

STUDY TITLE

Supplemental Information for Toxicity Similarity Assessment of AAD-12 Protein Expressed in Soybean Event DAS-68416-4 by Bioinformatic Analysis (Update, March 2010)

DATA REQUIREMENTS

N/A

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PERFORMING LABORATORY

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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 v1
(293 letters)

Database: /usr/local/blast/db/blastlibs/nr
10,606,545 sequences; 3,615,943,919 total letters

Searching.....done

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Sequences producing significant alignments:	(bits)
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emb CAF32813.1 (S)-2-(2,4-dichlorophenoxy)propionate, 2-oxoglutarate...	369
e-100	
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1e-82	
gb ABL97633.1 2,4-dichlorophenoxyacetate alpha-ketoglutarate dio...	271
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gb ADC34025.1 TfdA-like protein [uncultured bacterium]	266
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dbj BAB92964.1 alpha KG dependent 2,4-D dioxygenase [alpha prot...	162
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ref NP_990895.1 TfdA [Achromobacter denitrificans] >gi 44937736...	148
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gb ACF35465.1 TfdA [Burkholderia sp. TFD36] >gi 194245695 gb AC...	148
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dbj BAD15039.1 hypothetical protein [Bradyrhizobium sp. ApB16] 7e-05	52
ref XP_001526184.1 hypothetical protein LELG_02742 [Lodderomyce... 7e-05	52
ref XP_001201468.1 PREDICTED: hypothetical protein, partial [St... 7e-05	52
ref XP_001211559.1 conserved hypothetical protein [Aspergillus ... 7e-05	52
ref XP_002472100.1 predicted protein [Postia placenta Mad-698-R... 7e-05	52
ref ZP_06192176.1 hypothetical protein SOD_f01220 [Serratia odo... 8e-05	52
dbj BAD15041.1 hypothetical protein [Bradyrhizobium sp. BDV5329] 9e-05	52
ref XP_382474.1 hypothetical protein FG02298.1 [Gibberella zeae... 9e-05	52
gb ABI95434.1 2,4-D/alpha-ketoglutarate dioxygenase [uncultured... 1e-04	52
ref XP_001598964.1 hypothetical protein SS1G_01054 [Sclerotinia... 1e-04	52
ref XP_001216869.1 hypothetical protein ATEG_08248 [Aspergillus... 1e-04	52
ref ZP_03827804.1 pyoverdine biosynthesis protein PvcB [Pectoba... 1e-04	51
ref ZP_02383058.1 pyoverdine biosynthesis protein PvcB [Burkhol... 1e-04	51
emb CAY25731.1 alpha-KG-dehydrogenase [uncultured bacterium] 1e-04	51

gb EEQ91806.1 alpha-ketoglutarate-dependent taurine dioxygenase...	51
1e-04	
ref XP_001217671.1 hypothetical protein ATEG_09049 [Aspergillus...	51
1e-04	
gb ABD39113.1 alpha-ketoglutarate dioxygenase [uncultured bacte...	51
1e-04	
ref YP_001848583.1 oxidoreductase [Mycobacterium marinum M] >gi...	51
1e-04	
gb ABD39121.1 alpha-ketoglutarate dioxygenase [uncultured bacte...	51
1e-04	
dbj BAF81036.1 2,4-D dioxygenase [Burkholderia sp. M36-VN10-2W]	50
2e-04	
ref ZP_06474867.1 Taurine catabolism dioxygenase TauD/TfdA [Fra...	50
2e-04	
ref YP_001476938.1 taurine catabolism dioxygenase TauD/TfdA [Se...	50
2e-04	
ref XP_001224283.1 hypothetical protein CHGG_05069 [Chaetomium ...	50
3e-04	
gb EEH58672.1 predicted protein [Micromonas pusilla CCMP1545]	50
3e-04	
gb ACB21020.1 TfdA [uncultured bacterium]	50
3e-04	
ref XP_002476351.1 predicted protein [Postia placenta Mad-698-R...	50
4e-04	
ref XP_001947612.1 PREDICTED: hypothetical protein, partial [Ac...	50
4e-04	
emb CAY25780.1 alpha-KG-dehydrogenase [uncultured bacterium]	50
4e-04	
ref XP_001594485.1 hypothetical protein SS1G_04292 [Sclerotinia...	50
4e-04	
ref YP_003262840.1 Taurine catabolism dioxygenase TauD/TfdA [Ha...	49
4e-04	
ref XP_001548982.1 hypothetical protein BC1G_12213 [Botryotinia...	49
4e-04	
ref XP_001552854.1 hypothetical protein BC1G_09036 [Botryotinia...	49
5e-04	
ref XP_002621709.1 alpha-ketoglutarate-dependent taurine dioxyg...	49
5e-04	
ref XP_001727715.1 hypothetical protein [Aspergillus oryzae RIB...	49
6e-04	
gb EEY53775.1 taurine dioxygenase, putative [Phytophthora infes...	49
6e-04	
emb CAY25739.1 alpha-KG-dehydrogenase [uncultured bacterium]	49
7e-04	
gb AAB08969.1 alpha ketoglutarate dioxygenase [Variovorax parad...	49
8e-04	
gb AAX51275.1 TdfA [uncultured bacterium]	49
9e-04	
gb ACB21019.1 TfdA [uncultured bacterium]	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	

ref ZP_01630848.1 taurine dioxygenase [Nodularia spumigena CCY9... 0.001	48
gb ACB21023.1 TfdA [uncultured bacterium] 0.001	48
ref ZP_04588004.1 taurine dioxygenase [Pseudomonas syringae pv.... 0.001	48
gb ACB21028.1 TfdA [uncultured bacterium] 0.001	48
gb AAB18140.1 2,4-dichlorophenoxyacetate dioxygenase [Halomonad... 0.001	48
gb AAX51279.1 TdfA [uncultured bacterium] 0.001	48
gb ABE68889.1 TfdA [Burkholderia glathei] 0.001	48
gb ACB21024.1 TfdA [uncultured bacterium] 0.001	48
ref ZP_05883092.1 PvcB protein [Vibrio metschnikovii CIP 69.14]... 0.001	48
ref ZP_06188335.1 PvcB [Legionella longbeachae D-4968] >gi 2891... 0.002	48
gb AAX51272.1 TfdA [uncultured bacterium] >gi 61661373 gb AAX51... 0.002	48
ref XP_001559770.1 hypothetical protein BC1G_01926 [Botryotinia... 0.002	48
gb AAF02720.2 alpha ketoglutarate dependent dioxygenase [Ralsto... 0.002	47
ref XP_001391648.1 hypothetical protein An07g05690 [Aspergillus... 0.002	47
ref YP_125606.1 hypothetical protein lp10237 [Legionella pneumo... 0.002	47
gb ABI94568.1 TfdA [Burkholderia hospita] 0.002	47
gb AAX51288.1 TdfA [uncultured bacterium] 0.002	47
gb AAX51276.1 TdfA [uncultured bacterium] 0.002	47
gb EEQ42086.1 alpha-ketoglutarate-dependent sulfonate dioxygena... 0.003	47
ref XP_002419465.1 alpha-ketoglutarate-dependent sulfonate diox... 0.003	47
ref XP_657819.1 hypothetical protein AN0215.2 [Aspergillus nidu... 0.003	47
ref XP_713065.1 potential taurine catabolic dioxygenase [Candid... 0.003	47
gb AAX51287.1 TdfA [uncultured bacterium] 0.003	47
gb EEQ44600.1 hypothetical protein CAWG_02874 [Candida albicans... 0.003	47
ref XP_001937063.1 taurine dioxygenase family protein [Pyrenoph... 0.003	47
ref ZP_02357712.1 pyoverdine biosynthesis protein PvcB [Burkhol... 0.003	47
ref ZP_02364837.1 pyoverdine biosynthesis protein PvcB [Burkhol... 0.003	47

ref XP_002383259.1 alpha-ketoglutarate-dependent sulfonate diox...	47
0.004	
ref YP_001629703.1 Alpha-ketoglutarate-dependent taurine dioxyg...	46
0.004	
gb EEQ44372.1 hypothetical protein CAWG_02639 [Candida albicans...	46
0.004	
ref YP_003018467.1 Taurine catabolism dioxygenase TauD/TfdA [Pe...	46
0.005	
ref XP_720183.1 potential taurine catabolic dioxygenase [Candid...	46
0.005	
ref YP_094229.1 pyoverdine biosynthesis protein PvcB [Legionell...	46
0.005	
ref XP_714705.1 potential taurine catabolic dioxygenase [Candid...	46
0.005	
gb ACG80556.1 TfdA [uncultured bacterium]	46
0.006	
gb EEY21481.1 alpha-ketoglutarate-dependent sulfonate dioxygena...	45
0.006	
ref YP_122580.1 hypothetical protein lpp0237 [Legionella pneumo...	45
0.007	
gb ADC33970.1 TfdA-like protein [uncultured bacterium]	45
0.007	
ref XP_387766.1 hypothetical protein FG07590.1 [Gibberella zea...	45
0.008	
ref ZP_02484143.1 pyoverdine biosynthesis protein PvcB [Burkhol...	45
0.008	
gb AAX51278.1 TdfA [uncultured bacterium]	45
0.008	
gb AAX51283.1 TdfA [uncultured bacterium] >gi 61661369 gb AAX51...	45
0.008	
gb ADC33968.1 TfdA-like protein [uncultured bacterium]	45
0.008	
ref ZP_04522600.1 PvcB [Burkholderia pseudomallei MSHR346] >gi ...	45
0.009	
gb EEU33690.1 hypothetical protein NECHADRAFT_98371 [Nectria ha...	45
0.010	
gb AAZ39276.1 oxygenase [uncultured organism]	45
0.011	
ref ZP_04896071.1 pyoverdine biosynthesis protein PvcB [Burkhol...	45
0.011	
ref ZP_03454489.1 pyoverdine biosynthesis protein PvcB [Burkhol...	45
0.012	
ref ZP_02405336.1 pyoverdine biosynthesis protein PvcB [Burkhol...	45
0.013	
ref ZP_02449958.1 pyoverdine biosynthesis protein PvcB [Burkhol...	45
0.013	
ref YP_106451.1 pyoverdine chromophore biosynthetic protein Pvc...	45
0.014	
ref ZP_02495768.1 pyoverdine chromophore biosynthetic protein P...	44
0.015	
ref XP_001903241.1 unnamed protein product [Podospira anserina]...	44
0.015	
gb AAX51281.1 TdfA [uncultured bacterium]	44
0.015	

gb ABD39114.1 alpha-ketoglutarate dioxygenase [uncultured bacte... 0.016	44
ref XP_002484628.1 conserved hypothetical protein [Talaromyces ... 0.017	44
gb AAX51277.1 TdfA [uncultured bacterium] 0.017	44
gb ACB21022.1 TfdA [uncultured bacterium] 0.018	44
ref ZP_06035601.1 PvcB protein [Vibrio cholerae RC27] >gi 26202... 0.018	44
gb EEU35932.1 hypothetical protein NECHADRAFT_49706 [Nectria ha... 0.019	44
ref ZP_01680907.1 PvcB protein [Vibrio cholerae V52] >gi 147673... 0.019	44
dbj BAD15044.1 hypothetical protein [Sphingomonas sp. B6-5] 0.020	44
ref ZP_05476509.1 Alpha-ketoglutarate-dependent taurine dioxyge... 0.022	44
ref XP_002395867.1 hypothetical protein MPER_04001 [Moniliophth... 0.024	44
ref ZP_01767510.1 pyoverdine biosynthesis protein PvcB [Burkhol... 0.024	44
ref XP_001214255.1 hypothetical protein ATEG_05077 [Aspergillus... 0.025	44
ref YP_001249599.1 pyoverdine biosynthesis protein PvcB [Legion... 0.029	44
ref YP_001061325.1 pyoverdine biosynthesis protein PvcB [Burkho... 0.032	43
emb CAY25794.1 alpha-KG-dehydrogenase [uncultured bacterium] >g... 0.033	43
ref ZP_04967066.1 pyoverdine biosynthesis protein PvcB [Burkhol... 0.034	43
ref ZP_01981895.1 PvcB protein [Vibrio cholerae 623-39] >gi 148... 0.038	43
ref ZP_06050330.1 PvcB protein [Vibrio cholerae CT 5369-93] >gi... 0.038	43
ref ZP_05419250.1 PvcB protein [Vibrio cholera CIRS 101] >gi 26... 0.043	43
ref ZP_04418422.1 PvcB protein [Vibrio cholerae 12129(1)] >gi 2... 0.044	43
emb CAY67029.1 Alpha-ketoglutarate-dependent sulfonate dioxygen... 0.044	43
ref XP_001224155.1 hypothetical protein CHGG_04941 [Chaetomium ... 0.048	43
ref NP_231578.1 PvcB protein [Vibrio cholerae O1 biovar El Tor ... 0.049	43
ref ZP_04961829.1 PvcB protein [Vibrio cholerae AM-19226] >gi 1... 0.050	43
ref ZP_01677582.1 PvcB protein [Vibrio cholerae 2740-80] >gi 15... 0.055	42
ref ZP_02458135.1 pyoverdine chromophore biosynthetic protein P... 0.058	42
ref YP_001074272.1 pyoverdine biosynthesis protein PvcB [Burkho... 0.060	42

ref YP_003018783.1 Taurine catabolism dioxygenase TauD/TfdA [Pe... 0.061	42
gb ABR27314.1 TfdA [uncultured bacterium] 0.062	42
ref YP_106166.1 taurine dioxygenase-related protein [Burkholder... 0.072	42
ref XP_001389856.1 hypothetical protein An01g14680 [Aspergillus... 0.080	42
ref ZP_01909755.1 pyoverdine biosynthesis protein [Plesiocystis... 0.090	42
ref YP_438432.1 pyoverdine biosynthesis protein PvcB [Burkholde... 0.094	42
ref XP_001936735.1 taurine catabolism dioxygenase TauD [Pyrenop... 0.097	42
ref YP_051469.1 pyoverdine biosynthesis protein [Pectobacterium... 0.098	42
ref YP_336837.1 pyoverdine chromophore biosynthetic protein Pvc... 0.14	41
ref YP_110182.1 siderophore biosynthesis-related protein [Burkh... 0.17	41
ref YP_003258525.1 Taurine catabolism dioxygenase TauD/TfdA [Pe... 0.17	41
ref ZP_02369596.1 pyoverdine biosynthesis protein PvcB [Burkhol... 0.18	41
emb CAY25744.1 alpha-KG-dehydrogenase [uncultured bacterium] 0.22	40
gb AAX51280.1 Tdfa [uncultured bacterium] 0.22	40
emb CAY25788.1 alpha-KG-dehydrogenase [uncultured bacterium] 0.27	40
gb ACF09926.1 alpha-ketoglutarate-dependent taurine dioxygenase... 0.30	40
ref XP_772077.1 hypothetical protein CNBM2340 [Cryptococcus neo... 0.31	40
ref ZP_05225172.1 putative taurine dioxygenase [Mycobacterium i... 0.32	40
ref ZP_05073584.1 taurine catabolism dioxygenase TauD/TfdA [Rho... 0.33	40
ref ZP_01038110.1 hypothetical protein ROS217_03160 [Roseovariu... 0.43	40
ref ZP_01881466.1 hypothetical conserved membrane protein [Rose... 0.50	39
emb CAI47587.1 alpha-ketoglutarate dependent xanthine dioxygena... 0.52	39
tpe CBF89386.1 TPA: Alpha-ketoglutarate dependent xanthine diox... 0.57	39
ref XP_658092.1 hypothetical protein AN0488.2 [Aspergillus nidu... 0.61	39
ref XP_001214157.1 conserved hypothetical protein [Aspergillus ... 0.75	39
gb AAX51274.1 Tdfa [uncultured bacterium] 0.93	39

>gb|AAP88277.1| S-2,4-dichlorophenoxypropionate/alpha-ketoglutarate
dioxygenase

[Delftia acidovorans]
Length = 292

Score = 596 bits (1537), Expect = e-169, Method: Compositional matrix
adjust.

Identities = 291/291 (100%), Positives = 291/291 (100%)

Query: 3 QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK

Sbjct: 2 QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 61

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA

Sbjct: 62 RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
121

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAY
182

VFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAY

Sbjct: 122 VFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAY
181

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQAPR
242

IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQAPR

Sbjct: 182 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQAPR
241

Query: 243 VHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAALV 293

VHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAALV

Sbjct: 242 VHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAALV 292

>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%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
I P AT GA VTGV LA LDDAG+ L AAWL++ALL+FP QHL+ +QQI FA+RF

Sbjct: 5 FDIAPLDATFGAVVTGVKLDLDDAGWLDLQAAWLEYALLVFPDQHLTREQQIAFARRF 64

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
125

+E ++ AISNV+ DG++R S + DDMMK++ GNM WHADSTYMPV A+GAVFS

Sbjct: 65 PLEF----EMAAISNVRPDGSLRVES--DNDDMMKILKGNMGWHADSTYMPVQAKGAVFS
118

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQAGSA-YIG
184

AEVVP+VGG+T FADMRAAYDALDE +A V ARHSL YSQSKLGH +A Y G
Sbjct: 119 AEVVPVAVGGRTCFADMRAAYDALDEDLKARVETLQARHSLHYSQSKLGHQTKAADGEYSG
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+MWHRSR+AG P +E A

Sbjct: 239 HHDWAPGDAVLWDNRCLLHQATPDMTQKRIMWHSRIAGDPASETA 284

>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 TFGAIVTDIRLNELDNRFQFSALYQAWLEYGLLIFPGQYLSDAEQQTFAARFGDL--IKGV 73

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVG
133

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

Query: 134 GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG-HVQAGSAYIGYGMDDTTAT
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 PLRPLLKIHPETGRKSLAIGRHAFGIPEMSEGESSKFLADLMDFATGDPQRTYQYQWTKG
250

Query: 252 DVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGA 290
D VVWDNRCLLHRA WD+ PRVM HSR+AG PETE A

Sbjct: 251 DAVVWDNRCLLHRACSWDYSEPRVMLHSRIAGDPETESA 289

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

Score = 271 bits (694), Expect = 5e-71, Method: Compositional matrix
adjust.

Identities = 135/288 (46%), Positives = 184/288 (63%), Gaps = 9/288 (3%)

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

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
125

A+E D+ ISNV+ DG++R A DD++K + GNM WH DSTYMP+ A+GAVF+
Sbjct: 61 ALE----FDLSPISNVRNDGSIRD---ANDDDIVKSLRGNMEWHHDSTYMPIQAKGAVFT
113

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQ-SKLGHVQQAGSAYIG
184

A VP+ GG T +ADMRAAY+ALD++ + +++ SA HS +SQ + GH S +
Sbjct: 114 AHKVPSHGGETGWADMRAAYEALDQSMKDKINELSAHSYEWVSQKERFGHKDPKVSEFNS
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 YHHAWVEVGDAVIWDRCLMHQASMWDLSEGRIMYHSRIEGDPIAEAS 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 PVMAQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHV
175

PV A+GAVFSAEVVP+VGGRT +ADMRAAYDALD+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 DYSGYGFHDGPFVPLRPLVKSHPETGRKSSLLIGRHAHNIPNMDKDESERLLQALV
174

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCL 261
D+ACQ PR++ H W GD VVWDNRC+

Sbjct: 175 DFACQPPRIYHHTWTPGDAVVWDNRCV 201

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

Score = 162 bits (410), Expect = 4e-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-----KPLPKDHRTHLFLNGLNCLWHS DSSFRPIPAKFSLLSARVVNPKGGNTEFADM
147

Query: 142 RAAYDALDEATRALLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVH
201

RAAYDALD+ T+ + HSL+YS+ LG + Y + L+ LV+ H
Sbjct: 148 RAAYDALDDETKTEIDDMICEHSLMYSRGLGFLD-----YTDEEKEMFKPVLQRLVRTH
202

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL
261

P GR SL + HA AI GM E+ L L + A Q V+ H+W D+V+WDNR
Sbjct: 203 PAHGRKSLYLSSHAGAIRGMSMPPEARLLLLRDLTEHATQPEFVYVHKWTVHDLVMWDNRQT
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 = 5e-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 IEAGMDKYAVLVFHGQDISDDQQMAFALNFGGERENARGGTVTKKEDYRLSSGLNDVSNLG 92

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
141

DG P D + +GN WH+DS++ P+ A+ ++ SA VV GG T FADM
Sbjct: 93 KDG-----KPLPKDHRTHLFLNCLWHS DSSFRPIPAKFSLLSARVVNPKGGNTEFADM
147

Query: 142 RAAVDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVH
201

RAAYDALD+ T+ + HSL+YS+ LG + Y + L+ LV+ H
Sbjct: 148 RAAVDALDDETKTEIDDMICEHSLMYSRGLGFLD-----YTDEEKEMFKPVLQRLVVRTH
202

Query: 202 PETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL
261

P GR SL + HA AI GM E+ L L + A Q V+ H+W D+V+WDNR
Sbjct: 203 PAHGRKSLYLSSHAGAIRGMSPEARLLLLRDLTEHATQPEFVYVHKWTVHDLVMWDNRQT
262

Query: 262 LHRAEPWDFKLPRVMWHSRLAG 283
+HR +D PR M + +AG

Sbjct: 263 VHRVRRYDQSQPRDMRRATVAG 284

>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-----KPLPKDHRTHLFLNCLWHS DSSFRPIPAKFSLLSARVVNPKGGNTEFADM
147

Query: 142 RAAVDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVH
201

RAAYDALD+ TRA + HSL+YS+ LG + Y L+ LV+ H
Sbjct: 148 RAAVDALDDETRAEIDDMICEHSLMYSRGLGFLD-----YTDEEKQMFKPVLQRLVVRTH
202

Query: 202 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL
261

P GR SL + HA AI GM E+ L L + A V+ H+W D+V+WDNR

Sbjct: 203 PGHGRRSLYLSSHAGAIRGMSVPEARVLLRDLNEHATSPEFVYVHKWTVHDLVMWDNRQT
262

Query: 262 LHRAEPWDFKLPRVMWHSRLAG 283
+HR +D PR M + +AG

Sbjct: 263 MHRVRRYDQSQPRDMRRATVAG 284

>ref|YP_001203232.1| alpha-ketoglutarate-dependent 2, 4-
dichlorophenoxyacetate

dioxygenase [Bradyrhizobium sp. ORS278]

emb|CAL74995.1| Alpha-ketoglutarate-dependent 2, 4-dichlorophenoxyacetate
dioxygenase (EC 1.14.11.-) (2,4-D dioxygenase)

[Bradyrhizobium sp. ORS278]

Length = 295

Score = 158 bits (400), Expect = 7e-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--AELQAAIDHYAVLVFHDQDIGDEQQALAFALNFGDREKARGGTV 73

Query: 76 VA-----ISNVKADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGA
122

+SN+ DG P D + +GN WH+DS++ P+ A+ +

Sbjct: 74 TKKEDYRLTTGLNDVSNLKGKG-----KPLPPDHRTHLFLNCLWHSDDSFRPIPAKYS
128

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

+ SA +V GG T FADMRAAYDALDE T+A + + HSL+YS+ LG +

Sbjct: 129 ILSARIVNPKGGNTEFADMRAAYDALDEQTKAEIDDLVSEHSLMYSRGS LG-----F
180

Query: 183 IGYGMDTTATPLRP----LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC
238

+ Y D +P LV+ HP GR SL + HA A+ GM E L L + A

Sbjct: 181 LDY-TDEEKMKFKPVRQRLVRTHPAHGRKSLYLSSHAGAVVGMSPPEGRLLLRDLTEHAT
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

dioxygenase [Bradyrhizobium sp. BTAi1]
 gb|ABQ38852.1| Alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
 dioxygenase [Bradyrhizobium sp. BTAi1]
 Length = 295

Score = 157 bits (398), Expect = 9e-37, 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-VGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFA
 139

+ DG P D + +GN WH+DS++ P+ A+ ++ SA +V GG T FA
 Sbjct: 91 LGKDG-----RPLPRDHRTHLFLNGLNCLWHSDDSSFRPIPARYSILSARIVNPKGGNTEFA
 145

Query: 140 DMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRP-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 = 3e-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 MALSIRPINPKRDDFVAEVTGLDIAAGVSKAVAEIEIDAINRYAVLVFPEQRVNDQDQYV 60

Query: 60 FAKRFGAIERIGGG-----DIVAISNVKADGTVRQHSPAEWDDMMKVI-VGNMA
 107

F+ FG +E G DI ISN+ +G V Q DD ++ +GNM

Sbjct: 61 FSTHFGPMETATGDIAAQGDRRLSMDINDISNLKNGQVLQR-----DDRRRLFGLGNML
115

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
167

WH DS++ A+ ++ SA +P GG T FADMRAA+D LD T+A + A HS +Y
Sbjct: 116 WHTDSSFKATPAKFSLLSARTIPGEGGNTEFADMRAAWDDLDPKTQADLMPLVAEHSQLY
175

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
227

S+ LG Q + P R +V+ HP +GR S+ + HA I G E+
Sbjct: 176 SRGLLGFQFTDEERAKWA----PVPQR-MVRRHPGSGRLSVFLASHAGTIQGWPIPEAR
230

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLA 282
F+ L + A Q +AH+W D+V+WDNR ++HRA +D PR M + +A

Sbjct: 231 MFIRDLTEHATQREYTYAHRWRQYDLVMWDNRVAVMHRARRYDHTQPRDMHRTTVA 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 = 3e-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 SSLELTPHPLFAAEARGIDIRQPLSPSEVKQINAAMNRYAVLVWRGQPLTGQQQIDFAK 61

Query: 63 RFGAI-----ERIGGGDIVAISNVKADGTV-RQHSPAEWDDMMKVIVGNMAWHA
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 KLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFL
230

LG AY + PL + HP +GR L +G HA I G AE FL
Sbjct: 177 LLG-----DEAYTDDQKKAIPPAVWPLAQTHPGSGRKLFLVGVHAREIIGWPVAEGRMFL
231

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

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

Score = 151 bits (382), Expect = 7e-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 VESAMDKYAVLVFHDQDITDEQQMAFALNFGQREDARGGTVTKEKDYRLQSGLN DVSNLG 92

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

Query: 142 RAAVDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVH
 201
 RAAVDALD+ T+A + HSL+YS+ LG + Y L+ LV+ H
 Sbjct: 148 RAAVDALDDETKAEIEDLVCEHSLMYSRGS LGFTE-----YTDEEKQMFKPV LQRLV RTH
 202

Query: 202 PETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL
 261
 P R SL + HA I M E L L + A Q V+ H+W D+V+WDNR
 Sbjct: 203 PVHRRKSLYLSSHAGKIASMSVPEGRL LRLDLNEHATQPEFVYVHKWKLHDLVMW DNRQT
 262

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

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

Score = 151 bits (382), Expect = 8e-35, Method: Compositional matrix
 adjust.

Identities = 96/295 (32%), Positives = 149/295 (50%), Gaps = 30/295 (10%)

Query: 3 QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
 ++++I PTGA LGA V V L LDD FA+L A+ H++L+ GQ+L++ I F++

Score = 149 bits (377), Expect = 3e-34, Method: Compositional matrix adjust.

Identities = 97/298 (32%), Positives = 150/298 (50%), Gaps = 32/298 (10%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 ++I PT +LGA + V L LDDA FAA+ A+ H++L+ GQHLS+ I F++RF

Sbjct: 15 NIEIVPTDRSLGAEIRNVDLRQLDDAAFAAVLRAFHTHSVLLVRGQHLSQDLIAFSRRF 74

Query: 65 GAIE-----RIGGG--DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
 113

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

Query: 114 YMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
 173

Y+ + A +P VGG T F M A YDAL + + +H Y+ G
 Sbjct: 125 YLETPPIASALYALEIPPVGGNTSFCSMYAVYDALPTELKHRIADLKIKHDGTYN--G
 182

Query: 174 HVQQAGSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFL
 230

V+Q + D ++P + PLV HP++GR L +GR +A + G++ AESE L
 Sbjct: 183 FVRQG----VTPTDDPRSSPGAVHPLVCTHPDSCRQMLYLGRRRNAYLVGLELAESEALL
 238

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG--RPE 286

+ L + + H W GD+V+WDNR +HR +P+D + R+M +++ G RP+
 Sbjct: 239 DELWTYVARPEFAWEHVWQVGDLDVIWDNRSTMHRRDPFDDQARRIMHRTQIKGTERPQ 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 = 6e-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 LAITRRHPLIGTEVRGIDLTKPLDRDGLDRLNSIWMEHPMLVFPNQKITDEQQIVFARNF 67

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP
 116

G +E ++ +SNV G + EW + + WH DS++
 Sbjct: 68 GELEVHPSVAHRSSKNPEVYRVSINVDEQGNILPSESKEW----QYLELTWLWHTDSSFRE
 123

Query: 117 VMAQQAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS---LVYSQSKLG
173

 + + G++ VP GG T FA+M AAY+AL + T+A + + RHS ++ +KL
Sbjct: 124 IPSMGSILHGIEVPKDGGDTLAFANMYAAYEALSDGTKAEIEGLTVRHSHTDAVIARS AKLS
183

Query: 174 HVQQAGSAYIGYGMDDTATPL-RPLVKVHPETGRPSLLIGRHA-HAIPGMDAAESERFLE
231

 Q G+ T P+ +PLV+ HP TGR SL + H I GM + L+
Sbjct: 184 ARQDKGTY-----TELPPVEQPLVRRHPVTGRRSLFLSPHTMDGIVGMPNDKGFALLD
236

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWH 278

 L A V+ H W DV++WDNRC +H P+D R + H
Sbjct: 237 DLT KHATHERFVYRHSWHQDDVIMWDNRCTMHAVMPYDSANQRRIMH 283

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

Score = 148 bits (374), Expect = 7e-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 QKAVLVFRGQPLDQDQQIAFARNFGQLEGGFIKVNQRPSRFKYAELADISNVSVDGKVRE 98

Query: 90 HSPA EWDDMMKVIVGNMA---WHADSTYMPVMAQGA VFSAEVVPAVGGRTCFADMRAAYD
146

 E +VGN A WH+DS++ A+ ++ SA V+P GG T F DMRAAYD
Sbjct: 99 RDARE-----VVGNFANQLWHS DSSFQQPAARYSMLS AIVLPPSGGDTEFCDMRAAYD
151

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR-PLVKVHPETG
205

 L E + + A H + S+ LG + S P+ PLV+ H +G
Sbjct: 152 DLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWPLVRTHAGSG
205

Query: 206 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA
265

 R L IG HA I G AE L L++ A Q V+ H W GD+V+WDNRC+LHR
Sbjct: 206 RKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFFVYRHSWKVGDLMWDNRCVLRH
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]

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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 = 8e-34, 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 DQQI FA+ FG +E R ++ ISNV DG V +
Sbjct: 39 QKAVLVFRGQPLDQDQQIAFARNFGQLEGGFIKVNQRPSRFKYAELADISNVSVDGKVAE 98

```

```

Query: 90 HSPA EWDDMMKVIVGNMA---WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYD
146

```

```

          E +VGN A WH+DS++ A+ ++ SA V+P GG T F DMRAAYD
Sbjct: 99 RDARE-----VVGNFANQLWHS DSSFQOPAARYSMLS AIVLPPSGGDTEFCDMRAAYD
151

```

```

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR-PLVKVHPETG
205

```

```

          L E + + A H ++S+ LG + + S P+ PL++ H +G
Sbjct: 152 DLPEDFKKELQGLRAEHYALHSR FILGDTEYSES-----QRNAMPPVSWPLIRTHAGSG
205

```

```

Query: 206 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA
265

```

```

          R L IG HA I G AE L L++ A Q V+ H W GD+V+WDNRC+LHR
Sbjct: 206 RKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQPKFVYRHSWKVGD LVMWDNRCV LHRG
265

```

```

Query: 266 EPWDFKLPRVMWHSRLAGR 284

```

```

          +D R + + GR
Sbjct: 266 RRYDVTARRELRRATTLGR 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 QKAVLVFRGQPLDQDQQIAFARNFGQLEGGFIKVNQRPSRFKYAELADISNVSVGKV-- 96

Query: 90 HSPAEWDDMMKVIVGNMA---WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYD
 146

AE D + +VGN A WH+DS++ A+ ++ SA V+P GG T F DMRAAYD
 Sbjct: 97 ---AEAD--AREVVGNFANQLWHS DSS FQQAARYSMLS AIVLPPSGGDTEFCDMRAAYD
 151

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR-PLVKVHPETG
 205

L E + + A H ++S+ LG + + S P+ PL++ H +G
 Sbjct: 152 DLPEDFKKELQGLRAEHYALHSR FILGDTEYSES-----QRNAMPPVSWPLIRTHAGSG
 205

Query: 206 RPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA
 265

R L IG HA I G AE L L++ A Q V+ H W GD+V+WDNRC+LHR
 Sbjct: 206 RKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQPKFVYRHSWKVGD LVMWDNRCV LHRG
 265

Query: 266 EPWDFKLPRVMWHSRLAGR 284

+D R + + GR
 Sbjct: 266 RRYDVTARRELRRATTLGR 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 DQQI FA+ FG +E R ++ ISNV DG V Q
Sbjct: 39 EKSVLVFRGQPLSQDQQIAFARNFGPLEGGFIKVNQRPSRFKYAELADISNVSLDGKVAQ 98

Query: 90 HSPA EWDDMMKVIVGNMA---WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYD
146
E +VGN A WH+DS++ A+ ++ SA VVP GG T F DMRAAYD
Sbjct: 99 RDARE-----VVGNFANQLWHS DSSFQQPAARYSMLS AVVPPSGGDTEFCDMRAAYD
151

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR-PLVKVHPETG
205
AL ++ + A H + S+ LG + + P+ PLV+ H +G
Sbjct: 152 ALPRDLQSELEGLRAEHYALNSRFL LGD TDYSEA-----QRNAMPPVNWPLVRTHAGSG
205

Query: 206 RPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA
265
R L IG HA + G+ AE L L++ A Q V+ H+W GD+V+WDNRC+LHR
Sbjct: 206 RKFLFIGAHASHVEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGD LVMWDNRCVLRHG
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 = 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 DQQI FA+ FG +E R ++ ISNV DG V Q
Sbjct: 39 EKSVLVFRGQPLSQDQQIAFARNFGPLEGGFIKVNQRPSRFKYAELADISNVSLDGKVAQ 98

Query: 90 HSPA EWDDMMKVIVGNMA---WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYD
146
E +VGN A WH+DS++ A+ ++ SA VVP GG T F DMRAAYD
Sbjct: 99 RDARE-----VVGNFANQLWHS DSSFQQPAARYSMLS AVVPPSGGDTEFCDMRAAYD
151

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR-PLVKVHPETG
205
AL ++ + A H + S+ LG + + P+ PLV+ H +G
Sbjct: 152 ALPRDLQSELEGLRAEHYALNSRFL LGD TDYSEA-----QRNAMPPVNWPLVRTHAGSG
205

gb|ACF35484.1| TfdA [Pseudomonas sp. TFD50]
Length = 287

Score = 145 bits (366), Expect = 6e-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 DQOI FA+ FG +E R ++ ISNV DG V +
Sbjct: 39 QKAVLVFRGQPLDQDQQIAFARNFGQLEGGFIKVNQRPSRFKYAELADISNVSVDGKVAE 98

Query: 90 HSPAEDDMMKVIVGNMA---WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYD
146

E +VGN A WH+DS++ A+ ++ SA V+P GG T F DMRAAYD
Sbjct: 99 RDARE-----VVGNFANQLWHS DSSFQQPAARYSMLS AIVLPPSGGDTEFCDMRAAYD
151

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVHPETG
205

L E + + A H + S+ LG + S P+ PLV+ H +G
Sbjct: 152 DLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWPLVRTHAGSG
205

Query: 206 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA
265

R L IG HA I G AE L L++ A Q V+ H W GD+V+WDNRC+LHR
Sbjct: 206 RKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFFVYRHSWKVGDLMWDNRCVLRHG
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 = 1e-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 SRTTARFQPLSATMGADTSDIDVSHADAVPMDDVLA AFRQHLLLSFRGQTLTDEQIYNFA 66

Query: 62 KRFGAIE----RIGGGDIVA----ISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADST
113

+FG +E R G ++A I+N+ ADG P+ D+ + N WH+D +
Sbjct: 67 AKFGPVEQNKRRYADGTVMASVHGITNLDADG-----KPSSRPDVRE----NYYWHS DKS
117

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
173

+ V A + +P GG T FADM AY AL T+ + HS Y + +
 Sbjct: 118 HQEVPALTTMLYGVEIPPAGGETEFADMTRAYAALPPETKRRIDDLKVEHSWGYMRETV-
 176

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL
 233

AG A + + PLV++HP+TG SL +G + + GMD +E L+ +
 Sbjct: 177 ----AGLAPTEEEKLKSPVVIHPLVRIHPDTGAKSLYVGMYSRVIGMDVSEGRELLKEM
 232

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 +D A + + ++W GD+V+WDNRCL+HRA

Sbjct: 233 IDHATRPEFLFRYKWRQGDLVMWDNRCLVHRA 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 = 6e-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--DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY
 114

FG IE R G ++ +SNV+ DGT + E D + N WH+DST+
 Sbjct: 62 LFGPIEDRKADERKPGEAFFVPEVSNVQKDGT----TSGEMDLHTLNLKSNFLWHSdstf
 117

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
 174

+P A + VV GG T A RAA+ A+ E ++ + R H +S+ K+
 Sbjct: 118 LPTPALTNILIGRVVTTTEGGATELASTRAAWAAMPEELKSRIRGRGIWHRYSHSRRKIS-
 176

Query: 175 VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
 234

+ A D + + P +P GR L I HA + G D AES+ L+ L+
 Sbjct: 177 PELAKLPMFNKWPdqHWSAVWP----NPVNGREGLYIASHAFKVDGYDEAESQELLDELm
 232

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 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 TIQIKPLTGSVAAAVTGVDLNQP LDDASFEILHRAFLEHGVLVFRGQQLQPAAQVAFARR 62

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

+G + + G ++ G A+ + K AWH+DS Y V + ++
Sbjct: 63 WG--KPVQGNPLLK-----GLTEFPPELAQVTRIPKETASTEAWHSDSIYTEVPPKISI
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 SRRPFVEVRPLHPALGAEIAGITL EEA VGEAVFAE IYDVFLERGLILFHDVDLPPATQVAF 72

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHAD
111

A+RFG ++ +I ++N+ ADG P DM G M WH D

Sbjct: 73 ARRFGEVQVHVMNQYHGYADHPEIYRLANLDADGNPNKGHP-----DM-----GTMYWHTD
123

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSK
171

++ P + +E+VP+ GG T FADM AY++L + + A H+L +S+++
Sbjct: 124 GSWRPTTGHATMMYSEMVPSEGGETHFADMYGAYESLSPQWKERLGLKAFHNLDLFSRTR
183

Query: 172 LGHVQQAGSAYIGYGMTTATPL-RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFL
230

+ G + P+ P+V+ HPETGR SL +G HA I GMD AE +
Sbjct: 184 -----RHGHDPMTTEEQKAKVPPVAHPVVRTHPETGRKSLFLGDHAEWIDGMDYAEGRALI
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 = 2e-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+FPGQ L+ +Q I FAK

Sbjct: 3 ISIYPITQNFAAEVGDVDLSKPLSADDS--EAIKEAFWRYAVLVFPGQSLTPEQHIAFAK 60

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVI-----VGNM
106

FG +E G + S D T + HS +E D+ + +GN
Sbjct: 61 EFGPLE---GENPTIASYRNRDVTTKSHS-SELADVSNLSPKNEVWTSRARMFHLGNQ
116

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLV
166

WH DS++ V A+ ++ A + +GG T FAD RAAVDAL EA + + A HS+
Sbjct: 117 LWHTDSSFHHVPARASLLYAREIAPIGGHTEFADERAAVDALPEAMKRRIEGLIAEHSIF
176

Query: 167 YSQSKLGHVQQAGSAYIGYGMTTATP--LRPLVKVHPETGRPSLLIGRHAHAIPGMDAA
224

+S++K+G+ + A P L LV+ PE+ R SL + H I + A
Sbjct: 177 HSRKIGYTDFFEE-----ERRALPPALHVLVRTIPESHRRSLYLAHITRIVEISDA
229

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD 269

ES+ L+ L + A Q V+ H+W D+V+WDNRC +HR + +D
 Sbjct: 230 ESQSLLEDELTEHATQRQFVYTHRWRQHDLVMWDNRC TMHRGKDFD 274

>ref|ZP_02186680.1| hypothetical protein BAL199_17688 [alpha
 proteobacterium BAL199]
 gb|EDP66917.1| hypothetical protein BAL199_17688 [alpha proteobacterium
 BAL199]

Length = 290

Score = 139 bits (351), Expect = 3e-31, Method: Compositional matrix
 adjust.

Identities = 93/272 (34%), Positives = 142/272 (52%), Gaps = 20/272 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 +QITP + VTG+ L T DDA FA + A+ + ++L+F Q +S++ QI F++RF
 Sbjct: 2 IQITPLHPLFASEVTGLDLVTGPDDATFAQIEDAFRRRSVLFVREQAISDEIQIRFSQRF 61

Query: 65 GAIE--RIG----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
 118

G +E ++G G +V +SN+ +G Q P M+ N WH DS++ P
 Sbjct: 62 GPLETTKVGVTNGAGSHLVLSNIGPEG---QIVPPTSRQMLNN-RANQFWHTDSSFKPNP
 117

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
 178

A+ ++ SA +P GG T + MRA Y AL E R V R A H +S+S++
 Sbjct: 118 ARASMLSARAIPLTGGDTQYCCMRVY TALPERLRDAVEGRVAIH DYTHSR SRI-----
 171

Query: 179 GSAYIGYGMDDTTATPLR-PLVKVH-PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW
 236

+ P+R +V H PE GR SL +G HA + GM ++ L+ +
 Sbjct: 172 DPELVTVEERKAVPPVRQAMVLDHGPELGR-SLYLGAAHA AKVEGMSDDAGRSLIDELMAF
 230

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRAEPW 268

A + V+ HQW D+++WDNR +LHRA P+
 Sbjct: 231 ATRDRFVYTHQWRPFDLILWDNR AVLHRATPF 262

>ref|YP_001354176.1| taurine dioxygenase [Janthinobacterium sp. Marseille]
 gb|ABR88626.1| taurine dioxygenase [Janthinobacterium sp. Marseille]

Length = 297

Score = 139 bits (349), Expect = 5e-31, Method: Compositional matrix
 adjust.

Identities = 90/271 (33%), Positives = 134/271 (49%), Gaps = 21/271 (7%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
 T I A LGA + G+ L LDDA F+ +H A L H LL+F Q ++ QQI F++R
 Sbjct: 16 TFTIQFLDAPLGAELIGLDLTRPLDDADFSRVHQAHLDHLLVFRDQQITPAQQIDFSRR 75

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM
115

FGA++ G +I+ ISN+K +G P D WH+D +Y+
Sbjct: 76 FGALQIHVLHQFQLPGHPEILIISNIKENG-----QPIGLGD-----AGHFVHSDLSYV
124

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV
175

+ + G++ A+ +PA GG T FA+M A+D LD R V A HS + ++L
Sbjct: 125 DIPSLGSMHLHAQELPAEGGDTLFANMHLAWDTLDVHLRNKVANLKAESYLAQYAE LQRR
184

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLV
234

+ L+P+V+ HPETGR +L + H I G+ ES L L
Sbjct: 185 NPWRPNLSEEQIAKVKPVLQPVVVTHPETGRKALFVSEHFTTRIDGLPEDES RDLLNQLF
244

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ + + V+ H+W D++ WDNR L+H A
Sbjct: 245 EHSVKPEHVYRHRWQPHDLIFWDNRSLMHLA 275

>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-ALHAAWLQHALLIFPGQHLSNDQQITF 60

+L++ P A V +G+ L + A A+ AA ++A+L+F GQ L+ DQQ+ F
Sbjct: 14 SLEVVPIAARADDFVGLASGIDLTSPVSERLACAIDAAMNRYAVLVFRGQPLTQDQQ LAF 73

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA--
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 LWHS DSSFQQPAARYSMLHAVVVPESGGETE FADMRAAWDALDPREQRELEGLEAEHYAL
186

Query: 167 YSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGRHHAHAIPGMDAAE
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 GRVLLMDLLEHATARRRFVYSHRWLPGLVIWDNRCTLHRGRRHDLSVRREL 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 SDITVRPLGYAAGAAVSGIDLRQALQPEQLARLRAAWHEHLVLFPGQDLNAPQLIDFTR 61

Query: 63 RFGAIERIGG-----GDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADST
113

FG +ER +++ ++N DG P++ + + WH+D +
Sbjct: 62 HFGDVERNDSVPYYRDPDYPEVLLVTNKPRDG-----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 YTDRPAKGSVLMCKEKPVGDMTFANMYQAYESLSAPFKRFVDGLHAVHDISLIKGFDR
170

Query: 172 LGHVQQAGSAYIGYGMDDTATPL-RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFL
230

Q A + P+ P+V++HPETGR L + GM ES L
Sbjct: 171 RDPEQTAA-----LKRRNPPIAHPVVRIPHETGRKCLFVSDRVRTFVGMTEEEESRPIL
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 = 5e-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 MDIRKVTANIGADVHGVVLSQPLDKGVVAELRAALLEHLVLFVRGQRKLSVEEHVRFGRY 60

Query: 64 FGAIE----RIGGG---DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
116

FG I+ R +++ + G G +WHAD+TYMP
Sbjct: 61 FGDIDPPLFRTASSPAPEVIVLDQKNPKGE-----GADSWHADNTYMP
103

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ
176

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

Query: 177 QAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGM DAAESERFLEGLVD
235

A + +D L P+V VHPETGR L + + AI GM AES+ L L D
Sbjct: 164 ---GASLRDKVDQWPPVLHPVVAVHPETGRRLN NVNANWTVAIDGMSRAESDALLRLLYD
220

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWH-----SRLAGRPETEG
289

++P +W GDV WDNR + H A D++ R+M +R+ G P+ E
Sbjct: 221 -HVRSP EFQVRLRWNTGDVAFWDNRSVQHYAVA-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 = 6e-30, Method: Compositional matrix adjust.

Identities = 83/219 (37%), Positives = 111/219 (50%), Gaps = 23/219 (10%)

Query: 56 QQITFAKRFGAIERIGGGDIVA-----ISNVKADGTVRQHSPA EWDDMMKVI-
102

QQI FA FG E GG+I +SN+ DG P D +
Sbjct: 1 QQIAFALNFGERENARGGNITKKEDYRLTTGLNDVSNL GKD G-----KPLPRDSRAHLFN 55

Query: 103 VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSAR
162

+GN WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A +

Sbjct: 56 LGNCLWHSDDSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAYDALDDDTKAEIDDLICE
115

Query: 163 HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMD
222

HSL+YS+ LG + Y L+ LV+ HP R SL + HA AI GM
Sbjct: 116 HSLMYSRGSLSGLFD-----YTDEEKAMFKPVLQRLVVRTHPVHRRKSLYLSSHAGAIQGMT
170

Query: 223 AAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

E+ L L + A Q V+ H+W D+V+WDNRC+
Sbjct: 171 MPEARLLLLRDLTEHATQPEFVYVHKWTLHDLVMWDNRV 209

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

Score = 135 bits (339), Expect = 6e-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+

Sbjct: 2 TIEIKPLTGSV GASVTGVNLNDPINDATFKVLHQAFLEHGVLVFRGQFLKPAAQVAFARL 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVI-----VGNMAWHADSTYMPV
117

+G G AE+ ++ +V AWH+DS Y PV
Sbjct: 62 WGT-----PVQGNPLLKGLAEFPELFQVTKIPKETASTEAWHSDSIYTPV
106

Query: 118 MAQGA VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
177

+ ++ S +P VGG T + + +Y+ L A + L+ AR +S +L +
Sbjct: 107 PPKISILSGVTIP-VGGDTMWCNQYLSYERLSPAMQRLIEGLRAR----FSGGRLAKMT-
160

Query: 178 AGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR--HAHAIPGMDAAESERFLEGLVD
235

G D + + P+V+ HPETGR +L +G A I GM AES L+ L +
Sbjct: 161 -----GSDKVPSAVHPIVVRTHPETGRKALYVGHDPDQAQCIEGMTEAESRPLLDFLYE
212

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ V+ H W GDV++WDNRC +H A
Sbjct: 213 HSTTPDNVYRHMWQEGDVLMDNRCTMHYA 242

>gb|ADC34036.1| TfdA-like protein [uncultured bacterium]
Length = 210

Score = 135 bits (339), Expect = 7e-30, Method: Compositional matrix
adjust.

Identities = 84/221 (38%), Positives = 115/221 (52%), Gaps = 26/221 (11%)

Query: 56 QQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKV
101
 QQI FA+ FG +E R+G G + +SN+ DG + W K+
Sbjct: 1 QQIAFARNFGELNYNTSGTVRKREDNRLGPG-MADLSNLT KDGIISADDRVW--FFKL 57

Query: 102 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSA
161
 G+ WH+DS++ PV A+ ++ S VP GG T FADMRAAYDALD+ T+A V
Sbjct: 58 --GDRLWHS DSSFRPVPKYSLLSGRTVPGWGGNTEFADMRAAYDALDDRTKA EVAGLVC
115

Query: 162 RHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPG
220
 HSL+YS+ +G + + P+R PLV+V TGR SL + HA I G
Sbjct: 116 EHSLLYSRQAVGFSEFTAEEISNF-----QPVRHPLVRVQKATGRKSLYLSAHAGVIVG
169

Query: 221 MDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
 ES FL L + A + V++H W D+VVWDNRC+
Sbjct: 170 WSVPE SRAFLRDLTEHATRPEFVYSHSWRLHDLVVWDNRCV 210

>ref|YP_001413770.1| taurine dioxygenase [Parvibaculum lavamentivorans DS-1]
gb|ABS64113.1| Taurine dioxygenase [Parvibaculum lavamentivorans DS-1]
Length = 285

Score = 134 bits (336), Expect = 2e-29, Method: Compositional matrix adjust.

Identities = 93/296 (31%), Positives = 142/296 (47%), Gaps = 30/296 (10%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+++ PTGA LGA V G+ L+ L F A+ AW H +L+F GQ +S+D I F++ F
Sbjct: 3 IEVIPTGAALGAEVRGLDLSKPLSADDFEAVQQAWYDHIVLLFRGQKISDDDLIRFSQHF 62

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGN-----MAWHADST
113
 G + DI S G + P W ++ ++ N WH D +
Sbjct: 63 GEL-----DIAPASATDMAGGQEKSRPEIW--IISNVIENGKPIGALGDKEAEWHTDMS
114

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLG
173
 Y+ +V + +P+ GG T FA+M A + L RA + R H S + +G
Sbjct: 115 YVAQPPMASVLYSLEIPSAGGDTSFANMYKALEELPADLRAAIETRMVNHDA--STTSVG
172

Query: 174 HVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEG
232
 ++ A + + T P ++ HP TG +L +GR + I G ESE+ L+
Sbjct: 173 ELRAGADAVLD--VRTAPGAKHPAIRTHPATGGKALYLGRRNLNGYIEGCSVEESEKLLDR
230

Query: 233 LVDWA-CQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
 L WA C P H+WA GD++VWDNR +HR +D + RVM +++ G RP
 Sbjct: 231 L--WAHCAKPEFSWTHKWAVGDLLVWDNRSAIHRRASFDGRERRVMHRTQIKGDRP 284

>ref|YP_586272.1| taurine catabolism dioxygenase TauD/TfdA [Ralstonia metallidurans

CH34]

gb|ABF11003.1| taurine dioxygenase (TauD/TfdA family) [Cupriavidus metallidurans

CH34]

gb|EEF10497.1| predicted protein [Populus trichocarpa]

Length = 308

Score = 133 bits (335), Expect = 2e-29, Method: Compositional matrix adjust.

Identities = 92/288 (31%), Positives = 139/288 (48%), Gaps = 21/288 (7%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 +I P GA LGA V GV L L F +H A L H +L+F Q ++ QQI F++RF
 Sbjct: 28 FEIRPLGAALGAEVIGVDLGRPLSHGDFQRIHQAHLDHHVLFVFRDQRITPAQQIAFSRRF 87

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP
 116

G ++ G +++ +SNV +G P D WH+D +Y

Sbjct: 88 GPLQIHVLNQFQLPGHPEVLIVSNVIENG-----KPIGLGD-----AGHFWHSDLSYKE
 136

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
 176

+ G++ A +PA GG T FA+M A+++L EA + V +A H+ + ++L

Sbjct: 137 TPSLGSLHARELPAEGGDTLFANMHTAWESLPEALQRKVADLTAEHTYLARYAELQARS
 196

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD
 235

+ + P+V+ HPETGR +L + H I G+ AES L+ L

Sbjct: 197 PWRPNLTPEQIAQVKPVVHPVVRTHPETGRRALFVSEHFTTRIVGLPDAESRAILDDELFA
 256

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ + V+ HQW D+V WDNR LLH A +L RVM+ + + G

Sbjct: 257 HSVKPEHVYRHQWREHDLVFWDNRSLLHLAAGTPDQLRRVMYRTTIEG 304

>ref|NP_641182.1| taurine dioxygenase [Xanthomonas axonopodis pv. citri str. 306]

gb|AAM35718.1| taurine dioxygenase [Xanthomonas axonopodis pv. citri str. 306]

Length = 286

Score = 133 bits (335), Expect = 2e-29, Method: Compositional matrix adjust.

Identities = 86/275 (31%), Positives = 135/275 (49%), Gaps = 21/275 (7%)

Query: 1 MAQTTLQITPTGATLGATVTVGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
M ++++I P A LGA V G+ LA LD A FA +H A L H +L+F Q ++ QQ+
Sbjct: 1 MQTSSVRIVPFDAPLGAEVIGLDLAQPLDAATFARIHRAHLDDHVLVFRDQRITPAQQVE 60

Query: 60 FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHAD
111
F++RFG ++ G +++ +SN+K +G P D WH+D
Sbjct: 61 FSRRFGPLQIHVLRNFQLRGQPEVLVVSNIKENG-----EPIGLGD-----AGHYWHSD
109

Query: 112 STYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK
171
+Y + G++ A+ +P+ GG T FA+ A+ L E+ + V A HS + +
Sbjct: 110 LSYKQTPSLGSLHAQELPSEGGDTLFANQHLAWQTLPESLKRTVQDLRAEHSYLAKYEE
169

Query: 172 LGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL
230
L A + P+V+ HPETGR +L + H I G+ ES L
Sbjct: 170 LRARNPWRPALTPEQIAEVTVPVQHPVVRTHPETGRKALFVSEHFTTRIVGLPEDESRA
229

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ L + + QA V+ H+W D+V WDNR ++H A
Sbjct: 230 QTLFEHSTQAALVYRHRWQPHDMVFDNRSMVHMLA 264

>ref|YP_001773839.1| taurine catabolism dioxygenase TauD/TfdA
[Burkholderia cenocepacia
MC0-3]

gb|ACA95344.1| Taurine catabolism dioxygenase TauD/TfdA [Burkholderia
cenocepacia
MC0-3]
Length = 305

Score = 133 bits (334), Expect = 3e-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 SLEVPIDAARPDFVGLASGVDLTAPVSEPLACAIDAAMNRYAVLVFRAQPLTQDQQLAF 61

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

Query: 108 -WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
166
WH+DS++ A+ ++ A VVP GG T +ADMRAA+DALD + + A H +

Sbjct: 115 LWHS DSS FQQ PAARY SMLHAVVVPEWGGETEYADMRAAWDALDPREQCELDGFEEHAYL
174

Query: 167 YSQSKLGHVQAGSAYIGYGMDDTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAE
225

+S+ LG + + P+R PLV+ H +GR L IG HA + G AE
Sbjct: 175 HSRFLLGDDTDYSDA-----QRNALPPVRWPLVREHAGSGRRHLFIGAHATHVVGRTLAE
228

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
L L++ A V++H+W GD+V+WDNRC LHR D + R +

Sbjct: 229 GRVLLMDLLEHATARRFVYSHRWQPGDLVIWDNRCTLHRGRRHDL SVRREL 279

>ref|ZP_05728014.1| Taurine dioxygenase [Pantoea sp. At-9b]
gb|EEW03731.1| Taurine dioxygenase [Pantoea sp. At-9b]
Length = 284

Score = 133 bits (334), Expect = 3e-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-----RIGGGDIVAISNVKADGTVRQHS PAEWDDMMKIVIGNMAWHADSTYMP
116

G ++ ++ +SNVK DG + W+ WH+D +Y
Sbjct: 62 GELQVHVLSQYLTPPELYVLSNVKQDGKPIGNHKEGWN-----WHSDWSYYE
110

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ
176

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

Query: 177 QAGSAYIGYGMDDTATP--LRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGL
233

+ SA ATP + PLV+ H ETGRPSL +G+ I G+ ES L L
Sbjct: 171 EPLSA-----EQKAATPDVVHPLVRRHQETGRPSL FVGQDIVKEIVGLTPEESTALLARL
225

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPW-DFKLPRVMWHSRLAG--RPE 286
A + H+W A D+++WDNRC +H+A P+ D RVM + + G RP+

Sbjct: 226 NAHAISSETFTYRHKWQAHDLLIWDNRCTMHQATPYDDVAYRRVMHRATVKGSERPQ 281

>ref|YP_002800232.1| taurine catabolic dioxygenase protein [Azotobacter
vinelandii DJ]
gb|ACO79257.1| taurine catabolic dioxygenase protein [Azotobacter
vinelandii DJ]
Length = 273

Sbjct: 115 LWHS DSS FQQ PAARY SML HAVV VPEWGG ETEYADMRAAWDALDPREQLDGLAEAEHYAL
174

Query: 167 YSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAE
225

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

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276

L L++ A V++H+W GD+V+WDNRC LHR D + R +
Sbjct: 229 GRVLLMDLLEHATARRFVYSHRWRPGDLVIWDNRCTLHRGRRHDL SVRREL 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 = 4e-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 -VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSA
161

+GN+ WH+DS++ P A ++ A V+P VGG T F D R A+D L + T+A + A
Sbjct: 54 NLGNLLWHS DSSFKPTPAYWSMLQARVI PPVGGNTEFLDTRVAWDHLPQETKAEIKDLIA
113

Query: 162 RHSLVYSQSKLGHVQQAGSAYIGYGMD-TTATPLRPLVKVHPETGRPSLLIGRHAHAIPG
220

HSL+YS+++LG A+ + T P R LV++H E+GR ++ + H AI G
Sbjct: 114 YHSLIYSRAQLGF-----EAFSPPEEQERCTPVPQR-LVRLHQESGR LAVYLSAHIGAIEG
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 = 4e-29, Method: Compositional matrix
adjust.

Identities = 90/295 (30%), Positives = 140/295 (47%), Gaps = 27/295 (9%)

Query: 2 AQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60

Sbjct: 20 A + P +GA + G+ L L D FA + A L+H +++F Q ++ Q I F
 ADQDFDVRPLPGGIGAEIVGIDLGRPLGDGDFARVRRAHLEHHVVVFRDQRITPQQHIDF 79

Query: 61 AKRFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
 112

Sbjct: 80 ++RFG + G +I+ +SN+ DG P D K WH+D
 SRRFGKLMVHVLHQFHLPGHPEILIVSNIIEDG-----KPVGLGDAGKY-----WHSDI
 128

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKL
 172

Sbjct: 129 +Y P+ + G++ A+ +PA GG T FADM AYD L R + R A HS + +K
 SYKPLPSLGSLLHAQELPAEGGDTLFAFMHKAYDTLPAHLRQAIAGRRRAVHSYL---AKY
 185

Query: 173 GHVQQAGSAYIGYGMDDTA---TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESER
 228

Sbjct: 186 G +Q+ G+ D A + P+V+ HPETGR +L + I G+ ES +
 GQMQKEGNWRPNLSADQLAQVQEVVHPVVRTHPETGRKALFVSEGFTTRIEGLPEDESRQ
 245

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
 L+ L + + ++ H W D+V WDNR L+H A L R ++ + + G

Sbjct: 246 VLDELFAHSIRPEHIYRHAWRERDLVFDNRALIHLAGCPHLLRRKLYRTTIEG 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 = 5e-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 VRPLNDALGAEIVGIDLARALSVADFARVRRALDHHLVFRDQRITPRQHIDFSRRFRGR 88

Query: 67 I-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
 118

Sbjct: 89 + +I+ +SN+ +G +P D K WH+D +Y P+
 LMIHVLHQFHLAHNPEILVVSNIIVENG-----APVGLGDAGKY-----WHSDISYKPLP
 137

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQA
 178

Sbjct: 138 + G++ A+ +PA+GG T FA+M AY+ L A R V R A HS + +K G +Q+
 SLGSLHHAQELPAIGGDTLFANMHRAYETLPRALREAVDGRRRAVHSYL---AKYQLQKE
 194

Query: 179 GS---AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV
234

G+ + P+V+ HPETGR +L + I G+ A ES + L+ L
Sbjct: 195 GNWRPTLSAAQLAQVQEVVAHPVVRTHPETGRRALFVSEGFTTRIEGVAADESRQILDELF
254

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 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 = 6e-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 TIEIKPLTGSV GASVTGVNLNDPINDATFKVLHQAFLEHGMLVFRGQFLQPAAQVAFARL 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVI-----VGNMAWHADSTYMPV
117

+G G AE+ ++ +V AWH+DS Y V
Sbjct: 62 WGT-----PVQGNPLLKGLAEFPELFQVTKIPKETASTEAWHSDSIYTAV
106

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
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 -----GSDKVPSAVHPIVVRTHPETGRKALYVGHPTAECIEGMTEAESRPLLDFLYE
212

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 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 = 7e-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 SLNVEAAHPFIAARIHGLDLSKPLSDERIVEIEQASGQYPVLIFPRQYIDDDQLLAFAAG 61

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHAD
111

FG ++ R+ I ISN+ + + P + M + + WH+D
Sbjct: 62 FGPLQVAVSYSTRPEDHRLAPM-INDISNLSKENQT--YRPGDRRRMNNLT--SRRWHSD
116

Query: 112 STYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK
171

++Y+P+ A+ + + +VPAVGG+T FADMRAAYD L + R +V S + ++ S++
Sbjct: 117 ASYLPLPARYSFLLSYIVPAVGGQTQFADMRAAYDKLPDHLRKVVEGLSCHYDIMASRAA
176

Query: 172 LGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE
231

G + A + LV+ HP +GR SL + HA + G E L
Sbjct: 177 AGFYDASDEE-----RKALAPCIHELVRTHPISGRKSlyLSSHATHVVGWPEPEGRDLLR
231

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEP 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 = 9e-29, 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 SLEVPIDAARPDFVGLASGIDLTAPVSEPLACAIDAAMNRYAVLVFRAQPLTQDQQQLAF 73

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA--
107

A+ G ++ R+ ++ ISNV G + D + IVGN+A
Sbjct: 74 ARALGPLDVGFKRVARPHARLAYQELADISNVDESGQI-----ADRAHRRIVGNLANQ
126

Query: 108 -WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
166

WH+DS++ A+ ++ A VVP GG T +ADMRAA+DALD + + A H +

Sbjct: 127 LWHSDDSSFQQPAARYSMLHAVVVPEWGGETEYADMRAAWDALDPREQRELDGLEAEHYAL
186

Query: 167 YSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAE
225

+S+ LG + P+R PLV+ H +GR L IG HA + G AE
Sbjct: 187 HSRFLLGDTDYTDA-----QRNALPPVRWPLVREHAGSGRRHLFIGAHATHVVGRTLAE
240

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
L L++ A V++H+W GD+V+WDNRC LHR D + R +

Sbjct: 241 GRVLLMDLLEHATARRFVYSHRWRPGDLVIWDNRCTLHRGRRHDLSVRREL 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 = 9e-29, 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 ++ DQQI F++R

Sbjct: 14 SFEIRAFDAPLGAEVLGLDLGQPLGDDDFARIHRAHLDDHHVLFVREQRITPDQQIAFSRR 73

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
115

FG ++ G +++ +SN+ +G P D WH+D +Y
Sbjct: 74 FGPLQIHVLHQFGLSGYSEVLVVSNIIEENG-----KPIGLGD-----AGHYWHSDDL SYK
122

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV
175

+ G++ A+ +PA GG T FA+M A+D L R+ V RSA H+ + ++L
Sbjct: 123 DKPSLGSLLHAQELPAEGGDTL FANMHLAWDTLPSHLRS AVEGRSAEHTYLAKY AELQKR
182

Query: 176 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLV
234

+ + P+V+ HPETGR +L + H + G+ ES L+ L
Sbjct: 183 SPWRPNLSAEQIAQVRPVVHPIVIRTHPETGRKALFVSEHFTTRVIGLPEDES RALLDEL F
242

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ + ++ H+WAA D+V WDNR L+H A L R ++ + + G
Sbjct: 243 AHSVRPEHLYRHRWAAHDMVFWDNRSMLHLAAGTPDHLRRKLYRTTIEG 291

>ref|YP_002008624.1| taurine dioxygenase, 2-oxoglutarate-dependent
[Cupriavidus
taiwanensis]
emb|CAQ72572.1| taurine dioxygenase, 2-oxoglutarate-dependent
[Cupriavidus

taiwanensis]
Length = 309

Score = 131 bits (329), Expect = 9e-29, 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 NFEIRPLDAPLGAEVIGLDLSQPLSDADFARIHRAHLDYHVVVFRDQQITPAQQIGFSRR 87

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM
115
FG ++ G +++ +SNV +G P D WH+D +Y
Sbjct: 88 FGPLQIHVLHQFQLPGHPEVLVVSNNVENG-----KPIGLGD-----AGHFWHSDLSYK
136

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV
175
+ G++ A +PA GG T FA+M A+D L A + V A H+ + ++L
Sbjct: 137 EKPSLGSLLHARELPAEGGDTLFANMHLAWDTLPAALQRAVDGLQAEHTYLARYAELQQR
196

Query: 176 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLV
234
+ L+P+V+ HPETGR +L + H I G+ ES L+ L
Sbjct: 197 SPWRPNLTPEQVAQVRPVLQPVVVRTHPETGRKALFVSEHFTTRIVGLPEDESRLDLLDQLF
256

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ + ++ HQW D+V WDNR LLH A +L RVM+ + + G
Sbjct: 257 AHSVKPAHIYRHQWQPHDLVFDNRSLHLAAGCPPPELRRVMYRTTIEG 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 = 1e-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 TFEIRPFSGAVGAEIIGLDLTRPVNDEDFASIHRAHLDHVVVFRDQRITPQQQIDFSRR 76

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA--WHADST
113
FG ++ +I+ +SN+ +G + +G+ WH+D +

Sbjct: 77 FGVLQIHVLKQFLLANHPEILIVSNIVENG-----QNIGLGDAGKFWHSDLS
123

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
173

Y + + G++ A+ +P GG T FADM A+D+L +A R V RSA HS S+
Sbjct: 124 YKELPSLGSMLHAQELPPEGDTLFDAMHKAWDSLDPDALRKAVEGRSAAHSYTARYSETK
183

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG
232

+ A + P+V+ HPE GR +L + I G+ ES++ L+
Sbjct: 184 FEGNWRPTLTPEQLAQVAEVVHPVVRTHPENGRKALFVSEGFTTRIVGLPEDESKQLLDE
243

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + ++ HQW D+V WDNR L+H A L R ++ + + G

Sbjct: 244 LYAHSVLPQNIYRHQWQPHDLVFDNRSLIHLAAGCPAHLRRKLYRTTIQG 294

>ref|YP_257284.1| taurine catabolism dioxygenase TauD [Pseudomonas
fluorescens Pf-5]
gb|AA95549.1| taurine dioxygenase, TauD/TfdA family [Pseudomonas
fluorescens
Pf-5]
Length = 295

Score = 130 bits (328), Expect = 1e-28, Method: Compositional matrix
adjust.
Identities = 86/290 (29%), Positives = 139/290 (47%), Gaps = 25/290 (8%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+I P +GA + G+ L+ ++D FA +H A L H +++F Q +S +QQI F++RF

Sbjct: 15 FEIRPLNGAVGAEIVGLDLSRPVNDQDFARIHRAHLDDHHVVVFRDQRISPEQQIAFSRRF 74

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMA--WHADSTY
114

G ++ G +I+ +SN+ +G + +G+ WH+D +Y
Sbjct: 75 GVLQIHVLKQFLLAGHPEILIVSNIIENG-----QSIGLGDAGKFWHSDLSY
121

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
174

+ + G++ A+ +PA GG T FA+M A+D L EA R V RSA HS S+
Sbjct: 122 KELPSLGSMLHAQELPAEGDTLFDANMHQAWDNLPEALRKAVEGRSAAHSYTARYSETKF
181

Query: 175 VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL
233

+ A + P+V+ HPE GR +L + I G+ ES + L L
Sbjct: 182 EGNWRPTLTPEQLAQVAEVVHPVVRTHPENGRKALFVSEGFTTRIVGLPEDESAQLLAE
241

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ ++ HQW D+V WDNR L+H A L R ++ + + G
 Sbjct: 242 YAHSVLPDNIYRHQWQPHDLVFWDNRS LIHLAAGCPSHLRRKLYRTTIQG 291

>ref|YP_001666439.1| taurine dioxygenase [Pseudomonas putida GB-1]
 gb|ABY96103.1| Taurine dioxygenase [Pseudomonas putida GB-1]
 Length = 299

Score = 130 bits (328), Expect = 1e-28, Method: Compositional matrix
 adjust.

Identities = 89/293 (30%), Positives = 147/293 (50%), Gaps = 31/293 (10%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 +I P +GA + G+ LA ++ FA +H A L H +L+F Q +S QQITF++RF
 Sbjct: 19 FEIRPFSGAVGAEIIGLDLARPVNVEDFARIHRAHLDDHHVLVFRDQRISPQQQITFSRRF 78

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA--WHADSTY
 114

G ++ G +I+ +SN+ +G + +G+ WH+D +Y
 Sbjct: 79 GELQIHVLKQFLLTGHPEILIVSNIVENG-----QNIGLGDAGKFWHSDLSY
 125

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLV--YSQSKL
 172

+ + G++ A+ +P+ GG T FADM A+DA+ +A R +V RSA HS Y+++K
 Sbjct: 126 KALPSLGSMLHAQELPSEGGDTL FADMHKAWDAVPDALRKKVVEGRSAAHSYTARYAETKF
 185

Query: 173 -GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL
 230

G+ + +A + + P+V+ HPE GR +L + I G+ ES L
 Sbjct: 186 EGNWRPTLTA---EQLAQVQEV IHPVVRTHPENGRKALFVSEGFTTRIVGLPDDDES RDVL
 242

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ L + ++ HQW D+V WDNR L+H A L R ++ + + G
 Sbjct: 243 QQLYALSVLEKNIYRHQWQPHDLVFWDNRS LIHLATGCPAHLRRKLYRTTIQG 295

>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 FEVRPFNAPVGAEIVGLDISKPINDEDFARIHRAHLDDHHVLVFRNQQITPAEHIEFSRRF 66

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
 116

G +E +I+ +SN+K +G P D + WH+D +Y P

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
 + + ++ H+WA D+V WDNR L+H A L R ++ + + G
 Sbjct: 246 AHSVRPEHLYRHRWAEHDMVFWDNRSMLMHLAAGTPDHLRRKLYRTTIEG 294

>ref|ZP_06464322.1| taurine dioxygenase [Burkholderia sp. CCGE1003]
 gb|EFD38063.1| taurine dioxygenase [Burkholderia sp. CCGE1003]
 Length = 305

Score = 129 bits (323), Expect = 5e-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 IASQPIEIRPFDPVGAEVLRLDLSKPLNQDFARIHRAHLDHHVLVFRDQRITPDEQIA 79

Query: 60 FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHAD
 111
 F++RFG ++ G +++ +SN+ +G P D WH+D
 Sbjct: 80 FSRRFGPLQIHVLHQFQLPGYPEVLVVSNIIVENG-----KPIGLGD-----AGHYWHS
 128

Query: 112 STYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK
 171
 +Y + G++ A+ +PA GG T FA+M A+D L R+ V R+A H+ + +K
 Sbjct: 129 LSYKEKPSLGLLHAQELPAEGGDTLFANMHLAWDTLPAHLRSVEGRTAEHTYL---AK
 185

Query: 172 LGHVQQAGSAYIGYMDTTA--TPLR-PLVKVHPETGRPSLLIGRH-AHAIPGMDAAESE
 227
 +Q+ + A P++ P+V+ HPETGR +L + H + G+ ES+
 Sbjct: 186 YAELOKRSPWRPNLSPEQIAQVKPVQHPIVRTHPETGRKALFVSEHFTTRVIGLPEDESK
 245

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
 + L+ + + +A V+ H+WA D+V WDNR L+H A L R ++ + + G
 Sbjct: 246 QLLDEIFAHSVRAEHVYRHRWAEHDMVFWDNRSMLMHLAAGTPDHLRRKLYRTTIEG 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 = 6e-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 TFDIRPFPGAVGAEIVGLDLARPVNVEDFTRIHRALDHHVLFVFRDQRI SPEQQIAFSRR 77

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA--WHADST
113

FG ++ G +I+ +SN+ DG V +G+ WH+D +

Sbjct: 78 FGELQIHVLKQFLLAGHPEILIVSNIVEDGR-----NVGLGDAGKFWHSDLS
124

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSK
171

Y + + G++ A+ +P+ GG T FADM A+DA+ +A R +V R A HS Y+++K

Sbjct: 125 YKELPSLGSMLHAQELPSEGGDTL FADMHKAWDAVPDALRKVVEGRDAAHSYTARYAETK
184

Query: 172 L-GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGM DAAESERF
229

G+ + +A + + P+V+ HPE GR +L + I G+ ES

Sbjct: 185 FEGNWRPTLTA---EQLAQVQEVVHPVVRTHPENGRKALFVSEGFTTRIVGLPDDES RDV
241

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

L+ L + ++ HQW D+V WDNR L+H A L R ++ + + G

Sbjct: 242 LQQLYALS VLEQHIYRHQWQPNDLVFWDNRSLIHLAAGCPAHLRRKLYRTTIQG 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 = 8e-28, 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 TFEIRPFSGAVGAEIIGLDLAKPVNAEDFSLIHRALHLEHHVLFVLRDQRI SPEQQIAFSRR 77

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM
115

FG ++ G +I+ +SN+ +G H+ D WH+D +Y

Sbjct: 78 FGQLQIHVLKQFLLKGHPEILIVSNIIENG----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 ELPSLGSMLHAQELPSEGGDTL FADMHKAWDAVPQALRKQVEGRSAAHSYTARYAETKFE
186

Query: 173 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGM DAAESERFLE
231

G+ + SA + + P+V+ HPE GR +L + I G+ ES L+

Sbjct: 187 GNWRPTLSA---EQLAQVQEVVHPVVRTHPENGRKALFVSEGFTTRIVGLPDDES RDVLQ
243

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 TFEIRPLPGSVGAEIIGLDLTRAINDKDFARIHRAHLDDHHVVVFRDQRITPEQQIAFSRR 75

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA--WHADST
113

FG ++ +I+ +SN+ +G + +G+ WH+D +
Sbjct: 76 FGVLQIHVLKQFLLANHPEILIVSNIIENG-----QSIGLGDAGKFWHSDLS
122

Query: 114 YMPVMAQGA VFSAEV VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
173

Y + + G++ A+ +P+ GG T FADM A+D L E R V RSA HS S+
Sbjct: 123 YKELPSLGSMLHAQELPSEGGDTL FADMHKAWDQLPEHLR NAVEGRSAAHSYTARYSETK
182

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGM DAAESERFLEG
232

+ A + P+V+ HPE GR +L + I G+ ES L
Sbjct: 183 FEGNWRPTLTPEQLAQVAEVVHPIV RTHPENGRKALFVSEGFTTRIVGLPEDES RDLLAQ
242

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

L + ++ HQW D+V WDNR L+H A L R ++ + + G
Sbjct: 243 LYAHSVLPQNIYRHQWQPHDLV FWDNRSLIHLAAGCPSHLRRKLFRTTIQG 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 TKPKVTPLTGSIGASVEGIDL NKPVDDATFAALHDAFLTHCVLVYRGQQLQPAAQVEFAR 61

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

+G I +++++ + Q + + K AWH DS Y+PV + +
Sbjct: 62 CWGTPLNTNP----LIKHIESHPEIVQVT-----KIPKATASTEAWHYDSPYIPVPPKIS
112

Query: 123 VFSAEV VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY
182

+ SA VP GG T + + +YD L + + + + +LG + A +A
Sbjct: 113 ILSAVTVP H-GGDTMWCNQCLS YDRLSPTMKGALEGLRVK----FVGLRLGRMMGADAAS
167

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQ 89
 + A+L+F GQ L DQOI FA+ FG +E R ++ ISNV DG V
 Sbjct: 39 KKAVLVFRGQPLDQDQQIAFARNFGQLEGGFIKVNQRPSRFKYAELADISNVSVDGKV-- 96

Query: 90 HSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-YDAL
 148

+ E + + N WH+DS++ A+ ++ SA V+P +GG T F D+ A
 Sbjct: 97 -ADREARESVGNFANNQLWHS DSSFQAAARYSMLSASVLPPLGGDTEFWDIHATNLGGR
 155

Query: 149 DEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR-PLVKVHPETGRP
 207

D+ R L R+ R+ L S+ LG + S P+ PLV+ H +GR
 Sbjct: 156 DDLPRELQGLRAERY-LQNSRFILGDTDYSES-----QRNAMPPVSWPLVRTHAGSGRK
 208

Query: 208 SLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEP
 267

L IG HA I G AE L L++ A Q V+ H+W GD+V+WDNRC+LHR
 Sbjct: 209 FLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFFVYRHRWKVGDLMWDNRCVLRHGRG
 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 = 1e-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 MEIVASGPGFAAELRGVTIADVAASPDVYAQVRAAFEEHSVLIFRDQHVSDAQLAFSRR 60

Query: 64 FGAIE--RIG----GGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPV
 117

FG +E ++G G +V + + DG V P + ++ N WH DS++ V
 Sbjct: 61 FGPLEVTKVAVGRGSHLVVLKTLDDDDGNV---VPTDHRLELEN-KANQLWHTDSSFKR
 116

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQ
 177

A +V S+ +VP GG T + R A++ LD R V A H YS+ K+
 Sbjct: 117 PALASVLSSRIVPGRGGETEYVSTRIAFERLDPGLRERVENSFAWHEYAYSRGKI-----
 171

Query: 178 AGSAYIGYGMDDTTATPLR--PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
235

+ + + A P + LV +P GR +L + HA+ I GM+ A + L L +
Sbjct: 172 --APDLARPEERAALPPQCWRLVWRNPVNGRKALYLASHAYGIEGMEPAAARELLAALTE
229

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLA 282

A + H W AGDVV+WDNR +HR PW PR M S +A
Sbjct: 230 AATAPGASYLHWSWRAGDVMMWDNRATMHRGRPWPAHQPRYMVRSTIA 276

>ref|ZP_03397512.1| dioxygenase, TauD/TfdA family [Pseudomonas syringae
pv. tomato T1]

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 ASQSFQVDPFTGKVGAEIVGLDLRPLNDADFAFVHRAHLDHHVVVFRDQQITPQQQIDF 73

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
112

++RFG ++ +I+ +SN+ V P D K WH+D
Sbjct: 74 SRRFGVLQIHVLKQFLLANHPEILIVSNI-----VENEKPVGLGDAGKY-----WHS DL
122

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
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 -----GHNAVNWRPTLTAEQLAQVVEVSHPIVIRTHPENGRKALFVSEGFTTH-ILGLPE
234

Query: 224 AESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

ES + L L + + ++ HQW A D+V WDNR L+H A
Sbjct: 235 DESRQILGELYAHSVRPEHIYRHQWQANDMVFWDNRS 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.

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKL
172

+Y + G++ A+ +PA GG T FA+M A+D L EA R V R A H+ + ++L
Sbjct: 116 SYKRRPSLGSLLHAQELPAEGGDTLFANMHLAWDTLPEALRRAVEGRRAEHTYLARYAEL
175

Query: 173 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE
231

+ + P+V+ HPETGR +L + H I G+ ES L+
Sbjct: 176 QARSPWRPNLSAEQIAQVEPVVHPVVRTHPETGRRALFVSEHFTTRIVGLPDDESRRALLD
235

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + +A + H+W D+V WDNR LLH A L R ++ + + G

Sbjct: 236 ELFAHSVRAEHQYRHRWRDHDLVFWDNRSLHLAAGTPDHLRRKLYRTTIEG 287

>ref|ZP_06485157.1| taurine dioxygenase [*Xanthomonas campestris* pv.
vasculorum

NCPB702]
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 LQSSSVRIVPFDGPLGAEVIGLDLSQPLDADTFARIHRAHLDDHHVLVFRDQRITPAQQVE 79

Query: 60 FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHAD
111

F++RFG ++ G +++ +SN+K +G P D WH+D
Sbjct: 80 FSRRFGPLQIHVLRNFQLRGHPEVLVVSNIKENG-----EPIGLGD-----AGHYWHSD
128

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSK
171

+Y + G++ A+ +P+ GG T FA+ A+ L E+ + V A HS + +
Sbjct: 129 LSYKETPSLGSLLHAQELPSEGGDTLFANQHLAWQTLPESLKRTVQDLRAEHSYLAKYEE
188

Query: 172 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL
230

L A + + P+V+ HPETGR +L + H I G+ ES L
Sbjct: 189 LRARNPWRPALMPEQIAEVTVPVQHPVVRTHPETGRKALFVSEHFTTRIVGLPKDESRRALL
248

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ L + + +A V+ H+W D+V WDNR ++H A
Sbjct: 249 QTLFEHSTRAALVYRHRWQPHDMVFDNRSMVHLA 283

>ref|YP_555428.1| taurine dioxygenase [*Burkholderia xenovorans* LB400]

gb|ABE36078.1| Taurine dioxygenase [Burkholderia xenovorans LB400]
Length = 302

Score = 126 bits (317), Expect = 2e-27, Method: Compositional matrix adjust.

