)

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
G V + P V G +D L A++ VH + + ++ +AG
Sbjct: 117 GVVKVGNIAPRVSGVRLDRLEPGEFDGLFTASK--VHGSAGPRFAIGDVQRVDDTARAGK 174

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHA-HAIPGMDAAESERFLEGLVDWACQ 239
A+ L PLV HP TGR L + + G+ AE+ +E L
Sbjct: 175 AF-----LHPLVHTHPLTGRKGLVVSACPLTGVLADAEAAELIEQLFRQVV- 222

Query: 240 APR-VHAHQWAAGDVVVWDRCLLHRA 265
APR V +WAAG VV+ DNRC+ H A
Sbjct: 223 APRFVSRVWAAGLVVMIDNRCVQHYA 249

>emb|CBJ20074.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 130

Score = 42.7 bits (99), Expect = 0.054, Method: Compositional matrix adjust.
Identities = 36/136 (26%), Positives = 56/136 (41%), Gaps = 15/136 (11%)

Query: 122 AVFSAEVVPAVGGRTCFAD-MRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
++ A V+PA GG T F++ R D D AL R+ + S+
Sbjct: 8 SMLLARVIPAYGGDTMFSNAYRVFADLSGLKDALRGMRLHQGTTELAMSR----- 58

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVDWACQ 239
G +D T + P+V HPETGR L + G + + G ES+ L +
Sbjct: 59 ---GLSLDDITT-VHPVVARHPETGRELLNVNGAYVKHLDGWTVEESDLLLRYIYGLFGH 114

Query: 240 APRVHAHQWAAGDVVV 255
+ H W GD+++
Sbjct: 115 PEYTYRHHWQVGDLLI 130

>emb|CBJ18991.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 42.7 bits (99), Expect = 0.055, Method: Compositional matrix adjust.
Identities = 35/112 (31%), Positives = 47/112 (41%), Gaps = 7/112 (6%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVH 201
A YD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 AVYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPVSWPLVRTH 54

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR L IG HA I G AE L L++ A Q V+ H GD+
Sbjct: 55 AGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFFVYRHSRKVGDL 106

>ref|ZP_05419250.1| PvcB protein [Vibrio cholera CIRS 101]
ref|ZP_06029145.1| PvcB protein [Vibrio cholerae INDRE 91/1]
gb|EET92527.1| PvcB protein [Vibrio cholera CIRS 101]
gb|EEY48847.1| PvcB protein [Vibrio cholerae INDRE 91/1]
Length = 282

Score = 42.7 bits (99), Expect = 0.055, Method: Compositional matrix adjust.
Identities = 61/308 (19%), Positives = 108/308 (35%), Gaps = 50/308 (16%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG-QHLSNDQQIT 59
M + P G + +H+ LD L +L+ L++ G + + +Q
Sbjct: 1 MPYKITALQPFQVIVEPKHAPIHVNELD---IDELRELFRLREQLVLLRGFETFEHSEQFA 57

Query: 60 -FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
+ +R+G + G ++ + + G D + M W D Y P +
Sbjct: 58 DYCERWGEVSVWPFGRVLDLVQKEDPG-----DHIFDSSYMPMHW--DGMYPQV 105

Query: 119 AQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ +F +P GGRT F+ A Q + + L Q GH Q
Sbjct: 106 PEYQIFQCVKAPLPGHGGRTTFSHTMLAL-----QHAPQPDLELWQQVTGHIY 153

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDAA 224
+ Y + + P+V HP P L+ ++ G+
Sbjct: 154 RKMEFY-----HSKTVSPIVMQHPYRDYQVIRYNPHFEENGDLLNPPDVSLSGITPE 206

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR 284
++ F + L +AH+W GD+V+ DN LLH E + PR + ++
Sbjct: 207 QAIEFHKSLRRALYDPRNFYAHEWQTGDIVITDNFSLHGREAFSTHTPRHRRVQVLSN 266

Query: 285 PETEGAAL 292
P +L
Sbjct: 267 PPYNNPSL 274

>ref|ZP_04418422.1| PvcB protein [Vibrio cholerae 12129(1)]
gb|EEN98292.1| PvcB protein [Vibrio cholerae 12129(1)]
Length = 287

Score = 42.7 bits (99), Expect = 0.056, Method: Compositional matrix adjust.
Identities = 61/308 (19%), Positives = 108/308 (35%), Gaps = 50/308 (16%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG-QHLSNDQQIT 59
M + P G + +H+ LD L +L+ L++ G + + +Q
Sbjct: 6 MPYKITALQPFQVIVEPKHAPIHVNELD---IDELRELFRLREQLVLLRGFETFEHSEQFA 62

Query: 60 -FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
+ +R+G + G ++ + + G D + M W D Y P +
Sbjct: 63 DYCERWGEVSVWPFGRVLDLVQKEDPG-----DHIFDSSYMPMHW--DGMYPQV 110

Query: 119 AQGAVFSAEVVPAVG--GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ +F P +G GRT F+ A Q + + L Q GH Q
Sbjct: 111 PEYQIFQCVKAPLLGHGGRTTFSHTMLAL-----QHAPQPDLELWQQVTGHIY 158

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDAA 224
+ Y + + P+V HP P L+ ++ G+
Sbjct: 159 RKMEFY-----HSKTVSPIVMQHPYRDYQVIRYNPHFEENGDLLNPPDVSLSGITPE 211

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR 284
++ F + L +AH+W GD+V+ DN LLH E + PR + ++
Sbjct: 212 QAIEFHKSLRRALYDPRNFYAHEWQTGDIVITDNFSLHGREGFTSHTPRHRRVQVLSN 271

Query: 285 PETEGAAL 292
P +L
Sbjct: 272 PPYNNPSL 279

>emb|CAY67029.1| Alpha-ketoglutarate-dependent sulfonate dioxygenase [Pichia
pastoris]
Length = 405

Score = 42.7 bits (99), Expect = 0.056, Method: Compositional matrix adjust.
Identities = 64/270 (23%), Positives = 99/270 (36%), Gaps = 54/270 (20%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
++TP G+ V G+ L+ L + L Q +++F Q+L D+ ++ K+FG
Sbjct: 113 KLTPK---FGSVVEGIQLSELSNDQKDDLALFVAQRGVVFRDQNLK-DKSLSEVKKFGQ 168

Query: 67 -----IERIGG---GDIVAINVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPV 117
I + G G + K G R + V M WH+D TY +
Sbjct: 169 HFGPLHIHQTSGAPEGHPEFHISYKRSGRTRS-----FEKKVSAMTWHS DVTYE-L 218

Query: 118 MAQGAVF-SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
G F P VG L +R + AR G+Q
Sbjct: 219 QPPGTTFFLEFWKAPRVG-----EIQLLQIPSRHMRDLSLAR-----GSIQ 258

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW 236
+ T+ + PLV+ HP G+ S+ I G+ ES+ L+ + +
Sbjct: 259 RK-----KFTSENVHPLVRYHPVLGKKSIFAKAFGTRIIGLKQEESDLILQFIENH 309

Query: 237 ACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
A + + G VV WDNR LH A
Sbjct: 310 IATALDLQLRASYPEGTVVAWDNRRLHSA 339

>ref|XP_001224155.1| hypothetical protein CHGG_04941 [Chaetomium globosum CBS 148.51]
gb|EAQ88322.1| hypothetical protein CHGG_04941 [Chaetomium globosum CBS 148.51]
Length = 287

Score = 42.7 bits (99), Expect = 0.060, Method: Compositional matrix adjust.
Identities = 53/223 (23%), Positives = 85/223 (38%), Gaps = 32/223 (14%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQI 58
A T +TPT +G V G+ L+TL AG L + ++ F Q ++ D+ +
Sbjct: 73 AVTVTNLTPT---IGTEVRGIQLSTLTAKGKDELARFVAERKVVAFRDQDFADLPIDEAL 129

Query: 59 TFAKRFGA--IERIGGG-----DIVAINVKADGTVRQHSPAEDDDMMKVIVGNMAWHAD 111
+ FG I G +I + D + + ++AWH+D
Sbjct: 130 EYGSYFGRHHIHPTSGAPEGYEPIHLVHRGAGDTSA-----EAFFAKRTSSVAWHS 181

Query: 112 STYMPVMAQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK 171
+Y PA GG T FAD AY L + +H A HS
Sbjct: 182 VSYEQQPPGTTFLYVLDRLPATGGDTLFAADAAEAYRRLSPLFQQRLHGLRATHSA----- 235

Query: 172 LGHVQQAGSAYIGYGMDTTATPLR--PLVKVHPETGRPSLLIG 212
V+QA ++ G+ + P+V+ HP TG ++ +
Sbjct: 236 ---VEQAAASLARGGVQRREP VINEHPVIRTHPVTGEKAIYVN 275

>ref|NP_231578.1| PvcB protein [Vibrio cholerae O1 biovar El Tor str. N16961]
ref|ZP_01950742.1| PvcB protein [Vibrio cholerae 1587]
ref|ZP_01971420.1| PvcB protein [Vibrio cholerae NCTC 8457]
ref|ZP_01975160.1| PvcB protein [Vibrio cholerae B33]
ref|YP_002810625.1| PvcB protein [Vibrio cholerae M66-2]
ref|ZP_04397466.1| PvcB protein [Vibrio cholerae BX 330286]
ref|ZP_04401281.1| PvcB protein [Vibrio cholerae B33]
ref|ZP_04408383.1| PvcB protein [Vibrio cholerae RC9]
ref|YP_002878154.1| PvcB protein [Vibrio cholerae MJ-1236]
ref|ZP_05238381.1| pyoverdine biosynthesis protein PvcB [Vibrio cholerae MO10]
ref|ZP_07007827.1| pyoverdine biosynthesis protein PvcB [Vibrio cholerae MAK 757]
gb|AAF95092.1| PvcB protein [Vibrio cholerae O1 biovar El Tor str. N16961]
gb|EAY32805.1| PvcB protein [Vibrio cholerae 1587]
gb|EAY73310.1| PvcB protein [Vibrio cholerae NCTC 8457]
gb|EAY77190.1| PvcB protein [Vibrio cholerae B33]
gb|ACP06174.1| PvcB protein [Vibrio cholerae M66-2]
gb|EEO08604.1| PvcB protein [Vibrio cholerae RC9]

gb|EE016708.1| PvcB protein [Vibrio cholerae B33]
gb|EE020387.1| PvcB protein [Vibrio cholerae BX 330286]
gb|ACQ60584.1| PvcB protein [Vibrio cholerae MJ-1236]
gb|EET23150.1| pyoverdine biosynthesis protein PvcB [Vibrio cholerae MO10]
gb|EFH78403.1| pyoverdine biosynthesis protein PvcB [Vibrio cholerae MAK 757]
Length = 287