Identities = 84/288 (29%), Positives = 138/288 (47%), Gaps = 21/288 (7%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++I +GA V G+ L L FA +H A L H +L+F Q ++ DQQ+ F++RF
Sbjct: 22 IEIRAFDGPVGAIEVFGGLDLGQPLSPEDFARIHRAHLDHHVLFVFRDQRITPDQQVAFSRRF 81

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP
116
G ++ G +++ +SN+ DG P D WH+D +Y
Sbjct: 82 GPLQIHVLHQFQLPGYPEVLVVSNIWEDG-----KPIGLGD-----AGHYWHS DLSYKE
130

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
176
+ G++ A+ +PA GG T FA+M A+D L R V RSA H+ + ++L
Sbjct: 131 KPSLGSLLHAQELPAEGGDTLAFANMHLAWDTLPAHLRTAVEGRSAEHTYLAKYAELQKRS
190

Query: 177 QAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD
235
+ + + P+V+ HPETGR +L + H + G+ ES+ L+ L
Sbjct: 191 PWRPNLSAEQIASVKPVVHPIVRTHPETGRKALFVSEHFTTRVIGLPEDESQTLLDELFA
250

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ + ++ H+WA D+V WDNR L+H A L R ++ + + G
Sbjct: 251 HSVRPEHLRHRWAEHDMVFWDNRSLMHLAAGTPDHLRRKLYRTTIEG 298

>ref|YP_001941299.1| taurine dioxygenase [Burkholderia multivorans ATCC
17616]

dbj|BAG47309.1| taurine dioxygenase [Burkholderia multivorans ATCC 17616]
Length = 309

Score = 126 bits (317), 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: 25 APQRFEIVPFDAPLGAIEVVGIDLSQPLDADAFARIRRAHLDHHVLFVFRDQRITPDEHVAF 84

Query: 61 AKRFGAIER-----IGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS
112
++RFG ++ G +++ +SN+ +G P D WH+D
Sbjct: 85 SRRFGPLQTHVLHQFALPGHPEVLIVSNIVENG-----KPIGLGD-----AGYFWHSDL
133

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKL
172

+Y + G++ A+ +PA GG T FA+M A+D L EA R V R A H+ + ++L
Sbjct: 134 SYKRRPSLGSLLHAQELPAEGGDTLFANMHLAWDTLPEALRRAVEGRRAEHTYLARYAEL
193

Query: 173 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE
231

+ + P+V+ HPETGR +L + H I G+ ES L+
Sbjct: 194 QARSPWRPNLSAEQIAQVEPVVHPVVRTHPETGRRALFVSEHFTTRIVGLPDDESRRALLD
253

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

L + +A + H+W D+V WDNR LLH A L R ++ + + G
Sbjct: 254 ELFAHSVRAEHQYRHRWRDHLVFDNRSLHLAAGTPDHLRRKLYRTTIEG 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 LQSSSVRIVPFDGPLGAEVIGLDLSQPLDADTFARIHRAHLDDHHVLVFRDQRITPAQQME 79

Query: 60 FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHAD
111

F++RFG ++ G +++ +SN+K +G P D WH+D
Sbjct: 80 FSRRFGPLQIHVLRNFQLRGHPEVLVVSNIKENG-----EPIGLGD-----AGHYWHSD
128

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSK
171

+Y + G++ A+ +P+ GG T FA+ A+ L E+ + V A HS + +
Sbjct: 129 LSYKETPSLGSLLHAQELPSEGGDTLFANQHLAWQTLPESLKRTVQDLRAEHSYLAKYEE
188

Query: 172 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL
230

L A + + P+V+ HPETGR +L + H I G+ ES L
Sbjct: 189 LRARNPWRPALMPEQIAEVTVPVQHPVVRTHPETGRKALFVSEHFTTRIVGLPKDESRRALL
248

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ L + + +A V+ H+W D+V WDNR ++H A
Sbjct: 249 QTLFEHSTRAALVYRHRWQPHDMVFDNRSMVHLA 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 = 3e-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 MEIVASGPGFAAELRGVTIADVAASPDVYAQVRAAFEEHSVLVFRDQHVSDEAQLAFSRR 60

Query: 64 FG--AIERIG----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
 117

FG + ++G G +V + + DG V PA+ ++ N WH DS++ V
 Sbjct: 61 FGPLGVTKVGAVGHGSHLVVLKTLDDDGNV---VPADHRLALEN-KANQLWHTDSSFKR
 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 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLA 282

A + H W AGDVV+WDNR +HR PW PR M S +A
 Sbjct: 230 AATAPGASYLHSWRAGDVVMWDNRATMHRGRPWPAHQPRCMVRSTIA 276

>ref|ZP_04948709.1| Probable taurine catabolism dioxygenase [Burkholderia dolosa

AUO158]

gb|EAY71880.1| Probable taurine catabolism dioxygenase [Burkholderia dolosa

AUO158]

Length = 310

Score = 126 bits (316), Expect = 3e-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 AAQSFDIVPFDAPLGAEVVGIDLSRPLADADFACIHRALDHHVLVFRDQRITPDEHVAF 85

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
112

++RFG ++ G +++ +SN+ +G P D WH+D
Sbjct: 86 SRRFGPLQIHVLHQFALAGHPEVLIVSNIVENG-----KPIGLGD-----AGHFWHSDL
134

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
172

+Y + G++ A+ +PA GG T FA+M A+D L R V R A H+ + ++L
Sbjct: 135 SYKEKPSLGSLLHAQELPAEGGDTLFANMHLAWDTLPAHLRRAVEGRRAEHTYLARYAEL
194

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE
231

+ + P+V+ HPETGR +L + H I + ES L+
Sbjct: 195 QARSPWRPNLSPEQIAQVKPVVHPVVRTHPETGRKALFVSEHFTTRIVDLPDDES RALLD
254

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDRNCLLHRAEPWDFKLPRVMWHSRLAG 283

L + +A ++ H+W D+V WDRN 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 = 3e-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 MEIVASGPGFAAELRGVTIADVAASPDVYAQVRAAFEESHVSVLFRDQHVSDAQLAFSRR 60

Query: 64 FGAIE--RIG----GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV
117

FG + ++G G +V + + DG V PA+ ++ N WH DS++ V
Sbjct: 61 FGPLRVTKVGA VGHGSHLVVLKTLDDDDGNV---VPADHRLALEN-KANQLWHTDSSFKRV
116

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
177

A +V S+ +VP GG T + R A++ LD R V A H YS+ K+
Sbjct: 117 PALASVLSSRIVPGRGGETEYVSTRIAFERLDPGLRERVENSFAWHEYAYSRGKI-----
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 AATAPGASYLHSWRAGDVVMWDNRATMHRGRPWPAHQPRCMVRSTIA 276

>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 = 3e-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 ADVPLQIRALDAAFGEVLGLDLGLPLAAEDFRRIHRAHLDHHLVLFREQRITPAQQIAF 70

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
 112

++RFG ++ G +I+ +SN+ +G P D K WH+D

Sbjct: 71 SRRFGELQIHVLKQFLLPGHPEILIVSNIVENG-----QPVGLGDAGKF-----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 SYKELPSLGSMLHAQELPEEGDTLFADMHKAWDSLPEALRKAIEGRRTAAHSYTARYSEP
 179

Query: 171 KL-GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESER
 228

+ G+ + SA + + P+V+ HPE+GR +L + I G+ A ES +

Sbjct: 180 RFEGNWRPTLSA---AQLAEVREVVHPIVIRTHPESGRKALFVSEGFTTRILGLPADESAQ
 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 = 3e-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 VFEVRPFSGAVGAEIIGLDLAKPVSAEDFTRIHRALDHHVLFVFRDQRISPEQQIAFSRR 77

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMA--WHADST
113

FG ++ G +I+ +SN+ +G + +G+ WH+D +

Sbjct: 78 FGELQIHVLKQFLLTGHPEILIVSNIIENG-----QNIGLGDAGKFWHSDLS
124

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSK
171

Y + + G++ A+ +P+ GG T FADM A+DA+ + R +V RSA HS Y+++K

Sbjct: 125 YKELPSLGSMLHAQELPSEGGDTLFADMHKAWDAVPDTLRKVVVEGRSAAHSYTARYAETK
184

Query: 172 L-GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDDAAESERF
229

G+ + +A + + P+V+ HPE GR +L + I G+ ES

Sbjct: 185 FEGNWRPTLTA---EQLAQVKEVIHPVVRTHPENGRKALFVSEGFTTRIVGLPDDESRDV
241

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L+ L + ++ HQW D+V WDNR L+H A L R ++ + + G

Sbjct: 242 LQQLYALSIVLEQNIYRHQWQPHDLVFDNRSLIHLATGCPAHLRRKLYRTTIQG 295

>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 = 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 ADVPLQIRALDAAFGEVLGLDLGLPLAAEDFRRIHRALDHHVLFVFRDQRITPAQQIAF 70

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS
112

++RFG ++ G +I+ +SN+ +G P D K WH+D

Sbjct: 71 SRRFGELQIHVLKQFLLPGHPEILIVSNIVENG-----QPIGLGDAGKF-----WHSDL
119

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLV--YSQS
170

+Y + + G++ A+ +P GG T FADM A+D+L EA R + R+A HS YS+
Sbjct: 120 SYKELPSLGSMLHAQELPEEGDTLFADMHKAWDSLPEALRKAIEGRTAAHSYTARYSEP
179

Query: 171 KL-GHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESER
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 LLAELYAHSVRPEHIYRHRWQAHDLVFWDNRSLIHLAGGCPAHLRRKLYRTTIQG 291

>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 = 4e-27, Method: Compositional matrix
adjust.

Identities = 87/289 (30%), Positives = 136/289 (47%), Gaps = 21/289 (7%)

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-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
115

FG ++ G +++ +SNV +G P D WH+D +Y
Sbjct: 88 FGPLQIHVLHQFQLPGHAEVLVSNVVENG-----KPIGLGD-----AGHFWHSDLSYK
136

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHV
175

+ G++ A +PA GG T FA+M A+D L A + V A H+ + ++L
Sbjct: 137 EKPSLGSLLHARELPAEGDTLFANMHLAWDTLPSALQRAVDGLHAEHTYLARYAELQQR
196

Query: 176 QQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLV
234

+ L+P+V+ HPETGR +L + H I G+ ES L+ L
Sbjct: 197 SPWRPDLTPEQIAQVRPVLQPVVIRTHPETGRKALFVSEHFTTRIVGLPEQESRDLDDQLF
256

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ + ++ HQW D+V WDNR LLH A + RVM+ + + G
Sbjct: 257 AHSVKPAHIYRHQWQPHDLVFDNRSLHLAAGCPPEQRRVMYRTTIEG 305

>gb|AAT51290.1| PA2310 [synthetic construct]

Length = 296

Score = 125 bits (315), 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 ADVPLQIRALDAAFGEVLGLDLGLPLAAEDFRRIRHRAHLDHHLVLFREQRITPAQQIAF 70

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
 112

++RFG ++ G +I+ +SN+ +G P D K WH+D
 Sbjct: 71 SRRFGELQIHVLKQFLLPGHPEILIVSNIVENG-----QPIGLGDAGKF-----WHS DL
 119

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLV--YSQS
 170

+Y + + G++ A+ +P GG T FADM A+D+L EA R + R+A HS YS+
 Sbjct: 120 SYKELPSLGSMLHAQELPEEGD TLFADMHKAWDSLPEALRKAIEGR TAAHSYTARYSEP
 179

Query: 171 KL-GHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESER
 228

+ G+ + SA + + P+V+ HPE+GR +L + I G+ A ES +
 Sbjct: 180 RFEGNWRPTLSA---AQLAEVREV VHP I V R T H P E S G R K A L F V S E G F T T R I V G L P A D E S A Q
 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 = 4e-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 FDVRPFTGKVGAEIVGLDLSMPLNDADFARVHQAHLDHVVVFRDQQITPQQQVDFSRRF 77

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP
 116

G ++ +I+ +SN+ V P D K WH+D +Y
 Sbjct: 78 GVLQIHVLKQFLLANHP E I L I V S N I -----VENEKPVGLGDAGKY-----WHS D L S Y K E
 126

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ
 176

+ + G++ A+ +P+ GG T FADM A+D L + R V RSA HS ++ +
 Sbjct: 127 LPSLGSMLYAQELPSEGGDTLFDADMHQAWDTLPQHLDRAVEGRSAVHSYTARYAEGHNAA
 186

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD
 235

 + P+V+ HPETGR +L + I + ES + L +
 Sbjct: 187 NWRPTLTAEQLAQVVEVSHPIVRTHPETGRKALFVSEGFTRILDLPEDSRQILNEIYA
 246

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

 + + ++ HQW A D+V WDNR L+H A L R ++ + + G
 Sbjct: 247 HSVKPEHIYRHQWQANDMVFDNRSLIHLAAGCPAHLRRKLYRTTIQW 294

>ref|YP_002908767.1| Taurine dioxygenase [Burkholderia glumae BGR1]
 gb|ACR31532.1| Taurine dioxygenase [Burkholderia glumae BGR1]
 Length = 305

Score = 125 bits (314), Expect = 5e-27, Method: Compositional matrix
 adjust.

Identities = 85/288 (29%), Positives = 137/288 (47%), Gaps = 21/288 (7%)

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 FDIVPFDGPLGAEVVGLDLSQPLGEAAFARIHRAHLDHLLLVFREQRITPEQQVAFSRRF 84

Query: 65 GAIER-----IGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP
 116

 G ++ G +++ +SN+ +G P D WH+D +Y
 Sbjct: 85 GPLQTHVLHQFALPGHPEVLIVSNIVENG-----KPIGLGD-----AGHFWHSDLSYKE
 133

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
 176

 + G++ A+ +P GG T FA+M A++ L EA + V R A H+ + ++L
 Sbjct: 134 KPSLGSLLHAQELPTEGGDTLFDANMHLAWETLPEALKQAVRGRRAEHTYLARYAELQARS
 193

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD
 235

 + +P+V+ HPETGR +L + H I G+ ES L+ L
 Sbjct: 194 PWRPNLSAEQLAQVKAVQQPIVRTHPETGRRALFVSEHFTTRIVGLPEDESRALLDELFA
 253

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

 + + V+ H+W D+V WDNR L+H A L R ++ + + G
 Sbjct: 254 HSVRDEFVYRHRWREHDLVFDNRSLMHLAAGTPDHLRRKLYRTTIEG 301

>ref|YP_001117391.1| taurine dioxygenase [Burkholderia vietnamiensis G4]
 gb|ABO57926.1| Taurine dioxygenase [Burkholderia vietnamiensis G4]
 Length = 309

Score = 125 bits (314), Expect = 5e-27, Method: Compositional matrix adjust.

Identities = 86/292 (29%), Positives = 138/292 (47%), Gaps = 21/292 (7%)

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 AAQRFDIIPLDAPVGAEEVVGIDLSQPLDAAAFARIHRAHLDHHLVFRDQRITPEQHIAF 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 SYKEKPSLGSLLHAQELPADGGDTLAFANMHLAWDTLPAHLRRAVEGRRAEHTYLARYAEL
193

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE
231

+ + + P+V+ HPETGR +L + H I + A ES L+
Sbjct: 194 QARNRWRPVLSAEQLAQVEAVVHPIVRTHPETGRKALFVSEHFTTRIVDLPADSRALLD
253

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

L + + ++ H+W D+V WDNR L+H A L R ++ + + G
Sbjct: 254 ELFAHSVRDEHLYRHRWRDHDLVFWDNRSMLHLAAGTPDHLRRKLYRTTIEG 305

>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 = 6e-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-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY
114

RFG ++ G +++ +SN+K +G P D WH+D +Y
Sbjct: 83 RFGPLQIHVLRNFLRGHPEVLVSNIKENG-----EPIGLGD-----AGHYWHSDSL
131

>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 = 6e-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 ADFPLQIRALDAAFGEVLGLDLGLPLAAEDFRRIHRAHLDHHVLFVRFREQRITPAQQIAF 70

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
 112

++RFG ++ G +I+ +SN+ +G P D K WH+D

Sbjct: 71 SRRFGELQIHVLKQFLLPGHPEILIVSNIVENG-----QPIGLGDAGKF-----WHS DL
 119

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS LV--YSQS
 170

+Y + + G++ A+ +P GG T FADM A+D+L EA R + R+A HS YS+

Sbjct: 120 SYKELPSLGSMLHAQELPEEGD TLFADMHKAWDSLPEALRKAIEGRTAAHSYTARYSEP
 179

Query: 171 KL-GHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESER
 228

+ G+ + SA + + P+V+ HPE+GR +L + I G+ A ES +

Sbjct: 180 RFEGNWRPTLSA---AQLAEVREVVHPIVIRTHPESGRKALFVSEGFTTRIVGLPADES AQ
 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_02468555.1| Taurine dioxygenase [Burkholderia thailandensis MSMB43]

Length = 309

Score = 125 bits (314), Expect = 6e-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 FDIVPFDAPLGAEVVGIDLSQPLDAADFARIHRAHLDHHVLFVFRDQRITPDKHIAFSRRF 88

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP
 116

G ++ +++ +SN+ DG P D WH+D +Y

Sbjct: 89 GPLQIHVLHQFALAAHPEVLIVSNIVEDG-----KPIGLGD-----AGHFWHSDLSYKE
 137

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
176

+ G++ A+ +PA GG T FA+M A+D L R V R A H+ + ++L

Sbjct: 138 KPSLGSLHQAQELPAEGGDTLAFNMHLAWDTLPAHLRRAVEGRRAEHTYLARYAELQARS
197

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD
235

+ + P+V+ HPETGR +L + H I + ES L+ L

Sbjct: 198 PWRPNLSAEQIAQVEAVVHPVVRTHPETGRRALFVSEHFTTRIVDVPEDESRALLDELFA
257

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAG 283

+ +A +H H W D+V WDNR L+H A L R ++ + + G

Sbjct: 258 HSVRAEHLHRHHWRDHDLVFWDNRSLMHLAAGTPDHLRRKLYRTTIEG 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 = 6e-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 TIQIEPIGGSIGAVIHGVDLGAPLSNRQAKEVHDAFLEHSVVFFRDQKLDDPERQKRAAR 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 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS---LVYSQSKL-G
173

A G++ A VP+ GG T FAD AAY+ L + R L+ +A HS SQSK G

Sbjct: 117 PALGSLLYALQVPSRGGDTLAFADQYAAAYETLSDGMRRLLDGLTAVHSGRSYGSQSKFQG
176

Query: 174 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEG
232

Q+ S I D P+V+ HPETGR L + + + M AES+ L+

Sbjct: 177 GKNQSVSMTIDANADGDRLVEHPVVRTHPETGRKCLFVNPNYTLRLKDMTEAESKPLLDL
236

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

L A + + +W AG V VWDNRC +HRA

Sbjct: 237 LYAHAIRDEFICRFRWQAGSVAVWDNRCTMHRA 269

>ref|YP_001437971.1| hypothetical protein ESA_01880 [Enterobacter sakazakii ATCC

BAA-894]

gb|ABU77134.1| hypothetical protein ESA_01880 [Cronobacter sakazakii ATCC BAA-894]

Length = 294

Score = 125 bits (313), Expect = 7e-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 TTLNATPVAAQPFTITPFARLGAIEITGLDLRLPVNNADFARIHQAHLDHHVVVFRDQKIT 62

Query: 54 NDQQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGN 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 --WHSLSYKTLPSLGSMLYAQELPEEGGDTLFDADMELAYETLPADLKRAIEGKKAVHSY 171

Query: 166 V--YSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGM 221

YS+ K G + P+++ HPETGR +L + G H I G+

Sbjct: 172 TATYSRPKFG--SHWRPQLTEQQLAEVQAVSHPVMRTHPETGRKALFVSEGFTTH-IEGL 228

Query: 222 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRL 281

AES LE L + + ++ HQW GD+V WDNR L+H A L R ++ + +

Sbjct: 229 PEAESRDILEALWAHSVRPEHLYRHQWQPGDMVFDNRSLIHLATGCPAHLRRKLYRTTI 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 = 7e-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 ++ +QQI F++RF
 Sbjct: 19 FEVRPFSGAVGAEILGLDLAKPVSAEDFTRIHRALDHHVLFVFRDQRITPEQQIAFSRRF 78

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA--WHADSTY
 114

G ++ G +I+ +SN+ +G + +G+ WH+D +Y
 Sbjct: 79 GELQIHVLKQFLLTGHPEILIVSNIIENG-----QNIGLGDAGKFWHSDLSY
 125

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLV--YSQSKL
 172

+ + G++ A+ +P+ GG T FADM A+DA+ + R +V RSA HS Y+++K
 Sbjct: 126 KELPSLGSMLHAQELPSEGGDTLAFADMHKAWDAVPDTRLKVVVEGRSAHSTARYAETKF
 185

Query: 173 -GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL
 230

G+ + +A + + P+V+ HPE GR +L + I G+ ES L
 Sbjct: 186 EGNWRPTLTA---EQLAQVKEVIHPVVRTHPENGRKALFVSEGFTTRIVGLPDDESRLV
 242

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ L + ++ HQW D+V WDNR L+H A L R ++ + + G
 Sbjct: 243 QQLYALSVLEQNIYRHQWQPYDLVFDNRSLIHLATGCPAHLRRKLYRTTIQG 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 = 7e-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--DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY-----
 114

+R G I+ G + I V D + ++S A + + WH D
 Sbjct: 62 RRLGEIDFSSDGHRVAGIYPVTLDKS--KNSSAAY-----LRATFDWHIDGCTPTGDD
 113

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGH
 174

P MA V SA+ V GG T FA AAYDAL +A + HSL SQ +

Sbjct: 114 YPQMA--TVLSAKQVAESGGETEFASSYAAYDALTDAEKQRFASLRVVHSLEASQRR---
168

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
234

V S T PLV H TGR SL++G A I GMD E L L+
Sbjct: 169 VNPDPSPPEELARWRARPTHEHPLVWTH-RTGRKSLVLGASADYIVGMDPEEGRALLSELL
227

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

D A A +V++H WA GD V+WDNR +LHRA +D PR M + + G
Sbjct: 228 DRATTADKVYSHHWAVGDTVWIDNRGVLHRAARYDENSPREMLRTTVLG 276

>gb|ADC34043.1| TfdA-like protein [uncultured bacterium]
Length = 207

Score = 124 bits (312), Expect = 9e-27, Method: Compositional matrix
adjust.

Identities = 76/221 (34%), Positives = 116/221 (52%), Gaps = 29/221 (13%)

Query: 56 QQITFAKRFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVG
104

QQI FA+ +G + ER +I+ ISNV +G V + S +
Sbjct: 1 QQIAFARHYGPLNVGLKKAGKRRERYANREIIDISNVDEGRVYERS-----HTATIS 53

Query: 105 NMA---WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSA
161

N+A WH+DS++ + ++ SA VVP GG+T FAD+RAA+D+L + + + ++A
Sbjct: 54 NLANQLWHSDDSSFQKPAMKYSMLSAVVVPENGGQTEFADLRAAFDRLPDEMRELKGGKAA
113

Query: 162 RHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPG
220

H +S+ LG A T P++ PLV+ HP +GR L +G H +PG
Sbjct: 114 EHYAWHSREWLGDITITPEQA-----ETFPVQWPLVRKHGSGRDVLFVGIHCTKVPG
166

Query: 221 MDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

M AE + GL++ A Q V+ H+W GD+V+WDNRC+
Sbjct: 167 MTLAEGRMLIAGLLEHATQRELVRHEWRPGDLVMWDNRCV 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 = 9e-27, 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 IAGQPIEIRAFDGPLGAEVLGLDLSKPLAQADFARIHRAHLDYHVLVFRDQRITPDEQIA 82

Query: 60 FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHAD
111

F++RFG ++ +++ +SN+ +G P D WH+D
Sbjct: 83 FSRRFGPLQIHVLHQFQLPDYPEVLVSNIVENG-----KPIGLGD-----AGHYWHSD
131

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSK
171

+Y + G++ A+ +PA GG T FA+M A+D L R+ V R+A H+ + ++
Sbjct: 132 LSYKEKPSLGSLLHAQELPAEGGDTLFANMHLAWDTLPAHLRS AVEGRTAEHTYLAKYAE
191

Query: 172 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGM DAAESERFL
230

L + + P+V+ HPETGR +L + H + G+ ES + L
Sbjct: 192 LQKRSPWRPNLSPEQIAQVKPVVHPIVRTHPETGRKALFVSEHFTTRVIGLPEDES RQLL
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 ASQSFEVRPFTEKVGAEIVGLDLSRPLNDADFARVHQAHLDHVVVFRDQQITPQQQIDF 73

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
112

++RFG ++ +I+ +SN+ V P D K WH+D
Sbjct: 74 SRRFGVLQIHVLKQFLLANHPEILIVSNI-----VENDKPVGLGDAGKY-----WHSDL
122

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKL
172

+Y + + G++ A+ +P+ GG T FADM A++ L + R V RSA HS ++
Sbjct: 123 SYKELPSLGSMLYAQELPSEGGDTLFADMHLAWETLPQHRLDAVEGRSAVHSYTARYAEG
182

Query: 173 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGM DAAESERFLE
231

+ + P+V+ HPE GR +L + I G+ ES + L
Sbjct: 183 HNAANWRPPLTAEQLAQVVEVSHPIVRTHPENGRRALFVSEGFTRILGLPEDES RQILN
242

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 + + + ++ HQW A D+V WDNR L+H A
 Sbjct: 243 EIYAHSVKPEHIYRHQWQANDMVFDNRSLIHLA 276

>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 ASQEFEIIRRLPAPLGAEVLGLDLAQPLSDADFDRIILRAHWEHVVLVFRNQIRITPAQQVAF 73

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
 112
 ++RFG ++ G +++ +SN++ + P D G++ WH+D
 Sbjct: 74 SRRFGPLQIHVQRKFALQGHPEVLVVSNIIRDENG-----EPTGLGD-----AGSL-WHSDL
 123

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
 172
 +Y + G++ A+ +P VGG T FAD AAYDAL EAT+ + A HS + +L
 Sbjct: 124 SYKDKPSLGSLLHAQELPNVGGDTLFDADQYAAAYDALPEATQQRIAHLRAEHSYLARYEEL
 183

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE
 231
 + A + P+V+ HP TGR +L + H I + ES L+
 Sbjct: 184 RQRNPWRPRLTPAQIAEVAPAVHPVVRTHPATGRKALFVSEHFTTRILDLPEEESRALLQ
 243

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 L + + V+ HQW D+V WDNR +LH A
 Sbjct: 244 ELFAASVRPEFVYRHQWQPHDLVFDNRRAVLHLA 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 MQIRALDAAFGEVLGLDLGLPLAAEDFRRIHRAHLDDHVLVLFREQRITPAQQIAFSRRF 60

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP
 116

Sbjct: 61 G ++ G +I+ +SN+ +G P D K WH+D +Y
 109 GELQIHVLKQFLLPGHPEILIVSNIVENG-----QPVGLGDAGKF-----WHSDLSYKE

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLV--YSQSKL-G
 173

+ + G++ A+ +P GG T FADM A+D+L EA R + R+A HS YS+ + G
 Sbjct: 110 LPSLGSMLHAQELPEEGGDTLFAFMHKAWDSLPEALRKAIEGRRTAAHSYTARYSEPRFEG
 169

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG
 232

+ + SA + + P+V+ HPE+GR +L + I G+ A ES + L
 Sbjct: 170 NWRPTLSA--AQLAEVREVHPIVRTHPESGRKALFVSEGFTRIVGLPADESAQLLAE
 226

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLAG 283

L + + ++ H+W A D+V WDNR L+H A L R ++ + + G
 Sbjct: 227 LYAHSVRPEHIYRHRWQAHDLVFDNRSLIHLAGGCPAHLRRKLYRTTIQG 277

>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 = 1e-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 APQRFEIVPFDAPLGAEVVGDLSQPLDADAFARIRRAHLDDHVLVFRDQRITPDEHVAF 70

Query: 61 AKRFGAIER-----IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
 112

++RFG ++ G +++ +SN+ +G P D WH+D
 Sbjct: 71 SRRFGPLQTHVLHQFALPGHPEVLIVSNIVENG-----RPIGLGD-----AGYFWHSDL
 119

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKL
 172

+Y + G++ A+ +PA GG T FA+M A+D L A R V R A H+ + ++L
 Sbjct: 120 SYKRRPSLGSLLHAQELPAEGGDTLFAFMHMLAWDTLPAALRRAVEGRRAEHTYLARYAEL
 179

Query: 173 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE
 231

+ + P+V+ HPETGR +L + H I G+ ES L+

Sbjct: 180 QARSPWRPNLSAEQIAQVEPVVHPVVRTHPETGRRALFVSEHFTTRIVGLPDDESRALLD
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 = 1e-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 APQRFEIVPFDAPLGAEEVVGIDLSQPLDADAFARIRRAHLDHHVLFVFRDQRITPDEHVAF 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 SYKRRPSLGSLLHAQELPAEGGDTLFANMHLAWDTLPAALRRAVEGRRAEHTYLARYAEL
193

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE
231

+ + P+V+ HPETGR +L + H I G+ ES L+

Sbjct: 194 QARSPWRPNLSAEQIAQVEPVVHPVVRTHPETGRRALFVSEHFTTRIVGLPDDESRALLD
253

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + +A + H+W D+V WDNR LLH A L R ++ + + G

Sbjct: 254 ELFAHSVRAEHQYRHRWRDHDLVFWDNRSLHLAAGTPDHLRRKLYRTTIEG 305

>ref|ZP_01894021.1| Taurine catabolism dioxygenase TauD/TfdA [Marinobacter
algiticola
DG893]

gb|EDM47914.1| Taurine catabolism dioxygenase TauD/TfdA [Marinobacter
algiticola

DG893]
Length = 275

Score = 124 bits (310), Expect = 2e-26, Method: Compositional matrix adjust.

Identities = 81/268 (30%), Positives = 126/268 (47%), Gaps = 29/268 (10%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
T Q P LGA V GV L +DDA L+ WL+H +L+ ++ D+ + FA+ F
Sbjct: 2 TYQTLPLSPALGAEVVRGVDLTHIDDAHAQELNELWLKHHVLRVIRDSVTEDELVEFAQSF 61

Query: 65 GAIERIGG-----GDIVAINVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPV
117
G+IE +I+ ISN++ P G + WH D + V
Sbjct: 62 GSIENARKMSPLATRPEIMVISNIREGEAALGALPD-----GELFWHFDRIHQKV
111

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQ
177
+ V + +P+ GG T F+ M AY+AL E T+ + +A ++ Y Q+ + Q
Sbjct: 112 PNKAGVLHSIELPSKGGETRFSSMCQAYEALPEETKRKLEGLTALNTYQYQQTNAANKQL
171

Query: 178 AGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW
236
+ + + P+V+ PETG+ +L + R I + AESE L L D
Sbjct: 172 TKD-----SPSAVHPVVRTIPETGKKALYVCRLMTDRILELPEAESEALLAELFD-
221

Query: 237 ACQAPR-VHAHQWAAGDVVVDNRCLLH 263
C+ P ++ H W GD ++WDNRC+LH
Sbjct: 222 HCERPEFIYEHSWRLGDTLIWDNRCVLH 249

>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 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY
167
WH+DS++ P+ A+ ++ SA +V GG T FADMRAAYDALD+ T+A + HSL+Y
Sbjct: 2 WHSDSSFRPIPAKFSLLSARIVNPKGGNTEFADMRAAYDALDDETKAEIEDMVCEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
227
S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+
Sbjct: 62 SRGSLGFLD-----YTDEEKEMFKPVLQRLVVRTHPVHGRKSLYLSSHAGAIRGMSMPPEAR
116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHR 264

L L + A Q V+ H+W D+V+WDNR +HR
 Sbjct: 117 LLLRDLTEHATQPEFVYVHKWTVHDLVMWDNRQTVHR 153

>ref|ZP_06458047.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv. aesculi str.

NCPB3681]

ref|ZP_06481584.1| TauD/TfdA family dioxygenase [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 FDVRPFTGKVGAEIVGLDLRPLNDADFARVHQAHLDHHVVVFRDQQITPQQQVDFSRRF 77

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP
116

G ++ +I+ +SN+ V P D K WH+D +Y

Sbjct: 78 GVLQIHVLKQFLLANHPEILIVSNI-----VENEKPVGLGDAGKY-----WHSDL SYKE
126

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ
176

+ + G++ A+ +P+ GG T FADM A+D L + R V RSA HS ++ +

Sbjct: 127 LPSLGSMLYAQELPSEGGDTL FADMHQAWDTLPQHLRDAVEGRSAVHSYTARYAEGHNAA
186

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD
235

+ P+V+ HPETGR +L + I + ES + L +

Sbjct: 187 NWRPTLTAEQLAQVVEVSHPIVTRTHPETGRKALFVSEGFTRILDLPEDSRQILNEIYA
246

Query: 236 WACQAPRVHAHQWAAGDVVWDNRCLLHRA 265

+ + ++ HQW A D+V WDNR L+H A

Sbjct: 247 HSVKPEHIYRHQWQANDMVFWDNRS LIHLA 276

>gb|ABD16700.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. Ppar1-31]

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 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVY
167

WH+DS++ P+ A+ ++ SA +V GG T FADMRAAYDALD+ T+A + HSL+Y

Sbjct: 2 WHSDSSFRPIPAKFSLLSARIVNPKGGNTEFADMRAAYDALDDETKAEIDDMICEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESE
227

S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+
Sbjct: 62 SRGSLGFLD-----YTDEEKEMFKPVLQRLVVRTHPVHGRKSPLYLSSHAGAIRGMSMPEAR
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. on192.10]

Length = 153

Score = 123 bits (309), Expect = 2e-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 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESE
227

S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+
Sbjct: 62 SRGSLGFLD-----YTDEEKQMFKPVLQRLVVRTHPVHGRKSPLYLSSHAGAIRGMSMPEAR
116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264

L L + A Q V+ H+W D+V+WDNR +HR
Sbjct: 117 LLLRDLTEHATQGEFVYVHKWTVHDLVMWDNRQTVHR 153

>gb|ABD16698.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. Vgn-2]

Length = 153

Score = 123 bits (309), Expect = 2e-26, Method: Compositional matrix
adjust.

Identities = 66/157 (42%), Positives = 90/157 (57%), 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 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESE
227

S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+
Sbjct: 62 SRGSLGFLD-----YTDEEKEMFKPVLQRLVVRTHPVHGRKSLYLSSHAGAIRGMSMPEAR
116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVVDNRCLLHR 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
dioxygenase [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 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESE
227

S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+
Sbjct: 62 SRGSLGFLD-----YTDEEKEMFKPVLQRLVVRTHPVHGRKSLYLSSHAGAIRGMSMPEAR
116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVVDNRCLLHR 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 ++ DQQI F++RF

Sbjct: 22 IEIRAFDGPVGAEVLGLDLGRPLSQHDFERIHRAHLDDHHVLFVFRDQRITPDQQIAFSRRF 81

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP
116

G ++ G +++ +SN+ +G P D WH+D +Y

++ ++ 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 = 3e-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 MTDTGFTIDPVSPTLGAEVRGLDLSQPLSPATTSVLADALDRHLVLFVFRDQTLSDADLVR 60

Query: 60 FAKRFGAIERI-----GGGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAW
 108

+ FG +++ G ++ ISN+ A+G + + G W
 Sbjct: 61 VSGHFGPLDKAPITENGR LHAPGYEEVYVISNITANGR-----PIGALGAGESVW
 110

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
 168

HAD TY+ + A VP GG T F M AAYDAL E + V S +H +
 Sbjct: 111 HADMTYLETPPYASSLYALEVPVEGGDTGFLSMFAAYDALPEPLKRRVEGLSIKHDSTTN
 170

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESE
 227

G+++Q + T+ + PLV HP TG +LL+GR HA IPG+ ESE
 Sbjct: 171 SG--GYLRQGFAPPANVA--TSPGTVHPLVITHPVGTGARALLLGRRPHAHIPGLSVP ESE
 226

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLA 282

L+ + A + H+W GD+V+WDNR +HR +P+ R M +++A
 Sbjct: 227 ALLDEIWATAVRPELAWHHRWRVGD LV MW DNRW TMHRRDPFPDSQRRRMHRTQIA 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 = 3e-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 TLAIIPSGQACGAHVTVGVDLAHPLDPGTIAAIRAAWLDHHLVLAFPDQKMSDDDLERFTAY 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 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGS
180

G +P VGG T FA+ AA DA+ RA + A HS + G G+
Sbjct: 111 GTCLFGITIPPVGGNTEFANQHAALDAMPAGLRARIEGLRAIHSARAGYAPSG---MYGA
167

Query: 181 AYIGYGMDTTA-----TPLRPLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGL
233

G MD + T L P V+ HPETGR L + GMD AE+ L L
Sbjct: 168 NDRGRSMDIRSDDAALETQLHPFVRAHPETGRLGLFGCAGYIIGFEGMDDAEARPLLHEL
227

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ W + ++H+W +V+WDNR +LHRA
Sbjct: 228 IQWQGREEFRYSHRWEFDMLVMWDNRSVLHRA 259

>gb|ABD16701.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. aeky3]
Length = 153

Score = 122 bits (307), Expect = 3e-26, Method: Compositional matrix
adjust.

Identities = 66/157 (42%), Positives = 89/157 (56%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY
167

WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A + HSL+Y
Sbjct: 2 WHSDSSFRPIPAKFSLLSARVVNPPGGNTEFADMRAAYDALDDETKAEIEDMICEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
227

S+ LG + Y L+ LV+ HP GR SL + HA AI GM E+
Sbjct: 62 SRGSLGFLD-----YTDEEKQMFKPVLRVLRTHPVGHRKSLYLSSHAGAIRGMSMPEAR
116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264

L L + A Q V+ H+W D+V+WDNR +HR
Sbjct: 117 LLLRDLTEHATQGEFVYVHKWTVHDLVMWDNRQTVHR 153

>ref|YP_233447.1| taurine dioxygenase [Pseudomonas syringae pv. syringae
B728a]

gb|AAAY35409.1| Taurine dioxygenase [Pseudomonas syringae pv. syringae
B728a]

Length = 298

Score = 122 bits (306), 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 ++ QQI F++RF

Sbjct: 18 FEVRPFTEKVGAEIVGLDLSRPLNDADFARVHQAHLDHHVVVFRDQQITPQQQIDFSRRF 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 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ
176

+ + G++ A+ +P+ GG T FADM A++ L + R V RSA HS ++ +
Sbjct: 127 LPSLGSMLYAQELPSEGGDTL FADMHLAWETLPQH LRDAVEGRSAVHSYTARYAEGHNAA
186

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVD
235

+ P+V+ HPE GR +L + I G+ ES + L +
Sbjct: 187 NWRPTLTAEQLAQVVEVSHPIVRTHPENGRKALFVSEGFTTRILGLPEDESRQILNEIYA
246

Query: 236 WACQAPRVHAHQWAAGDVVWDNRCLLHRA 265

+ + ++ HQW A D+V WDNR L H A
Sbjct: 247 HSVKPEHIYRHQWRANDMVFWDNRS LTHLA 276

>ref|ZP_06234909.1| Taurine dioxygenase [Frankia sp. Eu1lc]

gb|EFA63826.1| Taurine dioxygenase [Frankia sp. Eu1lc]

Length = 303

Score = 122 bits (306), Expect = 4e-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 NLQIRPLNAAFGEITGVDLRGPLDAETVAALRQAWLDYQVVFFPEQHLTIDQQVAFTRN 67

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

FG E I+A + V S ++ +KV + WH D T+ G+V
Sbjct: 68 FG--ELTAPSAILAPVDADHREV VAFDSREFREEYVKV-GRHHGWHVDITFQATPPAGSV
124

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYI
183

F+ +P VGG T FA +AAY+ L L+ A HS G +AG
Sbjct: 125 FNIVKLPPVGGATLFASAQAAYETLSPPIHLLDGLVAIHS-----FGRPSRAGGGIS
177

Query: 184 GYGMDTTATPL-----RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW
236

 G+ P+ P+V VHPETGR L + AI G+ ES LE L D
Sbjct: 178 ATGV-WEDEPVDGGFVEHPVAVHPETGRKGLFVNPGF'TRAIKGLSPRESAALLELLYDH
236

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLH-RAEPWDFKLPVMMWHSRLAGRPET 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 = 4e-26, Method: Compositional matrix
adjust.

Identities = 86/288 (29%), Positives = 136/288 (47%), 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 FDIVPFDAPLGAEVIGLNLSQLGADDFARIHRAHLDHHVLFVFRDQRITPDEHIAFSRRF 87

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP
116

 G ++ G +++ +SN+ +G P D WH+D +Y
Sbjct: 88 GPLQIHVLHQFALAGHPEVLIVSNIVENG-----KPVGLGD-----AGHFWHSDLSYKE
136

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
176

 + G++ A+ +PA GG T FA+M A+D L R V R A H+ + ++L
Sbjct: 137 KPSLGSLHQAQELPAEGGDTLFANMHLAWDTLPAHLRRAVEGRRAEHTYLARYAELQARS
196

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD
235

 + A + P+V+ HPETGR +L + H I G+ ES L+ L
Sbjct: 197 PWRPNLSPEQIAQVAAVVHPIVRTHPETGRKALFVSEHFTTRIVGLPDDESRALLDELFA
256

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAG 283

 + +A ++ H W D+V WDNR L+H A L R ++ + + G
Sbjct: 257 HSVRAEHLYRHAWRDHDLVFWDNRSMLHLAAGTPDHLRRKLYRTTIEG 304

>ref|YP_202406.1| taurine dioxygenase [Xanthomonas oryzae pv. oryzae
KACC10331]

gb|AAW77021.1| taurine dioxygenase [Xanthomonas oryzae pv. oryzae
KACC10331]

Length = 359

Score = 122 bits (306), Expect = 5e-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: 74 VQRSGVRIAPFDGPLGAEVIGLNLSQPLDADAFARLHRAHLDDHVLVFRDQRISPAQQVE
 133

Query: 60 FAKRFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHAD
 111

F++RFGA+ + G +++ +SN+K +G P D WH+D
 Sbjct: 134 FSRRFGALQIHVLRNFQMRGHPEVLVVSNIKENG-----EPIGLGD-----AGHDWHSD
 182

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSK
 171

+Y + G++ A+ +P+ GG T FA+ A+ L E+ V A HS +
 Sbjct: 183 LSYKETPSLGSLLHAQQLPSEGGDTLFANQHLAWQTLPESLTRTVQDLRAEHSYLVRYEA
 242

Query: 172 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL
 230

L A + P+V+ HPETGR +L + H I G+ ES L
 Sbjct: 243 LRARNPWCALTPAQIAEVTVPVHPVVRTHPETGRKALFVSEHFTTRILGLPEDESRAAL
 302

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ L + + V+ H+W D+V WDNR ++H A
 Sbjct: 303 QTLFAHSTRPALVYRHRWQPYDMVFDNRSVMHLA 337

>ref|YP_001507295.1| taurine catabolism dioxygenase TauD/TfdA [Frankia sp.
 EAN1pec]

gb|ABW12389.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp.
 EAN1pec]

Length = 281

Score = 122 bits (306), Expect = 5e-26, Method: Compositional matrix adjust.

Identities = 93/287 (32%), Positives = 138/287 (48%), Gaps = 20/287 (6%)

Query: 4 TTLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
 TT+ P AT+GA V+GV L DD A+ A Q+ +L+F G HL+ + Q+ F

Sbjct: 3 TTISCEPLAATVGAEVSGVDAGQLAHDVTAVLEALEQYGVVFRGLHLAPETQVAFG 62

Query: 62 KRFGAIERIGGGDIVA-ISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQ
 120

+R G I+ G V+ I V D + +++ A++ + WH D P+ +
 Sbjct: 63 RRLGEIDYEQGHHPVSGIYRVTLDTSS--KNTSADY-----LRATFEWHMDGC-TPLHGE
 113

Query: 121 -----GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
 176

+ SA+ V GG T FA+ AAY+AL + + H++ SQ + V
 Sbjct: 114 PPQKATILSAKAVATSGGETEFANTYAAAYEALSDGEKEEFGSLRVVHTMEASQRR---VT
 170

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSELLIGRHAHAIPGMDAAESERFLEGLVDW
 236

 + T PLV H TGR SL+IG +A + GM E L+ L+D
 Sbjct: 171 PDPTPEQLQRWRNRPTSTHPLVWTH-RTGRRSLVIGANASHVVGMLNEGPSLLQELLDR
 229

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

 A RV+ HQW+ GD V+WDN ++HRA P+D PR M + + G
 Sbjct: 230 ATAPDRVYRHQWSVGDTVIWDNTGVVHRAAPYDSHSPREMLRRTTVFG 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 = 6e-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 ALQTFDIVAFDAPVGAEVLGLDLNEPLSADDFARIHRAHLDYHVLVLFREQRITPEQHVAF 79

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
 112

 ++RFG ++ G +++ +SN++ +G P D WH+D
 Sbjct: 80 SRRFGPLQIHVLRQFQLPGHPEVLIVSNIRENG-----QPIGLGD-----AGHFWHSDL
 128

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
 172

 +Y + G++ A+ +P+ GG T FA+M A+D L E R V R+A H+ + ++L
 Sbjct: 129 SYKEKPSLGSLLHAQELPSEGGDTLAFANMHLAWDTLPEHLRKAVEGRTAEHTYLAKY AEL
 188

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSELLIGRHAHA-IPGMDAAESERFLE
 231

 + + P+V+ HPETGR +L + H I G+ ES L
 Sbjct: 189 QKRSPWRPNLSAEQVAEVKPVVHPVVRTHPETGRKALFVSEHFTTHIVGLPEDESRLDG
 248

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

 L + + ++ HQWA D+V WDNR L+H A L R ++ + + G
 Sbjct: 249 ALFVHVRDEHIYRHQWAEHDLVFWDNRSMLHLAGTPDHLRRLKLYRTTIEG 300

>gb|ABD16697.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
 dioxygenase [Bradyrhizobium elkanii]
 Length = 153

Score = 122 bits (305), Expect = 6e-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 WHS DSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAYDALDDETKAEIEDMICEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLRP-----LVKVHPETGRPSLLIGRHAHAIPGMDA
223

 S+ LG ++ Y D RP LV+ HP GR SL + HA AI GM
Sbjct: 62 SRGSLG-----FLDYT-DEEKQMFRLVQLRVRTHPVHGRRSLYLSSHAGAIRGMSM
112

Query: 224 AESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 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
PXO99A]

gb|ACD57751.1| taurine dioxygenase [Xanthomonas oryzae pv. oryzae PXO99A]
Length = 305

Score = 122 bits (305), Expect = 6e-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 VQRSGVRIAPFDGPLGAEVIGLNLSQLDADAFARLHRAHLDDHHVLFVFRDQRISPAQQVE 79

Query: 60 FAKRFGAI-----ERIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHAD
111

 F++RFGA+ + G +++ +SN+K +G P D WH+D
Sbjct: 80 FSRRFGALQIHVLRNFQLRGHPEVLVVSNIKENG-----EPIGLGD-----AGHDWHS
128

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK
171

 +Y + G++ A+ +P+ GG T FA+ A+ L E+ V A HS +
Sbjct: 129 LSYKETPSLGSLLLHAQQLPSEGGDTLFANQHLAWQTLPELSTRVQDLRAEHSYLARYEA
188

Query: 172 LGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL
230

 L A + P+V+ HPETGR +L + H I G+ ES L
Sbjct: 189 LRARNPWCALTPAQIAEVTVPVHHPVVRTHPETGRKALFVSEHFTTRILGLPEDES RALL
248

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

 + L + + V+ H+W D+V WDNR ++H A
Sbjct: 249 QTLFAHSTRPALVYRHRWQPYDMVFDNR SVMHLA 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 = 6e-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 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
176

V G++ A +P GG T FA+M AAY+AL E+ + + S S+ +

Sbjct: 111 VPPAGSMLHALEIPPEGGDTWFANMFAAYEALPESVKQRIEDLKVIIISRTQSRPYNYPDR
170

Query: 177 QAGSAY-IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLV
234

A SA + +D +PLV+ H +GR +L G + I G+ ES + L

Sbjct: 171 PAPSAQELAWEVDVA----QPLVRRHEVSGRKALYAGGNVPWRIEGLPLEESAPLITFLQ
226

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGR 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 = 7e-26, Method: Compositional matrix adjust.

Identities = 64/157 (40%), Positives = 89/157 (56%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY
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-----YTDEEKEMFKPVLQRLVLRTHPVHGRKSLYLSSHAGAIRGMSMPEAR
 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
 dioxygenase [Bradyrhizobium sp. Lh10]
 Length = 153

Score = 121 bits (304), Expect = 7e-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 WHSDSSFRPIPAKFSLLSARIVNPKGGNTEFADMRAAYDALDDETKTEIDDMICEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
 227

S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+
 Sbjct: 62 SRGSLGFLD-----YTDEEKEMFKPVLQRLVLRTHPVHGRKSLYLSSHAGAIRGMSMPEAR
 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264

L L + A Q V+ H+W D+V+WDNR +HR
 Sbjct: 117 LLLRDLTEHATQPEFVYMHKWTVHDLVMWDNRQTVHR 153

>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 = 8e-26, 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 EVTGLDPDALAGDEALGAAVLEALEDNGVLFVFPGLHLDLPQAQVEFC 61

Query: 62 KRFGAIERIGGG--DIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTY-----
 114

+R G ++ G + I V D + ++S A + + WH D
 Sbjct: 62 RRLGEVDHSSDGHPVAGIYPVTLDKS--KNSSAAY-----LRATFDWHIDGCTPTGDE
 113

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
174

P MA V SA V GG T FA AYD LD+ + + HSL SQ +
Sbjct: 114 YPQMA--TVLSARQVAESGGETEFASSYGAYDHLDDDEKQRLASLRVVSLEASQRR---
168

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSELLIGRHAHAIPGMDAAESERFLEGLV
234

V S + + T PLV H +GR SL++G A I GMD E L L+
Sbjct: 169 VTPDPPELLARWRSRPTHEHPLVWTH-RSGRKSLLVVGASADYIVGMDLDEGRALLADLL
227

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLAG 283

D A Q V++H W+ GD V+WDNR +LHRA P+ PR M + + G
Sbjct: 228 DRATQPELVYSHTWSVGDTVIWDNRGVLHRAAPYPENSPREMLRRTTVLG 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 = 9e-26, 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 TVLTINKLTASVGAEVVTGLDPDALAGDEALGAAVLEALEDNQVLFVFPGLHLDPPQAQVEFC 61

Query: 62 KRFGAIERIGGG--DIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTY-----
114

+R G ++ G + I V D + ++S A + + WH D
Sbjct: 62 RRLGEVDHSSDGHPVAGIYPVTLDKS--KNSSAAY-----LRATFDWHIDGCTPTGDE
113

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
174

P MA V SA V GG T FA AYD LD+ + + HSL SQ +
Sbjct: 114 YPQMA--TVLSARRVAESGGETEFASSYGAYDHLDDDEKQRLASLRVVSLEASQRR---
168

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSELLIGRHAHAIPGMDAAESERFLEGLV
234

V S + + T PLV H +GR SL++G A I GMD E L L+
Sbjct: 169 VTPDPPELLARWRSRPTHEHPLVWTH-RSGRKSLLVVGASADYIVGMDLDEGRALLADLL
227

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLAG 283

D A Q V++H W+ GD V+WDNR +LHRA P+ PR M + + G
 Sbjct: 228 DRATQPELVYSHTWSVGDTVIWDNRGVLHRAAPYPENSPREMLRRTTVLG 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 = 9e-26, 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 APQRFEIVPFDAPLGAEVVGDLSQPLDADAFARIRRAHLDLHVLFVFRDQRITPDEHVAF 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 SYKRRPSLGSLLHAQELPAEGGDTLAFANMHLAWDTLPDALRRAVEGRRAEHTYLARYAEL
 193

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE
 231
 + + P+V+ HPETGR +L + H I G+ ES L+
 Sbjct: 194 QARSPWRPNLSAEQIAQVEPVVHPVVRTHPETGRRALFVSEHFTTRIVGLPDDESRRALLD
 253

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
 L + +A + H+W D+V WDNR LLH A L R ++ + + G
 Sbjct: 254 ELFAHSVRAEHQYRHRWRDHDLVFWDNRSLLHLAAGTPDHLRRKLYRTTIEG 305

>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 APLGAEVLGLGDASDLSDADIAAIRQAWLAHDGLLVFRDVEFTPQAQVAFSRRRFGPQQVH 85

Query: 67 -----IERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
 122

G +I+ +SNV +G P D + WH+D +Y P+ + G+
 Sbjct: 86 VLNQFHLSGYPEILVVSINVVENG-----KPIGLGDAGR-----DWHSLSYKPLPSLGS
 134

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
 182

+ +P GG T FA+M AY+ L + ++ R A HS VY +L +
 Sbjct: 135 MLLTRELPEEGGDTLAFANMVRAYETLPANLKRVIIEGRRVHSYVYRYDRLRALSTWRPPL
 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 WHADSTYMPVMAQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY
 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-----YTDEEKEMFKPVLQRLVVRTHPVHGRKSLYLSSHAGAIRGMSMPEAR
 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 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR₁₆₉ALVHQRSARHSLVYSQ

ADSTYMPV A+GAVFSAE VP+VGGRT FADMRAAYDALD A +A + +A HSL YSQ

Sbjct: 1 ADSTYMPVQAKGAVFSAEEVPSVGGRTGFADMRAAYDALDPAIKARIEGLNAYHSLHYSQ 60

Query: 170 SKLGH-VQQAGSAYIGYGMDDTTATPLRPLVKVHPET 204

++GH ++ Y GYG+ PLRPLVK+HPET

Sbjct: 61 GRVGHQTKKLDGEYSGYGLHDGPVPLRPLVKIHPET 96

>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 = 1e-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 FDIVPFDAPLGV₈₇EVIGLNLSQPLGADDFARIHRAHLDHHVLFVFRDQRITPDEHIAFSRRF

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHS₁₁₆PAEWDDMMKVIVGNMAWHADSTYMP

G ++ G +++ +SN+ +G P D WH+D +Y

Sbjct: 88 GPLQIHVLHQFALAGHPEVLIVSNIVENG-----KPVGLGD-----AGHFWHSDLSYKE 136

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR₁₇₆ALVHQRSARHSLVYSQS₁₇₆KLGHVQ

+ G++ A+ +PA GG T FA+M A+D L R V R A H+ + ++L

Sbjct: 137 KPSLGSL₁₉₆LHAQELPAEGGDTLFANMHLAWDTLPAHLRRAVEGRRAEHTYLARYAELQARS

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGM₂₃₅DAAESERFLEGLVD

+ A + P+V+ HPETGR +L + H I G+ ES L+ L

Sbjct: 197 PWRPNLSPEQIAQVA₂₅₆AVVHPIVRTHPETGRKALFVSEHFTTRIVGLPDDESRALLDEL₂₅₆FV

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 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
dioxxygenase [Bradyrhizobium sp. Tep5]
Length = 153

Score = 120 bits (302), Expect = 1e-25, Method: Compositional matrix
adjust.

Identities = 64/157 (40%), Positives = 89/157 (56%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY
167

WH+DS++ P+ A+ ++ SA +V GG T FADMRAAYDALD+ T+ + HSL+Y

Sbjct: 2 WHSDSSFRPIPAKFSLLSARIVNPKGGNTEFADMRAAYDALDDETKTEIDDMICEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESE
227

S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+

Sbjct: 62 SRGSLGFLD-----YTDEEKEMFKPVLQRLVVRTHPVHGRKSLYLSSHAGAIRGMSMPEAL
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 dioxxygenase,
putative

[Talaromyces stipitatus ATCC 10500]

gb|EED18830.1| alpha-ketoglutarate-dependent taurine dioxxygenase,
putative

[Talaromyces stipitatus ATCC 10500]

Length = 290

Score = 120 bits (302), Expect = 1e-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 LTIVANKVAGADVLGFDFTMPHQVQALRSAWLKYGILRFRGYDLTDEHQLNFKR-- 67

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVG-----NMAWHADSTYMP
116

E G A + K D V M +I G + WH DS +

Sbjct: 68 --EEDG-----APTTYKDDEKVTV-----MTNLINGVPSGAGSNVELEWHTDSWFE
112

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
176

G + A +P GG T +ADM A YDAL E R+ + R + VY+ G+++

Sbjct: 113 YPPVGEILRAMELPQTGGDTYWADMYAVYDALPEDLRSTIEGRLIQFDTVYNGH--GNLR
170

Query: 177 QAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHA---IPGMDAAESERFLEGL
233

+ A P+++ HPE+GR ++ +G+ H I G+ ES+ L +
Sbjct: 171 KGKEAPKTDDFRLWEHIRHPIIRTHPESGRKAVFVVGQSKHEKNWIVGLPLEESKEILAKI
230

Query: 234 VDWACQAPRVHAHQ-WAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276

+ + + P HQ W GD V+WDNRC +HR E W R+M
Sbjct: 231 LSY-VEKPEFQLHQKWQPGDTVIWDNRCTMHRRETWPDDQTRIM 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--VQAGSAYIGYGMDDTATPLRPLVKVHPET 204

SKLGH +++ Y GYG P R L+KVHPET
Sbjct: 61 SKLGHQPKKSDGEYSGYGFHDGPVRRALIKVHPET 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-TLDDAGFAALHAAWLQHALLIFPGQHLNSNDQQITFA 61
Q T + PT GA V+ ++ T + A+ A W +H LL+F Q+L + ++F+

Sbjct: 16 QNTRSLAPT---FGAEVSDYTISSTTSNEENTAIKALWAKHKLKLLFRNQNLDDEETLVSFS 72

Query: 62 KRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
113

+ FG +E +++ +SN+K +G M + + WH D
Sbjct: 73 RVFGDLEIHVRTEYLSSAFPEVLYVSNMKNNG-----KMGILADTEVGWHYDQI
122

Query: 114 YMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
173

Y+P A G++ A +P GG T FADM AY L E + + A S S
Sbjct: 123 YLPRPAVGSLLMAHTLPPTGGNTEFADMTTAYSELPEEVKQQLEGARAVQSYEAFNSAYS
182

Query: 174 ----HVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSL-LIGRHAHAIPGMDAAESER
228

Q+ S I + P+V+ HP TG +L L I G +AA+S
Sbjct: 183 VPTSKEQKQKQSPDIAH-----PIVRTHPVTGEKALYLCPGMTTEIVGWEAADSRA
232

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276

L+ L +W Q V++H W GD ++WDN C +HR +P+D R+M
Sbjct: 233 MLDYLFWEWTVQPRYVYSHSWQPGDALLWDNACTMHRDRPFDQNHDRML 280

>gb|ABD16705.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. on192.6]

gb|ABD16706.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. ApT2]

gb|ABD16707.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [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 WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
167

WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A + HSL+Y
Sbjct: 2 WHSDSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAYDALDDETKAEIEDMICEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMTTAT---PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAA
224

S+ LG ++ Y + A L+ LV+ HP GR SL + HA AI M
Sbjct: 62 SRGSLG-----FLDYTDEEKAMFKPVLQRLVVRTHPVHGRKSLYLSSHAGAIRDMSMP
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 dioxygenase [Xanthomonas oryzae pv. oryzae MAFF
311018]

dbj|BAE70311.1| taurine dioxygenase [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 VQRSGVRIAPFDGPLGAEVIGLDDLQPLDADAFARLHRAHLDDHVLVFRDQRISPAQQVE 79

Query: 60 FAKRFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHAD
 111

F++RFGA+ + G +++ +SN+K +G P D WH+D
 Sbjct: 80 FSRRFGALQIHVLRNFQLRGHPEVLVSNIKENG-----EPIGLGD-----AGHDWHSD
 128

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSK
 171

+Y + G++ A+ +P+ GG T FA+ A+ L E+ V A HS +
 Sbjct: 129 LSYRETPSLGSLLLHAQQLPSEGGYTLFANQHLAWQTLPESLTRTVQDLRAEHSYLARYEA
 188

Query: 172 LGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL
 230

L A + P+V+ HPETGR +L + H I G+ ES L
 Sbjct: 189 LRARNPWCALTPEQIAEVTVPVHPVVRTHPETGRKALFVSEHFTTRILGLPEDESRAAL
 248

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ L + + V+ H+W D+V WDNR ++H A
 Sbjct: 249 QTLFAHSTRPALVYRHRWQPYDMVFWDNRSVMHLA 283

>ref|ZP_06411142.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp.
 EUN1f]

gb|EFC86045.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp.
 EUN1f]

Length = 281

Score = 120 bits (300), Expect = 2e-25, Method: Compositional matrix
 adjust.

Identities = 103/297 (34%), Positives = 143/297 (48%), Gaps = 42/297
 (14%)

Query: 5 TLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
 T+ P AT+GA V+GV L DDA A+ AA Q+ +L+F G L + Q+ F++

Sbjct: 4 TIICEPLAATVGAEVSGVDAEQLGQDDAVAGAVLAALEQYGVLVFRGLDLDPE SQVAFSR 63

Query: 63 RFGAIE-RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ-
 120

R G I+ G + I V D + ++S A++ + WH D P+ +
 Sbjct: 64 RLGEIDYEPGHHVPPIYRVTLAS--KNSSADY-----LKATFEWHMDGC-TPLHGEP
 114

Query: 121 ---GAVFSAEVVPAVGGRTCFADMRAAYDAL-DEATRVLVHQRSARHSLVYSQSKLGHVQ
 176

V SA+ V A GG T FA AAYDAL DE A R H++ SQ ++
 Sbjct: 115 PQKATVLSAKAVAATGGETEFASTYAAYDALGDEEKEAFAALRVV-HAMEASQRRVTP--
 171

Query: 177 QAGSAYIGYGMDDTTATPL-----RPLVKVHP-----ETGRPSLLIGRHAHAIPGMDDAAES
226

 D T L RP VHP TGR SL+IG A + MD AE
Sbjct: 172 -----DPTPEQLARWRARP-TSVHPLVWRRRTGRRSLVIGVQAGHVVDMDLAEG
219

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
R L+ L+D A RV+ H+W+ GD V+WDN ++HRA P+D + PR M + + G

Sbjct: 220 RRLQDLLDRATAPERVYRHRWSVGDTVIWDNTGVVHRAAPYDPRSPREMLRTTVFG 276

>ref|YP_778414.1| taurine dioxygenase [Burkholderia ambifaria AMMD]
gb|ABI92080.1| Taurine dioxygenase [Burkholderia ambifaria AMMD]
Length = 308

Score = 120 bits (300), Expect = 2e-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 FDIVPFDAPLGAEVVGIDLSQPLGAADFARVHRAHLDHHVLFVFRDQRITPDEHVAFSRRF 87

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP
116

 G ++ +++ +SN+ +G P D WH+D +Y
Sbjct: 88 GPLQIHVLHQFALAAHPEVLIVSNIVENG-----RPIGLGD-----AGHFWHSDLSYKE
136

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
176

 + G++ A+ +PA GG T FA+M A+D L R V R A H+ + ++L
Sbjct: 137 KPSLGSLHQAQELPAEGGDTLFANMHLAWDTLPAHLRRAVEGRRAEHTYLARYAELQARS
196

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDDAAESERFLEGLVD
235

 + + P+V+ HPETGR +L + H I + ES L+ L
Sbjct: 197 PWRPNLSAEQIAQVEAVVHPVVRTHPETGRKALFVSEHFTTRIVDLPEDESRALLDELFA
256

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

 + +A ++ H W A D+V WDNR L+H A L R ++ + + G
Sbjct: 257 HSVRAEHLYRHHWRAHDLVFWDNRSLMHLAAGTPDHLRRKLYRTTIEG 304

>ref|ZP_04590344.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv.
oryzae str.

1_6]
Length = 287

Score = 120 bits (300), Expect = 2e-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 LELVPITNLIGTEVRGIDVNSKLSDDVIEALYEAWISSTILLFRGQSMTPDQQLKFSRNF 61

Query: 65 GAI-----ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
116

G + +I+ +SN+ DG ++ V WH D Y+
Sbjct: 62 GELVSYTRSQFSEKTQPEILILSNITKDGK-----LIGSPVSGRVWHTDGHYLE
110

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ
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 EFSVQPQFTYRHRWVPGDIILWDNRSAMHKATVYDDKYRLLHRTTIGAR 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 = 2e-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 FDIVPFDAPLGAEVVGGIDLSQPLGAADFARVHRAHLDHHLVFRDQRITPDEHVAFSRRF 87

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
116

G ++ +++ +SN+ +G P D WH+D +Y
Sbjct: 88 GPLQIHVLHQFALAAHPEVLIVSNIVENG-----RPIGLGD-----AGHFWHSDLSYKE
136

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ
176

+ G++ A+ +PA GG T FA+M A+D L R V R A H+ + ++L
Sbjct: 137 KPSLGSLLHAQELPAEGGDTL FANMHLAWDTLPAHLRRRAVEGRRAEHTYLARYAELQARS
196

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ
169
ADSTYMPV A+GAVFSAE VP +GG T FADMRAAYDALDE RA + SA HSL YSQ
Sbjct: 1 ADSTYMPVQAKGAVFSAEEVPTIGGHTGFADMRAAYDALDEGMRAKLEGLSAFHSLYYSQ 60

Query: 170 SKLGH--VQQAGSAYIGYGMDDTTATPLRPLVKVHPET 204
SKLGH ++A Y GYG P R L+KVHPET
Sbjct: 61 SKLGHQPKKKADGEYSYGFHDGPVPRRALIKVHPET 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 = 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 LGA V G++L+ L FA +H A L H +L+F Q ++ D+ I F++RF
Sbjct: 28 FDIVPFDAPLGAEVIGLNLSQLGADDFARIHRAHLDHHVLFVFRDQRITPDEHIAFSRRF 87

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP
116
G ++ G +++ +SN+ +G P D WH+D +Y
Sbjct: 88 GPLQIHVLHQFALAGHPEVLTVSNIVENG-----KPVGLGD-----AGHFWHSDLSYKE
136

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS
176
+ G++ A+ +PA GG T FA+M A+D L R V A H+ + ++L
Sbjct: 137 KPSLGSLLHAQELPAEGGDTLFANMHLAWDTLPAHLRRAVEGLRAEHTYLARYAELQARS
196

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVD
235
+ A + P+V+ HPETGR +L + H I G+ ES L+ L
Sbjct: 197 PWRPNLSPEQIAQVAADVHPPIVTRTHPETGRKALFVSEHFTTRIVGLPDDESRALLDELFA
256

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +A ++ H W D+V WDNR L+H A L R ++ + + G
Sbjct: 257 HSVRAEHLRHAWRDHDLVFWDNRSLMHLAAGTPDHLRRLKLYRTTIEG 304

>ref|ZP_02466092.1| dioxygenase TauD/TfdA family protein [Burkholderia
thailandensis
MSMB43]
Length = 297

Score = 120 bits (300), Expect = 2e-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 STLCIRPLSAALGAQIDGVDARADLDADTVRAIRAAWLRFGLLVFRGQALDPARLVAFTR 64

Query: 63 RFGA-----IERIGGG--DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY
 114

RFG E G D++ +SN+ DG + + WH D +
 Sbjct: 65 RFGEPVVYTRAENACDGPDLVLSNIVKDGKP-----IGAAISGRYWHTDGHF
 113

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGH
 174

+ G + + PA GG TCF +M AAY AL RA + R+ V Q+ H
 Sbjct: 114 LACPPAGTLLFGDETPAEGGDTCFVNMATAAYRALPAWLRARIDGRTFVMDRV--QTLPFH
 171

Query: 175 VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGL
 233

+ A L+P+V+ HPETG+ +L IG I GM+ E + L
 Sbjct: 172 YPRR-PAPPPDQKRVWPDMLQPVVRTHPETGQNALYIGGVVWPWRIVGMERRYGEALMAHL
 230

Query: 234 VDWACQAPRV-HAHQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RP 285

A R + H+W AGD+++WDNRCL HRA +D + R M+ + +AG RP
 Sbjct: 231 HAIADFDEARFGYRHRWRAGDLLMWDNRCLAHRATDYDMARYRRTMYRTTIAGDRP 285

>gb|ADC33992.1| TfdA-like protein [uncultured bacterium]

Length = 208

Score = 120 bits (300), Expect = 2e-25, Method: Compositional matrix adjust.

Identities = 71/221 (32%), Positives = 113/221 (51%), Gaps = 28/221 (12%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVR-----QHSPAEWDDM---MKV
 101

QQI FA+ FG +E I ++ D +R H W + +
 Sbjct: 1 QQIAFARNFGPLE-----TTIKAIRKDAKLRLPAEIIDVSNLDHEAKRWTEQSRHRRF 53

Query: 102 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSA
 161

N WH DS++ V A+ ++ + VGG T FADMRAAYDALD+AT+ + A
 Sbjct: 54 EAANKLWHTDSSFKRVPKASLLYQRSIAPVGGHTEFADMRAAYDALDDATKQRLRGLVA
 113

Query: 162 RHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPL-RPLVKVHPETGRPSLLIGRHAHAIPG
 220

HS+ YS+++LG + + D P+ + +V+ HP++GR +L + HA I G
 Sbjct: 114 NHSIKYSRAQLGFDEYSEDE-----DIALQPVQVMVRRHPDGRMTLYLASHAGHIYG
 167

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
227

S+ LG + Y + L+ LV+ HP GR SL + HA AI GM E+
Sbjct: 62 SRGSLGFLD-----YTDEEKEMFKPVLQRLVVRTHPVHGRKSPLYLSSHAGAIRGMSMPEAR
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 = 3e-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 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
227

S+ LG + Y L+ LV+ HP GR SL + HA AI GM E+
Sbjct: 62 SRGSLGFLD-----YTDEEKQMFKPVLQRLVVRTHPVHGRKSPLYLSSHAGAIRGMSMPEAR
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 = 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 FDIVPFDAPLGAEVVGGIDLSQPLGAADFARVHRAHLDHHLVFRDQRITPDEHVAFSRRF 87

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP
116

G ++ +++ +SN+ +G P D WH+D +Y
Sbjct: 88 GPLQIHVLHQFALAAHPEVLIVSNIVENG-----RPIGLGD-----AGHFWHSDLSYKE
136

+Y + G++ A+ +P+ GG T FA+ A+ L E+ + V A HS +
 Sbjct: 129 LSYKETPSLGLSLHAQQLPSEGGDTLAFANQHLAWQTLPESLKRTVQDLRAEHSYLARYEA
 188

Query: 172 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL
 230

L A + P+V+ HPETGR +L + H I G+ ES L
 Sbjct: 189 LRARNPWCALTPAQIAEVTVPVHHPVRRHPETGRKALFVSEHFTTRILGLPEDESRLAL
 248

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 + L + + V+ H+W D+V WDNR ++H A

Sbjct: 249 QTLFAHSTRPALVYRHRWQPYDMVFDNRNSVMHLA 283

>gb|ABG66523.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
 dioxygenase [Bradyrhizobium canariense]
 Length = 153

Score = 118 bits (296), Expect = 6e-25, Method: Compositional matrix
 adjust.

Identities = 64/157 (40%), Positives = 87/157 (55%), 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 SQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
 227

S+ LG + Y L+ LV+ HP R SL + HA I GM E
 Sbjct: 62 SRGSLGFTE-----YTDDEKQMFKPVLQRLVVRTHPVHRRKSLYLSSHAGKIVGMSVPEGR
 116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264

L L + A Q+ V+ H+W D+V+WDNR +HR
 Sbjct: 117 LLLRDLNEHATQSEFVYVHKWKLHDLVMWDNRQTMHR 153

>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 = 6e-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 MQVLPQDAPCGALVGLDLKQALTDQAQVAEIRRHWLEHKVLAFTDQDLAIEDIERFASTI 62

Query: 65 GAIERIGGGD--IVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

G + G D AI VR+ D + + +WH+D +++

Sbjct: 63 GPL----GSDPYFTAI PGHPHVAQVRR-----DANERTPIFAESWHSWDSFLAQPPAAT
112

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLV--YS-QSKLGHVQQAG
179

V V+P VGG T FAD AA+DAL ++LV R HS YS Q G +

Sbjct: 113 VLYGNVIPPVGGDTLFDQYAAWDALPAELKSLVDGRQGVHSARRGYSRQAYGKDKGR
172

Query: 180 SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWAC
238

S I Y AT L P+ + HPETGR +L + + I GM E+ L L +

Sbjct: 173 SMAIRYSDSAMATQLHPIARKHPETGRTALFVSVGYTIGIDGMSDEEAAPILRALFEHQ
232

Query: 239 QAPRVHAHQWAAGDVVVDNRCLLHRA 265

+ V+ H+W+ G +VVVDNR+ H A

Sbjct: 233 RPEFVYRHRWSQGMLVVVDNRNVHAA 259

>ref|YP_837647.1| taurine dioxygenase [Burkholderia cenocepacia HI2424]
gb|ABK10754.1| Taurine dioxygenase [Burkholderia cenocepacia HI2424]
Length = 317

Score = 118 bits (295), Expect = 8e-25, 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 AAVPLQLRQVAGRIGAEISGVRLSATLDDATFDVHAALLRHKVLFFRQHHLLDDTAQEA 81

Query: 60 FAKRFGAIERIGGGDIVAISNVKA-DGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM
118

FA+RFG D VA V + DG+ + E D +WH D T++

Sbjct: 82 FARRFG-----DTVAHPTVPSVDGSA---ALLELDSAHGARAN--SWHTDVTTFVDAY
128

Query: 119 AQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQA
178

+ ++ A V+P GG T +A+ AY L + RAL A H+ Y + HV

Sbjct: 129 PKISILRAVVIPFVGGDTVWANTATAYANLPDPLRALADTLWALHTNAYDYAST-HVHAD
187

Query: 179 GSAYIGYGMDDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
235

+ Y T+T P+V+VHPETG +L++G I G+ + +S L+ L +

Sbjct: 188 DTQLKRYREVFTSTVYETEHPVVRVHPETGERTLVLGHFVQKIKGLSSQDSAHLLOVLHE
247

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 + W GDV +WDNR H A
 Sbjct: 248 HVTRLENTVRWNWQEGDVAIWDNRATQHYA 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 = 9e-25, 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 LKVTASGEACGATITGV DLSQDLDTETIAAIRAAWLEHHVVAFPDQSMSDEDLERFTLCF 62

Query: 65 GAIERIGGGDIVAISNVKADGTV-----RQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
 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 IATCLYGITIPPIGGDTL FANQHKAYDQMPDSLRSRVEGLT AIHSAEYAYAPRGVFDTEK
 169

Query: 176 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLL--IGRHAHAIPGMDAAESERFLEGL
 233
 + S I D A P ++ H ETGRP L +G + ++ A+S+ L+ L
 Sbjct: 170 EADRSMKIVLSEDAKQEHFPFIRNHSETGRPGLFSTLG-YIQGFVELEKADSDALLQEL
 228

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 D+ P V H+W +V+WDNR +LH A
 Sbjct: 229 YDYQGSEPFVFRHKWQPNMLVMWDNRSVLHMA 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 = 9e-25, 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 LQLRQVAGRIGAEISGVRLSATLDDATFDVAVHAALLRHKVLFFFRGQHHLDDTAQEAFAARR 85

Query: 64 FGAIERIGGGDIVAISNVKA-DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG D VA V + DG+ + E D +WH D T++ + +

Sbjct: 86 FG-----DTVAHPTVPSVDGSA---ALLELDSA HGARAN--SWHTDVTFV DAYPKIS
132

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAY
182

+ A V+P GG T +A+ AY L + RAL A H+ Y + HV +

Sbjct: 133 ILRAVVIPPFGGDTVWANTATAYANLPDPLRALADTLWALHTNAYDYAST-HVHADDTQL
191

Query: 183 IGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQ
239

Y T+T P+V+VHPETG +L++G I G+ + +S L+ L + +

Sbjct: 192 KRYREVFTSTVYETEHPVVRVHPETGERTLV LGHFVQKIKGLSSQDSAHL LQVLHEHVTR
251

Query: 240 APRVHAHQWAAGDVVVDNRCLLHRA 265

W GDV +W DNR H A

Sbjct: 252 LENTVRWNWQEGDVAIW DNRATQH YA 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 AAVPLQLRQVAGRIGAEISGVRLSATLDDATFDVAVHAALLRHKVLFFFRGQHHLDDTAQEA 81

Query: 60 FAKRFGAIERIGGGDIVAISNVKA-DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
118

FA+RFG D VA V + DG+ + E D +WH D T++

Sbjct: 82 FARRFG-----DTVAHPTVPSVDGSA---ALLELDSA HGARAN--SWHTDVTFV DAY
128

Query: 119 AQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQA
178

+ ++ A V+P GG T +A+ AAY L + RAL A H+ Y + HV

Sbjct: 129 PKISILRAVVIPPFGGDTVWANTAAAYANLPDPLRALADTLWALHTNAYDYAST-HVHAD
187

Query: 179 GSAYIGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVD
235

+ Y T+T P+V+VHPETG +L++G + G+ A +S L+ +

Sbjct: 188 DTQLKRYREVFTSTVYETEHPVVRVHPETGERTLV LGHFVQRLKGLSAQDSAHL LQVFHE
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 MKVTPFSPNCGAVVSDLQLATMND AQLEQLRDAFTEHGLLFFRDQQLPPEEHLRFANRFG 60

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
125
I S + A+ VR+ + + +G WH D +Y + A G++
Sbjct: 61 KIVVNKFFKTTEESPLIAE--VRK-----EKTQQTNIGG-GWHTDHSYDDIPALGSILV
111

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
185
A ++P GG T FA++ AAYDAL + + A HS + + G +
Sbjct: 112 ARILPETGGNTQFANLAAAYDALPNTLKRLEGLRAVHSNTHLYGENGLYRFTDLKDQLG
171

Query: 186 GMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVH
244
GMD P+V HP++GR L + H G + +S L+ L Q
Sbjct: 172 GMDRVGDATHPVVITHPQSGRKVLYVNP GHTIQFEGWEFDKSRELLD ELYAHVAQPQFTC
231

Query: 245 AHQWAAGDVVVWDNRCLLHRAE 266
+ W G V WDNRC H+A+
Sbjct: 232 SFNWQPGSVTFWDNRCTWHQAD 253

>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 WHS DSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAYDALDDETKAEVEDLVCEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMTTAT---PLRPLVKVHPETGRPSLLIGRHAHAIPGM DAA
224
 S+ LG + Y D A L+ LV+ HP R SL + HA I M
Sbjct: 62 SRGSLG-----FTEYTDDEKAMFKPVLQRLVVRTHPVHRRKSLYLSSHAGKIVSMSVP
113

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
 E L L + A QA V+ H+W D+V+WDNR +HR
Sbjct: 114 EGRLLLLRDLNEHATQAEFVYVHKWKLHDLVMWDNRQTMHR 153

>gb|ABD16695.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [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 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
167
 WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A + HSL+Y
Sbjct: 2 WHS DSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAYDALDDETKAEIEDLVCEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGM DAAESE
227
 S+ LG Y + L+ LV+ HP+ R SL + HA I M E
Sbjct: 62 SRGSLGFTD-----YTDDEKEMFKPVLQRLVVRTHPQHRRKSLYLSSHAGKIASMSVPEGR
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 dioxygenase [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 FEIRAFDGPLGAEVIGLDLSKPLDDAGFTRIHRALDHHVLFVRDQRITPERHVAFSRRF 79

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
116
 G ++ G +++ +SN+ +G P D WH+D +Y

>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-VQQAGSAYIGYGMDDTATPLRPLVKVHPET 204

++GH ++ Y GYG+ PLRPLVK+HPET
Sbjct: 61 GRVGHQTKKLDGEYSYGLHDGPVPLRPLVKIHPET 96

>ref|ZP_06210504.1| Taurine catabolism dioxygenase TauD/TfdA [Acidovorax avenae subsp.

avenae ATCC 19860]

gb|EFA40541.1| Taurine catabolism dioxygenase TauD/TfdA [Acidovorax avenae subsp.

avenae ATCC 19860]
Length = 306

Score = 116 bits (290), Expect = 4e-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 FEIRPLPGAPLGAEVLGLDLRSRPLGDADFARLHQAHLDHHVVVFRDQRITPRQHIDFSRR 83

Query: 64 FGAIE-----RIGGGDIVAISNVK-ADGTVRQHSPAEWDDMMKVIVGNMA--WHADS
112

FG ++ +I+ +SN+K A G + +G+ WH+D
Sbjct: 84 FGPLQIHVLKNFQLADHPEILVVSNIKDASG-----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 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLE
231

A + A + P+V+ HPETGR +L + H I G+ ES L
Sbjct: 191 RARSPWRPALTPAQIAEVAPAVHPVVRTHPETGRRALFVNEHFTTRIVGLPEDES RALLA
250

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
181

++ A +P GG T FA+M AY+ L + + R A HS VY +L +
Sbjct: 135 SLLLARELPQAGGDTLAFANMVRAYETLPAELKHSIEGRRAVHSYVYRYERLRALSARPP
194

Query: 182 YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-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 = 5e-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 TFAVEAIQIEPIAARITGLDLRQPLSAADAQAIDNVIAQYPVLVFPAQDIDDNQLLAFSEN 61

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
112

FG + E I ISNV D + A + M V WH+D
Sbjct: 62 FGPVQVSVQYATRQNEHRLQPRISDISNVGKDNETFK---AGDNRRMNTFVSR-RWHSDQ
117

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
172

+Y P+ A+ + VPA GG + FADMR YD+L + R + SA +++++
Sbjct: 118 SYQPIPARYSFLLNYSVPARGGESQFADMRLVYDSLQDLRETIENLSAEFDILHTRAMC
177

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRP----LVKVHPETGRPSLLIGRHAHAIPGMDAAESER
228

G + + + A L+P LVK HP +GR +L + HA + E
Sbjct: 178 G-----FTDFPEEERAM-LKPSIHRLVKTHPLSGRKTLYLSVHATHVVDWPIPEGRD
228

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264

L L+++A Q ++ H W D+V+WDNR L+HR
Sbjct: 229 LLRELMEFATQPQFIYTHHWTVKDLVMWDNRTLIHR 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 = 6e-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-----IVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
112

FG ++ + D + ISN+ + PA D + + WH D

Sbjct: 62 FGPLQPVVSFHTAKADHRLSPMVSDISNLDKNNRT---FPAG-DRRRMNFLSSRRWHTDG
117

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR LVHQRSARHSLVYSQSKL
172

+Y+P + ++ A V VGG+T FADMRAAYDAL LV + H++++S++

Sbjct: 118 SYLPTPNRYSMLLAYTVARVGGQTQFADMRAAYDALPAEWLELVEDLTLEHNVMSRAVA
177

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG
232

G + + LV+ HP +GR SL + HA + G E L

Sbjct: 178 GFTDFDEEERRRF-----PATHKKLVRRHPVSGRSLYLSGHASHVVGWVPVEGLDLLRE
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
dioxygenase [Bradyrhizobium sp. DcE2.8]

gb|ABD16696.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bradyrhizobium sp. Dp6.5]

 Length = 153

Score = 115 bits (288), Expect = 6e-24, Method: Compositional matrix
adjust.

Identities = 63/157 (40%), Positives = 85/157 (54%), Gaps = 5/157 (3%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR LVHQRSARHSLVY
167

WH+DS++ P+ A+ ++ SA VV GG T FADMRAAYDALD+ T+A + HSL+Y

Sbjct: 2 WHSDSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAYDALDDDTKAEIEDLVCEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESE
227

S+ LG + Y L+ LV+ HP R SL + HA I M E
Sbjct: 62 SRGSLGFTE-----YTDDEKQMFKPVLQRLVLRTHPVHRRKSLYLSSHAGKIVSMSVPEGR
116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264

L L + A Q V+ H+W D+V+WDNR +HR
Sbjct: 117 LLLRDLNEHATQGEFVYVHKWKLHDLVMWDNRQTMHR 153

>ref|NP_883162.1| putative taurine dioxygenase [Bordetella parapertussis
12822]

emb|CAE40240.1| putative taurine dioxygenase [Bordetella parapertussis]
Length = 260

Score = 115 bits (288), Expect = 6e-24, Method: Compositional matrix
adjust.

Identities = 78/255 (30%), Positives = 115/255 (45%), Gaps = 31/255 (12%)

Query: 44 LLIFPGQHLSNDQQITFAKRFGAIERIGG-----GDIVAINVKADGTVRQHSPA 94
+L+FPGQ L+ Q I F + FG +ER +++ ++N DG

Sbjct: 1 MLVFPGQDLNAPQLIDFTRHFGDVERNDSVPYYRDPDYEVLLVTNKPRDGKP----- 53

Query: 95 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRA
154

++ WH+D +Y A+G+V + P VGG T FA+M AY++L +
Sbjct: 54 ----LQTRNTGRNWHSDLSYTDRPAKGSVLMCKEKPPVGGDTMFANMYQAYESLSAPFKR
109

Query: 155 LVHQRSARH--SLVYSQSKLGHVQQAGSAYIGYGMTTATPL-RPLVKVHPETGRPSLLI
211

V A H SL+ + Q A + P+ P+V++HPETGR L +
Sbjct: 110 FVDGLHAVHDISLIKGFDRRDPEQTAA-----LKRRNPPIAHPVVRIPHETGRKCLFV
162

Query: 212 GRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEP-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

>ref|ZP_03585567.1| taurine dioxygenase [Burkholderia multivorans CGD1]

gb|EEE00159.1| taurine dioxygenase [Burkholderia multivorans CGD1]
Length = 314

Score = 115 bits (288), Expect = 6e-24, Method: Compositional matrix adjust.

Identities = 90/266 (33%), Positives = 126/266 (47%), 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 LQLRQVAGRIGAEISGVRLSATLDDATFDIAIQAALLRHKVLFFRGGHLLDAAQEAFARR 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 VFSAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAY
182

+ A V+P VGG T +A+ AAY L +A R L A H+ Y + HV +
Sbjct: 130 ILRAVVI PPVGGDTVWANTAAAYAHLPDALRTLADTLWAVHTNAYDYAST-HVHADETQL
188

Query: 183 IGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ
239

Y T+T P+V+VHPETG +L++G I G+ +S L+ + +
Sbjct: 189 KRYREVFTSTVYETEHPVVRVHPETGERTLVVLGHFVQRIKGLSTQDSAHL LQVFHEHVTR
248

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265

W GDV +WDNR H A
Sbjct: 249 LENTVRWSWQEGDVAIWDNRATQHYA 274

>gb|ADC34031.1| TfdA-like protein [uncultured bacterium]
Length = 210

Score = 115 bits (288), Expect = 6e-24, Method: Compositional matrix adjust.

Identities = 75/219 (34%), Positives = 107/219 (48%), Gaps = 22/219 (10%)

Query: 56 QQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVI
102

QQI FA+ FG I R+ +I ISN+ D V + D +
Sbjct: 1 QQIAFARHFGPIHSSAQRARHKS IKHRLASDEIADISNLDGDNKVMDQTARRRLDGL--- 57

Query: 103 VGNMAWHADSTYMPVMAQGA VFSAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSAR
162

N WH D+++ V ++ A VVP GG T FAD+RAAYDAL +A +A + A
Sbjct: 58 -ANRLWHTDASFRAVPGALSMLYAHVVPEEGDTEFADLRAAYDALPDARKAEIDGLIAE
116

Query: 163 HSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMD
222

HS+ +S+ +L + + P R +V+ HP + R +L I HA I GM
Sbjct: 117 HSIWHSRGLDVTKYSP EELASL----PPVPQR-VVRTHPGSRRKTLIASHASHIVGMP
171

Query: 223 AAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
 + L L++ A Q VHAH+W GD+V+WDNRC+
 Sbjct: 172 VPDGRLLLLDLIEHATQPRFVHAHRWRRGDLVIWDNRCV 210

>gb|ABD16689.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
 dioxygenase [Bradyrhizobium sp. Ppau3-41]
 Length = 153

Score = 115 bits (287), Expect = 7e-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---PLRPLVKVHPETGRPSLLIGRHAHAIPGMDDA
 224

S+ LG + Y D A L+ LV+ HP R SL + HA I M
 Sbjct: 62 SRGSLG-----FTEYTDDEKAMFKPVLQRLVTRTHPVHRRKSLYLSSHAGKIVSMSVP
 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 dioxygenase TauD/TfdA [Marinobacter
 algicola

DG893]

gb|EDM48213.1| Taurine catabolism dioxygenase TauD/TfdA [Marinobacter
 algicola

DG893]

Length = 290

Score = 115 bits (287), Expect = 7e-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 MKINPFANDFGAEITDVDLKDPSSEITERIYQAFLDHQMLVIRDQDLNPLEQVAFTERYG 60

Query: 66 AIE-----RIGGGD---IVAISN-VKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP
 116

+E + D ++ +SN ++ DGT + V+ WH+DS++
 Sbjct: 61 TLEWQENVKYAHPDHDKVLILSNEIRPDGTA-----VGVVDAGDFWHSDDSSHHE
 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 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-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 LFSYITDEARKYHYRHYYRTGDLVLWDNRCIVHRA 264

>ref|NP_936287.1| taurine catabolism dioxygenase [Vibrio vulnificus YJ016]
 dbj|BAC96257.1| probable taurine catabolism dioxygenase [Vibrio
 vulnificus YJ016]
 Length = 288

Score = 115 bits (287), Expect = 7e-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 IERETMKITPLATSFALVEDVQLSAINERQFEALYHAFHLYKVLFFRDQLLTAEQHLAL 63

Query: 61 AKRFGAIERI-----GGGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
 112

+RFG +E I +V I R+ P G WH D
 Sbjct: 64 GQRFGELEPIHPFFPHLADAPQVVVIE-----TREG LPP-----GESYWHTDL
 106

Query: 113 TYMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-VYSQSK
 171

T+ ++ A+ A+ P GG T + DM A + +LD++ + + A H+L + S+
 Sbjct: 107 TWKARPSKCALLHAQHCPPSGGDTIWTDM EAVWRS LDDSLKQQLRPLYATHALHAFENS
 166

Query: 172 LGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL
 230

H + G +Y+ P+V HPETG+ +L I I G++ A+S+ L
 Sbjct: 167 YDHKDEDES YVVKKSREFPAVHHPVVAQHPETGQETLYINEQFTRCIDGLEKAQSQALL
 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]
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 GAPLGAIEILGLSDAAGLSADAVAVIRRAWLAHDGLLVFRDVMLAPRAQVDFSRFRGPLQV 65

Query: 69 -----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
121

+I+ +SNV +G P D + WH+D +Y P + G
Sbjct: 66 HVLNQFHLDPDHPEILVVSNNVENG-----KPIGLGDAGR-----DWHS DLSYKQPQPSLG
114

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
181

++ A +P GG T FA+M AY+ L + ++ R A HS VY +L +
Sbjct: 115 SLLLARELPQAGGDTL FANMVRAYETLPAGLKRIIEGRRVHSYVYRYERLRALSAWRPP
174

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLI--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++ WDNR +H A
Sbjct: 234 PDNRYTHRWPQGDMLFWDNRSTIHFA 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 SIHVEPSGQACGATVRGLDLAQPLSSDTVQAIRAAWLEHHVLAFFPEQTLNDDDLERFTGY 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA-EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG G+ I+ V R+H A E + + AWH+D ++ G

Sbjct: 62 FGPF-----GEDPFIAPVPG-----REHVIAVERRAQEQAPLFAEAWHSDWSFQATPPIGT
112

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

+P GG T FA+ A D L A R + A H S + G + A A
Sbjct: 113 CLHGITIPPTGGDTLAFANQHKALDTLPSALRGRIEGLMAMHSAKVGYPDG-LYGAADAA
171

Query: 183 IGYGMDTTATP-----LRPLVKVHPETGRPSL--LIGRHAHAIPGMDAAESERFLEGLV
234

MD +P PL++ H ETGR SL +G + I GM E+ L L
Sbjct: 172 SDRSMDIRPSPEAQAVQSHPLIRRHSETGRASLYSCLG-YIVGIEGMPDEEAVELLMELY
230

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

W + ++ HQW G +++WDNRCLLHRA
Sbjct: 231 AWQTREENIYTHQWETGMLIMWDNRCLLHRA 261

>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%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
+ + P A+ GA + G L A+ AAW + +L F G ++ Q F+ FG

Sbjct: 1 MNVIPIQASCADIIIGFDFEHLYPDQVDVRAAWRDYGVLRFRGYDITTOQHAKFSNLFG 60

Query: 66 AIERIGG-----GDIVAINVKADGTVRQHSAPAEWDDMMKVIVGN--MAWHADSTYM
115

+ G +I ISN K DG P +GN + WH DS Y
Sbjct: 61 HYVPVKGTSIAHHDQKEITVISNAKVDG-----KPVG-----TLGNVDLEWHTDSWYF
108

Query: 116 PVMAQGA VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHV
175

G + A +P GG T + +M A YDAL E TR ++ R + ++VY +G V
Sbjct: 109 DKPPCGQILRALELPRTGGDTYWVNMVAVYDALPEFTRKIIIEGRLIQFNIVY--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 IYSLIDSGKFVQKQWQPNDIIMWDNRCTMHRRDGWNEDMRIM 270

>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 LGIRPLSAALGARIDGIDARAELDADTVRAIRAAWLRFGLLVFRGQALDPPRLVAFTRRF 66

Query: 65 G---AIERI-----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP
 116
 G R G +++ +SNV DG + + WH D Y+
 Sbjct: 67 GEPVYTRACNACDQPEVLVLSNVVKDGKPE-----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 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLVD
 235
 Q + P +P+V+ HPETG +L IG I GM+ S+ + L
 Sbjct: 174 QRPAPPPDQKQAWPDMP-QPVVTRHPETGENALYIGGVVWPRIVGMEQGLSDALMAHLHA
 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 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR_LVHQRSARHSLVYSQ
169

ADSTYMPV A+GAVFSAE+VPA G T +ADMRAAYDALDEATR L+ + A HSL YSQ
Sbjct: 1 ADSTYMPVQAKGAVFSAEIVPASGAPTGWADMRAAYDALDEATRELIADKLAYHSLYYSQ 60

Query: 170 SKLGHV---QQAGSAYIGYMDTTATPLRPLVKVHPET 204

+ G++ Q G Y YG LRPLVKVHPET
Sbjct: 61 GRAGYLPSKQNDGGGYDQYGYHDLEPSLRPLVKVHPET 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 LELRQVAGRIGAEIAGVRLSSTLDDATFDIAIQAAALLRHKVLFERNQEHLDAAQEAFARR 86

Query: 64 FGAIERIGGGDIVAISNVK-ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG D VA V ADG+ E D +WH D T++ + +
Sbjct: 87 FG-----DTVAHPTVPPADGSAHL---LELDSAHGARAN--SWHTDVTFVDAYPKVS
133

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATR_LVHQRSARHSLVYSQSKLGHVQQAGSAY
182

+ A V+P GG T +A+ AAY L E+ RAL A H+ Y + HV +
Sbjct: 134 ILRAVVIPPFGGDTVWANTAAAYAHLPESLRALADTLWALHTNAYDYAST-HVHADDTQL
192

Query: 183 IGYMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ
239

Y T+T P+V+VHPETG +L++G I G+ + +S L+ L + +
Sbjct: 193 KRYREVFTSTVYETEHPVVRVHPETGERTLVLGHFVQRIKGLSSQDSAHLQLQVLHEHVTR
252

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265

+W GDV +WDNR 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

W H D T + A V A +G G T F A+M A A Y L E+ R V A H L
 Sbjct: 125 FWHQDGTLLNPNQASAVLRAATAYRLGGDTGFANMAAAAYQGLPESLRTFVDGLRAVHRLG
 184

Query: 167 YSQSKLGHVQQAGSAYIGYGMDTTATP---LRPLVKVHPETGRPSLLIGR-HAHAIPGMD
 222

 +++ D A P + P+V+VHPETG +L + R I G+
 Sbjct: 185 IRDIPSEDIRK-----DIRAHPRSVIHPVVRVHPETGERALFVNRISTEDIIGLT
 234

Query: 223 AAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDF-----KLPRV
 275

 +S+R L+ L D + W G D V W D N R L H R P D + R+
 Sbjct: 235 MRQSQRILDLLFDETEKPEYAVYFHWKPGDVAFWDNRSSLHRG-PADLGKLGHTAETDRL
 293

Query: 276 MWHSRLAG 283

 ++H L G
 Sbjct: 294 LYHVALLG 301

>ref|ZP_02406371.1| dioxygenase TauD/TfdA family protein [Burkholderia
 pseudomallei

DM98]

Length = 297

Score = 114 bits (285), 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 L G A + G + A L D A + A A W L + L L + F G Q L + + F + R F

Sbjct: 7 LGIRPLSAALGARIDGIDARAELDADTVRAIRAAWLRFGLLVFRGQALDPPRLVAFTRRF 66

Query: 65 G---AIERI-----GGGDIVAI SNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMP
 116

 G R G +++ +SNV DG + + W H D Y+
 Sbjct: 67 GEPVVYTRACNACDQPEVLVLSNVVKDGKPE-----IGAALSGRYWHTDGHYLA
 115

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ
 176

 G + +PAVGG T F +M A A Y A L R + R+ V Q+ H
 Sbjct: 116 CPPAGTLLFGAEIPAVGGDTHFVNMTAAYRALPAWVRTQIDGRTFVMDRV--QTLPFHYP
 173

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLVD
 235

 Q + P +P+V+ HPETG +L I G I G M+ S+ + L
 Sbjct: 174 QRPAPPPDQKQAWPDMP-QPVVRTHPETGENALYIGGVVWPWRIVGMEQRLSDALMAHLHA
 232

Query: 236 WACQAPRV-HAHQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RPE-TEGAA
 291

A R + H+W AGD+++WDNRCL HRA +D + R M+ + +AG RP GAA
 Sbjct: 233 IAFDEARFGYRHRWRAGDLLMWDNRCLAHRAATDYDMVRHRRRTMYRTTIAGDRPRYVRGAA
 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 = 1e-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 LGIRPLSAALGARIDGIDARAELDADTVRAIRAAWLRFGLLVFRGQALDPPRLVAFTRRF 76

Query: 65 G---AIERI-----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP
 116

G R G +++ +SNV DG + + WH D Y+
 Sbjct: 77 GEPVVYTRACNACDQPEVLVLSNVVKDGKPE-----IGAALSGRYWHTDGHYLA
 125

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
 176

G + +PAVGG T F +M AAY AL R + R+ V Q+ H
 Sbjct: 126 CPPAGTLLFGAEIPAVGGDTHFVNMTAAYRALPAWVRTQIDGRTFVMDRV--QTLPFHYP
 183

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLVD
 235

Q + P +P+V+ HPETG +L IG I GM+ S+ + L
 Sbjct: 184 QRPAPPPDQKQAWPDMP-QPVVRTHPETGENALYIGGVVWPRIVGMEQRLSDALMAHLHA
 242

Query: 236 WACQAPRV-HAHQWAAGDVVVDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RPE-TEGAA
 291

A R + H+W AGD+++WDNRCL HRA +D + R M+ + +AG RP GAA
 Sbjct: 243 IAFDEARFGYRHRWRAGDLLMWDNRCLAHRAATDYDMVRHRRRTMYRTTIAGDRPRYVRGAA
 302

>gb|ABD16693.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
 dioxygenase [Bradyrhizobium sp. Lppb2]
 Length = 153

Score = 114 bits (285), Expect = 1e-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 WHS DSSFRPIPAKFSLLSARVVNPKGGNTEFADMRAAFDALDDDTKAEIEDLVCEHSLMY 61

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAEASE
227

 S+ LG + Y L+ LV+ HP R SL + HA I M E
Sbjct: 62 SRGSLGFTE-----YTDDEKQMFKPVLQRLVVRTHPVHRRKSLYLSSHAGKIVSMSVPEGR
116

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264

 L L + A Q V+ H+W D+V+WDNR +HR
Sbjct: 117 LLLRDLNEHATQGEFVYVHKWKLHDLVMWDNRQTMHR 153

>ref|YP_105432.1| TauD/TfdA family dioxygenase [Burkholderia mallei ATCC
23344]
 ref|YP_337565.1| TauD/TfdA family dioxygenase [Burkholderia pseudomallei
1710b]
 ref|YP_001024592.1| TauD/TfdA family dioxygenase [Burkholderia mallei
NCTC 10229]
 ref|YP_001078924.1| TauD/TfdA family dioxygenase [Burkholderia mallei
NCTC 10247]
 ref|YP_001075173.1| TauD/TfdA family dioxygenase [Burkholderia
pseudomallei 1106a]
 ref|ZP_01765536.1| dioxygenase TauD/TfdA family [Burkholderia
pseudomallei 305]
 ref|ZP_02414882.1| dioxygenase TauD/TfdA family protein [Burkholderia
pseudomallei 14]
 ref|ZP_03450025.1| dioxygenase, TauD/TfdA family [Burkholderia
pseudomallei 576]
 ref|ZP_04521659.1| dioxygenase, TauD/TfdA family [Burkholderia
pseudomallei MSHR346]
 ref|ZP_00442490.2| dioxygenase, TauD/TfdA family [Burkholderia mallei GB8
horse 4]
 ref|ZP_04812458.1| dioxygenase, TauD/TfdA family [Burkholderia
pseudomallei 1106b]
 ref|ZP_04889852.1| dioxygenase TauD/TfdA family [Burkholderia
pseudomallei 1655]
 ref|ZP_04899361.1| dioxygenase TauD/TfdA family [Burkholderia
pseudomallei S13]
 ref|ZP_04953910.1| dioxygenase, TauD/TfdA family [Burkholderia
pseudomallei 1710a]
 ref|ZP_04967610.1| dioxygenase TauD/TfdA family [Burkholderia
pseudomallei 406e]
 ref|ZP_04971897.1| dioxygenase, TauD/TfdA family [Burkholderia mallei
2002721280]
 gb|AAU47037.1| dioxygenase, TauD/TfdA family [Burkholderia mallei ATCC
23344]
 gb|ABA51696.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei
1710b]

gb|ABN00471.1| dioxygenase, TauD/TfdA family [Burkholderia mallei NCTC 10229]
 gb|ABN95133.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 1106a]
 gb|ABO02276.1| dioxygenase, TauD/TfdA family [Burkholderia mallei NCTC 10247]
 gb|EBA49323.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei 305]
 gb|EDK82772.1| dioxygenase, TauD/TfdA family [Burkholderia mallei 2002721280]
 gb|EDO87497.1| dioxygenase 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 = 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 LGIRPLSAALGARIDGIDARAELDADTVRAIRAAWLRFGLLVFRGQALDPPRLVAFTRRF 66

Query: 65 G---AIERI-----GGGDIVAI SNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMP
 116
 G R G +++ +SNV DG + + WH D Y+
 Sbjct: 67 GEPVVYTRACNACDQPEVLVLSNVVKGKPK-----IGAALSGRYWHTDGHYLA
 115

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR LVHQRSARHSLVYSQSKLGHVQ
 176
 G + +PAVGG T F +M AAY AL R + R+ V Q+ H
 Sbjct: 116 CPPAGTLLFGAEIPAVGGDTHFVNMTAAYRALPAWVRTQIDGRTFVMDRV--QTLPFHYP
 173

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGM DAAESERFLEGLVD
 235
 Q + P +P+V+ HPETG +L IG I GM+ S+ + L
 Sbjct: 174 QRPAPPPDQKQAWPDMP-QPVVRTHPETGENALYIGGVVPWRIVGMEQRLSDALMAHLHA
 232

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--HSPAEDW-DMMKVIVGNMAWHADSTYMP
116

FA+RFG + A TV +P D + K + WH D T++
Sbjct: 61 FARRFGEV-----TTAHTPTVPSLPDNPEVLDLNYGKTVARANNWHTDVTFVD
107

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLG-HV
175

G+V A V+P GG T +A+ AY+ L R L Q A HS Y + +
Sbjct: 108 SPPLGSVLRALVIPPSGGDTIWANSVTAYEDLPTHLRNLADQLWAVHSNAYDYAAATVDL
167

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
235

+ AY T L P+V+VHPE+G L IG I G+ ES+ ++ L
Sbjct: 168 PEEVRAYRAVFTSTVYETLHPVVRVHPESGERGLFIGGFVRRIRGLSQNESDEIVKLLQA
227

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRA 265

+ + +W GDV WDNR H A
Sbjct: 228 YVTRPENTVRWRWQVGDVAFWDNRATQHYA 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 = 1e-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 IDVQPIAGALGAEISGVDLSQPVPDETFAEIRSALHNNHQQVIFFRDQQLTPDQHKAFSARF 66

Query: 65 GAIERI-----GGGDIVAISNVKADGTVRQHSPAEDWDDMMKVIVGNMAWHADSTYMPV
117

G + + G +I+ + KA+ T R AWH D +Y +
Sbjct: 67 GDLLEVPFVRALEGHAEILPVMKGKAEQTKRNFG-----GAWHTDMSYAEI
112

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQ
177

G+ A V+P GG T +A M AYDAL + + ++ + A HS V S G V
Sbjct: 113 PPLGSALYARVIPPYGGDTMWASMYHAYDALSDGLKLVLDKLRVHSPVRSYGARGAVVN
172

Query: 178 AGSAYIGYGMT-----TATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFL
230

G + MD + L P+V+VHP TGR +L + + GM ES L
Sbjct: 173 NGDP--AHKMDVRTDDDRANSEVLHPVVRVHPATGRKALYVNSTYTMRFEGMTEEEESAPLL
230

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ L A + +W G + VWDNRC H A

Sbjct: 231 QYLYAHAARPEFTCRFRWTRGALAVWDNRCTQHLLA 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 = 1e-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 LGIRPLSAALGARIDGIDARAELDADTVRAIRAAWLRFGLLVFRGQALDPPRLVAFTRRF
100

Query: 65 G-----AIERIGG-GDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMP
116

G A G +++ +SNV DG + + WH D Y+
Sbjct: 101 GEPVVYTRACNACDQPEVLVLSNVVKDGKP-----IGAALSGRYWHTDGHYLA
149

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
176

G + +PAVGG T F +M AAY AL R + R+ V Q+ H
Sbjct: 150 CPPAGTLLFGAEIPAVGGDTHFVNMTAAYRALPAWVRTQIDGRTFVMDRV--QTLPFHYP
207

Query: 177 QAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLVD
235

Q + P +P+V+ HPETG +L IG I GM+ S+ + L
Sbjct: 208 QRPAPPPDQKQAWPDMP-QPVVRTHPETGENALYIGGVVPWRIVGMEQRLSDALMAHLHA
266

Query: 236 WACQAPRV-HAHQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RPE-TEGAA
291

A R + H+W AGD+++WDNRCL HRA +D + R M+ + +AG RP GAA
Sbjct: 267 IAFDEARFGYRHRWRAGDLLMWDNRCLAHRATDYDMVRHRRRTMYRTTIAGDRPRYVRGAA
326

>ref|YP_775305.1| taurine dioxygenase [Burkholderia ambifaria AMMD]
 gb|ABI88971.1| Taurine dioxygenase [Burkholderia ambifaria AMMD]
 Length = 318

Score = 114 bits (284), Expect = 1e-23, Method: Compositional matrix
 adjust.

Identities = 89/266 (33%), Positives = 126/266 (47%), Gaps = 20/266 (7%)

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 LQLRQVAGRIGAEIAGVRLSNTLDDATFDQAIQAALLRHKVLFVRNQEHLDDAAQEAFAARR 86

Query: 64 FGAIERIGGGDIVAISNVK-ADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGA
 122

FG D VA V ADG+ + E D +WH D T++ + +
 Sbjct: 87 FG-----DTVAHPTVPPADGSAQL---LELDSAHGARAN--SWHTDVTFVDAYPKVS
 133

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY
 182

+ A V+P GG T +A+ AY L E RAL A H+ Y + HV +
 Sbjct: 134 ILRAVVIPFPGGDTVWANTATAYAHLPEPLRALADTLWALHTNAYDYAST-HVHADDTQL
 192

Query: 183 IGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ
 239

Y T+T P+V+VHPETG +L++G I G+ + +S L+ L + +
 Sbjct: 193 KRYREVFTSTVYETEHPVVRVHPETGERTLVVLGHFVQKIKGLSSQDSAHLQLQVLHEHVTR
 252

Query: 240 APRVHAHQWAAGDVVVDNRCLLHRA 265

+W GDV +WDNR H A
 Sbjct: 253 LENTVRWRWQQGDVAIWDNRATQHAYA 278

>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 = 1e-23, Method: Compositional matrix
 adjust.

Identities = 87/282 (30%), Positives = 124/282 (43%), Gaps = 15/282 (5%)

Query: 4 TTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
 T I G +GA +TGV LA LD+ + AA L+H L+F Q+L ++ Q+ FA
 Sbjct: 6 TDFDIRRIGGRIGAEITGVDLAGNLDEGILKEVKAAALLEHKALVFRNQNLDDEGQLRFAS 65

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGA
 122

+FG + A V Q P + + + WH D T++ + +
 Sbjct: 66 QFGPLTS-----AHPTVPGIAEQPQILPVDSEGAANV-----WHTDVTFVQSPPKAS
 113

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
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 RDVVFSTKYRTAHPVVRVHPETGERGLFIGAFAQTIEGLSTTESKDVLRLLQAYVNRPEN
233

Query: 243 VHAHQWAAGDVVVWDNRCLLHRAEPWDFK-LPRVMWHSRLAG 283

V QW GDVV++DNR H A P D+ LPR + +AG
Sbjct: 234 VLRVQWNPBGDVVIFDNRITQHYA-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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
195

T F DMRAAYDALD+ + HS YSQ K+G +++ + M
Sbjct: 1 TEFCDMRAAYDALDDERKQQFEGLLGTHSYAYSQKVGGLLEEVFTPEARARMVDIE---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|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 SVLTINKLTASVGAEEVVGIDSERLATDDGIAAAVLDALDNGVLVFRGLYLEPEAQVAFS 61

Query: 62 KRFGAIERIGGG--DIVAISNVKADGTVRQHSPPAEWDDMMKVIVGNMAWHADSTYMPVM-
118

+R G ++R G + I + D T ++ AE+ + WH D P+
Sbjct: 62 QRLGEVDRSADGHPVSGIYPITLDQT--KNKAAEY-----LKATFDWHIDGC-TPLND
112

Query: 119 ---AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSAR----HSLVYSQSK
171

+ V SA V A GG T FA+ AAY++LD + QR AR HSL SQ +
Sbjct: 113 ECPQKATVLSAIEVAARGGETEFANAYAAYESLDADEK----QRYARLRVVSLEASQRR
168

Query: 172 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE
231

V +A T PLV H GR SL++G A I GMD E L+
Sbjct: 169 ---VYPDPTAEQRRRWAARPTHEENPLVWTH-RNGRKSIVLGASADHIVGMDRDEGRALLD
224

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
GL+ +V++H+W+ GD V+WDN+ +LHRA P++ PR M + + G

Sbjct: 225 GLLARTTTPDKVYSHKWSVGDTVIWDNQGVLHRAAPYEPDSPRHMLRRTTVLG 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 LQLRQVAGRIGAEISGVRLSATLDDATFDIAIQALLRHKVLFFRQGHLLDAAQEAFARR 82

Query: 64 FGAIERIGGGDIVAISNVKA-DGTVRQHSPPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG D VA V + DG+ E D + WH D T++ + +
Sbjct: 83 FG-----DTVAHPTVPSVDGSAHL---LELDSAHGARANS--WHTDVTTFVDAYPKIS
129

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

+ A V+P VGG T +A+ AAY L + R L A H+ Y + HV +
Sbjct: 130 ILRAVVIIPVGGDTVWANTAAAYAHLPDTLRRTLADTLWAVHTNAYDYAST-HVHADETQL
188

Query: 183 IGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ
239

Y T+T P+V+VHPETG +L++G I G+ +S L+ + +
Sbjct: 189 KRYREVFTSTVYETEHPVVRVHPETGERTLVLGHFVQRIKGLSTQDSAHLQLQVFHEHVTR
248

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265

W GDV +WDNR H A
Sbjct: 249 LENTVRWSWQEGDVAIWDNRATQHYA 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 = 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 LQLRQVAGRIGAEISGVRLSATLDDATFDIAIQALLRHKVLFVRGQHHLDDAAQEAFAARR 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 VFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

+ A V+P VGG T +A+ AAY L + R L A H+ Y + HV +
Sbjct: 130 ILRAVVIPPVGGDTVWANTAAAYAHLPDTRLTLADTLWAIHTNAYDYAST-HVHADETQL
188

Query: 183 IGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ
239

Y T+T P+V+VHPETG +L++G I G+ +S L+ + +
Sbjct: 189 KRYREVFTSTVYETEHPVVRVHPETGERTLVLGHFVQRIKGLSTQDSAHLQLQVFHEHVTR
248

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265

W GDV +WDNR H A
Sbjct: 249 LENTVRWSWQEGDVAIWDNRATQHYA 274

>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 = 2e-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-----TTAHTVPVSLTGHPEILDLDYGKTAARANNWHTDVTFVD
107

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLG-HV
175

G++ A +PA GG T + + AY L E R L + A HS Y ++ ++
Sbjct: 108 RPPLGSILRALEIPAYGGDTIWGNSVTAYRDLPEHLRQLADELWAVHSNAYDYAEAAVNL
167

Query: 176 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAESERFLEGLVD
235

+ AY T L P+V+VHPE+G L IG I G+ ES+ ++ L
Sbjct: 168 SEDLKAYREVFTSTVYETLHPVVRVHPESGEKGLFIGGFVRQIRGLSTTESDHIIQLLQS
227

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRA 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 = 2e-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---IGGGDIVAISNVKADGTVRQHS-PAEWDMMKVIVGNMAWHADSTYMPV
117

+ FG IE + D A + + R S WH D T+
Sbjct: 95 GRLFGEIESHPTVPAPDGTAFLELNSQHGGRADS-----WHTDVTFKAA
138

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYS-----QSK
171

+ V A +P GG T +A+ AAY+ L E R L Q A H Y Q+
Sbjct: 139 FPKVCVLRVAVTLPGHGGDTVWANTVAAYEGLPEPLRQLAEQLWAVHGNVDYDAENFRQNA
198

Query: 172 LGHVQQAGSA-YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESERFL
230

+ AG A Y T +PLV VHPETG +LL+G A I G+ A ES L
Sbjct: 199 ASQTETAGRASYRKVFTRKTIIESEQPLVHVHPETGEKALLLGHFAKRIKGLRANESTALL
258

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ + + QWA GDV +WDNR H A

Sbjct: 259 QLFNERIIRLENTVRWQWAQGDVAIWDNRATQHYA 293

>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 LGIRPLSAALGARIDGIDARAELDADTVRAIRAAWLRFGLLVFRGQALDPPRLVAFTRRF 66

Query: 65 G---AIERI-----GGGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
116

G R G +++ +SNV DG + + WH D Y+
Sbjct: 67 GEPVVYTRACNACDGQPEVLVLSNVVKDGKP-----IGAALSGRYWHTDGHYLA
115

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ
176

G + +PAVGG T F +M AAY AL R + R+ + Q+ H
Sbjct: 116 CPPAGTLLFGAEIPAVGGDTHFVNMTAAYRALPAWVRTQIDGRT--FVMDRLQTLFPHYH
173

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-AIPGMDDAAESERFLEGLVD
235

Q + P +P+V+ HPETG +L IG I GM+ S+ + L
Sbjct: 174 QRPAPPPDQKQAWPDMP-QPVVRTHPETGENALYIGGVVPWRIVGMEQRLSDALMAHLHA
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|ADC33990.1| TfdA-like protein [uncultured bacterium]

Length = 208

Score = 113 bits (282), Expect = 3e-23, Method: Compositional matrix adjust.

Identities = 71/219 (32%), Positives = 106/219 (48%), Gaps = 24/219 (10%)

Query: 56 QQITFAKRFGA-----IERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVI-
102

QQI FA+RF R+G + ISN+ +G + + DD ++
Sbjct: 1 QQIAFAQRFDGQLHTKTGISALRKNRLGNEALGDISNLDENGEL-----LKSDDRRRMYG 55

Query: 103 VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSAR
162

+GN WH D+++ + ++ +A+V+P VG T FADMRAAYDAL +A +
Sbjct: 56 LGNRLWHTDASFQDPPGRYSLA AKVLPVGAETEFADMRAAYDALPPDFQAQLEGLRVH
115

Query: 163 HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMD
222

HS+ +S+ LG A D + PL++ P + R SL + HA I
Sbjct: 116 HSIASRQMLGFEFSEKEA-----DLLKGAVHPLIRTLPHSQRSKSLYVASHASKIIDRP
169

Query: 223 AAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

E L L++ A Q V+ HQW GD+V+WDNRC+
Sbjct: 170 VPEGRLLLRELIEHATQPEFVYRHQWRMGDLVIWDNRCV 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 = 3e-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 LQLRQVAGRIGAEIAGVRLSGTLD DATFD AIQAALLRHKVLFFR GQHLLDDTAQEAFARR 85

Query: 64 FGAIERIGGGDIVAISNVK-ADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG DIVA V DG+ E D +WH D T++ + +
Sbjct: 86 FG-----DIVAHPTVPPVDGSAHL---LELDSA HGARAN--SWHTDVTFV DAYPKIS
132

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAY
182

+ A +P GG T +A+ AAY L + RAL A H+ Y + HV +
Sbjct: 133 ILRAVAIPFPGGDTVWANTAAAYTHLPDPLRALADTLWALHTNAYDYAST-HVHADDTQL
191

Query: 183 IGYGMDDTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ
239

Y T+T P+V+VHPETG +L++G + G+ A +S L+ + +

Sbjct: 192 KRYREVFTSTVYETEHPVVRVHPETGERTLVLGHFVQRLKGLSAQDSAHLLOVVFHEHVTR
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 = 3e-23, Method: Compositional matrix
adjust.

Identities = 57/124 (45%), Positives = 75/124 (60%), Gaps = 3/124 (2%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSAHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
195

T FADMRAAYDALD+ +A + HS YSQ K+G +++ + M
Sbjct: 1 TEFADMRAAYDALDDQRKAQLEGLLGHSHSYAYSQGVGGLEEVFTPEARARMVDVE---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 = 4e-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-----GGGDIVAIISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP
116

G R G +++ +SNV DG + + WH D Y+
Sbjct: 67 GEPVVYTRACNACDGQPEVLVLSNVVKDGKP-----IGAALSGRYWHTDGHYLA
115

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR₁₇₆LVHQRSARHSLVYSQSKLGHVQ

Sbjct: 116 CPPAGTLLFGAEIPAVGGDTHFVNMTSAYRALPAWVRTQIDGR₁₇₃TFVMDRV--QTLPFHYP

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR₂₃₅HAH-AIPGM₂₃₅DAAESERFLEGLVD

Sbjct: 174 QRPAPPPDQKQAWPDMP-QPVVRTHPETGENALYIGGV₂₃₂PWRIVGMEQRLSDALMAHLHA

Query: 236 WACQAPRV-HAHQWAAGDVVWVWVWVWVWVWVWVW₂₉₁DNRCLLHRAEPWDF-KLPRVMWHSRLAG-RPE-TEGAA

Sbjct: 233 IAFDEARFGYRHRWRAGDLLMWDNRCLAH₂₉₂RATDYDMVRHRRRTMYRTTIAGDRPRYVRGAA

>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 = 4e-23, Method: Compositional matrix adjust.

Identities = 85/272 (31%), Positives = 130/272 (47%), Gaps = 20/272 (7%)

Query: 2 AQTTLQITPTGATLGATVTGVH-LATLDDAGFAALHAAWLQ₆₀HALLIFPGQHLSNDQQITF

Sbjct: 14 AA₇₃EAFRITPLQAPLGA₇₃EV₇₃RGLDARRPLAPEQVLALKQALREHHILVFRQ₇₃QHL₇₃LDDEQY₇₃LR₇₃F

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHS₁₁₂PAEWDDMMKVI-----VGNMAW--HADS

Sbjct: 74 AT₁₂₃LF₁₂₃GS₁₂₃VF₁₂₃Q-PPADIPVLSS-GGDGKV-----PDIVKVANTGDGELGNFALPAHIDH

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR₁₇₂LVHQRSARHSLVYSQSKL

Sbjct: 124 Q₁₈₃WTPV₁₈₃PSSGSFLYALEVPSSGGETRFTNLARAYESLDEATREIDGLRLINYNPFIRLRE

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR₂₃₁HAHA-IPGM₂₃₁DAAESERFLE

Sbjct: 184 G₂₄₃GYGGGFATYRTPDIEPIQ₂₄₃GSEHPLVRTHPESGRRVLF₂₄₃LSA₂₄₃TEVEI₂₄₃PGYDPARGQALIG

Query: 232 GLVDWACQAPRVHAHQWAAGDVVWVWVWVWVWVWVWVW₂₆₃DNRCLLH

Sbjct: 244 RLREHLARPELSYSHAWSVGDIVWVWVWVWVWVWVWVW₂₇₅QAVLH

[Ralstonia solanacearum IPO1609]
emb|CAQ62397.1| alpha-ketoglutarate-dependent taurine dioxygenase protein
[Ralstonia solanacearum IPO1609]
Length = 281

Score = 112 bits (280), Expect = 4e-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 GAPLGAEILGLSDAAGLSADAVAVIRRAWLAHDGLLVFRDVMLAPRAQVDFSRFRGPLQV 65

Query: 69 -----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
121

+I+ +SNV +G P D + WH+D +Y P + G
Sbjct: 66 HVLNQFHLPDHPEILVVSNNVENG-----KPIGLGDAGR-----DWHSDL SYKQPQPSLG
114

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSA
181

++ A +P GG T FA+M AY+ L + ++ R A HS VY +L +
Sbjct: 115 SLLLARELPQAGGDTL FANMVRAYETLPAGLKRIIEGRRVHSYVYRYERLRALSAWRPP
174

Query: 182 YIGYGMDDTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGM DAAESERFLEGLVDWACQ
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 PDNRYTHRWPQSDMLFWDNRSTIHFA 259

>emb|CAY27207.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 121

Score = 112 bits (280), Expect = 5e-23, Method: Compositional matrix adjust.

Identities = 55/124 (44%), Positives = 76/124 (61%), Gaps = 3/124 (2%)

Query: 136 TCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
195

T FADMRAAYDALD+ +A + + HS YSQ K+G +++ + M
Sbjct: 1 TEFADMRAAYDALDDERKAQLERLLGTHSYAYSQKVGGLLEEVFTPEARARMIDVE---H 57

Query: 196 PLVKVHPETGRPSLLI GRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

P+V++HP TGR SL IGRH + + GM +++ LE L+ WACQ PR+ H W GD+V+
Sbjct: 58 PIVRIHPATGRKSLFGRHVYRVGTMTDDDAQAMLEELLAWACQPPRLFKHIWTVGDIVM
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 = 5e-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 GAPLGAIEILGLSDAAGLSADAVAVIRRAWLAHDGLLVFRDVMLAPRAQVDFSRFRGPLQV 85

Query: 69 -----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
 121
 +I+ +SNV +G P D + WH+D +Y P + G
 Sbjct: 86 HVLNQFHLPDHPEILVVSNNVENG-----KPIGLGDAGR-----DWHSDLSEYKQPPLG
 134

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
 181
 ++ A +P GG T FA+M AY+ L + ++ R A HS VY +L +
 Sbjct: 135 SLLLARELPQAGGDTLAFANMVRAYETLPAGLKRIIEGRRVHSHYVRYERLRALSARPP
 194

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLI--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 = 5e-23, Method: Compositional matrix adjust.

Identities = 83/271 (30%), Positives = 128/271 (47%), Gaps = 25/271 (9%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 + I P+GA GA V+G+ L+ L+DA +A+ +AWL+H +L F Q + +D F
 Sbjct: 1 MHIEPSGAACGARVSGIDLSVALEDADISAIRSAWLEHKVLAFADQQMDDDALERFTLAM 60

Query: 65 GAI-----ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
 118

G + I G + +A +AD T + N WH+D +++
 Sbjct: 61 GGFGE DPFDPIDGHEHIAAIKREADETS-----TLFAEN--WHS DWSFLRKP
 106

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLV--YSQSKL-GHV
 175

G A +P +GG T F+D AA+ AL + + + +A HS Y+ L G
 Sbjct: 107 PSGTCLMAVEIPPIGGDTLFS DQVA AFAALPDKRKDEL RAMTAVHSASRGYAPDGLYGDN
 166

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLV
 234

+ S I G A PLVK+HPETG +L + I GMD ++ + + L
 Sbjct: 167 DKGRSMSIRPGEAALARQSHPLVKLHPETGEEALFCSISYTVGIEGMDDMDAFQLIIELH
 226

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

W Q V+ H+W G +V+WDNR + H+A
 Sbjct: 227 QWCEQDRFVYRHKWQPGMLVIWDNRSVNHKA 257

>ref|ZP_05002612.1| taurine dioxygenase [Streptomyces sp. Mg1]
 gb|EDX27123.1| taurine dioxygenase [Streptomyces sp. Mg1]
 Length = 304

Score = 112 bits (280), Expect = 5e-23, Method: Compositional matrix
 adjust.

Identities = 80/269 (29%), Positives = 125/269 (46%), Gaps = 26/269 (9%)

Query: 4 TTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62

+T I G +GA VTGV L A L D+ F ++ A+L+H +L F Q ++++QQ+ FA
 Sbjct: 19 STFDIRKIGGRIGAEVTVGDLSAGLSDSVFGQINEAFLEHKVLFVRNQRDITDEQQALAFAG 78

Query: 63 RFGAIER----IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
 118

RFG + R + D A + DG ++ WH D ++
 Sbjct: 79 RFGPLTRKHPPMRAVDTAAPHVLAVDGEDQRAD-----HWHTDISFTTAP
 123

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ--
 176

+ G + V+P GG T A+ A Y L R + + A H+ Q +LG +
 Sbjct: 124 SLGTTLRVVLPPYGGDTLVANAAAGYRDLPAELRKIADRLWAVHTNHAEQPRLGTERGD
 183

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW
 236

+ A++ +T P+V+VHPE+G PSL +G A + GM+ ES ++ L +

Sbjct: 184 KVREAFLSRRFETA-----HPVVRVHPESGEPFLGGAQWLVGMEVRESRPIIDVLQSY
239

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ W GDV+V+DNR H A

Sbjct: 240 VRRPENTARWTWRPGDVLVFDNRSTQHYA 268

>ref|YP_002765055.1| dioxygenase [Rhodococcus erythropolis PR4]
dbj|BAH32316.1| putative dioxygenase [Rhodococcus erythropolis PR4]
Length = 331

Score = 112 bits (279), Expect = 6e-23, Method: Compositional matrix
adjust.

Identities = 83/267 (31%), Positives = 123/267 (46%), Gaps = 27/267 (10%)

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 VTPLGAHIGARIDGITLGEHLDPATISLIRQALLEHKVIFFRGQNHLNDSQYEFQQLG 87

Query: 66 AIERIGGGDIVAISNVKADGTVRQHS----PAEWDDMMKVIVGNMAWHADSTYMPVMAQG
121

+ A TV+ H P + D+ K +WH D T++ + +
Sbjct: 88 -----TPTTAHPTVKSHGAKVLPID-SDLGKA----NSWHTDVTFVDRIPKA
129

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVY---SQSKLGHVQQA
178

++ A +P GG T +A AAY+ L + +AL ARH+ VY + S +
Sbjct: 130 SILRAVQLPEYGGSTTWASGVAAYNGLPDPLKALAENLWARHTNVYDYAATSAERLTEDR
189

Query: 179 GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC
238

+AY T P+V+VHPETG +L++G G+ +S + L D A
Sbjct: 190 TAAYREEFQSTYFETEHPVVRVHPETGERTLVLGHFVKNFVGLSTEQSNVFKLLQDHAI
249

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ W AGDV +WDNR H A

Sbjct: 250 KLEYTTRWNWEAGDVVAIWDNRATQHYA 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 = 6e-23, Method: Compositional matrix
adjust.

Identities = 84/271 (30%), Positives = 128/271 (47%), Gaps = 24/271 (8%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
+I P +GA + G+ + TLDD AA+ AAWL + ++ FPGQHL+ + + FA+RF 65
Sbjct: 32 FEIVPLSGNIGAEIRGLDVRTLDDREVAAVRAAWLHYKVVFFPGQHLTPAEHLAFARRF 91

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA----WHADSTYMPVMAQG
121

E G ++ + + + +S A VG ++ WH D T++ G
Sbjct: 92 --EPTEGHPVIPGLDGOPEVFEIDYSKARELAAAYGRVGTVSRGLDWHTDVTFVKRPPLG
149

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRNLVHQRSARHSLVYSQSKLGHVQQAGSA
181

++ A VVP GG T F++ AA+ AL A + + +A H G Q G
Sbjct: 150 SILRAVVVPPAGGDTLFSNQEAFAALSPALQEFGLTTLTAVHD-----GEAQFKGIL
201

Query: 182 -YIGYGMDDTTATPLR-----PLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEG
232

+G G T +R P+V+ HPETG+ SL + G +H I +D AES+ L
Sbjct: 202 DLVGEGRWEGETFVRLEPAAHPVVRTHPETGKKSFLVNPFGTSH-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 = 6e-23, Method: Compositional matrix
adjust.

Identities = 59/97 (60%), Positives = 71/97 (73%), Gaps = 2/97 (2%)

Query: 110 ADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRNLVHQRSARHSLVYSQ
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 ARAGYMPSKNEKGSYGGYGYHDGEP SLRPLVKVHPET 97

>gb|ACG80550.1| TfdA [uncultured bacterium]

Length = 121

Score = 112 bits (279), Expect = 6e-23, Method: Compositional matrix
adjust.

Identities = 54/124 (43%), Positives = 76/124 (61%), Gaps = 3/124 (2%)

Query: 136 TCFADMRAAYDALDEATRNLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDALD+ + + HS YSQ K+G +++ + M
Sbjct: 1 TEF GDMRAAYDALD DERKQQLEGLLGH TSHYAYSQGVGGLEEVFTPEARARMVDVE---H 57

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

P+V+ HP+TGR SL IGRH + + GMD +++ LE L+ WAC+ PR+ H+WA GD+V+
Sbjct: 58 PIVRTHPQTGRKSLFIGRHVYRVVTGMDDDDAQAMLEELLAWACRPPRLFVKHKWAVGDIVM
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 = 6e-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--RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

+E ++V+ V T + ++P E WH D T+ ++GA+
Sbjct: 62 ELEPAHPFFPNVSSPQVSIIEETTKGNAPLE-----SYWHTDLTWREQPSKGAI
110

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
183

A+ VP GG T + M A +DALD + + Q SA HSL + + +
Sbjct: 111 LHAQHVPNTGGDTIWSMTAVFDALDNTMKTCLRQLSATHSLTAFEEVAEEDIELDWHHR
170

Query: 184 GYGMDDTATP-LRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAP
241

+ P + P++K+HPETG+ +L I I + E ++ L L A Q
Sbjct: 171 LLEVSHQHPPVVPVVIKIHPETGKETLFINEQFTRHINEVGHTEGKQLLNELFTIARQPE
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 = 6e-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--ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
117

FG E G+ + P D WH D+TY+
Sbjct: 61 LVAHFGTPIPEPFSAGN-----EPDPLTEGDFQTAKRATSVWHTDTTYVTE
106

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
177

A +P VGG TC+++M AAY+ L R ++ +A HS+ ++G +
Sbjct: 107 PPSLTALRAISLPPVGGDTCSNMYYAAYNTLSAPLRGMLDGLTAVHSVYPVIQRMGTAGK
166

Query: 178 AGSAY--IGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLV
234

A + + +G + + P+++VHPET R +L + I + AES L L
Sbjct: 167 AHADHSAPAHGFEN----VHPVIRVHPETERKALFVNEAWTTRIVELQPAESAHLALLLF
222

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285

+ ++WA D+ +WDNR + H A P D+ PRVM LAG RP
Sbjct: 223 EHVKSPDFTMRYRWAPNDLAIWDNRAVQHYAVP-DYDTPRVMQRVVLGDRP 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 = 7e-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 MAATTLTVKPVAGAIGAEVGGVDLSQKLSDAMVGAIRKALLDHLVIFFRDQELTPEQLMA 60

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
119

F+ RFG VA VK + +P + + G + WH+D+ Y V
Sbjct: 61 FSLRFG-----QPVAYPFVKGLDGFPEITPILKREEDRSNFGGL-WHSDTVYQQVPP
111

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG
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 HSSVGLKGDDELVS-RHPAVRTHPETGRKVLVNVVAHTTFEGMTEDESAPILEFLFRHQI
230

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLAG 283

++ QW G V WDNRC H R+M LAG
Sbjct: 231 KSELTCRFQWTKGAVAFWDNRCTQHNPINDYHGFRMMHRVTLAG 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 = 8e-23, Method: Compositional matrix
adjust.

Identities = 59/98 (60%), Positives = 69/98 (70%), Gaps = 3/98 (3%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ
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
Sbjct: 61 GRAGYLPSKQKEGGYDQYGYHDMEPSLRPLVKVHPET 98

Query: 256 WDNR 259
WDNR
Sbjct: 118 WDNR 121

>ref|ZP_01101038.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Congregibacter
litoralis KT71]
gb|EAQ99139.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Congregibacter
litoralis KT71]
Length = 281

Score = 111 bits (278), Expect = 9e-23, Method: Compositional matrix
adjust.

Identities = 85/270 (31%), Positives = 120/270 (44%), Gaps = 19/270 (7%)

Query: 5 TLQITPTGATLGATVTGVHLLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+ + P+G GA VTG+ L+ LD AL AWL+H +L FP Q +S+D F +
Sbjct: 2 SFNVEPSGQACGARVTGLDLSKNLDADTVRALRGAWLEHHVLAFPDQSISSDDLERFTQY 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA-EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122
FG G+ I+ + R+H A E + AWH+D ++ G
Sbjct: 62 FGPF-----GEDPFIPIPG-----REHVIAVERRAQETSPIFAEAWHSDWSFQATPPPIGT
112

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSAHSLVYSQSKLGHVQQAGSA-
181
+P GG T FA+ A D L R + A HS + G A +A
Sbjct: 113 CLHGVTIPPTGGDTLAFANQHKALDTPGDLRQRIEGCMAMHSAKAGYAPDGMYGDADAAG
172

Query: 182 ----YIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHAHAIPGMDAAESERFLEGLVD
235
I D A PL++ H ETGR SL +G + I GM E+ L L
Sbjct: 173 DRSMDIRPSPDAKAVQTHPLIRRHGETGRASLYSCLG-YIVGIEGMPDDEAIELLMELYG
231

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
W + ++ H+W G +++WDNRCLLHRA
Sbjct: 232 WQREENIYTHEWEEGMLIMWDNRCLLHRA 261

>ref|YP_001859330.1| taurine dioxygenase [Burkholderia phymatum STM815]
gb|ACC72284.1| Taurine dioxygenase [Burkholderia phymatum STM815]
Length = 316

Score = 111 bits (277), Expect = 1e-22, Method: Compositional matrix
adjust.

Identities = 87/270 (32%), Positives = 125/270 (46%), Gaps = 20/270 (7%)

Query: 2 AQTTLQITPTGATLGATVTGVHLLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQIT 59

Sbjct: 21 A TL + +GA + G+ L+ ++ F A+HAA L+H +L F GQ HL + Q
 APETLDVRRVAGRIGAEIRGIELSGSIGAPTFDAIHAALLKHKVLFRRGQQHLDDAAQEA 80

Query: 60 FAKRFGAIERIGGGDIVAISNVKA-DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
 118

Sbjct: 81 FA+RFG + VA V + DG+ E D +WH D T++
 FARRFG-----ETVAHPTVPSVDGS---RHLELDSQHGAN--SWHTDVTTFVDAY
 127

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQA
 178

Sbjct: 128 + ++ A V+P GG T +A+ AAY+ L E R L A H+ Y + HV
 PKISILRAVVIPFPGD TVWANTAAAYEHLPEPLRRLADTLWALHTNAYDYAS-SHVDAD
 186

Query: 179 GSAYIGYGMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
 235

Sbjct: 187 G Y T+T P+V+VHPETG SL++G + G+ A+ES L+ D
 GEQLKRYREVFTSTVYETEHPVVRVHPETGERSLVLGHFVQRLKGLSASESAHLLQVFHD
 246

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRA 265

Sbjct: 247 + W GDV +W DNR H A
 HVTRLENTVRWSWTQGDVAIWDNRATQHYA 276

>ref|YP_001505084.1| taurine dioxygenase [Frankia sp. EAN1pec]
 gb|ABW10178.1| Taurine dioxygenase [Frankia sp. EAN1pec]
 Length = 309

Score = 111 bits (277), Expect = 1e-22, Method: Compositional matrix
 adjust.

Identities = 87/292 (29%), Positives = 123/292 (42%), Gaps = 23/292 (7%)

Query: 3 QTTLQITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
 QT + + P GA + GV L LDDA A + +A L ++ F Q+L + QQ+ F

Sbjct: 8 QTLIDVRPLSGYTGAEIHGVDLREELDDATIAEIRSALLTWKVVFFRDQNL DHAQQVAFG 67

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQG
 121

Sbjct: 68 +RFG + + + +E KV N WH D T + G
 RRFGLTPAHPHETAPPEGFPEILPIDSRRYSEIIGKRKVTYDN-GWHTDVTALVNPPAG
 126

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQA GSA
 181

Sbjct: 127 ++ A++VP GG T + ++ AAY AL E R L ARHS G
 SILRADIVPPYGGDTAWTNLVAAYQALPEPLRTLADSLRARHSFNLQIFDGG-----
 179

Query: 182 YIGYGMDTTATPLR---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 EQIARPEFTVRFKWNPGDIAFWDNRATAHLG-PSDLGHLDLDFDRVLYRVTLEG 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 MEIIKSGLALGAEVKGMDSLSSNEVDQINKAWDENLVLVFKNQNLTDPLIKF'SKNF 60

Query: 65 GAIERIGGG-----DIVAISNVKADGTVRQHSPAEWDDMMKVIVGN--MAWHAD
111

G ++ +I ISNVK +G I+G+ WH+D

Sbjct: 61 GNLDHPAPNPFGINFSPEYPEINVISNVKKEGKPTG-----ILGDGEATWHS
108

Query: 112 STYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK
171

+Y V + + + VP G T FA+M AAY+ + + + + H ++

Sbjct: 109 MSYQDVPPKAGILYSLEVPKDQGDTHFANMIAAYEDMPDDLKNRIEGKILIHDSAHNS--
166

Query: 172 LGHVQQAGSAYIGYG--MDTTATP--LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAES
226

AG GY D + TP P+V P TG+ +L IGR HA + G++ +ES

Sbjct: 167 -----AGQLRKGYYEVS DPSKTPGAKHPIVFKDPNTGKKALFIGRRPHAYVIGLELSES
220

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR 284
E+ L+ + A Q +W A ++++W N +LH+ + +D RVM +++ G

Sbjct: 221 EKLLDDIWAHATQKKYTWTQRWQANELLMWKNLFLVHKKRDAFDPNTRRVMHRTQVTGE 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 IEIEKITPNIGACIHGVDLSTCKTEDLKKVYQALIDHQVFFDNQRISPDQQLNLAKFFG 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 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQA
178

++GA+ A+ VP GG T + M + +DALD+A + + SA HSL + V +

Sbjct: 106 SKGAILHAKHVPDAGGDTIWVSM TSVFDALDDAIKMKLRNLSATHSLTAFEDVDEEVIEL
165

Query: 179 GSAYIGYGMDDTTATP-LRPLVKVHPETGRPSLLIGRH-AHAIPGM DAAESERFLEGLVDW
236

+ + P + P+VKVHPETG+ +L I I M AE R L+ L

Sbjct: 166 DWHHRLREVSHQQRPV IHPVVKVHPETGKETLFINEQFTRCINEMRHAEGSRLLKELFAV
225

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRA 265

A Q +W G + +WDNR H A

Sbjct: 226 ARQPEHQVRFKWQKGLAIWDNR TTQHYA 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 AAVPLQLRQVAGRIGAEIADVRLSATLDDATFD AIQAALLRHKVLFFRQHHLLDDTAQEA 81

Query: 60 FAKRFGAIERIGGGDIVAISNVKA-DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
118

FA+RFG D VA V + DG+ + E D + WH D T++

Sbjct: 82 FARRFG-----DTV AHPTVPSVDGSA---ALLELDSA HGARANS--WHTDVTFV DAY
128

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQA
178

+ ++ A V+P GG T +A+ AAY L + RAL A H+ Y + HV

Sbjct: 129 PKISILRAVVIPPFGGDTVWANTAAAYAHLPDPLRALADTLWALHTNAYDYAST-HVHAD
187

Query: 179 GSAYIGYGMDDTTATPLR---PLVKVHPETGRPSLLIGRH AHAIPGM DAAESERFLEGLVD
235

+ Y T+T P+V+VHPETG +L++G + G+ A +S L+ +

Sbjct: 188 DAQLKRYREVFTSTVYETEHPVVRVHPETGERTLVLGHFVQRLKGLSAQDSAHLLQVFE
247

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ W GDV +WDNR H A

Sbjct: 248 HVTRLENTVRWNWREGDVAIWDNRATQHYA 277

>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 LELRQVAGRIGAEIAGVRLSSTLDDATFDIAIQAALLRHKVLFFRNQEHLDDAAQEAFARR 85

Query: 64 FGAIERIGGGDIVAISNVK-ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG D VA V ADG+ E D +WH D T++ + +
Sbjct: 86 FG-----DTVAHPTVPPADGSAHL---LELDSAHGARAN--SWHTDVTFVDAYPKVS
132

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
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 KRYREVFTSSVYETEHPVVRVHPETGERTLVLGHFVQKIKGLSSQDSAHLLQVLHEHVTR
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 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
 + + LGA ++G+ L D F ++ L+H ++ F Q ++N+QQI A +FG
 Sbjct: 1 MNVKLLSGALGAEISGIDLTDSDQNFKKINDLLEHKVIFFRDQPITNEQQIALAAKFG 60

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA-----WHADSTYMPVM
 118

+E ++ G ++ H +++++I G WH+D +Y
 Sbjct: 61 PLE-----THAYVKG-LKDHP-----EIVRIIKGKEEKNQWGENWHSADVSYNSKP
 104

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ-Q
 177

+ + + +P VGG TCF++M A++ LD ++ + + A HS + ++ + + +
 Sbjct: 105 TKAVILKSVKIPVGGDTCFSNMELAWETLDPKIQSKIINKKAVHSSLGAEFFIDNYKYM
 164

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDW
 236

G+ Y + + P+V+ HPETG+ L + + I G++ ES++ L+ + +
 Sbjct: 165 EGNEKRNYD---SYSNEHPIVRTHPETGKKILYVNWYTKQIIGLEKEESDQVLKEIFEH
 221

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEG 289

+ W V +WDR ++H A DF R + + R+ R EG
 Sbjct: 222 QARLDLTCRFSWTEDTVAIWDNRSVIHYAIA-DFFPGRGLGYERIMDRIAIEG 273

>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%)

Query: 3 QTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
 QT L++ P + GA + GV L+ L A+ A L H ++ F Q L+ +Q F
 Sbjct: 4 QTALEVRPLTGSCGAELFGVDLSQALSADTVKAIHQALLDHNVIFFREQTLTPEQHRAFT 63

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVI-----VGNMAWHADST
 113

++FG + +V +G + D+M VI +G+ WH+D +

Sbjct: 64 RQFGEV-----VVNPVYTHVEG-----YPDIMPVIKEPNDRYNI GD-TWHS DMS
106

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLG
173

YM G+V +P GG T FA+M AYD L EA R ++ R A HS Y S++
Sbjct: 107 YMQEPLG SVLYGRDIPEYGGDTL FANMYL AYDLLPEALRQMIDGRQAYHS DRYLTSRIS
166

Query: 174 HVQQAGSAYIGYGM DTTAT-PLRPLVKVHPETGRPSLLIG-RHAHAIPGM DAAESERFLE
231

S + D L P+V+ H ETGR L + I G+ ES L
Sbjct: 167 ERNAGRSTRLKADADAKENLALHPMVRTHEETGRKCLYVNF PFTWQIEGLSREESLPLLH
226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVW DNRCLLHRA 265

L A + +W G + WDNRC +H A
Sbjct: 227 QLYAHAARPEFACRFRWRKGS LAFWDNRCTMHYA 260

>ref|ZP_01894276.1| alpha-ketoglutarate-dependent 2,4-
dichlorophenoxyacetate

dioxygenase [Marinobacter algicola DG893]

gb|EDM47645.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate

dioxygenase [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%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHA AWLQHALLIFPGQHLSNDQQITFAKRF 64

+I P + GA + G+ LA + DA FAA+ A+ ++ ++ F Q + + F R+
Sbjct: 10 FRINPLTESFGAEILGLDLAKPISDATFAAIQEA FQKYHVICFRDQVMDEKAHLDFTLRW 69

Query: 65 GAIERIGGGD--IVAISNVKADGTVRQHSPA EWDDMMKVIVG-NMAWHADSTYMPVMAQG
121

G +E D A + T R+ DD + N WH DS+Y V +
Sbjct: 70 GELEVFPEEDKTTTAKTFY NVANTSREGEHLS EDDPRVLFQKVNARWHTDSSYRYVPSFA
129

Query: 122 AV-FSAEVV P--AVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQA
178

+V +S E++P A GG T F++M AAYDAL +A + H + + + A
Sbjct: 130 SVMYSTEILPDEARGGETEFSNMLAAYDALSDADKRRFEPLH MVHYEFGR----RLYP A
185

Query: 179 GSAYIGYGM DTTATPLRPLVKVHPE-TGRPSLLIGRHA-HAIPGM DAAESERFLEGLVDW
236

+ D PLV+VHP+ + SL +A + I GM E + + L ++
Sbjct: 186 LPPITPFERDAVPPVSHPLVRVHPDRDNQRSLFF TVNAGNEISGMSLEEGQALHKWLDEY
245

Query: 237 ACQAPRVHAHQWAAGDVVVW DNRCLLHRAEPWDF-KLPRVMWHSRLAG 283

A + +++H+W D+V+WDNR LLHRA +D K R + +AG
 Sbjct: 246 ASKPEFIYSHRWCENDLVMWDNRVLLHRATHYDMAKYRRAFRRRTTVAG 293

>ref|YP_001133737.1| taurine catabolism dioxygenase TauD/TfdA

[Mycobacterium gilvum

PYR-GCK]

gb|ABP44949.1| Taurine catabolism dioxygenase 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: 4 TTLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61

+ L I ++GA V GV L D++ AA+ A + +L+FP HL+ + Q+ F+

Sbjct: 2 SLLTINKLTPSVGAEVLGVDPVRLASDESLLAAVLDALDNGVLFVFPDLHLAPEAQVAFS 61

Query: 62 KRFGAIERIGGG--DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV--
 117

+R GA++ G + I V D + +++ A + + WH D P+

Sbjct: 62 RRLGAVDHSADGHPVAGIYPVTLDKS--KNASAAAY-----LRATFDWHIDGC-TPIGD
 112

Query: 118 --MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHV
 175

+ V SA V GG T FA+ AAY+A + + HSL SQS+ V

Sbjct: 113 ECPQRATVLSAVQVADRGGETEFANSYAAAYEAFSDEEKERYAALRVVHSLEASQSR---V
 169

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
 235

S + T PLV H +GR SL++G AH + GMD E L L+D

Sbjct: 170 NPDPSPEELARWRSRPTHEHPLVWTH-RSGRKSLVLGASAHYVVGMDYDEGRALLAELLD
 228

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

A Q V++H W+ GD V+WDN +LHRA P+D R M + + G

Sbjct: 229 RATQPELVYSHSWSVGDTVIWDNNGVLHRAAPYDPDSQREMLRRTTVLG 276

>emb|CAY27226.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 121

Score = 110 bits (275), Expect = 2e-22, Method: Compositional matrix
 adjust.

Identities = 56/124 (45%), Positives = 75/124 (60%), Gaps = 3/124 (2%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
 195

T FADMRAAYDALD+ +A + HS +SQ K+G +++ + M

Sbjct: 1 TEFADMRAAYDALDDQRKAQLEGLLGTSHYSAHSQKVGGLLEEVFTPEARARMVDVE---H 57

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

PLV+ HP TGR SL IGRH + + GM +++ LE L+ WACQ PRV H+W GD+V+
Sbjct: 58 PLVRTHPATGRKSLFIGRHVYRVVTGMTDDDAQAMLEELLAWACQPPRVFKHRWTVGDIVM
117

Query: 256 WDNR 259

WDNR

Sbjct: 118 WDNR 121

>ref|YP_002911540.1| Dioxygenase, TauD/TfdA family protein [Burkholderia
glumae BGR1]

gb|ACR28836.1| Dioxygenase, TauD/TfdA family protein [Burkholderia glumae
BGR1]

Length = 281

Score = 110 bits (275), Expect = 2e-22, Method: Compositional matrix
adjust.

Identities = 80/281 (28%), Positives = 127/281 (45%), Gaps = 41/281 (14%)

Query: 6 LQITPTGATLGATVTGVHLA-----TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
+++ P LGA V G+ L T DD + +H +L+FP +S++QQI

Sbjct: 1 MKVIPLSPALGAEVRGIDLTRPLSARTRDD-----IVGLLTHEQMLVFPDMSMSSEQQIA 55

Query: 60 FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
112

++ FG +E +I +SNV DG + + WH+D
Sbjct: 56 MSRNFGLEPHPMTTNTSPYPEITVVSNTTGDGKPLGYPTPPFQ-----LWHS DL
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 CYLERPAKMTLFYAESVPEQHGDWTFANMFRAYDTLPEHLKAALDGRNAVFSLDGSLVK-
164

Query: 173 GHVQQAGSAYIGYGMDDTATPLRPLV-----KVHPETGRPSLLIG-RHAHAIPGMDAAES
226

IG+ ++ A +P V +VHPE+ R S+ + H ++ G +S
Sbjct: 165 -----RCRKIGFDLNIAADDFKPTVSHPAIRVHPESLRRSIFVNWAHTDSVEGYSPEQS
218

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEP 267
E LE + ++ H++ AG++V+WDN ++H P

Sbjct: 219 EALLEQVFAHCLNEDFIYRHRYTAGELVIWDNASVIHTNSP 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 = 2e-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-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHAD
111

+ FGA+E +I +SNV DG + ++ WH+D
Sbjct: 55 AACRDFGALEPHPMTTNTSAFPEITVVSNTVDGKPVGYPTPPFE-----LWHSD
104

Query: 112 STYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK
171

Y+ A+ F AE VP G T FA+M AY+AL + + + R+A SL S
Sbjct: 105 LCYLEHPAKMTFFYAESVPEAHGDTWFANMFDAYEALPDDLKTAIEGRNAIFSL--DGSL
162

Query: 172 LGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFL
230

+ ++ G D T P V+ HPET + S+ + H I G ES+ L
Sbjct: 163 VKRCRKKGFDLNIAEEDFKPTVSHPAVRAHPETRKRSIFVNWAHTDRIEGYSPEESDDIL
222

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEP 267

+ + ++ H++AA D+V+WDN L+H P
Sbjct: 223 DRIFAHCTNEAFIYRHRYYAADLVIWDNASLIHTNSP 259

>ref|YP_002799309.1| Taurine catabolism dioxygenase, TauD/TfdA family
[Azotobacter

vinelandii DJ]

gb|ACO78334.1| Taurine catabolism dioxygenase, TauD/TfdA family

[Azotobacter

vinelandii DJ]

Length = 338

Score = 110 bits (274), Expect = 2e-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-----GDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWH
109

G + R G ++ I+N+ DGT P +D + + + WH

Sbjct: 87 GQPQEGANRLYIRAAGIAQEERFPALLPITNLGPDGT-----PVRENDGLGSL--EVVWH
139

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ
169

+D++Y+ G + A PA G T FA+ AY+ L E + + R A+H S+
Sbjct: 140 SDNSYIEAPPIGCLLYALEAPADSGFTSFANQFLAYERLSETLKRDIIEGRWAKHD--ASR
197

Query: 170 SKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRH----AHAI PGMDAAE
225

+ G ++ + P PLV P + R +L +GR + I G+ E
Sbjct: 198 NSAGMLRPG--LRTPSRPEEVPGPFHPLVIRQPGSARRALFLGRRRIFPSQYIEGLPGVE
255

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR-
284

SE L+ L A H+W GDV++WDN LH P D RVM ++ G+
Sbjct: 256 SEALLDALWAAATHPDITWTHRWT PGDVLWLDNCHTLHHRTPVDATRRRVMVRTQFQGQT
315

Query: 285 PETEG 289

P +G
Sbjct: 316 PRADG 320

>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 ATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG---AIE 68
A LGA + G+ A LD A+ AAWL+ LL+F GQ L + + F +RFG

Sbjct: 3 AALGARIDGIDARAELDADTVRAIRAAWLRFGLLVFRGQALDPPRLVAFTRRFGEPPVYT 62

Query: 69 RI-----GGGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

R G +++ +SNV DG + + WH D Y+ G +
Sbjct: 63 RACNACDGQPEVLVLSNVKDGKP-----IGAALSGRYWHTDGHYLACPPAGTL
111

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
183

+PAVGG T F +M AAY AL R + R+ V Q+ H Q +
Sbjct: 112 LFGAEIPAVGGDTHFVNMTAAYRALPAWVRTQIDGRTFVMDRV--QTLPFHYQPAPPP
169

Query: 184 YGMDTTATPLRPLVKVHPETGRPSLLIGRH AH-AIPGMDAAESERFLEGLVDWACQAPR
242

P +P+V+ HPETG +L IG I GM+ S+ + L A R

Query: 177 QAGSAYIGYGMDDTTATP-----LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESE
227

+ G G G T TP PLV+ HPE+GR L + H IPG D A +
Sbjct: 183 EGG---YGGGFATYRTPDIGPIQGSEHPLVRTHPESGRRVLFLSAHEVEVEIPGYDPARGQ
239

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH 263

+ L + + ++H W+ GD+V WDN+ +LH
Sbjct: 240 ALIGRLREHLARPELSYSHAWSVGDIVWWDNQAVLH 275

>ref|ZP_06236528.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp.
Eu11c]

gb|EFA62231.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp.
Eu11c]

Length = 281

Score = 109 bits (273), Expect = 3e-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+F G L + Q+ F +
Sbjct: 4 TLTCEPLAATVGAEVRGVDADQLAHDDAAAAAVLDALERFGVLVFRGLDLGPENQVAFCR 63

Query: 63 RFGAIE-RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ-
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 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

L+D A + H W+ GD V+WDN ++HRA P+D R + + + G
Sbjct: 225 RLIDHTTAAGLTYRHTWSVGDTVIWDNTGVVHRASPYDPNSSRELLRRTTVFG 276

>ref|ZP_02493282.1| dioxygenase [Burkholderia pseudomallei NCTC 13177]

Length = 286

Score = 109 bits (273), Expect = 3e-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 AALGARIDGIDARAELDADTVRAIRAALWLRFGLLVFRGQALDPPRLVAFTRRRFGEFVVYT 62

Query: 69 RI-----GGGDIVAIISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAV
 123
 R G +++ +SNV DG + + WH D Y+ G +
 Sbjct: 63 RACNACDGQPEVLVLSNVVKDGRP-----IGAALSGRYWHTDGHYLACPPAGTL
 111

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSAHSLVYSQSKLGHVQAGSAYI
 183
 +PAVGG T F +M AAY AL R + R+ V Q+ H Q +
 Sbjct: 112 LFGAEIPAVGGDTHFVNMATAAYRALPAWVRTQIDGRTFVMDRV--QTLPFHYPQRPAPPP
 169

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFLEGLVDWACQAPR
 242
 P +P+V+ HPETG +L IG I GM+ S+ + L A R
 Sbjct: 170 DQKQAWPDMP-QPVVRTHPETGENALYIGGVVPWRIVGMEQGLSDALMAHLHAIADFDEAR
 228

Query: 243 V-HAHQWAAGDVVVDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RPE-TEGAA 291
 + H+W AGD+++WDNRCL HRA +D + R M+ + +AG RP GAA
 Sbjct: 229 FGYRHRWRAGDLLMWDNRCLAHRAATDYDMVRHRRTMYRTTIAGDRPRYVRGAA 281

>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 = 3e-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 QSNNVLEIVPVAGRIGAEVGRVRLRADLDAATVSEIRKAWLRHKVIFFRGQHHLDDASQE 66

Query: 59 TFAKRFGA-----IERIGGGDIVAIISNVKADGTVRQHSPAEDDMMKVIVGNMAWHAD
 111
 FGA + + G D + + + G +WH D
 Sbjct: 67 ALTTLFGAKPVAHPTVPVNGTDYIHELDSREGGRAN-----SWHTD
 108

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSAHSLVYSQSK
 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 RKPNSADDVRRYQEVFTSTVYETEHPVVRVHPETGERSLVLGHFVKRLLGVSSHDSAHL
228

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ L + + +WAAGDV +WDNR H A
Sbjct: 229 FQVLQEHVTRLENTVRWRWAAGDVAIWDNRATQHYA 264

>ref|NP_880388.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bordetella pertussis Tohama I]
emb|CAE41952.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase [Bordetella pertussis Tohama I]
Length = 289

Score = 109 bits (273), Expect = 3e-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 FGAIERIGGGDIVAISNVKADGTVRQHSPAED-----DMMKV-IVGNMAW
108

FG + + +K + R H P D MK+ ++ N W
Sbjct: 62 FGPA-----IVTNTIKELTSRRSHRPHLLDITTVDEHGEPLKDRSFMKLYMLANQLW
113

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
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----FSDDSLNRRPPVQHSVVRTNPRTGRRSLYLSGHASHIIIGWPVEQGR
229

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPET
287

L+ L + A Q V+AH W D+V+W+N +HRA P+ PR++ R +G E
Sbjct: 230 ALLQQLTEHATQRQFVYAHAWQMDLLVMWNNAAASMRALPYTGTEPRLL---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 = 3e-22, Method: Compositional matrix
adjust.

Identities = 71/213 (33%), Positives = 105/213 (49%), Gaps = 25/213 (11%)

Query: 56 QQITFAKRFGAIER--IGGGDIVA-----ISNVKADGTVRQHSPAEWDDMMKVIVGNMAW
108

QQI FA++FG +ER + V ++N+ DG V + W
Sbjct: 1 QQIAFAEQFGTLERHVSNRGTVNPLVHIVTNLGPDKPSGK-----VASTQW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
168

H+D ++ P + + A V+P GG TCFADM AAY+AL EA +A + + HS S
Sbjct: 49 HSDKSFRPQPSLATILHALVMPPEGGETCFADMIAAYEALPEAEKAELERVRVHWSGLS
108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
228

Q+++G + I D + PLV+ PETGR +L +G A + G
Sbjct: 109 QARVG--IKVPPEEIIADAPDMS----HPLVRTIPETGRKALFMGERAVYLEGQPEEVGRA
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 = 4e-22, Method: Compositional matrix
adjust.

Identities = 73/213 (34%), Positives = 104/213 (48%), Gaps = 25/213 (11%)

Query: 56 QQITFAKRFGAIER---IGGGDIVA----ISNVKADGTVRQHSPAEWDDMMKVIVGNMAW
108

QQI FA++FG +ER + G + +SN+ ADG V + W
Sbjct: 1 QQIAFAEQFGTLERHMAMNRGTVHPLVHIVSNLGDGKPSGQ-----VASTLW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
168

H+D ++ P + + A V+P GG TCFADM AAY+AL +A +A + HS S
Sbjct: 49 HSDKSFRPQPSLATILHALVMPDGGGETCFADMIAAYEALPDAEKAELDGVRVHWSWEIS
108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
228

+++ AGS + PLV+ PETGR +L +G HA G
Sbjct: 109 RAR-----AGSKATPEEIIADAPPMTHPLVRRIPETGRKALFMGEHASYFEGQPEEVGRV
162

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

LE LV A Q V+ H+W GD+++WDNRC+
 Sbjct: 163 RLEKLVHAVQERFVYRHKWTMGDLLMWDNRCV 195

>ref|NP_763286.1| taurine catabolism dioxygenase [Vibrio vulnificus CMCP6]
 gb|AAO08276.1|AE016813_28 Probable taurine catabolism dioxygenase [Vibrio
 vulnificus CMCP6]
 Length = 288

Score = 109 bits (272), Expect = 4e-22, Method: Compositional matrix
 adjust.

Identities = 76/275 (27%), Positives = 125/275 (45%), Gaps = 27/275 (9%)

Query: 1 MAQTTLQITPTGATLGATVTVGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITF 60
 + + T++ITP + GA V V L+ +++ F AL+ A+L + +L F Q L+ +Q +
 Sbjct: 4 IERETMKITPLATSFALVEDVQLSAINERQFEALYQAFVHYKVLFFRDQLLTAEQHLAL 63

Query: 61 AKRFGAIERI-----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
 112

+RFG +E I +V I R+ P G WH D
 Sbjct: 64 GQRFGELEPIHPFFPHLADAPQVVVIE-----TREGLP-----GESYWHTDL
 106

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-VYSQSK
 171

T+ ++ A+ A+ P GG T + DM A + +LD++ + + A H+L + S+
 Sbjct: 107 TWKARPSKCALLHAQHCPPSGGDTIWTDM EAVWRSLLDSDLKQQLRPLYATHALHAFENSR
 166

Query: 172 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFL
 230

+ + G +Y+ P+V H ETG+ +L I I G++ A+S+ L
 Sbjct: 167 YDNKDEDGESYVVKKSREFPAVHHPVVAQHLETGQETLYINEQFTRCIDGLEKAQSQALL
 226

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

E L A +A QW A + +WDNR H A
 Sbjct: 227 EMLFAMAREAKFQVRFQWQANSLAIWDNRATQHFA 261

>ref|ZP_02501489.1| dioxygenase TauD/TfdA family protein [Burkholderia
 pseudomallei
 112]
 Length = 286

Score = 109 bits (272), Expect = 4e-22, Method: Compositional matrix
 adjust.

Identities = 96/293 (32%), Positives = 135/293 (46%), Gaps = 28/293 (9%)

Query: 13 ATLGATVTVGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG---AIE 68
 A LGA + G+ A LD A+ AAWL+ LL+F GQ L + + F +RFG
 Sbjct: 3 AALGARIDGIDARAELDADTVRAIRAAWLRFGLLVFRGQALDPPRLVAFTRRFGEPPVYT 62

Query: 69 RI-----GGGDIVAIISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

R G +++ +SNV DG + + WH D Y+ G +
Sbjct: 63 RACNACDGGQPEVLVLSNVVKDGKP-----IGAALSGRYWHTDGHYLACPPAGTL
111

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
183

+PAVGG T F +M AAY AL R + R+ V Q+ H Q +
Sbjct: 112 LFGAEIPAVGGDTHFVNMAAAYRALPAWVRTQIDGRTFVMDRV--QTLPFHYPQRPAPPP
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-HAHQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG-RPE-TEGAA 291

+ H+W AGD+++WDRCL HRA +D + R M+ + +AG RP GAA
Sbjct: 229 FGYRHRWRAGDLLMWDNRCLAHRATDYDMVRHRRTMYRTTIAGDRPRYVRGAA 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 = 4e-22, Method: Compositional matrix
adjust.

Identities = 84/264 (31%), Positives = 119/264 (45%), Gaps = 16/264 (6%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
+Q+TP G V+GV LA+ DA + A +H + +F Q S ITF KR+G

Sbjct: 1 MQMTPMAPKCGVEVSGVSLASCSDAEMQDIKNAIYEHGVAVFRDQEFQSKQDHITFGKRWG 60

Query: 66 AIERIGGGDIVAIISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
125

I+ + ++ A+ V + P D I G+ WH D +Y + A G+V
Sbjct: 61 GIDV---NNYFPLTEDYAEIAVVKKDP----DQQTNIGGD--WHTDHSYDQIPAMGSVLV
111

Query: 126 AEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQQAGSAYI
183

A +P GG T +A M AAYDAL + + + A H+ +Y L G +
Sbjct: 112 ARELPPKGGDTMWAHMGAAYDALSQDLKDEIEGLEAFHTADHIYKADGLYAQTMGRSLR
171

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIP--GMDAAESERFLEGLVDWACQAP
241

G+ + T A + P+V HP TGR L + R A I G ES L+ L D A

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
 L I G +GA ++ V L+ TL + AA+ A L+H ++ F Q HL++ +Q +F +
 Sbjct: 19 LDIHHVGGRIGAEISNVTLSSTLQPSIIAAIRQALLRHKVIFFRNQTHLTDVEQESFGRL 78

Query: 64 FGAIERIGGGDIVAISNVKA-DGTVRQHSPA EWDDMMKVIVGNMA--WHADSTYMPVMAQ
 120

G D+V V + +GT + E D G A WH D T+ +
 Sbjct: 79 LG-----DLVPHTVPSLEGT---QAILELDGAR----GERASSWHTDVTFRAAYPK
 123

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQ--SKLGHV-QQ
 177

++ VVP GG T +++ AY+ L E R + + A HS Y + G++ +
 Sbjct: 124 ISILRGHVPPERGGDTTWSNTEYAEELPEVFRDFIDKLWAVHSNEYDYVGD RGGNIPES
 183

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA
 237

A Y T PLV VH ETG+ SL+IG I G A+S+R + L D A
 Sbjct: 184 AIKRYKQIFTSTVYEAHPLVHVHSETGKRSLIIGHFVKRITGFGTADSQRIISILHDHA
 243

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRA-EPWDFKLPRVMWHSRLAG 283

+ +W+ GDV +WDNR LHRA + +D + PR++ + +AG
 Sbjct: 244 TRPENTVRWRWSVGDVAIWDNRATLHRAVDDYDDQ-PRIVRRTTIAG 289

>gb|ADC33995.1| TfdA-like protein [uncultured bacterium]
 Length = 195

Score = 108 bits (270), Expect = 7e-22, Method: Compositional matrix
 adjust.

Identities = 69/213 (32%), Positives = 104/213 (48%), Gaps = 25/213 (11%)

Query: 56 QQITFAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW
 108

QQI FA++FG +ER + + ++N+ ADG V + W
 Sbjct: 1 QQIAFAEQFGTLERHMASNRGTVNPLVHIVTNLGADGKPSGK-----VASTGW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYS
 168

H+D ++ P + + A+V+P GG TCFA+M AAY+AL EA +A + HS S
 Sbjct: 49 HSDKSFRPRPSLATILHAQVMPPDGGETCFANMIAAYEALPEAEKAELDGVRVVHSWEIS
 108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
 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 RLEKLTAAHAVEERFVYRHKWTAGDLLMWDNRCV 195

>gb|ADC34035.1| TfdA-like protein [uncultured bacterium]
Length = 205

Score = 108 bits (270), Expect = 7e-22, Method: Compositional matrix
adjust.

Identities = 74/215 (34%), Positives = 104/215 (48%), Gaps = 19/215 (8%)

Query: 56 QQITFAKRFGAIERIGGGD-----IVAINVKADGTVRQHSPA EWDDMMKVIVGNMA
107

QQI FA+ FG +E D I ++NV G + W + I +
Sbjct: 1 QQIAFARNFGKLEIHPSKDHSSRNPEIYRVANVDEQGGILPPKSEAW----RYINISWL 56

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
167

WH+DS++ V + G++ V GG T F ++ AY AL E+ R V R ARHS
Sbjct: 57 WHSDSSFREVPSLGSILHGIEVTDQGGETMFCNLYEAYAALSESLRKEVAGRRARHSHAT
116

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHA-HAIPGMDAAES
226

S+ G + + Y D PLV+ HPETGR SLLI H + G D A S
Sbjct: 117 VLSR-GQTL EHS AKY-----DPLKPVWHPLVRRHPETGRHSLISPHTMDLVEGCDEAAS
170

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

L+ L+ +A Q V+ H+WA D+++WDNRC+
Sbjct: 171 RALLDELIAFAQQDRFVYRHKWARDIIIMWDNRCV 205

>gb|ADC33991.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 108 bits (270), Expect = 7e-22, Method: Compositional matrix
adjust.

Identities = 73/213 (34%), Positives = 105/213 (49%), Gaps = 25/213 (11%)

Query: 56 QQITFAKRFGAIER--IGGGDIVA-----ISNVKADGTVRQHSPA EWDDMMKVIVGNMAW
108

QQI FA++FG +ER +G V ++N+ ADG V + W
Sbjct: 1 QQIAFAEQFGTLERHVVGNRGTVNPLVHIVTNLGADGKPSGK-----VASTQW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
168

H+D ++ P + + A V+P GG TCFADM AAY+AL EA +A + HS S
Sbjct: 49 HSDKSFRPQPSLATILHALVMPPQGGETCFADMIAAYEALPEAEKAELAGVRVHHSWELS
108

Query: 169 QSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
228

Q+++G + I D + PLV+ PETGR +L +G A + G

Sbjct: 109 QARVG--IKVPP EEIADAPDMS----HPLVRTIPETGRKALFMGERAVHLEGQPEDVGRA
162

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
LE L A Q V+ H+W GD+++WDNRC+

Sbjct: 163 RLEKLTAAHAVQERFVYRHKWTLGDLLMWDNRCV 195

>gb|ABB69741.1| Pla01 [Streptomyces sp. Tu6071]
Length = 288

Score = 108 bits (270), Expect = 7e-22, Method: Compositional matrix
adjust.