Score = 42.7 bits (99), Expect = 0.062, Method: Compositional matrix adjust.
Identities = 61/308 (19%), Positives = 108/308 (35%), Gaps = 50/308 (16%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG-QHLSNDQQIT 59
M + P G + +H+ LD L +L+ L++ G + + +Q
Sbjct: 6 MPYKITALQPFQVIVEPKHAPIHVNELD---IDELRELFLREQLVLLRGFETFEHSEQFA 62

Query: 60 -FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
+ +R+G + G ++ + + G D + M W D Y P +
Sbjct: 63 DYCERWGEVSVWPFGRVLDLVQKEDPG-----DHIFDSSYMPMHW--DGMYPQV 110

Query: 119 AQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ +F +P GGRT F+ A Q + + L Q GH Q
Sbjct: 111 PEYQIFQCCKAPLPGHGGRTTFSHTMLAL-----QHAPQPDLELWQQVTGHHY 158

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDAA 224
+ Y + + P+V HP P L+ ++ G+
Sbjct: 159 RKMEFY-----HSKTVSPIVMQHPYRDYQVIRYNPHFEENGDLLNPPDVSLSGITPE 211

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR 284
++ F + L +AH+W GD+V+ DN LLH E + PR + ++
Sbjct: 212 QAIEFHKSLRRALYDPRNFYAHEWQTGDIVITDNFSLHGREFTSHTPRHRRVQVLSN 271

Query: 285 PETEGAAL 292
P +L
Sbjct: 272 PPYNNPSL 279

>ref|ZP_04961829.1| PvcB protein [Vibrio cholerae AM-19226]
gb|EDN14976.1| PvcB protein [Vibrio cholerae AM-19226]
Length = 287

Score = 42.7 bits (99), Expect = 0.064, Method: Compositional matrix adjust.
Identities = 62/308 (20%), Positives = 110/308 (35%), Gaps = 50/308 (16%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG-QHLSNDQQIT 59
M + P G + +H+ LD L +L+ L++ G + + +Q
Sbjct: 6 MPYKITALQPFQVIVEPKHAPIHVNELD---IDELRELFLREQLVLLRGFETFEHSEQFA 62

Query: 60 -FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVM 118
+ +R+G + G ++ + V++ P D + M W D Y P +
Sbjct: 63 DYCERWGEVSVWPFGRVLDL-----VQKEDPG--DHIFDSSYMPMHW--DGMYPQV 110

Query: 119 AQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ +F +P GGRT F+ A Q + + L Q GH Q
Sbjct: 111 PEYQIFQCCKAPLPGHGGRTTFSHTMLAL-----QNAPQPDLELWQQVTGHHY 158

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDAA 224
+ Y + + P+V HP P L+ ++ G+
Sbjct: 159 RKMEFY-----HSKTVSPIVMQHPYRDYQVIRYNPHFEENGDLLNPPDVSLSGITPE 211

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR 284
++ F + L +AH+W GD+V+ DN LLH E + PR + ++
Sbjct: 212 QAIEFHKSLRRALYDPRNFYAHEWQTGDIVITDNFSLHGREFTSHTPRHRRVQVLSN 271

Query: 285 PETEGAAL 292

P +L
 Sbjct: 272 PPYNNPSL 279

```
>ref|ZP_01677582.1| PvcB protein [Vibrio cholerae 2740-80]
ref|ZP_01979042.1| PvcB protein [Vibrio cholerae MZO-2]
ref|ZP_02957750.1| PvcB protein [Vibrio cholerae MZO-3]
ref|ZP_04404788.1| PvcB protein [Vibrio cholerae TMA 21]
ref|ZP_04411279.1| PvcB protein [Vibrio cholerae TM 11079-80]
ref|ZP_04413368.1| PvcB protein [Vibrio cholerae bv. albensis VL426]
ref|ZP_04920074.1| PvcB protein [Vibrio cholerae V51]
ref|ZP_06941385.1| pyoverdine biosynthesis protein PvcB [Vibrio cholerae RC385]
gb|EAX58008.1| PvcB protein [Vibrio cholerae 2740-80]
gb|EAX49344.1| PvcB protein [Vibrio cholerae V51]
gb|EDM54044.1| PvcB protein [Vibrio cholerae MZO-2]
gb|EDT88250.1| PvcB protein [Vibrio cholerae MZO-3]
gb|EEO02561.1| PvcB protein [Vibrio cholerae bv. albensis VL426]
gb|EEO05792.1| PvcB protein [Vibrio cholerae TM 11079-80]
gb|EEO12992.1| PvcB protein [Vibrio cholerae TMA 21]
gb|EFH75884.1| pyoverdine biosynthesis protein PvcB [Vibrio cholerae RC385]
Length = 287
```

Score = 42.4 bits (98), Expect = 0.070, Method: Compositional matrix adjust.
 Identities = 61/308 (19%), Positives = 108/308 (35%), Gaps = 50/308 (16%)

```
Query: 1 MAQTTLQITPTGATLGATVTVGVHLATLDDAGFAALHAAWLQHALLIFPG-QHLSNDQQIT 59
M + P G + +H+ LD L +L+ L++ G + + +Q
Sbjct: 6 MPYKITALQPFVIVEPKHAPIHVNELD---IDELRELFLREQLVLLRGFETFEHSEQFA 62

Query: 60 -FAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM 118
+ +R+G + G ++ + + G D + M W D Y P +
Sbjct: 63 DYCERWGEVSVWPFGRVLDLVQKEDPG-----DHIFDSSYMPMHW--DGMYPQV 110

Query: 119 AQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ 176
+ +F +P GGRT F+ A Q + + L Q GH Q
Sbjct: 111 PEYQIFQCCKAPLPGHGGRTTFSHTMLAL-----QHAPQPDLELWQQVTGHYQ 158

Query: 177 QAGSAYIGYMDTTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDAA 224
+ Y + + P+V HP P L+ ++ G+
Sbjct: 159 RKMEFY-----HSKTVSPIVMQHPYRDYQVIRYNPHFEENGDLLNPPDVSLSGITPE 211

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR 284
++ F + L +AH+W GD+V+ DN LLH E + PR + ++
Sbjct: 212 QAIEFHKSLRRALYDPRNFYAHEWQTGDIVITDNFSLHGREGFTSHTPRHIRRVQVLSN 271

Query: 285 PETEGAAL 292
P +L
Sbjct: 272 PPYNNPSL 279
```

```
>ref|ZP_02458135.1| pyoverdine chromophore biosynthetic protein PvcB [Burkholderia
pseudomallei 9]
ref|ZP_03794324.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
Pakistan 9]
ref|ZP_04889417.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
1655]
gb|EDU10401.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
1655]
gb|EEH25223.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
Pakistan 9]
Length = 304
```

Score = 42.4 bits (98), Expect = 0.073, Method: Compositional matrix adjust.

Identities = 53/202 (26%), Positives = 74/202 (36%), Gaps = 41/202 (20%)

```
Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRAL---VHQRSARH 163
          H D Y+ + + VF      + A GGRT F+      A      RAL      H R R
Sbjct: 110 HWDGMYLETVPFQVQVQCVQAIGDAHGGRTTFSSTTEALRVATPEARALWQRAHGRYRRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL-----LI 211
          +YS +                                P+V+ HP      P L      I
Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPFTI 207

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDF 270
          ++A G+ +E + L G + A      PR H AH+W GDVV+ DN LLH E +
Sbjct: 208 NPSSYAFGGIADSERDALL-GSLTRALYDPAHYAHRWRTGDVVLTDNFTLLHGRERFTS 266

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292
          + R +      + G P      L
Sbjct: 267 RSGRHLRRVHIHGDPPLRNPHL 288
```

>emb|CBJ18859.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 104

Score = 42.4 bits (98), Expect = 0.074, Method: Compositional matrix adjust.
Identities = 31/96 (32%), Positives = 46/96 (47%), Gaps = 7/96 (7%)

```
Query: 144 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPE 203
          AYDA+DE +A +      A H      +S+ LG +      ++      + P+V+ P
Sbjct: 2   AYDAMDEDMKAFLDPLEAEHFHAFHSRELLGAMPTQEER-----NSIPPAVWPIVR-KPA 54

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239
          TGR S IG HAH + GM A+      L L++ A Q
Sbjct: 55 TGRSSFIGAHAKVIGMPLAQGRMLLLDLLEHATQ 90
```

>ref|YP_001074272.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei 1106a]
ref|ZP_02413867.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei 14]
ref|ZP_02473690.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei B7210]
ref|ZP_04812137.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei 1106b]
ref|ZP_04901820.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei S13]
gb|ABN93174.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei 1106a]
gb|EDS84832.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei S13]
gb|EES22762.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei 1106b]
Length = 304

Score = 42.4 bits (98), Expect = 0.076, Method: Compositional matrix adjust.
Identities = 53/202 (26%), Positives = 74/202 (36%), Gaps = 41/202 (20%)

```
Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRAL---VHQRSARH 163
          H D Y+ + + VF      + A GGRT F+      A      RAL      H R R
Sbjct: 110 HWDGMYLETVPFQVQVQCVQAIGDAHGGRTTFSSTTEALRVATPEARALWQRAHGRYRRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL-----LI 211
          +YS +                                P+V+ HP      P L      I
Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPFTI 207
```