Identities = 79/270 (29%), Positives = 120/270 (44%), Gaps = 45/270 (16%)

Query: 4 TTLQITPTGATLGATVTVGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAK 62
T ++ P + LGA + GV L + DA FA L L+H ++ P Q S + +I F +
Sbjct: 7 TAFEVRPLTSALGAEIHGVRLEDITDADFAELRRLLLKHLVIFIPDQEGWSAESRIAFGR 66

Query: 63 RFGAIER-----IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
116

RFG +E + G + I + + +G + WH D TY P
Sbjct: 67 RFGEELEHAYLPHLDGHPQIQIIDSEQNGKI-----PIWHTDMTYAP
108

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
176

G+V PA GG T +++ AY+ L R L+ +A HS+ H+
Sbjct: 109 NPPIGSVLQIVDGP AQGGDTMWSNQYLAYEGLSAPLRDLLDGLTAVHSI-----HIP
160

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD
235

G+D+ A P+V+VHPETGR +L + R H I ++ ES+ L+ L
Sbjct: 161 -----GLDSQAE--HPVVRVHPETGRRALFVNRAHTSHIAQLNRNESDALLQYLYR
209

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 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 = 7e-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 MEVRKLTGVIGAEELGIDLSRDLDPADVAAIRQALLDHQVIFFRDQTLTPEQHIAFARF 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 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS--LVYSQSKLGHVQQAG
 179

++ VP GG T +A+M AYD L + +A + A H+ + + SK + ++
 Sbjct: 109 SILYGRQVPETGGDTLWANMYRAYDTLSGGMKAKLANLRAVHTNDFLSANSKYRNSTRST
 168

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWAC
 238

G + T + P+V+ H ETGR L + ++ M ES L+ L +
 Sbjct: 169 KLRELVG---SITSVHPVVRTHEETGRKCLFVNHPFTYSFENMTREESLPLLQFLYQHS
 225

Query: 239 QAPRVHAHQWAAGDVVVDNRCLLHRA 265

+ +W G + WDNRC +H A
 Sbjct: 226 KPENTCRFRWRKGSMAFWDNRCMHYA 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 = 8e-22, 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--RIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
 123

+E ++ + V T + ++P E WH D T+ ++GAV
 Sbjct: 105 GLEPAHPFFPNVESSPQVSI IETTGNAPLE-----SYWHTDLTWREQPSKGAV
 153

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
 183

A+ VP GG T + M A +DALD + + Q SA HSL + + +
 Sbjct: 154 LHAQHVPNTGGDTIWSMTAVFDALDNTMKTCLRQLSATHSLTAFEVVAEEDIELDWHR
 213

+VVWDN +LHRA P+D R M + + G
 Sbjct: 233 LVVWDNTGVLHRAMPYDPTSERTMQRTTIVG 263

>ref|YP_003272551.1| Taurine dioxygenase [Gordonia bronchialis DSM 43247]
 gb|ACY20658.1| Taurine dioxygenase [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 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
 L + G + GA + G+ +A+ D A+ A +++ +++ QHL + I F +R G
 Sbjct: 28 LDVDEFGPSFGAELRGIDVASASDDEVRAIRRALIEYKVIVLRNQHLDDAAHIEFGRR 87

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNM-AWHADSTYMPVMAQGA 124

D+ V G V P E + G WH D T+MP G++
 Sbjct: 88 -----DLTVGHPVWDSGDV----PDEVYSLDSADNGFADVWHTDVTFMPRPPMGSIL 135

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG 184

V+P GG T +AD AY +L E R L+ A H ++ G
 Sbjct: 136 RPVVLPRNGGDTNWADAELAYLSLSEPVRTLIEGLRAVHDGSREFGYLQKRRGGKGN 195

Query: 185 YGMDTTATP--LRPLVKVHPETGRPSLLI--GRHAHAIPGMDDAESERFLEGLVDWACQA 240

G + T P P+V+VHPETGR SL + G +H I G+ AES L+ L +
 Sbjct: 196 DGREVTTELPPVTHPVVRVHPETGRKSLFVNPGFTSH-IEGVSDAESRGILDLLYAH 254

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAE 266

+ H+W GD+V+WDNR LH A
 Sbjct: 255 EHIVRHRWRLGDLVLWDNRNTLHYAN 280

>ref|XP_001394361.1| hypothetical protein An11g03620 [Aspergillus niger]
 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-VRQHSPAEWDDMMKVIVGNMA 107

A++FG ++ R+ ++ + N++ DG+ V +SP + GN

Sbjct: 72 ARKFGELDDVTPYNKAGRVHRLKYNELFDVGNIEIDGSIVDLNSPRG-----EANKGNSL
126

Query: 108 WHADSTYMPVMAQGAVFSAEVVP--AVGGRTCFADMRAAYDALDEATRVLVHQRS--ARH
163

+H DS++ P A ++ A +P GG T FADMR AY LD+ + +H R+ ARH
Sbjct: 127 FHTDSSFNPRRAGYSLLLAHELPPPGTGGSTAFADMRGAYRDLDDDFKRFLHDRNFVARH
186

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDA
223

S+++S+ A + L++ H TG P++ + +H H++ G+
Sbjct: 187 SILHSKK-----MAAPEHFVKDVNPTDHFMSRHLLQKHERTGIPTIYLAKHIHSLEGVSP
241

Query: 224 AESERFLEGLVDWACQAPRVHAHQW-AAGDVVVWDNRCLLHRAEPWDF 270

ES+ L+ L + + Q V +W + GD++VWDN C +HRA +F
Sbjct: 242 EESQGILDRLFEHSSQDKYVIEVEWISVGMIVWDNTCTMHRAISGEF 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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDALD+ +A + HS YSQ K+G +++ + M
Sbjct: 1 TEFGDMRAAYDALDDQRKAQLEGLLGTHSYAYSQKVGGLLEEVFTPEARARMVDVE---H 57

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

LV+ HP TGR SL IGRH + + GM +++ LE L+ WACQ PRV H+W GD+V+
Sbjct: 58 LLVRTHPATGRKSLFIGRHVYRVGTMTDDDAQAMLEELLAWACQPPRVFKHRWTVGDIVM
117

Query: 256 WDNR 259

WDNR

Sbjct: 118 WDNR 121

>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]

Sbjct: 133 GARVDPPAATILRAETVPPYGGDTTWSNLAAAYAGLSAPLREFADGLRAEHRL-----GV
187

Query: 173 GHVQQAGS-AYIGYGMDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFL
230

G+ + G AY+ + +D L PLV+VHPETG L + G + I G+ ES L
Sbjct: 188 GYQPRPGDDAYVRHLLDRQVATLHPLVRVHPETGERVLYVNGYYVEQIAGLSRPESGAIL
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]
gb|ABP45584.1| Taurine dioxygenase [Mycobacterium gilvum PYR-GCK]
Length = 309

Score = 107 bits (268), Expect = 1e-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 DVVKLGAAIGARIDGVDLARGIDAGTAAQINAALLEHKVIFFRGQHDLDGQLEFARAL 64

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVF
124

G A V + G + +D +WH D T++ + + ++
Sbjct: 65 GT-----PTTAHPTVTSRGAKVLPIDSRYDKAD-----SWHTDVTFFVDRIPKASLL
110

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY-----SQSKLGHVQQAG
179

A +PA GG T +A AAYD L RAL A H+ Y + ++L +
Sbjct: 111 RAVTLPAYGGTTAWASTEAAAYDRLPAPLRALTENLWAVHTNTYDYAADADARLVPLADTE
170

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ
239

Y + P+V+VHPETGR LL+G G+ AES L+ L + +
Sbjct: 171 RQYREEFVSDYYETEHPVVRVHPETGRKVVLLGHFVKHFVGLGQAESTALLQLLQNRVTK
230

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265

W GD+ VWDNR H A
Sbjct: 231 LENTIRWSWELGDIADVWDNRATQHYA 256

>ref|ZP_06238189.1| Taurine dioxygenase [Frankia sp. Eu11c]
gb|EFA60569.1| Taurine dioxygenase [Frankia sp. Eu11c]
Length = 302

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-----IVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAW
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+ L EA +A + HS S
Sbjct: 49 HSDKSFRPRPSLATILHAQVMPDGGGETCFANMIAAYETLPEAEKAELDGVRVVHSWEIS
108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
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 RLEKLTAAHAVEERFVYRHKWTAGDLLMWDNRCV 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 TIQVKPISGALGAEIEGVDSLKDLNETFDDIHQAFLDHVVIFFRDQQLSHEQHKAFGR 61

Query: 64 FGAIE-----RIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMP
116
FG + G +I+ I VK E +D + G WH+D +++
Sbjct: 62 FGTLNIHPYVKMEGHPEIMQI--VK-----EPEDRLNFGGG---WHS DMSFLE
105

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
176
A G++ A+ VP GG T +A+ AY+ L + +A + A H+ S+ G
Sbjct: 106 EPALGSILYAKEVPPYGGDTLWANQYLAYETLS DGMKATLDGLKAVHTAKGEYSERGASA
165

Query: 177 QA-GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLV
234
QA S + D T + P+V+ HPETGR +L + G ES L L

Sbjct: 166 QARKSMDVATAGDDTPSYEHPVVRTHPETGRKALYVNPAPFTEKFGVWTRRESRPLLNFLE
225

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
+ Q P +W A + WDNR H A

Sbjct: 226 EHCTQEPLTCRFRWTANALAFWDNRRAAQHFA 256

>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 ADSTYMP LQAKGAVFSAKVVPTGGETGWADMRAAYEALDENLRSKLEGLEAYHSLYYSQ 60

Query: 170 SK-LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET 204

K LG+ +AGSA YG+ PLR LVKVHPET

Sbjct: 61 GKVLGYAPKAGSA---YGLHEGPPPLRKLVKVHPET 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-HLSNDQQITFAKRF 65
+T GA +GA + G+ L LD A + + A L+H ++ F GQ HL ND Q FA G

Sbjct: 28 VTTLGAHIGARIDGITLGGHLDPATISLIRQALLEHKVIFFRGQDHLDNDSQYEFALLG 87

Query: 66 AIERIGGGDIVAISNVKADGTVRQHS----PAEWDDMMKVIVGNMAWHADSTYMPVMAQG
121

+ A TV+ H P + D+ K +WH D T++ + +
Sbjct: 88 -----TPTTAHPTVKSHGAKVLPID-SDLGKA-----NSWHTDVTFVDRI PKA
129

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY---SQSKLGHVQQA
178

++ A +P GG T +A AAY+ L + +AL ARH+ VY + S +
Sbjct: 130 SILRAVQLPEYGGSTTWASGVAAYNGLPDPLKALAENLWARHTNVYDYAATSAERLTEDR
189

Query: 179 GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC
238

+AY T P+V+VHPETG +L++G G+ +S + L D A
Sbjct: 190 TAAAYREEFQSTYFETEHPVVRVHPETGERTLVLGHFVKNFVGLSTEQSNVFKLLQDHAI
249

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ W AGDV +WDR H A
Sbjct: 250 KLEYTTRWNWEAGDVVAIWDNRATQHYA 276

>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-----IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW
108

QQI FA++FG +ER + + ++N+ ADG V + W
Sbjct: 1 QQIAFAEQFGTLERHMASNRGTVNPLVHIVTNLGDGKPSGK-----VASTGW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
168

H+D ++ P + + A+V+P GG TCFA+M AAY+AL E +A + HS S
Sbjct: 49 HSDKSFRPRPSLATILHAQVMPPDGGETCFANMIAAYEALPEVEKAELDGVRVVHSWEIS
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+++WDRNC+
Sbjct: 162 ARLEKLTAAHAVEERFVYRHKWTAGDLLMWDNRV 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 QRGVLVFPQIDFSDAEQIAFTRTLGTFCEASDQONITKISLDVK-----ENPAG--- 93

Query: 98 MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVH
157

+ + G++ WH D T V ++ S +V ++GG T F + AAY+AL A +
Sbjct: 94 -AEFLKGSLYWHIDGTSSDVPILASLLSCKVPASLGGNTGFCNTYAAYEALSSADK----
148

Query: 158 QRSARHSLVYS--QSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHA
215

QR R ++++ S L + + G A + M PLV H +GR SL++G A
Sbjct: 149 QRYERLRVIHAPWASLLLYNPEPGLAMLK-AMQAIGEKELPLVVRH-RSGRKSLLIGCTA
206

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRV
275

+ G+ A+S + L GL +WA ++H W GD+V+WDN +HRAE +D R+
Sbjct: 207 QQVVGVSLSAQSAQILVGLREWATAEAFSYSHAWQTGDLVIWDNTGTMHRAEAYDPACGRM
266

Query: 276 MWHSRLAGRPETE 288

M ++L G E
Sbjct: 267 MHR TKLQGE E PFE 279

>gb|AAT51068.1| PA3935 [synthetic construct]

Length = 278

Score = 107 bits (266), Expect = 2e-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 SLTIQPI SPALGATVSGIDLGAPLDDTGQRAIEQALLEHQVLFVRDQSLEPRSQARFAAR 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

FG + I + Q D + + N WH D T++ A GAV
Sbjct: 62 FGD LH-----IHPIYP-SVPEQPEVIVLDTAVTDVVDNAIWH TDVTFLETPALGAV
111

>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 = 3e-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 SVTVTPLGPHLGVEITGMSGDLPTTAAAAACLETLARHGVVIYREAHISDSLVSFSRL 61

Query: 64 FG--AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMK-VIVGNMAWHADSTYMPVMAQ
 120

G + G + I+ + D PA+ D + GN WH D + +
 Sbjct: 62 LGRVVLNPTGEHERAEIATITLD-----PAKTDATLAWYRKGNFLWHIDGATDQLPQK
 114

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLHQRSARHSLVYSQSKLGHVQQAGS
 180

+ +A V GG T FA AAY+AL + + + + HS +Q + H
 Sbjct: 115 ATLLTAREVDETGGDTEFASTYAAYEALPDTEKVALAEHHVLHSFAAAQRR-AHPDATDE
 173

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA
 240

+G T PLV GR SLL+G A + G+ AE E L+ L++W+ Q
 Sbjct: 174 QQADWGR--VPTRKHPLVWTR-GNGRRSLLLGGATAGEVVGLPPAEGEALLQRLLEWSTQP
 230

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

V H+W AGD+V+WDN +LHRA P+ R+M + L G
 Sbjct: 231 QFVLRHRWRAGDLVIWDNTGMLHRALPFAATSRRLMHRRTTLVG 273

>gb|ADC34015.1| TfdA-like protein [uncultured bacterium]

Length = 195

Score = 106 bits (265), Expect = 3e-21, Method: Compositional matrix adjust.

Identities = 69/214 (32%), Positives = 106/214 (49%), Gaps = 27/214 (12%)

Query: 56 QQITFAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW
 108

QQI FA++FG +ER + + ++N+ ADG V + W
 Sbjct: 1 QQIAFAEQFGTLERHMASNRGTVSPLVHIVTNLGADGKPSGK-----VASTGW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLHQRSARHSLVYS
 168

H+D ++ P + A+V+P GG TCFADM AAY+AL +A +A + + HS S

Sbjct: 49 HSDKSFRPQPPLATILHAQVMPPDGGETCFADMIAAYEALPDAEKAELDRVVRVVSWEIS
108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTATPL-RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
227

++++G +A I A P+ PLV+ PETG +L +G HA G
Sbjct: 109 RARMG--IKAPPEEIA-----DAPPMVHPLVRTIPETGSKALFMGEHAVYFQQGPPEEVGR
161

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

LE L A + ++ H+W GD+++WDNRC+
Sbjct: 162 ARLEKLTAAHAVEERFIYRHKWTVGDLLMWDNRCV 195

>gb|ADC33988.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 106 bits (265), Expect = 3e-21, Method: Compositional matrix
adjust.

Identities = 72/213 (33%), Positives = 104/213 (48%), 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 HSDKSFRPQPPLATILHALVMPPQGGETCFADMIAAYEALPEAEKAELAGVRVVSWEIS
108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
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 RLEKLTAAHAVQERFVYRHKWTLGDLLMWDNRCV 195

>gb|ADC34006.1| TfdA-like protein [uncultured bacterium]
Length = 213

Score = 106 bits (265), Expect = 3e-21, Method: Compositional matrix
adjust.

Identities = 74/224 (33%), Positives = 110/224 (49%), Gaps = 29/224 (12%)

Query: 56 QQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMM 99
QQI FA +G +E RI ++ +SN+ G + D

Sbjct: 1 QQIAFAGLYGPLEVAPPVQYKPGTFVETRIRHREVFDVSNLDEQGRILDG----DQRR 56

Query: 100 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQR
159

+GN WH DS++ A ++ A ++P GG T FAD RAAYDAL +AT+ +
Sbjct: 57 AYGLGNQLWHTDSSFRQKSATWSLLHARIIPDGGDTEFADTRAAYDALPQATKDRDLGL
116

Query: 160 SARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGRHAHA
217

A HS+ +S++KLG Y + A P P+V++ P +GR +L I HA
Sbjct: 117 IAEHSIWHSRALG-----GYTPTEERQARPPAQHPVRLRPGSGRKALYIASHASH
169

Query: 218 IPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

I G E L L+ +A Q V+ H+W++GD+V+WDNRC+
Sbjct: 170 IVGWPIEEGRALLAELLAFAFATQPQFVYTHRWSSGDLVIWDNRCV 213

>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 = 3e-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 LTKIRLRAVQHASNVCGDIEGFDFNDYDADDVAAVRKFQYGVVRFKKAGITDAQVQF 61

Query: 61 AKRFGAI-----ERIGGG-----DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNM--AW
108

++ FG + GG +I+ ISN DG P+ +GN W
Sbjct: 62 SRHFGEFVIHPKQLQEGGHPHPEILVISNAMKDG-----KPSG-----AMGNSEATW
109

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYS
168

H D+ + GA+ A VP GG T F AYD L + V R VY
Sbjct: 110 HTDTWFYERPPAGAILRAVAVPPSGGDYFLSTYIAYDTLPAPLKNVAVDGRQIFFQNVYD
169

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA--IPGMDAAES
226

K G ++ S + + PLV+ H ETGR +L +G I GM ES
Sbjct: 170 --KTGKRLRLGKSTPKSQDFREWSGIVHPLVRTHGETGRKALYLGTTTEGAWIVGMSRDES
227

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP
285

+ L L D + QW GD+++WDNRC +HR + +D R+M + +G RP

Sbjct: 228 DALLAELWDHTTNTKHIFVQQWDEGDIMMWDNRCTMHRDRSFDPASIRIMHRTTTSGERP
287

>ref|XP_002149830.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate

dioxygenase, putative [Penicillium marneffeii ATCC 18224]

gb|EEA21221.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate

dioxygenase, putative [Penicillium marneffeii ATCC 18224]

Length = 326

Score = 106 bits (264), Expect = 3e-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 VTFKPLHPTFGAECNGIDFSQPVEETVDIIRNGLAKYGILVFRGAELDDARHVALARQL 68

Query: 65 GAIER-----IGG-----GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHAD
111

G ++R + G ++ +SN++ DG++ Q + W ++ GN +H D

Sbjct: 69 GELDRSTVFMVMPGQKYRLAPFNE LT DVS NIEQDGSIIQKNSLSW----QIGQGNLSLFHVD
124

Query: 112 STYMPVMAQGAVFSAEVVP--AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ
169

+Y P A +V A +P GG T FAD R AYD LD+ R + HSL +S+

Sbjct: 125 CSYNPRRAGFSVLRRAHKLPPKGNNGGGTAFADSR TAYDDL DDEKREEIKDYIVCHSLWHSR
184

Query: 170 SKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
228

+ ++ Y + R LV++H + R ++ I HAH G ES+

Sbjct: 185 ----RLASPDCEFLKYMEPEKNSMARHKL VQMHEPSKRMNMYIAAH AHFDGWTHQESQP
240

Query: 229 FLEGLVDWACQAPRVHAHQWAA-GDVVVWDNRCLLHRAEPWDFK 271

++ L+ Q A W GD V+WDN C+LHRA DF+

Sbjct: 241 VIDDLMRHVTQDKYTF AVNWENDGDFVIWDNTCVLHRACGGDFE 284

>ref|YP_001505765.1| taurine catabolism dioxygenase TauD/TfdA [Frankia sp.
EAN1pec]

gb|ABW10859.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp.
EAN1pec]

Length = 276

Score = 106 bits (264), Expect = 3e-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 LTLNKLSTHVGAIEILGLDATTRLLSDETLPGAVLDALEENGLVFRNLHLDDATQVAFCRK 63

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

GA++ I I+ V D PA+ + + + G WH D T + + V
Sbjct: 64 LGAVQSWASHAIPEITVVSLE-----PAK-TAIAEYLKGTDFDWHIDGTVDVIPNKATV
115

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYI
183

+A + GG+T FA AY+ L + Q HS Q +++ +
Sbjct: 116 LTAHTLAEEGGQTEFASTYVAYENLTAEEKEQYALRVLHSFEALQ-----LRRNPNPTP
170

Query: 184 GYGMDTTATPLR--PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAP
241

D + P R PL+ H +GR SL++G A + G D A S++ L+GL+ +
Sbjct: 171 EVAADMKSREPQREHPLIWRHG-SGRNSLVLGATASHVVGWDDAASQQLLDGLLARSTAPQ
229

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

V+ H+W+ GD V+WDNR +LHR P+D PR M S L G
Sbjct: 230 LVYRHEWSLGDTVIWDNRGVLHRVSPYDPTSPREMHRSSTLLG 271

>gb|ADC33994.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 105 bits (263), Expect = 4e-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 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYS
168

H+D ++ P + + A+V+P G TCFADM AAY+AL +A + + + HS S
Sbjct: 49 HSDKSFRPQPSLATILHAQVMPPDRGETCFADMIAAYEALPDAEKTELDRVVRVVSWEIS
108

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATPL-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 ARLEKLTAAHAVEERFVYRHKWTAGDLLMWDNRCV 195

>ref|ZP_06234871.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. Eu11c]
 gb|EFA63788.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. Eu11c]

Length = 277

Score = 105 bits (263), Expect = 4e-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-DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ
 120

G + +GG D IS + D PA+ + G WH D V +
 Sbjct: 62 LGDVVAVPMGGQQDFPEIS AISLD-----PAQ-STLAAYRTGTFYWHIDGANDLVPQK
 113

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGS
 180

+ +A V GG T FA + AAYD+L + +A HS +Q + S
 Sbjct: 114 ATLLTALEVATEGGDTEFASLYAAYDSLSDDDKAQYAALRVVHSFAATQRL---ISPDAS
 170

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQA
 240

+ + + PLV GR SLL+G A I G+ A ES L+ L+DWA Q
 Sbjct: 171 DKVRASWEKVPSREHPLVWTR-RNGRKSLLVGT TADYIVGLPADES RALLDRLLDWATQP
 229

Query: 241 PRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

H WA GD+V+WDN +LHRA+P+ R+M + L G
 Sbjct: 230 RFALRHHWAPGDLVIWDNTGILHRAQPYTAASRRLMHR TLLG 272

>ref|YP_002798036.1| Taurine dioxygenase [Azotobacter vinelandii DJ]

gb|ACO77061.1| Taurine dioxygenase [Azotobacter vinelandii DJ]

Length = 298

Score = 105 bits (263), Expect = 4e-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----NSWHTDVTFVEDYPKIC
 117

>gb|ADC33996.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 105 bits (263), Expect = 5e-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 QQIAFAEQFGTLERHMASNRGTVNPLVHIVTNLGADGKPSGK-----VASTGW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
168

H+D ++ P + + A+V+P GG TCFADM AAY+AL +A +A + + HS S

Sbjct: 49 HSDKSFRPQPSLVTLHAQVMPDGGGETCFADMIAAYEALPDAEKAELDRVRVVSWEIS
108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPL-RPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESE
227

++++G +A I A P+ PLV+ PETG +L +G HA G

Sbjct: 109 RARMG--IKAPPEEIA-----DAPPMVHPLVRTIPETGSKALFMGEHAVYFQQPPEEVGR
161

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

LE L A + ++ H+W GD+++WDNRC+

Sbjct: 162 ARLEKLTAAHAVEERFIYRHKWTVGDLLMWDNRCV 195

>ref|YP_702048.1| taurine dioxygenase [Rhodococcus jostii RHA1]
gb|ABG93890.1| probable taurine dioxygenase [Rhodococcus jostii RHA1]
Length = 315

Score = 105 bits (263), Expect = 5e-21, Method: Compositional matrix
adjust.

Identities = 79/263 (30%), Positives = 122/263 (46%), Gaps = 19/263 (7%)

Query: 8 ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFG 65

+ GA +GA + GV L LD A + + A L+H ++ F GQ HL++D Q FA+ G

Sbjct: 22 VVKLGAHIGARIDGVRLLGGNLDPATVSLIRQALLEHKVIFFRGQEHLTDDSQYEFALLG 81

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
125

+ A V + GT + P + D K +WH D T++ + + ++

Sbjct: 82 S-----PTTAHPTVTSRGT--KVLPID-SDYGKA----NSWHTDVTFVDRIPKASILR
127

Query: 126 AEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
185

A +P GG T +A AAY+AL E + L A H+ VY + + Y

Sbjct: 128 AVQLPTYGGSTTWASGVAAYNALPEPLKVLADNLWATHTNVYDYAATSAERTQDEKSKEY
187

Query: 186 GMDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPR
242

+ +T P+V+VHPETG +LL+G ++ G+ + +S+ L D A
Sbjct: 188 RAEFQSTYFETEHPVVRVHPETGERTLLLGHFVKSLVGLSSTQSQUALFRVLQDHAISLEF
247

Query: 243 VHAHQWAAGDVVVWDNRCLLHRA 265

W +GDV +WDNR H A
Sbjct: 248 TTRWNWQSGDVAIWDNRATQHYA 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 = 5e-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 GAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF
124

G + + + + A + K + + WH D T + ++
Sbjct: 70 GKLTPAHPHEDAPPAGFPEILPIDSRRYARFFGTKKKVITYDNGWHTDVTALVNPPAASIL
129

Query: 125 SAEVVPVAVGGRTCFADMRAYDALDEATRVLVHQRSAHSLVYSQSKLGHVQQAGSAYIG
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 = 5e-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 LSTTRLDVIDCTPLIGSEIKTDLDLTLSSGREAEAIRAILEQRGVVFFRGLQISDEQQVTI 62

Query: 61 AKRFGAI-ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
 119

AK G+I + G G I IS D V Q + + + G++ WH D + P
 Sbjct: 63 AKTLGSIVQNEGEGGIYKIS---LDTNVNQRA-----EYKGSFLFWHFDGSLQPYPN
 111

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA-----LVHQRSARHSLVYSQSKLG
 173

+ A + GG+T F + AAY+ L EA + +VH SA S Y + +
 Sbjct: 112 LATLLRAMKLSDSGGQTEFCNTYAAYEELPEADKETIAGLRVH--SAERSQYYVRPEMS
 169

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL
 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 RDWATQPRYVYRHEWRLGDLLMWDNTGTMHRALPYAADSGRMLMHRTVLAG 271

>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 = 6e-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 SLTIQPISPALGAIIVSGIDLGAPLDDTGQRAIEQALLEHQVLFRRDQSLEPRSQARFAAR 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
 123

FG + I + Q D + + N WH D T++ A GAV
 Sbjct: 62 FGDH-----IHPIYP-SVPEQPEVIVLDTAVTDVVDNAIWHTDVTFLETALGAV
 111

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQQAGSA
 181

+A+ +P GG T +A AAY+AL R L+ +A H + + + + G V +A A

Score = 105 bits (262), Expect = 6e-21, Method: Compositional matrix adjust.

Identities = 69/214 (32%), Positives = 104/214 (48%), Gaps = 27/214 (12%)

Query: 56 QQITFAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW
108

QQI FA++FG +ER + + ++N+ ADG V + W

Sbjct: 1 QQIAFAEQFGTLERHMASNRGTVNPLVHIVTNLGADGNPSGK-----VASTGW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
168

H+D ++ P + + A+V+P GG TCFA+M AAY+AL A +A + HS S

Sbjct: 49 HSDKSFRPRPSLATILHAQVMPDGGGETCFANMIAAYEALPGAEGAELDGVRVVHSWEVS
108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPL-RPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESE
227

++++G A A P+ PLV+ PETG +L +G HA G

Sbjct: 109 RARMGITAPAEI-----ADAPPMVHPLVRSIPETGSKALFMGEHAVYFEGQPEEAGR
161

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCL 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 = 7e-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 LQAKGAVFSAKEVPTHGGETGWADMRAAYDALDEELRAKLEGLEAYHSLYYSQ 60

Query: 170 SK-LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET 204

K LG++ +A SA YG+ PLR LVKVHPET

Sbjct: 61 GKVLGYMPKANS---YGLHEGPPPLRKLVKVHPET 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 = 7e-21, Method: Compositional matrix adjust.

Identities = 83/281 (29%), Positives = 133/281 (47%), Gaps = 36/281 (12%)

Query: 12 GATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPG-QHLSNDQQITFAKRFGAIER 69

Sbjct: 12 G+ +GA V G + T+DD + A QH +L+F G + SND + FA+RFG + +
GSAIGAVVAGADFSGTIDDTQVEEIQALDQHLVLFVFRGHKDPNSDDLLMFARRFGHVPK 71

Query: 70 IG-----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGN---MAWHADSTYMPVM
118

Sbjct: 72 G +I+ ISN+ + + K+ VGN M WH D ++ P +
TGLTTGASPDHNEILLISNILDE-----NGQKIGVGNAEWMWDWHTDYSFRPRV
119

Query: 119 AQ-GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-----VYSQSK
171

Sbjct: 120 ++ G + + E+ P+ GG+T F DM AY++L + R +H ARHSL V +
SRIGFLAAVELPPSGGGQTLFTDMYTAYESLPDDLRLHSYRARHSLRSGYEDVIEEEY
179

Query: 172 LGHVQQAGSAYIGY--GMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESER
228

Sbjct: 180 G V G + D TAT + L+ +P TGR ++ + I +D S+
QGEVSIEGPTAKPFVAPEDGTAT-VHQLIARNPRTGRRAVYANPLNTRKRIELEDVTSSKE
238

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD 269

Sbjct: 239 L+ L + +AH+W GD+V+WD +H +D
VLQQLFAKPGPELTYAHEWLPGDIVMWDQLGTVHAKRAFD 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 = 8e-21, Method: Compositional matrix
adjust.

Identities = 93/291 (31%), Positives = 131/291 (45%), Gaps = 27/291 (9%)

Query: 4 TTLQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61

Sbjct: 2 + L IT ++GA VTG+ A L DD+ A+ A + +L+F G +L Q+ F
SLLTITKLTDVGAEVTVGLDPAALAHDDSVGEAVLDALEDNGVLVFRGLYLDPAQAQVAF 61

Query: 62 KRFGAIERIGGG-----DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP
116

Sbjct: 62 R G ++ G I I+ K+ + A +D WH D P
GRLGEVDHSSDGHPVPGIYPITLDKSKNASAAAYLKATFD-----WHIDGC-TP
109

Query: 117 V----MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
172

Sbjct: 110 + + V SA V GG T FA+ AAYDAL + + HSL SQ +
LGDECPQKATVLSAVRVAERGGGETEFANSYAAYDALTDDEKRRFGALRVVHSLEASQRR-
168

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG
232

V S + + T PLV H +GR SL++G A + GMD E LE

Sbjct: 169 --VYPDPSPPELVARWRSRRTHEHPLVWTH-RSGRKS LVLGASADYVVGMDLDEGRALLEE
225

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L+ A RV++H W+ GD V+WDNR +LHRA P+D R M + + G

Sbjct: 226 LLQRATVPERVYSHGWSIGDTVIWDNRGVLHRAAPYDPDSSREMLRRTTVLG 276

>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 = 8e-21, Method: Compositional matrix
adjust.

Identities = 84/288 (29%), Positives = 129/288 (44%), Gaps = 19/288 (6%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQOI 58
++Q+ ++ GA +GA V GV L LD A+ AA +H ++ F GQ HL+ D Q
Sbjct: 4 VSQSAVRAVKLGAIHIGAVVEGVRLCGDLDPETVTAVRAALHEHKVIFFRGQDHLTEDGQY 63

Query: 59 TFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
118

FA+ G A VK+ +H A +WH D T++ +
Sbjct: 64 EFAQLLGTPTTPHPTVTS A--GVKSLAIDSRHGRAN-----SWHTDVTFVDRV
109

Query: 119 AQQAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ--
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 ACQAPRVHAHQWAAGDVVVWDNRCLLHRA-EPWDFKLPRVMWHSRLAG 283
+ WA GDV +WDNR H A + +D R + LAG

Sbjct: 230 VTRLEHTTRWHWAPGDVAIWDNRATQHAYAIDDYDGSEHRRLTRITLAG 277

>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 = 9e-21, Method: Compositional matrix
adjust.

Identities = 86/285 (30%), Positives = 128/285 (44%), Gaps = 19/285 (6%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWL-QHALLIFPGQHLSNDQOITFAKR 63

Sbjct: 2 ++ +TP G LG + GV L A AA L +H ++I+ H+ + + F++
SVTVTPLGPLGVEIAGVSGGDLPTAEAAAECLELLARHGVIYREAHIKDGLVAFSRL 61

Query: 64 FGAI--ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMK-VIVGNMAWHADSTYMPVMAQ
120

G + G ++ I+ + D PA+ D + GN WH D + +
Sbjct: 62 LGEVVPNPTGEHELPEIATITLD-----PAKTDATLAWYRRGNFLWHIDGATDQLPQK
114

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGS
180

+ +A V GG T FA AAY+AL EA +A HS +Q + H
Sbjct: 115 ATLLTAREVDPAGGDTEFASTYAAAYEALPEAEKAAAFADLQVLHSFAAAQLR-AHPDATDE
173

Query: 181 AYIGYGMDDTTATPLR--PLVKVHPETGRPSLLIGRHAHAI PGMDAAESERFLEGLVDWAC
238

+G P+R PLV GR SLL+G A + G+ E E L L+DW+
Sbjct: 174 QKASWGR---VPVRRHPLVWTR-GNGRRSLLL GATAGEVIGLPPEEGEALLARLLDWST
228

Query: 239 QAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPVVMWHSRLAG 283

Q V H+W GD+V+WDN +LHRA P+ R+M + L G
Sbjct: 229 QPQFVLRHRWHTGDLVIWDNTGMLHRALPFTATSRRMLHRTTLVG 273

>ref|ZP_06494532.1| taurine catabolism dioxygenase TauD/TfdA [Pseudomonas
syringae pv.

syringae FF5]
Length = 279

Score = 104 bits (260), Expect = 9e-21, Method: Compositional matrix
adjust.

Identities = 81/249 (32%), Positives = 122/249 (48%), Gaps = 22/249 (8%)

Query: 41 QHALLIFPGQHLSDNDQQITFAKRFGAI--ERIGGGDIVAIS-NVKADGTVRQHSPA EWDD 97
Q +L+FP H S+ +QI F + G E G +I IS +VK + PA

Sbjct: 44 QRGVLVFPQIHFSDAEQIAFTRTLGTFCPEPGDQGNITRISLDVKEN-----PAG--- 93

Query: 98 MMKVIVGNMAWHADSTYM--PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR AL
155

+ + G++ WH D T P++A ++ S +V + GG T F + +AY+ L A R
Sbjct: 94 -AEFLKGS LYWHIDGTSSDSPILA--SLLSCKVPASWGGNTGFCNTYSAYEGLSSADRQ-
149

Query: 156 VHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHA
215

H S R S L + + G A + M PLV H +GR SL++G A
Sbjct: 150 -HYDSL RVIHAPWASLLYYNPEPGLAML-EAMQAI GEKELPLVWKH-RSGRKS LILGCTA
206

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPV
275

+ G+ A+S R L GL +WA ++H W GD+V+WDN +HRAE +D + R+

Sbjct: 207 QQVVGLSLAQ SARILVGLREWATSEAFSYSHAWQV GDLVIWDNTGTMHRAEAYDPECGRM
266

Query: 276 MWHSRLAGR 284
M ++L G

Sbjct: 267 MHR TKLQGE 275

>gb|ADC34008.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 104 bits (260), Expect = 9e-21, 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 QQIAFAEQFGTLERHVVSNRGTVNPLVHIVTNLGADGKPSGK-----VASTQW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
168

H+D ++ P + + A V+P GG TCFADM AAY+AL EA +A + HS S
Sbjct: 49 HSDKSFRPQPSLATILHALVMPPQGGETCFADMVAAYEALPEAEKAELAGVRVVHWSGLS
108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
228

Q+++G + I D PLV+ PETGR +L +G A + G
Sbjct: 109 QARVG--IKVPEEIADAPDIA----HPLVRTIPETGRKALFMGERAVHLEGQPEDVGRT
162

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

LE L A Q V+ H+W GD+++WDNRC+
Sbjct: 163 RLERLTAHAVQERFVYRHKWTLGDLLMWDNRCV 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 = 9e-21, Method: Compositional matrix
adjust.

Identities = 79/270 (29%), Positives = 116/270 (42%), Gaps = 18/270 (6%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
M L+I P +GA + + L L D + A +Q+ ++ F Q+L+ +QI

Sbjct: 1 MTYQHLKIKPIAGRIGAKILEIDLKQNLQDEVINEIRRALVQYKVIFFREQNLTAQE QIA 60

W +GDV +WDNR H A

Sbjct: 247 TTRWNWQSGDVAIWDNRATQHYA 269

>ref|ZP_05884985.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Vibrio

coralliilyticus ATCC BAA-450]

gb|EEX33578.1| alpha-ketoglutarate-dependent taurine dioxygenase [Vibrio
coralliilyticus ATCC BAA-450]

Length = 277

Score = 104 bits (260), Expect = 1e-20, Method: Compositional matrix
adjust.

Identities = 75/262 (28%), Positives = 114/262 (43%), Gaps = 11/262 (4%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKREG 65

+ +TP +GA V GV L+ L + F AL+ A+L+H +L F Q ++ QQI AKREG

Sbjct: 1 MNLTPLSEHIGALVEGVDLSNLSEQEFDALYQAYLKHKVLFVFRDQGMTPQQQIGLAKREG 60

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
125

+E + + + V + SP G WH D T+ + ++

Sbjct: 61 DLEPV--HPFFPHLDDEEQVVVIETSPGN-----PPGESFWHTDLTWQATPCRC SILQ
111Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-VYSQSKLGHVQQAGSAYIG
184

A+ P GG T + M A + +L + + +A H L + S+ V + G +++

Sbjct: 112 AQHCPHGGDTIWTSM EAVWSSLTSDDQHTLRGLTATHGLHAFEGSRYSVNEQGESHVA
171Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAPRV
243

PLV HPETG + + H I ++ ES + LE L A Q

Sbjct: 172 TVSQGYPPVKHPLVVRHPETGNLTAYVNEQFTHRINELEERESRKRLEQLFALARQPEYQ
231

Query: 244 HAHQWAAGDVVVWDNRCLLHRA 265

W G V +WDN 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 ADSTYMPVMAQGAVFSAEVVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ
169

ADSTYMP+ A+GAVFSAE++P+ GG T +ADMRAAY+ALD+ TRA + A HSL YSQ

Sbjct: 1 ADSTYMP LQAKGAVFSAEII PSEGGATGWADMRAAYEALDDDTRARIADLRAHHS LFYSQ 60

Query: 170 SKLGHV---QQAGSAYIGYGMTTATPLRPLVKVHPET 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 ADSTYMPVMAQGAVFSAEIVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ 169

ADSTYMPV A+GAVFSAE+VP+ G T +ADMRAAYDA+DE R + ARHSL YSQ

Sbjct: 1 ADSTYMPVQAKGAVFSAEIVPSEGAATGWADMRAAYDAMDEPMRERISAMRRARHSLWYSQ 60

Query: 170 SKLGHV---QQAGSAYIGYGMTTATPLRPLVKVHPET 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 SLLTITKLTDSVGA EVTGLDPAALAHDDSVGEAVLDALEDNGVLFVFRGLYLDPAAQVAF 61

Query: 62 KRFGAIERIGGG-----DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMP 116

R G ++ G I I+ K+ + A +D WH D P

Sbjct: 62 GRLGEVDHSSDGHPVPGIYPITLDKSKNASAAYLKATFD-----WHIDGC-TP 109

Query: 117 V----MAQGAVFSAEIVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL 172

+ + V SA V GG T FA+ AAYDAL + + HSL SQ +

Sbjct: 110 LGDECPQKATVLSAVRVAERGGETE FANSYAAYDALTDDEKRRFGALRVVHSLEASQRR- 168

Query: 173 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG
232

V S + + T PLV H +GR SL++G A + GMD E LE
Sbjct: 169 --VYPDPSPELMARWRSRRTHEHPLVWTH-RSGRKSLLVGLASADYVVGMDVDEGRALLEE
225

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

L+ A RV+ H W+ GD V+WDNR +LHRA P+D R M + + G
Sbjct: 226 LLQRATVPERVYRHGWSIGDVIWDNRGVLHRAAPYDPDSSREMLRTTVRG 276

>ref|YP_003490344.1| putative dioxygenase [Streptomyces scabiei 87.22]
emb|CBG71801.1| putative dioxygenase [Streptomyces scabiei 87.22]
Length = 325

Score = 104 bits (259), Expect = 1e-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--SPAEWDDMMKVIVGNMAWHADS
112

R G R+ G + + + T R+H AEW + + WHAD
Sbjct: 73 HRLGEPVRLRARGSVSPAAYPEIETTADRQELGRKHGMDQAEWLERRRHSTLR-GWHADH
131

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
172

T + AE VP GG T +A++ AY L E R A H L +
Sbjct: 132 TARIDPPALTLRAERVPPYGGDTTANLANLATAYAGLSEPVRRFADGLRAEHRL-----GV
186

Query: 173 GHVQQAG-SAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFL
230

G++ ++G Y+ + D + P+V+VHPETG L + + I + AES L
Sbjct: 187 GYLARSGPDPYLRHLQDHQVASVHPVVRVHPETGERILYVNPYYVEHIVDVSRAESRLLL
246

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAG-RP 285

E V+ + +W G V +WDNR +H A P D PR+M +AG RP
Sbjct: 247 EMFVEQITRPEYTVRFRWEPGSVALWDNRATVHLA-PSDAAHLDFPRIMHRVMIAGDRP 304

>gb|ADC33997.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 104 bits (259), 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 QQIAFAEQFGTLERHVVSNRGTVNPLVHIVTNLGADGKPSGK-----VASTQW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
168
 H+D ++ P + + A V+P GG TCFADM AAY+AL EA +A + HS S
Sbjct: 49 HSDKSFRPQPSLATILHALVMPPQGGETCFADMIAAYEALPEAEKAELAGVRRVHWSGIS
108

Query: 169 QSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
228
 Q+++G + I D PLV+ PETGR +L +G A + G
Sbjct: 109 QARVG--IKVPPEEIIADAPDMA----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 = 1e-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 LQAKGAVFSAEIIIPSEGGATGWADMRAAYEALDDDTRARIADLRAYHSLFYSQ 60

Query: 170 SKLGHV---QQAGSAYIGYMDTTATPLRPLVKVHPET 204
 + G++ Q Y YG LRPLVKVHPET
Sbjct: 61 GRSGYLPSKQNERGGYDMYGYHDEEPSLRPLVKVHPET 98

>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 = 1e-20, Method: Compositional matrix
adjust.

Identities = 81/271 (29%), Positives = 127/271 (46%), Gaps = 26/271 (9%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64

Sbjct: 11 +L + G GA + G+ +A+ D AA+ +A +H +L+ GQ L + I F +R
 SLTLDKFGPHFGAEIIGLDVASATDDEVAAIRSALTEHKVLVLRGQSLGDASHIEFGRRL 70

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPA--EWDDMMKVIVGNMAWHADSTYMPVMAQGA
 122

Sbjct: 71 G + A V G V Q A D+ + WH D T+M G+
 GRL-----TAGHPVHDSGDVAQEYALDSQDNGFADV-----WHTDVTFMKRPPLGS
 117

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHV---QQAG
 179

Sbjct: 118 + V+P GG T +AD + AY++L R ++ Q +A H + G+ ++ G
 ILRPVVLPPHGGDTNWADSQLAYESLSLPVRQ MIDQLTAVHD---GNREFGYLLAQKRG
 174

Query: 180 SAYIGYGMDTTA-TPLR-PLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVD
 235

Sbjct: 175 + G + TA P+ P+V+VHPETGR + + G +H I G+ AES L+ L
 KGNVWDGEEVTALVPVEHPVVRVHPETGRKGIFVNPFTSH-IAGVSEAESRGILDFLYA
 233

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAE 266

Sbjct: 234 + + H+W GD+V+WDNR H A
 HLTKEPHIVRHRWRLGDLVLWDNRSTAHYAN 264

>ref|ZP_06120739.1| Taurine dioxygenase [Caulobacter segnis ATCC 21756]
 gb|EEZ37224.1| 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----GDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
 115

Sbjct: 61 F ++FG + G D I + AD + V WH+D T
 FGRKFGNLAIHSGVPLPDHPEIVAIHADANSK-----FVAGENWHSDLTCD
 107

Query: 116 PVMAQGA VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHV
 175

Sbjct: 108 P G++ +V+P GG TCFA M AYD L + +A + SA H V
 PEPPLGSILYMKVLPDDGGDTCFASMYWAYDTLSDRMKAYLEGLSAVHD-----ANPV
 160

Query: 176 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLV
 234

+A I + + P+V+ HP +GR SL + + I G+ AES L L

Sbjct: 161 YKAIFPDIDRKYNCST---HPIVRTHPVSGRKSLEFVNPSYTHIAGLSKAESNAILNFLY
217

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDF 270
A +W V WDNRC H+A WD+

Sbjct: 218 QHASNPDFQVRFWRKPNNSVAFWDNRCTWHQAI-WDY 252

>ref|ZP_06467676.1| taurine dioxygenase [Burkholderia sp. CCGE1003]
gb|EFD34797.1| 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 ARASLNIRRLAGRIGAQVEGVTLSPDQPTFEAIEKALYTHKVLFFRGGHLDASQEG 78

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA----WHADSTYM
115

FA+RFG A TV H+ + D++ + + A WH D T++
Sbjct: 79 FARFG-----ETVAHPTVPSHAGSA--DLLDLSAHGARANSWHTDITFV
122

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY-----SQ
169

+ ++ A +P VGG T +A+ AAY+ + E RA A H+ Y ++
Sbjct: 123 DAYPKLSILRAITIPPVGGDTVWANTAAAYERVPEPLRAFADHARAIHTNAYDYASSHAE
182

Query: 170 SKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF
229

+ +++ +I +T P+V VHP TG +L++G A G+ A +S
Sbjct: 183 ADDTQLKRYREVFIKVVETE----HPVSVHPVTGERTLVLGHFQRFAGLSAQDSASL
238

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L+ L + + QWA GDV +WDNR H A

Sbjct: 239 LQVLHEHITRLENTVRWQWAEGDVAIWDNRATQHYA 274

>ref|ZP_06297656.1| Taurine dioxygenase [Burkholderia sp. CCGE1001]
gb|EFB07124.1| 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 AKASLNIRRVAGRIGAQIEGVRLSPELDQATFEAIEAALHTHKVLFFRGGHLDASQEG 78

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA--WHADSTYMPV
117

FA+RFG + A TV H+ + G A WH D T++
Sbjct: 79 FARRFG-----DTVAHPTVPSHAGGSRLLDLDSAHGARANSWHTDVTFFVDA
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----HPVVRVHPVTGERTLVLGHFVQRFIQLSTQESTALLQ
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 RYPVLIFPKQFINDDELLAFSANFGPVHTAMSYQTREKEHRLQPKITDISNLGKDNQTFK 98

Query: 90 HSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD
149

M V WH D++Y + A+ + A V GG T FADMRAAYD +
Sbjct: 99 RGDHR---RMNNEFVSK-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 RKTLYLSGHATHVVDWPIPEGRDLLRELMFATQPQFVYTHKWHERDLVMWDNRALMHR 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  RVVKLGANIGARIEGVRVGGGLDPVTVTAINALLEHKVIFFRGQHLLDDDGQLAFARRL 63
```

```
Query: 65  GAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGAVF
      124
      G          +      T R H      D          +WH D T++ + + ++
Sbjct: 64  GTP-----TTAHPVTSRGRHILPIDSRYD---KANSWHTDVTFFVDRIPKASLL
      109
```

```
Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHS--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 REYREEFVSEYFETEHPVVRHPETGRRVLLLGHFQFVGLGVAESTALLALLQNRVTK
      229
```

```
Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
      W  GD+ VWDNR  H A
Sbjct: 230 LENTVRWSWEPGDLAVWDNRATQHYA 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  +
```


V + + Y T T PLV VHPE G SL++G I G+ A+S+ L
 Sbjct: 172 VNVSEAGRERRYDEVFTKTVFETEHPVHVPENGERSLIVGHFIQRILGLTTADSQHLLA
 231

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
 D A + W GDV +WDNR +HRA + PRV+ + G

Sbjct: 232 IFHDHATRPENTVRWSWRITGDVAIWDNRATVHRAVDDYGEAPRVVRRVTIQG 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-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVG
 104

QQI FA+ FG ++ R+ + + ISNV DG + + + M +
 Sbjct: 1 QQIAFARAFGLDIGLKKVFKRPNRLKRDESIDISNVADDGRIASLATKK----MYSQLA 56

Query: 105 NMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
 164

N WH+DS++ A+ ++ + P GG T FAD+RAAYD L E T+ V A+H+
 Sbjct: 57 NQLWHSDDSSFDPPARYSMLYLSNPPKGGETEFAIDLRAAYDGLPEDTKREVEGLRAQHN
 116

Query: 165 LVYSQSKLGHVQQAGSAYIGYMDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDA
 223

++S+ LG P+ PLV+ HP + R L +G H + GM
 Sbjct: 117 ALHSRINLGD TDWTEE-----QKNAIPPVEWPLVVRTHPGSKRKLFLVGVHTTHVVMHML
 170

Query: 224 AESERFLEGLVDWACQAPRVHAHQWAAGDVVVVDNRCL 261

E L L++ A Q V+ H W GD+VVVDNRC+
 Sbjct: 171 GEGRLLLAELLEHATQREFVYRHSWRVGD LVVVDNRCV 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 = 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 FEVVPQARTIGAEIRGADLSRPLPPALREELNRALLEWKVLFVFRGAHLTSDQQQRFAGNW
 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 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG
179

GAV VP GG T +ADM AAYD L + V A H + G + G
Sbjct: 152 LGAVLQLREVPPFGGDTMWADMAAAYDNLPREVKERVDGALAVHDFI-----PGFARFYG
206

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWAC
238

+ D P+V+ HPETGR L + I G+D ES+R L L A
Sbjct: 207 PERLLPHQDLLPPVEHPVVRTHPETGRRMLFVNASFTTRITGVDRDESDRLLRFLFQQAH
266

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+W GDV WDNR H A
Sbjct: 267 VPEYQVRWRWQPGDVAFWDNRATQHYA 293

>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 = 2e-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 LTAEPLSRVLGAEIKGLDLSSPIADADREELLTLFWQHKVIVIRGQDVAPDGFIRFAEAF 61

Query: 65 GAIERI-----GGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMP
116

G IE I +SNV+ DG P D WH+DST+
Sbjct: 62 GTIEPFFISAYNLPHTHPQIYVLSNVRQDG-----KPIGRDG-----AGTHWHS DSTFTE
110

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA-----RHSLVYS---
168

+ + VP GG T F + AYD LD+ T+A + R A R VYS
Sbjct: 111 KPSSATLLHGVTVPDRGGDTL FVNTADAYDRLDDETKARIQGRRAIHRYQRKEFVYSGDR
170

Query: 169 ---QSKLGHVQQAGSAYIGYGMDTTATP-----LRPLVKVHPETGRPSLLIGRH
214

++ +++ + + A+P L P+V+ HP TG L +
Sbjct: 171 TIDDAERTEIERVKALRMAEAAAADAASPTAQRSNQEPDRLHPIVRTHPVTGSKGLYLNDE
230

Query: 215 AHA-IPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLP
273

I G+ E+ L L + A V ++W GDVVVWDN ++H A LP
 Sbjct: 231 MTVGIIEGIPDEEAVPLLRRLCEVATAPDPTVLRKWRQGDVVVWDNAAVIHSATFTFPDLP
 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 = 2e-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 AGSGVRVVKLGAHIGARVDGVRLGGDL D A G T V E A I R S A L L T H K V I F F R D Q G H L D D E S Q V A 73

Query: 60 FAKRFGAIE----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM
 115

 FA+ G + + G D I + +D +S A +WH D T++
 Sbjct: 74 FARLLGDLTLAHTVGRGRDNANILPIDSD-----YSKAN-----SWHTDVTFV
 116

Query: 116 PVMAQGAVFSAE VVPVAVGGRTCFADMR AAYDALDEATRALVHQRSARHSLVYS-----Q
 169

 + +V A +P GG T +A AAY+ L +ALV A H+ Y +
 Sbjct: 117 DRVPAISVLRVAVQLPEYGGTTTWASTVAAYEKLPAPLKALVDSLWAVHTNAYDYAANIDE
 176

Query: 170 SKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF
 229

 +++G V Y + P+V+VHPETG +LL+G + G+ ++ES
 Sbjct: 177 TRVGGVDVKFQ EYRREFVSNVYETEHPVVRVHPETGERALLLGHFVKRLVGLTSSESHTL
 236

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 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]

+SN+ +G H ++ WH D Y V ++ A VPA GG T
 Sbjct: 71 IVSNILENGVSIGHLGSK-----EAYWHTDMCYTDVPPITSILYAIEVPACGGNT
 120

Query: 137 CFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATP--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 HPIVRVHPVTQRPYLYLGRRLNAYVVGLPVGSEALLDELWRYTRLDGVTWTQRWEVGD
 234

Query: 254 VVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285

 ++WDNRC +HR + +D R+MW +++ P
 Sbjct: 235 MIWDNRCTMHRRAFDANARRLMWRTQIQADP 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]

gb|AAO56118.1| 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 = 2e-20, Method: Compositional matrix
 adjust.

Identities = 79/255 (30%), Positives = 118/255 (46%), Gaps = 26/255 (10%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAI--ERIGGGDIVAIS-NVKADGTVRQHSPAEWDD 97
 Q +L+FP H S+ +QI F + G E G +I IS +VK + PA

Sbjct: 44 QRGVLVFPKIHFSDAEQIAFTRTLGTFSPASDQGNITKISLDVKEN-----PAG--- 93

Query: 98 MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALLVH
 157

 + + G++ WH D T ++ S +V + GG T F + AAY+AL +A +
 Sbjct: 94 -AEFLKGSPLYWHIDGTSSDAPILASLLSCKVPASWGGNTGFCNTYAAYEALGDADKHRYE
 152

Query: 158 QRSARH----SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR
 213

 H SL+Y + G IG PLV H +GR SL++G
 Sbjct: 153 SLRVIHAPWASLLYYNPEPGLAMLKAMQAIG-----EKELPLVWKH-RSGRKSLLIGC
 204

Query: 214 HAHAI PGMDAAE SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLP
273

A + G A+S + L GL +WA ++H W GD+V+WDN +HRAE +D +
Sbjct: 205 TAQHVVGNSLAQSAQILVGLREWATAEAFSYSHTWQVGDVLIWDNTGTMHRAEAYDPECG
264

Query: 274 RVMWHSRLAGRPETE 288

R+M ++L G E
Sbjct: 265 RMMHRTKLQGEPPFE 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 = 2e-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-----SSALGSEVYGFDTFPYESDAVQTLIDAWHAGGICRLRQQLDMAEFVE 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 HTDMCYTDVPPIASILYAIEVPTRGGDTEFMNMYRVHDALPASLRKRIAGLSIKHDRSYT
165

Query: 169 QSKLGHVQQAGSAYIGYGMTTATP--LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAE
225

+G ++ + + D T P + P+V+VHP T RP L +GR +A + G+ E
Sbjct: 166 --AVGELRYGFESVV----DVTTCPGSVHPVIRVHPVTRRPYLYLGRRLNAYVVGLPVDE
219

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLP RVMWHSRLAGRP
285

SE L+ L + W GD+++WDNRC +HR + +D + R+MW +++ P
Sbjct: 220 SEALLDELWRYTRLDGVTWTQHWEVGDIMIWDNRCTMHRRAFDERARRLMWRTQIQADP
279

>ref|ZP_04700699.1| putative taurine catabolism dioxygenase [Streptomyces
albus J1074]

Length = 315

Sbjct: 119 LRPVVLPPHGGDTNWADSQLAYESLSLPIRQ MIDQLTAVHD---GNREFGYLLAQKRGK
175

Query: 181 AYIGYGMDDTTA-TPLR-PLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVDW
236

I G + TA P+ P+V+VHPETGR + + G +H I G+ AES L+ L
Sbjct: 176 GNIWDGEEVTALAPVEHPVVRVHPETGRKGFVNPGFTSH-IAGVSEAESRGILDFLYAH
234

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRAE 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 = 2e-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 KSQLRIEPLTPAIGAEILGVDLGKVTPELVEDVRVALLKYKVVFFRDQQISARQHIDFAR 65

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQ--HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ
120

FG +E A +AD + + H P NM WH+D T+ +
Sbjct: 66 EFGELEIHP-----ATPKNQADPEILRLAHGPDSKGS-----ENM-WHSDVTWREKPSL
113

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSL--VYSQSKLGHVQQA
178

G++ A VPAVGG T FA+M AY+ L +AT+ +H R A H + V+++ ++
Sbjct: 114 GSILRAVEVPAVGGDTLFANMAMAYERLS DATKEKIHNR IAVHDIARVFAKRLNKRPEEL
173

Query: 179 GSAYIGYGMDDTTATPL--RPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVD
235

Y PL P+V+ HPETG + + G I MD S+ L+ L
Sbjct: 174 HEQY-----PLMEHPVVRTHPETGEQVVVNGAFTSHIKDMDPQASKSLLDELYK
223

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RPETE 288

A +W A + WDNR H A F RVM +AG RP E
Sbjct: 224 SAWNPEIQCRFKWRANSIAFWDNRACQHFAASDYFPAVRVMERVTIAGDRPYFE 277

>ref|ZP_04953283.1| dioxygenase, TauD/TfdA family [Burkholderia
pseudomallei 1710a]
gb|EET02805.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei
1710a]

Length = 283

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
168

H D Y V ++ A VPA GG T F +M +DAL + R + S +H Y+
Sbjct: 106 HTDMCYTDVPPIASILYAIEVPAHGGNTEFMNMYRVHDALPASLRRQIAGLSIKHDRSYT
165

Query: 169 QSKLGHVQQAGSAYIGYGMDDTATP--LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAE
225

+G ++ + + D T P + P+V+VHP T RP L +GR +A + G+ E
Sbjct: 166 --AVGELRYGFDSVV----DVTTCPGSIHPIVVRVHPVTQRPYLYLGRRLNAYVVGLPVGE
219

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP
285

SE L+ L + +W GD+++WDNRC +HR + +D R+MW +++ P
Sbjct: 220 SEALLDELWRYTRLDGVTWTQRWEVGDIMIWDNRCTMHRRDAFDANARRLMWRTQIQADP
279

>ref|ZP_01616095.1| alpha-ketoglutarate-dependent taurine dioxygenase
[marine gamma

proteobacterium HTCC2143]

gb|EAW33178.1| alpha-ketoglutarate-dependent taurine dioxygenase [marine
gamma

proteobacterium HTCC2143]

Length = 281

Score = 103 bits (256), Expect = 3e-20, Method: Compositional matrix
adjust.

Identities = 82/274 (29%), Positives = 118/274 (43%), Gaps = 29/274 (10%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
+ I +G GA VTGV L+ LD+ ++ AWL+H +L FP Q +S+D F F

Sbjct: 3 IMIAASGQACGAEVTVGVDLSKPLDEKTVQSIRTAWLEHHVLSFPEQLMSDDDLERFTNYF 62

Query: 65 GA-----IERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM
118

G I I G + V AD T + A WH D ++
Sbjct: 63 GPFGDDPFILPIAGREHVIAIQRNADETSSLFAEA-----WHTDWSFQTNP
108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV---
175

G +P VGG T FA+ A + RA + + A HS + S G
Sbjct: 109 PSGTCLYGITIPPVGGDTLFANQHKALADMPAQLRAKIEGKLAIHSAAGAYSPEGAYGET
168

Query: 176 -QQAG-SAYIGYGMDDTATPLRPLVKVHPETGRPSL--LIGRHAHAIPGMDAAESERFLE
231

Q +G S I + T PL+K HPE+G+ L +G + I G+D ++ L
Sbjct: 169 DQDSGRSMLIKADDEAKETHKHPLIKAHPESGQECLYSLG-YIVGIDGLDQEQATELLA
227

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
 ++ + P+G GAT+ GV L+ LDDA + +AWL H +L F Q + +D F
 Sbjct: 2 SMIVEPSGQACGATIRGVDLSGKLDLITDVRSAWLTHRVLAFADQSMDDDALERFTLA 61

Query: 64 FGAIER-----IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
 116

G G G+I AI E D+ + N WH+D +++
 Sbjct: 62 MGGFGEDPFFDPIPRGNIAAILR-----EPDEKAPLFAEN--WHSDWSFSL
 106

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHS--LVYS-QSKLG
 173

G A +P VGG T FAD AA+ AL + + + +A HS L Y+ G
 Sbjct: 107 HPPAGTCLLAIEIPVGGDTL FADQIAAFAALS DERKQ LRALTAIHS AKLAYAPDGTYG
 166

Query: 174 HVQQAGSAYIGYGMDDTTATPLR--PLVKVHPETGRPSLL--IGRHAHAIPGM DAAESERF
 229

A + D +A ++ PL++ HPETG ++ +G + I GM AE+
 Sbjct: 167 EKDAAGRSM AIRPDESANAMQTHPLIQ AHPETGEEAIFSTLG-YIIGIEGMAQAEAIAL
 225

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 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 = 3e-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 QRGVLFVFPQIDFSDAEQIALTRTLGTFCEASDQGNITKISLDVK-----ENPAG--- 93

Query: 98 MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVH
 157

+ + G++ WH D T V ++ S +V + GG T F + AAY+AL A +
 Sbjct: 94 -AEFLKGSLYWHIDGTSSDVPVLASLLSCKVPASWGGNTGFCNTYAAAYEALSSADK----
 148

Query: 158 QRSARHSLVYS--QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHA
 215

QR R ++++ S L + + G A + M PLV H +GR SL++G A
 Sbjct: 149 QRYERLRVIHAPWASLLYYNPEPGLAMLK-AMQAI GEKELPLVVRH-RSGRKS LILGCTA
 206

Query: 216 HAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLP RV
 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 MHRTKLQGEEPFE 279

>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 = 3e-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-NVGVEVSGFDINEPLTDEIKAELKALWYEHAILVFRDQDISPEKQIEFSRIF 61

Query: 65 GAIE----RIGGGDIV-AISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
 119

G +E ++ D + ++ G + + A + + IVG + WH D Y

Sbjct: 62 GPLELHPLKVTTSDKYPELFVLQNGGPMDFQTAIFYKG--EEIVGRLDWHMDLHYTARPN
 119

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG
 179

GA+ A VV A G T F D+ AYDALD+ T+AL+ Q +S + + +V G

Sbjct: 120 HGALLRAVVVAAEDGMTGFGDLAKAYDALDDDTKALIEQLEVVYSFSMQRRHMRVYVNLGD
 179

Query: 180 -----SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH---AIP---GMDAAE
 225

+ G + P+V HP +GR L + P G+ E

Sbjct: 180 YEPGNSPTKPTDIGFPDFSDAAYPMVVTHTPISGRKVLEVVVEQFLDRVVTPQQFGLSNDE
 239

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH 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 EVTGLDPAALAHDDSVGEAVLDALEDNGVLVFRGLYLDPAQAFC 61

Query: 62 KRFGAIERIGGG-----DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
116

R G ++ G I I+ K+ + A +D WH D P
Sbjct: 62 GRLGEVDHSSDGHPVPGIYPITL DKSKNASAA YLKATFD-----WHIDGC-TP
109

Query: 117 V----MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
172

+ + V SA V GG T FA+ AYDAL + + HSL SQ +
Sbjct: 110 LGDECPQKATVLSAVRVAERGGETE FANSYGAYDALTDDEKQRF GALRVVHSLEASQRR-
168

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG
232

V S + + T PLV H +GR SL++G A + GMD E LE
Sbjct: 169 --VYPDPSPELVARWRSRRTHEHPLVWTH-RSGRKS LVLGASADYVVGMDVDEGRALLEE
225

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

L+ A RV+ H W+ GD V+WDNR +LHRA P+D R M + + G
Sbjct: 226 LLQRATVPERVYRHGWSIGDTVIWDNRGVLHRAAPYDPDSSREMLRRTTVLG 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 = 4e-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 FTLSPLTPLIGAEITGIDLKPLD TAALSALRQALLDWKVIFFRDQDITTDQHLAFARLF 72

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV
117

G +E + G +++AI++ + D R++ WH+D T+
Sbjct: 73 GELEVHPFAPHKQGYPEVLAI THDR-DRPGRENK-----WHSDVTWREC
115

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
177

+ G+V A VP VGG T FADM AAYD L E + + A H + + + + +

Sbjct: 116 PSLGSVLRAIEVPEVGGDTLFDADMYAAYDGLTEEVKEKIDGAVAIHDFAHFRAAM-RARG
174

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDW
236

A I P+V+ HPETGR + + I G++ AES+ L+ L
Sbjct: 175 KSEAEIEEMNRKYPMVEHPVVRTHPETGRKGIYVNVAFVQHVIVGLEKAESDALLKHLIYAQ
234

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRA 265

A +W + WDNR H A
Sbjct: 235 AAIPYQCRFRWQKNSIAFWDNRSSQHYA 263

>ref|ZP_05226007.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Mycobacterium
intracellulare ATCC 13950]
Length = 300

Score = 102 bits (255), Expect = 4e-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 ITVTKLGSRIGARIDGLSLGGHLDDAAVETIRRALLTHKVVFFRHQHHLDDDEQQQLDFARL 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 MSDAQRAFRAFEKPDFRTEHPVVRVHPETGERALLAGDFVVRGFVGLDNHESSVLELLQ
227

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRA-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 = 4e-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 LGTEVYGFDSPPPHDAEAVRALIEAWHAGGICRLRRQRLDMAEFVEFSRIFGRPERALNQ 69

Query: 74 D-----IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
 122
 + ++ +SN+ +G H ++ WH D Y V +
 Sbjct: 70 ERKLT SREDLP ELMIVSNILENGVSIGHLGSK-----EAYWHTDMCYTDVPPIAS
 119

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAY
182

+ A VPA GG T F +M +DAL + R + S +H Y+ +G ++ +
Sbjct: 120 ILYAIEVPAHGGNTEFMNMYRVHDALPASLRQIAGLSIKHDRSYT--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----DVTTCPGSIHPVIRVHPVTQRPYLYLGRRLNAYVVGLPVGESALLDELWRYTRL
233

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLAGRP 285

+W GD+++WDNRC +HR + +D R+MW +++ P
Sbjct: 234 DGVTWTQRWEVGDIMIWDNRCTMHRRAFDANARRLMWRTQIQADP 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 = 4e-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 ISVNPPIHPTFGAEVREVDVFSKPLTDEVFSEIYSAITKYGVLVFRNTGLTDEGHIAFAKRF 73

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQ-HSPA EWDDMMKVIVGNMAWHAD
111

G ++ R+ ++ +SNV+ DG++ SP + GN +H D
Sbjct: 74 GELDDITPYLALGRKNRLKYNELFDVSNVEFDGSILDPE SPRGQGNK-----GNGLFHVD
128

Query: 112 STYMPVMAQGAVFSAEVV--PAVGGRTCFADMRAAYDAL--DEATRVLVHQR SARHSLVY
167

S++ P A ++ + + P +GG T FAD R A+D L D + + A HS+ +
Sbjct: 129 SSFNPRRAGYSLLLSHELPPPGMGGATAFADTRTAFDEL PVDLKADLVANDYVAAHSIHH
188

Query: 168 SQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
227

S+ A + Y M +V+ H + R +L I H H I G+ S+
Sbjct: 189 SRKLAAP E FYADR NPLD YPMGR-----HKMVQRHEPSRRMNL YIAAHIHHIEGLGPEASQ
243

Query: 228 RFLEGLVDWACQAPRVHAHQWA-AGDVVVWDNRCLLHRA 265

+ + + QA V +W GD++ WDN C++HRA
Sbjct: 244 KLFDRVFTHTCTQAKYVTEVEWKQPGDLIAWDNTCVMHRA 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 = 4e-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 LRIRPAGPLIGAEITGVDLGAPLDEELKAELRDALLEWKVLFRRGRRVTGADQRRRLAEVW 93

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGAVF
124

G +E +S ++ VR E + WH+D+T+ P + GAV
Sbjct: 94 GKVE-----TFPFLSKGRSPDVVRFKHEERPGLNT-----WHS DATWHPTPSMGAVL
142

Query: 125 SAEVVPVAVGG-RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
183

A VPA GG T ++D+ AAYD LD ALV R A H + S+LG ++
Sbjct: 143 RAVEVPAGGGGDTIWSVAAAYDNLDPELAALVDGREAVHHFDWLYSRLGLLE-----
195

Query: 184 GYGMDTTAT---PLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC
238

G +D P+R P+V+ HP TGR + + R + G++ + L+D C
Sbjct: 196 GEELDRARADFPVVRHPVIRTHPVTGRKGIFVNRVFTGEGVVGLEHGAARE----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 = 4e-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 DAEAVRALIEAWHAGGICRLRRQRLDMAEFVEFSRIFGRPERALNQRKLSREDLPELM 70

Query: 77 AISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRT
 136

+SN+ +G H ++ WH D Y V ++ A VPA GG T
 Sbjct: 71 IVSNILENGVSIGHLGSK-----EAYWHTDMCYTDVPPIASILYAIEVPARGGNT
 120

Query: 137 CFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP--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 HPIVRVHPVTQRPYLYLGRRLNAYVVGLPVGSEALLDELWRYTRLDGVTWTQRWEVGD
 234

Query: 254 VVWDRCLLHRAEPWDFKLPRVMWHSRLAGRP 285

++WDRNC +HR + +D R+MW +++ P
 Sbjct: 235 MIWDRCTMHRRDANARRLMWRTQIQADP 266

>emb|CAJ89608.1| putative dioxygenase [Streptomyces ambofaciens ATCC
 23877]

Length = 312

Score = 102 bits (254), Expect = 5e-20, Method: Compositional matrix
 adjust.

Identities = 84/266 (31%), Positives = 109/266 (40%), Gaps = 25/266 (9%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 + P T+GA + GV L+ L A L+ A L+ +L F QHL++DQQ FA +

Sbjct: 44 FDVVPLARTIGAEIRGVDLSRPLGAALREELNRALLEWKVLFRAQHLTSDQORAFAGHW
 103

Query: 65 GAIER----IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
 120

G +E G + KAD + + WH D T+ A
 Sbjct: 104 GRLETNPLLAAGSREDVVRFDKADASTPTYE-----NVWHTDVTFRERPAL
 149

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGS
 180

GAV VP GG T +ADM AAYD L R V A H + G + G
 Sbjct: 150 GAVLQLREVPPFGGDTLWADMAAAYDNLPREVRDRVDGARAVHDFI-----PGFARFYGP
 204

Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ
239

+ D P+V+ HPETGR L + I GMD ES+R L L A
Sbjct: 205 ERLIPHQDAFPPVEHPVVRTHPETGRRMLFVNASFTTHITGMDRDESDRLLRFLFQQAHV
264

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265

+W GD+ WDNR H A
Sbjct: 265 PEFQVRFRWQPGDIAFWDNRATQHYA 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 = 5e-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 TFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNM-----AWHADST
113

FA+RFG + A TV S E +++ + G +WH D T
Sbjct: 61 AFARRFGEV-----TTAHTV--PSLPENPEVLDLNYGRTTSRANSWHTDVT
105

Query: 114 YMPVMAQGAVFSAEYVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
173

++ G++ A +P GG T +A+ AY L R L Q A HS Y +
Sbjct: 106 FVDRPPLGSILRALDIPPTGGDTIWANSVTAYQDLPIHLRNLADQLWAVHSNKYDYATAF
165

Query: 174 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL
233

+ + AY T L P+V+VHPE+G L IG G+ ES+ L L
Sbjct: 166 DLPEYAKAYRAVFTSTVYETLHPVVRVHPESGERGLFIGGFVRQFRGLSTTESDDILRLL
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 = 5e-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 SLTIQPISPALGAIIVSGIDLAAPLDDGGQRAIEQALLDHQVLFVRDQSLPKSQARFAAH 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

FG + I I A+ Q D + + N WH D T++ A GAV
Sbjct: 62 FGD LH-----IHPIYPSVAE----QPEVIVLDTAVTDVRD NAIWHTDVTFLETPALGAV
111

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQQAGSA
181

A+ +P GG T +A AAY+AL R L+ +A H + + + G V +A A
Sbjct: 112 LVAKQLPPYGGDTLWASSTAA YEALSAPLRRLLDGLTATHDIGKSFPRERFG-VTEADLA
170

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGM DAAESERFLEGLVDWACQA
240

+ P+V+ HP TGR L + I ++ AES+ L+ L A +
Sbjct: 171 RLEEARLKNPPRSHPVVRTHPVTGRKGLFVSDGFTTRINELEPAESDALLKFLFAHATRP
230

Query: 241 PRVHAHQWAAGDVVVW DNRCLLHRAEPWDFKLPRVMWH--SRLAGRP 285

+W DV W DNR H A D++ R + H + L RP
Sbjct: 231 EFTVRWRWQENDVA FWDNRVTQHYAVD-DYRPQRRVMHRATILGDRP 276

>gb|ADC34019.1| TfdA-like protein [uncultured bacterium]

Length = 195

Score = 102 bits (254), Expect = 5e-20, Method: Compositional matrix adjust.

Identities = 70/214 (32%), Positives = 105/214 (49%), Gaps = 27/214 (12%)

Query: 56 QQITFAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW
108

QQI FA++FG +ER + + ++N+ ADG V + +W
Sbjct: 1 QQIAFAEQFGTLERRIASNRGKTNPLVHIVTNLNADGKPSGK-----VASTSW 48

Query: 109 HADSTYMPVMAQGA VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
168

H+D ++ P + + A V+P GG TCFA+M AAY+AL A +A + A HS S
Sbjct: 49 HSDKSFRPQPSLATILHALVMPDGGGETCFANMIAAYEALPAAEKAELDGIRAVHSWEIS
108

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATPL-RPLVKVHPETGRPSLLIGRHAHAIPGM DAAESE
227

Q++ G +A I A P+ PLV+ PETG +L +G A G +
Sbjct: 109 QARAGF--KAPPEEIA-----DAPPMHPLVRTIPETGLKALFMGERAVFFEGHPPEEAGQ
161

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
LE L A + V+ H+W GD+++WDNRC+
Sbjct: 162 ARLEKLTAHAVEERFVYRHKWTLGDLLMWDNRCV 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 = 5e-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 SITVTPVSPAVGAEEVGLSGHQVDRQVAADSLAALDITYGVLIYRDANIGDDDLVAFSRL 61

Query: 64 FGAIERIGGGDIVA---ISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQ
120
G + G + + IS V D PA+ D+ WH D V +
Sbjct: 62 LGDVVVAPMGGLASHPEISPVSLD-----PAK-SDLANYRRSTFFWHIDGVNDDVDPQK
113

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGS
180
++ +A V GG T FA+ AYDAL + + + HS SQ L H +
Sbjct: 114 ASLLTARQVADEGGETEFTANTYATYDALPDDEKEYLATLRVVHSFAASQ-ILVHPHPSDK
172

Query: 181 AYIGYGMDDTTATPLR--PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC
238
+ P R PL+ +GR SLLIG + G+ A ES L+ L+ W+
Sbjct: 173 ERAAWNRR---VPSREHPLIWTR-RSGRKSLLIGATTDHVGLPARESRALLDKLLAWST
227

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
Q V H W GD+V+WDN +LHRA P+ PR+M + LAG
Sbjct: 228 QESFVLRHWDWRGDLVIWDNTGMLHRALPYQPTAPRLMHRRTLAG 272

>ref|YP_235431.1| taurine catabolism dioxygenase TauD/TfdA [Pseudomonas
syringae pv.
syringae B728a]
gb|AAAY37393.1| Taurine catabolism dioxygenase TauD/TfdA [Pseudomonas
syringae pv.
syringae B728a]
Length = 279

Score = 102 bits (254), Expect = 5e-20, Method: Compositional matrix
adjust.

Identities = 79/250 (31%), Positives = 120/250 (48%), Gaps = 24/250 (9%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMK
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 FLKGSPLYWHIDGTSSDSPILA--SLLSCKVRASWGGNTGFCNTYAAAYEGLSSADQQHYDG
153

Query: 159 RSARH----SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH
214
H SL+Y + G IG PLV H +GR SL++G
Sbjct: 154 LRVIHAPWASLLYYNPEPGLAMLEAMQVIG-----EKELPLVWKH-RSGRKSLLIGCT
205

Query: 215 AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPR
274
A + G+ A+S R L GL +WA ++H W GD+V+WDN +HRAE +D + R
Sbjct: 206 AQQVVGLSLAQ SARILVGLREWATSEAFSYSHAWQVGD LVIWDNTGTMHRAEAYDPECGR
265

Query: 275 VMWHSRLAGR 284
+M ++L G
Sbjct: 266 MMHRTKLQGE 275

>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 = 6e-20, Method: Compositional matrix
adjust.

Identities = 82/254 (32%), Positives = 112/254 (44%), Gaps = 31/254 (12%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAI---ERIGGGDIVAISNVKADGTVRQHSPAEWDD 97
+H +L+F +L Q+ F +R G + + D I + D PA +
Sbjct: 41 EHGVLFFRELNLDYATQVAFCRRLGELLTFPKTPPLDFPEIMEINWD-----PA--NP 91

Query: 98 MMKVIVGNMAWHADSTYMP-VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
156
GN AWH D P + +V S VV GG T FA AAYDAL
Sbjct: 92 RSDYFRGNTAWHLGDALDPGNPPKASVMSGGVVTDSSGGETEFASYAAYDAL-----
143

Query: 157 HQRSARHSLVYSQSKLGHVQQA--GSAYIGYGMDDTTATPLRPLVKVHP-----ETGRPSL
209
SA+ + + ++ H +A AY + A + K HP E+GR SL
Sbjct: 144 ---SAQEKEEFGKLRVIHTLEAILRPAYPNPTPEQRADWAKRPAKEHPLVWQHESGRRSL
200

Query: 210 LIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD
269

+ G I GMD AE L+ L A RV H W GD+V+WDNR L+HR P+D
Sbjct: 201 VFGSTTSHIAGMDEAEGRALLDELERRATTPDRVLQHTWTQGDMVIWDNRGLVHRVRFD
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 = 6e-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---AYIGYGMDTTATPLRPLVKVHPET 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 = 7e-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 QQIAFAEQFGTLERHIASNRGKTNPLVHIVTNLNADGKPSGK-----VASTSW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
168

H+D ++ P + + A V+P GG TCFA+M AAY+AL A +A + A HS S
Sbjct: 49 HSDKSFRPQPSLATILHALVMPDGGGETCFANMIAAYEALPAAEKAELDGIRAVHSWEIS
108

Query: 169 QSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
227

Q++ G A A P+ PLV+ PETG +L +G A G +
Sbjct: 109 QARAGFKAPAEI-----ADAPPMSHPLVRTIPETGLKALFMGERAVFFEGHPPEEVGQ
161

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
 LE L A + V+ H+W GD+++WDNRC+
 Sbjct: 162 ARLEKLTAAHAVEERFVYRHKWTLGDLLMWDNRCV 195

>ref|ZP_05537081.1| dioxygenase [Streptomyces griseoflavus Tu4000]
 Length = 321

Score = 102 bits (253), Expect = 7e-20, Method: Compositional matrix
 adjust.

Identities = 90/295 (30%), Positives = 125/295 (42%), Gaps = 22/295 (7%)

Query: 4 TTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
 T L++ P +GA +TGV LA LD A + AA L+ ++ F GQ L + + A+
 Sbjct: 12 TALEVRPAAGHIGAEITGVDLAGDLDGTVIAGIRAAVLRWKVVFFRQQLDHAHVALAR 71

Query: 63 RFG---AIERIGGGDIVAISNVKAD-----GTVRQHSPA EWDDMMKVIVGNMAWHADST
 113
 RFG + R G V+ G EW + + WH D
 Sbjct: 72 RFGEPVVLPRRGKASPPDFPEVETTADRLELGGFRFGMEHDEWLRRRRHTL-LRGWHCDHG
 130

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
 173
 + AE VP GG T +A++ AAY L R A H L +G
 Sbjct: 131 ARVDPPAATILRAETVPPYGGDTTANLAAAYAGLSAPVREFADGLRAEHRL-----GVG
 185

Query: 174 HVQQAGS-AYIGYGMDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGM DAAESERFLE
 231
 + + G AY+ + +D PLV+VHPETG L + G + I G+ ES LE
 Sbjct: 186 YQPRPGDDAYLRHLLDHQTASEHPLVRVHPETGERVLFVNGYYVEQISGLSRPESAAVLE
 245

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283
 L++ A + +W G V WDNR +H A P D PR+M LAG
 Sbjct: 246 MLLEQATRPEYTVRFRWEPEGSVAFWWDNRATIHILA-PGDTAHLGRPRIMHRVMLAG 299

>gb|ADC34018.1| TfdA-like protein [uncultured bacterium]
 Length = 195

Score = 102 bits (253), Expect = 7e-20, Method: Compositional matrix
 adjust.

Identities = 69/213 (32%), Positives = 102/213 (47%), Gaps = 25/213 (11%)

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 HSDKSFRPQPSLATILHALVMPPDGGETCFADMVTAYEALPEAEKVELAGVVRVHWSGLS
 108

Query: 169 QSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
 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 RLERLTAHAVQERFVYRHKWTLGDLLMWDNRCV 195

>gb|ACX54979.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-
 like protein

[uncultured bacterium]
 Length = 98

Score = 102 bits (253), Expect = 7e-20, Method: Compositional matrix
 adjust.

Identities = 56/98 (57%), 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 LQAKGAVFSAEIVPEGRAPTGWADMRAAYDALDDETRLRVEGMSAYHSLFYQS 60

Query: 170 SKLGHV---QQAGSAYIGYGMTTATPLRPLVKVHPET 204

+ G++ Q Y YG LRPLVKVHPET
 Sbjct: 61 DRAGYMPSKQNESGGYDQYGYHDMEPSLRPLVKVHPET 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 = 7e-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 FRLVPLGRVIGAEHLGVDLSRPLDAALRAELDRALLEWKVLFRRDQHLSRQQRAFAGYW
 100

Query: 65 GAIER---IGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
 121

G +E + GD ++ + D V WH D T+ A G

Sbjct: 230 YQVRFKWQPNTLAIWDNRSTQHYA 253

>ref|ZP_05218298.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Mycobacterium

avium subsp. avium ATCC 25291]

Length = 297

Score = 101 bits (252), Expect = 8e-20, 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 ITVTKLGSRIGARVDGVRLLGGDLDDATVEQIRRALLTHKVIFFRHQHLLDDSRQLEFARL 64

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSP-----AEWDDMMKVIVGNMAWHADSTYMPV
117

G I + A +H P +E+ + WH D T+
Sbjct: 65 LG-----TPIGHPAASALAAKHLPVITPIDSEYGKATR-----WHTDVTFAAN
107

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
177

++ A +P+ GG T +A AAY L E R L A H+ Y + +
Sbjct: 108 YPAASILRAVTLPSYGGSTLWASTVAAYQQLPEPLRHLTENLWALHTNRYDYVRTDPMND
167

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA
237

A+ P+V+VHPETG +LL G G+D ES LE L
Sbjct: 168 TQRAFRQAFEKPDFRTEHPVVRVHPETGERALLAGDFVRGFVGLDGHESSVLELLQRRRI
227

Query: 238 CQAPRVHAHQWAAGDVVVDNRCLLHRA-EPWDFKLPRVMWHSRLAG 283

WA GDV +WDNR HRA + +D + PR+M L G
Sbjct: 228 TMPENTVRWSWAPGDVAMWDNRATQHRAIDDYDDQ-PRLMHRITLMG 273

>ref|ZP_01765753.1| dioxygenase, TauD/TfdA family [Burkholderia
pseudomallei 305]

ref|ZP_02484793.1| dioxygenase, TauD/TfdA family protein [Burkholderia
pseudomallei

7894]

gb|EBA49540.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei
305]

Length = 270

Score = 101 bits (252), Expect = 8e-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 DAEAVRALIEAWHAGGICRLRRQRLDMAEFVEFSRIFGRPERALNQRKLTSSREDLPELM 70

Query: 77 AISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRT
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 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 HPIVRVHPVTQRPYLYLGRRLNAYVVGLPVGSEALLDELWRYTRLDGVTWTQRWEVGD
234

Query: 254 VVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285

++WDNRC +HR + +D R+MW +++ P

Sbjct: 235 MIWDNRCTMHRRAFDANARRLMWRTQIQADP 266

>gb|ADC34000.1| TfdA-like protein [uncultured bacterium]

gb|ADC34005.1| TfdA-like protein [uncultured bacterium]

Length = 195

Score = 101 bits (252), Expect = 8e-20, Method: Compositional matrix
adjust.

Identities = 69/213 (32%), Positives = 102/213 (47%), Gaps = 25/213 (11%)

Query: 56 QQITFAKRFGAIERIGGGD-----IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW
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 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
228

Q+++G + I D + PLV+ PETGR +L +G A + G

Sbjct: 109 QARVG--IKVPPEEIVDAPDMS----HPLVRTIPETGRKALFMGERAVHLEGQPEDVGRA
162

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVWDNRCL 261

LE L A Q V+ H+W GD+++WDNRC+

Sbjct: 163 RLERLTAHAVQERFVYRHKWTLGDLLMWDNRCV 195

>gb|ACX54982.1| putative (S)-2,4-dichlorophenoxypropionate dioxygenase-like protein

[uncultured bacterium]
Length = 98

Score = 101 bits (252), Expect = 8e-20, 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 = 8e-20, Method: Compositional matrix adjust.

Identities = 90/281 (32%), Positives = 130/281 (46%), Gaps = 25/281 (8%)

Query: 12 GATLGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIER 69
G +GA V G+ L D +A A ++ L+F G ++ Q+ F +R G +

Sbjct: 10 GEKVGAEVLGIDADRLNLDQDLPSACLTALEENGALLFRGLNIDPATQVAFCRRRLGELIS 69

Query: 70 IGGG---DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTY-MPVMAQGAVFS
125

DI I+ + D + H AE+ GN+AWH D + + +V +
Sbjct: 70 FPTSPPYDIPEINEINWDPS---HPRAEY-----FRGNVAWHIDGALDHDIPPKASVMT
120

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
185

AEVV GG T FA AAYD L +A + +R A +++ + V+ A
Sbjct: 121 AEVVTEQGGETEFASTYAAAYDDLTD A E K --- 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 VFSSWTAGDMVIWDNRGLVHRVRFDPQTEPRRMHRITLAG 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 = 9e-20, 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-----KADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
118

G I E G I N+ KAD T + +H+D ++MP+

Sbjct: 63 GEIGEDPFFGHIDGYPNICAIQRKADETT-----IFAETFHSDWSFMPPI
108

Query: 119 AQQAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHS--LVYS-QSKLGHV
175

+ + +P GG T FAD A+D + ++ R V +A HS L Y+ G

Sbjct: 109 PAATMLLSITIPPHGGDTLFDQVKAFDEMPDSLREVENLTAIHSALGYAPDGAYGDQ
168

Query: 176 QQAG--SAYIGYMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEG
232

Q+ S I T PLV+ H ETG+ +L + + M+ ++ L

Sbjct: 169 DQSNGRSMTIKPSESARETCNHPLVRTHRETGKKALFSSAAYIQSFSDMNLETAQALLME
228

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

L + Q ++ HQW +V+WDNR LLH A

Sbjct: 229 LYQYQTQEQLYRHQWQPNMLVMWDNRSLHAA 261

>gb|ADC34017.1| TfdA-like protein [uncultured bacterium]

Length = 195

Score = 101 bits (252), Expect = 9e-20, Method: Compositional matrix adjust.

Identities = 72/207 (34%), Positives = 102/207 (49%), Gaps = 13/207 (6%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
115

QQI FA++FG +ER VA + KA+ V + D V + WH+D ++

Sbjct: 1 QQIAFAEQFGTLERH-----VASNRGKANPLVHIVTNLGPDKPSGKVASTQWHSDKSF 55

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV
175

P + + A V+P GG TCFA+M AAY+AL A +A + HS SQ++ G
Sbjct: 56 PQPSLATILHALVMPPDGGETCFANMIAAYEALPAAEKAALDGVRVVSWEISQARAG--
113

Query: 176 QQAGSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
234

A I A P+ PLV+ PETGR +L +G A G LE L
Sbjct: 114 TPAPPEEIA-----DAPPMSHPLVRTIPETGRKALFMGERAVFFEHPHPEEAGRARLEKLT
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 = 9e-20, 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 TVTVTPCTRLIGAQISGIDLGEVPAPEVFAELDRALLEFKVLFFRGQSRVTAARHRDFAG 97

Query: 63 RFGAIE---RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
119

+G +E + GD+ I V+ + + R+ V N+ WHAD T+ A
Sbjct: 98 MWGELEIHPFLPQGDAEI--VRFKESEREAG-----VENV-WHADVTWREKPA
143

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY-----SQSKLG
173

G+V A VP GG TCFADM AAYD L E +A + R A H KL
Sbjct: 144 LGSVLRAVEVPEAGGDTCFADMAAYDCLPEQVKARIEGRVAVHDFTLPGIGMDPDKLK
203

Query: 174 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG
232

+Q+ A P+V+ HP TGR +L + I G+ ESE L+
Sbjct: 204 EMQEKYPVAV-----EHPVVRTHPRTGRRTLFVNAIFTTHIVGLPEQESEELLKV
252

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285

L A +W G + WDNR + H A F RVM + + G RP
Sbjct: 253 LFRQASVPEYQVRFKWEPGSI AFWDNRVAVQHYAVSDYFPRRRVMERAAAILGDRP 306

>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-HLSNDQQITFAKRF 65
 + P +GA + GV L L DA AA++ L+H ++ F Q HL + +Q FA+R G
 Sbjct: 16 VIPLTGRVGAIEIKGVRLGGDLSDATVAAINQLLLKHKVIFFRDQGHLEDESEQEAFARRLG 75

Query: 66 AI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
 118

+ G I+ + + + G Q WH D T++
 Sbjct: 76 DLVPHTQGPVAGTASILNLDSSRGGGRADQ-----WHTDVTFVDAY
 117

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG--HVQ
 176

+ +V V+PA GG T +++ AAY++L + L A HS Y + +
 Sbjct: 118 PKFSVLRGVVIPAAGGDTIWSNTHAAYESLPAPLKLLEAENLWAIHSNAYDYAAVRPRATA
 177

Query: 177 QAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIQRHAHAIPGMDAAESERFLEGLVDW
 236

+ + T P+V+VHPETG SLL+G + G+ ++S + E +
 Sbjct: 178 EEKKHFEEVFTSTIYETEHPVVRVHPETGERSLLLGNFVQRLVGLSKSDSAKLYEVFQSY
 237

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRA 265

+W AGDV +WDNR H A
 Sbjct: 238 VTAPENTVRWRWRAGDVVAIWDNRATQHYA 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 TLTVTPSDMACGAQVRGLDLSKPVTDLAAEIRDIWLKHQVLCFPEQNLSDDDLERFTLA 61

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA-----WHADSTYMPV
 117

FG GD I+ + R+H A +K G + WH+D ++

>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 LDIHPVTGRIGAEIRGVRLSSQLEAATVEAIRAALIRHKVIFFRGQTHLQDADQEAFAFL 71

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
 123

G E + + + + H + +WH D T++ Q ++
 Sbjct: 72 LG--EPVSHPTVPVVDGTDYLLLELDSHRGGRAN-----SWHTDVTFVVDAYPQASI
 119

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG----
 179

+PAVGG T +A+ AY+ L +AL Q A HS Y + V + G
 Sbjct: 120 LRGVTIPAVGGDTVWANTATAYEDLPPPLKALADQLWAVHSNDYDYANHTSVGERGRDAE
 179

Query: 180 -----SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL
 233

A++ +T P+V+VHPE+G +L++G + G+ + S LE L
 Sbjct: 180 AIRRHREAFVSTRYETE----HPVVRVHPESGEKTLILGHFVKSFVGLAPSASAHLLLELL
 235

Query: 234 VDWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265

+ + + +W AGDV +WDNR H A
 Sbjct: 236 QGYVTRHENIVRWRWQAGDVAIWDNRATQHAYA 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-HLSNDQQITFAKRF 65
 + P +GA + G+ L L DA AA++ L+H ++ F Q HL + +Q +FA+R G
 Sbjct: 16 VVPLTGRVGAIEIRGIRLGGDLSDATVAAINQLLLKHKVIFFRDQDHLGDSEQESFARRLG 75

Query: 66 AI-----ERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM
 118

+ G I+ + + + G Q WH D T++
 Sbjct: 76 DLVPHTQGPVAGTASILNLDSSRGGGRADQ-----WHTDVTFVVDAY
 117

Sbjct: 228 TMPENTVRWSWAPGDVAMWDNRATQHRAIDDYDDQ-PRLMHRITLMG 273

>ref|ZP_06216167.1| Taurine dioxygenase [Micromonospora aurantiaca ATCC 27029]

gb|EFA34747.1| Taurine dioxygenase [Micromonospora aurantiaca ATCC 27029]
Length = 287

Score = 100 bits (250), Expect = 1e-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 LGAEVHGIDLNTLTDEGFALIHLLLLKHQVVFLAGQTGLTPQAHVAFGRRFGELEVELHPYL 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 HQWAAGDVVVWDNRCLLHRA 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 = 1e-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 QQIAFAEQFGTLERHVSNRGTVNPLVHIVTNLGDGKPSGK-----VASTQW 48

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
168

H+D ++ P + + A V+P GG TCFADM AAY+AL EA +A + HS S

Sbjct: 49 HSDKSFRPQPSLATILHALVMPPQGETCFADMVAAYEALPEAEKALAGVVRVHWSGLS
108

Query: 169 QSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
228

Q+++G + I D LV+ PETGR +L +G A + G

Sbjct: 109 QARVG--IKVPPEEIADAPDIAHL----LVRTIPETGRKALFMGERAVHLEGQPEDVGRA
162

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

LE L A Q V+ H+W GD+++WDNRC+

Sbjct: 163 RLERLTAHAVQERFVYRHKWTLGDLLMWDNRVCV 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 = 1e-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 FGD LHTHP IYPQH PDAREIMVLD TDAVD-----LQDN AVWHTD VTFIE
104

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ
176

GAV +A +P +GG T +A AAY+AL + +A + SA H S +

Sbjct: 105 TPPLGAVLAARQLPELGGDTLWASGIAAYEALSASLKARLDGLSAVHDFAKSFPLARYGL
164

Query: 177 QAGSAYIGYGMDDTATPL-RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV
234

P+ PLV++HPE+GR +L + A+ + AE + L+ L

Sbjct: 165 TDDDRRRWDETRRKHPPI SHPLVRIHPESGRRALFVSEGF TVAVNDLPEAEGQALLQFLF
224

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ +W GDV WDNRC +H A

Sbjct: 225 AHQSRPEFSIRWRWQPGDVAFWDNRCTIHYA 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 = 1e-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 SSLNITPLSSALGAQISGVDISQPLNQEQRDAIEQALLKFQVLFRRNQPIEPSQQARFAH 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 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLV--YSQSKLGHVQQAG
 179

AV SA+++P GG T +A AAY+AL +AL+ +A H + + G+ QA
 Sbjct: 111 AVLSAKLLPEFGGDTLWASGIAAYEALSAPMKALLEGLTATHDFTRSFPLERYGNTFPQAL
 170

Query: 180 SAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWA
 237

+ + PL P+++ HP +GR SL + I + ESE L+ L A
 Sbjct: 171 AQW--EEARRKNPPLSHPVIRTHPVSGRRSLFVNEGFTSKINELSESEAVLKFLFAHA
 228

Query: 238 CQAPRVHAHQWAAGDVVVDNRCLLHRA 265

+ +W D+ WDNR H A
 Sbjct: 229 TRPEFTIRWRWQKDDIAFWDNRVTQHYA 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-----PAKTDAVRAWYRQGNFLWHIDGATEELPQKATLL
 118

[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%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 T+ TP T A +GV + + ++ +LIF L++ + + F
 Sbjct: 2 TINYTPLHPTFVAEASGVDFDNITPEVVEEIKKGLAKYGVLI FRKTGLNDKKHVEMSSFF 61

Query: 65 GA-----IERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIV--GNMAWHA
 110

G I R+ ++ +SNV A+G + Q + + I+ GN +H
 Sbjct: 62 GELDDVKPYNKLGRINRLAYDELFDVSNVDAEGNIFQPT-----GQRAIINRGNTIFHC
 115

Query: 111 DSTYMPVMAQGAVFSAEVVP--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----RVANPGEPLLDQEKFLPTSHPFKHKLVQVHEPSGRTNLYIANHAYKIESLPLEH
 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

>ref|ZP_03498565.1| Taurine dioxygenase [Rhizobium etli Kim 5]
 Length = 309

Score = 100 bits (249), Expect = 2e-19, Method: Compositional matrix
 adjust.

Identities = 73/269 (27%), Positives = 115/269 (42%), Gaps = 29/269 (10%)

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 IVPLTGRVGAIEIKGIRLGGELSDATVSAINQLLLKHKVIFFRDQGHLLDPEQEAFARRLG 75

Query: 66 AI-----ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
118

 + G I+ + + G Q WH D T++
Sbjct: 76 DLVPHTQGPIAGTASILNLDSSRGGGRADQ-----WHTDVTTFVDAY
117

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLG--HVQ
176

 + +V V+PA GG T +++ AAY++L + L A HS Y + +
Sbjct: 118 PKFSVLRGVVIPAAGGDTIWSNTHAAYESLAAPLKL LADNLWAIHSNAYDYAAVRPRATA
177

Query: 177 QAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW
236

 + + T P+V+VHPETG SLL+G + G+ ++S R E +
Sbjct: 178 EEKHFEEVFTSTIYETEHPVVRVHPETGERSLLLGNFVQRLVGLSKSDSARLYEVFQSY
237

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRA 265

 +W AGDV +W DNR H A
Sbjct: 238 VTAPENTVRWRWRAGDVAIW DNRATQHYA 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]
 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]
 Length = 295

Score = 100 bits (249), Expect = 2e-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 QQH L + +Q+ FA
 Sbjct: 5 ITVKKLGSRIGAQIDGVRLLGGDLDPAAVNEIRAALLAHKVVFFRGGQHQLDDAEQLAFAGL 64

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
 123
 G IG +A+++ D + +E+ + WH D T+ +V
 Sbjct: 65 LGT--PIGHPAAIALAD---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

>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 LQAKGAVFSAEIVPEGRAPTGWADMRAAYDALDDETRLRVEGMSAYHSLFY SQ 60

Query: 170 SKLGHV---QQAGSAYIGYGMDDTTATPLRPLVKVHPET 204

 + G++ + Y YG LRPLVKVHPET
 Sbjct: 61 DRAGYMPSKKNESGGYDQYGYHDMEPSLRPLVKVHPET 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 TKVKISPIDAPLGTIVTDLDASQAIAPREVILQLKQALRDRHILIFKDQKLSDKELLNFSL 66

Query: 63 RFGAIERIGGGDIVAISNVKADGT-VRQHSPAEWDDMMKVI-----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 WTPTPSSGSLLYALEIPSQGGNTYWLNTNLAYEALDETTK----ERIALDLQLITYNPFLLR
170

Query: 174 HVQQAGSAYIGYGMDTTATPL--RPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFL
230

S Y +P+ PLV+ HPE+G+ L + + G++ E + +
Sbjct: 171 DRNAPRSLYRLDKTIPLISPIFPHPVLRTHPESGKKHLYLDAATEVEVVGLEPEEESKLI
230

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
E L Q + H+W+ GD+V WDN+ LH + +D RV+ LAG RP

Sbjct: 231 EQLRQHLNQPKEYYQHKWSVGDIVYWDNQATLHYRQAFDPNERRVLKRVSLAGSRP 286

>ref|ZP_03421998.1| dioxygenase [Mycobacterium tuberculosis 94_M4241A]
Length = 295

Score = 100 bits (249), Expect = 2e-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 ITVKKLGSRIGAQIDGVRLGGDLDPAAVNEIRAALLAHKVVFFRGQHQLDDAEQLAFAGL 64

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

G IG +A+++ D + +E+ + WH D T+ +V
Sbjct: 65 LGT--PIGHPAAIALAD---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

>ref|ZP_02414516.1| dioxygenase, TauD/TfdA family protein [Burkholderia pseudomallei

14]

Length = 270

Score = 100 bits (248), Expect = 2e-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 DAEAVRALIEAWHAGGICRLRRQRLDMAEFVEFSLIFGRPERALNQERKLT SREDLPELM 70

Query: 77 AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRT
 136

+SN+ +G H ++ WH D Y V ++ A VPA GG T

Sbjct: 71 IVSNILENGVSIGHLGSK-----EAYWHTDMCYTDVPPIASILYAIEVPAHGGNT
 120

Query: 137 CFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATP--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 HPIVRVHPVTQRPYLYLGRRLNAYVVGLPVGESSEALLDELWRYTRLDGVTWTQRWEVGD
 234

Query: 254 VVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285

++WDNRC +HR + +D R+MW +++ P

Sbjct: 235 MIWDNRCTMHRRD AFDANARRLMWRTQIQADP 266

>gb|ADC34033.1| TfdA-like protein [uncultured bacterium]

Length = 195

Score = 100 bits (248), Expect = 2e-19, Method: Compositional matrix adjust.

Identities = 71/213 (33%), Positives = 102/213 (47%), Gaps = 25/213 (11%)

Query: 56 QQITFAKRFGAIER--IGGGDIVA-----ISNVKADGTVRQHSPA EWDDMMKVIVGNMAW
 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 QSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
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 RLERLTAHAGQERFVYRHKWTLGDLLMWDNRCV 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 IRVRPQPHAFGAIEITGLSISRPLPAPVLDEVKKAHAAHSVVYFPDQPLTHSELEAFTLQF 68

Query: 65 GAIERIGGGD--IVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

G G D IV I + +R+ E D+ K + WH+D ++ G

Sbjct: 69 GEF----GVDPYIVPIEDHPHILELRR----EADE--KAVNFGAQWHSDFQEEPPAGT
118

Query: 123 VFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHS--LVYSQSKL-GHVQQAG
179

+ ++V P VGG T +AD AYD L + + L+ A HS + Y + L +

Sbjct: 119 ILHSKVTTPVGGDTLYADGYRAYDELSDTMKRLLDGLVAIHSAGMPYKDGDFAKETETR
178

Query: 180 SAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC
238

S I D T PLV++HP T R +L + + I GM ES L L

Sbjct: 179 SMKIVVSEDADKTWPHPLVRLHPVTRRKALYVSPVYTQGIEGMTRGESAALLGYLYQHVM
238

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRAE-PWDFKLPRVMWHSRLAG-RP 285

+ V+ H+WA + +WDNRC LH A+ +D L RVM + +AG RP

Sbjct: 239 RDEYVYRHRWAPNMLTLWDNRCTLHNADGGYDGHL-RVMHRTTIAGERP 286

>ref|YP_001985889.1| putative 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 VVPLTGRVGAIEIKGIRLGGELSDATVAAINQLLLKHKVIFFRDQGHLLDSEQEAFARRLG 75

Query: 66 AI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
 118
 + G I+ + + + G Q WH D T++
 Sbjct: 76 DLVPHTQGPVSGTASILNLDSSRGGGRADQ-----WHTDVTTFVDAY
 117

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQA
 178
 + +V V+PA GG T +++ AAY++L + L A HS Y + + A
 Sbjct: 118 PKFSVLRGVVIPAAGGDTIWSNTHAAYESLPAPLKLADNLWAIHSNAYDYAAVRPRATA
 177

Query: 179 GSA--YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW
 236
 + T P+V+VHPETG SLL+G + G+ ++S + E +
 Sbjct: 178 EEKRHFEEVFTSTIYETEHPVVRVHPETGERSLLLGNFVQRLVGVSKSDSAKLYEVFQSY
 237

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
 +W AGDV +WDNR H A
 Sbjct: 238 VTTPENTVRWRWRAGDVVAIWDNRATQHYA 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 DAGTVQAIKDAVVRHKVFFRQKDLDDARHEGF 73

Query: 61 AKRFGAIERIGGGDIVAISNVK-ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
 119
 A FG + VA V A+G+ E D K +WH D T++
 Sbjct: 74 ASLFG-----EPVAHPTVPVAEGS---RYLLELDS--KEGYAASSWHTDVTTFVDSYP
 120

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQA
 179
 +G++ A VP GG T +A+ AY++L E+ R LV+ A H+ +Y + + + +
 Sbjct: 121 KGSILRAITVPEAGGDTVWANGETAYESLPESLRQLVNNLWAVHTNLYDYAAVLNAPKGD
 180

Query: 180 SA---YIGYGMDDTTATPL----RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG
232

 + + A+ + P+V+VHP +G+ SLL+G G++ A+S R +
Sbjct: 181 ETERERVNFHKSVMFASTVYETEHPVVRVHPVSGQRSLLLGHFVKQFVGLNQADSSRLFQI
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 LTVTPAGPVLGAEISSVDLRQPLAPEIVAAIRAALLRHKKVFFRDQDISHEDHVRFGRYF 77

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
117

 G +E G +I+ I ADG + +++++ ++ WH D T+ P
Sbjct: 78 GDLEGHPVTAHVPGFPEILLIE--AADGMKLR-----EEIVPLVRVANKWHTDVTFRPA
129

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
177

 + G V +P +GG T FAD A Y L +A +A + A H ++ QS V +
Sbjct: 130 PSMGGVLRMRQMPPLGGDTLFADTAAIYRDLDPALKARIADLQAEHDIL--QSYGYRVDE
187

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW
236

 A + A P+V+ HPETG L + + I G+ E+ R L L+D
Sbjct: 188 AKRQELRAAHPVQA---HPVVRTHPETGKHLFVNKVFTRILGLPEDEAARLLADLLDR
244

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

 +W +V WDNR H A
Sbjct: 245 VKTPEYQVRFRWTPNAIVFWDNRATQHYA 273

>ref|ZP_06234277.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp.
Eu11c]

gb|EFA64736.1| 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-IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
120

G + +GG + +S + D PA+ + G WH D V +
Sbjct: 62 LGEVVVAPMGEEEEFPPEVSAISLD-----PAQ-SALAAVRTGTFYWHIDGANDLVPQK
113

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGS
180

+ +A V GG T FA++ AAY+ L +A HS +Q +L H S
Sbjct: 114 ATLLTALEVATEGGDTEFANLYAAYEGLSAEDKARFADLRVVHSFAATQ-RLAHPD--AS
170

Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA
240

+ + + PLV GR SLL+G A I G+ ES L+ L+DWA Q
Sbjct: 171 DKVRASWEKVPSREHPLVWTR-RNGRKSLLVGATADHIVGLPEDESRAALLDRLLDWATQP
229

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

HQW+ GD+V+WDN +LHRA+P+ R+M + L G
Sbjct: 230 RFSLRHQWSRGDLVIWDNTGILHRAQPYTALSRRMLMHRRTTLVG 272

>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 = 3e-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 IDVRPLSGHTGAEIHGVDLSQQQLDDATIAEIRSALLRWKVVFFRDQSIGHAEQIAFGARF 69

Query: 65 GAIERI-----GGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
115

G I G I+ I + + + + + I + WH D T +
Sbjct: 70 GKITPAHPHEDAPPEGFPQILPIDSRRYEKKFGK-----RKITYDNGWHTDVTAL
119

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHV
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---YGEKIASNPLLAHPVVRVHPETGERALFVSPFTTSGENEIIGFSTRQSHR
229

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFK---LPRVMWHSRLAG 283
L+ + + +W+ GDV WDNR H P D RV++ L G

Sbjct: 230 ILDLFYEQIARPEYTVRFRWSPGDVAFWDNRATAHLG-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 = 3e-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 MTYDVLVDVKPMTRRIGAEIFGVDLGQPLSNRQFEEVHQALTQYQVLFVRDQEMTHDAHKA 60

Query: 60 FAKRFGAIERIGG-----GDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
112

F ++FG + G +IVAI H+ A+ K + G WH+D
Sbjct: 61 FGRKFGDLAIHSGVPGLPEHPEIVAI-----HADAD----SKFVAGE-NWHS DL
104

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
172

T P G++ +V+P GG TCFA M AAY+ L + +A + SA H
Sbjct: 105 TCDPEPPLGSILYMKVLPDDGGDTCFASMYAAYETLSDRMKAYLEGLSAVH-----
155

Query: 173 GHVQQAGSAYIGYGMDD---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 ILGFLYQHASNPDFQVRFWRKNSVAFWDNRCTWHQAI-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 = 3e-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 LGAEIRGIDFSQPLSSQTRDDIIGLLSEHQLLVFPFGQRLSCEQQVAACRDFGELEPHPM 69

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
126

++ +SNV DG + ++ WH+D Y+ A+ F A
Sbjct: 70 TNTSSFPEMTIVSNVTTDGKPVGYPTPPFE-----LWHS DLCYLEHPAKMTFFYA
119

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
186

E VP G T FA+M AAY+ L + ++ + R+A SL S + ++ G
Sbjct: 120 ESVPDAHGDTWFANMFAAYETLPDELKSAIDGRNAIFSL--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 = 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: 5 LGAEIRGIDFSQPLSSQTRDDIIGLLSEHQLLVFPFGQRLSCEQQVAACRDFGELEPHPM 64

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
126

++ +SNV DG + ++ WH+D Y+ A+ F A

Sbjct: 65 TNTSSFPEMTIVSNVTTD GKPVGYPTPPFE-----LWHS DLCY LEHPAKMTFFYA
114

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG
186

E VP G T FA+M AAY+ L + ++ + R+A SL S + ++ G
Sbjct: 115 ESVPDAHGDTWFANMFAAYETLPDELKSAIDGRNAIFSL--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 = 4e-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 LKQALAEHLILIFKNQTLDDLQYLAFASYFGSIFRPSADNPVLASQTDGTGVPDPVVPVSN 78

Query: 81 VKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFAD
140

G H G + HAD + P+ + G++ A +P GG+T + +
Sbjct: 79 AVGGQNYTGH-----GELTPHADHQWTPLPSEFGSLLYALELPQDGGQTSWFN
125

Query: 141 MRAAYDALDEATRALVHQRS--ARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTA--TPLRP
196

AYDAL + + + Q + V +QS G+ S Y + T P
Sbjct: 126 TIKAYDALPDDVKKQIDQLQLITYNPFVRAQSNTGNTGYGDSPPYRFKDQPILGHTYPHP
185

Query: 197 LVKVHPETGRPSL-LIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

LV+ HPE+GR +L L R + +D +E + L + + HQW GD+V
Sbjct: 186 LVRTHPESGRKALWLNTRSEVELLNVDSEGSSELIAALRAHILKPEFRYKHWETGDIVF
245

Query: 256 WDNRCLLHRAEPWDFKLPVMMWHSRLA-GRP 285
 WDN+ LH P+ R++ LA GRP
 Sbjct: 246 WDNQVTLHSRRPFPVDQRLLKRISLAGGRP 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 = 4e-19, Method: Compositional matrix
 adjust.
 Identities = 85/291 (29%), Positives = 125/291 (42%), Gaps = 33/291 (11%)

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 LKITPLGPYIGALVENVVLARPLGDGQFEQLYHALLKHQVLFVRNQPITPLQQRDLAAGR 64

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIV-----GNMAWHADSTYM
 115
 G + I V T D+ ++IV N WH D T++
 Sbjct: 65 GDLH-----IHPVYPHAT-----DVEEIIIVLDTHDDNPPDNDNWHTDVTFI
 105

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV
 175
 QGA+ +A+ +P+ GG T +A AAY+AL E R L+ A H S + H+
 Sbjct: 106 ENPPQGAILAAKTLPSFGGDTLWASGIAAYEALSEPFRQLLAGLKAHDFTKSFPEHKHL
 165

Query: 176 QQAGSAYIGYGMDDTATP--LRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEG
 232
 + + + + P L P+V+ HP +GR +L + I + ESE L
 Sbjct: 166 -SSEEEHQRWQVAKQKNPPLLHPVVRTHPVSGRQALFVNEGFTTRIVDLAPKESEALLNF
 224

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAG 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 = 4e-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 LPLTPLGPSFGAEIRGIDLGRLLDDQVLALREALVRYKVLVFRGQDGLDDAAQIEFGRRL 72

D + QW GDV +WDNR H A PRV+ +AG
 Sbjct: 240 DAVARPENTVRWQWKTGDVAIWDNRSTQHYAVNDYNDAPRVVHRVTVAG 288

>ref|ZP_06281660.1| Taurine dioxygenase [Streptomyces sp. ACT-1]
 gb|EFB79297.1| Taurine dioxygenase [Streptomyces sp. ACT-1]
 Length = 307

Score = 99.4 bits (246), Expect = 5e-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 FRLVPLGRVIGAEELHGVDLSRPLDAAALRAELDRALLEWKVLFVRDQHLTSRQQRAFAGYW
 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 + + V A H + ++ ++ +
 Sbjct: 146 AVLQREVPPTGGDTLWADMAAAYDNLDPDEVKERVEGARAVHDFIPGFARFSPPERLAAH
 205

Query: 182 YIGYGMDDTTATPLR-PLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ
 239
 + P+ P+V+ HP TGR ++ + I G + ES+R L L A
 Sbjct: 206 QEEF-----PPVEHPVRRHPVTGRRTIFVNASFTTRIVGFEREESDRLRLRLFQQA-H
 258

Query: 240 APRVHAH-QWAAGDVVVDNRCLLHRA 265
 AP W AGDV WDNR H A
 Sbjct: 259 APEFQVRFSWRAGDVAFWDNRRATQHYA 285

>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 = 5e-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 TGIEVEPVAGHIGAEIRGVDLAAGLDAAQVAAVRSVAVLRWKVVFVRDQRLDHAGHVAFAFAR 78

Query: 63 RFG---AIERIGGGDIVAISNVKAD-----GTVRQHSPAEWDDMMKVIVGNMAWHADST
 113

FG + R G ++ G EW + + WH D
 Sbjct: 79 LFGEFVVLPRRGKASPAGFPEIETTADRLELGGFRFGMEHDEWLRRRRRTL-LRGWHCDHG
 137

Query: 114 YMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLG
 173

V AE VP GG T +A++ AAY L RALV A H L +G
 Sbjct: 138 ARVDPPAATVLRRAETVPPYGGDTTWANLAAAYAGLSAPLRALVDTLRAEHRL-----GVG
 192

Query: 174 HVQQAG-SAYIGYGMDDTATPLRPLVKVHPETGRPSLLI-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 LLVEQATRPEYTVRFRWEFGSVAFWDNRATIHLA-PGDHAHLDPRTMHRVMLTG 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 = 5e-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 TMQIEPLTPHIGALIHVVLDLVHCNDTTFEAVYQAWFTHQVIFRFREQVLSPPQQLTIAARF 61

Query: 65 GAIERIGG--GDIVAI SNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
 122

G +E + V TV+ P E WH D T+ ++ +
 Sbjct: 62 GELEPHFPFFPHVAQAPQVSIIETVKGKPPLE-----SFWHTDLTWRRQPPSKAS
 110

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLV-YSQSKLGHVQQAGSA
 181

V A+ VP GG T + M A + L E + L+ + SA H+L + + + +
 Sbjct: 111 VLHAQHVPHCGGDTLWCSMTAVFRQLPEQDKILLRRLSAMHALFAFDGIESSEITEDWQQ
 170

Query: 182 YIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQA
 240

+ T P++ HP+TG L I I GM+ +S L L A Q
 Sbjct: 171 DVLAVSATNPPVSHPVITRHPDTGEEILFINEQFTRYIIGMNRDDSALLAKLFAMARQP
 230

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRA 265

+W A + +WDNR H A
 Sbjct: 231 EYQVRFKWQANSLAIWDNRSTQHYA 255

>ref|ZP_05521054.1| taurine catabolism dioxygenase [Streptomyces
 hygroscopicus ATCC
 53653]
 Length = 300

Score = 99.0 bits (245), Expect = 5e-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 TGFDIRRIGGRIGAEVLGVALSDDLDPALVSDINSALLEHKALVFRDQQLDDAAQLRFAS 64

Query: 63 RFG-----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
 115

FG + + G +I V A+ +R + WH D T++
 Sbjct: 65 LFGELTTAHTVPSVDGQP--SILPVNAEEGIRANR-----WHTDVTFV
 106

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV
 175

+ + VVP GG T A+ AAY L + R L + A H+ Y +
 Sbjct: 107 RSPPKVSTLRGIVVPPYGGNTLIANAGAAYQDLPQPLRELADKLWAVHTNDYDYAAPPKD
 166

Query: 176 QQAG---SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG
 232

++A +I T P+V+VHPE+G L IG A + G+ +ES L
 Sbjct: 167 EKAAEHRKRKFISRKYRTA----HPVVRVHPESGERGLFIGGFAQSFIGLGPSESRDLLRI
 222

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAG 283

+ + + W+ GDVVV+DNR H A P D+ LPR++ +AG
 Sbjct: 223 FQSYVIRPENIVRIAWSPGDVVVFDNRITQHYA-PDDYGDLPRLLHRVTVAG 273

>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 = 5e-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 MNENRFDVRPVSGALGAEVVRGVPDLALDSDFTAVRELLLEHLVLFPPDAAGLEPGAHA 60

Query: 60 FAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
113
F +RFG +E ++ G D + + + + Q + A+ WH D T

Sbjct: 61 FGRRFGELEVHPFLPKLPGHDELVVDSE-----QGARAD-----VWHTDVT
102

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
173
+ P +V P GG T +++ AY+AL R L+ +A H +

Sbjct: 103 FSPSPPIASVLQLV ECPPSGGDTMWSNQYLAYEALSAPVRELLDGLTAVHVFKHPNGSFR
162

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-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 LFEVSESPQRVCRYRWVPGAVAVWDNRVTQHYA 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 = 6e-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 IEVRPQPTGFGEVVRGLDLSRPLPPGVLEQVKA AAWARHAVLAFPNQPLSLDALEAFTLQI 67

Query: 65 GAIERIGGGDIVAISNVKADGTVRQ--HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122
G G+ I + V + P E K WH+D ++

Sbjct: 68 GPF-----GEDPFIKPM PGHPNVLELRREPDE-----KATNFGAGWHS DWSFQARPPAAT
117

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG---HVQQAG
179
+ +E+VP VGG T F D AY+AL + ++ A HS + G +

Sbjct: 118 ILRSEIVPPVGGDTLFC DGARAYEALSPTFORMLEGLRAVHSATRAYGTKGVFARETEKR
177

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWAC
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 KEAFVYRHKWRPGMVLWMDNRC TA HFAEGGYDGHL-RVMHRRTVAG 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 = 6e-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 TFQVRPVSIGSIGAEVYGVDLSTVDDEQFKEIHDLLVRHLVLFPEAGGLTPEAHQAFGSR 65

Query: 64 FGAIE-----RIGGGDIVAI----SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
113

FG +E ++ G + + + KAD WH D +
Sbjct: 66 FGELEVHPFLPKLEGHEHIVVLDSDKGAKAD-----VWHTDVS
103

Query: 114 YMPVMAQGA VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
173

Y+ +V + P GG T +++ AY+AL E R L+ +A H + Q
Sbjct: 104 YVKHPPITSVLQITLTP EAGGDTMWSNQYLAYEALSEP MRELLEGTTASHVFAHPQGT F-
162

Query: 174 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEG
232

+ P+V+VHP +GR SL + R I + ES LE
Sbjct: 163 -----RSEVEHPVVRVHPVSGRKS LYVNRMF TKRILQLSRGES AALLEH
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 = 6e-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 RTDISVTKIGGNIGARIDGVWLGGDLDEATVARIRAALLEHKVVFFRQQHHLDDAGQQAF 67

Query: 61 AKRFG-----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
113

+ G + +G G+I+ I AE+ +WH+D T
Sbjct: 68 GRLLGELTQPHTVRSVGLGNILPID-----AEYGRAN-----SWHSDVT
107

Query: 114 YMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQS---
170

++ + +V A +P GG T +A+ AY L ++ +AL + A H+ +Y S
Sbjct: 108 FVDRIPAFVSVLRAVTIPPYGGSTVWANTATAYANLPDSLKALAEKLWAVHTNLYDYSRHV
167

Query: 171 ---KLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESE
227

++G + Y P+V+VHPETG LL+G + G+ +AES
Sbjct: 168 DERRIGGIDVKERDYRDEFRSEVYETEHPVVRVHPETGERVLLLGHFVKHLVGLSSAESN
227

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLH 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 = 6e-19, Method: Compositional matrix adjust.

Identities = 65/211 (30%), Positives = 102/211 (48%), Gaps = 25/211 (11%)

Query: 56 QQITFAKRFGAIERI----GGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHAD
111

QQI FA+R+G I G D I +K +P E + VGN AWH D
Sbjct: 1 QQIAFARRWGNIHYPPLSPGLPDHPEILEIKK-----TPEEEKN-----VGN-AWHTD 47

Query: 112 STYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSK
171

+ P A + A+ VP GG T F++ AAY++L A + ++ S++
Sbjct: 48 QMFAPKPAMATMLYAKEVPRYGGDTMFSNQYAAYESLSSAMQQMLAGLKTVCVSL-----
102

Query: 172 LGHVQQAGSAYIGYGM-TTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESERFL
230

V+ +G Y +++ + PL++ HPETGR +L IG HA + GM ES+ L
Sbjct: 103 --DVRNSSGGNYNADAPVNSKTVSMHPLIRTHPETGRRALYIGNHARSFDGMTEEEESKPLL
160

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261
 + L+ + + + +W G + +WDNRC+
 Sbjct: 161 DYLIQHSTRPETICRFRWRPGSMAIWDNRCV 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 = 6e-19, Method: Compositional matrix
 adjust.

Identities = 77/275 (28%), Positives = 117/275 (42%), Gaps = 38/275 (13%)

Query: 6 LQITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 64
 + + P GA + G+ L LDDA A + +A Q ++ F QH+ + QQ+ F +RF
 Sbjct: 11 IDVRPLSGHTGAEIHGIDLREELDDATVAEIRSALHQWKVVFFRDQHIDHAQQVAFGRRF 70

Query: 65 GAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
 115
 G + +G +I+ I + + V A +D+ WH D T +
 Sbjct: 71 GRLTPAHPHEEAPPVGFPEILPIDSRRY-AKVFGRKATYDN-----GWHTDVTAL
 120

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV
 175
 ++ +V+P GG T + ++ AAY+ L E R L ARHS G+
 Sbjct: 121 VNPPTASILRGDVIIPPYGGDTAWTNLVAAYEGLPEPLRNLADGLRARHS-----FGNF
 173

Query: 176 QQAGSAYIGYGMDDTTATPL---RPLVKVHPETGRPSLLIGRHAHA----IPGMDAAESER
 228
 YG A PL P+V+VHPETG +L + A I G +S +
 Sbjct: 174 PSDSE----YGRRVAANPLVAIHVVVRVHPETGERALFVSPSFTAKDGEIIGFSPKQSRQ
 229

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH 263
 L+ D ++ +W GDV WDNR H
 Sbjct: 230 ILDVFYDQISRSEFTVRFKWNQGDVAFWWDNRATAH 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 = 6e-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 MRIEPMTCAIGAELLGVRLADAVRDDALFSEIRAALLRHKVLFLRDQGLTRAHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG +E VA S+ + G VR + +P + +D + +WH D+T+ G
Sbjct: 61 FGELE----DHPVAGSDPEHPGLVRIYRTPEQPNDRYE-----NSWHCDATWREAPPMGC
111

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAY
182

V P VGG T +A+M AY+ L +A +AL+ ARHS+ + +++ +
Sbjct: 112 VLHCVECPPVGGDTLWANMALAYERLPDAVKALIAPLRARHSIECTFGAAMPIERRLALK
171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGM DAAESERF-----LEGLVD
235

Y P+V+ HPETG L + + R GL+
Sbjct: 172 AQY-----PDAEHPVVRTHPETGEKVL FVNGFTTHFTNFHTPANVRVGQDFTQGASGLLQ
226

Query: 236 WACQAPRVHAHQ----WAAGDVVVWDNRCL LHRA 265

+ + +Q W AG V +WDNR H A
Sbjct: 227 YLIGQAAIPEYQVRWRWRAGSVAIWDNRATQH YA 260

>ref|YP_003329314.1| TauD [Sinorhizobium meliloti]
gb|ABA55987.1| TauD [Sinorhizobium meliloti]
Length = 317

Score = 98.6 bits (244), Expect = 6e-19, Method: Compositional matrix
adjust.

Identities = 75/276 (27%), Positives = 117/276 (42%), Gaps = 43/276 (15%)

Query: 8 ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRF G 65

+ P +GA V GV L L D AA++ L++ ++ F GQ HL +Q FA+R G
Sbjct: 16 VVPLTGRVGA EVRGVRLGGDLS DVAIAAINQLLLKYKVIFFRGQEHLDEVEQELFARRLG 75

Query: 66 AI-----ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
118

+ G I+ + + + G Q WH D T++
Sbjct: 76 DLVPHPTQGPTAGTASILNLDSSRGGGRADQ-----WHTDVTTFV DAY
117

Query: 119 AQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVY-----SQ
169

+ +V V+P GG T +++ AAY++L + L A HS Y S
Sbjct: 118 PKFSVLRGVVIPTAGGDTIWSNTHAAYESLPAPL KLLADNLWAIHSNAYDYAAVRPRASA
177

Query: 170 SKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGM DAAESERF
229

+ H ++ ++ I Y + P+V+VHPETG SLL+G + G+ ++S +
Sbjct: 178 EEKKHFEEVFTSTI-YETE-----HPVVRVHPETGEKSLLLGNFVQRLVGLSKSDSAKL
230

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL LHRA 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 = 7e-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-LQIRRIAGALGAEISGVDLSQDLDPDQTIAAIRRALVEHQVIFFRGQALTPERQVA 59

Query: 60 FAKRFGAIE---RIGG--GDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTY
 114
 F RFG + + G G + +K + +V G WH+D ++
 Sbjct: 60 FGARFGPLNVHPFVAGMAGQPAVMEI IK-----EPQDRVNF GG-GWHS DMSF
 105

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGH
 174
 + + G++ A VP GG T FA AA++AL + + +A HS S GH
 Sbjct: 106 LERPSIGSILYAVEVPDFGGDTL FASQAAAFEALSPGLQKTLEGLNAVHSASREYSARGH
 165

Query: 175 VQQAGSAY-IGYGMDTTATPLRPLVKVHPETGRPSLLIG-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 = 7e-19, Method: Compositional matrix
 adjust.

Identities = 82/291 (28%), Positives = 121/291 (41%), Gaps = 35/291 (12%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61

Sbjct: 165 AELLAKAGSGSKYVREFGATHFETHHPVVRVHPETGEKALLLGNFVKRILDVSASESQAL
224

Query: 228 -RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
R + V W R W GDV +WDNR H A PR M LAG

Sbjct: 225 FRMFQDRVTWLENTIR---WSWELGDVAMWDNRATQHYAISDYGDQPRRMHRVTLAG 278

>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 = 9e-19, Method: Compositional matrix
adjust.

Identities = 72/269 (26%), Positives = 119/269 (44%), Gaps = 25/269 (9%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG 65
L+I +GA + GV LAT ++ A + H ++ Q LS +Q + A+RFG

Sbjct: 2 LKIEQVTPHIGARIHGVDLATCSVTELDEVYQALISHQVIFLGDQILSPEQHLMIAERFG 61

Query: 66 AIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
118

+E R+ V++ T R ++P E WH D T+ V
Sbjct: 62 QLELAHPFFPRVESAPQVSVIE-----TTRGNAPME-----SYWHTDLTWRKVP
105

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLV-YSQSKLGHVQQ
177

++ ++ A+ +P+ GG T + M A +D+LDE + + SA HSLV + + ++
Sbjct: 106 SKASLLHAQHIPSTGGDTIWCSMTAVFDSLDEDMKVKLRGLSATHSLVAFEGVEPDQIEL
165

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDW
236

+ + P+V+ HPETG+ +L I I +D ES+ L L +
Sbjct: 166 DWHKSLKTAQQNPPVIHPVVQSHPETGKETLYINEQFTRYINELDRQESDILLNQLFEI
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 = 9e-19, 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 + AKRF

Sbjct: 2 LKIEPITPHIGARIHGLNLSGCSESELDDVYQALVITYQVVFDEQSLSPHQHLALAKRF 61

Query: 66 AIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
118

+E R+ V++ T R ++P E WH D T+ +
Sbjct: 62 ELEPAHPFFPRVERAPQVSIE-----TTRGNAPME-----SYWHTDLTWRELP
105

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLV-YSQSKLGHVQQ
177

++ ++ A+ VP VGG T + M A +D+LDE+ + + SA HSLV + + ++
Sbjct: 106 SKASLLHAQHVPDVGGDTIWCSMTAVFDSLDESMDKLRGLSATHSLVAFEGLESDQIEL
165

Query: 178 AGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDW
236

+ PLV++HPETG+ +L I I ++ E + L L +
Sbjct: 166 DWHKSLKTAQENPPVKHPLVQLHPETGKETLYINEQFTRYINELEREEGDALLSQLFEI
225

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRA 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 TGIEVEPVAGHIGAEIRGVDLAAGLDAAQVA AVRSVLRWKVVFVRDQRLDHAGHVA FAR 78

Query: 63 RFG---AIERIGGGDIVAISNVKAD-----GTVRQHSPA EWDDMMKVIVGNMAWHADST
113

FG + R G ++ G EW + + WH D
Sbjct: 79 LFGEVVLPRRGKASPAGFPEIETTADRLELGGRFGEHDEWLRRRRHTL-LRGWHCDHG
137

Query: 114 YMPVMAQGA VFSAEV VPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLG
173

V AE VP GG T +A++ AAY L RA V A H L +G

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG
179

G++ A VP GG T FA+M AY++L R L+ +A S S V +
Sbjct: 113 MGSMLLAAEVPPFGGDTLAFANMFLAYESLSARMRELLDGLTA-----ISSSAKADVSRTR
167

Query: 180 SAYI----GYGMDTTATPLRPLVKVHPETGRPSLLIG--RHAHAIPGMDAAESERFLEGLV
234

I G G T P+V+ HPE+GR L + H GM A ESE L L
Sbjct: 168 EDRIASNPGGGAKTVYEAHEPVRTHPESGRKGLYVNIHAHTVRFGGMTAESEPLLAFLF
227

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLH 263

+ +W G + WDNR H
Sbjct: 228 RHQTKPEFTCRFRWQPGSLAFWDNRSTQH 256

>ref|XP_001397270.1| hypothetical protein An15g07490 [Aspergillus niger]
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%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63

TL P TLGA GV + + DA L AA ++ +L+F L + + FA++
Sbjct: 19 TLTFRPLHPTLGAECEGVDFSKPVPDAVIEQLRAAMAKNGILVFRATGLDDARHTAFARQ 78

Query: 64 FG-----AIERIG-----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHA
110

G A+ + G G+++ I NV DG + S W +++ G +H
Sbjct: 79 LGPEMVDSAVGKPGVFNRLDPKGELMDIGNVDGDGRIL--STTSWRS--QLLRGTRLFHV
134

Query: 111 DSTYMPVMAQGAVFSAEVVPP--AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
168

D +Y A ++ A +P GG T FAD R AY L E T+ + HSL+ S
Sbjct: 135 DGSYFQRRAGYSLLRAHQQLPPRGTGGATAFADTRTAYADLAEETKNEIQNHVLWHSMLMQS
194

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAES
226

+ LG A ++ + AT LV++H + R +L +G HA+ I G A+S
Sbjct: 195 R-YLG----APENWLIRLLPEAATSRGRHQLVQLHKPSNRMNLYLGSAYQIDGWSRADS
249

Query: 227 ERFLEGLVDWACQAPRVHAHQWA-AGDVVVWDNRCLLHRA 265

+ +E L+ A Q V W GD+++WDN C++HR+
Sbjct: 250 KPVIEALMRHASQDKYVLTVDWQNNGDMIMWDNTCVMHRS 289

>ref|ZP_06239536.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp.
Eu11c]
gb|EFA59126.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp.
Eu11c]

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%)

Query: 15 LGATVTGVHLATL--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGG 72
+GA V V + + DD A A ++ +L+F ++ ++ QI F ++ G + +I G

Sbjct: 13 VGAEVVDVDVDRMLHDDDLPTACLRALALEENGVLLFRELNIDDEAQIAFGRKLGRLAQIPG 72

Query: 73 ---GDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVS
129

+++ IS A+ Q+ P+ N WH D + + A+ A+ SA V+
Sbjct: 73 YRSPEVMEISFDPANPNA-QYFPS-----NDHWHFDGSMDDIPAKAALMSARVI
120

Query: 130 PAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT
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-ESGRRSLVFGASAARVIGMDVEESRALLADLERRSTAPDRVLRHSWS
236

Query: 250 AGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

GD+V+WDN L+HRA P+D PR M + LAG
Sbjct: 237 VGDVVIWDLGLVHRACPFDRTPRRMHRRTTLAG 270

>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 LTITKLTESVGAEVAGLGPTTELADDSVGAAVLDALEDNGVLFVFRGLHLDPVAQVGFRCRL 63

Query: 65 GAIERIGGG--DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM---PVMA
119

G ++ G + I + D + +++ A + + WH D

Sbjct: 64 GEVDHSSDGHHPVAGIYPITLDKS--KNASAA-----LKATFDWHIDGCTPLGDECPQ
115

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDAL-DE-----ATRALVHQRSARHSLVYSQSKLG
173

+ V SA V GG T FA+ AAYD L DE T +VH A VY

Sbjct: 116 KATVLSAVRVAEWGGETEAFANSYAAYDDLTDDEEKQRFGLRVVHSLEASQRRVYPDPSPE
175

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL
233

VQ+ S T PLV H +GR SL++G A + GM+ E L+ L

Sbjct: 176 QVQRWRS-----RRTHEHPLVWTH-RSGRKSIVLGASADYVVGMELEDEGRALLDEL
225

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAGRPETE 288
+ A +V++H W+ GD V+WDNR +LHRA P+D R M + + G E

Sbjct: 226 LARATTPEKVYSHSWSVGDTVIWDNRGVLHRAAPYDPSQREMLRRTTVLGDEPIE 280

>ref|ZP_02374281.1| dioxygenase, TauD/TfdA [Burkholderia thailandensis
TXDOH]

Length = 292

Score = 97.8 bits (242), 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 TLEIRPLSGTIGAQVRNRTLGGVVESEGRVDEIRQALLRYKVLFFTNQPDLSVETQIAFGK 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
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 ILCVKETPASGGDTMWADLEAAYAALSPGMQAFLEGQRAVHDMMPQYAQRPGAFQTQGR
173

Query: 181 AYIGYGMDDTAT--PLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWA
237

+ MD + P+V+VHPETGR L + + I G +AES L L

Sbjct: 174 S-----DMDLSEVFGAEHPVVRVHPETGRKCLFVNPFLLTSHITGFHSAESATILNYLYALM
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 marneffeii ATCC 18224]

gb|EEA19475.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase, putative [Penicillium marneffeii ATCC 18224]

Length = 336

Score = 97.8 bits (242), Expect = 1e-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 QLGALELNPVWGNTTRVNNQYLFVSNLEADGSVAKRGSRRWAHSL----GNALWHTDSA
124

Query: 114 YMPVMAQGAVFSAEVPVAVG-GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
172

+ A+ ++ A VP G G+T FAD R A+ LDE + + H L +S+

Sbjct: 125 FNQHRAKYSLLLAHSVPGEGKGTTFADTRRAWRELDEERKGELKDVVVEHELWHSRRLA
184

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAE---SERF
229

+ + G A LV+ P + + HA + D E S++

Sbjct: 185 APEEYSELTPEERGGKPPA--YHRLVQRTPNGEEETFFLAAHAKRFLFSKDGELEDSQKK
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 = 1e-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 TLEIRPLSGTIGAQVRNCTLAGVVESEGRVDEIRQALLRYKVLFFFTNQPDLSVETQIAFGK 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG +E D + + K DG Q +D + ++ WH D + +

Sbjct: 63 LFGELET----DFPSFT-AKPDG---QPEVTVFDGAVSTGRASI-WHTDLSIAKRPSAMG
113

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQ--SKLGHVQQAGS
180

+ + P GG T +AD+ AAY AL +A + + A H ++ Q + G Q G
Sbjct: 114 ILCVKETPDSGGDTMWADLEAAYAALSPGMQAFLEGQRAVHDMMPQYAERPQAFQTQGR
173

Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQ
239

+ + + P+V+VHPETGR L + + I G +AES L L +
Sbjct: 174 SDMD--LSNVFGAEHPVVRVHPETGRKCLFVNPFLTSHITGFHSAESAMILNHLYALMER
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 = 1e-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 MGTTRKITPNTGTEFSGLKGTQLV---DKGVADDALAALEETGVVVFSEADIDDESIVA 57

Query: 60 FAKRFGAIERI--GGGDIVAINVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPV
117

FA+ G + + G I I + D + Q A + + WH D T V
Sbjct: 58 FARLLGNVLPMPGSHKIKEIQRITRDAS--QSKLAAAYRE-----ATFYWHIDGTTGEV
109

Query: 118 MAQGAVFSAEVSPA-VGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQ--SKLGH
174

+ + +A + G T FA+ AAY+AL + +A + A HS SQ +
Sbjct: 110 PDKATLLTARRISGDPEGDTEFANTYAAAYEALSDEEKAQLEGVRALHSFTASQLVANPNP
169

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
234

+ +A+ D T +P+V GR SLL+G A + G+ A E L+ L+
Sbjct: 170 SPEERAAW-----DRNPTREQPIVWTR-RNGRKSLLVGSTAGEVVGLPADEGRALLDRLL
223

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

DWA Q V H+W GD+V+WDN +LHRA P+ R+M + LAG

Sbjct: 224 DWATQPQFVLRHRWTQGD LVIWDNTGMLHRALPYGPSSSRLMHRASLAG 272

>ref|ZP_06121187.1| Taurine dioxygenase [Caulobacter segnis ATCC 21756]
 gb|EEZ36857.1| Taurine dioxygenase [Caulobacter segnis ATCC 21756]
 Length = 295

Score = 97.4 bits (241), Expect = 1e-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 LTVTPAGTVLGA EISGIDL RAPLKPEIVA AIRAALLRYKVVFFRDQDISYEDHVRFRGRYF 77

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV
 117

G +E G +I+ I ADG + +D++ ++ WH D T+
 Sbjct: 78 GDLEGHPVTSHVPGFPEILHIE--AADGMKLR-----EDIVPIVRAANKWHTDVTFRE
 129

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
 177

+ G V +P +GG T FAD A Y L + + +A H ++ QS V +
 Sbjct: 130 PSMGGVLRMRQMPPLGGDTLFADTAAIYRDLPPKLDQIADLTAEHDII--QSYGYRVDE
 187

Query: 178 AGSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLV
 234

A + A P + P+V+ HPETG L + + I G+ E++ L L+
 Sbjct: 188 AKRQEL-----RAAYPPMVHPVVRTHPETGEKHLFVNKVFTRILGLPEDEAKALLNELL
 242

Query: 235 DWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

D +AP +W +V WDNR 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 NSLHITPLGPHIGAEISGISLAGPLDEGQFAQLQQALLTHQVLFRRDQPITPRQORALAN 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIV-----GNMAWHADST
113

RFG + V H+P + ++IV N WH D T
Sbjct: 63 RFGDLH-----IHPVYPHAP----EAE E I I V L D T H D D N P P D N D N W H T D V T
103

Query: 114 YMPVMAQGAVFSAE V V P A V G G R T C F A D M R A A Y D A L D E A T R A L V H Q R S A R H S L V Y S Q S K L G
173

++ A+ +A+ +P VGG T +A AA++ L + L+ A H +++S
Sbjct: 104 FIETPPALAILAAKQLPPVGGDTLWASGIAAFEG LSPRLQQLLTGLEAEHD--FTKSFPA
161

Query: 174 HVQQAGSAYIGYGM DTTA--TPLR-PLVKVHPETGRPSLLIGR-HAHAIPGM DAAESERF
229

H A A + A PLR P+++ HP +GR +L + +P + A ESE
Sbjct: 162 HRHNASPAEYQRWQEAAARHPPLRHPVIRTHPLSGRQALFVNEGFTTRLPLPAQESEAL
221

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAE 266

L L + +W D+ +W DNR H A
Sbjct: 222 LTFLFRHVTKPEYQVRWRWREHDIAIWDNRVTQHYAN 258

>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 TPLAPAIGSVVEGLDLSRDMSEPTMRLLALLFDRGVVVI PGQTIDDAAYVRFASFFGTP 65

Query: 67 ----IERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

I D AI + D +PA D G + WH+DS+Y V
Sbjct: 66 LDFFIPEHRNADFP A I I R I N N D P A ----TPAAMRD-----GAVHWHSDSSYESVPGCVT
115

Query: 123 VFSAEVVPVAVGGRTCFADMR AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY
182

+ + P GG T FA AAY L EATRA + ARH L + G + +
Sbjct: 116 MLFGKEAPDQGGETHFASTSAAYADLPEATRARIDGLVARHELGRAPWIEGETRPDPN--
173

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQAPR
242

T P PLV VHP TGR + A+AI GMD AE+ + L + +

Sbjct: 174 --RPPRKTDA PSHPLVMVHPVTGRKGIFTS GTAY AIDGMDDAEATALIRELREHVAKPAY
231

Query: 243 VHAHQWAAGDVVVWDNRCLLHRAEPWDFK 271
+++ GD+V+WDN +H A P ++

Sbjct: 232 RISYKARPGDIVLWDFNGTVHCASPIEYS 260

>ref|NP_822287.1| taurine catabolism dioxygenase [Streptomyces avermitilis
MA-4680]

dbj|BAC68822.1| putative taurine catabolism dioxygenase [Streptomyces
avermitilis

MA-4680]

Length = 306

Score = 97.1 bits (240), Expect = 2e-18, Method: Compositional matrix
adjust.

Identities = 90/291 (30%), Positives = 125/291 (42%), Gaps = 22/291 (7%)

Query: 8 ITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG- 65
+ P +GA + GV LA +DD+ A + AA L+ ++ F Q L + + FA+RFG

Sbjct: 1 MKPVAGHIGAEIRGVDLAGPMDDSVVAEIRAAVLRWKVVFREQRDLHTSHVAFARRFGE 60

Query: 66 --AIERIGGGDIVAISNVK--AD----GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV
117

++ G V+ AD G AEW + WH D

Sbjct: 61 PVSLRSRGSASPPDFPEVETTADRLELGERYGMDHAEWL-RRRRHSLLRGWHCDHGARID
119

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-VYSQSKLGHVQ
176

V AE VP GG T ++++ AAY L + R V A H L V Q++ G

Sbjct: 120 PPAATVLR AETVPPYGGDTTWSNLAAAYAGLSKPV RDFVDGLRAEHLGVGYQARPG---
176

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGM DAAESERFLEGLVD
235

AY+ + +D PLV+VHPETG L + G + I + ES L+ L+

Sbjct: 177 --DDAYVRHLLDHQTASEHPLVRVHPETGERVLFVNGYYVEQIQDVSRTESRALLDMLLG
234

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283
A + +W G V WDNR +H A P D PRVM LAG

Sbjct: 235 EATRPEYTVRFRWEPGSVAFWDNRATIHLA-PSDTAHLDPVMHRVMLAG 284

>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 = 2e-18, Method: Compositional matrix adjust.

Identities = 87/271 (32%), Positives = 126/271 (46%), Gaps = 21/271 (7%)

Query: 5 TLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+++T +G + GA V GV L+ L A + AWLQH +L FPGQ LS+D F

Sbjct: 20 NIEVTASGQSCGAEVVRGVDLSRELAPTLVAQIREAWLQHQVLSFPGQSLSDDDLRLRFTLC 79

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGA
122

FG GD I+ + T R+H A D + + WH+D ++ QG
Sbjct: 80 FGPF-----GDDPFIAP I-----TGRKHIIAVQRDAGETTSLFAEQWHSDFQARPPQGT
130

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

+P GG T FAD AA A+ ++ R + + A HS + S G + A A
Sbjct: 131 CLYGV TIPPTGGDTL FADQVAAAAAMPKSLRDKLEGKRAVHSAIMGYSPAGILGDADKA-
189

Query: 183 IGYGMDT-----TATPLRPLVKVHPETGRPSLL--IGRHAHAIPGMDAAESERFLEGLV
234

G MD AT ++ HPETGR S+L +G + I G++ E L L
Sbjct: 190 AGRSMDIRPSDNAAATQSHLIIFSHPETGRDSILGTVG-YMIGIEGLEGEERALLTELY
248

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+W + + H W G +++WDNR +LH A
Sbjct: 249 EWQTREEFRYRHHWEQGTLMLMWDNRVAVLHSA 279

>ref|YP_002417336.1| Probable taurine catabolism dioxygenase [Vibrio
splendidus LGP32]

emb|CAV18911.1| Probable taurine catabolism dioxygenase [Vibrio
splendidus LGP32]

Length = 271

Score = 97.1 bits (240), Expect = 2e-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 LKIEQVTPHIGAQIHGVNLTCSVTELDEVYQALITHQVIFLGDQVLSPEQHLMIAERFG 61

Query: 66 AIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
118

+E R+ V++ T R ++P E WH D T+ V
Sbjct: 62 KLEPAHPFFPRVESAPQVSVE-----TTRGNAPME-----SYWHTDLTWRKVP
105

Query: 119 AQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLV-YSQSKLGHVQQ
177

++ ++ A+ +P+ GG T + M A +++LDE +A + SA HSLV + + ++

Sbjct: 106 SKASLLHAQHIPSTGGDTIWCSMTAVFESLDEDMKAKLRGLSATHSLVAFEGVESDQIEL
165

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDW
236

+ + P+V+ HPETG+ +L I I +D +S+ L L +
Sbjct: 166 DWHKSLKTAQKNPPVVIHPVVQSHPETGKETLYINEQFTRYINELDRQDSDVLLYQLFEI
225

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRA 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 = 2e-18, Method: Compositional matrix
adjust.

Identities = 52/125 (41%), Positives = 73/125 (58%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
195

T FADMRA YDALD+ T+ +V HS ++S++K+G + P+R
Sbjct: 1 TEFADMRAAYDALDDETKDIVEDLVCEHSQIFSRKMGFTDLTPEERERF-----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 QRLVRVHPVTGRKSLFLASHAGSILGWVPEAQTFMLDLTEIATQRQFVYAHEWSVGDV
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 = 2e-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-SNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
120

RFG + I I NV V D + + N WH D T++P A

Sbjct: 60 ARFGDLH-----IHPIYPNPETPQV-----LILD TAVTDVRDNAVWHTDVTFLPTPAL
108

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQA
178

GAV SA+ +PA GG T +A AA++AL R ++ +A H + + G +
Sbjct: 109 GAVLSAKQLPAYGGDTLWASGIAAFEALSAPLREMLDGLTATHDFTKSFPLERFGTTPED
168

Query: 179 GSAYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW
236

+ + + PL P+V+ HP +GR +L + I ++ ESE L+ L
Sbjct: 169 LARWEATRNN--PPLSHPVVRTHPVSGRKALFVNEGFTTRINELNEQESEALLKLLFAH
226

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

A + +W DV WDNR H A
Sbjct: 227 ATRPEFSIRWRWQENDVAFWDNRV TQHFA 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 ITVKKLGSRIGAQVDGVS LGADLDAAVDQIRAALLEHKVIFFRNQHHLDDQQQLQFAGL 64

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV
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 LRAVTLPNYGGSTLWANTATAYAE LPEPLKCLVENLWALHTNRYDYVANEAVQAL TDTQQ
172

Query: 184 GYGMDDTTATPLR---PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA
240

+ R P+V+VHPETG +LL G G+D+ ES E L

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 ++I A +GA V GV LA LD+ AAL A H L+F HL ++ Q FA+ F
 Sbjct: 4 IEIRKVTANIGAQVFGVDLAEPLDEETAALRDALNTHKALVFSVDVHLDDEGQQAFARHF 63

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA---WHADSTYMPVMAQG
 121

G + A V A P + + G A WH D T++ Q
 Sbjct: 64 GDL-----TTAHPTVPAVDGAPNVLPVDSE-----GGRAANHWHTDVTFVNLNPPQA
 109

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYS---QSKLGHVQQ
 177

+ + +P GG T A+ AAY L E R L A H+ Y + L Q
 Sbjct: 110 STLRSLTIPPYGGETLIANSAAAYRDLPEPLRRLADDLWAEHTNDYDYAVPEETLDEEQA
 169

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA
 237

A A + P+V+VHP TG L IG A I G+ ES + L+ L +
 Sbjct: 170 ARRAQF---TSIKYRTVHPVVRVHPLTGERGLFIGGFAQRIVGLSTGESRKLDDLQSYV
 226

Query: 238 CQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPVMMWHSRLAG 283

+ + H+W+ +V++DNR H A LPR + +AG
 Sbjct: 227 TRPENLLRHRWSENQLVLFDNRITQHYAVDNYDGLPRRLHRVTVAG 272

>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 = 3e-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 EAELRISPLSAHIGAEISGVYLTRPLDQKQIQAIRAALLKWRVVFREQFLSHEQHVAFS 68

Query: 62 KRFGAIERIG---GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
 118

+FG + +G G + + + +R+ + E +++ G WH D T
 Sbjct: 69 AQFGELT-VGHPVFGHVEGHPQIYSISKLRATRFEGPPLLRPWTG---WHTDVTA AVNP
 124

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQA
 178

++ +P GG T + ++ AY+ L E R V H Q G
 Sbjct: 125 PFASILRGVTIPPYGGDTQWTLNVIAYEKLSEPLRKFVDGLRGVHRFAPPQGAAG-----
 179

Query: 179 GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA
 237

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 = 3e-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 LDVHPVAGRIGAEIRGVKLSPLDAATVEAIQAALVRHKVIFFRGQTHLDDQSQEGFAKL 74

Query: 64 FGAIERIGGGDIVAISN----VKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
 119

G E + + + ++ DG Q + +WH D T++
 Sbjct: 75 LG--EPVAHPTVPVVDGTRYLLQLDGAQGQRA-----NSWHTDVTFVEAYP
 118

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----G
 173

+ ++ + V PA GG T +A+ AAY L E R L + A HS Y + L

>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 = 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 LDVHPVAGRIGAEIRGVKLSPLDAATVEAIQAALVRHKVIFFRGQTHLDDQSQEGFAKL 74

Query: 64 FGAIERIGGGDIVAISN----VKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
119

G E + + + ++ DG Q + +WH D T++

Sbjct: 75 LG--EPVAHPTVPVVDGTRYLLQLDGAQGQRA-----NSWHTDVTVEAYP
118

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKL-----G
173

+ ++ + V PA GG T +A+ AAY L E R L + A HS Y + L

Sbjct: 119 KASILRSVVAPASGGDTVWANTAAAYQELPEPLRELADKLWAVHSNRYDYASLKPDPIDPA
178

Query: 174 HVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL
233

+++ + +T P+V+VHP +G +L +G I G A+S+ L

Sbjct: 179 KLERHRKVFTSTVYETE----HPVVRVHPISGERALQLGHFVKRIKGYSLADSQHLFAVL
234

Query: 234 VDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ +W AGDV +WDNR H A PR++ LAG

Sbjct: 235 QGHVTRLENTVRWRWEAGDVAIWDNRATQHYAVDDYGTQPRIVRRVTLAG 284

>ref|ZP_05483905.1| putative taurine catabolism dioxygenase [Streptomyces sp. AA4]

Length = 308

Score = 96.3 bits (238), Expect = 4e-18, Method: Compositional matrix adjust.

Identities = 82/263 (31%), Positives = 113/263 (42%), Gaps = 24/263 (9%)

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHP-----ETGRPSLLIGRHAHAIPGMDAAESERFLE
231

A T A R + HP +GR SLL+G + G A ES L+
Sbjct: 165 ----AEPDASERTRALWARVPAREHPLVWTRRSGRSLLVGATTDHVVGWPADESRRALLD
220

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L++W+ Q V H W GD+V+WDN +LHRA P+ R+M + L G

Sbjct: 221 RLEWSTQPRFVLRHHWHRGDLVIWDNTGMLHRAIPYTATSRRMLHRTTLVG 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 = 4e-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 MPENQLTISRIVAGRIGAEISGIDLAEPLLEHTVAAIRAALLEHKVVFVFRQRLDHGSQIA 60

Query: 60 FAKRFGAI-----ERIGGGDIVAISNVKADGTVRQHSPPAEWDDMMKVIVGNMA-WHADS
112

FA++FG + E I + D +++ + K + WH D
Sbjct: 61 FARQFGELTHAHPHEDAPPEQFPQILTIDPDRYAQKYGEDFRQEYRKRQYSYFSGWHTDV
120

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-VYSQSK
171

T G++ AE VP GG T + ++ AAY+ L + L A H + ++ +
Sbjct: 121 TAAVNPPAGSILRAEAVPEFGGDTQWTNLAAAYEGLSAPLQRLAESLRVHRFRIPAE
180

Query: 172 LGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERF
229

++ + + P+V+VHPETG L + G H + G+ A ES R
Sbjct: 181 SKRAERVNANLL-----IAEHPVVRVHPETGERVLFVNPFGFTDHIV-GLSAVESRRV
231

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVVDNRCLLHRA 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 = 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 IDVIPLAGRIGAQINGVELSSHLNPEVLNQIRQSLLEHKVIFFRNQEHLTDQEQEKFAEL 73

Query: 64 FG-----AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV
 117

G + G + + DG WH D T++
 Sbjct: 74 LGQPISHPTVPVAEGSTYIFELDSRHDGRAD-----VWHTDVTFVSN
 115

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATR LVHQRSARHS--LVYSQSKLGHV
 175

+ ++ A P GG T +A+ AAYD L E + L +Q A H+ Y +
 Sbjct: 116 YPKISILRAVTTPHRGGDTTWANTEAAYDELPEPLKLLANQLRAIHTNDFDYGGFRPSAS
 175

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
 235

+ + T PLV+VHPETG+ +L++G+ G+ A ES + E D
 Sbjct: 176 DEVVKRHQKIFASTVYEAHPLVRVHPETGKRTLILGQFFKRFVGLTAKESNKLFEIFQD
 235

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPVMMWHSRLAG 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 = 4e-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 LGAEIRGIDFSKPLSSQARDDVIGLLSEHQLLVFPGQRLSCEQQIAACGAFGELEPHPMPT 69

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
 126

++ +SNV +DG + ++ WH+D Y+ A+ F A
 Sbjct: 70 TNTSSFPEMTIVSNVTS DGKPVGYPTPPFE-----LWHS DLCYLEHPAKMTFFYA
 119

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATR LVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG
 186

E VP G T FA+M AY+ L + +A + + A SL S + ++ G
 Sbjct: 120 ESVPDAHGDTWFANMFRAYETLPDELKAAIDGKRAVFSL--DSSLVKRCRKIGFDL NIAE
 177

Length = 270

Score = 95.9 bits (237), Expect = 5e-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 GVEVSGVQLASCTDAEMEDIKQSIYEHGVAVFRDQEFSDHIFRFGKRWGGI-----DI 59

Query: 76 VAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGR
135

+ D E D+ + AWH D +Y + A G+V A +P GG
Sbjct: 60 NNYFPLDDDYGEIAIVKKEADESTNI---GGAWHTDHSYDQIPAMGSVLVARDLPPSGGD
116

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T +A M AAYDAL + +A + A H+ + G Q G D +
Sbjct: 117 TEWAHMGAAAYDALPDDLKAEIEGLEAFHTADHVYKTDGLYAQTDMGKNLRGQDLKTGAVH
176

Query: 196 PLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

P+V HP TGR L + I G ES LE L A QW G V
Sbjct: 177 PVVIRHPHTGRKLLYVNSAFTINIVGKTREESLPLLEKLYAAALTGDNQCRLQWKPGTVA
236

Query: 255 VWDNRCLLHRA 265

+WDNR H A

Sbjct: 237 IWDNRRTTWHNA 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 = 5e-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-SNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG + I I NV V D + + N WH D T++P A GA
Sbjct: 62 FGDH-----IHPIYPNPVETPQV-----LVLDTAVTDVRDNAVWHTDVTFLPTPALGA
110

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLV--YSQSKLGHVQQAGS
180

V SA+ +PA GG T +A AA++AL R ++ +A H + + G + +

Sbjct: 111 VLSAKQLPAYGGDTLWASGIAAFEALSVPLREMLDGLTATHDFTKSFPLERFGTTPEDLA
170

Query: 181 AYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWAC
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 RPEFSIRWRWQENDVAFWDNRVTQHFA 255

>ref|ZP_01770198.1| dioxxygenase TauD/TfdA family [Burkholderia
pseudomallei 305]

gb|EBA45341.1| dioxxygenase TauD/TfdA family [Burkholderia pseudomallei
305]

Length = 327

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: 56 LGAEIRGIDFSKPLSSQARDDVIGLLSEHQLLVFPGQRLSCEQQIAACGAFGELEPHPM
115

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
126

++ +SNV +DG + ++ WH+D Y+ A+ F A
Sbjct: 116 TNTSSFPEMTIVSNVTS DGKPVGYPTPPFE-----LWHS DLCYLEHPAKMTFFYA
165

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG
186

E VP G T FA+M AY+ L + +A + + A SL S + ++ G
Sbjct: 166 ESVPDAHGDTWFANMFRAYETLPDELKAAIDGKHAVFSL--DSSLVKRCRKIGFDLNIAE
223

Query: 187 MDDTTATPLRPLVKVHPETGRPSLLIG-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 dioxxygenase TauD/TfdA [Frankia sp.
EUN1f]

gb|EFC83067.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp.
EUN1f]

Length = 277

Score = 95.9 bits (237), Expect = 5e-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--VDKGVAADALAALEESGVVVFREADIDDESLVAF 58

Query: 61 AKRFGAIERI--GGGDIVAI SNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVM
118

+ G + + GG + I + D + Q A + + WH D T V
Sbjct: 59 GRLLGDVLPMPGGHRLKEIQRITRDAS--QSKLAAYRE-----ATFYWHIDGTTGEVP
110

Query: 119 AQGAVFSA-EVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ--SKLGHV
175

+ + +A ++ + G T FA+ AAY+AL + +A + A HS SQ +
Sbjct: 111 DKATLLTARQISGSTEGDTEFANTYAAEALSDEDKASLEGVRALHSFTASQLVANPDPS
170

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
235

+ +A+ D T +P+V GR SLL+G A + G+ A E L+ L+D
Sbjct: 171 PEERA AW-----DRNPTREQPVVWTR-RNGRKSLLVGSTAGEVVGLPADEGRALLDRLLD
224

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 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 = 5e-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 SLTITPLSPALGAQISGVDISRDITAEERDAIEQALLQHQVLFVRDQPINPQQQARFAAR 61

Query: 64 FGAIERIGGGDIVAI-SNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG + I I NV V D + + N WH D T++P A GA
Sbjct: 62 FGD LH-----IHPIYPNPVETPQV-----LILD TAVTDVRDNAVWHTDVTF LPTPALGA
110

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLV--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 RWEATRNN--PPLSHPVVRTHPVSGRKALFVNEGFTTRINELSELESEALLKLLFAHAT
228

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ +W DV WDNR H A
Sbjct: 229 RPEFSIRWRWQENDVAFWDNRVTQHFA 255

>ref|ZP_04522662.1| taurine dioxygenase [Burkholderia pseudomallei
MSHR346]

gb|EEP51576.1| taurine dioxygenase [Burkholderia pseudomallei MSHR346]
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 LGAEIRGIDFSKPLSSQARDDVIGLLSEHQLLVFPQQLSCEQQIAACGAFGELEPHPMPT 69

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
126

++ +SNV +DG + ++ WH+D Y+ A+ F A
Sbjct: 70 TNTSSFPEMTIVSNVTSDGKPVGYPTPPFE-----LWHS DLCYLEHPAKMTFFYA
119

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
186

E VP G T FA+M AY+ L + +A + + A SL S + ++ G
Sbjct: 120 ESVPDAHGDTWFANMFRAYETLPDELKAAIDGKHAVFSL--DSSLVKRCRKIGFDLNIAE
177

Query: 187 MDDTTATPLRPLVKVHPETGRPSLLIG-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_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
                    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 = 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: 56  LGAEIRGIDFSEPLSSQARDDVIGLLSEHQLLVFPGQRLSCEQQIAACGAFGELEPHPM
115

```

```

Query: 69  --RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
126
          ++ +SNV +DG      +      ++              WH+D Y+  A+  F A

```

```

Sbjct: 116 TNTSSFPEMTIVSNVTSDGKPVGYPTPPFE-----LWHS DLCYLEHPAKMTFFYA
165

```

```

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATR LVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
186
          E VP  G T FA+M AY+ L +  +A +  + A SL      S +  ++ G

```

```

Sbjct: 166 ESVVPAHGDTWFANMFRAYETLPDELKAAIDGKHAVFSL--DSSLVKRCRKIGFDLNIAE
223

```


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: 5 LGAEIRGIDFSKPLSSQARDDVIGLLSEHQLLVFPQGRLSCEQQIAACGAFGELEPHPM 64

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
126

++ +SNV +DG + ++ WH+D Y+ A+ F A
Sbjct: 65 TNTSSFPEMTIVSNVTSKGKPVGYPTPPFE-----LWHS DLCYLEHPAKMTFFYA
114

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
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|ZP_02356184.1| dioxygenase, TauD/TfdA [Burkholderia oklahomensis
E0147]

Length = 292

Score = 95.5 bits (236), Expect = 6e-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 TLEIRPLSGTIGAQVRNRTLGGVVESEGRVDEIRQALLRYKVLFFFTNQPDLSVETQIAFGR 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG +E D + + K DG Q +D + ++ WH D + +
Sbjct: 63 LFGELET----DFPSFT-AKPDG---QPEVTVFDGAVSTGRASI-WHTDLSIAKRPSAMG
113

Query: 123 VFSAEVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ--SKLGHVQQAGS
180

+ + P GG T +AD+ AAY AL +A + + A H ++ Q + G Q G
Sbjct: 114 ILCVKETPDSGGDTMWADLEAAYAALSPGMQAFLEGQRAVHDMMPQYAERPQAFQTQGR
173

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQ
239

 + + + P+V+VHPETGR L + + I G +AES L L +
Sbjct: 174 SDMD--LSNVFGAEHPVVRVHPETGRKCLFVNPFLLTSHITGFHSAESAMILNHLIALMER
231

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265

 V W+ GDV +WDNRC +H A
Sbjct: 232 PQYVVRWHWSNGDVALWDNRCTMHTA 257

>ref|ZP_03546154.1| Taurine dioxygenase [Comamonas testosteroni KF-1]
gb|EED70440.1| Taurine dioxygenase [Comamonas testosteroni KF-1]
Length = 329

Score = 95.5 bits (236), Expect = 6e-18, Method: Compositional matrix
adjust.

Identities = 79/284 (27%), Positives = 122/284 (42%), Gaps = 14/284 (4%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
++ITP A +GA ++GV+L L A + +A L+ ++ F QHLS++QQI F+++F
Sbjct: 27 IRITPQSAHIGALISGVNLKQALSAAEVHTIRSALLRWKVIFFRDQHLSHEQQIAFSRQF 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 LRGVTIPPYGGDTQWTNLAAAYEALSKPLQAFLOGLRGEHRFSAPQGA-----TASQEYL
199

Query: 184 GYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPR
242

 D T PLV +HPETG L I +I + ES LE L + A +
Sbjct: 200 DLVRDNTLISEHPLVTIHPETGKVLVYISPGFLKSIVELSTRESRVLLELLWEHAVSSEF
259

Query: 243 VHAHQWAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283

 +W G + WDNR H A P D + R ++ + L G
Sbjct: 260 TVRFKWEPSLAFWDNRSTAHVA-PQDIFALEFDRQLYRTTLVG 302

>ref|YP_111178.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia
pseudomallei K96243]

ref|ZP_02415379.1| dioxygenase TauD/TfdA family protein [Burkholderia
pseudomallei 14]

ref|ZP_02459626.1| dioxygenase TauD/TfdA family protein [Burkholderia
pseudomallei 9]

ref|ZP_02475125.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei

B7210]

ref|ZP_02502025.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei

112]

ref|ZP_02509863.1| dioxygenase TauD/TfdA family protein [Burkholderia pseudomallei

BCC215]

emb|CAH38633.1| putative alpha-ketoglutarate-dependent taurine dioxygenase

[Burkholderia pseudomallei K96243]

Length = 281

Score = 95.5 bits (236), 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: 10 LGAEIRGIDFSEPLSSQARDDVIGLLSEHQLLVFPQRLSCEQQIAACGAFGELEPHPM 69

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
 126

++ +SNV +DG + ++ WH+D Y+ A+ F A
 Sbjct: 70 TNTSSFPEMTIVSNVTS DGKPVGYPTPPFE-----LWHS DLCYLEHPAKMTFFYA
 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 = 6e-18, Method: Compositional matrix adjust.