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDF 270
++A G+ +E + L G + A PR H AH+W GDVV+ DN LLH E +
Sbjct: 208 NPSSYAFGGIADSERDALL-GSLTRALYDPRAHYAHRWRTGDVVLTDNFTLLHGRERFTS 266

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292
+ R + + G P L
Sbjct: 267 RSGRHLRRVHIHGDPLRNPHL 288

>emb|CBJ20175.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 42.4 bits (98), Expect = 0.077, Method: Compositional matrix adjust.
Identities = 41/141 (29%), Positives = 60/141 (42%), Gaps = 11/141 (7%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS + G + QA +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHS---ATRVFGSLYQAQNRR 65

Query: 183 IGYG---MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
I MD A + PLV HP +GR L + + + I GM AES+ L+ L
Sbjct: 66 ISNTSVKVMVDAGDRETVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLY 125

Query: 235 DWACQAPRVHAHQWAAGDVVV 255
+ A + +W V+V
Sbjct: 126 EHATRFDFTCRVRWKKDQVLV 146

>ref|YP_003018783.1| Taurine catabolism dioxygenase TauD/TfdA [Pectobacterium
carotovorum subsp. carotovorum PC1]
gb|ACT14247.1| Taurine catabolism dioxygenase TauD/TfdA [Pectobacterium
carotovorum subsp. carotovorum PC1]
Length = 284

Score = 42.4 bits (98), Expect = 0.077, Method: Compositional matrix adjust.
Identities = 81/302 (26%), Positives = 117/302 (38%), Gaps = 65/302 (21%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG--QHLSNDQQIT-FAKRF 64
++P G L G +ATL L A +H LL+ G S+ + +T +A +
Sbjct: 13 LSPFGVLLTPVEEGQGIATLP---IDTLRALAREHHLLVLRGFSSGFSDPETLTEYAGHW 69

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGN--MAWHADSTYMPVMAQGA 122
G I G A+ +VK + H I N + H D Y P + +
Sbjct: 70 GEIMMWPFPG---AVLDVKEHADTKDH-----IFDNSYVPLHWDGMYKPTIPEFQ 115

Query: 123 VFSAEVVPAV--GGRTCFADMRAAYDALDEATRALVHQ-RSARHSLVYSQSKLGHVQQAG 179
+F P GGRT F D L EA L + R+ S+ Y + H
Sbjct: 116 LFHCVSAPGQDQGGRITTFVDTRL---LAEADTQLADKWRTV--SITYRIKAVVH----- 165

Query: 180 SAYIGYGMTTATPLRPLVKVHPE-TGR-----PS---LLIGRHA----HAIPGMDAA 224
YG + T+ PLV HP TG P+ + +HA + P A
Sbjct: 166 -----YGGEVTS---PLVIPHPNGTGEIMRYNEPTEGERFLNQHALEYHNVTTPETQNA 216

Query: 225 ESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
S+ + L D PR + AH+W GDVV+ DN LLH E + + R + + G
Sbjct: 217 FSQTLRQHLYD----PRYYYAHKWLGQDVVIADNFSLLHGREAFTAQSARHLQRVHIQ 271

Query: 284 RP 285
P
Sbjct: 272 TP 273

>gb|ABR27314.1| TfdA [uncultured bacterium]
Length = 92

Score = 42.4 bits (98), Expect = 0.079, Method: Compositional matrix adjust.
Identities = 33/97 (34%), Positives = 43/97 (44%), Gaps = 7/97 (7%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR-P 196
F DMRAAYDAL ++ + A H + S+ LG + + P+ P
Sbjct: 2 FCDMRAAYDALPRDLQSELEGLRAEHYALNSRFLLGDTDYSEA-----QRNAMPPVSWP 55

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL 233
LV+ H +GR L IG HA I G AE L L
Sbjct: 56 LVRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAEL 92

>emb|CBJ18850.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 42.0 bits (97), Expect = 0.091, Method: Compositional matrix adjust.
Identities = 30/111 (27%), Positives = 52/111 (46%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHP 202
AA+DAL + + SL++S+++G A+ + + LV+ H
Sbjct: 1 AAWDALPQKLKDECFDLVTDPSLIFSRAQMGF-----EAFSAEELARCEPVPQRLVRRHA 55

Query: 203 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
+GR SL + H I G E+ + L ++A Q V+AH W+ GD+
Sbjct: 56 GSGRQSLYLSAHIGEIHGWARPEALALIRELTEFATQPQFVYAHHWSVGDL 106

>ref|YP_106166.1| taurine dioxygenase-related protein [Burkholderia mallei ATCC
23344]
ref|ZP_00439368.1| alpha-ketoglutarate-dependent taurine dioxygenase
(2-aminoethanesulfonate dioxygenase) (Sulfate
starvation-induced protein3) (SSI3) [Burkholderia mallei
GB8 horse 4]
ref|YP_001025812.1| taurine dioxygenase-related protein [Burkholderia mallei NCTC
10229]
ref|YP_001077895.1| taurine dioxygenase-related protein [Burkholderia mallei NCTC
10247]
ref|ZP_02268184.1| taurine dioxygenase-related protein [Burkholderia mallei PRL-20]
ref|ZP_04883144.1| taurine dioxygenase-related protein [Burkholderia mallei ATCC
10399]
ref|ZP_04907400.1| taurine dioxygenase-related protein [Burkholderia mallei FMH]
ref|ZP_04911353.1| taurine dioxygenase-related protein [Burkholderia mallei JHU]
ref|ZP_04975391.1| taurine dioxygenase-related protein [Burkholderia mallei
2002721280]
gb|AAU45787.1| taurine dioxygenase-related protein [Burkholderia mallei ATCC
23344]
gb|ABO02644.1| taurine dioxygenase-related protein [Burkholderia mallei NCTC
10247]
gb|EDK55722.1| taurine dioxygenase-related protein [Burkholderia mallei FMH]
gb|EDK61650.1| taurine dioxygenase-related protein [Burkholderia mallei JHU]
gb|EDK86266.1| taurine dioxygenase-related protein [Burkholderia mallei
2002721280]
gb|EDP87498.1| taurine dioxygenase-related protein [Burkholderia mallei ATCC
10399]
gb|EEP84764.1| alpha-ketoglutarate-dependent taurine dioxygenase
(2-aminoethanesulfonate dioxygenase) (Sulfate
starvation-induced protein3) (SSI3) [Burkholderia mallei
GB8 horse 4]
gb|EES44143.1| taurine dioxygenase-related protein [Burkholderia mallei PRL-20]
gb|ABN00124.2| taurine dioxygenase-related protein [Burkholderia mallei NCTC

10229]
Length = 103

Score = 42.0 bits (97), Expect = 0.092, Method: Compositional matrix adjust.
Identities = 33/102 (32%), Positives = 44/102 (43%), Gaps = 22/102 (21%)

Query: 196 PLVKVHPETGRPSLLIGR----HAHAIPGMDAAESERFL-----EGLVDWACQAPRVH 244
P+V+ HPETGR +L + +P + A RFL E + W
Sbjct: 11 PVVRTHPETGRKTLFVNEGFTTEIDELPEEEGAALLRFLFAHQSRPEFTLRW----- 62

Query: 245 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
+W GDV WDNR +H A K RVM + + G RP
Sbjct: 63 --RWQPGDVAFWDNIRSTIHYAVNDYGKAHRVMHRATIVGDRP 102

>emb|CBJ20438.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxxygenase
[uncultured bacterium]
Length = 146

Score = 42.0 bits (97), Expect = 0.096, Method: Compositional matrix adjust.
Identities = 41/141 (29%), Positives = 60/141 (42%), Gaps = 11/141 (7%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS + LG + QA +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHS---ATRVLGSLYQAQNR 65

Query: 183 IGYG---MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
MD A + PLV HP +GR L + + + I GM AES+ L+ L
Sbjct: 66 FSNTSVKVMVDVAGDRETVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLY 125

Query: 235 DWACQAPRVHAHQWAAGDVVV 255
+ A + +W V+V
Sbjct: 126 EHATRFDFTCRVRWKKDQVLV 146

>ref|YP_004022174.1| hypothetical protein RBRH_04238 [Burkholderia rhizoxinica HKI 454]
emb|CBW76655.1| unnamed protein product [Burkholderia rhizoxinica HKI 454]
Length = 415

Score = 42.0 bits (97), Expect = 0.100, Method: Compositional matrix adjust.
Identities = 29/115 (25%), Positives = 51/115 (44%), Gaps = 13/115 (11%)

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQR----- 159
H++S Y+P + + F E P +GG T D+ Y+ L E + + Q+
Sbjct: 128 HSESYYPDVPRFISFFCEKPLLGGETGLFDICKIYNDLPERLKEKLEQQRYLAGIFSI 187

Query: 160 ---SARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI 211
+ R++L Y +K ++ + + Y D A +P V HP T S++I
Sbjct: 188 WQIAKRYNLPYEVAK-DFCEKIDMSMVDYHGDQYAFMYKPSVAEHPTTKEKSI 241

>gb|EFZ38396.1| alpha-ketoglutarate-dependent taurine dioxxygenase domain protein
[Escherichia coli EPECa14]
Length = 85

Score = 42.0 bits (97), Expect = 0.10, Method: Compositional matrix adjust.
Identities = 23/63 (36%), Positives = 34/63 (53%), Gaps = 1/63 (1%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVFLRDQTIAPQQQRALAQR 64

Query: 65 GAI 67
G +
Sbjct: 65 GEL 67

>emb|CAK44165.1| unnamed protein product [Aspergillus niger]
Length = 369

Score = 42.0 bits (97), Expect = 0.10, Method: Compositional matrix adjust.
Identities = 26/84 (30%), Positives = 41/84 (48%), Gaps = 7/84 (8%)

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIG----RHAHAIPGM---DAAESERFLEGLVDWACQ 239
+D + + P+V +P TG+P+L I R H G D + L A
Sbjct: 256 IDESKIQILPMVWKNPVTGKPALQIHPSAVRKIHRKDGTVIDDLGRVREIVYKLQRPAS 315

Query: 240 APRVHAHQWAAGDVVVWDNRCLLH 263
P V+AH W GD+V+++NR ++H
Sbjct: 316 PPHVYAHDWQEGDLVLFNNRGVIH 339

>emb|CBJ20437.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 42.0 bits (97), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRATDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVDAGDRETIVHPLVTHPGSGRGLYVNVQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V
Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>emb|CBJ20463.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 42.0 bits (97), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVDAGDRETIVHPLVTHPGSGRGLYVNVQVYCQIEGMSDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V
Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>ref|ZP_01909755.1| pyoverdine biosynthesis protein [Plesiocystis pacifica SIR-1]
gb|EDM77310.1| pyoverdine biosynthesis protein [Plesiocystis pacifica SIR-1]
Length = 666

Score = 42.0 bits (97), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 42/168 (25%), Positives = 64/168 (38%), Gaps = 26/168 (15%)

Query: 104 GNMAWHADSTYMPVMAQGAVFSA-EVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSAR 162
G + H D ++ VF E P GG T F + + E A +
Sbjct: 61 GPVPVHWDGAFLLHTPPHYIVFQCDEAGPGCGGETTFVNTVELMKGISEEELAAWDE---- 116

Query: 163 HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET-----GRPSLLIGRHA 215
+++ Y K+ H YG D A+ ++ HP T P L+

Sbjct: 117 YTVTYLTKKVH-----YGGDFMAS----IIGEHPVTKERTLRYAEPVELLNPKV 162

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLH 263
I GM E F+E + + ++AH+W GD+V+ DN LLH

Sbjct: 163 VFIHGMPVDEHSGFIETMKERLYDPSVLYAHRWVEGDIVLADNHALLH 210

>ref|YP_438432.1| pyoverdine biosynthesis protein PvcB [Burkholderia thailandensis
E264]
ref|ZP_02383525.1| pyoverdine biosynthesis protein PvcB [Burkholderia thailandensis
Bt4]
ref|ZP_05589737.1| pyoverdine biosynthesis protein PvcB [Burkholderia thailandensis
E264]
gb|ABC36029.1| pyoverdine biosynthesis protein PvcB [Burkholderia thailandensis
E264]
Length = 303

Score = 41.6 bits (96), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 51/195 (26%), Positives = 69/195 (35%), Gaps = 41/195 (21%)

Query: 109 HADSTYMPVMAQGAVFSA--EVVPVAVGGRTCFADMRAAYDALDEATRAL---VHQRSARH 163
H D Y+ + + VF + A GGRT F+ A TRAL H R R

Sbjct: 110 HWDGMYLETVPEFQVQVQQAIGEADGGRTTFSSTAEALRIATPQTRALWQRAHGRYQRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----LI 211
+YS + P+V+ HP P L I

Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPSIADDPTFI 207

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVDNRCLLHRAEPWDF 270
+ G+ E + L G + A PR H AH+W GDV DN LLH E +

Sbjct: 208 NPSRYTFGGIADGEQDALL-GSLKRALYDPAHYAHRWQTGDVAFTDNFTLLHGRERFTS 266

Query: 271 KLPRVMWHSRLAGRP 285
+ R + + G P

Sbjct: 267 RTGRHLRRVHIHGEP 281

>ref|XP_001936735.1| taurine catabolism dioxygenase TauD [Pyrenophora tritici-
repentis
Pt-1C-BFP]
gb|EDU49322.1| taurine catabolism dioxygenase TauD [Pyrenophora tritici-repentis
Pt-1C-BFP]
Length = 272

Score = 41.6 bits (96), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 20/57 (35%), Positives = 28/57 (49%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARH 163
WH+D T+ PV + A+ +PA GG T +A YD L A R + +A H

Sbjct: 161 GWHSDITFEPVPSDYAMLKIHTLPATGGDTLWASGYEIDRLSPAMRNFLQSLTATH 217

>ref|YP_051469.1| pyoverdine biosynthesis protein [Pectobacterium atrosepticum

SCRI1043]
emb|CAG76278.1| pyoverdine biosynthesis protein [Pectobacterium atrosepticum
SCRI1043]
Length = 310

Score = 41.6 bits (96), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 76/301 (25%), Positives = 110/301 (36%), Gaps = 63/301 (20%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG--QHLSNDQQIT-FAKRF 64
++P GA L G +ATL L ++ LL+ G S+ + +T +A +
Sbjct: 39 LSPFGALLTPVEAGQGIATLP---IDTLRELAREYHLLVLRGFSSGFSDPETLTEYAGHW 95

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGN--MAWHADSTYMPVMAQGA 122
G I G A+ +VK + H I N + H D Y P + +
Sbjct: 96 GEIMMWPFG---AVLDVKEHADTKDH-----IFDNSYVPLHWDGMYKPTIPEFQ 141

Query: 123 VFSAEVVPAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS 180
+F P GGRT F D D A + + R S+ Y + H
Sbjct: 142 LFHCVSAPGQDQGGRITTFVDITRLLAGAD-----APLVEEWRRVSITYRIKAVVH----- 191

Query: 181 AYIGYGMDDTATPLRPLVKVHPE-----TGRPSLLIGRHA----HAIPGMDAAE 225
YG + T+ PLV HP + + +HA H P
Sbjct: 192 ----YGGEVTS----PLVIPHPNGVGEIMRYNEPPTKGERFLNQHALEYHHIAPEAQNTF 243

Query: 226 SERFLEGLVDWACQAPRVH-AHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGR 284
S+ + L D PR + AHQW GDVV+ DN LLH E + R + + G
Sbjct: 244 SQTLRQHLYD----PRYYAHQWLQGDVVIADNFSLLHGREAFTHASARHLQRVHIQGT 298

Query: 285 P 285
P
Sbjct: 299 P 299

>ref|XP_003188569.1| hypothetical protein ANI_1_3376014 [Aspergillus niger CBS 513.88]
Length = 141

Score = 41.6 bits (96), Expect = 0.13, Method: Compositional matrix adjust.
Identities = 26/84 (30%), Positives = 41/84 (48%), Gaps = 7/84 (8%)

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIG---RHAHAIPGM---DAAESERFLEGLVDWACQ 239
+D + + P+V +P TG+P+L I R H G D + L A
Sbjct: 28 IDESKIQILPMVWKNPVTGKPALQIHPSAVRKIHRKDGTVIDDLGRVREIVYKLQRP AIS 87

Query: 240 APRVHAHQWAAGDVVVDNRCLLH 263
P V+AH W GD+V+++NR ++H
Sbjct: 88 PPHVYAHDWQEGDLVLFNNRGVIH 111

>emb|CBJ20176.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 41.6 bits (96), Expect = 0.13, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVMSATRVFGSLYQAQNRFSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVADGRETVDHPLVVTHTPGSGRKGLYVNVQVYQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V
Sbjct: 129 TRFNFTCRVRWKKDQVLV 146

>emb|CBJ20300.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 41.6 bits (96), Expect = 0.14, Method: Compositional matrix adjust.
Identities = 39/137 (28%), Positives = 56/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS S L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFSSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVDAGDRETVDHPLVVTHPGSGRKGLCVNQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+
Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>emb|CBJ20465.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 41.2 bits (95), Expect = 0.15, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVDAGDRETVDHPLVVTHPGSGRKGLVYNQVYCQRIEGMSDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V
Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>emb|CBJ20432.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 41.2 bits (95), Expect = 0.16, Method: Compositional matrix adjust.
Identities = 40/141 (28%), Positives = 60/141 (42%), Gaps = 11/141 (7%)

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS + G + QA +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHS---ATRVFGSLYQAQNR 65

Query: 183 IGYG----MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
+ MD A + PLV HP +GR L + + + I GM AES+ L+ L
Sbjct: 66 LSNTSVKVMVDVDAGDRETVDHPLVVTHPGSGRKGLVYNQVYCQRIEGMTDAESKPLLQFLY 125

Query: 235 DWACQAPRVHAHQWAAGDVVV 255
+ A + +W V+V
Sbjct: 126 EHATRFDFTCRVRWKKDQVLV 146

>emb|CBJ20446.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 41.2 bits (95), Expect = 0.16, Method: Compositional matrix adjust.
Identities = 40/141 (28%), Positives = 59/141 (41%), Gaps = 11/141 (7%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS + G + QA +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHS---ATRMFGSLYQAQNR 65

Query: 183 IGYG----MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
MD A + PLV HP +GR L + + + I GM AES+ L+ L
Sbjct: 66 FSNTSVKMDVDAGDRETVHPLVVTHPGSGRKGLYVNVQVCQRIEGMTDAESKPLLQFLY 125

Query: 235 DWACQAPRVHAHQWAAGDVVV 255
+ A + +W V+V
Sbjct: 126 EHATRFDFTCRVRWKKDQVLV 146

>emb|CBJ20166.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20425.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 41.2 bits (95), Expect = 0.16, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMHTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDAGDRETVHPLVVTHPGSGRKGLYVNVQVCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V
Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>emb|CBJ20456.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 41.2 bits (95), Expect = 0.17, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMCAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDAGDRETVHPLVVTHPGSGRKGLYVNVQVCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V
Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

```
>ref|YP_336837.1| pyoverdine chromophore biosynthetic protein PvcB [Burkholderia
pseudomallei 1710b]
ref|ZP_02500515.1| pyoverdine chromophore biosynthetic protein PvcB [Burkholderia
pseudomallei 112]
ref|ZP_04954350.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
1710a]
gb|ABA52768.1| pyoverdine chromophore biosynthetic protein PvcB [Burkholderia
pseudomallei 1710b]
gb|EET03872.1| pyoverdine biosynthesis protein PvcB [Burkholderia pseudomallei
1710a]
Length = 304
```