Identities = 81/268 (30%), Positives = 121/268 (45%), Gaps = 20/268 (7%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFA-ALHAAWLQHALLIFPGQ-HLSNDQQITFAK 62

Sbjct: 3 TL+I P T+GA V LA + ++G A + A L++ +L F Q LS + QI F +
 TLEIRPLSGTIGAQCVCNRTLADVVEGRADEIRQALLRYKVLFFFTNQPELSVETQIAFGR 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
 122

Sbjct: 63 FG +E K DG Q +D + ++ WH D + +
 LFGELE-----TNFPSFTAKPDG---QPEVTVFDGAVSTGRASI-WHTDLSIAKTFSAMG
 113

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQ--SKLGHVQQAGS
 180

Sbjct: 114 + + P GG T +AD+ AAY AL +A + + A H ++ Q + G Q G
 ILCVKETPDSGGDTMWADLEAAYAALSPGMQAFLEGQRAVHDMMPQYAQRPGAFQTRGR
 173

Query: 181 AYIGYGMDDTTAT--PLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWA
 237

Sbjct: 174 + MD + P+V+VHPETGR L + + + G +AES L L
 S----DMDLSEVFGAEHPVVRVHPETGRKCLFVNPFLTSHLVGFHSAESATILNYLYALM
 229

Query: 238 CQAPRVHAHQWAAGDVVVDNRCLLHRA 265

Sbjct: 230 + V W+ GDV +WDNRC +H A
 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 = 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: 5 LGAEIRGIDFSEPLSSQARDDVIGLLSEHQLLVFPGQRLSCEQQIAACGAFGELEPHPM 64

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA VFSA
 126

Sbjct: 65 ++ +SNV +DG + ++ WH+D Y+ A+ F A
 TNTSSFPEMTIVSNVTSDGKPVGYPTPPFE-----LWHS DLCYLEHPAKMTFFYA
 114

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
 186

Sbjct: 115 E VP G T FA+M AY+ L + +A + + A SL S + ++ G
 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 = 6e-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 GPLTPAHPIALGLPEHPEIWERKAAEYKENHRSDLSIPTAKPPRDYKQWHIDITFVANPN
134

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG
179

 + ++ +P GG T ++++ AYD L +ALV A H S G
Sbjct: 135 RYSILRGVEIPPYGGDTLWSNLECAVDGLSPTIKALVDGLQAVHRTSSYDS-----G
186

Query: 180 SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI--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-AGPIDYAHFDLPRVRRITVAG 293

>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 = 7e-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 MVSTRLTFDPLHATFAAKCLGVDFQAALPAKTVEEIRCGLATYGVLVFRHAQLDDARHVA 60

Query: 60 FAKRFGAIE----RIGGG-----DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNM
 106
 FA + G ++ I G ++ +SN+ DG + + ++ +GN
 Sbjct: 61 FAAQLGELDDSTPYIKAGRKHRLAPYTELFDVSNLDDDGNIIVSTDLSRF----QLGLGNG
 116

Query: 107 AWHADSTYMPVMAQGAVFSAEVVP--AVGGRTCFADMRAAYDALDEATRVLVHQRSARHS
 164
 +H DS + P A +V A +P GG T FAD R AY LDE T+ + HS
 Sbjct: 117 LFHVDSAFNPRRAGYSVLRAHELPPKGTGGATAFADTRTAYADLDEVTKGRIKDHVVSHS
 176

Query: 165 LVYSQSKLGHVQQAGSAYI-GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDA
 223
 L +S+ + ++ G + LV+ H +GR +L I HAH I G+
 Sbjct: 177 LWHSRR----LAAPDCEFLQGMPKEEHFMARHRLVQTHEASGRTNLYIAHHAHHIDGLSQ
 232

Query: 224 AESERFLEGLVDWACQAPRVHAHQWAA-GDVVVWDNRCLLHRAEPWDFK 271
 + + L+ A Q +W + GD+++WDN C++H A F+
 Sbjct: 233 DVGQEVIRNLLSHATQEKYTIIEVEWESNGDIIIWDNTCMHAARRGAFE 281

>ref|ZP_04690003.1| dioxygenase [Streptomyces ghanaensis ATCC 14672]
 Length = 324

Score = 95.1 bits (235), Expect = 7e-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 VEVPRVAGHIGAEVTGVDLAGDLDEAVVAIRAALVLRWKVVFVRGQRLDHAGHVALARRF 76

Query: 65 G---AIERIGGG---DIVAISNVKADGTVRQHSPAEWDD--MMKVIVGNMAWHADSTYMP
 116
 G + R G D I + E D+ + WH D
 Sbjct: 77 GEPVVLPRRGKASPPDFPEIETTADRLELGGFRFGMEHDEWLRRRRHTLLRGWHCDHGARV
 136

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSL-VYSQSKLGHV
 175
 + AE VP GG T ++++ AAY L R + A H L V QS+ G
 Sbjct: 137 DPPAATILRAETVPPYGGDTTWSNLAAAYAGLSAPVREFADRLRAEHRLGVGYQSRPGD-
 195

Query: 176 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLV
 234

AY+ + +D PLV+VHPETG L + G + I G+ ES L+ L+
Sbjct: 196 ----DAYVRHLLDRQTASEHPLVRVHPETGERVLYVNGYYVEQITGLSRPESAAVLQMLL
251

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283
+ A + +W G V WDNR +H A P D PR+M LAG

Sbjct: 252 EQATRPEYTVRFRWEPGSVAFWWDNRATIHLA-PGDTAHLDDHPRIMHRVMLAG 302

>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]

Length = 292

Score = 95.1 bits (235), 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 TLEIRPLSGTIGAQVRNRTLADVVEGRADEIRQALLRYKVLFFFTNQPELSVETQIAFGR 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
 122
 FG +E K DG Q +D + ++ WH D + +
 Sbjct: 63 LFGELE-----TNFPSFTAKPDG---QPEVTVFDGAVSTGRASI-WHTDLSIAKTSPSAMG
 113

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQ--SKLGHVQQAGS
 180
 + + P GG T +AD+ AAY AL +A + + A H ++ Q + G Q G
 Sbjct: 114 ILCVKETPDSGGDTMWADLEAAYAALSPGMQAFLEGQRAVHDMMPQYAQRPGAFQTRGR
 173

Query: 181 AYIGYGMDDTTAT--PLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWA
 237
 + MD + P+V+VHPETGR L + + + G +AES L L

Sbjct: 174 S-----DMDLSEVFGAEHPVVRVHPETGRKCLFVNPFLLTSHLVGFHSAESATILNYLYALM
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 = 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+FPGQ LS +QQI FG +E

Sbjct: 10 LGAEIRGIDFSEPLSSQARDDVIGLLSEHQLLVFPGQRLSCEQQIAACGAFGELEPHPM 69

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
126

++ +SNV +DG + ++ WH+D Y+ A+ F A
Sbjct: 70 TNTSSFPEMTIVSNVTSKPKVGYPTPPFE-----LWHS DLCYLEHPAKMTFFFYA
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 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 = 8e-18, 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 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLG-HVQQA
178

+ ++ + V P GG T +A+ AAY L E R L + A HS Y + + V A

Sbjct: 119 KASILRSVVAPTSGGDTVWANTAAAYQELPEPLRELADKLWAVHSNEYDYASIKPDVDPA
178

Query: 179 G-SAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA
237

Y T P+V+VHP +G +L +G I G A+S+ L

Sbjct: 179 KLERYRKVFTSTVYETEHPVVRVHPISGERALQLGHFVKRIKGYSLADSQHLFAVLQGHV
238

Query: 238 CQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPVMMWHSRLAG 283

+ +W GDV +WDNR H A PRV+ LAG

Sbjct: 239 TRLENTVRWRWQVGDVAIWDNRATQHYAVDDYGTQPRVRRVTLAG 284

>ref|YP_002799405.1| Taurine dioxygenase protein [Azotobacter vinelandii
DJ]

gb|ACO78430.1| Taurine dioxygenase protein [Azotobacter vinelandii DJ]
Length = 318

Score = 95.1 bits (235), Expect = 8e-18, 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 AAEAIVVTPLSLYIGAQVDGVDLSRPLPSAQREAIRAALLRWKVLFFHDQHLDAHQVAF 73

Query: 61 AKRFG--AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
118

++FG + G + + + G R A + D +++ WH D +

Sbjct: 74 GRQFGEPTVGHVPVFGHVVEGHPEIYSVG--RDRFKARFTDE-RLVRPWSGWHTDVSAALNP
130

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
178

A+ +P GG T + D+ AAY+ L RA V H +

Sbjct: 131 PAAAILRGVDIPPYGGDTQWTDLVAAYNGLSPTLRAFVDGLRGEHRFTPE-----G
182

Query: 179 GSAYIGYMDTTATPL---RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLV
234

A G+ PL PLV+VHPETG +L + I G+ ESE+ LE L

Sbjct: 183 AEARPGFSEPLAVRPLVSEHPLVRVHPETGEKALFVSPTFLKRIVGLSPRESEQLLELLELF
242

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDF---KLPRVMWHSRLAG 283
+ A + +W G + WDNR H+ P D LPR ++ L G

Sbjct: 243 EHAIRPEYTVRFKWRPGSLAFWDNRVTAHQP-PSDIHATDLPRQLYRITLVG 293

>ref|YP_335290.1| TauD/TfdA family dioxxygenase [Burkholderia pseudomallei
1710b]

ref|ZP_04899972.1| dioxxygenase TauD/TfdA family [Burkholderia
pseudomallei S13]

gb|ABA52694.1| dioxxygenase, TauD/TfdA family [Burkholderia pseudomallei
1710b]

gb|EDS82984.1| dioxxygenase TauD/TfdA family [Burkholderia pseudomallei
S13]

Length = 327

Score = 95.1 bits (235), Expect = 9e-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 LGAEIRGIDFSKPLSSQARDDVIGLLSEHQLLVFPGQCLSCEQQIAACGAFGELEPHPM
115

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
126

++ +SNV +DG + ++ WH+D Y+ A+ F A

Sbjct: 116 TNTSSFPEMTIVSNVTSKGKPVGYPTPPFE-----LWHS DLCYLEHPAKMTFFYA
165

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYG
186

E VP G T FA+M AY+ L + +A + + A SL S + ++ G

Sbjct: 166 ESVPDAHGDTWFANMFRAYETLPDELKAAIDGKHAVFSL--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_04954431.1| dioxxygenase, TauD/TfdA family [Burkholderia
pseudomallei 1710a]

gb|EET03953.1| dioxxygenase, TauD/TfdA family [Burkholderia pseudomallei
1710a]

>emb|CAY27508.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 94.7 bits (234), Expect = 1e-17, Method: Compositional matrix adjust.

Identities = 53/124 (42%), Positives = 68/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALD+ T+A + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFADMRAAYDALDDETKAEIEDMICEHSLMYSRGS LGFLD-----YTDEEKELFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

LV+ HP GR SL + HA AI GM E+ L L + A Q VH H+W D+V+
Sbjct: 56 RLVTRHPVHGRKSLYLSSHAGAIKGMTPEARVLLRDLNEHATQPEFVHVHKWTLHDLVM
115

Query: 256 WDNR 259

WDNR

Sbjct: 116 WDNR 119

>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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFADMRAAYDALDDETKVEIEDMICEHSLMYSRGS LGFLD-----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 RLVTRHPSTGRKSLYLASHAGAIVGWPVPEARALLRDLIEHATQRKFVYVAHEWKQWDLVM
115

Query: 256 WDNR 259

WDNR

Sbjct: 116 WDNR 119

>ref|ZP_06210503.1| Taurine catabolism dioxygenase TauD/TfdA [Acidovorax
avenae subsp.

avenae ATCC 19860]

gb|EFA40540.1| Taurine catabolism dioxygenase TauD/TfdA [Acidovorax
avenae subsp.

avenae ATCC 19860]

Length = 318

Score = 94.4 bits (233), Expect = 1e-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 LRIRRVAGALGGEVLDLELSAGLDDATIGHLTAALVRHKVLFVRGQHQQLDDARHQAFGER 75

Query: 64 FG-----AIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPV
117

G + G I + K G +WH D T++
Sbjct: 76 LGRTVSHPTVPAREGTRIFELDASKGGGRAD-----SWHTDVTFLDA
117

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS-----LVYS
168

+ + A VPA GG T +A+ AAY+ L E + L A HS LV
Sbjct: 118 FPKYGILRAVTVPAYGGDTVWANTAAAYERLPEDLKRLADSLWAVHSNNYDYGADRLVVD
177

Query: 169 QSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
228

+++L H + ++ + Y + PLV VHP +G +LL+G I G + ES R
Sbjct: 178 ETRLRHHRDVFASEV-YEAE-----HPLVHVHPVSGERALLLGHFIQRIQGFSSTESAR
230

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285

E L + + W DV +WDNR H A + PRV+ + G P
Sbjct: 231 LFELLQNRVTRLENTVRRWSWRQNDVAIWDNRATQHIAVNDYGRQPRVVRRVTVHGDP 287

>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 = 1e-17, Method: Compositional matrix adjust.

Identities = 79/285 (27%), Positives = 119/285 (41%), Gaps = 21/285 (7%)

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 LNITPLGPYIGALVENVNLRPLGDGQFEQLYHALLKHQVLFRLNQIPITPLQQRNLAGRF 64

Query: 65 GAIE----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
120

G + D+ I + H+P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPQAADVKEIIVLD----THDHNPPDNDN-----WHTDVTFIENPPL
110

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV-QQAG
179

GA+ +A+ +P+ GG T +A AAY+AL E R L+ A H S + H +

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 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
 195

T FADMRAAYDALD+ T+A + RHS +YS+ KLG V+ + P+R
 Sbjct: 1 TEFADMRAAYDALDDRTKADIENLVCRHSNMYSRGKLGLEVEFTDEERAVF-----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 QLLVRRHPVSGRKSFLSAHAGEIEGMPTPQARMLLLDLTEFATREPFVYSHVWRVNDLV
 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 TVHVAVPAGHIGADITGVDLREPLTDPQVEAITSALHTYKVLFFRDQHIGHAEHVAFSRR 72

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
 123

FGA+ D A ++ V + + K N WH D + + ++
 Sbjct: 73 FGAVTPSHPYDDDAPTTYPEILAVDTRLYEKRFVGRKASYTNQ-WHTDVSPLINPPAASI
 131

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYI
 183

AE+ P GG T + ++ AAY+ L E+ R V A H + G + A S
 Sbjct: 132 LRAEIAPERGGDTRWTNLVAAYEHLPELRRFVDGLQAEH-----RFGGSRPAWSTDS
 184

Query: 184 GYGMDDTTATPL---RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQ
 239

Y A PL P+V+VHP TG +L + I G+ A+S+ L L D

>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 MRIEQLTCSIGAEALTGVDLADAVHDDGLFAEIRAALLKHRVFLRDQEITRAQHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
 122

FG +E +A S+ + G VR + +P + +D + AWH D+T+ G
 Sbjct: 61 FGELE----DHPIAGSDPEHPGLVRIYKTPDQPNDRYE-----NAWHTDATWRAAPPFGC
 111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAY
 182

V P VGG T +A+M AY+ L E + + ARHS+ S +++ +
 Sbjct: 112 VLRCVECPPVGGDTMWANMVLAYENLPEHVKTQIADLRARHSIEASFGAAMPIEKRHALK
 171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEG-----LVD
 235

Y P+V+ HPETG L + E RF + L+
 Sbjct: 172 AQY-----PDAEHPVVRTHPETGEKVLVNAFTTHFTNYHTPERVRFQDANPGASMLLS
 226

Query: 236 WACQAPRVHAHQ----WAAGDVVVWDNRCLLHRA 265

+ V +Q W + +WDNR H A
 Sbjct: 227 YLVSQAYVPEYQVRWRWRKNSIAIWDNRSTQHAYA 260

>ref|ZP_05374097.1| Taurine dioxygenase [Geobacillus sp. Y4.1MC1]
 gb|EET69258.1| Taurine dioxygenase [Geobacillus sp. Y4.1MC1]
 Length = 310

Score = 94.0 bits (232), Expect = 2e-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 FEVKPLSPIIGAEIIGVDLREPITPELQAE LNRALLEWKVLFVRNQKITSEQQRAFARLW
 100

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVF
 124

G +E I + + R H ++++ WHAD T+ A+ AV
 Sbjct: 101 GELEVHPFYPIIEGQSKEIVRFSRDHKQGGFENI-----WHADVTFRANPAKAAVL
 151

Length = 277

Score = 93.6 bits (231), Expect = 2e-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--AIEQALLQHQVLFRRDQPITPEQQAHFA 59

Query: 62 KRFGAIERIGGGDIVAI-SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ
120

RFG + I I NV V D + + N WH D T++P A
Sbjct: 60 ARFGDLH-----IHPIYPNVPQTPQV-----LILD TAVTDVRDNAVWHTDVTF LPTPAL
108

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLV--YSQSKLGHVQQA
178

GAV SA+ +PA GG T +A AA+ AL R ++ +A H + + G +
Sbjct: 109 GAVLSAKQLPAYGGDTLWASGIAAFQALSAPLREMLDGLTAMHDFTKSFPLERFGTTPED
168

Query: 179 GSAYIGYGMDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDW
236

+ + + PL P+++ HP +GR +L + I + ESE L+ L
Sbjct: 169 LARWEATRNN--PPLSHPVIRTHPVSGRKALFVNEGFTTRINELSELESEALLKLLFAH
226

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRA 265

A + +W DV WDNR H A
Sbjct: 227 ATRPEFSIRWRWQENDVAFWDNRVTQHFA 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 = 2e-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 --RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
126

A++ + D V + AWH D T+ P + A+ A

Sbjct: 109 PLLPANSAESALARFQKDANVSGY-----ENAWHHDVTRPEPSILAILHA
154

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG
186

VP +GG T FADM AAYD+LD+ T+A + + A H Y L ++ +
Sbjct: 155 IEVPPIGGDTLFDADMYAAYDSLDDTKAEIDRLDAAHDFYYLRGLVPDEKIAELQAAHP
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 +WDR + H A + R+M + + G
Sbjct: 267 QVRFWRAPDSVAIWDNRAVQHYAASGYWPHTRIMERASVTG 307

>emb|CAY27276.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 93.6 bits (231), Expect = 2e-17, Method: Compositional matrix
adjust.

Identities = 50/124 (40%), Positives = 68/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
195

T FADMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFADMRAAYDALDDTKVEIEDMICEHSLMYSRGS LGFLD-----YTDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

LV++HP GR SL + HA AI GM E+ L L + A + V+ H+W D+V+
Sbjct: 56 RLVRIHPVHGRKSLYLSSHAGAIKMSVPEARLLLRNLTEHATKPEFVYVHKWTLHDLVM
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 = 2e-17, Method: Compositional matrix
adjust.

Identities = 53/124 (42%), Positives = 72/124 (58%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
195

T FADMRAAYDALDE TRA V + HSL++S+ +G SA+ ++ L+
Sbjct: 1 TEFADMRAAYDALDERTRAEVEELICEHSLLRGAIGF-----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 RLVRFHPATGRKSLFLSAHIGTIIGWPQPEAMAFIRDLIEHATQPQFVYHRWTQHDLVM
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 = 2e-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+++ 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 QRLVRTHPVTGRKSLFLSAHAGGIVGWPVPEARAFRLDMVEHATQPRFVYSHKWRQWDLV
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 = 2e-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 SLTITPLSPALGAQISGVDISRDISAERDAIEQALLQHQVLFRLDQPINPEQQARFAAR 61

Query: 64 FGAIERIGGGDIVAI-SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG + I I NV V D + + N WH D T++P A GA

Sbjct: 62 FGD LH-----IHPIYPNVPDTPQV-----LVLDTAVTDVRDNAVWHTDVTF LPTPALGA
110

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLV--YSQSKLGHVQQAGS
180

V SA+ +PA GG T +A AA++AL R ++ +A H + + G Q +
Sbjct: 111 VLSAKQLPAYGGDTLWASGIAAFEALSAPLREMLDGLTATHDFTKSFPLERFGTTPQDLA
170

Query: 181 AYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWAC
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 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 = 2e-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 TLEIRPLSGTIGAQVRNRTLADVVEGRADEIRQALLRYKVLFFFTNQPELSVETQIAFGR 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG +E K DG Q +D + ++ WH D + +
Sbjct: 63 LFGELE-----TNFPSFTAKPDG---QPEVTVFDGAVSTGRASI-WHTDLSIAKTSPSAMG
113

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQ--SKLGHVQQAGS
180

+ + P GG T +AD+ AAY AL +A + + A H ++ Q G Q G
Sbjct: 114 ILCVKETPDSGGDTMWADLEAAYAALS PGMQAFLEGQRAVHDMMPQYAQHPGAFQTRGR
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 = 2e-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 TPLSPAIGAIIVSGVNLAQSLTAKTESRLRELLLRHQVLFVRNQNITPRQQRNFAQRFGPL 92

Query: 68 ERIGGGDIVA-ISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
126

+ VA + + T E +D+ N WH D T+ GAV +A

Sbjct: 93 HQHPYPTVADVPEIIVLDT-----EQNDLK----DNALWHTDVTFSQTPPLGAVLAA
141

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRVLVHQR SARHSLVYS--QSKLGHVQQAGSAYIG
184

+P GG T +A AAYDAL + + + +A H +S S+ G + ++
Sbjct: 142 RHLPPSGGDTLWASATAAYDALSDGMKLRLEHLTALHDFTHSFPLSRFGRTEAEKQKWL-
200

Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQAPRV
243

+ P++++HPET + ++ + + G++ ES L L +
Sbjct: 201 RTREQQPPVEHPVIRIHPETNKRAIFVNEGFTTEVCGLEIEESAALLRFLFQHLSKPEFS
260

Query: 244 HAHQWAAGDVVVWDNRCLLHRA 265

W GDV WDNR H A
Sbjct: 261 VRWTWREGDVAFWDNRRATQHYA 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 = 2e-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 TLEIRPLSGTIGAQVRNRTLADVVEGRADEIRQALLRYKVLFFFTNQPELSVETQIAFGR 62

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG +E A + + TV +D + ++ WH D + +
Sbjct: 63 LFGELE-TNFPSFTAKPEGQPEVTV-----FDGAVSTGRASI-WHTDLSIAKTSPSAMG
113

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQR SARHSLVYSQ--SKLGHVQQAGS
180

+ + P GG T +AD+ AAY AL +A + + A H ++ Q + G Q G
Sbjct: 114 ILCVKETPDSGGDTMWADLEAAYAALSPGMQAFLEGQRAVHDMMPQYAQRPGAFQTRGR
173

Query: 181 AYIGYGMDDTTAT--PLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWA
237

+ MD + P+V+VHPETGR L + + + G +AES L L
Sbjct: 174 S-----DMDLSEVFGAEHPVVRVHPETGRKCLFVNPFLLTSHLVGFHSAESATILNYLYALM
229

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ V W+ GDV +WDNRC +H A
Sbjct: 230 ERPQYVVRWHWSRGDVALWDNRCTMHTA 257

Query: 232 GLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRV 275
 L C P H +W V WDNRC H A WD+ P+V
 Sbjct: 215 MLYK-HCANPNFHVRFWRKPKSVAFWDNRCTWHLAV-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 = 3e-17, Method: Compositional matrix
 adjust.

Identities = 50/124 (40%), Positives = 68/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
 195

T FADMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
 Sbjct: 1 TEFADMRAAYDALDDETKVEIEDMICESHLSMYSRGSLSGFLD-----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

>emb|CAY27510.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 93.2 bits (230), Expect = 3e-17, Method: Compositional matrix
 adjust.

Identities = 52/124 (41%), Positives = 67/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
 195

T FADMRAAYDALD+ T+A + HSL+YS+ LG + Y + L+
 Sbjct: 1 TEFADMRAAYDALDDETKAEIEDLVCEHLSMYSRGSLSGFLD-----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 = 3e-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-----GGGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHAD
 111

+++FG + G I+A+ + K + + K + WH D
 Sbjct: 75 SRKFGDVTSPHPYDDEAPEGFPQILAVDSRKYEKRFGR-----KKYSYDNKWHTD
 124

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK
 171

T + G + A +VP GG T + ++ AAY+ L ++ + LV A H +
 Sbjct: 125 VTALINPPAGTILRAHIVPEQGGDTQWTNLVAAAYEGLPDSLKGLVDGLRAEH-----R
 177

Query: 172 LGHVQQAGSAYIGYGMDDTTATPL---RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESE
 227

G + Y + T PL P+V+VHP TG +L + I G+ ++S+
 Sbjct: 178 FGGRHPQWAEDSSYALKTRENPLVTEHPVVRVHPVTGERALFVTPGFTSRIVGVSPSQSD
 237

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD---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 = 3e-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 LDPAAVNEIRAALLAHKVVFFRGQHQLDDAEQLAFAGLLGT--PIGHPAAIALAD---DA 60

Query: 86 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAY
 145

+ +E+ + WH D T+ +V A +P+ GG T +A+ AAY

Sbjct: 61 PIITPINSEFGKANR-----WHTDVTFAANYPAASVLRVSLPSYGGSTLWANTAAAY
113

Query: 146 DALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETG
205

L E + L A H+ Y + A A+ P+V+VHPETG
Sbjct: 114 AELPEPLKCLTENLWALHTNRYDYVTTKPLTAAQRAFRQVFEKPDFRTEHPVVRVHPETG
173

Query: 206 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA
265

+LL G + G+D+ ES E L WA GDV +WDNR HRA
Sbjct: 174 ERTLLAGDFVRSFVGLDSHESRVLFEVLQRRITMPENTIRWNWAPGDVAIWDNRATQHRA
233

>emb|CAY27216.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 92.8 bits (229), Expect = 3e-17, Method: Compositional matrix
adjust.

Identities = 54/128 (42%), Positives = 71/128 (55%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
195

T FADMRAAYDALD+AT+A V HS+VYS+ ++G A + A LR
Sbjct: 1 TEFADMRAAYDALDDATKAEVEDLVTEHSIVYSREQIGFNDYA-----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 PVQHRLVITHPVVTGRKSLYLSSHIGGIVGWPMPEARAFIRD LIEHATQPEFVYSHKWRVN
111

Query: 252 DVVVWDNR 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 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRNLVHQRSARHSLVYSQ
169
ADSTYMPV A+ ++ SA VV GG T +ADMRAA DALD R+ V SA HS+ YSQ
Sbjct: 1 ADSTYMPVSAKASML SARVVTTKGGETEWADMRAALDALDTEARSRVADLSAYHSIAYSQ 60

Query: 170 SKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET 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 TCFADMRAAYDALDEATRNLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195
T FADMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFADMRAAYDALDDETKVEIEDMICEHSLMYSRGLGFLD-----YTDEEKEMFEPVLQ 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

>emb|CAY27440.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 92.8 bits (229), Expect = 4e-17, Method: Compositional matrix
adjust.

Identities = 53/125 (42%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRNLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195
T FADMRAAYDALDE T+A + HSL+YS+ LG + + T TP+R
Sbjct: 1 TEFADMRAAYDALDEKTKAEEDLACEHSLIYSRGTGTFTE-----LSEEERKTFTPVV 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
254
LV+ HP TGR SL + H I G E+ F+ L + A Q +AH+W D+V
Sbjct: 55 QRLVRTHPVTGRKSLYLSSHIGTIVGWPMPEARAFIRDLEHATQPRFTYAHKWRQFDLV
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 = 4e-17, Method: Compositional matrix
 adjust.

Identities = 80/278 (28%), Positives = 117/278 (42%), Gaps = 14/278 (5%)

Query: 1 MAQTTLQITPTGATLGATVTVGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59
 + T +TPT T+GA ++G+ L+ L D + L A L+ +L F Q + +
 Sbjct: 2 LPYTRFTLTPTTPTIGAEISGIQLSGQLSDETMSELRRALLEWKVLFVRDQTIDRSEHRD 61

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMA
 119

FA R+G++E+ +AD D M + N WH D ++ +
 Sbjct: 62 FASRWGSLEQHPFFKYTQPGQSEADIVTLAK-----DAMTGGVENN--WHNDVSWHEFPS
 114

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAG
 179

AV A VP VGG T +AD AAY+ L E + + Q A H + S K H+ +
 Sbjct: 115 FAAVLRAVEVPPVGGDTLWADTGAAYELLPEGIKERIDQLVAEHDWINSFGK--HMDPST
 172

Query: 180 SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDDAESERFLEGLVDWAC
 238

A + P+V+V PETGR L + I G+ AES+ L L
 Sbjct: 173 VAKLRPQFP AVR---HPVVRVIPETGRKVLVFNLSFTQRIVGVSEAESDELLTLLYRHVH
 229

Query: 239 QAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVM 276

+ +W + WDNR H A F RVM
 Sbjct: 230 RPEFQVRLKWRNTTIAFDNRNRTCQHYAASDYFPARRVM 267

>emb|CAY27211.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 92.8 bits (229), Expect = 4e-17, Method: Compositional matrix
 adjust.

Identities = 55/125 (44%), Positives = 70/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
 195

T FADMRAAYDALDE T+ LV HS +YS+ LG + P+R
 Sbjct: 1 TEFADMRAAYDALDEETKDLVADLVCEHSQLYSRQLLGFDFTEERERF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDDAESERFLEGLVDWACQAPRVHAHQWAAGDVV
 254

LV+ HP TGR SL + HA +I G E+ FL+ L + A Q V+AH+W GD+V
 Sbjct: 55 QRLVRTHPVTGRKSLYLSSHAGSIVGWVPEARAFLKDLNEHATQREFVYHRWRVGDV
 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 = 4e-17, Method: Compositional matrix
adjust.

Identities = 51/125 (40%), Positives = 71/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALD+ T+A + RHS +YS+ KLG V+ + P+R
Sbjct: 1 TEFADMRAAYDALDDRTKADIENLVCRHSNMYSRGKLG LVEFTDEERAVF-----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 QLLVRRHPVSGRKSFLSAHVGEIEGMPTPQARMLLLDLTEFATREPFVYSHVWRVNDLV
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 = 4e-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 IEVEPAAGHIGAEIHGVDLAGGLDAAQVAAVRAAVLRWKVVFVRDQHLDHAGHVAFARLF 81

Query: 65 G---AIERIGGGDIVAISNVKAD-----GTVRQHSPEWDDMMKVIVGNMAWHADSTYM
115

G + R G ++ G EW + + WH D
Sbjct: 82 GDPVTLPRRGKASPAGFPEIETTADRLELGGFRFGMEHDEWLRRRRHTL-LRGWHCDHGAR
140

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHV
175

+ AE VP GG T ++++ AAY L RA V A H L +G+
Sbjct: 141 VDPPAATILRAETVPPYGGDTTWSNLAAAYAGLSAPMRAFDGLRAEHRL-----GVGYQ
195

Query: 176 QQAG-SAYIGYGMDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGL
233

+ G AY+ + +D + PLV+VHPETG L + G + I G+ ES LE L
Sbjct: 196 PRPGDDAYVRHLLDHQ TASVHPLVRVHPETGERVLFVNGYYVEQIVGLSRPESAAVLELL
255

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKL--PRVMWHSRLAG 283

++ A + +W G V WDNR +H A + L PR M LAG
Sbjct: 256 LEHATRPEYTVRFRWQPGSVAFWDNRATIHLAPSDNAHLDPRTMHRVMLAG 307

>emb|CAY27393.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 92.8 bits (229), Expect = 4e-17, Method: Compositional matrix
adjust.

Identities = 54/125 (43%), Positives = 70/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
195

T FADMRAAYD LDEAT+A Q HSL+++ LG + T P+R
Sbjct: 1 TEFADMRAAYDGLDEATKAETEQLVCEHSLMFSRGALGFSDLSKEER-----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 QRLVRTHPVTGRKSLFLSTHAGGIVGWPVPEARAFLRDMVEHATQPRFVYSHKWRQWDLV
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 = 4e-17, Method: Compositional matrix
adjust.

Identities = 86/297 (28%), Positives = 131/297 (44%), Gaps = 52/297 (17%)

Query: 7 QITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65

++TP +GA + GV L+ L A + A+L++ +L+F QHL +Q F + FG
Sbjct: 27 RLTPV---IGAEIGGVDSRPLAAEQLAIEIRRAFLNHVLFVFRDQHL DVEQHKAFGRFLG 83

Query: 66 AIERIG----GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQG
121

+ + GD + ++A+ R V WH D T + G
Sbjct: 84 ELRALPLDDIDGDDPELVVIRANAQSR-----FVAGETWHTDGTADLEPSMG
130

Query: 122 AVFSAEVPVAVG--GRTC FADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAG
179

++ + PA+G G T FA+M A + L A +A + +A H
 Sbjct: 131 SMLYVKETPAIGTGGDTLFFANMHLALEMLSPAMQAFGLTTLTAIHD-----GE
 177

Query: 180 SAYIGY----GMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGL
 233

+ GY G+ T P+V HP+TGRPSL + G +H + + A ES+ L L
 Sbjct: 178 MPWKGYTPPPGLPKTE---HPVVVRHPQTGRPSLFFVNSGFTSHIV-QLSAGESQMLLNLL
 233

Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPVVMWHSR---LAGRPE 286
 D + P + +WA G +V WDNRC H A WD+ P + R L GRP+

Sbjct: 234 FDLVAREPVLSCRVRWAPGTLVFWDNRCTQHHAV-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 = 5e-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 MQVKQITCSLGAELVGVNLADAVRDDGLFAEIRALLLQHRVLFRLDQNISRADHVAFARR 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 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSAHSLVYSQSKLGHVQQAGSAY
 182

V P VGG T +A+M AY+ L E +A + ARHS+ S +++ +
 Sbjct: 112 VLRCVECPCPVGGDTMWANMALAYERLPEHIKAQIADLRARHSIEASFGAAMPIEKRLALK
 171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE-----GLVD
 235

Y P+V+ HPETG L + A RF + L+
 Sbjct: 172 AQY-----PDAEHPVVRTHPETGEKILYVNAFTTHTNFHTANRVRFGQDANPGAPDLLR
 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 = 5e-17, Method: Compositional matrix adjust.

Identities = 53/95 (55%), Positives = 62/95 (65%), Gaps = 6/95 (6%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQ
169

ADSTYMPV A+ ++ SA VV GG T +ADMRAA DALD R+ V SA HS+ YSQ
Sbjct: 1 ADSTYMPVSAKASML SARVVTTKGGETEWADMRAALDALDPEARSRVADLSAHHSIAYSQ 60

Query: 170 SKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET 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 = 5e-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 LDIHPVAGRIGAEIRGVQLSGDLDAATVEAIRQALVQYKVIFFRGQTHLDDQSQEAFSHL 74

Query: 64 FGAIERIGGGDIVAISNVKA-DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

G + VA V DGT E D +WH D T++ + +
Sbjct: 75 LG-----EPVAHPTVPVRDGT---RYLMELDGAQGQRAN--SWHTDVTFVDAYPKAS
121

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHS--LVYSQSKLGHVQQAGS
180

+ + V PA GG T +A+ AY+ L R L + A HS Y+ +K +
Sbjct: 122 IILRSVVPASGGDTVWANTATAYNELSAELRELADKLWAVHSNEYDYAGAKPDVSAEKLE
181

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQA
240

Y T P+V+VHPE+G SL++G I G A+S L +
Sbjct: 182 RYRKVFTSTVFETEHPVIRVHPESGEKSLVLGHFVKRIKGYSQADSAHLFGLLQSHVTRL
241

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRA 265

+W+AGDV +WDNR H A
Sbjct: 242 ENTVRWRWSAGDVVAIWDNRSTQHYA 266

>emb|CAY27418.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 119

Score = 92.4 bits (228), Expect = 5e-17, Method: Compositional matrix adjust.

Identities = 52/125 (41%), Positives = 71/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDALD+AT+A + HSL++S+ LG + + T P+R
Sbjct: 1 TEFGDMRAAYDALDDATKAEIEDLVCEHSLIFSRGSLGFTE-----LSEEEERATFRPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

LV+ HP TGR SL + H AI G E+ FL L++ A Q V++H+W D+V
Sbjct: 55 QRLVRAHPVTGRKSLFLSSHGGAILGWVPEARAFLRDLMEHATQPQFVYSHKWRQWDLV
114

Query: 255 VWDNR 259

+WDNR

Sbjct: 115 MWDNR 119

>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 = 5e-17, Method: Compositional matrix adjust.

Identities = 89/298 (29%), Positives = 127/298 (42%), Gaps = 46/298 (15%)

Query: 7 QITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64

QITP +GA ++GVHL A D A FA + AA L H +L F Q ++ + + FA RF
Sbjct: 5 QITPA---IGAEISGVHLGDAARDAALFADIRAALLTHRVLFFRDQDITRAEHVAFASRF 61

Query: 65 GAIERIGGGDIVAISNVKADGTVRQH---SPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
121

G +E VA S+ + G VR + P +++ WH D + P A G
Sbjct: 62 GPLE----DHPVAGSDPEHPGLVRIYRSDDPHSYEN-----TWHCDGLWRPNPAMG
108

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSA
181

AV P +GG T + +M AY+ L E S + S+ ++K G G+
Sbjct: 109 AVLRCIECPPIGGDTIWNMVKAYEELPE-----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 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

L + P W GDV VWDNR H A + PR M + + G

Sbjct: 220 AALLMNYLISRATIEPYQVRWSWKPGDVAVWDRNSTQHIALNDYYPAPRRMERAGIVG 277

>emb|CAY27497.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 92.4 bits (228), Expect = 5e-17, Method: Compositional matrix
adjust.

Identities = 51/124 (41%), Positives = 66/124 (53%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSAHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRA YDALD+ TRA + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFGDMRAGYDALDDETRAEIEDMVCEHSLMYSRGSGLGFLD-----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 RLVVRTHPVHGRKSLYLSSHAGAIQGMSPEARLLLRDLTEHATQPEFVYVHKWTLHDLVM
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 = 5e-17, Method: Compositional matrix
adjust.

Identities = 53/125 (42%), Positives = 70/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSAHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALD T+A V + HSL++S+ +G Q + P+R
Sbjct: 1 TEFADMRAAYDALDARTKAEVEELVCEHSLLSRGAIGFTQFTPEEIEINF-----RPVR 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 QRLVRTHPQTGRKSLFLSSHAGAIEGWTIPEARSFLRDLTEHATQREFVYSHPWQRHDLV
114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>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 = 5e-17, Method: Compositional matrix adjust.

Identities = 53/95 (55%), Positives = 62/95 (65%), Gaps = 6/95 (6%)

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR_LVHQ_SSARHSLVYSQ
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 = 5e-17, Method: Compositional matrix adjust.

Identities = 53/127 (41%), Positives = 68/127 (53%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATR_LVHQ_SSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---
192

T F DMRAAYDALD+ T+A + HSL+YS+ LG ++ Y D A
Sbjct: 1 TEFGDMRAAYDALDDDTKAEIEDMICEHSLMYSRGS LG-----FLDYTDDEKAMFKP 52

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGM_DAAESERFLEGLVDWACQAPRVHAHQWAAGD
252

L+ LV+ HP R SL + HA AI GM E+ L L + A Q VH H+W D
Sbjct: 53 VLQRLV_RTHPVHRRKSLYLSSHAGAIKGMSPPEARLLLLRDLTEQATQREFVHIHKWTVHD
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 = 6e-17, Method: Compositional matrix adjust.

Identities = 54/125 (43%), Positives = 70/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATR_LVHQ_SSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDALDEAT+A Q HSL++S+ LG + T P+R
Sbjct: 1 TEFGDMRAAYDALDEATKAETEQLVCEHSLMFSRGALGFSDLSKEER-----TMFRPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGM_DAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

LV+ HP TGR SL + HA I G E+ FL +V+ A Q V++H+W D+V
Sbjct: 55 QRLVRTHPVTGRKSLFLSAHAGGIVGWVPEARAFLRDMVEHATQPRFVYSHKWRQWDLV
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 = 6e-17, Method: Compositional matrix
adjust.

Identities = 49/124 (39%), Positives = 68/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFADMRAAYDALDDETKVEIEDMICEHSLMYSRGS LGFLD-----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 = 6e-17, Method: Compositional matrix
adjust.

Identities = 51/122 (41%), Positives = 66/122 (54%), Gaps = 5/122 (4%)

Query: 138 FADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPL
197

FADMRAAYDALD+ T+A + HSL+YS+ LG + Y + L+ L
Sbjct: 2 FADMRAAYDALDDETKAEIEDLICEHSLMYSRGS LGFLD-----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 VRTHPAHGRKSLYLSSHAGAIRGMSMPEGRLLRDLTEHATQPEFVYVHRWTVHDLVMWD
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 = 6e-17, Method: Compositional matrix
adjust.

Identities = 52/127 (40%), Positives = 70/127 (55%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---
192

T FADMRAAYDALD+ T+A + HSL+YS+ LG ++ Y + A
Sbjct: 1 TEFADMRAAYDALDDETKAEIEDMICESHLSMYSRGLG-----FLDYSDEEKAMFKP 52

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD
252

L+ LV+ HP GR SL + HA AI GM E+ L L + A + V+ H+W D
Sbjct: 53 VLQRLVVRTHPVHGRKSLYLSSHAGAIKMSVPEARLLLRDLTEHATKPEFVYVHKWTLHD
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 = 6e-17, Method: Compositional matrix
adjust.

Identities = 60/207 (28%), Positives = 97/207 (46%), Gaps = 10/207 (4%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYM
115

QQI FA+R G I V +G + + + +G WH D +Y
Sbjct: 1 QQIAFARRLGRI-----VVNKFFPENGHAPEIAEVRKEKEQRTNIGG-GWHTDHSYD 51

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHV
175

P+ A G++ A +P GG T FA++ AAYDAL + + + A+HS + + G
Sbjct: 52 PIPALGSILVARELPESGGDTMFANLYAAYDALSDGLKRTLSTLRKHSNRHLYGENGLY
111

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV
234

+++ A G + + + P+V HPE+GR +L + H G A+S L+ L
Sbjct: 112 RKSDLASQLKGPEGVSDAVHPVVITHPESGRRALYVNPGHLLHFEGWSEADSRPLLKHLV
171

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCL 261

+ A + +WA G + WDNRC+

Sbjct: 172 EHASRPEFTCRFRWAPGSIAFWDNRV 198

>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 = 7e-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--FSAIRDAFAEYSVIVLRGQTAGPGDHAFARRFG 58

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNM-----AWHADSTYMPV
117

+ NV R P E + ++ WH D +Y

Sbjct: 59 PV-----NVN-----RFFKPVEGHPEIATVLKEKDQTEAVGEGWHTDHSYDQE
101

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSL--VYSQSKLGHV
175

A G++ A +P GG T F M AAY+AL E R + +A HS V+ + +

Sbjct: 102 PAMGSILHAIEMPPYGGDTLFFVSMGAAYEALSEPMMRFLDGLTAVHSSRHVFGAAAMDS-
160

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV
234

+ S +G T P+V HP +GR L + I G++ ES L ++

Sbjct: 161 EAVKSGRLGNAAEATQDVRHPVVITHPLSGRRGLFVNPVFTTRIEGLNPEESSALL-AML
219

Query: 235 DWACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285

CQ P +W AGD+ +WDNR H+A R+M + G P

Sbjct: 220 YAHCCQPEFQCRVRWRAGDITMWDNRATRHKAINDYHGFRLMHRVTVEGGP 271

>gb|AAS64583.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
Length = 119

Score = 92.0 bits (227), Expect = 7e-17, Method: Compositional matrix
adjust.

Identities = 53/127 (41%), Positives = 70/127 (55%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---
192

T FADMRAAYDALD+ T+A + HSL+YS+ LG ++ Y + A

Sbjct: 1 TEFADMRAAYDALDDDTKAEIEDMICEHSLMYSRGLG-----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 VLQRLVRTHPVRHRRKSLYLSSHAGAIQGMSVPEARLLLLRDLTEHATQREFVYAHKWTLHD
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 = 7e-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 MRAQPLTCNIGAEVSGVSLADAARDDALFAEIKSLLLTHKVLFLRDQEISRADHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVI VGNMAWHADSTYMPVMAQGA V
123

FG +E VA S+ G V+ + + ++ ++H D ++ G V

Sbjct: 61 FGELE----DHPVAGSDPDHPGLVQIYRSDKRENYEN-----SYHTDGSWRET PPMGC V
110

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY I
183

P VGG T + +M AAY+ L E + + A+HS+ +S ++ S

Sbjct: 111 LRCIECPPVGGDTIWNMAAAYEHLPEEIKQRIAGLRAKHSIEHSFGAAMSPEKRASLAA
170

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LEG
232

Y M P+V+ HPETG +L + + E+ R+ L

Sbjct: 171 QYPMVE----HPVVRTHPETGEKALYVCGFSTHFANFHTPENVRYGQDKTPGASHLLNY
225

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L+ A +W V +WDNRC H A + PR M + + G

Sbjct: 226 LISQAAIPEYQVRFRWQPNSVAIWDNRCTQHYAVQDYWPAPRKMERAAIIG 276

>ref|ZP_06237516.1| Taurine dioxygenase [Frankia sp. Eu11c]

gb|EFA61131.1| Taurine dioxygenase [Frankia sp. Eu11c]

Length = 261

Score = 91.7 bits (226), Expect = 8e-17, Method: Compositional matrix
adjust.

Identities = 81/277 (29%), Positives = 114/277 (41%), Gaps = 41/277 (14%)

Query: 7 QITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
 I P LG A V GV LA +DDA AL AA+ +H +L+F Q L+ D + + F
 Sbjct: 9 DIRPASPVLGAEVVGVDLAGGVDDATAEALRAAFWKHKVLFVFRDQDLAPDAHVRVAVRIFD 68

Query: 66 A-----IERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
 118

+ R +V + N++ G AWH T+
 Sbjct: 69 EPFDHPQWLYRHEDNRLVYVFNLEKAGNA-----AAWHVGGTWRNPP
 110

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
 178

+ +VVP +GGRT +AD++AAYD L E + L+ +A V A
 Sbjct: 111 FTIESLTYQVVPEIGGRTLWADLQAAYDGLSEPFKQLLESVNA-----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 CQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPR 274

+ W GD V+WDN+ H A D+ PR
 Sbjct: 218 SSPNYTVSFGWKPGDFVIWDNQATWHYAVN-DYDGPR 253

>ref|ZP_05001574.1| taurine dioxygenase [Streptomyces sp. Mg1]
 gb|EDX26085.1| taurine dioxygenase [Streptomyces sp. Mg1]
 Length = 325

Score = 91.7 bits (226), Expect = 8e-17, 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 STTSITRLGGRIGAEELGGIRLAGDLPA GTVAEIRGALLAHKVVFFRGQDHLDEAGHEAFA 79

Query: 62 KRFGAIERIGGGDIVAISNVKADGT----VRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
 117

+ GA + + ADG + H A + WH D T++P
 Sbjct: 80 RLLGA-----PVAHPTVPSADGRYALGIDSHHGARANQ-----WHTDVTFVPA
 122

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGH--V
 175

+V A +P GG T +A+ AY L E R L A H+ Y + L +
 Sbjct: 123 YPAFVSLRAVTIPPYGGNTLWANTATAYAHLPEPLRVLADSLRAVHTNEYDYAALKPDAL
 182

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
 235

+A + Y T P+V+VHPETG +LL+G I G+ +S ++
 Sbjct: 183 PEALAQYREVFTSTKFLTEHPVVRVHPETGERTLLLGNFVQRIKGLTGQDSRALIDLFP
 242

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLH 263

+ QW AGDV +WDNR H
 Sbjct: 243 HVERPENTVRWQWRAGDVAIWDNRATQH 270

>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 = 8e-17, 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 TDIRPLTPAIGAEIHGIDLGAPNVAERIAEVRAALLKYGVIFFRDQDLTQEAHIAFARH 73

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMA-----WHADSTYMPV
 117

FG +E + Q +P +++++ G + WH+D T+
 Sbjct: 74 FGELE-----IHPATPKDQANP----EVLRIAHGPKSRGQENNWHS DVTWREE
 117

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARH--SLVYSQSKLGHV
 175

+ G++ A VP GG T FA+M AY+ L E + +A H S V+++ +LG
 Sbjct: 118 PSLGSILLAREVPECGGDTL FANMHLAYERLSEQMQRFCESLTAVHDISRVFAK-RLGKA
 176

Query: 176 QQAGSAYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGL
 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 YATAKDVEIQCRFRWQAGSVAFWDNRVCQHLAVSDYFPARRVMERVTIAG 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 = 8e-17, Method: Compositional matrix
 adjust.

Identities = 52/128 (40%), Positives = 70/128 (54%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
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 PVQHRLVITHPVTGRKSLYLSSHIGGIVGWPVPEARAFIRDLMEHATQRRFVYAHEWRVN
111

Query: 252 DVVVWDNR 259
D+V+WDNR
Sbjct: 112 DLVMWDNR 119

>gb|ACG80584.1| TfdA [uncultured bacterium]
Length = 119

Score = 91.7 bits (226), Expect = 9e-17, Method: Compositional matrix
adjust.
Identities = 52/126 (41%), Positives = 70/126 (55%), Gaps = 13/126 (10%)

Query: 138 FADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-
196
FADMRAAYDALD+AT+A + HS+V+S+ ++G A + A LRP
Sbjct: 3 FADMRAAYDALDDATKAEIENLVTEHSIVFSREQIGFTDYA-----EGNADKLRPV 53

Query: 197 ---LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV
253
LV HP TGR SL + H I G E+ F+ L++ A Q V+AH+W D+
Sbjct: 54 QHRLVITHPVTGRKSLYLSSHIGGIVGWPVPEARAFVVDLMEHATQRQFVYAHEWRVNDL
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 = 9e-17, Method: Compositional matrix
adjust.
Identities = 49/124 (39%), Positives = 67/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195
T F DMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFGDMRAAYDALDDETKVEIEDMICEHSLMYSRGSLSGLFD-----YTDEEKEMFKPALQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

LV++HP GR SL + HA AI GM E+ L L + A + V+ H+W D+V+
 Sbjct: 56 RLVRIHPVHGRKSLYLSSHAGAIKGMSPPEARLLLRDLTEHATKPEFVYVHKWTPHDLVM
 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 = 9e-17, 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 MGYKHIEVKPVSGFIGAEIGGVLDSTHLQDETIQEIRKALLKWKVVFVRNQNIDHAAQIA 60

Query: 60 FAKRFGAI-----ERIGG-GDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHA
 110

F RFG + E I G I+ I S E + ++ WH
 Sbjct: 61 FTGRFGEVTYAHPHEDEPIEGYSQILPID-----RSRYERRNGLRRSSYESRWHT
 110

Query: 111 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-----
 165

D T G++ A VP++GG T + ++ AAY+ L R L + A H
 Sbjct: 111 DVTAAINPPAGSILRAVNVPSIGGDTQWTNLVAAAYEGLSAPVRELADKLLKAEHRFNARLR
 170

Query: 166 VYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLI--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-PQDLDHLEVERVLYRRT
 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 = 9e-17, Method: Compositional matrix adjust.

Identities = 49/124 (39%), Positives = 67/124 (54%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFGDMRAAYDALDDETKVEIEDMICEHSLMYSRGS LGFLD-----YTDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSELLIGRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
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]
gb|ABG68462.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Escherichia coli
536]
gb|EDV65797.1| taurine dioxygenase [Escherichia coli F11]
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-TLDDAGFAALHA AWLQHALLIFPGQHLSNDQQITFAKRF 64
L ITP G +GA +TG L L D F L+ A L+H ++ Q ++ QQ A+RF

Sbjct: 5 LSITPLGPYIGAQITGADLTRPLSDNQFEQLYHAVLRHQVVFLRDQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
118

G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIQTP
108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHVQQA
178

GA+ +A+ +P+ GG T +A AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWASGIAAYEALSVPFRQLLSGLRAEHDFRKSFPYKY-RKT
167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSELLIGR-HAHAIPGM DAAESERFLEGLVD
235

+ + + P L P+V+ HP TG+ +L + I + ESE L G +
 Sbjct: 168 EAEHQRWREAVAKNPPLLHPVVRTHPVTGKQALFVNEGFTTRIVDVSEKESALL-GFLF
 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

P +W D+ +WDNR H A R+M + + G
 Sbjct: 227 AHITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 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 SIQVNPLSAHIGAEIHGVDLTQKLDARQVAEIRAALLRWRVVFREQFLTQHQHIAFSAQ 70

Query: 64 FGAIERIG---GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
120

FG + +G G + + + RQ + E +++ G WH D T
 Sbjct: 71 FGELT-VGHPVFGHVDGHAEIYSISKYRQATRFEGQTLLRPWTG---WHTDVTAAVNPPW
 126

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGS
180

++ +P GG T + ++ AAY L RA V H G
 Sbjct: 127 ASILRGVTIPPYGGDTQWTNLMAAYQKLSAPLRAFVDGLRGLHRFAPPAGASG-----TE
 181

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ
239

A++ PLV+VHPETG +L + +I G+ ES+ LE L + +
 Sbjct: 182 AFVKAVEQRILVTEHPLVRVHPETGERALYVSPSFLKSIVGVTPRESQALLELLWEHVTR
 241

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA--EPWDFKLPRVMWHSRLAG 283

+W AG V WDNR H A + +D + R ++ + L G
 Sbjct: 242 PEFTVRFKWEAGSVAFWDNRATAHLAPSDIFDLEFDRQLYRTTLVG 287

>ref|YP_002327887.1| taurine dioxygenase [Escherichia coli O127:H6 str.
 E2348/69]

emb|CAS07856.1| taurine dioxygenase, 2-oxoglutarate-dependent
 [Escherichia coli
 O127:H6 str. E2348/69]

dbj|BAI53872.1| taurine dioxygenase [Escherichia coli SE15]
 Length = 283

Score = 91.7 bits (226), Expect = 1e-16, Method: Compositional matrix adjust.

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

 LV+ HP TGR SL + HA I G E+ FL L + A Q V+AH W D+V
Sbjct: 55 QLVRRHPTTGRLSLYLASHAGEIEGWPVPEARAFRLRDLNEHATQRQFVYAHVWRLHDLV
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 KVVRIGGRIGAEIIGADLTDPDAFPTEEINRLLLEHKALIFRDAGLDEAGHRDFAARFGA 62

Query: 67 IERI-----GGGDIVAIISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
121

+ R + + V AD R + WH D T++ +
Sbjct: 63 LTRAHPTVPSAEGLEPEVLAVDADTGHAN-----VWHTDVTFFVRTPPKI
106

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSA
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---HPVVREHPETGERTLFIGGFAQRIVGLSGTESRDILRILQSYVTRPE
222

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRAEPWDF-KLPRVMWHSRLAGRPET 287

+ +W GD+VV+DNR H A P D+ PR++ +AG P T
Sbjct: 223 NIVRVRWNVGDVLFVFDNRITQHYA-PDDYDDRPRLLHRTVAGGPVT 268

>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.

Sbjct: 53 VLQRLVRTHPVHRRKSLYLSSHAGAIKMSMPEARLLLLRDLTEHATQPEFVHVHKWTVHD
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
UTI89]
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]
Length = 283

Score = 90.9 bits (224), 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 LSITPLGPYIGAQITGADLTRPLSDNQFEQLYHAVLRHHVFLRDQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVM
118

G + G D + + + D +P + D+ WH D T++

Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIQTP
108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
178

GA+ +A+ +P+ GG T +A AAY+AL R L+ A H S + + ++

Sbjct: 109 PAGAILAAKELPSTGGDTLWASGIAAYEALSVPFRQLLSGLRAEHDFRKSFPPEYKY-RKT
167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD
235

+ + + P L P+V+ HP TG+ +L + I + ESE L G +

Sbjct: 168 EAEHQRWREAVAKNPPLLHPVVRTHPVVTGKQALFVNEGFTTRIVDVSEKESEALL-GFLF
226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G

Sbjct: 227 AHITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>gb|ACG80564.1| TfdA [uncultured bacterium]
Length = 118

Score = 90.9 bits (224), Expect = 1e-16, Method: Compositional matrix
adjust.

Identities = 52/125 (41%), Positives = 67/125 (53%), Gaps = 11/125 (8%)

Query: 138 FADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTAT---PL
194

F DMRAAYDALD+ T+A + HSL+YS+ LG ++ Y D A L
Sbjct: 2 FGDMRAAYDALDDDTKAEIEDMICEHSLMYSRGLG-----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 QRLVRTHPVHRRKSLYLSSHAGAIKGMSPPEARLLLRDLTEHATQREFVHIHKWTVHDLV
113

Query: 255 VWDNR 259
+WDNR

Sbjct: 114 MWDNR 118

>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 = 1e-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 VTVTKLGAHIGARIDGVRVGGDLSPATVSAINAALLEHKVIFFSGQDHLDDAGQLEFAEL 62

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNM----AWHADSTYMPVMA
119

G TV + AE + + I +WH D T++ +
Sbjct: 63 LGT-----PTVAHPTLAEGAEQLLPIDSRDKANSWHTDVTDFVDRIP
104

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY-----SQSKL
172

+ ++ A +P+ GG T +A AAY L R L A H+ + S +
Sbjct: 105 KASLLRAVTLPSYGGTTAWASTEAAQQLPAPLRTLADNLWAVHTNRFDYADSAISAEQR
164

Query: 173 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG
232

G+ Q+ S Y Y ++ P+V+VHPETG LL+G + G+ ES
 Sbjct: 165 GYRQRFESDY--YEVE-----HPVVRVHPETGERVLLLGHFVKSFVGLKDTESAALFRL
 216

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 D + W GD+ +WDNR H A

Sbjct: 217 FQDRITRLENTVRWSWKPGDLAIWDNRATQHYA 249

>emb|CAY27454.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 90.9 bits (224), Expect = 1e-16, Method: Compositional matrix
 adjust.

Identities = 52/125 (41%), Positives = 70/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
 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 QRLVVRTHPVTGRKSLFLSAHAGTIVGWPVPEARAFRLDLIEHATQPQLVYSHQWRQWDLV
 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 = 1e-16, Method: Compositional matrix
 adjust.

Identities = 54/125 (43%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
 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 QRLVRRHPTTGRLSLYLASHAGGIEGWPVPEARAFRLDLTEHATQRQFVYAHVWRLHDLV
 114

Query: 255 VWDNR 259
 +WDNR

Sbjct: 115 MWDNR 119

>emb|CAY27428.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 90.9 bits (224), Expect = 1e-16, Method: Compositional matrix
adjust.

Identities = 51/125 (40%), Positives = 70/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYD LDE T+A + HSL++S+ LG + + + + P+R
Sbjct: 1 TEFADMRAAYDTLDERTKAEIEDLVCEHSLMFSRGLLGFTEMSEAEREMF-----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 QRLVRTHPVTGRKSLFLSAHAGTIVGWPVPEARAFRLDLIEHATQPQLVYSHQWRQWDLV
114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>emb|CAY27538.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 90.9 bits (224), Expect = 2e-16, Method: Compositional matrix
adjust.

Identities = 52/124 (41%), Positives = 69/124 (55%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALD TRA V HSL++S+ +G S + ++ +
Sbjct: 1 TEFADMRAAYDALDARTRAEVEDLICEHSLLHSRGAIGF-----SEFTPEEIIENFRPVRQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

LV+ HP+TGR SL + HA AI G E+ FL L + A Q V++H W D+V+
Sbjct: 56 RLVVRTHPQTGRKSLFLSSHAGAIEGWTIPEARSFLRDLTEHATQREFVYSHPWQRHDLVM
115

Query: 256 WDNR 259
WDNR

Sbjct: 116 WDNR 119

>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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

Sbjct: 1 T FADMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
TEFADMRAAYDALDDETKVEIEDMICEHSLMYSRGSLSGLFD-----YTDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

Sbjct: 56 LV++HP R SL + HA AI GM E+ L L + A + V+ H+W D+V+
RLVRIHPVHDRKSLSYLSSHAGAIKMSVPEARLLLLRDLTEHATKPEFVYVHKWTLHDLVM
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 VGARITLDPARIGDPALTDALRRAFADHGVLFFPRIGTSPDIHVALSRCFGTLQVHPVVK 71

Query: 70 ---IGGGDIVAISNVKAD--GTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVF
124

Sbjct: 72 G ++V +S G + H A + + + G + WH D +YM + G++
NQVEGFPEVVDMSYTPPSRPGDLSYH--AVYRIEGRELAGWLPWHFDLSYMAEINHGSML
129

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIG
184

Sbjct: 130 A VP GGRT F D Y+ L + + + + K + + A A +
RALEVPPEGGRTGFMDRIRLYELLPDDLKRRIEGLGVVYRFQPDMMKRRYCRPADMALVA
189

Query: 185 YGM-----DTTATPL-RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG
232

Sbjct: 190 M D P+ P+V +TGR L + A I GMD E + L
PSMKAGMFDGDVLDLDRDFPPVHHPMVYTERDTGRKVLNVAPLFAVGIAGMDDPEGDALLGA
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

dioxygenase, putative [Talaromyces stipitatus ATCC 10500]

gb|EED24625.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate dioxygenase, 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-TLDDAGFAALHAAWLQHALLIFPGQHLSND 55
M +L + P + GA V+GV ++ +A A L ++ +LIF L N
Sbjct: 20 MQYGSLTVIPVLRSEDSVFGAEVSGVDWNRISIPEATVAQLVELQDKYGVLIFFRETGLDNA 79

Query: 56 QQITFAKRFGA-----IERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIV 103

+ I F+++ GA +R+G + + N++ D T+ + W +

Sbjct: 80 RHIAFSQQLGAELEVNPFYYGRENDRLGEPLLFVGNIEMDRTLKVPDSRRWHHSL---- 135

Query: 104 GNMAWHADSTYMPVMAQGAVFSAEVPVAVGGR-TCFADMRAAYDALDEATRALLVHQRSAR 162

GN WH DS+Y ++ ++ + P GG T FAD R AY L + + +

Sbjct: 136 GNALWHTDSSYHQRRSKYSILLSHGPNPVKGGSWTHFADTRRAYADLPDTKKKEIEDLVVE 195

Query: 163 HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMD 222

H L +S+ KL G+ + + + LV+ P+ GR +L + HA I G

Sbjct: 196 HDLWHSR-KLASPIVYGNP-LPHELAAKPPAYHRLVQKAPD-GRQTLYLAAHAKLILGWS 252

Query: 223 AAESERFLEGLVDWACQAPRVHAHQWAAG-DVVVWDNRCLLHRAEPW 268

ES++ + L+D Q+ V + +W +G D+V WDNR +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 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR 195

T FADMRAAYDALD T+A + HSL++S+ LG + + T P+R

Sbjct: 1 TEFADMRAAYDALDGDTKAEIEGLVCEHSLIFSRGSLGFTE-----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 QRLVRTHPVTGRKSLFLSSHGGTIVGWPVPEARAFRLRDLVEHATQRRFVYSHKWRQWDLV
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 ISPVAGRIGAEVSGVRLGGDLPAETVQEIARAALLRHKVIFFRGQEHLDERGQVAFAGLLG 65

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
125

+ A V A ++ + KV WH D T++ +V
Sbjct: 66 DL-----TTAHTVPALNGNSSILDLDYSNGHKV----DRWHTDVTFVDRPPLASVLR
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 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM DTTAT---
192

T F DMRAAYDALD+ T+A + HSL+YS+ LG ++ Y + A
Sbjct: 1 TEFCDMRAAYDALDDDTKAEIEDMICEHSLMYSRGS LG-----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 VLQRLVRTHPVHRRKSLYLSSHAGAIQGMSPPEARLLLRNLTEHATQREFVHVHKWTLHD
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 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFG--AIERIGG 72
+GA ++ ++L L + +L++++F Q L+ A +G +I +

Sbjct: 9 IGAELSNINLNDLSKDEVHMIKKYFLDYSVIVFRNQSLAPKDLKDIASFWGGASIHVFK 68

Query: 73 G-----DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
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 EVPKEGGDTLFSSQYLAYDELKTDLKSCLADKKAHS-----NLGVLMLSGG-----DT
160

Query: 188 DTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH
246

T P+ + HPETG+ +L + I MD+ ES++ LE L A ++ H
Sbjct: 161 KNAKTVEHPVFRHPETGKKALYVTEAFVKEIKNMDSNESQKILEYLYRHASNEDYIYRH
220

Query: 247 QWAAGDVVVWDNRCLLHRAE 266
+W+ GD+VVWDNR + H AE

Sbjct: 221 KWSGDGLVVWDNRSVQHAYE 240

>ref|YP_001267994.1| taurine dioxygenase [Pseudomonas putida F1]
gb|ABQ78810.1| Taurine dioxygenase [Pseudomonas putida F1]

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 MHIEQLTCAIGAEVSGVNLADAIHDDDELFAQLRQQLLQHRVFLFRDQHFSTRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHS-PAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG +E VA S+ + G V+ + P + +D + AWH D+T+ G
Sbjct: 61 FGELE----DHPVAGSDPEHPGLVQIYKRPDQPNDRYE-----NAWHTDATWREAPPMGC
111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSAHSLVYSQSKLGHVQQAGSAY
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--HPVVRTHPETGEQVLFVNAFTTHFSNYHTPQVRVFGQDANPGAGDLLR
226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265

L+ A +W V +WDNR H A
Sbjct: 227 YLISQAYLPEYQVRWRWKPNSVAIWDNRSTQHYA 260

>ref|YP_002008631.1| taurine dioxygenase, 2-oxoglutarate-dependent
[Cupriavidus

taiwanensis]

emb|CAQ72579.1| taurine dioxygenase, 2-oxoglutarate-dependent
[Cupriavidus

taiwanensis]

Length = 321

Score = 90.5 bits (223), 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: 15 LDIHPVAGRIGAEIRGVALHGDLPATFAAIRAALLRHKVLFVFRDQVHLDDAAQQGFARL 74

Query: 64 FGAIERIGGGDIVAISNVKA-DGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG D V V + DGT E D +WH D T+ +
Sbjct: 75 FG-----DTPHPPTVPSRDGT----QLLELDSQHGGGRAN--SWHTDVTFDLAYPAVS
120

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQR SARHS--LVYSQSKLGHVQQAGS
180

V A VPA GG T +A+ AAY L E R L + A H+ Y+ +++ +
Sbjct: 121 VLRAVTVPAAGGDTVWANTAAAYQDLPEPLRELADKLWALHTNDYDYAATRNVNPSDEGLK
180

Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA
240

Y P+V+VHPETG +L++G + +A+S + L +
Sbjct: 181 RYREVFTSALYETEHPVVRVHPETGERTLVLGHFVKKLLDYASADSAHLIAVLQGHVHRL
240

Query: 241 PRVHAHQWAAGDVVVVDNRCLLHRA 265

+W AGDV +WDNR H A
Sbjct: 241 ENTVRWRWRAGDVVAIWDNRATQHYA 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 = 2e-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 TELRIAPIAGYIGAEVSGVDLAGDLDEAAAARLRQALLDHKVLFFRDQPLDHAAQIRFSR 71

Query: 63 RFGAIERI-----GGGDIVAISNVK--ADGTVRQHSPA EWDDMMKVIVGNMAWHAD
111

FG + G +I+ + + K A G R++S A + WH D
Sbjct: 72 HFGKVTPAHPYDYNAP EGYPEILEVDSRKYAARGGARKYSYANF-----WHTD
119

Query: 112 STYMPVMAQGA VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSK
171

+ + +E+VP VGG T + ++ AAY L E+ + V A H +
Sbjct: 120 VSALVNPPAITFLRSELVPDVG GDTAWTNLAAAYANLPESLKT FVDGLRAEH-----R
172

Query: 172 LGHVQQAGSAYIGYGMDTTATPL---RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESE
227

G Q+ A + T P+ P+V+VHPETG L + I G+ A+S+
Sbjct: 173 FGGRQKRWEAGSDAEQNVTTKPIVTEHPVVRVHPETGERGLFVTPGFTSRILGVSPAQSD
232

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVVDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283

R L+ L + +W + VWDNR H A P D + RV++ + + G
Sbjct: 233 RILDLLFEEVTNPAYTVRVRWQNN SIGVWDNRITAH LA-PADLDHLDVVRVLYRTTVEG 290

>ref|ZP_02509143.1| putative alpha-ketoglutarate-dependent taurine
dioxygenase

[Burkholderia pseudomallei BCC215]
Length = 346

Score = 90.1 bits (222), Expect = 2e-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---IGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVM
118
+ FG I + +GG AI + + R +S WH D T+
Sbjct: 119 QAFGEIVKHPTMGGKTSAILLHSHEGGRANS-----WHTDVTFGLRP
162

Query: 119 AQQAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVY----SQSKLGH
174
+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
Sbjct: 163 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSSLQDLVDKLVAVHGNDFDYAASRVLLH
222

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
234
A Y T P+V++HPETG SLL+G +A D +S R E L
Sbjct: 223 DPVAKEYRKKYAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRFVQYDTHDSNRLYEILQ
281

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
+ WAAGDV +WDR H A
Sbjct: 282 AHITRLENTVRWHWAAGDVVAIWDNRSTQHYA 312

>emb|CAY27536.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 90.1 bits (222), Expect = 2e-16, Method: Compositional matrix adjust.

Identities = 51/124 (41%), Positives = 70/124 (56%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195
T F DMRAAYDALD AT+A + HSL+YS+ +LG SA++ A +
Sbjct: 1 TEFGDMRAAYDALDAATKAEIEDLVCEHSLIYSRQLGF-----SAFLPDERVAMAPVRQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
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

>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 = 2e-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--ITQALLTHRVIFFRRQHHLDDRAQELFA 66

Query: 62 KRFGAIER---IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
118

+ FG I + +GG AI + + R +S WH D T+

Sbjct: 67 QAFGEIVKHPTMGKKTGSAILELHSHEGGRANS-----WHTDVTFGLRP
110

Query: 119 AQQAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY----SQSKLGH
174

+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H

Sbjct: 111 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSLQDLVDKLVAVHGNDYDAAASRVELLH
170

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
234

A Y T P+V++HPETG SLL+G +A D +S R E L

Sbjct: 171 DPVAKEYRKKYAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRFVQYDTHDSNRLYEILQ
229

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265

+ WAAGDV +WDNR H A

Sbjct: 230 AHITRLENTVRWHWAAGDVVAIWDNRSTQHVA 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 = 2e-16, Method: Compositional matrix
adjust.

Identities = 74/271 (27%), Positives = 115/271 (42%), Gaps = 33/271 (12%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWL-QHALLIFPGQHLSNDQOITFAKRF 64
+Q+ LGA + GV L + + L +H +L F Q + QQ A F
Sbjct: 1 MQVKRIAGALGAEIKGVDLQILTPEISIVIRDLLNEHEVLFFRQQAIEPAQQORDLAAIF 60

Query: 65 GAIE-RIGGGDIVAISNVKA-DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

G ++ G + I V + TV + S E WH+D T+

Sbjct: 61 GPLQTHPAYGTVAGIPEVMILESTVDKPSKIE-----VWHSDMTFRQHPPSVT
108

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQS-KLGHVQQAGSA
181

V V+P VGG T FA M +AYDAL E + + A H ++Q + + G

Sbjct: 109 VLRGMVIPNVGGDTL FASMTSAYDALSEG MKVYLEGLVAVHD--FAQGFRESLAEPGGRE
166

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIG----RHAHAIPGMDAAESERFLEGLVDWA
237

+G ++ P+V+VHPETG+ L + H +P ++++ L+D+

Sbjct: 167 RLGAALEENPPVRHPVVQVHPETGKKVLFVNALFTTHIEGLPPLESS-----ALLDFL
219

Query: 238 CQAPRVHAH----QWAAGDVVVWDNRCLLHR 264

CQ + H QW VV+WDNR H+

Sbjct: 220 CQHAALPEHTCRFQWTFDSVVLWDNRSTQHK 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 = 2e-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 LDIQPVAGRIGAQIRGVKLSADLDAATVA AIQAALVQYKVIFFRGQAHLDDLDSQEGFAKL 74

Query: 64 FGAIERIGGGDIVAISN----VKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMA
119

G E + + + ++ DG Q + +WH D T++

Sbjct: 75 LG--EPVAHPTVPVVDGTSYLLQLDGAEGQRA-----NSWHTDVT FVVDAYP
118

Query: 120 QGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLG-HVQQA
178

+ ++ + V PA GG T +A+ AAY L E R L + A HS Y + + V A

Sbjct: 119 KASILRSVVAPASGGDTVWANTAAAYQELPEPLRELADKLWAVHSNEYDYASIKPDVDPA
178

Query: 179 G-SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA
237

Y T P+V+VHP +G +L +G I G A+S+ L

Sbjct: 179 KLERYRKVFTSTVYETEHPVVRVHPISGERALQLGHFVKRIKGYSLADSLQHLFALLQGHV
238

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAG 283
 + +W AGDV +WDNR H A PR++ LAG
 Sbjct: 239 ARLENTVRWRWEAGDVVAIWDNRATQHYAVDDYGTQPRIVRRVTLAG 284

>ref|ZP_05011745.1| taurine dioxygenase [Streptomyces pristinaespiralis ATCC 25486]
 gb|EDY64309.1| taurine dioxygenase [Streptomyces pristinaespiralis ATCC 25486]

Length = 287

Score = 90.1 bits (222), Expect = 3e-16, Method: Compositional matrix adjust.

Identities = 80/282 (28%), Positives = 115/282 (40%), Gaps = 34/282 (12%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLA--TLDDAGFAALHAAWLQHALLIFPQHLNSNDQOI 58
 M + ++++ P TLGA ++GV LA DD F + L++ +L Q +S + +
 Sbjct: 1 MLRGSIEVEPLTCTLGAEISGVSLADAARDDDLFTEIKGLLLRYKVLFLRDQDISRAEHV 60

Query: 59 TFAKRFGAIERIGGGDIVAISNVKADGTVRQH----SPAEWDDMMKVIVGNMAWHADSTY 114
 FA+RFG +E VA S+ G VR + SPAE + A H D T+
 Sbjct: 61 AFARRFGELE----DHPVAGSDPDHPGLVRIYKDLDSPAEHYEN-----ALHTDGTW 108

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRNLVHQRSARHSLVYSQSKLGH 174
 + GAV P VGG T + DM AY+ L E R + ARHS+ ++ G
 Sbjct: 109 RENPSMGAVLRCVESPVGDDTIWVDMAQAYNRLPEHIRTQIEDLRARHSI---EATFGA 165

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF----- 229
 V + A P+V+ HPETG L + + RF
 Sbjct: 166 VLPEEKRHAKAQFPDAE--HPVVRTHPETGEKILFVNAFTHFVNYHTPRNVRFVFGQDYA 223

Query: 230 -----LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 L L+ A +W V +WDNR H A
 Sbjct: 224 PGSGLLLNYLISQAAVPEYQVRFWRKNSVAIWDNRSTQHYA 265

>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 TCFADMRAAYDALDEATRNLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR 195
 T FADMRAAYDALD+ T+A + RHS +YS+ KLG + P+R
 Sbjct: 1 TEFADMRAAYDALDDRTKADIENLVCRHNSMYSRGLGLADFTTEERRVFK-----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

>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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
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 RLVTRHPKTGRKSLYLSSHAGRIVGWPVPEAMLLLRELTEHATQREFVYSHKWRVGDLMV
114

Query: 256 WDNR 259
WDNR

Sbjct: 115 WDNR 118

>ref|ZP_02406094.1| putative alpha-ketoglutarate-dependent taurine
dioxxygenase

[Burkholderia pseudomallei DM98]
Length = 381

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: 96 LSIRPLSGHIGAEVQGIQLGSQMAPNDIRF--ITQALLTHRVIFFRRQHHLDDRAQELFA
153

Query: 62 KRFGAIER---IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
118

+ FG I + +GG AI + + R +S WH D T+
Sbjct: 154 QAFGEIVKHPTMGGKTGSAILELHSHEGGRANS-----WHTDVTFLGRP
197

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVY----SQSKLGH
174

+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
Sbjct: 198 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSLQDLVDKLWAVHGNDFDYAASRVELLH
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 DWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265

+ WAAGDV +WDNR H A
Sbjct: 317 AHITRLENTVRWHWAAGDVAIWDNRSTQHYA 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 = 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: 96 LSIRPLSGHIGAEVQGIQLGSQMAPNDIRF--ITQALLTHRVIFFRRQHHLDDRAQELFA
153

Query: 62 KRFGAIER---IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
118

+ FG I + +GG AI + + R +S WH D T+
Sbjct: 154 QAFGEIVKHPTMGGKTGSAILELHSHEGGRANS-----WHTDVTFGLRP
197

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVY----SQSKLGH
174

+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
Sbjct: 198 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSLQDLVDKLWAVHGNDFDYAASRVELLH
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 DWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265

+ WAAGDV +WDNR H A
Sbjct: 317 AHITRLENTVRWHWAAGDVAIWDNRSTQHYA 347

>gb|ACG80549.1| TfdA [uncultured bacterium]
Length = 119

Score = 90.1 bits (222), Expect = 3e-16, Method: Compositional matrix
adjust.
Identities = 52/128 (40%), Positives = 69/128 (53%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
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 PVQHRLVITHPVVTGRKSLYLSSHIGGIVGWPVPEARAFIRDLMEHATQRRFVYAHEWRVN
111

Query: 252 DVVVWDNR 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 = 3e-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 MRFNPLFPPTIGTELGTGVTFNDILSDALFPELDHALRQHQLLVIRGLQLTPEQQQLLLARKE 60

Query: 65 G-----AIERIGGGD---IVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMP
116
G + R D ++ SN DG + VGN WH DS++
Sbjct: 61 GHPIPFVMSRYHHPDHPPELMISSNEVKDGGK-----PLGVARVGNF-WHQDSSFTQ
109

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQR SARHSLVYS-QSKLGHV
175
A + +P G T FA Y L E + + ARH++ + + HV
Sbjct: 110 DPAAYTMLYGINIPPRSGDTLFAS AIDLRYRLPEEWKRRIAGLQARHTVSKRFRIRAEHV
169

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV
234
+ + T L PLV++ ++G+P L + + + G+D A S+ FL+ L+

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

Sbjct: 1 T FADMRAAYDALD+ T+ + HSL+YS+ LG + Y + L+
TEFADMRAAYDALDDETKVEIEDMICEHSLMYSRGS LGFLD-----YTDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

Sbjct: 56 LV++HP GR SL + HA AI GM E+ L L + A + V+ H+W +V+
RLVRIHPVHGRKSLYLSSHAGAIKMSVPEARLLLLRDLTEHATKPEFVYVHKWTLHGLVM
115

Query: 256 WDNR 259

WDNR

Sbjct: 116 WDNR 119

>ref|ZP_05805002.1| Taurine dioxygenase [Streptomyces flavogriseus ATCC
33331]

gb|EEW71330.1| Taurine dioxygenase [Streptomyces flavogriseus ATCC 33331]
Length = 311

Score = 89.7 bits (221), Expect = 3e-16, Method: Compositional matrix
adjust.

Identities = 80/267 (29%), Positives = 108/267 (40%), Gaps = 25/267 (9%)

Query: 4 TTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62

T + P G +GA + G L L A + A L+ +L F GQH S QQ FA+

Sbjct: 43 TLFDVVPLGPVIGAEIRGADLTRPLAPAVREEIDRALLEWKVLFVRGQHPSPAQQRAFAR
102

Query: 63 RFGAIER---IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
119

+G +E + GD ++ R +P+ WH D T+ A

Sbjct: 103 NWGELETNPLLAAGDDPEVARFD-----RSSAPS-----FENVWHTDVTFRERPA
147

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAG
179

GAV VP GG T +ADM +AYD L + + A H V ++ ++

Sbjct: 148 LGAVLHLREVPPYGGDTMWADMASAYDNLAPEVKERLEGARAVHDFVPGFARFTPEER--
205

Query: 180 SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWAC
238

I + D P+V+ HP TGR L + I G D ES+R L L A

Sbjct: 206 --LIPF-QDRFPPVEHPVVRTHPVTGRRMLFVNTSFTTRIVGWDRDESDRMLRLLFQQA
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 = 3e-16, Method: Compositional matrix adjust.

Identities = 51/125 (40%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDALD+A +A + Q HSL++S+ LG + + P+R
Sbjct: 1 TEFGDMRAAYDALDDAMKAEIEQVVCEHSLMFSRGALGFSE-----LNEQEAMFRPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

LV+ HP TGR SL + HA I E+ FL L++ A Q V++HQW D+V
Sbjct: 55 QRLVRTHPVTGRKSLFLSAHAGGIVNWPVPEARAFRLDLIEHATQPQLVYSHQWQQWDLV
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 = 3e-16, Method: Compositional matrix adjust.

Identities = 51/125 (40%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYD LDE T+A + HSL++S+ LG + + + P+R
Sbjct: 1 TEFGDMRAAYDTLDERTKAEIEDLVCEHSLMFSRGLLGFAMSEAEREMF-----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 QRLVRTHPVTGRKSLFLSAHAGTIVGWVPEARAFRLDLIEHATQPQSVYSHQWRQWDLV
114

Query: 255 VWDNR 259

+WDNR

Sbjct: 115 MWDNR 119

>gb|ACG80558.1| TfdA [uncultured bacterium]

Length = 119

Score = 89.7 bits (221), Expect = 3e-16, Method: Compositional matrix adjust.

Identities = 52/127 (40%), Positives = 68/127 (53%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---
192

Sbjct: 1 T F DMRAAYDALD+ T+A + HSL+YS+ LG ++ Y + A
TEFGDMRAAYDALDDDTKAEIEDMICEHSLMYSRGS LG-----FLDYTDDEEKAMFKP 52

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD
252

Sbjct: 53 L+ LV+ HP R SL + HA AI GM E+ L L + A Q VH H+W D
VLQRLVRTHPVHRRKSLYLSSHAGAIQGMSPPEARLLLLRDLTEHATQREFVHVHKWTLHD
112

Query: 253 VVVDNR 259
+V+VDNR

Sbjct: 113 LVMVDNR 119

>emb|CAY27353.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 89.7 bits (221), Expect = 3e-16, Method: Compositional matrix
adjust.

Identities = 50/125 (40%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

Sbjct: 1 T FADMRAAYDALDDRTKAEIEDLVCEHSLIYSRGT LG + + + TP+R
TEFADMRAAYDALDDRTKAEIEDLVCEHSLIYSRGT LGFTLSEEEKRMF-----TPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

Sbjct: 55 LV+ HP TGR SL + H I G E+ F+ L + A Q ++H+W D+V
QRLVRTHPVVTGRKSLYLSSHIGMIVGWPMPPEARAFIRDLTEHATQKQFTYSHKWRQYDLV
114

Query: 255 VVDNR 259
+VDNR

Sbjct: 115 MVDNR 119

>gb|ACG80569.1| TfdA [uncultured bacterium]
Length = 118

Score = 89.7 bits (221), Expect = 3e-16, Method: Compositional matrix
adjust.

Identities = 51/122 (41%), Positives = 63/122 (51%), Gaps = 5/122 (4%)

Query: 138 FADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPL
197

Sbjct: 2 F DMRAAYDAL + T+A + HSL+YS+ LG V Y L+ L
FGDMRAAYDALHDETKAEIEDLVCEHSLMYSRGS LGFVD-----YTDEEKQMFKPVLRQL 56

Query: 198 VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVD
257

Sbjct: 57 V+ HP GR SL + HA AI GM E L L + A Q V+ HQW D+V+WD
VRTHPVHGRKSLYLSSHAGAIRGMSVPEGRLLRDLTEHATQPEFVYVHQWTVHDLVMWD
116

Query: 258 NR 259
NR
Sbjct: 117 NR 118

>ref|ZP_03504692.1| Taurine dioxygenase [Rhizobium etli Brasil 5]
Length = 313

Score = 89.7 bits (221), Expect = 3e-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 IDVVPLTGRVGAIEIKGIRLGGELSDATVAAVNQLLKHKVIFFRDQGHLDSDAQEAFARR 76

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP
116
G + G I+ + + + G Q WH D T++
Sbjct: 77 LGDLVPHTQGPVSGTASILNLDSSRGGGRADQ-----WHTDVTFVD
118

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGH--
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 PILTFTAPENTVRWRWRAGDVAIWDNRATQHYA 270

>gb|ACG80568.1| TfdA [uncultured bacterium]
gb|ACG80586.1| TfdA [uncultured bacterium]
Length = 119

Score = 89.7 bits (221), Expect = 3e-16, Method: Compositional matrix
adjust.
Identities = 51/122 (41%), Positives = 63/122 (51%), Gaps = 5/122 (4%)

Query: 138 FADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPL
197
F DMRAAYDAL + T+A + HSL+YS+ LG V Y L+ L
Sbjct: 3 FGDMAAYDALHDETKAEIEDLVCEHSLMYSRGLGFVD-----YTDEEKQMFKPVLRQL 57

Query: 198 VKVHPETGRPSELLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWD
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 = 3e-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-DGTVRQHSPAEDDMMKVIVGNMA--WHADSTYMPVMAQGA
122

D+V V A GT S E D G A WH D T++ + A
Sbjct: 83 -----DLVPHPTVGAIKGTA---SILELDSGRG---GGRADSWHTDVTFVDAYPKAA
128

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY-----SQSKLGHVQ
176

V V+P GG T +++ AAY L + L + A HS Y S++ +
Sbjct: 129 VLRGVVIPEFGGDTIWSNTAAAYQDLPAPLQRLADELWAVHSNAYDYAATRSRATEDR
188

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSELLIGRHAHAIPGMDDAAESERFLEGLVDW
236

+ G +T P+V+VHPETG +LL+G G+ A+ ++ + +
Sbjct: 189 HFEEVFTGTIYETE----HPVVRVHPETGERTLLLGNFVQRFVGIKADGQKLFDFQSY
244

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLH 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 = 4e-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-----NSWHTDVTFVDAYP
 118

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLG-HVQQA
 178

+ ++ + V PA GG T +A+ AAY L E R L A HS Y + + V A
 Sbjct: 119 KASILRSVVPASGGDTVWANTAAAYQELPEPLRVLADTLWAVHSNEYDYASVKPDVDP
 178

Query: 179 G-SAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA
 237

Y T P+V+VHP +G +L +G I G A+S+ L
 Sbjct: 179 KLERYRKVFTSTVYETEHPVVRVHPISGERALQLGHFVKRIKGYSLADSQHLFALLQGHV
 238

Query: 238 CQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPVMMWHSRLAG 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 = 4e-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 SIQVTPLSAHIGAEIHGVDLTQKLDARQIAEIRAALLKWRVFFREQFLTQHVAFSAQ 70

Query: 64 FGAIERIG---GGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
 120

FG + +G G + V + R+ + E + + G WH D T
 Sbjct: 71 FGELT-LGHPVFGHVDGYPEVYSISKYRKATRFEGQTLQRPWTG---WHTDVTAALNPPW
 126

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGS
 180

++ +P GG T + ++ AAY L R V H G
 Sbjct: 127 ASILRGVTIPPYGGDTQWTLVAAYQKLSAPLRGFVDGLRGLHRFTPPAGASG-----TE
 181

Query: 181 AYIGYMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ
 239

A+ T PLV+VHPETG +L + +I G+ ES+ LE L + +

Query: 176 QQAGSAYIGYGMDDTTATPL-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 = 4e-16, Method: Compositional matrix
adjust.

Identities = 50/123 (40%), Positives = 70/123 (56%), Gaps = 7/123 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALD+ T+A + RHS +YS+ KLG V+ + P+R
Sbjct: 1 TEFADMRAAYDALDDRTKADIENLVCRHSNMYSRGKLG LVEFTDEERAVF-----RPVR 54

Query: 196 PL-VKVHPETGRPSLLIGRHAHAIPGMDDAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

L V+ HP +GR SL + HA I GM ++ L L ++A + P V++H W D+V
Sbjct: 55 QLLVRRHPVSGRKSFLSAHAGEIEGMPTPQARMLLLDLTEFATREPFVYSHVWRVNDLV
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 = 4e-16, Method: Compositional matrix
adjust.

Identities = 51/125 (40%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYD LDE T+A + HSL++S+ LG + + + P+R
Sbjct: 1 TEFADMRAAYDRTLDERTKAEIEDLVCEHSLMFSRGLLGFTAMSEAEREMF-----RPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDDAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

LV+ HP TGR SL + HA I G E+ FL L++ A Q V++HQW D+V
Sbjct: 55 QRLVTRHPVTGRKSFLSAHAGTIVGWPVPEARAFRLDLIEHATQPQLVYSHQWRQWDLV
114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>gb|AAP21654.1| Shy7 [Streptomyces hygrosopicus subsp. yingchengensis]
Length = 251

>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 = 4e-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---IGAEISGVNLGEGARDPALFAEIKAAALLKHRVLFVRKQEITRADHVAFASAF 61

Query: 65 GAIERIGGGDIVAISNVKAD----GTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQ
 120
 G +E D + +V R +P +++ ++H D + P A
 Sbjct: 62 GKLE-----DHPVVGSVPDHPGLVKVYRSDNPHSYEN-----SYHCDGLWRPNPAM
 107

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGS
 180
 GAV P +GG T + +M AYD L E + ++ AR S+ +S G V +
 Sbjct: 108 GAVLRCLCEPEIGGDTIWNMVKAYDELPEEIKRKINGLRARASIEHS---FGAVMTPEN
 164

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIP-----GMDAAESERF
 229
 D A P+V+ HPETG L +G ++ P G+D +
 Sbjct: 165 R-AKLAQDHPAVE-HPVVRTHPETGEKILFVGASFTTHTFTNYSTPDNVRHGIDKSPGASL
 222

Query: 230 LEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
 L + P W GDV VWDNR H A + PR M + + G
 Sbjct: 223 LLNYLTSRATIEPYQVRWAWQEGDVAVWDNRSTQHYAVNDYYPAPRKMERAGIVG 277

>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 = 4e-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 LNITPLGPYIGAQITGADLARPLSDNQFEQLYHAVLRHQVVFLREQVITPQQQRALALRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVM
 118
 G + G D + + + D +P + D+ WH D T++
 Sbjct: 65 GDLHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIDTP
 108

LV+ HP TGR SL + H I G E+ F+ L + A Q+ +AH+W D+V
 Sbjct: 55 QRLVRTHPVTGRKSPLYLSSHIGTIVGWPMPEARAFIRDLTEHATQSRFTYAHKWRQFDLV
 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 = 4e-16, Method: Compositional matrix
 adjust.

Identities = 82/274 (29%), Positives = 110/274 (40%), Gaps = 31/274 (11%)

Query: 7 QITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKREG 65
 I P LGA V GV LA +DDA AL A+ QH +L+F QHLS D + + F
 Sbjct: 10 DIRPASVPLGAEVVGVDLAGGVDDATAEALREAFWQHVKLVFRDQHLSPDAHVQAVRIFD 69

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEE--WDDMMKVI VGNMAWHADSTYMPVMAQGAV
 123

+ +H +D ++ G WH T+
 Sbjct: 70 -----EPFDHPKWLYRHEDNRLVYDFQLEKAGGASTWHVGGTWRTPPFHLES
 116

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
 183

+ +VVP +GGRT +AD++AAYD L E + L+ SA V A
 Sbjct: 117 LTYQVVPDIGGRTLWADLQAAYDGLSEPFQHLLLESVSA-----VYNADPGDG
 163

Query: 184 GYGM-DTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPR
 242

Y T T P+V+ H TGR L + A + G+ AE L L+ A
 Sbjct: 164 TYNRPPVTETVEHPVVRTHRHTGRKGLFLSSALRLTGVGPAEGAALLPFLLAHASSPNY
 223

Query: 243 VHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276

+ W GD V WDN H A D+ PRV
 Sbjct: 224 TVSFGWKPGDFVTWDLATWHFAVN-DYDGPRVY 256

>ref|YP_110680.1| alpha-ketoglutarate-dependent taurine dioxygenase
 [Burkholderia
 pseudomallei K96243]
 emb|CAH38124.1| putative alpha-ketoglutarate-dependent taurine
 dioxygenase
 [Burkholderia pseudomallei K96243]
 Length = 298

Score = 89.4 bits (220), Expect = 4e-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: 13 LSIRPLSGHIGAEVQGIQLGSQMAPNDIRF--ITQALLTHRVIFFRRQHHLDDLAQELFA 70

Query: 62 KRFGAIER---IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
 118
 + FG I + +GG AI + + R +S WH D T+
 Sbjct: 71 QAFGEIVKHPTMGGKTGSAILELHSHEGGRANS-----WHTDVTFLGRP
 114

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVY----SQSKLGH
 174
 + +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
 Sbjct: 115 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSLQDLVDKLWAVHGNDFDYAASRVELLH
 174

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
 234
 A Y T P+V++HPETG SLL+G +A D +S R E L
 Sbjct: 175 DPVAKEYRKKYAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRVQYDTHDSNRLYEILQ
 233

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
 + WAAGDV +WDR H A
 Sbjct: 234 AHITRLENTVRWHWAAGDVAIWDRSTQHYA 264

>gb|AAM87510.1|AE014000_14 taurine dioxygenase [Yersinia pestis KIM 10]
 gb|AAS60461.1| putative taurine dioxygenase [Yersinia pestis biovar
 Microtus str.
 91001]
 Length = 288

Score = 89.4 bits (220), Expect = 4e-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: 11 LIVTPLGPHIGALVENINIAHPLGDSQFEQLYHVLLKHQVLFRRNQIPITPLQQRDLAGRF 70

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
 118
 G + + + + D +P + D+ WH D T++
 Sbjct: 71 GDLHIHPVYPHTQECEEIIVLDTADD-----NPPDNDN-----WHTDVTFIETP
 114

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGH--VQ
 176
 GA+ +A+ +P GG T ++ AAYDAL + L+ A H S + H
 Sbjct: 115 PLGAILAAKQLPTTGGDTLWSSGIAAYDALSAPFKQLLAGLQAEHDFTKSFPEHKHRTTP
 174

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD
235

+ ++ G + L P+++ HP +GR +L + I G+ ESE L G +
Sbjct: 175 EEHQRWLQ-GKEKNPPLLHPVIRTHPVSGRQALFVNEGFTTRIIGLSDKESEALL-GFLF
232

Query: 236 WACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
P +W DV +WDNR H A RVM + + G RP

Sbjct: 233 AHHTKPEFQVRWRWQQDDVAIWDNRVTQHYANADYLPQRRVMHRATILGDRP 284

>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 = 4e-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---IGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVM
118

+ FG I + +GG AI + + R +S WH D T+
Sbjct: 67 QAFGEIVKHPTMGGKTGSAILELHSHEGGRANS-----WHTDVTFGLRP
110

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY----SQSKLGH
174

+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
Sbjct: 111 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSLQDLVDKLVAVHGNDFDYAASRVELLH
170

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
234

A Y T P+V++HPETG SLL+G +A D +S R E L
Sbjct: 171 DPVAKEYRKKYAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRFVQYDTHDSNRLYEILQ
229

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
+ WAAGDV +WDNR H A

Sbjct: 230 AHITRLENTVRWHWAAGDVVAIWDNRSTQHVA 260

>ref|YP_001412108.1| taurine dioxygenase [Parvibaculum lavamentivorans DS-
1]

gb|ABS62451.1| Taurine dioxygenase [Parvibaculum lavamentivorans DS-1]

Sbjct: 103 QNPPLGCVLQAIKIPVGGDTLWSSGVAAFAALDQSLQQKLGKLTATHDIRQSYPIERFA
162

Query: 174 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG
232

H + + P+V+ HP TG+ L + I +D +ES L+
Sbjct: 163 H-NDVERKKLEETFKRNPVHVHPVVRTHPVTGQSILFVSEGFTTRINELDESESAELLQY
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]
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 CO92]
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|EEO74798.1| putative taurine dioxygenase [Yersinia pestis Nepal516]
gb|EEO82489.1| 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]
 Length = 282

Score = 89.4 bits (220), Expect = 4e-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 LIVTPLGPHIGALVENINIAHPLGDSQFEQLYHVLLKHQVLFVRNQPITPLQQRDLAGR 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
 118
 G + + + + D +P + D+ WH D T++
 Sbjct: 65 GDLHIHPVYPHTQECEEIIVLDTADD-----NPPDNDN-----WHTDVTFIETP
 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGH--VQ
 176
 GA+ +A+ +P GG T ++ AAYDAL + L+ A H S + H
 Sbjct: 109 PLGAILAAKQLPTTGGDTLWSSGIAAYDALSAPFKQLLAGLQAEHDFTKSFPEHKHRTTP
 168

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD
 235
 + ++ G + L P+++ HP +GR +L + I G+ ESE L G +
 Sbjct: 169 EEHQRWLQ-GKEKNPPLLHPVIRTHPVSGRQALFVNEGFTTRIIGLSDKSESEALL-GFLF
 226

Query: 236 WACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
 P +W DV +WDNR H A RVM + + G RP
 Sbjct: 227 AHTTKPEFQVRWRWQQDDVAIWDNRVTQHYANADYLQRRVMHRATILGDRP 278

>emb|CAY27414.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 89.4 bits (220), Expect = 4e-16, Method: Compositional matrix
 adjust.

Identities = 51/124 (41%), Positives = 66/124 (53%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
 195
 T FADMRAAYDALD+ T+A + HSL+YS+ LG + Y L+
 Sbjct: 1 TEFADMRAAYDALDDDTKAEIEDLVCEHSLMYSRGS LGFTE-----YTDEKQMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

 LV+ HP R SL + HA AI GM E+ L L + A Q V+ H+W D+V+
Sbjct: 56 RLVRTHPVHRRKSLYLSSHAGAILGMSVPEARLLLLRDLTEHATQPEFVYVHKWTLHDLVM
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 = 5e-16, Method: Compositional matrix
adjust.

Identities = 50/124 (40%), Positives = 65/124 (52%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

 T F DMRA YDALD+ T+A + HSL+YS+ LG + Y L+
Sbjct: 1 TEFGDMRAGYDALDDETKAEIEDMICEHSLMYSRGSGLGFLD-----YTDEEKQLFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

 LV+ HP GR SL + HA AI GM E+ L L + A Q V+ H+W D+V+
Sbjct: 56 RLVRTHPVHGRKSLYLSSHAGAIKGMTPEARLLLLRDLNEHATQPEFVYVHKWTLHDLVM
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 = 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---IGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVM
118

 + FG I + +GG AI + + R +S WH D T+
Sbjct: 67 QAFGEIVKHPTMGGKTGSAILELHSHEGGRANS-----WHTDVTFGLRP
110

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY----SQSKLGH
174

+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
Sbjct: 111 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSLQDLVDKLWAVHGNDFDYAASRVELLH
170

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
234

A Y T P+V++HPETG SLL+G +A D +S R E L
Sbjct: 171 DPVAKEYRKKYAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRVQYDTHDSNRLYEILQ
229

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ WAAGDV +WDNR H A
Sbjct: 230 AHITRENTVRWHWAAGDVAIWDNRSTQHYA 260

>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 = 5e-16, Method: Compositional matrix
adjust.

Identities = 75/268 (27%), Positives = 105/268 (39%), Gaps = 29/268 (10%)

Query: 7 QITPTGATLGATVTGVHL-ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQOITFAKRFG 65
I P +GA V GV L A L L AA L H +L F Q +S + A+ FG

Sbjct: 4 SIHPLTPPVGAEVRGVDLRAPLSAEQSEFLEAALLAHGVLFVRDQDISPADHLALARAFAFG 63

Query: 66 -----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
119

+ + G D V I V D + + WH D T++
Sbjct: 64 EPVPHPSFSPVPGFDAVNILRVTPDEEPKIDT-----WHTDMTFLEAPP
107

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG
179

G++ A V+ GG T F AAYD+L + + A HS + H
Sbjct: 108 LGSILRARVLTECGGDTLFGSTIAAYDSLSPMKRRLEGLRAAHSFTHG---FRHSLAEP
164

Query: 180 SAYIGYGMDDTTATPLR--PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW
236

A A P R P+V+VHP +G+P L + R I + ES+ L L +
Sbjct: 165 DASPRLRAAAKAHPPRVHPVVRVHPRSGKPLFVNRLFTTHILDLPRESDSLAYLYEH
224

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHR 264

Q +W+ + WDNRC +HR
Sbjct: 225 LEQPEHTCRFRWSPNAIAFWDNRCTIHR 252

Query: 256 WDNR 259
WDNR
Sbjct: 115 WDNR 118

>ref|YP_001669049.1| taurine dioxygenase [Pseudomonas putida GB-1]
gb|ABY98713.1| Taurine dioxygenase [Pseudomonas putida GB-1]
Length = 282

Score = 89.0 bits (219), Expect = 6e-16, Method: Compositional matrix
adjust.
Identities = 80/281 (28%), Positives = 113/281 (40%), Gaps = 42/281 (14%)

Query: 6 LQITPTGATLGATVTGVHLATL--DDAGFAALHAAWLQHALLI FPGQHLSNDQQITFAKR 63
+ I +GA V+GV+LA DD FA L LQH +L QH S + + FA+R
Sbjct: 1 MHIEQLTCAIGA EVSGVNLADAIHDDDLFAQLRQQLLQHRVLF LRDQHFSRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHS-PAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122
FG +E VA S+ + G V+ + P + +D + AWH D+T+ G
Sbjct: 61 FGELE----DHPVAGSDPEHPGLVQIYKRPDQPNDRYE-----NAWHTDATWREAPPMGC
111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYS-----QSKLGHV
175
V P VGG T +A+M AY+ L +A + ARHS+ S + +L
Sbjct: 112 VLRCVECPPVGGDTLWANMVLAYENLPSEVKANIEGLRARHSIEASFGAAMPLEKRLALK
171

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----
229
Q A P+V+ HPETG L + + RF
Sbjct: 172 AQFPDAE-----HPVVRTHPETGEQVLFVNAFTTHFSNYHTPQVRVRFQDANP
219

Query: 230 -----LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L L+ A +W V +WDNR H A
Sbjct: 220 GAGDLLRYLISQAYLPEYQVRWRWKPN SVAIWDNRSTQH YA 260

>ref|YP_337380.1| putative alpha-ketoglutarate-dependent taurine
dioxygenase
[Burkholderia pseudomallei 1710b]
ref|ZP_04955608.1| dioxygenase, TauD/TfdA family [Burkholderia
pseudomallei 1710a]
gb|ABA53737.1| putative alpha-ketoglutarate-dependent taurine dioxygenase
[Burkholderia pseudomallei 1710b]
gb|EET05130.1| dioxygenase, TauD/TfdA family [Burkholderia pseudomallei
1710a]
Length = 381

Score = 89.0 bits (219), 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: 96 LSIRPLSGHIGAEVQGIQLGSQMAPNDIRF--ITQALLTHRVIFFRRQHHLDDLAQELFA
153

Query: 62 KRFGAIER---IGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVM
118
+ FG I + +GG AI + + R +S WH D T+
Sbjct: 154 QAFGEIVKHPTMGGKTGSAILELHSHEGGRANS-----WHTDVTFGLRP
197

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVY----SQSKLGH
174
+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
Sbjct: 198 PKLSVLRALALPDAGGDTVWANTVAAYQHL PSSLQDLVDKLVAVHGNDFDYAASRVELLH
257

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
234
A Y T P+V++HPETG SLL+G +A D +S R E L
Sbjct: 258 DPVAKEYRKKYAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRVQYDTHDSNRLYEILQ
316

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
+ WAAGDV +WDNR H A
Sbjct: 317 AHITRLENTVRWHWAAGDVVAIWDNRSTQHYA 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 = 6e-16, Method: Compositional matrix
adjust.
Identities = 51/125 (40%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
195
T FADMR AYD LD TRA + HSL+YS+ +G + + P+R
Sbjct: 1 TEFADMRNAYDTLDAKTRAQIENLVCEHSLIYSRGSMGFTE-----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]
 gb|ABB60709.1| taurine dioxygenase [Shigella dysenteriae Sd197]
 Length = 283

Score = 89.0 bits (219), Expect = 6e-16, Method: Compositional matrix
 adjust.

Identities = 74/288 (25%), Positives = 122/288 (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 LSITPLGPYIGAQISGADLTRSLSDNQFEQLYHAVLRHQVVFLRDQAITPQQORALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVM
 118

G + G D + + + D +P + D+ WH D T++
 Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP
 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
 178

GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++
 Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPPEYKY-RKT
 167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVD
 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 HITKPEFQVRWRWQPNDIAIWDNRVTVQHYANADYLPQRRIMHQATILG 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 = 6e-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 LPYTRFTLTPTTPTIGAEISGISLSGQLSDETMSELRRALLEWKVLFRRDQTIERSEHRD 97

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMA
 119

FA R+G++E+ +AD D M + N WH D ++ +

Sbjct: 98 FASRWGSLEQHPPFFKYTQPGQSEADIVTLAK-----DAMTGGVENN--WHNDVSWHEFPS
150

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG
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 VAKLRPQFP AVR---HPVVRVIPETGRKVLVFNLSFTQRI VGVPEAESNELLTLLYRHHVH
265

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLAG-RP 285
+ +W + WDNR H A F RVM + G RP

Sbjct: 266 RPEFQVRLKWRDTIAFWDNRTCQHYAASDYFPARRVMDRISIVGDRP 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 = 6e-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 LDIHPVAGRIGAEIRGIRLSGDLDAATVEAIQQALVQYKVVFFREQTHLDDQSQEAF AHL 74

Query: 64 FGAIERIGGGDIVAISNVK----ADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMA
119

G E I + + DGT Q + + WH D T++
Sbjct: 75 LG--EPIAHPTVPVRDGTRELFMELDGTGRQRANS-----WHTDVT FVDA YP
118

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG
179

+ +V + + P GG T +A+ +AY+ L RAL A HS Y + L A
Sbjct: 119 KASVLRVSLAPKSGGDTVWANTSSAYNDLSVELRALADNLWAVHSNEYDYAALKPDVSAE
178

Query: 180 --SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA
237

AY T P+V+VHP +G +LL+G + G A+S + L
Sbjct: 179 RLEAYRKVFTSTVYETEHPVVRVHPVSGEKTLLLGHFVKRLKGY SQADSTQLFNLLQSHV
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 = 6e-16, Method: Compositional matrix
adjust.

Identities = 51/125 (40%), Positives = 66/125 (52%), Gaps = 11/125 (8%)

Query: 138 FADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---PL
194

F DMRAAYDALD+ T+A + HSL+YS+ LG ++ Y D A L
Sbjct: 2 FGDMAAYDALDDDTKAEIEDMICEHSLMYSRGLG-----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 QRLXRTHPVHRRKSLYLSSHAGAIKGMSPPEARLLLRDLTEHATQREFVHIHKWTVHDLV
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 = 6e-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 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFLRDQTITPQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM
118

G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP
108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
178

GA+ +A+ +P+ GG T + AAY+AL R L++ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGLAAYEALSVPFRQLLNGLRAEHDFRKSFPYKY-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 AHITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 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 = 6e-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 LSITPLGPYIGALVSGADLTRPLSDNQFEQLYHAVLRHQVVFVFLREQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
 118

 G + G + + + + D +P + D+ WH D T++
 Sbjct: 65 GDLHIHPVYPHAEGVEEIIIVLDTHND-----NPPDNDN-----WHTDVTFIETP
 108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSL--VYSQSKLGHVQ
 176

 GA+ +A+ +P+ GG T +A AAYDAL E R L+ A H + + K
 Sbjct: 109 PAGAILAAKELPSSGGDTLWASGIAAYDALSEPFRQLLSGLRAEHDFRKSFPYKYRKT
 168

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVD
 235

 + ++ + L P+V+ HP +G+ +L + I + ESE L G +
 Sbjct: 169 EEHQRWLE-AVAKHPPLLHPVVRTHPVSGKLALFVNEGFTTRIVDVTEKESEALL-GFLF
 226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 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 = 7e-16, Method: Compositional matrix
 adjust.

Identities = 75/268 (27%), Positives = 111/268 (41%), Gaps = 13/268 (4%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59

Sbjct: 4 +A TL +TP +GA V G+ L L D+ AAL A + H +L F Q L+ Q
IALPTLVLTVPSPAIGARVEGLDLTRPLSDSEAAALERALVAHQVLFENQPLTPQAQRA 63

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMA
119

Sbjct: 64 FAARFGQLHVHPIYPKVPEQPEIMVLDTGPHNPSD-----NDVWHTDVTICIENPP
113

Query: 120 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAG
179

Sbjct: 114 AIVALSGKLIPPVGGDTVWASNIAAYNGLSEPIRRLLEPLKALHDFTRSFPEWRHNGDPE
173

Query: 180 S-AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWA
237

Sbjct: 174 THARWKAAREKHPPVHVHPVIRTHPVSGAKALFVNENFTSRIVGLSDRESAAILDFLYDHV
233

Query: 238 CQAPRVHAHQWAAGDVVVDNRCLLHRA 265

Sbjct: 234 SRPEFTVRWRWKTDDLVLWDNRSTQHYA 261

>emb|CAY27424.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 88.6 bits (218), Expect = 7e-16, Method: Compositional matrix
adjust.

Identities = 51/127 (40%), Positives = 68/127 (53%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---
192

Sbjct: 1 TEFGDMRAAYDALDDETKAEIEDMICESHLSMYSRGS LG ++ Y + A
TEFGDMRAAYDALDDETKAEIEDMICESHLSMYSRGS LG-----FLDYSDEEKAMFKP 52

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD
252

Sbjct: 53 VLQRLVRTHPVHRRKSLYLSSHAGAIQGMSPPEARLLLLRDLTEHATQREFVYVHKWTLHD
112

Query: 253 VVVWDNR 259
+V+WDNR

Sbjct: 113 LVMWDNR 119

>ref|YP_002411171.1| taurine dioxygenase [Escherichia coli UMN026]
emb|CA11623.1| taurine dioxygenase, 2-oxoglutarate-dependent
[Escherichia coli
UMN026]

emb|CBG33235.1| alpha-ketoglutarate-dependent taurine dioxygenase
 [Escherichia coli
 042]
 Length = 283

Score = 88.6 bits (218), Expect = 7e-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 LSITPLGPYIGAQITGADLTRPLSDNQFEQLYHAVLRHQVVFLREQAITPQQORALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVM
 118
 G + G D + + + D +P + D+ WH D T++
 Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP
 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
 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 EEEHQRWREAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESALLSFLFA
 227

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
 + +W D+ +WDNR H A R+M + + G
 Sbjct: 228 HITKPEFQVRWRWQPNDIAIWDNRVTDHYANADYLPQRRIMHRATILG 275

>gb|ACG80581.1| TfdA [uncultured bacterium]
 gb|ACG80582.1| TfdA [uncultured bacterium]
 Length = 118

Score = 88.6 bits (218), Expect = 7e-16, Method: Compositional matrix
 adjust.

Identities = 51/123 (41%), Positives = 66/123 (53%), Gaps = 7/123 (5%)

Query: 138 FADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAAGSAYIGYGMDDTTATPLRP-
 196
 F DMRAAYDALD T+A V HSL+YS+ +G + P+R
 Sbjct: 2 FGDMAAYDALDARTKAEVEDLICEHSLIYSREAIGFNALTEEEIAAF-----KPVRQR 55

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVD
 256
 LV+ HP TGR SL + HA AI G E+ FL L + A Q V++H+W D+V+W
 Sbjct: 56 LVRTHPVTGRKSLFLSSHAGAIVGWTIPEARMFLRDLTEHATQPAFVYSHEWRPHDLVMW
 115

Query: 257 DNR 259
 DNR
 Sbjct: 116 DNR 118

>ref|YP_001610738.1| putative taurine dioxygenase [Sorangium cellulosum
 'So ce 56']
 emb|CAN90258.1| putative Taurine dioxygenase [Sorangium cellulosum 'So ce
 56']

Length = 327

Score = 88.6 bits (218), Expect = 7e-16, Method: Compositional matrix
 adjust.

Identities = 76/291 (26%), Positives = 119/291 (40%), Gaps = 28/291 (9%)

Query: 6 LQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 +Q+ P +GA + G ++ L D A+ AA L+ ++ F Q L + +QI FA RF
 Sbjct: 10 IQVKPLAGHIGAEIHGADISKPLPDEAVTAIRAALLKWKVVFFRNQPLGHAEQIAFAARF 69

Query: 65 GAIERIGGGDIVAISNVKADGTVRQH-----SPAEWDDMMKVIVGNMAWHADSTYMPV
 117

G V ++ D +H S + WH D T
 Sbjct: 70 GE-----VTYAHPEDEPFDEHPEILAIIDSRRYDRRYGRRFSYENRWHTDVTAAVN
 120

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQ
 177

++ A ++P GG T + ++ AAY+ L RALV A H + Q
 Sbjct: 121 PPAASILRAHILPPYGGDTTWTNLVAAAYEGLSAPVRALVDGLRAEHRFGLRFAP----QD
 176

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEGLVD
 235

S Y+ + + P+V+VHPETG +L + G +H + G+ ES L+ L +
 Sbjct: 177 QDSPYLKRVRENPLISIHVVRVHPETGERALFVSPGFTSHIV-GLSPRESSAILDLLFE
 235

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWD---FKLPRVMWHSRLAG 283

+ +W G + WDNR H P D + RV++ L G
 Sbjct: 236 QISRPAYTVRFRWEPGSIAFWDNRATAHLG-PQDLGHLDVERVLYRVTLTG 285

>emb|CAY27514.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 88.6 bits (218), Expect = 8e-16, Method: Compositional matrix
 adjust.

Identities = 50/125 (40%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
 195

T FADMRAAYDALD+AT+A + HSL++S+ LG + + T P+R
 Sbjct: 1 TEFADMRAAYDALDDATKAEIEDLVCEHSLIFSRGSLGFTE-----LSEEEERATFRPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

 LV+ HP TGR L + H I G E+ FL L++ A Q ++H+W D+V
Sbjct: 55 QRLVRAHPVTGRKPLFLSSHGTTILGWVPPEARAFRLRDLMEHATQPQFAYSHKWRQWDLV
114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>ref|XP_002151041.1| alpha-ketoglutarate-dependent 2,4-
dichlorophenoxyacetate

 dioxygenase, putative [Penicillium marneffei ATCC 18224]
gb|EEA20041.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
 dioxygenase, putative [Penicillium marneffei ATCC 18224]
 Length = 337

Score = 88.6 bits (218), Expect = 8e-16, 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 NSAFGAEVSGVDWENPVPAETVAQLVALQDKYGVLIFFRETGLDNARHIAFSQQLGESLEV 99

Query: 68 -----ERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVM
118

 +R+G + + N++ D T+ ++ W + GN WH DS+Y
Sbjct: 100 NPFYYGRENDRLEPPLFDVGNIELDRTLVKNESRRWHHSL----GNALWHTDSSYHQQR
155

Query: 119 AQGAVFSAEVPVAVGGR-TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
177

 ++ ++ + P GG T FAD R AY L E + + H L +S+ KL
Sbjct: 156 SKYSILLSHGPNPVKGGSWTHFADTRRAYADLPETKKKEIEDLIVEHDLWHSR-KLASPIV
214

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA
237

 G + + + LV+ P GR +L + HA I G ES++ + L+D
Sbjct: 215 YGDP-LPHELAAKPPAYHRLVQTAP-NGRRTLYLAAHAKLILGQSFEESSQKLIWELIDHC
272

Query: 238 CQAPRVHAHQWAAG-DVVVWDNRCLLHRAEPW 268

 Q V + +W +G D+V WDNR +HRA P+
Sbjct: 273 TQPKYVFSMEWLSGGDMVWWDNRQSMHRANPY 304

>emb|CAY27257.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 88.2 bits (217), Expect = 9e-16, Method: Compositional matrix adjust.

Identities = 51/125 (40%), Positives = 70/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALD+A +A + Q HSL++S+ LG + + P+R
Sbjct: 1 TEFADMRAAYDALDDAMKAEIEQVVCEHSLMFSRGALGFSE-----LNEQEQA MFRPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

LV+ HP TGR SL + HA I E+ FL L++ A Q V++H+W D+V
Sbjct: 55 QRLVRTHPVTGRKSLFLSAHAGGIVNWPVPEARAFRLDLMEHATQPRFVYSHKWRQWDLV
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 = 9e-16, Method: Compositional matrix adjust.

Identities = 51/125 (40%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALDE + + HS +YS+ KLG T + P+R
Sbjct: 1 TEFADMRAAYDALDERLKQQIEDLVCLHSNMYSRGKLGGLADFTDEER-----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 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEGRMLLLDLTEFATREQFVYSHMWRVNDV
114

Query: 255 VWDNR 259

+WDNR

Sbjct: 115 MWDNR 119

>emb|CAY27220.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 118

Score = 88.2 bits (217), Expect = 9e-16, Method: Compositional matrix adjust.

Identities = 49/124 (39%), Positives = 69/124 (55%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALD T+AL+ HS ++S+ LG ++ + A +
Sbjct: 1 TEFADMRAAYDALDAKTKALIEDLVCEHSRIFSKGALGF-----SFTEEEVKAFAPVRQ 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

 LV+ HP+TGR SL + +A I G E+ L L + A Q V++H+W GD+V+
Sbjct: 55 RLVTRHPKTGRKSLEYLSSYAGRIVGWPVPEAMLLLRELTEHATQREFVYSHKWRVGDLM
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 = 9e-16, 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--QIHGLERAHLTDAAVREELNRLWIRHGLVVFRGMDDSDDELHIELSRVFGP 66

Query: 67 IE----RIGGGDI--VAISNVKADGTVRQHSPA EWDDMMKVIVGN-----MAWHADSTYM
115

 + + G D + I+NV Q+ P + + G + H D Y
Sbjct: 67 FQLHPIKQGNTPSRLEITNV-----QYEPGGENGNVYTVNGVDLGGWLPLHFDLVYF
119

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL-DEATR-----ALVHQRSARHSLVYSQ
169

 + G + V+P G T F D AAY+ L DE R +V+ S + +
Sbjct: 120 DKVNHGGLLRPRVIPPEMGGTVFLDKIAAYETLPDELKRRRAEGLEVYDFYMDISTMKNS
179

Query: 170 SKLGHVQQAGSAY--IGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDDAAES
226

 + + G + I D+ + PLV E+GR L + A + G+D AE
Sbjct: 180 VDDIRLVRMGKKFRDIQQREDSYPRSIHPLVYAQKESGRKMLNLSPWFADELLGLDKAEG
239

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE 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 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
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 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMLLLLDLTEFATREPFVYSHAWRVNDLV
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 LSITPQGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFLRDQTITPQQORALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM
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 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPYKY-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 AHITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 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 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-
196

FADMRAAYDALDE T+A V HSL+++ +G + P+R
Sbjct: 3 FADMRAAYDALDERTKAEVQDLVCEHSLLSRAAVGFTEFTPEEVANF-----RPVRQR 56

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAEESERFLEGLVDWACQAPRVHAHQWAAGDVVVW
256

LV+ HP +GR SL + HA I G E+ FL L + A Q V++H W D+V+W
Sbjct: 57 LVRTHPASGRKSLFLSSHAGTIVGWTVPEARSFLRDLTEHATQREFVYSHAWRQHDLVMW
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 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALD+ T+A V HSL+YS+ +G + P+R
Sbjct: 1 TEFADMRAAYDALDDRTKAEVAGLVCEHSLLSRQAVGFDFTEFTPEEISNF-----QPVR 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAEESERFLEGLVDWACQAPRVHAHQWAAGDVV
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 TCFADMRAAYDALDEATR^LVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALD+ TRA Q HS +++ LG S + A +
Sbjct: 1 TEFADMRAAYDALDDETRAECEQLICEHSQ^LFSRAILGF-----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 RLVRRHPVTGRRSLFLASHAGAILGWPVPEARAF^LRDLTEHATQRRFVYAHVWKQWDLVM
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 TCFADMRAAYDALDEATR^LVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALDE + + HS +YS+ KLG + P+R
Sbjct: 1 TEFADMRAAYDALDERLKNQIEDLVCLHSNMYSR^GKLGLADFTDEERRVF-----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 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARM^LLLDLTEFATREPFVYSHVWRLNDFV
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 NLNIEVIKPTIGAIIHNLNIDLNALNEQTTQQIQQALLDHQVIFFRKQQLAPQAQADLARSF 66

Query: 65 G-----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
 115

G +IE + +++ + + K D + N WH D T+
 Sbjct: 67 GTLHVHPIYPSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFS
 107

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRNLVHQRSARHSL--VYSQSKLG
 173

G V A +P VGG T ++ AA+ L + + +A H + + +
 Sbjct: 108 KTPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQKRLRGLTATHDIRKSFPLERFA
 167

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG
 232

H ++ + + P+V+ HP TG P L + I + ESE+ L
 Sbjct: 168 HNEEEREKLLQ-TFKRNPPVHPVVRTHPVTGEPLELVSEGFTRINELPEQESEQLLNF
 226

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

L + A Q +W GDV +WDRNC H+A
 Sbjct: 227 LFEHATQEQFHLRRKWQDGDVAIWDNRCTQHKA 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 TCFADMRAAYDALDEATRNLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
 195

T FADMRAAYDAL++ TR + HSL+YS+ LG + Y L+
 Sbjct: 1 TEFADMRAAYDALNDETRTEIEDMICHSLSMRGSLGFLD-----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 RLVTRHPVHGRKSLYLSSHAGGIIGMSVPEARVLLRDLNEHATQPEFVYVHKWTLHDLVM
 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 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
 + I P LGA + G + +D F+A+ A+ ++++++ GQ + FA+RF 65
 Sbjct: 1 MDILPMTGGLGAEILGADIRSED--FSAIRDAFAEYSVIVLRGQTAGPGDHLAFARRF 58

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNM-----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 PAMVSILHAIEMPPYGGDTLFVSMGAAYEALSEPMMRFLDGLTAVHSSRHVFGAAAMDS-
 160

Query: 176 QQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLV
 234
 + S +G T P+V HP +GR L + I G++ ES L ++
 Sbjct: 161 EAVKSGRLGNAAATQDVRHPVITHPLSGRRGLFVNPVFTTRIEGLNTEESSALL-AML
 219

Query: 235 DWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
 CQ P +W AGD+ +WDNR H+A R+M + G P
 Sbjct: 220 YAHCCQQPEFQCRVRWRAGDITMWDNRATWHKAINDYHGFRLMHRVTVEGGP 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 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR
 195
 T F DMRAAYDAL++ TR + HSL+YS+ LG + Y L+
 Sbjct: 1 TEFGDMRAAYDALNDETRTEIEDMICEHSLMYSRGSGLGFLD-----YTEEEKQMFKPVLQ 58

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
 255
 LV+ HP GR SL + HA I GM E+ L L + A Q V+ H+WA D+V+
 Sbjct: 56 RLVTRTHPVHGRKSLYLSSHAGGIIGMSVPEARVLLRDLNEHATQPEFVYVHKWALHDLVM
 115

Query: 256 WDNR 259
 WDNR
 Sbjct: 116 WDNR 119

>ref|YP_587247.1| taurine catabolism dioxygenase TauD/TfdA [Ralstonia 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 MRIEPMASIGAEELVGVRLSDAIHDDGLFDEIRAALLRHKVLFLRDQDISRAEHVAFER 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHS-PAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
 122

FG +E VA S+ G V+ + P + D + AWH D+T+ G
 Sbjct: 61 FGKLE----DHPVAGSHPDHPGLVQIYKRPDQPMDRYE-----NAWHTDATWREAPPLGC
 111

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
 182

V P +GG T +A+M AY+ L + + ARHS+ S +++ +
 Sbjct: 112 VLRCVESPEIGGDTMWANMVLAYENLPAHVKTQIAGLRARHSIEASFGAAMPIEKRLALK
 171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMD----AAESER
 228

Y P P+V+VHPETG L + AH G D A E R
 Sbjct: 172 AQY-----PDPEHPVVRVHPETGKVLVFNFTTHFSNFHTPAHVRYGQDYNPGAGELLR
 226

Query: 229 FL-----EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 +L E V W +W A + +WDNR H A

Sbjct: 227 YLISQAFIPEYQVRW-----RWKANSMAIWDNRSTQHVA 260

>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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTAT---
 192

T F DMRAAYDALD+ T+ + HSL+YS+ LG ++ Y + A

Sbjct: 1 TEFGDMRAAYDALDDDTKTEIEDMICEHSLMYSRGSIG-----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 VLQRLVRTHPVHRRKSLYLSSHAGAIQGMSIPEARLLLRDLTEHATQPEFVHVHKWTLHD
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--QPDQPMDDRYEN--AWHTDATWREAPPMGCV
112

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
183

PAVG T +A+M AY+ L + + ARHS+ S +++ +
Sbjct: 113 LRCVEGPAVGADTMWANMVLAYENLPAHVKTEIAGLRARHSIEASFGAAMPIEKRLALKE
172

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LEG
232

Y P P+V++HPETG L + A R+ L
Sbjct: 173 QY-----PDPEHPVVRIPHETGEKVLVFNFTTFTNFHTAAHVRYGQDYNPGGADLLRY
227

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

LV A +W + +WDNR H A
Sbjct: 228 LVSQAFIPEYQVRWRWKPNMAIWDNRSTQHVA 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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---
192

T FADMRAAYDALD T+A + HSL+YS+ LG ++ Y + A
Sbjct: 1 TEFADMRAAYDALDNDTKAEIDDMICEHSLMYSRGS LG-----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 VLQRLVVRTHPVHRRKSLYLSSHAGAIQGMSPPEARLLLRDLTEHATQPEFVYVHKWTLHD
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 MRVEPLTCAIGAELSGVSLADAVHDDGLFAEIRALLLKHVRVLFRLDQDITRAEHVAFARR 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 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

V P VGG T +A+M AY+ L + + ARHS+ S + + +
Sbjct: 112 VLRCVACPPVGGDTMWANMALAYENLPGHVKRQIDGLRARHSIEASFGAAMPIDKRLALK
171

Query: 183 IGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LE
231

Y P+V+ HPETG L + E RF L+
Sbjct: 172 TQY-----PDAEHPVVRTHPETGEKILYVNAFTTHFTNFHTPERVRFQDANPGAGQLLQ
226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

L+ A +WA V +WDNR H A
Sbjct: 227 YLISQAYIPEYQVRWRWAKHSVAIWDNRSTQHVA 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 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFLRDQTITPQQORALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVM
118

G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP
108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
178

GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + +
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPYKYRKYRTE
168

Query: 179 GSAYIGYGMDTTATP-LRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDW
236

+ P L P+V+ HP +G+ +L + I + ESE L G +
Sbjct: 169 EEHQRWHEAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESALL-GFLFA
227

Query: 237 ACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

P +W D+ +WDNR H A R+M + + G
Sbjct: 228 HITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 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
O103:H2 str. 12009]
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
O103:H2 str. 12009]
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 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFLRDQTITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
118

G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP
108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
178

GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPPEYKY-RKT
167

Query: 179 GSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVD
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 AHITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|YP_586764.1| taurine catabolism dioxygenase TauD/TfdA [Ralstonia 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 MQVNPLTCSIGAELAGVSIADVARDDTLFAEIKALLLKHRLVFFRDQDISRADHVAFKR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

FG +E VA S + G + + + D +H D+++ +GAV
Sbjct: 61 FGDLE----DHPVANSVPEHPGLIEIYKSEKRDHFEN-----TYHTDASWRACPPKGAV
110

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYI
183

P VGG T + +M AY L E + + A+H + +S + ++
 Sbjct: 111 LRCISCPDVGGDTIWVNMVEAYKHLPEDIKVKIAGLRAKHGIEHSFGAIMTTEEREEL--
 168

Query: 184 GYGMDDTTATPL--RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----L
 230

PL P+V+ HPETG L +G + E+ RF L
 Sbjct: 169 -----VRKNPLVDHPVVRTHPETGEKILYVGGPFSTHFINYHTPENVRFGQDKTPGASLLL
 223

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285
 L+ A +W V +WDN H A + PR M + + G RP

Sbjct: 224 NYLISQAAIPEYQVRFRWKPNSVALWDNVSTQHYAVSDYWPAPRRMERATIKGDRP 279

>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---IGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVM
 118

+ FG I + +GG AI + + R +S WH D T+
 Sbjct: 224 QAFGEIVKHPTMGGKTGSAILELHSHEGGRANS-----WHTDVTFGLRP
 267

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVY----SQSKLGH
 174

+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
 Sbjct: 268 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSLQDLVDKLVAVHGNDFDYAASRVELLH
 327

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
 234

A Y T P+V++HPETG SLL+G +A D +S R E L
 Sbjct: 328 DPVAKEYRKKYAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRVQYDTHDSNRLYEILQ
 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 LAVRPLQPTIGAEISGVDLRYPLTDEVDRDQIRATILKYKVVFFRDQELTREEHEAFARF 74

Query: 65 GAIERIGGGDIVAISNVKADGT-VRQHSAPAEWDDMMKVIV---GNMAW---HADSTYMPV
117
G + G +++ T + + + A++ D + + +W H D+++ V
Sbjct: 75 GPLYPHPSGPKAPLNSAGRATSIHRIAADFKDYERARATADADESWDAYHTDTSWRLV
134

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
177
GAV A +P +GG T + D AY+AL + + + R H +
Sbjct: 135 PTWGAVLRAVTLDPDIGDGIWVDAGLAYNALSDDVKERLAGRHVTHDF-----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 ACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
+ W G V WDNR +H A PRV+ +A P
Sbjct: 241 YRKPEHQVRFVSWRPGSVAFWDNRATVHYAVRNYGDFPRVLERILIAEEP 289

>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 = 1e-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 LSITSLGPYIGAQITGADLTRPLSDNQFEQLYHAVLRHHVVFRLRDQTITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM
118
G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIQTP
108

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
178

GA+ +A+ +P+ GG T +A AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWASGIAAYEALSVPFRQLLSGLRAEHDFRKSFPPEYKY-RKT
167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD
235

+ + + P L P+V+ HP TG+ +L + I + ESE L G +
Sbjct: 168 EAEHQWRREAVAKNPPLLHPVVRTHPVTGKQALFVNEGFTTRIVDVSEKESEALL-GFLF
226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

P +W D+ +WDNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|ZP_04332111.1| Probable taurine catabolism dioxygenase [Nocardiopsis
dassonvillei

subsp. dassonvillei DSM 43111]

gb|EEK36424.1| Probable taurine catabolism dioxygenase [Nocardiopsis
dassonvillei

subsp. dassonvillei DSM 43111]

Length = 303

Score = 87.8 bits (216), Expect = 1e-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: 5 TDLSLRPVAGRIGAEISGVRLGPDLDGATVASIRAALLAHKVVFFRDQRHLTDETQAGFA 64

Query: 62 KRFGAIER-----IGGGD--IVAINVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
112

G + GGD ++ I + + +WH D
Sbjct: 65 ALLGPLTTPHPTTGAAFGGDHHLVLPIDSERGKAN-----SWHTDV
104

Query: 113 TYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY-----
167

T++ Q +V A +P GG T +A+ AY L + + L A H+ Y
Sbjct: 105 TFVDRPPQASVLRVHLLPPRGDVTWANTATAYQDLPQPLKDLADGLRAVHTNDYDYAAV
164

Query: 168 --SQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAE
225

+ G +++ A++ T P+V+VHPETG L +G A G+ + +
Sbjct: 165 APEREPTGDLRKYREAFVSTLFKTE----HPVVRVHPETGERVFLGHFAQHFTGLSSKD
220

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ L +A W GDV VWDNR H A

Sbjct: 221 FHHLFDLLQQRVTRAENTVRWSWREGDVAVWDNRATQHYA 260

>ref|ZP_06120735.1| Taurine dioxygenase [Caulobacter segnis ATCC 21756]
 gb|EEZ37220.1| Taurine dioxygenase [Caulobacter segnis ATCC 21756]
 Length = 285

Score = 87.8 bits (216), Expect = 1e-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 FGAEISGIDLASAPDAALDQVVDTFHRHGAIALRGQKMT PDDLRFIFRFGDPEDHTQTR 75

Query: 70 ---IGGGDIVAISNVKADGT-VRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
 125

G I +SN DG + H+ + WH D +Y P +
 Sbjct: 76 FTLPGYPKIFILSNRVVDGKPIGAHN-----DGVGWHTDYSYKPEPVMLTMLY
 123

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVY--SQSKLGHVQQAGSAYI
 183

A VP G T AD AA++AL +AL+ HS + + + G Q
 Sbjct: 124 AVEVPDEGSDTLLADGCAAWNALPADKQALLEGRLRHHSYKHFMATRQFGQQQTLSPLE
 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 = 1e-15, Method: Compositional matrix
 adjust.

Identities = 61/209 (29%), Positives = 94/209 (44%), Gaps = 10/209 (4%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
 115

QQI FA+ FG I+ ++ + GTVR+ + + GN WH D ++
 Sbjct: 1 QQIAFAQGFGFEIDVDPTAGMLPVPGYPEIGTVRKEP-----EQTRNTGGN--WHTDHSFD 53

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHV
 175

P+ G++ A +P GG T FA M AAYDAL + + + +A H+ + + L

Sbjct: 54 PIPPLGSILVARDLPDTGGDTLFASMYAAYDALSDGLKKTLEGMNAVHAKTRAFALPKE
113

Query: 176 QQAGSAYIGYGMDDTTAT--PLRPLVKVHPETGRPSLLIG--RHAHAIPGMDAAESERFLEG
232

+Q +A A + P+V HPE+GR L + + G ES L+
Sbjct: 114 RQVSAAEHAEIQARFAARDAIHPVVPRHPESGRRLLFVNPNYTTRFEGWTEQESAPLLDY
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 = 1e-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 GTAIGATVEGFDHATASDADIAALKSTVYTKKIAVLKQDLSPQEFLELGKRLGRPETYY 67

Query: 72 G-----GDIVAISNVKADGTVRQHSPAEWDDMMKVI VGNMAWHADSTYMPVMAQGAV
123

+I SNV +G + V WHAD +MP +
Sbjct: 68 EPMYHHPEVTEIFVSSNVPENK-----QIGVPKTGKFWHADYQFMPDPFGITL
116

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL-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(DE3)]
ref|YP_003043545.1| taurine dioxygenase [Escherichia coli B str. REL606]
ref|YP_003076385.1| taurine dioxygenase, 2-oxoglutarate-dependent [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]
gb|AAG54718.1|AE005216_6 taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli O157:H7 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| tauD [Escherichia coli BL21(DE3)]
 gb|ACT30293.1| Taurine dioxygenase [Escherichia coli BL21(DE3)]
 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]
 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-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVM 118
 G + G D + + + D +P + D+ WH D T++
 Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA 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 EEEHQRWREAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESALL-GFLF 226

Query: 236 WACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
 P +W D+ +WDNR H A R+M + + G
 Sbjct: 227 AHITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|ZP_06234914.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. Eu11c]
 gb|EFA63831.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp. Eu11c]

Length = 304

Score = 87.8 bits (216), Expect = 1e-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 PLSDRFGVEVRGLNLANVTDEDSSSLRGLLLRHGVVAVPDQILDPDQHIALAARFG---R 88

Query: 70 IGGGDIVAIISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVS
 129
 + V +A ++ WD G AWH+ YMP A V V
 Sbjct: 89 VTPSSAVIPGLNRAYPQIKVIDSRRWDG-----GLDAWHSVMQYMPEPAAVLVLYLRVA
 142

Query: 130 PAVGGRTCFADMRAAYDALDEATRA-LVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
 188
 P G + +AYDALD +A L R H+ + +++ G
 Sbjct: 143 PPGGTTLRWLSRESAYDALDPDLKARLRGVRGVHHPALDE----YLRAFPGPRWNGRTI
 198

Query: 189 TTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH
 246
 T P+ P+V+VHPETGR L I A+ G+ AA+ R LE LVD ++
 Sbjct: 199 TRVDPVEHPVVRVHPETGRLGLFIDPWSTQALVGVPAQAQRLLERLVDHLTSPEHEASY
 258

Query: 247 QWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 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]

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
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]
Length = 283

Score = 87.8 bits (216), Expect = 1e-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 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFLRDQAITPQQORALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
118

G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP
108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQA
178

GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPPEYKY-RKT
167

Query: 179 GSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVD
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

>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 = 1e-15, Method: Compositional matrix adjust.

Identities = 78/287 (27%), 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: 3 VTPLGPHIGALVENINIARPLGDGQFEQLYHALLKHQVLFVRNQPITPLQQRELAGRFGD 62

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMA
119

+ +I+ + ++P + D+ WH D T++
Sbjct: 63 LHIHPVYPHTKECEEIIVLD-----THDNNPPDNDN-----WHTDVTFIDHPP
105

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYS--QSKLGHVQQ
177

GA+ +A+ +PA GG T ++ AAYDAL + L+ A H +S + K +
Sbjct: 106 LGAILAAKQLPATGGDTLWSSGVAAYDALSAFQKQLLAGLRAEHDFAHSFPEHKNRGTPE
165

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW
236

++ + L P+V+ HP TGR +L + I + A ES+ L L
Sbjct: 166 EHQRWL-LAKERNPPLLHPVVRTHPVTGRQALFVNEGFTTRIVDLSAKESDAILRLLFAH
224

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPVVMWHSRLAG 283

A + +W DV +WDNR H A RVM + + G
Sbjct: 225 ATKPEFQVRWRWQQDDVAIWDNRVTQHYANADYLPQRRVMHRATILG 271

>ref|ZP_02493042.1| putative alpha-ketoglutarate-dependent taurine
dioxxygenase

[Burkholderia pseudomallei NCTC 13177]
Length = 381

Score = 87.8 bits (216), Expect = 1e-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--ITQALLTHRVIFFRRQHHLDDLAQELFA
153

Query: 62 KRFGAIER---IGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVM
118

+ FG I + +GG AI + + R +S WH D T+
Sbjct: 154 QAFGEIVKHPTMGGKTGSAILELHSHEGGRANS-----WHTDVTFFGLRP
197

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVY----SQSKLGH
174

+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
Sbjct: 198 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSLQDLVDKLVAVHGNDYDFAASRVELLH
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 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 = 1e-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 SIQVKPLSAHIGAEHLGVDLTRKLDPSEVAQIRAALLRWRVVFREQFLTHEQHVAFSAQ 70

Query: 64 FG--AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
 121

FG + G + V + R+ + E +++ G WH D T
 Sbjct: 71 FGEPTLGHVPVFGHVDGHPEVYSISKYRKATRFEGQALLRPWTG---WHTDVTAAALNPPWA
 127

Query: 122 AVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
 181

++ +P GG T + ++ AY+ L RA V H G A
 Sbjct: 128 SILRGVTIPPYGGDTQWTNLALAYEKLSAPLRAFVDGLRGVHRFTPPAGASG-----TEA
 182

Query: 182 YIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQA
 240

++ PLV+VHPETG L + +I G+ ESE LE L + A +
 Sbjct: 183 FVKAVEQRVLVTEHPLVRVHPETGERVLYVSPSFLKSIVGVTPRESEALLELLWEHATRP
 242

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRA--EPWDFKLPRVMWHSRLAG 283

+W AG V WDNR H A + +D R ++ + L G
 Sbjct: 243 EFTVRFKWEAGSVAFWWDNRATAHLAPTDFDLDFDRQLYRTTLVG 287

>ref|YP_587420.1| taurine catabolism dioxygenase TauD/TfdA [Ralstonia
 metallidurans
 CH34]

gb|ABF12151.1| taurine dioxygenase [Cupriavidus metallidurans CH34]
 Length = 281

Score = 87.8 bits (216), Expect = 1e-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---RQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
 120

G +E D + +V G V R +P +++ ++H D + P A
 Sbjct: 62 GKLE-----DHPVVGSPDPYPLVGVYRSDNPHSFEN-----SYHCDGLWRPNPAM
 107

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGS
180

GAV P +GG T + +M AY+ L + ++ + AR S+ +S + +
Sbjct: 108 GAVLRCLCEPEIGGDTIWNMVKAYEELPDEIKSKIDGLRARASIEHSFGAVMTPENRAK
167

Query: 181 AYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGRH-----AHAI PGMDAAESER
228

+ P+ P+V++HPETG L +G A+ G+D +
Sbjct: 168 -----LAQDHPPEVHPVVRHPETGEKILFVGASFTTHTFTNYSTPANVRHGIDKSPGAS
221

Query: 229 FLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

L + P W GDV VWDNR H A + PR M + + G
Sbjct: 222 LLLNYLTSRATIPEYQVRWAWQEGDVAVWDNRSTQHYAVNDYYPAPRKMERAGIVG 277

>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]
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 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFLRDQTIAPQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM
118

G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP
108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAA
178

GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGLAAYEALSVPFRQLLSGLRAEHDFRKSFPYKY-RKT
167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVD
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 AHITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>emb|CAY27347.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 87.4 bits (215), Expect = 1e-15, Method: Compositional matrix
adjust.

Identities = 52/128 (40%), Positives = 72/128 (56%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

 T FADMRAAYDALD+AT+A HSL+++S+ +LG + + D +R
Sbjct: 1 TEFADMRAAYDALDDATKAETEGLVCEHSLMFSREQLG-----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 PVRQRLVVRTHPVVTGRKSLFLAAHIGSIVGWPVPEARAFIRDLMEHATQPRFVYHRWQQW
111

Query: 252 DVVVWDNR 259

 D+V+WDNR
Sbjct: 112 DLVMWDNR 119

>ref|ZP_04002432.1| taurine dioxygenase [Escherichia coli 83972]
gb|EEJ49179.1| taurine dioxygenase [Escherichia coli 83972]
Length = 283

Score = 87.4 bits (215), Expect = 1e-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 LSITSLGPYIGAQITGADLTRPLSDNQFEQLYHAVLRHHVVFRLDQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVM
118

 G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIQTP
108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
178

 GA+ +A+ +P+ GG T +A AAY+AL R L+ A H S + + ++

Sbjct: 109 PAGAILAAKELPSTGGDTLWASGIAAYEALSVPFRQLLSGLRAEHDFRKSFPPEYKY-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 AHITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>emb|CAY27376.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 117

Score = 87.4 bits (215), Expect = 1e-15, Method: Compositional matrix
adjust.

Identities = 49/123 (39%), Positives = 68/123 (55%), Gaps = 6/123 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
195

 T FADMRAAYDALD T+AL+ HS ++S+ LG ++ + A +
Sbjct: 1 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 RLVVRTHPKTGRKSLYLSSHAGRIVGWPVPEAMLLLRELTEHATQREFVYSHKWRVGDLMV
114

Query: 256 WDN 258

WDN

Sbjct: 115 WDN 117

>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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
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 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDALD+ T+A + HSL+YS+ LG + Y + L+
Sbjct: 1 TEFCDMRAAYDALDDETKAEIDDLVCEHSLMYSRGLGFTE-----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 RLVRTHPVHRRKSLYLSSHAGKIVGMSVPEGRLLLRDLNEHATQSEFVYVHKWKLHDLVM
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 MQINPLTCAIGAELVDVQLADALRDDGLFAEIKAAALLKHKVLFRLRHQRISRAEHVGFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG +E V S+ G V+ + +P + D + +WH D+T+ V G
Sbjct: 61 FGELE----DHPVVGSDPDHPGLVQIYKTPDKPLDRYE-----NSWHCDATWREVPPMGC
111

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSL--VYSQSKLGHVQQAGS
180

V P VGG T +A+M AY+ L + ++ ARHS+ + + H + A
Sbjct: 112 VLRCVECPPVGGDTMWANMALAYEMLPSHIKDVIAPLRARHSIECTFGAAMPAHKRLALK
171

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-----RHAHAIPGMDAAE-SERF
229

A P+V+ HPETG L + A+ G D + S
Sbjct: 172 AQFPDAE-----HPVVRTHPETGKVLVSVGFTTHTFTNFHTPANVRVVGQDFTQGSSSL
224

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

L+ L+ A +W G + +WDNR H A
Sbjct: 225 LQFLISQAAIPEYQVRWRWEPGSAIWDNRATQHYA 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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
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 RLVVRTHPKTGRKSLYLLSHAGRIVGWPVPEAMLLLRELTEHATQREFVFSHKWRVGDLMV
114

Query: 256 WDNR 259

WDNR
Sbjct: 115 WDNR 118

>ref|ZP_05520940.1| putative 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 IERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
126

R+ G + + ADG R P + + + WH D T++P ++ A
Sbjct: 69 FGRLGEPVAHPTVPSADG--RYAFPIDNEHGGRA----NQWHTDVTTFVPAYPAFSILRA
122

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRAL-----VHQRSARHSLVYSQSKLGHVQQAGS
180

EV+P GG T +++ AAY L E R L VH ++ + +++ +
Sbjct: 123 EVIPPYGGNTLWSNTAAAY AHLPEPLRVLADSLRGVHTNDYDYAATRPDASAAALERHLT
182

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA
240

+ T P+V+VHPETG +L++G + G + +S ++ L +
Sbjct: 183 VFTAIFQTE----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]
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 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFLRDQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVM
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 PAGAILAAKELPSTGGDTLWTS GIIAAYEALSVPFRQLLSWLRAEHDFRKSFPYKY-RKT
167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD
235

+ + P L P+V+ HP +G+ +L + I + ESE L G +
Sbjct: 168 EEEHQRWREAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESALL-GFLF
226

Query: 236 WACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
P +W D+ +WDNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---
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 VLQRLVVRTHPVHRRKSLYLSSHAGAIQGMSVPEGRLLLRDLNEHATRPEFVYAHKWTLHD
112

Query: 253 VVVDNR 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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
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 RLVVRTHRKTGRKSLYLTSAGRIVGWPVPEAMLLRELTEHATQREFVYSHKWQVGD 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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDAL++ TR + HSL+YS+ LG + Y L+
Sbjct: 1 TEFADMRAAYDALNDETRTEIEDMICEHSLMYSRGLGFLD-----YTEEEKQMFKPVVQ 55

Query: 196 PLVKVHPETGRPSELLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

LV+ HP GR SL + HA I GM E+ L L + A Q V+ H+W D+V+
Sbjct: 56 RLVTRHPVHGRKSLYLSSHAGGIIGMSVPEARVLLRDLNEHATQPESVYVHKWTLHDLVM
115

Query: 256 WDNR 259

WDNR

Sbjct: 116 WDNR 119

>gb|ACI70549.1| taurine dioxygenase [Escherichia coli]

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 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFVLRDQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM
118

G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP
108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
178

GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHYFRKSFPEYKY-RKT
167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSELLIGR-HAHAIPGMDAAESERFLEGLVD
235

+ + P L P+V+ HP +G+ +L + I + ESE L G +
Sbjct: 168 EEEHQRWREAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESALL-GFLF
226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

P +W D+ +WDNR H A R+M + + G
Sbjct: 227 AHITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 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 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
 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 QRLVRTHPVTGRKSLFLSAHAGTIVGWPVPEARASLRDLIEHATQPQLVYSHQWRQWDLV
 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---LGAIVDDVDLSNATDALRDDIRAALAHHQVLFVFRGQRLSAAHRDFAAAGFGD 59

Query: 67 I-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
 119

+ +I+ + N D + N WH D T+
 Sbjct: 60 LHVHPIYPSPDAREIMVLDNAVFD-----LQDNAIWHTDVTFETETPP
 102

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGHVQQ
 177

+ ++ +A +P GG T + AAYDAL E +A + +A+H + + G V
 Sbjct: 103 RASILAAHTLPETGGDTLWGSFGFAAYDALSERVKAQLDGLTAQHDFTKSFPLKRFG-VTA
 161

Query: 178 AGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDALD T+AL+ HS ++S+ LG ++ + A +
Sbjct: 1 TEFGDMRAAYDALDGKTKALIEDIVCEHSRIFSKGALGF-----SFSEEEVKAFAPVRQ 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

LV+ HP+TGR SL + HA I G E+ L L + A Q V++H+W GD+V+
Sbjct: 55 RLVRTHPKTGRKSLYLSSHAGRIVGWPVPEAMLLRELTEHATQREFVYSHKWRVGDLMV
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 LRTRPLMPGFGVEIFDVDLKTAGSDARQKVVDLPHANGAILLRQDMDPDDLMSFIGLFG 66

Query: 66 AIER-----IGGGDIVAISNVKADGT-VRQHSPAEWDDMMKVIVGNMAWHADSTYMP
116

E G I +SN DG + H+ + WH D +Y
Sbjct: 67 EAEDHTQTQFTLPGYSKIFLLSNKIVDGKPIGAHNDG-----VGWHTDYSYKE
114

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
176

+ A VP G T AD+ AAYD+L +A + HS + S +
Sbjct: 115 EPVMCTMLYAVEVPDEGSDTLLADLCAAYDSLPRERQAQLDGLVLHHSYQHLMS----TR
170

Query: 177 QAGSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGL
233

Q G + M A P PLV+ HP GR +L + I GM E++ ++ L
Sbjct: 171 QFGRMELSEEM-KAANPDVHFHPLVRTHPADGRKALWVSTGTVKGI VMPDDEA QALIDEL
229

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD 269
V++ P VH H+W GD+++WDNRC LH +D

Sbjct: 230 VEFVTSEPFVHRHKWHVGDILMWDNRCTLHTGTGTVFD 265

>ref|ZP_04900578.1| putative alpha-ketoglutarate-dependent taurine
dioxxygenase

[Burkholderia pseudomallei S13]

gb|EDS83590.1| putative alpha-ketoglutarate-dependent taurine dioxxygenase

[Burkholderia pseudomallei S13]

Length = 277

Score = 87.0 bits (214), Expect = 2e-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 TRLTTLRLTPALGAI VDDVDLSNATDALRDDIRAALAHHQVLF FRGQRLS AARHRDFAAG 61

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMP
116

FG + +I+ + N D + N WH D T+

Sbjct: 62 FGDLHVHPIYP SHPDAREIMVLDNAVFD-----LQDNAIWHTD VTFTE
104

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGH
174

+ ++ +A +P GG T + AAYDAL E +A + +A+H + + G

Sbjct: 105 TPPRASILAAHTLPETGGDTLWGS GF AAYDALSERVKAQLDGLTAQHDFTKSFPLKRFG-
163

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR----HAHAI PGMDAAESERFL
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-----RWQPGDVAFW DNRSTIHYAVNDYGKAHRVMHRATIVG
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 = 2e-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 LVVTPGLPHIGALIENVNIRPLGDSQFEQLYHALLKHQVLFVRNQPITPLQQRDLAGRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
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 PPLGAILAAKQLPTTGGDTLWSSGIAAYEALSVPFKQLLAGLQAEHDFTHSFPEHKH-RA
166

Query: 178 AGSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLV
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 [Freymyella diplosiphon Fd33]

Length = 320

Score = 87.0 bits (214), Expect = 2e-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 MSNKHIEVKPVAGHIGAEIGGVDLRPLSDKAVAEIRQALLKWKVIFFRNQNIDHAAQIA 79

Query: 60 FAKRFGAI-----ERIGG-GDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHA
110

F RFG + E I G +I+ I S E + ++ WH

Sbjct: 80 FTSRFGEVITYAHPHEDEPIEGFAEILPID-----RSRYERKNGLRRSSYENRWHT
129

Query: 111 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSL-----
165

D T + G++ A VP+ GG T + ++ AAY+ L +AL A+H

Sbjct: 130 DVTAVVNPPAGSILRAVNVPSFGGDTQWTNLVAAAYEGLSAPVKALADTLKAQHFNARLR
189

Query: 166 VYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDA
223

+ S SKL A + P+V+VHPETG +L + G +H I +

Sbjct: 190 LSSSSKLAKRIAANP-----QVSIHPVVRVHPETGERALFVNPGFTSH-ILDVSP
238

Query: 224 AESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDF---KLPRVMWHSR
280

ES+ LE + + GD+ WDNR H A P D ++ RV++ +

Sbjct: 239 QESDLLLELFFNQITKPAYTTRFHGNNGDIAFWDNRATAHLA-PQDLDHIEVERVLYRTT
297

Query: 281 LAG 283

+ G

Sbjct: 298 ITG 300

>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 = 2e-15, Method: Compositional matrix
adjust.

Identities = 74/257 (28%), Positives = 110/257 (42%), Gaps = 20/257 (7%)

Query: 13 ATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIG 71
A LGA V+GV L LDD A + L+H +L F Q L+ Q + FA+RFG E +G

Sbjct: 8 AALGAEVSGVDLTQPLDDDALAIVRGGLLEHQVLFREQALTPAQHLAFARRFG--EPVG 65

Query: 72 GGDIVAIISNVKADGTVRQ--HSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV
129

+ A + P + D WH D T++ G++ V+

Sbjct: 66 HPAYPHVDGYPAINILENTPERPPKID-----TWHTDMTFLERPPLGSILRGVVI
115

Query: 130 PAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT
189

P GG T +A + A+DAL + + A HS + + + G + +

Sbjct: 116 PR-GGDTQWASLALAWDALARMQRYLEGLEALHSFAHG-FRHSLAEPGGFERLERAVRD
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 WAAGDVVVWDNRCLLHR 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 = 2e-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-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
118

G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP
108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQA
178

GA+ +A+ +P+ GG T + AAY+ L R L+ A H S + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYETLSVPFRQLLSGHRAEHDFRKSFPYK-SRKT
167

Query: 179 GSAYIGYGMDDTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD
235

+ + P L P+V+ HP +G+ +L + I + ESE L G +
Sbjct: 168 EEEHQWRWREAAAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALL-GFLF
226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

P +W D+ +WDNR H A R+M + + G
Sbjct: 227 THITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 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 = 2e-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 NLNIEVIKPTIGAIIHDLNALNEQTTQQIQQALLDHQVIFFRKQQLAPQAQADLARSF 66

Query: 65 G-----AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM
 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 KTPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQKRLRGLTATHDIRKSFPLERFA
 167

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR----HAHAIPGMDAAESERF
 229

H ++ + + P+V+ HP TG P L + H + +P ESE+
 Sbjct: 168 HNEEEREKLLQ-TFKRNPPVHPVVRTHPVTGEPLELFVSEGFTTHINELP---EQESEQL
 223

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

L L + A Q +W GDV +WDRNC 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 = 2e-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 NLNIEVIKPTIGAIIHDLNALNEQTTQQIQQALLDHQVIFFRKQQLAPQVQADLARSF 66

Query: 65 G-----AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM
 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 KTPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQQKLRGLTATHDIRKSFPLERFA
167

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-----HAHAIPGMDAAESERF
229

H ++ + + P+V+ HP TG P L + H + +P ESE+
Sbjct: 168 HNEEEREKLLQ-TFKRNPPVHPVVRTHPVTGEPPLLFVSEGFTTHINELP---EQESEQL
223

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L L + A Q +W GDV +WDNRC H+A

Sbjct: 224 LNFLFEHATQEQFHLRWKWDGDVAIWDNRCTQHKA 259

>ref|ZP_06227021.1| taurine dioxygenase [Burkholderia sp. CCGE1002]
gb|EFA53668.1| taurine dioxygenase [Burkholderia sp. CCGE1002]
Length = 282

Score = 87.0 bits (214), Expect = 2e-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 MRVEQLTYSIGAELTGVNVAHAHDDGLFAEIRSALLKHRVLFRLDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG +E VA S+ + G VR + +P + +D + AWHAD+T+ GA
Sbjct: 61 FGELE-----DHPVAGSDPENPGLVRIYKTPDQPNDRYE-----NAWHADATWREKPFQGA
111

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

V P VGG T +A+M AY+ L +A + ARHS+ S +++ +
Sbjct: 112 VLRCVECPPVGGDTMWANMVLAYENLPAYVKAQIADLRARHSIEASFGAAMPIEKRLALK
171

Query: 183 IGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE-----GLVD
235

+ P+V+ HPET L + E RF + L+
Sbjct: 172 AQF-----PDAEHPVVRTHPETEEKVLFVSAFTSHFTNFHTPERVRFQDANPGAGDLLR
226

Query: 236 WACQAPRVHAHQ----WAAGDVVVWDNRCLLHRA 265
+ + +Q W + +WDNR H A

Sbjct: 227 YLISQAYIPEYQVRWRWQKNSIAIWDNRSTQHAYA 260

>emb|CAY27436.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 87.0 bits (214), Expect = 2e-15, Method: Compositional matrix
adjust.

Identities = 50/127 (39%), Positives = 70/127 (55%), Gaps = 12/127 (9%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGH--VQQAGSAYIGYGMDDTATP
193

T F DMRAAYDALD T+AL+ HS ++S+ LG ++ A++ P
Sbjct: 1 TEFADMRAAYDALDAKTKALIEDLVCEHSRIFSKGTLGFSFTEEELKAFV-----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 VRQILVRTHRKTGRKSLYLSSHAGRIVGWPVPEAMLLRELTEHATQREFVYSHKWQVGD
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 = 2e-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 NLNIEVIKPTIGAIIHDLNLANEQTTOQIQQALLDHQVIFFRKQQLAPQAQADLARSF 66

Query: 65 G-----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
115

G +IE + +++ + + K D + N WH D T+
Sbjct: 67 GTLHVHPIYPSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFS
107

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSL--VYSQSKLG
173

G V A +P VGG T ++ AA+ L + + +A H + + +
Sbjct: 108 KTPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQQLRGLTATHDIRKSFPLERFA
167

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR----HAHAIPGMDAAESERF
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 LNFLFEHATQEQFHLRWKWQGDVAIWDNRCTQHKA 259

>ref|ZP_02501235.1| putative alpha-ketoglutarate-dependent taurine
dioxygenase

[Burkholderia pseudomallei 112]
Length = 393

Score = 87.0 bits (214), Expect = 2e-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---IGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYM--P
116
+ FG I + +GG AI + + R +S WH D T + P
Sbjct: 167 QAFGEIVKHPTMGGKTSAILLHSHEGGRANS-----WHTDVTCLRPP
210

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY----SQSKL
172
++ V A +P GG T +A+ AAY L + + IV + A H + S+ +L
Sbjct: 211 KLS---VLRALALPDAGGDTVWANTVAAYQHLPSSLQDLVDKLWAVHGNDFDYAASRVEL
267

Query: 173 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG
232
H A Y T P+V++HPETG SLL+G +A D +S R E
Sbjct: 268 LHDPVAKEYRKKYAAQVIKTE-HPVVQIHPETGEKSSLLGHYAQRFVQYDTHDSNRLYEI
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 = 2e-15, Method: Compositional matrix adjust.

Identities = 79/287 (27%), Positives = 114/287 (39%), Gaps = 31/287 (10%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQOITFAKRFGA 66
++TP LGA V V L+ DA + AA H +L F GQ LS + FA FG
Sbjct: 3 RLTPA---LGAIVDDVDLSNATDALRDDIRAALAHHQVLFRRGQRLSAAHRDFAAAGFGD 59

Query: 67 I-----ERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMA
119
+ +I+ + N D + N WH D T+
Sbjct: 60 LHVHPIYPSHPDAREIMVLDNAVFD-----LQDNAIWHTDVTFTETPP
102

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLV--YSQSKLGHVQQ
177

+ ++ +A +P GG T + AAYDAL E +A + +A+H + + G V
 Sbjct: 103 RASILAAHTLPETGGDTLWGSFGFAAYDALSERVKAQLDGLTAQHDFTKSFPLKRFG-VTA
 161

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-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 = 2e-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-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM
 118

G + G + + + + D +P + D+ WH D T++
 Sbjct: 65 GDLHIHPVYPHAEGVEEIIIVLDTHND-----NPPDNDN-----WHTDVTTFIDTP
 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQA
 178

GA+ +A+ +P+ GG T + AAY+AL E R L+ A H S + + +
 Sbjct: 109 PAGAILAAKELPSAGGDTLWTSGIAAYEALSEPFRQLLSGLRAEHDFRKSFFQYKRYRKT
 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 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALDE + + HS +YS+ KLG + P+R
Sbjct: 1 TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLGADFTTEERRVF-----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 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMLLLLDLTEFATRPYVYSHVWRLNDFV
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 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDAL++ TR + HSL+YS+ LG + Y L+
Sbjct: 1 TEFADMRAAYDALNDETRTEIEDMICEHSLMYSRGS LGFLD-----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 RLVTRHPVHGRKSLYLSSHAGGIIGMSVPEARVLLRDLNEHATQPEFVYVHKWTLHDLVM
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-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64

L ITP G +GA ++G L L D F L+ A L+H ++ Q ++ QQ A+RF
Sbjct: 5 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFLRDQAITPQQORALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
118

G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEVGVDEIIVLDTHND-----NPPDNDN-----WHTDVTFIETP
108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQA
178

GA+ +A+ +P+ GG T + AAY+AL R L+ A H S + + ++
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFP EYKY-RKT
167

Query: 179 GSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAE SERFLEGLVD
235

+ + P L P+V+ HP +G+ L + I + ESE L L
Sbjct: 168 EEEHQRWREAVAKNPPLLHPVVRTHPVSGKQVLFVNEGFTTRIVDVSEKESEALLSFLFA
227

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLP RVMWHSRLAG 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]
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-ALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63

LQI P GA + GV L A L A L+ ++ F GQ+ + D Q+ +
Sbjct: 43 LQIEPLTPHFGAVIGGVDLTRPVTGTLADELRQALLEWKVIFFRGQNGFTPDHQLALSGL
102

Query: 64 FGAIER---IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ
120

+G E IS + D K WH+D ++M +
Sbjct: 103 WGPPEPNPFFATTGTAGISRLAKDA-----KAAGNKNIWHS DHSFMANPSL
148

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQA
180

GAV A VPAVGG T +ADM AAYD L E + + +A H S L + +Q +
Sbjct: 149 GAVLRAVEVPAVGGDTMWADMAAAYDNLPEDLKERIEDLTAVHDWEASWGALMNEEQKAA
208

Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQ
239

+ P+V HP +GR +L + I G+ AES L+ LV Q
Sbjct: 209 FRANWPQVE-----HPVVVRHPRSGRRTLYVNEPFTRYIKGLSDAESRELLDILV---LQ
260

Query: 240 APRVHAHQ----WAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAGRP 285
A R+ +Q W G + VWDN + H A F RVM +AG P

Sbjct: 261 A-RIPEYQIRFHWEPSIAVWDNIAVQHYAINDYFPQRRVMERIAIAGVP 309

>emb|CAY27330.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.7 bits (213), Expect = 3e-15, Method: Compositional matrix
adjust.

Identities = 50/125 (40%), Positives = 67/125 (53%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
195

T FADMRAAYDALDE + + HS +YS+ KLG + P+R
Sbjct: 1 TEFADMRAAYDALDEWLKNQIEDLVCLHSNMYSRGKLGGLADFTDEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

LV+ HP TGR SL + HA I GM ++ L L ++A + P V++H W D+V
Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPKARMLLLDLTEFATREPFVYSHAWRVNDLV
114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>ref|ZP_02450703.1| putative alpha-ketoglutarate-dependent taurine
dioxxygenase

[Burkholderia pseudomallei 91]
Length = 381

Score = 86.7 bits (213), Expect = 3e-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--ITQALLTHRVIFFRRQHLLDDLAQELFA
153

Query: 62 KRFGAIER---IGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM
118

+ FG I + + G AI + + R +S WH D T+
Sbjct: 154 QAFGEIVKHPTMDGKTGSAILELHSHEGGRANS-----WHTDVTFGLRP
197

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY----SQSKLGH
174

+ +V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
Sbjct: 198 PKLSVLRALALPDAGGDTVWANTVAAYQHLPSLQDLVDKLWAVHGNDFDYAASRVELLH
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 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ WAAGDV +WDNR H A
Sbjct: 317 AHITRENTVRWHWAAGDVVAIWDNRSTQHYA 347

>ref|YP_001603688.1| Alpha-ketoglutarate-dependent taurine dioxygenase
[Gluconacetobacter diazotrophicus PA1 5]
ref|YP_002277264.1| Taurine dioxygenase [Gluconacetobacter diazotrophicus
PA1 5]
emb|CAP57402.1| Alpha-ketoglutarate-dependent taurine dioxygenase
[Gluconacetobacter diazotrophicus PA1 5]
gb|ACI52649.1| Taurine dioxygenase [Gluconacetobacter diazotrophicus PA1
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 IERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA--WHADSTYMPVMAQGAVF
124

+ + + A GT +K G A WHAD T+M + ++
Sbjct: 74 L-----VAHPTVASAKGTNHIFE-----LKAQKGRAANTWHADMTFMATYPKASIL
119

Query: 125 SAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLV-YSQSKLGHVQQAGSAYI
183

+ GG T +A+ AY AL + + L + A H+ Y + L V + +I
Sbjct: 120 RSVHTAPYGGATLWANTATAYQALPQLQELADKLWAIHTNDDYDHTDL--VVERDWDIFI
177

Query: 184 GYGMDTTATPL----RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ
239

+ + A + PLV+VHPETG SL++G + + +S L+ + + +
Sbjct: 178 RWSANVFAARIFETRHPVVRVHPETGEKSLILGNFVKRLVDFNLPDSRALLDLFLSYVTR
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 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIIVGNMAWHADSTYMPVMAQGAV
 123
 FG +E V S+ + G V+ + + KV ++H D+T+ G V
 Sbjct: 61 FGELE-----DHPVVGSDEHPGLVQIYKSPD-----SKVEHYENSFHCDATWRQAPPMGCV
 112

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYI
 183
 PAVGG T + +M AY L + +A + A+HS+ ++ ++ +
 Sbjct: 113 LRCVETPAVGGDTIWWNMGEAYRRLPQDIKARIEGLRAKHSIEHTFGANMPPEKRAALAA
 172

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE-----GLVDW
 236
 + M P+V+ HPETG L + + RF + L+ +
 Sbjct: 173 QFPMVE-----HPVVRTHPETGEKVLVFNRAFTSHFANYHRDDVVRFGKDFMPGAGDLLHY
 227

Query: 237 ACQAPRVHAHQ----WAAGDVVVWDNRCLLHRA 265
 C + +Q W V +WDNRC H A
 Sbjct: 228 LCAQAEIPEYQVRWRWKKNSVAIWDNRCTQHVA 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 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
 195
 T F DMRAAYDALD+ T+A V HSL+YS+ +G + P+R
 Sbjct: 1 TEFGDMRAAYDALDDRTKAEVAGLVCEHSLLYSRQAVGFTDFTPEEISNF-----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|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 = 3e-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 VSPISPEVGVVAGLRGHQLVDPAAAAECQALLEKHGVVYRELNIDDADLVAFSRMLGT 64

Query: 67 IERIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
126

+ G I + V PAE + G WH D + + + +A
Sbjct: 65 VVVAPTGGIEGLPEVSKITL----DPAE-SVLAAYRKGTFFWHIDGANDELPQKATLLTA
119

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYG
186

V GG T FA+ AAYDAL + +A HS SQ A
Sbjct: 120 RQVSDEGGDTEFANTYAAAYDALTDDEKAQFATLRVVHSFAASQRL-----AEPDAS
170

Query: 187 MDTTATPLRPLVKVHP-----ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAP
241

T A R + HP +GR SLL+G + G ES L+ L+ W+ Q
Sbjct: 171 EKTRALWARVPSREHPLVWTRRSGRKSLLVGATTSHVVGWPEEESRALLDRLLAWSTQPR
230

Query: 242 RVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

V H W GD+V+WDN +LHRA P+ R+M + L G
Sbjct: 231 FVLRHHWRPGDLVIWDNTGMLHRAIPYTATSRRMLMHRRTTLVG 272

>gb|ACG80570.1| TfdA [uncultured bacterium]

Length = 119

Score = 86.7 bits (213), Expect = 3e-15, Method: Compositional matrix
adjust.