Score = 41.2 bits (95), Expect = 0.17, Method: Compositional matrix adjust.
Identities = 52/202 (25%), Positives = 73/202 (36%), Gaps = 41/202 (20%)

```
Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRAL---VHQRSARH 163
      H D Y+ + + VF + A GGRT F+ A RAL H R R
Sbjct: 110 HWDGMYLETVPFQVQVCQAIGDAHGGRTTFSSTTEALRVATPEARALWQRAHGRYRRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL-----LI 211
      +YS + P+V+ HP P L I
Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPFTFI 207

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDF 270
      ++ G+ +E + L G + A PR H AH+W GDVV+ DN LLH E +
Sbjct: 208 NPSSYTFGGIADSERDALL-GSLTRALYDPAHYAHRWRTGDVVLTDNFTLLHGRERFTS 266

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292
      + R + + G P L
Sbjct: 267 RSGRHLRRVHIHGDPPLRNPHL 288
```

```
>emb|CBJ20468.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146
```

Score = 41.2 bits (95), Expect = 0.18, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

```
Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
      V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRFSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
      MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVDAGDRETVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
      + +W V+V
Sbjct: 129 TRFDLTCRVRWKKDQVLV 146
```

```
>emb|CBJ20110.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20161.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20164.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20165.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20167.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
```


[uncultured bacterium]
emb|CBJ20480.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20481.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20483.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20484.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 41.2 bits (95), Expect = 0.18, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRFSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L+ A
Sbjct: 69 TSVKVMVDAGDRETIVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V
Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>emb|CBJ20112.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 41.2 bits (95), Expect = 0.18, Method: Compositional matrix adjust.
Identities = 43/144 (29%), Positives = 58/144 (40%), Gaps = 17/144 (11%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEDGGDTGFLSMYTAWETLSPTMQATIEGLNIVHSATRVFGSLYQAQNRFRFSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL---- 233
MD A + PLV HP +GR L + + + I GM AES+ L+ L
Sbjct: 69 TSVKVMVDAGDRETIVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 234 --VDWACQAPRVHAHQWAAGDVVV 255
D+ C RVH W V+V
Sbjct: 129 TRFDFTC---RVH---WKKDQVLV 146

>emb|CBJ20454.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 41.2 bits (95), Expect = 0.20, Method: Compositional matrix adjust.
Identities = 37/132 (28%), Positives = 54/132 (40%), Gaps = 5/132 (3%)

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG-M 187
VP GG T F M A++ L +A + + HS L Q + M
Sbjct: 15 VPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRFSNTSVKVM 74

Query: 188 DTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRV 243
D A + PLV HP +GR L + + + I GM AES+ L+ L+ A +
Sbjct: 75 DVDAGDRETIVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYEHATRFDFT 134

Query: 244 HAHQWAAGDVVV 255

+W V+V
 Sbjct: 135 CRVRWKKDQVLV 146

>emb|CBJ20455.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 146

Score = 40.8 bits (94), Expect = 0.20, Method: Compositional matrix adjust.
 Identities = 37/132 (28%), Positives = 54/132 (40%), Gaps = 5/132 (3%)

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY-M 187
 VP GG T F M A++ L +A + + HS L Q + M
 Sbjct: 15 VPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFSNTSVKVM 74

Query: 188 DTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRV 243
 D A + PLV HP +GR L + + + I GM AES+ L+ L + A +
 Sbjct: 75 DVDAGDRETVHPLVVTHPGSGRKGlyVNVQVYCQRIEGMTDAESKPLLQFLYEHA TRFDFT 134

Query: 244 HAHQWAAGDVVV 255
 +W V+V
 Sbjct: 135 CRVRWKKDQVLV 146

>emb|CBJ20282.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 145

Score = 40.8 bits (94), Expect = 0.21, Method: Compositional matrix adjust.
 Identities = 39/137 (28%), Positives = 56/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
 V A VP GG T F M A++ L A +A + + HS L Q +
 Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLS PAMQATIEGLNVVHSATRVFGSLYQAQNRFSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
 MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
 Sbjct: 69 TSVKVMVDVAGDRETVHPLVVTHPGSGRKGlyVNVQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
 + +W V+
 Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>emb|CBJ20447.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 146

Score = 40.8 bits (94), Expect = 0.21, Method: Compositional matrix adjust.
 Identities = 40/141 (28%), Positives = 59/141 (41%), Gaps = 11/141 (7%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
 V A VP GG T F M A++ L +A + + HS + G + QA +
 Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHS---ATRVFGSLYQAQNR 65

Query: 183 IGYG----MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
 MD A + PLV HP +GR L + + + I GM AES+ L+ L
 Sbjct: 66 FSNTCVKVMVDVAGDRETVHPLVVTHPGSGRKGlyVNVQVYCQPIEGMTDAESKPLLQFLY 125

Query: 235 DWACQAPRVHAHQWAAGDVVV 255
 + A + +W V+V
 Sbjct: 126 EHATRFDFTCRVRWKKDQVLV 146

>emb|CBJ20177.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 40.8 bits (94), Expect = 0.21, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFSLMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVDAGDREAVHPLVVTHPGSGRKGLYVNVQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V
Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>emb|CBJ20204.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 40.8 bits (94), Expect = 0.21, Method: Compositional matrix adjust.
Identities = 39/137 (28%), Positives = 56/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + +A HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFSLMYTAWETLSPTMQATIEGLNAVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVDAGDRETIVHPLVVTHPGSGRKGLYVNVQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+
Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>emb|CBJ20485.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 40.8 bits (94), Expect = 0.21, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 57/138 (41%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFSLMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTAT---PLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A+ + PLV HP +GR L + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVDASDRETIVHPLVVTHPGSGRKGLYANQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
++ +W V+V
Sbjct: 129 TRSDFTCRVRWKKDQVLV 146

>ref|YP_110182.1| siderophore biosynthesis-related protein [Burkholderia pseudomallei
K96243]

emb|CAH37606.1| putative siderophore biosynthesis-related protein [Burkholderia
pseudomallei K96243]
Length = 304

Score = 40.8 bits (94), Expect = 0.21, Method: Compositional matrix adjust.
Identities = 52/202 (25%), Positives = 73/202 (36%), Gaps = 41/202 (20%)

Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRAL---VHQRSARH 163
H D Y+ + + VF + A GGRT F+ A RAL H R R
Sbjct: 110 HWDGMYLETVPFQVQVQVQAIGDAHGGRTTFSSTTEALRVATPEARALWQRAHGRYRRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL-----LI 211
+YS + P+V+ HP P L I
Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPTFI 207

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDF 270
++ G+ +E + L G + A PR H AH+W GDVV+ DN LLH E +
Sbjct: 208 NPSSYTFGGIADSERDALL-GSLTRALYDPRAHYAHRWRTGDVVLTDNFTLLHGRRERFTS 266

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292
+ R + + G P L
Sbjct: 267 RSGRHLRRVHIHGDPPLRNPHL 288

>ref|YP_003258525.1| taurine catabolism dioxygenase TauD/TfdA [Pectobacterium
wasabiae
WPP163]
gb|ACX86918.1| Taurine catabolism dioxygenase TauD/TfdA [Pectobacterium wasabiae
WPP163]
Length = 279

Score = 40.8 bits (94), Expect = 0.22, Method: Compositional matrix adjust.
Identities = 77/299 (25%), Positives = 113/299 (37%), Gaps = 59/299 (19%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG--QHLSNDQQIT-FAKRF 64
++P GA L G + TL L +H LL+ G S+ + +T +A +
Sbjct: 8 LSPFGALLTPVEAGQSIVTLP---IDTLRELAREHLLVLRGFSSGFSDFPETLTEYAGHW 64

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF 124
G I G AI +VK + H +D+ + H D Y P + + +F
Sbjct: 65 GEIMMWPFG---AILDVKEHAGTKDHI---FDN-----SYVPLHWDGMYKPTIPEFQLF 112

Query: 125 SAEVVPVAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
P GGRT F D L EA LV + R S+ Y + H
Sbjct: 113 HCVSAPGQDQGGRRTTFVDTRL---LAEADAQLVDEWR-RVSITYRIKAVVH----- 160

Query: 183 IGYGMDDTATPLRPLVKVHPE-----TGRP---SLLIGRHA----HAIPGMDAAESE 227
YG + T+ PL+ HP P + +HA + P +A S+
Sbjct: 161 --YGGEVTS----PLIIPHPNGVGEIMRYNEPPTEGERFLNQHALEYHNVTPAQSAFSQ 214

Query: 228 RFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
+ L D PR + AH+W DVV+ DN LLH E + R + + G P
Sbjct: 215 TLRQHLYD-----PRYYYAHKWLQSDVVIADNFSLLHGREAFTAHSARHLQRVHIQGTP 268

>emb|CBJ20223.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 40.8 bits (94), Expect = 0.22, Method: Compositional matrix adjust.
Identities = 38/137 (27%), Positives = 55/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182

Sbjct: 9 V A VP GG T F M A++ L +A + + HS L Q +
VMRAIDVPEYGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A

Sbjct: 69 TSVKVMVDVDAGDRET VHPLVVTHPGSGRKGLYVNVQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+

Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>ref|ZP_02369596.1| pyoverdine biosynthesis protein PvcB [Burkholderia thailandensis
TXDOH]
Length = 303

Score = 40.8 bits (94), Expect = 0.23, Method: Compositional matrix adjust.
Identities = 50/183 (27%), Positives = 67/183 (36%), Gaps = 17/183 (9%)

Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRAL---VHQRSARH 163
H D Y+ + + VF + A GGRT F+ A TRAL H R R

Sbjct: 110 HWDGMYLETVP EFQVFCVQAIGEADGGRTTFSSTAEALRIATPQTRALWQRAHGRYQRT 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDA 223
+YS + A I P+ L P I + G+

Sbjct: 170 VELYSNTV-----EALIVERHPRREFPI--LRFCEPPIADDPTFINPSRYTFGGIAD 219

Query: 224 AESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLA 282
E + L G + A PR H AH+W GDV DN LLH E + + R + +

Sbjct: 220 GEQDALL-GSLKRALYDPRAHYAHRWQTGDVAFTDNFTLLHGRERFTSRTGRHLRRVHIH 278

Query: 283 GRP 285
G P

Sbjct: 279 GEP 281

>emb|CBJ20471.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 40.8 bits (94), Expect = 0.24, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +

Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A

Sbjct: 69 TSVKVMVDVDAGDRET VHPLVVTHPGSGRKGLYVNVQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V

Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>emb|CBJ20162.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 40.8 bits (94), Expect = 0.25, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVDAGDRETIVHPLVVTHPGSGRKGLYVNVQVYCQRIEGMTDAESKPLLQLLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V
Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>emb|CBJ20459.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 40.4 bits (93), Expect = 0.26, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSAAARVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVDAGDRETIVHPLVVTHPGSGRKGLYVNVQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V
Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>emb|CBJ20443.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 40.4 bits (93), Expect = 0.26, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVDAGDRETIVHPLVVTHPGSGRKGLYMNQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V
Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>emb|CBJ20436.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 40.4 bits (93), Expect = 0.27, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVAGDRETVHPLVVTHTPGSGRKGLYVNVQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V
Sbjct: 129 TRFDFTCRVRWKRQDVLV 146

>emb|CAY25744.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 40.4 bits (93), Expect = 0.27, Method: Compositional matrix adjust.
Identities = 26/90 (28%), Positives = 43/90 (47%), Gaps = 18/90 (20%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVK 82
+ A ++A+L+F GQ ++++QQ+ FA FG E GG + +SN+
Sbjct: 16 IEAGMDKYAVLLFRGQDVTDEQQALAFALNFGEREHARGGTVTKKEDYRLTSGLNDVSNLG 75

Query: 83 ADGTVRQHSPAEDDDMMKVI-VGNMAWHAD 111
DG +P D + +GN WH+D
Sbjct: 76 KDG-----NPLPRDHRTHLNLGNCLWHSD 100

>gb|AA51280.1| TdA [uncultured bacterium]
Length = 105

Score = 40.4 bits (93), Expect = 0.28, Method: Compositional matrix adjust.
Identities = 22/53 (41%), Positives = 27/53 (50%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQW 248
PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W
Sbjct: 53 PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRFVYRHSW 105

>emb|CBJ20479.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 40.4 bits (93), Expect = 0.28, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 55/138 (39%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRFSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES L+ L + A
Sbjct: 69 TSVKVMVDVAGDRETVHPLVVTHTPGSGRKGLYVNVQVYCQRIEGMTDAESRPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V
Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>emb|CBJ20252.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 40.4 bits (93), Expect = 0.29, Method: Compositional matrix adjust.
Identities = 38/137 (27%), Positives = 55/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVSGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVAGGRETVHPLVVTHPGSGRGLYVNVQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+
Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>emb|CBJ20427.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 40.4 bits (93), Expect = 0.29, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVAGDRETIVHPLVVTHPGSGRGLYVNVQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V
Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>emb|CBJ20231.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 40.0 bits (92), Expect = 0.34, Method: Compositional matrix adjust.
Identities = 38/137 (27%), Positives = 55/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVAGDRETIVHPLVVTHPGSGRGLYVNVQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+
Sbjct: 129 TRFDFTCCVRWKKDQVL 145

>emb|CAY25788.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 115

Score = 40.0 bits (92), Expect = 0.34, Method: Compositional matrix adjust.
Identities = 28/105 (26%), Positives = 51/105 (48%), Gaps = 7/105 (6%)

Query: 30 AGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIE-----RIGGGDIVAISNVKA 83
A AA+ A ++A+L+F Q ++++QQI F++ G +E R G + +
Sbjct: 11 ATMAAIGEADRYAVLVFHDQRITDEQQIAFSRGLGPLETTIKAYRPGHKPRLDLHISDV 70

Query: 84 DGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAE 127
Q DD ++ +GN WH DS++ + A+ ++ SA
Sbjct: 71 SNLDEQSRVLAADRRRMNGLGNRLWHTDSSFKAI PARYSLLSAR 115

>gb|ACF09926.1| alpha-ketoglutarate-dependent taurine dioxygenase [uncultured
marine group III euryarchaeote KM3-28-E8]
Length = 407

Score = 40.0 bits (92), Expect = 0.38, Method: Compositional matrix adjust.
Identities = 27/82 (32%), Positives = 35/82 (42%), Gaps = 8/82 (9%)

Query: 194 LRPLVKVHPETGRPSLLIG-----RHAHAIPGMDAAESERFLEGLVDWACQAPRVHA 245
L PLV+ P +G SL R + GM ES FL+ L Q +
Sbjct: 270 LAPLVRTDPRSGTKSLHSPVWASRPGVRPPIEVGMTPEESREFLDRLEKHVLPQPFYD 329

Query: 246 HQWAAGDVVVWDNRCLLHRAEP 267
H A GDV +W+N LH + P
Sbjct: 330 HLHAQGDVTIWNMYMTLHTSPP 351

>ref|XP_772077.1| hypothetical protein CNBM2340 [Cryptococcus neoformans var.
neoformans B-3501A]
gb|EAL17430.1| hypothetical protein CNBM2340 [Cryptococcus neoformans var.
neoformans B-3501A]
Length = 363

Score = 40.0 bits (92), Expect = 0.39, Method: Compositional matrix adjust.
Identities = 51/243 (20%), Positives = 89/243 (36%), Gaps = 29/243 (11%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQH-----SPA EW 95
Q ++ F Q ++ D Q T KR G + S D T+ H S ++
Sbjct: 78 QRGVVFFRAQDINVDDQKTLGKRLGEL-----SGKPGDSTLHIHPTTELSSSKG 126

Query: 96 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV--VPAVGGRTCFADMRAAYDALDEATR 153
D + + + + + PV + +V P GG T +A AY L
Sbjct: 127 DHISVITISSDTLISRLSLSPVTTTPSSKPPGQVHTAPPSGGDTIWASAYEAYSRLSPHFT 186

Query: 154 ALVHQRSARHSLVY---SQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLL 210
+ + A H + + + G + G + + + P+++V+P TG L
Sbjct: 187 KFLEGKEAFHEAAFFSKAAEQYGIELRTGERGSPLNEGPSLSAHPVIRVNPVTGWKGLY 246

Query: 211 IGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAG-----DVVVWDNRCLL 262
+ + I G+ ES+ L+ L + +W DV +WDNR
Sbjct: 247 VNQGFTRRILGVTKDESDFILDYLFKVTQNNHDLQVRFKWGINYPTGIADVALWDNRSTS 306

Query: 263 HRA 265
H A
Sbjct: 307 HSA 309

>emb|CBJ20265.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 40.0 bits (92), Expect = 0.40, Method: Compositional matrix adjust.
Identities = 38/137 (27%), Positives = 56/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L + +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPSMQATIEGLNVVHSATRVFGSLYQAQNRFRS 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237

MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVAGDRET VHP LVVTHPGSGRKG LYV NQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254

+ +W V+
Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>ref|ZP_05225172.1| putative taurine dioxygenase [Mycobacterium intracellulare ATCC
13950]
Length = 153

Score = 40.0 bits (92), Expect = 0.41, Method: Compositional matrix adjust.
Identities = 25/79 (31%), Positives = 36/79 (45%), Gaps = 2/79 (2%)

Query: 194 LRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252

+ P+V+VHPET + + + I + ES L L + + +W G
Sbjct: 39 IHPVVRVHPETNERVVYV NQFFTK EIVDLSPRESRHVLG LLFEQISRPEYSVRFKWEPGS 98

Query: 253 VVVWDNRCLLHRAEPWDFK 271

V WDNR LH A P DF+
Sbjct: 99 VAFWDNRATLHLA-PRDFE 116

>emb|CBJ20466.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 40.0 bits (92), Expect = 0.41, Method: Compositional matrix adjust.
Identities = 39/142 (27%), Positives = 59/142 (41%), Gaps = 11/142 (7%)

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181

V A VP GG T F M ++ L +A + + HS + G + QA +
Sbjct: 8 VVMRAIDVPEHGGDTGFLSMYTVWETLSPTMQATIEGLNVVHS---ATRVFGSLYQAQNR 64

Query: 182 YIGYG----MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL 233

+ MD A + PLV HP +GR L + + + I GM AES+ L+ L
Sbjct: 65 RLSNTSVKVMVDVAGDRET VHP LVVTHPGSGRKG LYV NQVYCQRIEGMTDAESKPLLQFL 124

Query: 234 VDWACQAPRVHAHQWAAGDVVV 255

+ A + +W V+V
Sbjct: 125 YEHATRFDFTCRVRWKKDQVLV 146

>ref|ZP_05073584.1| taurine catabolism dioxygenase TauD/TfdA [Rhodobacterales
bacterium
HTCC2083]

gb|EDZ41244.1| taurine catabolism dioxygenase TauD/TfdA [Rhodobacteraceae
bacterium HTCC2083]
Length = 155

Score = 40.0 bits (92), Expect = 0.42, Method: Compositional matrix adjust.
Identities = 28/86 (32%), Positives = 44/86 (51%), Gaps = 11/86 (12%)

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-VYSQSKLGHVQQAGSAYIGYGM 187

+P GG FA M AAY+ L +A + +A HS +++SK+G + SA+
Sbjct: 16 LPPFGGDALFASMTAAYEGLSTGLKATLLNLNAIHSDGSFAESKVG-IDAETSAF----- 69

Query: 188 DTTATPLR-PLVKVHPETGRPSLLIG 212

P++ P+V HP+TG P L +
Sbjct: 70 ---RAPIKHPVVIAHPDTGAPCLYVN 92

>emb|CBJ20277.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 40.0 bits (92), Expect = 0.42, Method: Compositional matrix adjust.
Identities = 38/137 (27%), Positives = 55/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDAGDRET VHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYERA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+
Sbjct: 129 TRLDFTCRVRWKKDQVL 145

>emb|CBJ20409.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 40.0 bits (92), Expect = 0.43, Method: Compositional matrix adjust.
Identities = 38/137 (27%), Positives = 55/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGNSVVHSATRVFGSLYQAQNRFSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDAGDRET VHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+
Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>emb|CBJ20286.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20361.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 39.7 bits (91), Expect = 0.45, Method: Compositional matrix adjust.
Identities = 39/140 (27%), Positives = 59/140 (42%), Gaps = 11/140 (7%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS + G + QA +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHS---ATRVFGSLYQAQNR 65

Query: 183 IGYG----MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
+ MD A + PLV HP +GR L + + + I GM AES+ L+ L
Sbjct: 66 LSNTSVKVMVDAGDRET VHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLY 125

Query: 235 DWACQAPRVHAHQWAAGDVV 254
+ A + +W V+
Sbjct: 126 EHATRFDTCRVRWKKDQVL 145

>emb|CBJ20478.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase

[uncultured bacterium]
Length = 146

Score = 39.7 bits (91), Expect = 0.47, Method: Compositional matrix adjust.
Identities = 39/138 (28%), Positives = 55/138 (39%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A+ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWXTLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDAGDRETVDHPLVVTHTPGSGRGLYVNVQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V
Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>emb|CBJ20349.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 39.7 bits (91), Expect = 0.47, Method: Compositional matrix adjust.
Identities = 37/137 (27%), Positives = 57/137 (41%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ---AG 179
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 180 SAYIGYGMDT-TATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
++ G+D + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMGVDAGDRETVDHPLVVTHTPGSGRGLYVNVQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+
Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>emb|CBJ20420.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 39.7 bits (91), Expect = 0.47, Method: Compositional matrix adjust.
Identities = 38/137 (27%), Positives = 55/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDAGDRETVDHPLVVTHTPGSGRGLYVNVQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+
Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>emb|CBJ20276.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 39.7 bits (91), Expect = 0.47, Method: Compositional matrix adjust.
Identities = 39/140 (27%), Positives = 58/140 (41%), Gaps = 11/140 (7%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS + G + QA +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHS---ATRVFGSLYQAQNRR 65

Query: 183 IGYG----MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
MD A + PLV HP +GR L + + + I GM AES+ L+ L
Sbjct: 66 FSNSSVKVMDVDAGDRETVMHPLVVTHPGSGRKGLYVNVQVYCQRIEGMTDAESKPLLQFLY 125

Query: 235 DWACQAPRVHAHQWAAGDVV 254
+ A + +W V+
Sbjct: 126 EHATRFDFTCRVRWKKDQVL 145

>emb|CBJ20328.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20396.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 39.7 bits (91), Expect = 0.48, Method: Compositional matrix adjust.
Identities = 38/137 (27%), Positives = 55/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRRFSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVAGDRETVMHPLVVTHPGSGRKGLYVNVQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+
Sbjct: 129 TRFDFTCLVRWKKDQVL 145

>emb|CBJ20375.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 39.7 bits (91), Expect = 0.50, Method: Compositional matrix adjust.
Identities = 37/137 (27%), Positives = 57/137 (41%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ---AG 179
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRRFSN 68

Query: 180 SAYIGYGMT-TATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
++ G+D + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVGVDAGDRETVMHPLVVTHPGSGRKGLYVNVQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+
Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>emb|CBJ20186.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20236.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 39.7 bits (91), Expect = 0.50, Method: Compositional matrix adjust.
Identities = 38/137 (27%), Positives = 55/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L+ A
Sbjct: 69 TSVKVMVDVAGDRETIVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+
Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>emb|CBJ20188.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20190.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20192.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20196.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20198.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20212.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20217.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20218.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20219.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20221.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20225.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20230.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20232.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20235.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20240.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20243.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20246.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20247.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20249.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20250.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20251.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20253.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20261.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]

[uncultured bacterium]
 emb|CBJ20385.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 emb|CBJ20390.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 emb|CBJ20391.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 emb|CBJ20401.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 emb|CBJ20407.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 emb|CBJ20411.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 emb|CBJ20510.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 emb|CBJ20511.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 145

Score = 39.7 bits (91), Expect = 0.54, Method: Compositional matrix adjust.
 Identities = 38/137 (27%), Positives = 55/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
 V A VP GG T F M A++ L +A + + HS L Q +
 Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
 MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
 Sbjct: 69 TSVKVMVDVAGDRETVHPLVVTHTPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
 + +W V+
 Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>ref|YP_003743530.1| Taurine dioxygenase, C-terminal fragment [Erwinia billingiae
 Eb661]
 emb|CAX61683.1| Taurine dioxygenase, C-terminal fragment [Erwinia billingiae Eb661]
 Length = 101

Score = 39.7 bits (91), Expect = 0.55, Method: Compositional matrix adjust.
 Identities = 20/74 (27%), Positives = 33/74 (44%), Gaps = 1/74 (1%)

Query: 194 LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD 252
 L P+++ HP +G+P+L + I + ES+ L L + +W D
 Sbjct: 2 LHPVIRTHPFSGKPALFVNEGFTTRIVDVSQKESDALLNFLFAHVTKPEFQVRWRWQEND 61

Query: 253 VVVWDNRCLLHRAE 266
 + +WDNR H A
 Sbjct: 62 IAIWDNRVTQHYAN 75

>emb|CBJ20255.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 145

Score = 39.7 bits (91), Expect = 0.55, Method: Compositional matrix adjust.
 Identities = 38/137 (27%), Positives = 55/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
 V A VP GG T F M A++ L +A + + HS L Q +
 Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWERLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVAGDRETVDHPLVVTHPGSGRKGGLYVNVQVYQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+
Sbjct: 129 IRFDFTXRVRWKKDQVL 145

>ref|ZP_01038110.1| hypothetical protein ROS217_03160 [Roseovarius sp. 217]
gb|EAQ23334.1| hypothetical protein ROS217_03160 [Roseovarius sp. 217]
Length = 487

Score = 39.7 bits (91), Expect = 0.55, Method: Compositional matrix adjust.
Identities = 29/105 (27%), Positives = 50/105 (47%), Gaps = 6/105 (5%)

Query: 101 VIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRS 160
+I+G A Y A A S++V PA+G RT FA+ +A +AL + A+VH+++
Sbjct: 14 LILGACAAAVPGIYTEPKAGFANISSQVTPAIGKRTAFAETQAENEALKKQVHAMVHRKT 73

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYGMDDT-----ATPLRPLVKV 200
Q L + + ++Y G+ +TP P+V +
Sbjct: 74 ISADTAV-QVALLNNKGLQASYANVGLSAAEAWQQSTPENPIVSI 117

>emb|CBJ20206.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
emb|CBJ20419.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 39.7 bits (91), Expect = 0.56, Method: Compositional matrix adjust.
Identities = 38/137 (27%), Positives = 55/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVAGDRETVDHPLVVTHPGSGRKGGLYVNVQAYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+
Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>emb|CBJ20444.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 39.7 bits (91), Expect = 0.57, Method: Compositional matrix adjust.
Identities = 38/138 (27%), Positives = 56/138 (40%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I G+ AES+ L+ L + A
Sbjct: 69 TSVKVMVDVAGDRETVDHPLVVTHPGSGRKGGLYVNVQVYQRIEGITDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255

+ +W V+V
Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>emb|CBJ20163.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 146

Score = 39.3 bits (90), Expect = 0.62, Method: Compositional matrix adjust.
Identities = 38/139 (27%), Positives = 59/139 (42%), Gaps = 7/139 (5%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQQAGS 180
V A VP GG T F M A++ L +A + + HS V+ ++ +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSPYQAQNRFRFSN 68

Query: 181 AYIGYGMDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW 236
+ MD A + PLV HP +GR L + + + I GM AES+ L+ L +
Sbjct: 69 TSVKVMVDVAGDRETIVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYEH 127

Query: 237 ACQAPRVHAHQWAAGDVVV 255
A + +W V+V
Sbjct: 128 ATRFDFTCRVRWKKDQVLV 146

>ref|ZP_01881466.1| hypothetical conserved membrane protein [Roseovarius sp. TM1035]
gb|EDM30048.1| hypothetical conserved membrane protein [Roseovarius sp. TM1035]
Length = 487

Score = 39.3 bits (90), Expect = 0.63, Method: Compositional matrix adjust.
Identities = 29/105 (27%), Positives = 50/105 (47%), Gaps = 6/105 (5%)

Query: 101 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRS 160
+I+G A Y A A S++V PA+G RT FA+ +A +AL + A+VH+++
Sbjct: 14 LILGACATAVPGIYTEPKAGFANISSQVTPAIGKRTAFAETQAENEALKKQVHAMVHRKT 73

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYGMDTT-----ATPLRPLVKV 200
Q L + + ++Y G+ +TP P+V +
Sbjct: 74 ISADTAV-QVALLNNKGLQASYANVGLSAAEAWQQSTPENPIVAI 117

>emb|CBJ20273.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 39.3 bits (90), Expect = 0.64, Method: Compositional matrix adjust.
Identities = 37/128 (28%), Positives = 52/128 (40%), Gaps = 11/128 (8%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRFSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL---- 233
MD A + PLV HP +GR L + + + I GM AES+ L+ L
Sbjct: 69 TSVKVMVDVAGDRETIVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYKHA 128

Query: 234 --VDWACQ 239
D+ C+
Sbjct: 129 TRFDFTCR 136

>emb|CBJ20337.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 39.3 bits (90), Expect = 0.66, Method: Compositional matrix adjust.
Identities = 38/137 (27%), Positives = 55/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDVAGDRET VHPLVVTHPGSGRKGLYVNQVYCQHIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+
Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>emb|CAI47587.1| alpha-ketoglutarate dependent xanthine dioxygenase [Emericella
nidulans]
Length = 370

Score = 39.3 bits (90), Expect = 0.66, Method: Compositional matrix adjust.
Identities = 27/86 (31%), Positives = 44/86 (51%), Gaps = 11/86 (12%)

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIG---RHAHAIPGMDAAESERFLEGLVDWACQAP- 241
+D +A + P+V +P TG+P+L I R H G + ++ E + + Q P
Sbjct: 257 IDESAIQILPMVWKNPATGKPALQIHPSAVRKIHCGDGTVIDDLKKVRE--IAYKLQRP 314

Query: 242 ----RVHAHQWAAGDVVVWDNRCLLH 263
V+AH W GD+V++ NR +LH
Sbjct: 315 ISPQYVYAHDWEEGDLVLFHNRGV LH 340

>emb|CBJ20281.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 39.3 bits (90), Expect = 0.67, Method: Compositional matrix adjust.
Identities = 37/130 (28%), Positives = 52/130 (40%), Gaps = 11/130 (8%)

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA 181
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 8 VVMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRS 67

Query: 182 YIGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL--- 233
MD A + PLV HP +GR L + + + I GM AES+ L+ L
Sbjct: 68 NTSVKVMVDVAGDRET VHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYEHA 127

Query: 234 ---VDWACQA 240
D+ C+
Sbjct: 128 VTRFDFTCRV 137

>emb|CBJ20279.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 39.3 bits (90), Expect = 0.68, Method: Compositional matrix adjust.
Identities = 37/128 (28%), Positives = 52/128 (40%), Gaps = 11/128 (8%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL---- 233
 MD A + PLV HP +GR L + + + I GM AES+ L+ L
 Sbjct: 69 TSVKVMVDVAGDRET VHPLVVT HPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYEHG 128

Query: 234 --VDWACQ 239
 D+ C+
 Sbjct: 129 TRFDFTCR 136

>emb|CBJ20296.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 145

Score = 39.3 bits (90), Expect = 0.69, Method: Compositional matrix adjust.
 Identities = 38/137 (27%), Positives = 55/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
 V A VP GG T F M A++ L +A + + HS L Q +
 Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQAAIEGLNVVHSATRVFGSLYQAQNRFRFSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
 MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
 Sbjct: 69 TSVKVMVDVAGDRET VHPLVVT HPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
 + +W V+
 Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>emb|CBJ20470.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 146

Score = 39.3 bits (90), Expect = 0.71, Method: Compositional matrix adjust.
 Identities = 38/138 (27%), Positives = 55/138 (39%), Gaps = 5/138 (3%)

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
 V A VP GG T F M A++ L +A + + H L Q +
 Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHRATRVFGSLYQAQNRFRFSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
 MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
 Sbjct: 69 TSVKVMVDVAGDRET VHPLVVT HPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
 + +W V+V
 Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>emb|CBJ20336.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
 [uncultured bacterium]
 Length = 145

Score = 39.3 bits (90), Expect = 0.71, Method: Compositional matrix adjust.
 Identities = 39/140 (27%), Positives = 58/140 (41%), Gaps = 11/140 (7%)

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
 V A VP GG T F M A++ L +A + + HS + G + QA +
 Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHS--ATR VFGSLYQAQNR 65

Query: 183 IGYG----MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV 234
 MD A + PLV HP +GR L + + + I GM AES+ L+ L

Sbjct: 66 FSNTSVRVMDVDAGDRETVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLY 125

Query: 235 DWACQAPRVHAHQWAAGDVV 254

+ A + +W V+

Sbjct: 126 EHATRFDFTCRVRWKKDQVL 145

>emb|CBJ20292.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 39.3 bits (90), Expect = 0.71, Method: Compositional matrix adjust.
Identities = 38/137 (27%), Positives = 55/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182

V A VP GG T F M A++ L +A + + HS L Q +

Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRFSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237

MD A + PLV HP +GR L + + + I GM AES+ L+ L+ A

Sbjct: 69 TSVKVMVDVDAGDRETVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQLLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254

+ +W V+

Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>gb|EFZ46473.1| alpha-ketoglutarate-dependent taurine dioxygenase domain protein
[Escherichia coli E128010]
Length = 158

Score = 39.3 bits (90), Expect = 0.72, Method: Compositional matrix adjust.
Identities = 33/127 (25%), Positives = 52/127 (40%), Gaps = 6/127 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATP--LRPLVKV 200

AAY+AL R L+ A H S + + ++ + + P L P+V+

Sbjct: 8 AAYEALSVPRQLLSGLRAEHDFRKSFPYKY-RKTEEEHQWRWEAVAKNPPLLHPVVRT 66

Query: 201 HPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDN 258

HP +G+ +L + I + ESE L G + P +W D+ +WDN

Sbjct: 67 HPVSGKQALFVNEGFTTRIVDVSEKESEALL-GFLFAHITKPEFQVRWRWQPNDIAIWDN 125

Query: 259 RCLLHRA 265

R H A

Sbjct: 126 RVTQHYA 132

>emb|CBJ20397.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 39.3 bits (90), Expect = 0.72, Method: Compositional matrix adjust.
Identities = 38/137 (27%), Positives = 55/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182

V A VP GG T F M A++ L +A + + HS L Q +

Sbjct: 9 VMRAIDVPEHGGDTGFLGMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRFSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237

MD A + PLV HP +GR L + + + I GM AES+ L+ L+ A

Sbjct: 69 TSVKVMVDVDAGDRETVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254

+ +W V+
Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>tpe|CBF89386.1| TPA: Alpha-ketoglutarate dependent xanthine dioxygenase
[Source:UniProtKB/TrEMBL;Acc:Q4QZZ9] [Aspergillus
nidulans FGSC A4]
Length = 354

Score = 39.3 bits (90), Expect = 0.72, Method: Compositional matrix adjust.
Identities = 27/86 (31%), Positives = 44/86 (51%), Gaps = 11/86 (12%)

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIG---RHAHAIPGMDAAESERFLEGLVDWACQAP- 241
+D +A + P+V +P TG+P+L I R H G + ++ E + + Q P
Sbjct: 241 IDESAIQILPMVWKNPATGKPALQIHPSAVRKIHCGDGTVIDDLKKVRE--IAYKLQRP 298

Query: 242 ----RVHAHQWAAGDVVVDNRCLLH 263
V+AH W GD+V++ NR +LH
Sbjct: 299 ISPQYVYAHDWEEGDLVLFHNRGV LH 324

>emb|CBJ20344.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 39.3 bits (90), Expect = 0.74, Method: Compositional matrix adjust.
Identities = 38/137 (27%), Positives = 55/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +
Sbjct: 9 VMRAIDVPEHGGGTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSVKVMVDAGDRETVDHPLVVTHTPGSGRGLYVNQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+
Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>emb|CBJ20239.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 38.9 bits (89), Expect = 0.75, Method: Compositional matrix adjust.
Identities = 39/137 (28%), Positives = 56/137 (40%), Gaps = 5/137 (3%)

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ-QAGSA 181
V A VP GG T F M A++ L +A + + HS L Q + S
Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 182 YIGYGMDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
MD A + PLV HP +GR L + + + I GM AES+ L+ L + A
Sbjct: 69 TSAKVMVDAGDRETVDHPLVVTHTPGSGRGLYVNQVYCQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVV 254
+ +W V+
Sbjct: 129 TRFDFTCRVRWKKDQVL 145

>emb|CBJ20241.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]

Query: 123 VFSAEVVPVAVGGRTCFADMR AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ---AG 179
V A VP GG T F M A++ L +A + + HS L Q +

Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 180 SAYIGYGMDT-TATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA 237
++ +D + PLV HP +GR L + + + I GM AES+ L+ L + A

Sbjct: 69 TSVKVMVAVDAGDRETVDHPLVVTHPGSGRKGLYVNVQVYQRIEGMTDAESKPLLQFLYEHA 128

Query: 238 CQAPRVHAHQWAAGDVVV 255
+ +W V+V

Sbjct: 129 TRFDFTCRVRWKKDQVLV 146

>emb|CBJ20205.1| 2-(2,4-dichlorophenoxy)propionate,2-oxoglutarate dioxygenase
[uncultured bacterium]
Length = 145

Score = 38.9 bits (89), Expect = 0.87, Method: Compositional matrix adjust.
Identities = 37/128 (28%), Positives = 52/128 (40%), Gaps = 11/128 (8%)

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY 182
V A VP GG T F M A++ L +A + + HS L Q +

Sbjct: 9 VMRAIDVPEHGGDTGFLSMYTAWEMLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSN 68

Query: 183 IGYG-MDTTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL---- 233
MD A + PLV HP +GR L + + + I GM AES+ L+ L

Sbjct: 69 TSVKVMVDAGDRETVDHPLVVTHPGSGRKGLYVNVQVYQRIEGMTDAESKPLLQFLYGHA 128

Query: 234 --VDWACQ 239
D+ C+

Sbjct: 129 TRFDFTCR 136

>emb|CBJ18807.1| alpha-ketoglutarate dioxygenase-like protein [uncultured bacterium]
Length = 106

Score = 38.9 bits (89), Expect = 0.89, Method: Compositional matrix adjust.
Identities = 22/58 (37%), Positives = 28/58 (48%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253
PL + +GR L IG HA I G AE L L++ A Q V+ H W GD+

Sbjct: 49 PLCLPNAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFFVYRHSWKVGDL 106

Database: /usr/local/blast/db/blastlibs/nr
Posted date: Apr 13, 2011 11:46 AM
Number of letters in database: 4,621,495,809
Number of sequences in database: 13,473,798

Lambda	K	H
0.321	0.133	0.419

Gapped		
Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 13473798
Number of Hits to DB: 2,778,827,635
Number of extensions: 116470082
Number of successful extensions: 250030
Number of sequences better than 1.0: 2252
Number of HSP's gapped: 246605

Number of HSP's successfully gapped: 2286
Length of query: 293
Length of database: 4,621,495,809
Length adjustment: 137
Effective length of query: 156
Effective length of database: 2,775,585,483
Effective search space: 432991335348
Effective search space used: 432991335348
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 (21.9 bits)
S2: 89 (38.9 bits)