Identities = 50/128 (39%), Positives = 64/128 (50%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
195

T F DMRAAYDALDE + + HS +YS+ KLG + D T +
Sbjct: 1 Tefgdmraaydalderlkqqiedlvclhsnmysrgklg-----LADFTDEERTAFK 51

Query: 196 P-----LVKVHPETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAG
251

P LV+ HP TGR SL + HA I GM E L L ++A + V++H W
Sbjct: 52 PVRQRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEGRLMLLDLTFATREQFVYSHMWRVN
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 = 3e-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 NLNIEVIKPTIGAIHHDIDLNALNEQTTQQIQQALLDHQVIFFRKQQLAPQAQADLARSF 66

Query: 65 GA-----IERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYM
115

G+ IE + +++ + + K D + N WH D T+
Sbjct: 67 GSLHVVHPIYPSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFS
107

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYD----ALDEATRALVHQRSARHSLVYSQSK
171

G V A +P VGG T ++ AA+ L + R L R S + +
Sbjct: 108 KNPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQDKLRGLTATHDIRKS--FPLER
165

Query: 172 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDDAAESERFL
230

H ++ + + P+V+ HP TG P L + I + ESE+ L
Sbjct: 166 FAHNEEECEKLLQ-TFKRNPPVHPVVRTHPVTGEPLLFVSEGFTRINELSEQEQQL
224

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

L + A Q +W GDV +WDNRC H+A

Sbjct: 225 NFLFEHATQEKFHRLRWKWDGDVAIWDNRCTQHKA 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 = 3e-15, Method: Compositional matrix
 adjust.

Identities = 51/125 (40%), Positives = 66/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
 195

T FADMRAAYDALDE + + HS +YS+ KLG + P+R
 Sbjct: 1 TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLGADFTTEERRVF-----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 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMLLLLDLTEFATRDPPFVYSHVWRLNDFV
 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 = 3e-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 MTPLGPYIGAVVENINIARPLGDGQFEQLYHALLKHQVLFERNQPITPLQQRELGRFGD 60

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMA
 119

+ +I+ + ++P + D+ WH D T++
 Sbjct: 61 LHIHPVYPHTKECEEIIVLD-----THDNNPPDNDN-----WHTDVTFIENPP
 103

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS--QSKLGHVQQ
 177

GA+ +A+ +PA GG T ++ AAY+ L + L+ A H +S + K +

Sbjct: 104 LGAILAAKQLPATGGDTLWSSGIAAYETLSAPFKQLLAGLRAEHDFAHSFPEHKNRGTPE
163

Query: 178 AGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW
236

++ + L P+V+ HP TGR +L + I + A ES+ L L
Sbjct: 164 EHQRWL-LAKENNPPLLHPVVRTHPVTGRQALFVNEGFTTRIVDLSAKESDAILRFLFAH
222

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-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 = 3e-15, Method: Compositional matrix
adjust.

Identities = 50/128 (39%), Positives = 64/128 (50%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
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 DVVVWDNR 259
D V+WDNR

Sbjct: 112 DFVMWDNR 119

>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 dioxxygenase
 [Burkholderia pseudomallei 406e]
 emb|CAH39048.1| alpha-ketoglutarate-dependent taurine dioxxygenase
 [Burkholderia pseudomallei K96243]
 gb|ABN93706.1| putative alpha-ketoglutarate-dependent taurine dioxxygenase
 [Burkholderia pseudomallei 1106a]
 gb|EBA46669.1| putative alpha-ketoglutarate-dependent taurine dioxxygenase
 [Burkholderia pseudomallei 305]
 gb|EDO88031.1| putative alpha-ketoglutarate-dependent taurine dioxxygenase
 [Burkholderia pseudomallei 406e]
 gb|EDO90258.1| putative alpha-ketoglutarate-dependent taurine dioxxygenase
 [Burkholderia pseudomallei Pasteur 52237]
 gb|EEC31743.1| putative alpha-ketoglutarate-dependent taurine dioxxygenase
 [Burkholderia pseudomallei 576]
 gb|EEH27989.1| putative alpha-ketoglutarate-dependent taurine dioxxygenase
 [Burkholderia pseudomallei Pakistan 9]
 gb|EES23667.1| putative alpha-ketoglutarate-dependent taurine dioxxygenase
 [Burkholderia pseudomallei 1106b]
 Length = 277

Score = 86.7 bits (213), Expect = 3e-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 TRLTTLRLTPALGAIVDDVDLSNATDALRDDIRAALAHHQVLFRRGQRLSAARHRDFAAG 61

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP
 116
 FG + +I+ + N D + N WH D T+
 Sbjct: 62 FGDHLVHPIYPSHPDAREIMVLDNAVFD-----LQDNAIWHTDVTFTTE
 104

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLV--YSQSKLGH
 174
 + ++ +A +P GG T + AAYDAL +A + +A+H + + G
 Sbjct: 105 TPPRASILAAHTLPETGGDTLWGSFGAAYDALSGRVKAQLDGLTAQHDFTKSFPLKRFG-
 163

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGL
 233
 V A T + P+V+ HPETGR +L + I G+ E L L
 Sbjct: 164 VTAEDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNEGFTEIDGLPEEEGAALLRFL
 223

Query: 234 VDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG-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 = 3e-15, Method: Compositional matrix adjust.

Identities = 51/125 (40%), Positives = 66/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALDE + + HS +YS+ KLG + P+R
Sbjct: 1 TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLGADLFTEERRVF-----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 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMLLLLDLTEFATRDPFVYSHIWRLNDFV
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 = 3e-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 LIITPLGPNIGAQVAGLDVTRPLSDNQFEQLYHAVLRHQVVFLREQAISPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVM
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 PAGAILAAKQLPETGGDTLWASGIAAFEALSAPFRALLSGLRAEHDFKKSFFQYKY-RNS
167

Query: 179 GSAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD
235

+ + P L P+V+ HP TG+ +L + I + ESE L G +
Sbjct: 168 DEEHQRWQEAQAKHPPLLHPVVRTHPVTGKQALFVNEGFTTRIVDVSEKESALL-GFLF
226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 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 = 3e-15, Method: Compositional matrix
adjust.

Identities = 47/124 (37%), Positives = 66/124 (53%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADM AYDALD T+ + HS +YS+ +LG + + ++
Sbjct: 1 TEFADM PGAYDALDSETKDEIEDLVCEHSQIYSRQQLGFTDFTEEERVRF-----KPVIQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

LV+ HP TGR SL + HA I G E+ FL+ L + A Q V++H+W GD+V+
Sbjct: 56 RLVRTHTPTGRKSLYLSSHAGGIVGWPVPEARAFKDLNEHATQRQFVYSHKWRVGDLMV
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 = 3e-15, Method: Compositional matrix
adjust.

Identities = 48/125 (38%), Positives = 66/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYD LD T+A + HSL+YS+ LG + + TP+R
Sbjct: 1 TEFADMRAAYDGLDTKTKAEIEDLVCEHSLSIYSRGTGFTTELSDEERRMF-----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 QRLVRAHPVTGRKSLYLSSHIGTIVGWPMPPEARAFIRDLEHATQKQFTYSHKWRQYDLV
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 = 3e-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 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY--SQSKLGH
174

+ A VP G T AD AA++AL +A + S HS + + + G
Sbjct: 117 EPVMLTMLYAVEVPDEGSDTLLADGCAAWNALSPEKQAEELLPLSLHHSYKHFMATRQFGQ
176

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL--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 LVEFMTGDDFVYRHKWAKGDLMLMWDNRCTLHTGTLYD 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 = 3e-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 MQINPLTCAIGAELVDVQLADALRDDGLFAEIKTALLKHKVFLRRQSI SRAEHVGFARR 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 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

V P VGG T +A+M AY+ L + ++ ARHS+ + G A
Sbjct: 112 VLRCVECPVGGDTMWMANMALAYEMLPSHIKDVIAPLRARHSI---ECTFGAAMPAQKRL
168

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIG-----RHAHAIPGMDAAE-SERFLE
231

A P+V+ HPETG L + A+ G D + S L+
Sbjct: 169 ALKAQFPDAE--HPVVRTHPETGEKVLVSGFTTHFTNFHTPANVRVGQDFTQGSSSLQ
226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

L+ A +W G + +WDNR H A
Sbjct: 227 FLISQAAIPEYQVRWRWEPGSIWIWDNRATQHYA 260

>emb|CAY27543.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.3 bits (212), Expect = 3e-15, Method: Compositional matrix
adjust.

Identities = 51/127 (40%), Positives = 69/127 (54%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTA--TP
193

T FADMRAAYD LD+ T+A + HSL+YS+ LG ++ + D P
Sbjct: 1 TEFADMRAAYDDLDEETKAEIEPMICEHSLMYSRGLG-----FLDFTTEDEKRMFKP 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 = 3e-15, Method: Compositional matrix
adjust.

Identities = 51/124 (41%), Positives = 65/124 (52%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
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 RLVRRHPVTGRRSLFLSSHAGTIVGWPVEARALLRDLTEHATQREFVYHRWRQYDLVM
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 = 3e-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 SSIRVEPLTCTIGAELSNVNLGAAAEDDGQMAEIRALLLKHRVLFVRDQDITRAQHVAFA 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 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
177

 G V P VGG T + +M AY+ L E + + ARHS+ S +++
Sbjct: 127 PPLGCVLRCIIECPPVGGDTMWNMVEAYNQLPEEIKTKIGSLRARHSIEASFGAAMPIEK
186

Query: 178 AGSAYIGYMDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERF-----
229

 + Y P+V++HPETG L + G + + RF
Sbjct: 187 RLALKAQY-----PDAEHPVVRHHPETGKVLVFNNGSFTTHTNYNVPANVRFGLDKSPG
241

Query: 230 LEGLVDWACQAPRVHAHQ----WAAGDVVVWDNRCLLHRA 265

 L+++ + +Q W V WDNR H A
Sbjct: 242 ASNLLNYLTSQAMIPEYQVRFWRKKNVAFWDNRSTQHAYA 281

>ref|XP_381837.1| hypothetical protein FG01661.1 [Gibberella zeae PH-1]
Length = 380

Score = 86.3 bits (212), Expect = 3e-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 TIGTEVEGVQLSSLS DAGKDELARYVAERKVVAFRNQDFA-DLP ISEALKFGGY---FGR
 158

Query: 74 DIVAISNVKADGTVRQH-----SPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA VFSAE
 127
 + ++ +G H ++D K V ++AWH+D TY
 Sbjct: 159 HHIHPTSGSPEGHPEIHLVHRSAGDKSYEDFFKTRVSSVAWHSDITYEQPPGTTFLYVL
 218

Query: 128 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
 187
 P GG T FA+ AY+ L + L+H A HS + + +A + G
 Sbjct: 219 DNPDTGGDTLFANTVEAYNRLSPTFQKLLHGLKATHSGI-----EQVNASVKKGS
 268

Query: 188 DTTATPL---RPLVKVHPETGRPSLLIG-RHAHAIPGM DAAESERFLEGLVDWACQAPRV
 243
 P+ P+V+ HP TG SL + + +I G+ ES+ L L +
 Sbjct: 269 IKRREPVVNEHPIVRTHPVTGKSLYVNPQFTRSIVGLKKEESDAILNFLFEHIAWGADF
 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 = 3e-15, Method: Compositional matrix
 adjust.

Identities = 53/125 (42%), Positives = 67/125 (53%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM DTTATPLR
 195
 T FADMRAAYDALD+ T+A V HSL+YS+S +G + P+R
 Sbjct: 1 TEFADMRAAYDALDDRTKAEVAGLVCEHSLLYSRSVAVGFTDFTPEEVS NF-----QPVR 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
 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

>emb|CAY27448.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 86.3 bits (212), Expect = 3e-15, Method: Compositional matrix adjust.

Identities = 49/124 (39%), Positives = 65/124 (52%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
195

T F DMRAAYDALD+ +A + HSL+YS+ LG Y + L+
Sbjct: 1 TEFGDMRAAYDALDDEMKAIEDLICEHSLMYSRGS LGFTD-----YSDEEKEMFKPVLQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

LV+ HP GR SL + HA A+ GM E L L + A + V+AH+W D+V+
Sbjct: 56 RLVRTHPVHGRKSLYLSSHAGAVRGMSVPEGRLLLRDLNEHATRPEFVYAHKWLHDLVM
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 = 3e-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 ITVEKLGEGHIGARVNGIELRGDLSADRVEAIRLALAINKVLVFTQHHLLDDAGQYAF-- 72

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

R+ G + V++ GT +++ + WH D T++ + + +V
Sbjct: 73 -----RLLGEPTLPHTVRSHT-----E L L N L E G A A N G W H T D V T F V D R I P K A S V
117

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY----SQSKLGHVQQAG
179

+P+ GG T +A AAY+ L + R+LV A H+ +Y S + G +
Sbjct: 118 LRPVTLPSYGGATTWASTVAAYEQLPKPLRSLVDDLWATHTNLYDYASSGASGGVSAERR
177

Query: 180 SAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ
239

+AY + + P+V+VHPETG SLL+G+ + + +AE + L +
Sbjct: 178 AAYYTEFTSSRYETVHPVVRVHPETGERSLLLGQFVKSFQDLPSAEFASLFLQLLQARITK
237

Query: 240 APRVHAHQWAAGDVVVWDNRCLLH 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 = 3e-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 ARIGAEIRNVKLSADLPDRITAAINGLVLEHKVVFRRDQGHLLDAGQERFALRFGKLSPY 80

Query: 71 --GGGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA VFSAEV
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 IPLVGGDTVWSNTAAAYLDLPLPLQRLANELWAVHSFPGS-----YLRSSSTEPNTGPMIE
177

Query: 189 TTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQW
248

T P+V+VHPETG +L++G + G+ + +R L+ +W
Sbjct: 178 TE----HPVVRVHPETGERTLVLVGVYVTRFVGVISKYDQRLLDLDFESHVTAQENTVVRWKW
233

Query: 249 AAGDVVVWDNRCLLHRA 265

GD+ +WDNR +H A
Sbjct: 234 KEGDIAIWDNRATMHCA 250

>ref|ZP_05531495.1| 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 IEIHKV TANIGARVEGVDITRPLDEETYALREALNAHKALVFDAEGLDDAGQQAFVRHF 62

Query: 65 GAIERIGGGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMA--WHADSTYMPVMAQGA
122

G I A V A P + + G A WH D T++ Q +

Sbjct: 63 GDI-----TTAHTVPAVDGAPNVLVDSEG-----GRAANHWHTDVTFVLNPPQAS
109

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS-KLGHVQQAGSA
181

+ VP GG T A AAY L ++ R+L A H+ Y + V +A
Sbjct: 110 SLRSITVPPYGGETLIASSAAAYRNLPDSLRLADTLWAEHTNDYDYAVPEESVDDEQAA
169

Query: 182 YIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAP
241

+ P+V+VHP TG L IG A I G+ ES + L+ L + +
Sbjct: 170 RRAQFTSIKYRTVHPVVRVHPLTGERGLFIGGFAQRIVGLSPGESRKILLQAYVTRPE
229

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRA-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 LDIQPVAGRIGAEIRGVTLGELDAATVEAIQAALVRHKVIFFRGQSQLDDQTQEAF AHL 73

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

G + VA V + R + + + +WH D T++ + ++
Sbjct: 74 LG-----EPVAHTVPSREGTRFLLELDGAEGRRA----NSWHTDVTFVEAYPKASI
121

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL---GHVQQAGS
180

+ V P GG T +A+ +AY L R L + A HS Y + + V+Q +
Sbjct: 122 LRSVAPESGGDTVWANTASAYADLPAELRELADRLWAVHSNEYDYAGVKPSASVEQLEN
181

Query: 181 AYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA
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 PR++ L G

Sbjct: 241 ENTVRWRWQAGDVAIWDNRATQHAYAIDYGNQPRMVRRTLGG 283

>ref|XP_001383599.2| hypothetical protein PICST_43041 [Pichia stipitis CBS 6054]

gb|ABN65570.2| predicted protein [Pichia stipitis CBS 6054]
Length = 383

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix adjust.

Identities = 76/270 (28%), Positives = 108/270 (40%), Gaps = 15/270 (5%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQOI 58
A T ++ LG+ V G+ L+ LDD G L Q + IF Q S+ + +
Sbjct: 78 ANGTHKVKVTPKLGSEVHGIQLSQLDDKGNLALFLAQRGVAIFRDQDFSSYGPEFAV
137

Query: 59 TFAKRFGAIE-RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
117
+ K FG + G + T R S E D + N+ WH+D +Y
Sbjct: 138 EYGKYFGPLVHPTSGSPEGFPQLHI--TFRGASQNELDSAFETRNNIGWHSVSYELN
195

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
177
Q FS P GG T FAD + AY L + ++ H L S+ + H+ Q
Sbjct: 196 PPQITFFSVLEGPESSGGDTIFADTQEAYKRLSPTMQKML---EGLHVLHTSEDQ-AHINQ
251

Query: 178 AGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDW
236
A G + + PLV+ HP T L + R I + ESE LE L +
Sbjct: 252 AAG---GICRRAPVSNIHPLVRQHPVTKEKFLFLNREFGRRIVELKEESENLEFLFNH
308

Query: 237 ACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
A + W VV+WDNR +H A
Sbjct: 309 VESAHDLQLRANWEPNTVVLWDNRRTVHSA 338

>emb|CAY27338.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix adjust.

Identities = 49/125 (39%), Positives = 67/125 (53%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
195
T FAD+RAAYDAL+E + + HS +YS+ KLG + P+R
Sbjct: 1 TEFADIRAAAYDALEEGLKNQIEDLVCLHSNMYSRGKLGGLADFTDEERRVF-----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 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 = 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: 60 TRLTLRLTPALGAIVDDVDLSNATDALRDDIRAALAHHQVLFVRGQRLSAAHRDFAAG
 119

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP
 116

FG + +I+ + N D + N WH D T+
 Sbjct: 120 FGDLVHVPYPSHPDAREIMVLDNAVFD-----LQDNAIWHTDVTFTTE
 162

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGH
 174

+ ++ +A +P GG T + AAYDAL +A + +A+H + + G
 Sbjct: 163 TPPRASILAAHTLPETGGDTLWGSFGAAYDALSGRVKAQLDGLTAQHDFTKSFPLKRFG-
 221

Query: 175 VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGL
 233

V A T + P+V+ HPETGR +L + I G+ E L L
 Sbjct: 222 VTAEDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNEGF'TTEIDGLPEEEGAALLRFL
 281

Query: 234 VDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285

+ +W GDV WDNR +H A K RVM + + G RP
 Sbjct: 282 FAHQSRPEFTLRWRWQPGDVAFWDNRSTIHYAVNDYGKAHRVMHRATIVGDRP 334

>emb|CAY27534.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix
 adjust.

Identities = 51/128 (39%), Positives = 69/128 (53%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

Sbjct: 1 T FADMRAAYDALD+AT+A + HS+V+S+ ++G + A LR
TEFADMRAAYDALDDATKAEIEDLVTEHSIVFSREQIGFSDYEAAH-----ADKLR 51

Query: 196 P-----LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG
251

Sbjct: 52 P LV HP TGR SL + H I G E+ F+ L++ A Q V+ H+W
PVRHRLVVTHPVTGRKSLFLAAHIGTILGWPQPEAMAFIRDLMEHATQPQFVYVHRWTRH
111

Query: 252 DVVVWDNR 259
D+V+WDNR

Sbjct: 112 DLVMWDNR 119

>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 = 4e-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 MTPLGPYIGALVENINIARPLGDSQFEQLYHALLKHQVLFRRNQPITPLQQRDLAQRFGD 60

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
119

Sbjct: 61 LHIHPVYPHAKECEEIIVLD-----THDNNPPDNDN-----WHTDVTFIENPP
103

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG
179

Sbjct: 104 LGAILAAKQLPTTGGDTLWSSGIAAYEALSAPFKQLLAGLRAEHDFVHSFPEHKH-RATP
162

Query: 180 SAYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW
236

Sbjct: 163 EDHQRWLLAKEKNPPLLHPVVRTHPVSQRSLFVNEGFTTRIVDLSDKESDALLRFLFAH
222

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W DV +WDNR H A R+M + + G

Sbjct: 223 TTKPEFQVRWRWQDDVAIWDNRVTQHYANADYLPQRRIMHRATILG 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 = 4e-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 IEVTRLAPEIGAEISGYTGRDLVNEAAAAACKAALDRYGVLVYREVHIEDGDLVRFSRLL 62

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHPAEWDDMMKVIVG----NMAWHADSTYMPVMAQ
120

G V + V G + + D V+ G N WH D + +
Sbjct: 63 GE-----VVVPKVNDPGEHPEIARITLDPEKSVLAGYRQGNFLWHIDGATDELPQK
113

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGS
180

+ +A V GG T FA+ AAY+AL + +A + HS +Q ++ + A
Sbjct: 114 ATLLTAREVDPAGGDTEFANTYAAAYEALSDEEKAEIADLQVVHSFAIAQ-RIAYPDAADK
172

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQA
240

+ + T + PLV GR SLLIG A + G L+ L+ W+
Sbjct: 173 QRASW--EKVPTRVHPLVWTRA-NGRKSLLIGATAGMVVGRSEDRGRTLLDRLLQWSTSP
229

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR 284

HQW GD+V+WDN +LHRA P++ R+M + L G+
Sbjct: 230 RFTLRHQWRRGDLVIWDNTGVLHRALPFEPTSRRMLHRTTLVGQ 273

>emb|CAY27434.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 86.3 bits (212), Expect = 4e-15, Method: Compositional matrix
adjust.

Identities = 49/125 (39%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDALDE + + + HS +YS+ KLG + + + P+R
Sbjct: 1 TEFGDMRAAYDALDERLKQQIEELVCLHSNMYSRGKLGLEFSDERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

LV+ HP TGR SL + HA I GM E L L ++ Q V++H W D V

Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEGRMLLLDLTEFGTQHGFVYSHTWRVNDVF
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 = 4e-15, Method: Compositional matrix
adjust.

Identities = 49/124 (39%), Positives = 65/124 (52%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALDE + + HS +YS+ KLG + + +
Sbjct: 1 TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLGGLADSTEEERRVF-----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 RLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMLLLDLTEFATRDPFVYSHVWRNLDFVM
115

Query: 256 WDNR 259
WDNR

Sbjct: 116 WDNR 119

>gb|AAT51233.1| PA0193 [synthetic construct]
Length = 301

Score = 86.3 bits (212), Expect = 4e-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 LDIRPVAGRIGAEIRGVTLGELDAATVEAIQAALVRHKVIFFRDQSHLDDQTQEAF AHL 73

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

G + VA V + R + + + +WH D T++ + ++
Sbjct: 74 LG-----EPVAHPTVPSREGTRFLELDGAEGRRA-----NSWHTDVTFVEAYPKASI
121

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL---GHVQQAGS
180

+ V P GG T +A+ +AY L R L + A HS Y + + V+Q +
Sbjct: 122 LRSVVAPESGGDTVWANTASAYADLP AELRELADRLWAVHSNEYDYAGVKPSASVEQLEN
181

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
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 = 4e-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 LDIRPVAGRIGAEIRGVTLGELDAATVEAIQAALVRHKVIFFRDQSHLDDQTQEAF AHL 73

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

G + VA V + R + + + +WH D T++ + ++
Sbjct: 74 LG-----EPVAHPTVPSREGTRFLELDGAEGRR-----NSWHTDVTFVEAYPKASI
121

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL---GHVQQAGS
180

+ V P GG T +A+ +AY L R L + A HS Y + + V+Q +
Sbjct: 122 LRSVVAPESGGDTVWANTASAYADLPAELRELADRLWAVHSNEYDYAGVKPSASVEQLEN
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 ENTVRWRWQAGDVVAIWDNRATQHYAIDDYGDQPRVVRVTLGG 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 = 5e-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 IRIQALGPHIGALVSDINLSRPLSDAQFEQLYHALIRHQVFLFRDQPLTPHQQRQLASRF 64

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIV-----GNMAWHADSTYM
115

G + V H+P D+ ++IV N WH D T++
Sbjct: 65 GDLHI-----HPVYPHAP----DVEEIIIVLDTHDDNPPDNDNWHTDVTFI
105

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHV
175

GA+ +A+ +PA GG T +A AA+DAL +AL+ H S + +
Sbjct: 106 ETPPAGAILAAKQLPASGGDTLWASGIAAWDALSAPLQALLDGLQGEHDFRKSFQEYKY-
164

Query: 176 QQAGSAYIGYGMDDTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG
232

+ + + + P L P+V+ HP +G+ +L + + G+ ES+ L
Sbjct: 165 RSSAEEHQRWQQAVAKNPPVLPVVRTHPVSGKKALFVNEGFTTRLIGLKEKESDALLNF
224

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L + +W DV +WDNR H A R+M + + G

Sbjct: 225 LFAHITKPDFQVRWRWQQDDVAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>ref|YP_002319044.1| taurine dioxygenase [Acinetobacter baumannii AB0057]
ref|YP_002325944.1| Alpha-ketoglutarate-dependent taurine dioxygenase
[Acinetobacter

baumannii AB307-0294]

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 = 5e-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 NLNIEVIKPTIGAIIHNLNALNEQTTQQIQQALLDYQVIFFRKQQLAPQAQADLARSF 66

Query: 65 G-----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
 115

G +IE + +++ + + K D + N WH D T+
 Sbjct: 67 GTLHVHPIYPSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFS
 107

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRNLVHQRSARHSL--VYSQSKLG
 173

G V A +P VGG T ++ AA+ L + + +A H + + +
 Sbjct: 108 KTPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQQKLRGLTATHDIRKSFPLERFA
 167

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR----HAHAIPGMDAAESERF
 229

H ++ + + P+V+ HP TG P L + H + +P ESE+
 Sbjct: 168 HNEEEREKLLQ-TFKRNPPVHPVVRTHPVTGEPLLFVSEGFTTHINELP---EQESEQL
 223

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRA 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 = 5e-15, Method: Compositional matrix adjust.

Identities = 49/125 (39%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRNLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
 195

T FADMRAAYDALD+AT+A V HS+V+S+ ++G A G + P++
 Sbjct: 1 TEFADMRAAYDALDDATKAEVEDLVTEHSIVFSREQIGFSDYAS-----GNEERLRPVQ 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
 254

LV HP +GR SL + H I G E+ + L++ A Q V+ H+W D+V
 Sbjct: 55 HRLVITHPVSGRKSLYLSSHIGGIVGWPVPEARALIRDLMEHATQRQFVYTHEWRVNDLV
 114

Query: 255 VWDNR 259
 +WDNR

Sbjct: 115 MWDNR 119

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 AHITKPEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILG 275

>emb|CAN89617.1| putative taurine dioxygenase [Streptomyces collinus]
Length = 307

Score = 85.9 bits (211), Expect = 5e-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 TSIEVERLTCAIGAELRGVNIADAVRDDDLFAEIKSLLEHRVLFRLDQDLSRAEHVAF 83

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
121

 RFGA+E VA S+ G VR + E D + A H D T+ + G
Sbjct: 84 SRFGALE----DHPVAGSDPDHPGLVRIYK--ELDSAPEHY--ENALHTDGTWRVNPSMG
135

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSA
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--HPVVRTHPETGEKILFVNAFTTHTFTNFHTPANVRFQDYAPGASHLL
250

Query: 235 DWACQAPRVHAHQ----WAAGDVVVWDNRCLLHRA 265

 + V +Q W G V +WDNR H A
Sbjct: 251 SYLISQAAVPEYQVRWRWTPGSVAIWDNRSTQHYA 285

>emb|CAY27492.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 85.9 bits (211), Expect = 5e-15, Method: Compositional matrix
adjust.

Identities = 50/125 (40%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

Sbjct: 1 T FADMRAAYDALDE + + HS +YS+ KLG + P+R
TEFADMRAAYDALDERLKHRIEDLVCLHSNMYSRGKLGLTDFDTDDERSAF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

Sbjct: 55 LV+ HP TGR SL + HA I GM E L L ++A + V++H W D+V
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 = 6e-15, Method: Compositional matrix
adjust.

Identities = 48/125 (38%), Positives = 70/125 (56%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

Sbjct: 1 T FADMRAAYDAL T+A + HS ++S+ ++G A + P+R
TEFADMRAAYDALPAETKAEIEDLVCEHSQIFSRQQIGFFDLAEEERARF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

Sbjct: 55 +V+ HP TGR S + HA AI G E+ FL L++ A + V++H+W+ GD+V
QCMVRTHPVTGRKSAYLASHAGAIVGWPVPEARIFLRDLIEHATRREFVYSHKWSVGDV
114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>emb|CAY27416.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 85.5 bits (210), Expect = 6e-15, Method: Compositional matrix
adjust.

Identities = 50/125 (40%), Positives = 68/125 (54%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

Sbjct: 1 T F DMRAAYD LDE T+A + HSL++S+ LG + + + P+R
TEFWDMRAAYDTLDERTKAEIEDLICEHSLMFSRGLLGFTAMSEAEREMF-----RPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

Sbjct: 55 LV+ HP T R SL + HA I G E+ FL L++ A Q V++HQW D+V
QRLVTRHPVTRRKSFLSAHAGTIVGWPVPEARAFRLDLIEHATQPQLVYSHQWRQWDLV
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 = 6e-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---IGAEVGGVDLSQPLSAKQLTEIRRAFLENHVLVFRDQHLTVEQHKAFGR 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--GGRTCFAADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHV
175
+ G++ + PA+ GG T FA+M A + L A +A + + +A H G +
Sbjct: 124 PSMGSMYLVKETPAIGTGGDTLAFANMHLAIEMLSPAMQAFELGELTAIHD-----GEI
175

Query: 176 QQAGSAYIGYGMDDTATPLR-PLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEG
232
+ GY P+V HPETGR SL + G +H + + A ES L
Sbjct: 176 -----PWKGYQPPANLPKSEHPVVVVRHPETGRSLFVNSGFTSHIV-QLSAGESRTLLNM
229

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSR---LAGRPE 286
L D + P + +W +V WDNRC H A WD+ P + R L GRP+
Sbjct: 230 LFDLIAREPSLSCRVRWEPNTLVFWDNRCTQHHAV-WDY-FPHSRYGERVTILGGRPK 285

>gb|ADC34020.1| TfdA-like protein [uncultured bacterium]
Length = 196

Score = 85.5 bits (210), Expect = 6e-15, Method: Compositional matrix adjust.
Identities = 59/214 (27%), Positives = 98/214 (45%), Gaps = 26/214 (12%)

Query: 56 QQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW
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 HSDVTWRLEPSLGSILRSIEIPVGGDTLFADMYAAAYEGLSDTVKAKIEGRTAIHDFAFF
103

Query: 169 QSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESE
227

+ L ++ + Y P+V+ HPETGR + + I G++A ES

Sbjct: 104 RKGLRKAGKSEAEIEAYNKKFPPAE-HPVVRTHPETGRKGIYVNAaftQNIvGLEADESA
162

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

L+ L A +W+ + WDNRC+

Sbjct: 163 SLLKHYAQAAIPEYQCRFRWSVNALAFWDNRcv 196

>ref|ZP_05639075.1| TauD/TfdA family dioxygenase [Pseudomonas syringae pv.
tabaci ATCC

11528]

Length = 289

Score = 85.5 bits (210), Expect = 6e-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---IGAEVGGVDLSQPLSAEQKKEIRRAFLENHVLVFRDQHLTVEQHKAFGR 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 MAQGAVFSAEVVPAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV
175

+ G++ + PA+ GG T FA+M A + L A +A + + +A H G +

Sbjct: 127 PSMGSMlyVKETPAIGTGGDTLFANMHLAIEMLSpAMQAFLGELTAIHD-----GEI
178

Query: 176 QQAGSAYIGYGMDDTATPLR-PLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFLEG
232

+ GY P+V HPETGR SL + G +H + + A ES L

Sbjct: 179 -----PWKGYQPPANLPKSEHPVVVRHPETGRRSLFVNSGFTSHIV-QLSAGESRTLLNM
232

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSR---LAGRPE 286
L D + P + +W +V WDNRC H A WD+ P + R L GRP+

Sbjct: 233 LFDLIAREPSLSCRVRWEPNTLVFWDNRCTQHHAHV-WDY-FPHSRYGERVTILGGRPK 288

>gb|ACG80553.1| TfdA [uncultured bacterium]
gb|ACG80576.1| TfdA [uncultured bacterium]
Length = 119

Score = 85.5 bits (210), Expect = 6e-15, Method: Compositional matrix
adjust.

Identities = 47/124 (37%), Positives = 69/124 (55%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSAHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
195

T F DMRAAYDALD+ T+A V HS ++S+ +G + + + L+
Sbjct: 1 TEFGDMRAAYDALDDETKAEVENMVCEHSQMFSRQIIGF-----TDFTDEERERFRPVLQ 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 CMVRVNPVTGRKSLYLSSHAGGIVGWPMPEARGLRDLIEHATQREFVYTHKWRIGDLVM
115

Query: 256 WDNR 259

WDNR

Sbjct: 116 WDNR 119

>ref|ZP_02474390.1| putative alpha-ketoglutarate-dependent taurine
dioxxygenase

[Burkholderia pseudomallei B7210]

Length = 380

Score = 85.5 bits (210), Expect = 6e-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--ITQALLTHRVIFFRRQHHLDDLAQELFA
153

Query: 62 KRFGAIER---IGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHAD--STYMP
116

+ FG I + +GG AI + + R +S WH D S+ P
Sbjct: 154 QAFGEIVKHPTMGGKTGSAILELHSHEGGRANS-----WHTDVTSSSAP
197

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSAHSLVY----SQSKL
172

++ V A +P GG T +A+ AAY L + + LV + A H + S+ +L
Sbjct: 198 KLS---VLRALALPDAGGDTVWANTVAAYQHLPSLQDLVDKLVAVHGNDYDFYAAASRVEL
254

Query: 173 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG
232

H A Y T P+V++HPETG SLL+G +A D +S R E

Sbjct: 255 LHDPVAKEYRKKYAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRFVQYDTHDSNRLYEI
313

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L + WAAGDV +WDNR H A

Sbjct: 314 LQAHITRLENTVVRWHWAAGDVVAIWDNRSTQHYA 346

>emb|CAY27213.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 85.5 bits (210), Expect = 6e-15, Method: Compositional matrix
adjust.

Identities = 48/125 (38%), Positives = 68/125 (54%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDALD+AT+A V HS+V+S+ ++G A G + P++
Sbjct: 1 TEFADMRAAYDALDDATKAEVEDLVTEHSIVFSREQIGFSDYAA-----GNEERLRPVQ 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

LV HP +GR SL + H I G E+ F+ L++ Q V+ H+W D+V
Sbjct: 55 HRLVITHPVSGRKSLLSSHIGGIVGWPVPEARAFIRDLMEHVTQRQFVYTHEWRVNDLV
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 = 6e-15, Method: Compositional matrix
adjust.

Identities = 48/123 (39%), Positives = 67/123 (54%), Gaps = 6/123 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
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 RLVTRTHPKTGRKSLLSSHAGRIVGWPVPEAMLLRELTEHATQREFAYSHKWRVGDVLM
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]
 Length = 311

Score = 85.5 bits (210), Expect = 6e-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 NLNIEVIKPTIGAIIHNLNALSNEQTTQQIQQALLDYQVIFFRKQQLAPQAQADLARSF 84

Query: 65 G-----AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
 115

G +IE + +++ + + K D + N WH D T+
 Sbjct: 85 GTLHVHPIYPSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFS
 125

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYD----ALDEATRALVHQRSARHSLVYSQSK
 171

G V A +P VGG T ++ AA+ L + R L R S + +
 Sbjct: 126 KTPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQQKLRGLTATHDIRKS--FPLER
 183

Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR----HAHAIPGMDAAESE
 227

H ++ + + P+V+ HP TG P L + H + +P ESE
 Sbjct: 184 FAHNEEEREKLLQ-TFKRNPPVVHPVVRTHPVTGEPLELVSEGFTHINELP---EQESE
 239

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ L L + A Q +W GDV +WDNRC H+A
 Sbjct: 240 QLLNFLFEHATQEQFHLRWKWDGDVAIWDNRCTQHKA 277

>emb|CAY27480.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 85.5 bits (210), Expect = 6e-15, Method: Compositional matrix
 adjust.

Identities = 52/125 (41%), Positives = 67/125 (53%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
 195

T FADMRAAYDALDE + HS ++S+S LG + P+R
 Sbjct: 1 TEFADMRAAYDALDEEIKTECENLICEHSQFSLRSILGSTDFDERRRFA-----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

>emb|CAY27505.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 85.5 bits (210), Expect = 7e-15, Method: Compositional matrix
adjust.

Identities = 49/124 (39%), Positives = 67/124 (54%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
195

T FADMRAAYDALD T+AL+ HS ++S+ LG ++ + A +
Sbjct: 1 TEFADMRAAYDALDAETKALIEDLVCEHSRIFSKGALGF-----SFTEEEELRAFAPVRQ 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

LV+ H +T R SL + HA I G E+ L L + A Q V+AH+W GD+V+
Sbjct: 55 RLV RTHRKT SRKSLYLSSHAGRIVGWPVPEAMLLLRELTEHATQREFVYAHKWQVGDVLM
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 = 7e-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 TIGAIIHDIIDLNALNEQTTQQIQQALLDHQVIFFRKQQLAPQAQADLARSFGTLHVHPIY 64

Query: 66 -AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVF
124

+IE + +++ + + K D + N WH D T+ G V
Sbjct: 65 PSIEDVP--EVMVLDSWKQD-----LRDNELWHTDVTFSKTPPLGCVL
105

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQR SARHSL--VYSQSKLGHVQQAGSAY
182

A +P VGG T ++ AA+ L + + +A H + + + H ++
Sbjct: 106 QAIKIPVGGDTLWSSNTAAFKGLPLELQOKLRGLTATHDIRKSFPLERFAHNEEEREKL
165

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGR----HAHAIPGMDAAESERFLEGLVDWAC
238

+ + P+V+ HP TG P L + H + +P ESE+ L L + A
Sbjct: 166 LQ-TFKRNPPVVPVVRTHPVTGEPLLFVSEGFTHINELP---EQESEQLLNFLFEHAT
221

Query: 239 QAPRVHAHQWAAGDVVVWDNRCLLHRA 265

Q +W GDV +WDNRC H+A
Sbjct: 222 QEQFHLRWKQDGDVAIWDNRCTQHKA 248

>emb|CAY27266.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 85.5 bits (210), Expect = 7e-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 TEFADMRAAYDALDERLKHQTEDLVCLHSNMYSRGKLGGLADFTEEERRVF-----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|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 = 7e-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---IGAEIGGVLDLSQPLSDEQLTEIRRAFLENHVVVFRDQHLTVDEHKAFGR 80

Query: 63 RFGA-----IERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
117

FG +E I G D + ++A+ R V WH D T
Sbjct: 81 LFGELRALPVEDIDGDDPELVV-IRANAQSR-----YVAGETWHTDGTADLA
126

LV+ HP+TGR SL + HA I G E+ L L + A Q V +H+W GD+V+
 Sbjct: 55 RLVRTHPKTGRKSLYLSSHAGRIVGWPVPEAMLLRELTEHATQREFVFSHKWRVGDLMV
 114

Query: 256 WDNR 259
 WDNR

Sbjct: 115 WDNR 118

>ref|ZP_01363100.1| hypothetical protein PaerPA_01000192 [Pseudomonas
 aeruginosa PACS2]
 ref|ZP_04936624.1| hypothetical protein PA2G_04110 [Pseudomonas
 aeruginosa 2192]
 gb|EAZ60743.1| hypothetical protein PA2G_04110 [Pseudomonas aeruginosa
 2192]

Length = 300

Score = 85.1 bits (209), Expect = 7e-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 LDVRPVAGRIGAEIRGVTLGELDAATVEAIQAALVRHKVIFFRDQSHLDDQTQEAF AHL 73

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
 123
 G + VA V + R + + + +WH D T++ + ++
 Sbjct: 74 LG-----EPVAHPTVPSREGTRFLLELDGAEGRR-----NSWHTDVTFVEAYPKASI
 121

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL---GHVQQAGS
 180
 + V P GG T +A+ +AY L R L + A HS Y + + V+Q +
 Sbjct: 122 LRSVVAPESGGDTVWANTASAYADLPAELRELADRLWAVHSNEYDYAGVKPSASVEQLEN
 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 = 7e-15, 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 NNFNVYPLAGRIGAEIVGLDLKQTLSDETIHDRQVLIKYKVIFFRQQLTEISQVAFAR 78

Query: 63 RFGAIERI-----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY
 114
 +FG + G +I + D Q WH D T+
 Sbjct: 79 QFGILTTHAHLSSLPGHPEIFDFDYGRMDNRTNQ-----WHTDVTF
 120

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGH
 174
 + ++ A +PAVGG T +A+ AY + R +Q A HS Y+ LG
 Sbjct: 121 IDRPPFASILRAVEIPAVGGDTIWANTVTAYQDMPIPLRNFANQLWAVHSNTYN-DYLGA
 179

Query: 175 V-----QQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESE
 227
 Q+ G + T L P+V+V P++G L IG + G ES
 Sbjct: 180 TANISKKRQELGKIFTSIEYQT----LHPVVQVVPDSGERGLFIGAFVRQLQGFSSINESM
 235

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLH 263
 + L+ L + + W GD+ WDNR H
 Sbjct: 236 QILKILQSYIIRPENTVRWHWEQGDIAFWDNRVTQH 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 = 8e-15, 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 SIEVTPLSAHIGAEIHGVDLTQKLEARQIAEIRAALLKWRVFFREQFLTQHVAFSAQ 70

Query: 64 FGAIERIG---GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
 120
 FG + +G G + V + R+ + E + + G WH D T
 Sbjct: 71 FGELT-LGHPVFGHVEGHPEVYSISKYRKATRFEGQTLQRPWTG---WHTDVTA AVNPPW
 126

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGS
 180
 ++ +P GG T + ++ AAY L R+ V H G

Sbjct: 127 ASILRGVTIPPYGGDTQWTNLVAAAYQKLSAPLRSFVDGLRGIHRFTPPAGASG-----TQ
181

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ
239

A++ PLV+VHPETG +L + +I G+ ES+ LE L + +
Sbjct: 182 AFVEAVEQRILVTEHPLVRVHPETGERALYVSPSFLKSIVGVSPRESQVLELLELWEHVTR
241

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA--EPWDFKLPVMMWHSRLAG 283
+W AG V WDNR H A + +D R ++ + L G

Sbjct: 242 PEFTVRFKQAGSVAFWDNRATAHLAPTDIFDLDFDRQLYRTTLVG 287

>ref|YP_002008878.1| Putative taurine dioxygenase [Cupriavidus taiwanensis]

emb|CAQ72826.1| Putative taurine dioxygenase [Cupriavidus taiwanensis]
Length = 282

Score = 85.1 bits (209), Expect = 8e-15, 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 MHAEPLTCTIGAELTGVS LADASRDAGLFAEIKALLLQYKVLFLRDQDITRAEHVAFARQ 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123
FG +E V S+ + G V+ + + KV A+H D+T+ G V
Sbjct: 61 FGELE----DHPVVGS DPEHPGLVQIYKSPD----SKVEHYENAFHCDATWRQAPPMGCV
112

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
183
PAVGG T + +M AY L + +A + A+HS+ ++ ++ +
Sbjct: 113 LRCVETPAVGDDTIWVNMGEAYRRLPQDIKARIEGLRAKHSIEHTFGANMAPEKRAALAA
172

Query: 184 YGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE-----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 = 8e-15, 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-----IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
112

+ FG + G G+ I I++ + H+P DD+ + +H D+
Sbjct: 70 RHFGPLYTHPGAGNAGPDISPSIHRIASEDFKKYEKAHTPQAGDDVWE-----PYHTDT
123

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKL
172

++ V GAV A +P VGG T + D AY L + +A + H + +
Sbjct: 124 SWRLVPTWGAVLRAVNLPEVGGDTIWVDAALAYQGLPDDVKARLEGHHVTHDYRAALHQS
183

Query: 173 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLE
231

GH + P+V++ ETG +L + I G+D AES L
Sbjct: 184 GHDYPVVA-----HPVRLHRETGEKTLWVNFTQRPTIVGLDRAESRELLT
229

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276

++D + W G V WDNR +H A PR++
Sbjct: 230 AVIDQYRKPANQVRFSWRPGSVAFWDNRATVHYAVRNYGTFPRL 274

>ref|ZP_04662843.1| taurine dioxygenase [Acinetobacter baumannii AB900]
Length = 293

Score = 85.1 bits (209), Expect = 8e-15, Method: Compositional matrix adjust.

Identities = 68/276 (24%), Positives = 110/276 (39%), 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 NLNIEVIKPTIGAIHIDIDLNALNEQTTQIQQALLDHQVIFFRKQQLAPQAQADLARSF 66

Query: 65 G-----AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM
115

G +IE + +++ + + K D + N WH D T+
Sbjct: 67 GTLHVHPIYPSIEDVP--EVMVLDSWKQD-----LRDNELWHIDVTFS
107

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSL--VYSQSKLG
173

G V A +P VGG T ++ AA+ L + + +A H + + +
Sbjct: 108 KTPPLGCVLQAIKIPVGGDTLWSSNTAAFKGLPLELQQLRGLTATHDIRKSFLERFA
167

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-----HAHAIPGMDAAESERF
229

H ++ + + P+V+ HP TG P L + H + +P ESE+
Sbjct: 168 HNEEEREKLLQ-TFKRNPPVHPVVRTHPVTGEPPLLFVSEGFTTHINELP---EQESEQL
223

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

L L A Q +W GDV +WDNRC H+A
Sbjct: 224 LNFLFGHATQEQFHLRWKQDGDVAIWDNRCTQHKA 259

>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 = 8e-15, 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 FTLTPVTPFIGAEISDIDLDRPSEEQIEDVRRALLEWKVFFFRDQPISSVNRDFAAHWG 98

Query: 66 AIE---RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGA
122

+E + G++ A+ + + SP WH D T+ G+
Sbjct: 99 ELEVHPLLPOGEVPAVVRFERG-----EDSPG-----TENIWHVDVDTWTKTPPLGS
144

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSK---LGHVQQAG
179

V A VP GG T +ADM A+D L + + L+ + A H V S + ++Q
Sbjct: 145 VLRAIDVPPAGGDTLWADMGNADFCLPDEIKDLIDGKDAIHDFVPSFGRGMSPEKLEQMK
204

Query: 180 SAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV-----
234

Y L P+V+ HPETGR +L + IP MD E L L
Sbjct: 205 EQYPPV-----LHPMVRKHPETGRKTLFVNSLFTTHIPDMDPVEGNDLLNLLFAQVK
256

Query: 235 --DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276

D+ C+ +WA + WDNR H A F RVM
Sbjct: 257 VPDFQCR-----FKWAPNSIAFWDNRATQHYYAASDYFPHRRVM 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 = 9e-15, Method: Compositional matrix adjust.

Identities = 74/284 (26%), Positives = 113/284 (39%), Gaps = 41/284 (14%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKREG 65
+TP +GA ++ + L + + A L+ ++ F Q +S+ FA +G

Sbjct: 16 FTLTPVTPFIGAEISDIDLDRPSEEQIEDVRRALLEWKVVFRRDQPISSLNHRDFAAHWG 75

Query: 66 AIE---RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

+E + G++ A+ + + SP WH D T+ G+
Sbjct: 76 ELEVHPLLPOGEVPAVVRFERG----EDSPG-----TENIWHVDVTWTKTPPLGS
121

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSK---LGHVQQAG
179

V A VP GG T +ADM A+D L + + L+ + A H V S + ++Q
Sbjct: 122 VLRAIDVPPAGGDTLWADMGNAFDCLPDEIKDLIDGKDAIHDFVPSFGRGMSPEKLEQMK
181

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV----
234

Y L P+V+ HPETGR +L + IP MD E L L
Sbjct: 182 EQYPPV-----LHPMVRKHPETGRKTLFVNSLFTTHIPDMDPVEGNDLLNLLFAQVK
233

Query: 235 --DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276

D+ C+ +WA + WDNR H A F RVM
Sbjct: 234 VPDFQCR-----FKWAPNSIAFWDNRATQHYYAASDYFPHRRVM 271

>emb|CAY27496.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 85.1 bits (209), Expect = 9e-15, Method: Compositional matrix adjust.

Identities = 51/125 (40%), Positives = 67/125 (53%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
195

T FADMRAAYDALDE + HS ++S+S LG + P+R
Sbjct: 1 TEFADMRAAYDALDEEIKTECENLICEHSQSFERSILGFTDFTDDERRRFA-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

LV+ HP TGR SL + HA AI G E+ FL L++ + Q V++HQW D+V
Sbjct: 55 QRLVRRHPVTGRRSLYLASHAGAILGWLVPPEARAFRLDLIEHSTQPQLVYSHQWRQWDLV
114

Query: 255 VWDNR 259

+WDNR
Sbjct: 115 MWDNR 119

>ref|ZP_04891715.1| putative alpha-ketoglutarate-dependent taurine dioxxygenase

[Burkholderia pseudomallei 1655]

gb|EDU12699.1| putative alpha-ketoglutarate-dependent taurine dioxxygenase

[Burkholderia pseudomallei 1655]

Length = 277

Score = 85.1 bits (209), Expect = 9e-15, 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 TRLTLTRLTPALGAIVDDVDLSNATDALRDDIRGALAHHQVLFFRGQRLSAARHRDFAAG 61

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP 116

FG + +I+ + N D + N WH D T+

Sbjct: 62 FGDLVHVPYPSHPDAREIMVLDNAVFD-----LQDNAIWHTDVTFTE 104

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLV--YSQSKLGH 174

+ ++ +A +P GG T + AAYDAL +A + +A+H + + G

Sbjct: 105 TPRASILAAHTLPETGGDTLWGSQFAAYDALSGRVKAQLDGLTAQHDFTKSFPLKRFG- 163

Query: 175 VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGL 233

V A T + P+V+ HPETGR +L + I G+ E L L

Sbjct: 164 VTAEDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNEGFTTEIDGLPEEEGAALLRFL 223

Query: 234 VDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285

+ +W GDV WDNR +H A K RVM + + G RP

Sbjct: 224 FAHQSRPEFTLRWRWQPGDVAFWDNRSTIHYAVNDYGKAHRVMHRATIVGDRP 276

>ref|ZP_04520779.1| alpha-ketoglutarate-dependent taurine dioxxygenase (2-aminoethanesulfonate dioxxygenase) (Sulfate starvation-induced protein3) (SSI3) [Burkholderia pseudomallei MSHR346]

gb|EEP49693.1| alpha-ketoglutarate-dependent taurine dioxxygenase

(2-aminoethanesulfonate dioxxygenase) (Sulfate starvation-induced protein3) (SSI3) [Burkholderia pseudomallei MSHR346]

Length = 277

Score = 85.1 bits (209), Expect = 9e-15, 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 TRLTLTRLTPALGAIVDDVDLSNATDALRDDRVALAHHQVLFFRGQRLSAAHRDFAAG 61

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
116

FG + +I+ + N D + N WH D T+

Sbjct: 62 FGDLHVHPIYPSHPDAREIMVLDNAVFD-----LQDNAIWHTDVTFTE
104

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLV--YSQSKLGH
174

+ ++ +A +P GG T + AAYDAL +A + +A+H + + G

Sbjct: 105 TPPERASILAAHTLPETGGDTLWGS GFAAYDALSGRVKAQLDGLTAQHDFTKSFPLKRFG-
163

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGL
233

V A T + P+V+ HPETGR +L + I G+ E L L

Sbjct: 164 VTAEDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNEGFTTEIDGLPEEEGAALLRFL
223

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLP RVMMWHSRLAG-RP 285

+ +W GDV WDNR +H A K RVM + + G RP

Sbjct: 224 FAHQSRPEFTLRWRWQPGDVAFWDNRSTIHYAVNDY GKAHRVMHRATIVGDRP 276

>gb|ADC34028.1| TfdA-like protein [uncultured bacterium]

Length = 197

Score = 84.7 bits (208), Expect = 9e-15, 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-----EPVEYPQLKGLPESPFITPVV KLEHERNNFGGI-WHSDTTYL 51

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQR---SARHSLVYSQSKL
172

PV G++ A VP GG T FA+ AY+ L R + SA ++++

Sbjct: 52 PVPPMGSMMLLAREVPPYGGDTL FANQYLAYETLSAGLRRTLDGLIGVSASSKADVTKTRE
111

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAI PGMDAAESERFLE
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

>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 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDAL E +A + A HS+ YS+ +LG + G + +
Sbjct: 1 TEFADMRAAYDALPEDMKARLEGLQAHHSIAYSQRQLGF-----EFGSDEAERLKGAVH 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 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDALDE + + HS +YS+ KLG + P+R
Sbjct: 1 TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLGGLADFTEEECRVF-----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|YP_003491531.1| putative dioxygenase [Streptomyces scabiei 87.22]
emb|CBG72991.1| putative dioxygenase [Streptomyces scabiei 87.22]
Length = 305

Score = 84.7 bits (208), Expect = 1e-14, Method: Compositional matrix
adjust.

Identities = 76/289 (26%), Positives = 115/289 (39%), Gaps = 30/289 (10%)

Query: 5 TLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLI FPGQHLSNDQQITFAKR 63
 T++I A +GA V+GV ++ L + AAL A H L+ +L + +F +
 Sbjct: 2 TIEIQKVTARIGARVSGVDISRPLGEETVAALREALNVHKALVLDVNLDDASHQSFVRH 61

Query: 64 FGAIERI-----GGGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM
 115

FG I G ++ + + + WH D T++
 Sbjct: 62 FGDITTAHPTVA AVEGAASVLPVDSERGRAN-----HWHTDVTFV
 101

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHV
 175

Q + +P GG T A+ AAY L E R L A H+ Y +
 Sbjct: 102 LNPPQATTLRSITIPPYGGETLIANAAAAYRDLPEPLRRLADGLWAEHTNDYDYAVPDEE
 161

Query: 176 QQAGSAYIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
 234

A A + T + P+V+VHP TG L IG A I G+ ES + L+ L
 Sbjct: 162 IDAERAEQRARFTSITYRTVHPVVRVHPLTGERGLFIGGFAQRIVGLSLGESRKILDLLQ
 221

Query: 235 DWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ + V H+W+ +VV+DNR H A LPR + +AG
 Sbjct: 222 SYVTRPENLVRHRWSENQLVVF DNRI TQHYAIDNYDGLPRRLHRVTVAG 270

>emb|CAY27379.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 118

Score = 84.7 bits (208), Expect = 1e-14, Method: Compositional matrix
 adjust.

Identities = 51/124 (41%), Positives = 66/124 (53%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
 195

T FADMRAA+D LD T+ALV HS +YS+ +LG + A +
 Sbjct: 1 TEFADMRAAWDTLDADTKALVRDMLCEHSRLYSRGELG F-----RFTEEEEEKKFAPVQQ 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
 255

LV+ HP TGR SL + H AI G E+ L L + A Q RV+AH+W D+V+
 Sbjct: 55 RLVR RHPSTGRLSLYLSSHGGAITGWPLPEARALLRELTEHATQRERVYAHKWQRYDLVM
 114

Query: 256 WDNR 259

WDNR

Sbjct: 115 WDNR 118

>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]
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 MRIEPLTCAIGAELVGVCLADAAHDDGLFAEIRAALLAHRVLFRLDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVI VGNMAWHADSTYMPVMAQGA V
 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 GYGMDDTATPLRPLVKVHPETGRPSLLIGRH-----AHAI PGMDAAESERFLEGL
 233
 A P+V+ HPETG L + A G DA L G
 Sbjct: 170 LKAQFPDAE--HPVVRTHPETGKVLVFNFTTHTFTNYHTPARVRVGDANPGAALLLGY
 227

Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
 + P +W V +WDNR H A
 Sbjct: 228 LLSQAYIPEYQVRWRWRKNSVAIWDNRSTQHVA 260

>ref|YP_002780830.1| putative 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----SPA EWDDMMKVIVGNMAWHADSTYMPVM
 118

RFG +E VA S+ G VR + SPAE + A+H D+T+
 Sbjct: 82 RFGPLE----DHPVAGSDPAHPGLVRIYKDLDSPAEHYEN-----AFHC DATWREN P
 129

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQA
 178

G V A P VGG T + +M AY+ L + + + ARHS+ ++ G Q
 Sbjct: 130 PMGCVLRAVETPPVGGDTIWNMALAYEKL PDGVKKQIEGLRARHSI---EASFGAAQTE
 186

Query: 179 GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LE
 231

+ A P+V+ HP+TG L + A ++ R+
 Sbjct: 187 EQRRALHQRFPAE--HPVVRTHPDTGEKILFVNSFATHFVNYHTPDNIRY GIDYAPGSS
 244

Query: 232 GLVDWACQAPRVHAHQ----WAAGDVVVDNRCLLHRA 265

L+++ + +Q W V +WDR H A
 Sbjct: 245 NLLNYLISQASIPEYQVRWRWTPNSVAIWDNRSTQH YA 282

>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--DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 63
 +Q+ P ++GA +TGV L + DD+ A + A L+H +L F Q ++ D + FAKR

Sbjct: 1 MQVNPLTCSIGAELTGVQLGNVARDDSLHAEIKALLLKH RVLFFRDQEMTRDDHVAF AKR 60

Query: 64 FGAIERIGGGDIVA-----ISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
 118

FG +E + V I VK++ R H +H+D+++
 Sbjct: 61 FGDLEDHPVANTVPGYPGLIEIVKSEK--RDHF-----ENTYHSDASWRAN P
 105

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQA
 178

+GAV P VGG T + +M AY L E + + A+H + +S + ++
 Sbjct: 106 PRGAVLRCISCPEVGGDTIWNMVDAYKNLPEEIKQKIEGLRAKHGIEHSFGAIMSTEER
 165

Query: 179 GSAYIGYGMDDTTATPL--RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG-----
 232

PL P+V+ HP+TG L + + E+ RF +
Sbjct: 166 EEL-----VRKHPLVDHPVVRTHPDTGEKILYVTFPFSTHFINYHTPENVRVRFQDKTPG
218

Query: 233 ---LVDWACQAPRVHAHQ----WAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-R
284

L+++ + +Q W V +WDN H A + PR M + + G R
Sbjct: 219 ASLLLNILLSQAAIPEYQVRFWRPNSVAIWDNMATQHYAVSDYWPAPRRMERATIMGDR
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 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+ +Q+ PTG LGA V V L + DD FA+ A L+H +L+ Q L++ F++R

Sbjct: 14 SLVQVLPTGKALGAEVCNVDLRSFDDWAFASFMRALLKHQVLLVVRWQRLTDRDIAAFSRR 73

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV-MAQGA
122

FG HAD Y +G
Sbjct: 74 FG-----HADLHYTSYGTTTRGE 90

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAY
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 -----PVHPLVGLHADTGRSMLALGQRRHSYVVGLEQDESEALLNDLWQLAERPE
185

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276
H GD++VWD RC +HR E D +PR++

Sbjct: 186 FSWHTHCRGGDLIVWDTRCTIHRHEAPD--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 = 1e-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 MQVKPLTCAIGAELVGVNLDADAIKSDDLFAEIRAQLLKHRVVFRLDQTFSSRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG +E VA S+ + G VR + SP + +D + AWH+D+T+ GA
Sbjct: 61 FGELE----DHPVAGSDPEHPGLVRIYKSPDQPNDRYE-----NAWHSDDTTWREAPQFGA
111

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

V P VGG T +A+M AY+ L + ++ + ARHS+ S + +++ +
Sbjct: 112 VLRCVECPPVGGDTMWANMALAYENLPDHKSQIADLRARHSIEASFGAVMPIEKRLALK
171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE-----GLVD
235

Y P+V+ HP+TG L + RF + L+
Sbjct: 172 ERY-----PDAEHPVVRTHPDTGEKILYVNAFTTHFTNYHTPARVRFQDGNPGATDLLR
226

Query: 236 WACQAPRVHAHQ----WAAGDVVVWDNRCLLHRA 265

+ + +Q W V +WDN H A
Sbjct: 227 YLISQAYIPEYQVRWRWQPNVVAIWDNTATQHYA 260

>ref|YP_788349.1| hypothetical protein PA14_02420 [Pseudomonas aeruginosa UCBPP-PA14]

gb|ABJ15148.1| putative alkylsulfatase [Pseudomonas aeruginosa UCBPP-PA14]

Length = 300

Score = 84.7 bits (208), Expect = 1e-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 LDVRPVAGRIGAEIRGVTLSGELDAATVEAIQAALVRHKVIFFRDQSHLDDQTQEAF AHL 73

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
123

G + VA V + R + + + +WH D T++ + ++

Sbjct: 74 LG-----EPVAHPTVPSREGTRFLELDGAEGRRA----NSWHTDVTFVEAYPKASI
121

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQS--KLGHVQQAGSA
181

+ V P GG T +A+ +AY L R L + A HS Y + K +
Sbjct: 122 LRSVVAPESGGDTVWANTASAYADLPAELRELADRLWAVHSNEYDYAGVKPSASLEQLEN
181

Query: 182 YIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAP
241

Y T P+V+VHP++G +LL+G + G+ +S L +
Sbjct: 182 YRKVFTSTVYETEHPVVRVHPQSGERTLLLGHFVKRLKGLSQHDSAHLFAVLQGHVTRLE
241

Query: 242 RVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+W AGDV +WDNR H A PRV+ L G

Sbjct: 242 NTVRWRWQAGDVAIWDNRATQHYAIDDYGDQPRVRRVTLGG 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 = 1e-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 SLEVNPLTCSIGAELSNVHLGAAAEEDEGLMAEIRQALLKHRVIFFRDQDITRAEHVAFAR 79

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

+FG +E V S+ + G V+ + + + +WH D+T+ G
Sbjct: 80 KFGELE----DHPVVGSHPEHPGLVQIYKTPD----NPLDRNENSWHTDATWREQPPMGC
131

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

V P VGG T + +M AY+ L + + + ARHS+ S + +++ +
Sbjct: 132 VLRCVECPPVGGDTMWNMVMAYENLPDDIKVKIEHLRARHSIEASFGAVMPIEKRLALK
191

Query: 183 IGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-----AHAIIPGMDAAE-SERFL
230

Y P+V++HPETG L + A+ G+D + S + L
Sbjct: 192 AQY-----PDAEHPVVRVHPETGKILFVNSSFTTHTNYNTPANVRFGLDKSPGSSQLL
246

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 L A +W+ V WDNR H A
 Sbjct: 247 NYLTSQAMIPEYQVRFKWSKNSVAFWDNRSTQHYA 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 = 1e-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 LAITPLAGALGAQIHGLDLSQDLSEGDAAKLRQLLNEYEVIFFRDQDISGERQDLALAF 61

Query: 65 GAIE-RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIIVGNMAWHADSTYMPVMAQGA
 123
 G ++ + I + T+ + +P ++ K+ AWH+D T+ G V
 Sbjct: 62 GPLQVHPAYKTVEGIPEL-----TILESTP----ENPTKI-----EAWHSDMTFREHPPMGTV
 110

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYI
 183
 + VVP GG T +A M AYDAL A ++ + +A H + K + G +
 Sbjct: 111 LKSVVPPKGGDTMWASMTTAYDALSPAMQSFLGGLTAVHDFSWG-FKESIAEPGGRELR
 169

Query: 184 GYGMDDTATPLRPLVKVHPETGRPSLLIGR-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 = 1e-14, Method: Compositional matrix
 adjust.

Identities = 85/298 (28%), Positives = 129/298 (43%), Gaps = 48/298 (16%)

Length = 283

Score = 84.3 bits (207), Expect = 1e-14, Method: Compositional matrix adjust.

Identities = 73/288 (25%), Positives = 123/288 (42%), Gaps = 27/288 (9%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 + ITP G +GA V+ ++LA L D+ F L+ A ++H +L Q ++ QQ A RF
 Sbjct: 5 ITITPLGPYIGALVSDINLARPLSDSQFEQLYHALIRHQVLFVRDQPITPQQORALAMRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVM
 118

G + G + + + D +P + D+ WH D T++
 Sbjct: 65 GDLHIHPVYPHAEGVEEIIIVLDTHND-----NPPDNDN-----WHTDVTFIDTP
 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGH--VQ
 176

GA+ +A+ +P GG T + AA++AL + L+ A H S + H +
 Sbjct: 109 PAGAILAAKALPPTGGDTLWTSGIAAFEALSAPFQQLSGLRAEHDFRKSFPPEWKHTKTE
 168

Query: 177 QAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVD
 235

+ +I ++ L P+V+ HP +G+ +L + I + ES+ L L
 Sbjct: 169 EEHQRWIT-AVEKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSPKESDALLNFLFA
 227

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ +W DV +WDNR H A RVM + + G
 Sbjct: 228 HITKPEFQVRWRWQENDVALWDNRVTQHYANADYLPARRVMHRATILG 275

>ref|ZP_04636549.1| Alpha-ketoglutarate-dependent taurine dioxygenase
 [Yersinia

intermedia ATCC 29909]

gb|EEQ19297.1| Alpha-ketoglutarate-dependent taurine dioxygenase
 [Yersinia

intermedia ATCC 29909]

Length = 285

Score = 84.3 bits (207), Expect = 1e-14, Method: Compositional matrix adjust.

Identities = 76/289 (26%), Positives = 125/289 (43%), Gaps = 28/289 (9%)

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 VTPLGPHIGALVENINIARPLGDSQFEQLYHALLKHQVLFVRNQPITPLQQRELGRFGD 62

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQ
 120

+ + + + D +P + D+ WH D T++
 Sbjct: 63 LHIHPVYPHTKECEEIIVLDTHND-----NPPDNDN-----WHTDVTFIANPPL
 106

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS
180

GA+ +A+ +P+ GG T ++ AAY+AL + L+ A H +S + H +
Sbjct: 107 GAILAAKQLPSTGGDTLWSSGIAAYEALSAPFKQLLAGLQAEHDFAHSFPEHKH-RVTPE
165

Query: 181 AYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA
237

+ + + P L P+V+ HP +GR +L + I + ES+ L L
Sbjct: 166 EHQRWLLAKKNNPILHPVVRTHPVSGRQALFVNEGFTTRIVELSDKESDALLRFLFAHT
225

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285

+ +W DV +WDNR H A RVM + + G RP
Sbjct: 226 TKPEFQVRWRWQDDVAMWDNRVTQHYANADYLPQRRVMHRATILGDRP 274

>ref|ZP_04632718.1| Alpha-ketoglutarate-dependent taurine dioxygenase
[Yersinia frederiksenii ATCC 33641]
gb|EEQ14605.1| Alpha-ketoglutarate-dependent taurine dioxygenase
[Yersinia frederiksenii ATCC 33641]
Length = 276

Score = 84.3 bits (207), Expect = 1e-14, Method: Compositional matrix
adjust.

Identities = 75/290 (25%), Positives = 123/290 (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 MTPLGPHIGALVENINIRPLGDGQFEQLYHALLKHQVLFVRNQPITPIQORLLASRFGD 60

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMA
119

+ +I+ + ++P + D+ WH D T++
Sbjct: 61 LHIHPVYPHTKECEEIIVLD-----THDNNPPDNDN-----WHTDVTFIENPP
103

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG
179

GA+ +A+ +P GG T ++ AAY+AL + L+ A H +S + H +
Sbjct: 104 LGAILAAKQLPPTGGDTLWSSGIAAYEALSAPFKQLLAGLQAEHDFTHSFPEHKH-RDTP
162

Query: 180 SAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW
236

+ + + P L P+V+ HP +GR +L + I + ES+ L L
Sbjct: 163 EEHQRWLLAKEKNPPLHPVVRTHPVSGRQALFVNEGFTTRIVDLSDKESDALLHFLFAH
222

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285

+ +W DV +WDNR H A R+M + + G RP

Sbjct: 223 TTKPEFQVRWRWQQDDVAIWDRVTQHYANADYLPQRRIMHRATILGDRP 272

>emb|CAY27365.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 84.3 bits (207), Expect = 1e-14, Method: Compositional matrix
adjust.

Identities = 51/124 (41%), Positives = 66/124 (53%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAA+D LD T+ALV HS +YS+ +LG + A +
Sbjct: 1 TEFADMRAAWDTLDADTKALVRDMLCEHSRLYSRGELGF-----RFTEEEEEKKFAPVQQ 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

LV+ HP TGR SL + H AI G E+ L L + A Q RV+AH+W D+V+
Sbjct: 55 RLVRHPSTGRLSLSYLSSHGGAIIGWPLPEARALLRELTEHATQRERVYAHKWQRYDLVM
114

Query: 256 WDNR 259
WDNR

Sbjct: 115 WDNR 118

>emb|CAY27555.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 84.3 bits (207), Expect = 1e-14, Method: Compositional matrix
adjust.

Identities = 50/124 (40%), Positives = 65/124 (52%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMR A+D+LD T+ALV HS +YS+ +LG + A R
Sbjct: 1 TEFADMARGAWDSLNETKALVRDMVCEHSRLYSRGELGF-----RFTEEEEEKKFAPAQR 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

LV+ HP TGR SL + H AI G E+ L L + A Q V+AH+W D+V+
Sbjct: 55 RLVRHPSTGRLSLSYLSSHGGAITGWPLPEARALLRELTEHATQRRHVYAHKWQRYDLVM
114

Query: 256 WDNR 259
WDNR

Sbjct: 115 WDNR 118

>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]

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 = 1e-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---LGAIVDDVDLSNATDALRDDIRAALAHHQVLFVFRGQRLSARHRDFAAGFGD 59

Query: 67 I-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
119

+ +I+ + N D + N WH D T+
Sbjct: 60 LHVHPIYPSHPDAREIMVLDNAVFD-----LQDNAIWHTDVTFETETPP
102

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLV--YSQSKLGHVQQ
177

+ ++ +A +P GG T + AAYDAL +A + +A+H + + G V
Sbjct: 103 RASILAAHTLPETGGDTLWGSFGFAAYDALSGRVKAQLDGLTAQHDFTKSFPLKRFG-VTA
161

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW
236

A T + P+V+ HPETGR +L + I G+ E L L
Sbjct: 162 EDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNEGFTTEIDGLPEEEGAALLRFLFAH
221

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285

+ +W GDV WDNR +H A K RVM + + G RP
Sbjct: 222 QSRPEFTLRWRWQPGDVAFWVDNRSTIHYAVNDYGKAHRVMHRATIVGDRP 271

>emb|CAY27346.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 84.3 bits (207), Expect = 1e-14, Method: Compositional matrix adjust.

Identities = 51/125 (40%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMR AYDALDE + + HS +YS+ KLG + I + P+R
Sbjct: 1 TEFADMRTAYDALDERLKHQIVDLVCLHSSMYSRGKLGLETFTEERIVFK-----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 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMLLLDLTFATREHFVCAHVWRINDFV
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 = 1e-14, Method: Compositional matrix
adjust.

Identities = 49/125 (39%), Positives = 64/125 (51%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
195

T FADMRAAYDALD+ T+A HSL+YS+ LG + + P+R
Sbjct: 1 TEFADMRAAYDALDDETKAETEDLICEHSLMYSRGSGLGFTDYSEEEKQMFK-----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 QRLVVRTHPVHRRKSLYLSSHAGKVIGMTVPEGRLLLRDLTEHATQREFVYVHRWTVHDLV
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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
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 PVRQCMVRTHPVVTGRKSLYLSSHAGGIVGWPMPEARGLYLRDLIEHATQREFVYTHKWQVG
111

Query: 252 DVVVDNR 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 IKVTPNKNNVGAII EA-ELSKFNNDIIEEVKDVLA EYGVVFFRNQRLDSEYIKFAKQFG 63

Query: 66 AIERIGGGDIVAISNVK--ADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123
+ + + ++ ++ TV + P E +++ G WH DSTY + +
Sbjct: 64 PL-----AEYPMLKGLEGYSEITVVEKKPNE-----EIMFGE-GWHTDSTYTKEPPRFM
112

Query: 124 FSAEVVPAVG-GRTCFADMRAAYDALDEATR ALVHQRSARHSL--VYSQSKLGHVQQAGS
180
+ P G G T FA +Y+ LDE T+ + A S S+++ V + G+
Sbjct: 113 LYSIKTPEKKGNTMFASQYKSYETLDEKTKKKIENLKALFSADGPISKTRKNRVDEKGT
172

Query: 181 AYIGYGMD-TTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC
238
G+D + + P+V+ + + SL + HA I +D ES+ ++ L+D
Sbjct: 173 -----GIDPKSLNAIHPIVRKNERNNKKS LYLSPGHAIKICDLDENESKTLMKRLMDHQV
227

Query: 239 QAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVM 276
+ V+ +W + +W N +LH DF RVM
Sbjct: 228 KDEFVYGFWEWPNCLALWSNYSVLHNPTN-DFNAHRVM 264

>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 MRVEPLTCSIGAELVGVSLADAIHDDGLFAGIREALLKHRVLFVVRGQDITAGEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-SPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122
FG +E VA S+ + G VR + SP E + +WH D+T+ +
Sbjct: 61 FGELE----DHPVAGSDPEHPGLVRIYKSPEEPTPRYE-----NSWHTDATWREAPPLAS
111

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAY
182

+ P VGG T +++M AY+ L + + + ARHS+ S +++ +
Sbjct: 112 ILRCRECPPVGGDTMWSNMVLAYENLPQH IKDQIAGLRARHSIEASFGAAMPIEKRHALR
171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPR
242

+ P+V+ HP+TG L + E RF + A R
Sbjct: 172 AQF-----PDAEHPVVRTHPDTGEKVLVNGFTTHFTNFHTPEHVRFGQDFNPGAADLLR
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 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
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 MRIEPLTCAIGAELVGVCLADAHDDDLFAEIRAALLAHRVLFRLDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
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-----AHAI PGMDAAESERFLEGL
233

A P+V+ HPETG L + A G DA L G

Sbjct: 170 LKAQFPDAE--HPVVRTHPETGEKVLVFNFTTHTFTNYHTPARVRVGDANPGAALLGY
227

Query: 234 VDWACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
+ P +W V +WDNR H A

Sbjct: 228 LLSQAYIPEYQVRWRWRKNSVAIWDNRSTQHVA 260

>ref|ZP_05731065.1| Taurine dioxygenase [Pantoea sp. At-9b]
gb|EEW00579.1| 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 FTALGPNIGAQVSDVDLSRPLSDAQFEQLYHGLLRHQVLFRLNQVITPEQQRALAVRFGD 66

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMA
119

+ G +I+ + Q +P + D+ WH D T++

Sbjct: 67 LHIHPVYPHAPGVEEIIIVLD-----THQDNPPDNDN-----WHTDVTFITTPP
109

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG
179

A+ +++++P GG T +A AAY+AL E + L+ A H S + + ++

Sbjct: 110 AIALASKLLPESGGDTLWASGIAAYEALSEPFKTLLSGLQAEHDFKKSQEFKY-RKTE
168

Query: 180 SAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW
236

+ + P P+++ HP +GR +L + + G+ ES+ L L

Sbjct: 169 EEHQRWQQAVAKHPPVTHPVIRTHPVSGRKALFVNEGFTTRLIGLQEKESDALLNFLFAH
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 LSITPLGPYIGAQVTGADLTRPLSDNQFEQLYHAVLRHQVVFVFLREQNITPAQQRDALRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
 118

G + G + + + + D +P + D+ WH D T++

Sbjct: 65 GDLHIHPVYPHAPGVEEIIIVLDTHND-----NPPDNDN-----WHTDVTFIDTP
 108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQA
 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 AEHRRWQEAVAKHPPLLHPVVRTHPVTGKQALFVNEGFTTRIVEVSEKESAALLNFLFAH
 228

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ +W DV +WDNR H A R+M + + G

Sbjct: 229 VTKPEFQVRWRWQPNDVAIWDNRVTQHYANADYLPQRRIMHRATILG 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 TCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F+DMR AYD LD T+A V HSLVYS+ +G + + P+R
Sbjct: 1 TEFSDMRNAYDTLDAKTKAQVEGLVCEHSLVYSRGSMTGTE-----LTEDEKAMMKPVR 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

LV+ HP TGR SL + HA I G ES L L + A Q V+ H+W D+W
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 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
T L +T LGA V V L+ DA + AA H +L F GQ LS + FA

Sbjct: 2 TRLTTLRLTPALGAI VDDVDLSNATDALRDDIRAALAHHQVLFRRGQLSARHRDFAAG 61

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMP
116

FG + +I+ + N D + N WH D T+
Sbjct: 62 FGD LHVHPIYP SHPDAREIMVLDNAVFD-----LQDNAIWHTDVTFTTE
104

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQR SARHSLV--YSQSKLGH
174

+ ++ +A +P GG T + AAYDAL +A + +A+H + + G
Sbjct: 105 TP PRASILAAHTLPETGGDTLWGS GFAAYDALSGRVKAQLDGLTAQHDFTKSFPLKRFG-
163

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR----HAHAIPGMDAAESERFL
230

V A T + P+V+ HPETGR +L + +P + A RFL
Sbjct: 164 VTAEDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNEGFTTEIDELPEEEGAALLRFL
223

Query: 231 -----EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAG
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 MRVEQLTYSIGAELIGVNVARAIHDDGLFAEIRAALLKHRVLFRLDQAITRAEHVAFARR 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 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

 V P+VGG T +A+M AY+ L + + ARHS+ S +++ +
Sbjct: 112 VLRCVECPSVGGDTMWANMVLAYENLPAHVKTQIAGLRARHSIEASFGAAMPIEKRLALK
171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE-----GLVD
235

 + P+V+ HPET L + E RF + L+
Sbjct: 172 AQF-----PDAEHPVVRTHPETDEKVLVNAFTSHFTNFHTPERVRFVFGQDANPGAGDLLR
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 GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVA
 131

G I +++ + R S A+ WH D T++ + AV V+P
 Sbjct: 83 LGAIKGTASIIELDSTRAGSRAD-----LWHTDGTTFVDAYPKIAVLRGIVMPP
 130

Query: 132 VGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTA
 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 YRTEHPVVRVHPETGERTIVLGALVQNFVGLPKYDQKLFDFQSHITALENTVRWSWRD
 250

Query: 251 GDVVVWDNRCLLHRA 265

GDV +WDNR H A
 Sbjct: 251 GDVAIWDNRATQHYA 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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR
 195

T F DMRAAYDALD T+AL+ HS ++S+ LG ++ + A +
 Sbjct: 1 TEFGDMRAAYDALDAETKALIEDLVCEHSRIFSKGALGF-----SFTEEELRAFAPVRQ 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDVVV
 255

LV+ H +T R SL + HA I G E+ L L + A Q V+AH+W GD+V+
 Sbjct: 55 RLVTRHRKTSRKSLYLSSHAGRIVGWPVPEAMLLLRELTEHATQREFVYAHKWQVGDLMV
 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 TRCLKLTRLTPAIGAIVDDVDLSNATDDLRRDDLRAALARHQVLFRRGQRLSAVQHRDFAAG 96

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADSTYMP
116

FG + +I+ + N D + N WH D T++
Sbjct: 97 FGD LHVHPIYPSPHPDAREIMVLDNAVFD-----LKD NAIWHTDVTFVE
139

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR LVHQRSARHSLV--YSQSKLGH
174

+ ++ +A +P GG T + AAYDAL + + + +A+H + + G
Sbjct: 140 T PPRASILAARTLPETGGDTLWGS GFAAYDALSDRVKTQLDGLTAQHDFTKSFPLKRFGL
199

Query: 175 VQQAGSAYIGYGMDTTAT---PLRPLVKVHPETGRPSLLIGR----HAHAIPGM DAAESE
227

+ + + +T AT P+V+ HPE GR +L + + +P ++A
Sbjct: 200 TAEDRARW----EETRATHPGVTHPVV RTHPENGRHALFVNEGFTTEINELPDEESAALL
255

Query: 228 RFL-----EGLVDWACQAPRVHAHQWAAGDVVVW DNRCLLHRAEPWDFKLPRVMWHSR
280

RFL E + W +W GDV WDNR +H A K RVM +
Sbjct: 256 RFLFAHQSRPEFTLRW-----RWQPGDVAFW DNRSTIHYAVNDYGKTHRVMHRAT
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 TCFADMRAAYDALDEATR LVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
195

T FADMRAAYDALDE + + HS +YS+ KLG + P+R
Sbjct: 1 TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLG LADFTEEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

LV+ HP TGR SL + HA I GM E+ L L ++A + P V++ W D V
Sbjct: 55 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARM LLLDLTEFATRDPFVYSRVWRLNDFV
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 LTITPLGPHIGAQISGLDVARPLSDNQFEQLYHAVLRHQVVFLREQAVTAQQQRALALRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVM
118
G + G + + + + D +P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPHAEGVEEIIIVLDTHND-----NPPDNDN-----WHTDVTFIETP
108

Query: 119 AQQAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSKLGHVQ
176
GA+ +A+ +P GG T + AA++AL E + L+ A H + + K +
Sbjct: 109 PAGAILAAKQLPETGGDTLWTSGVAAFNALSEPFKQLLSGLRAEHDFRKS FQEYKYRKTE
168

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVD
235
+ ++ + L P+++ HP TG+ +L + I + ESE L L
Sbjct: 169 EEHQRWLE-AVAKHPPLLHPVIRTHPVGTGKQALFVNEGFTTRIVDVSEKESETLLTFLFA
227

Query: 236 WACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W D+ +WDNR H A R+M + + G
Sbjct: 228 HITKPEFQVRWRWQQNDLAIWDNRVTOHYANADYLPQRRIMERATILG 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 = 2e-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 QSPLAVRPLQPTIGAEIAGVDLSQPLSPAVRDEIRATVTLKYKVVFFRNQELTQEGHENFA 65

Query: 62 KRFGAIERIGGGD-----IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
113

+FG + G I IS+ D + H+P DD+ +H D++
Sbjct: 66 GQFGPLYTHPGAAKADARTTAIHRISADFDKVAKVHTPQADDDIWD-----PYHTDTS
119

Query: 114 YMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
173

+ V GAV A +P VGG T + D AY L + + + R H + G
Sbjct: 120 WRLVPTWGAVLRAVQLPEVGGDTI WVDAAALAYQGLSDEVKERLDGRHVTHDFRAALHASG
179

Query: 174 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGM DAAESERFLEG
232

H + P++++H ETG + I G+D AES+ L
Sbjct: 180 HDYPVVA-----HPVIRIHRETGEKIAWVNFTQRPTIIGLDRAESKELLTA
225

Query: 233 LVDWACQAPRVHAHQWAAGDVVVW DNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285

++D + W G V W DNR +H A PR++ +A P
Sbjct: 226 VIDQYRKPENQVRFTWRPGSVAFW DNRRAAVHYAVRNYGSAPRLLERILIADEP 278

>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 = 2e-14, Method: Compositional matrix
adjust.
Identities = 70/266 (26%), Positives = 113/266 (42%), Gaps = 27/266 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKR 63
+ + G +GA + GVHL+ L + A++ A H ++ F GQH L + Q FA
Sbjct: 22 ITVHKVGELIGARIDGVHLSGDLSEETAYAINYALAAHKVVFFRQGHLLD DTSQYEFAGT 81

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

G VK+ G D ++ + +WH D T++ + + ++
Sbjct: 82 LGT-----QTPHPTVKS RG-----DKLLVLDRAANSWHTDVT FVD RIPKASI
124

Query: 124 FSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG----
179

A +P GG T +A AAYD L + + LV A H+ Y +++ V QA
Sbjct: 125 LRATTIPEYGGATTWASTTAA YDQLPSSLKVLVENLRVHTNAYDYAEV--VDQANPVDA
182

Query: 180 --SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWA
237

AY P+V++HP TG +LL+G G+ +ES + L
 Sbjct: 183 QRQAYYAEFTREIYETEHPVVRHPATGEKTLGHHFFKEFVGLKPSVALYQILQARI
 242

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLH 263
 + W+AGD+ +WDN+ H

Sbjct: 243 IKLENTVRWNWSAGDLAIWDNQATQH 268

>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 = 2e-14, Method: Compositional matrix
 adjust.

Identities = 69/279 (24%), Positives = 121/279 (43%), Gaps = 35/279 (12%)

Query: 5 TLQITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
 ++++ P ++GA ++ VHL A D+ A + A L+H ++ F Q ++ + + FA+
 Sbjct: 20 SVEVNPLTCSIGAELSNVHLGAAAEDEGLMAEIRQALLRHRVIFFRDQDITRAEHVAFAR 79

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQH----SPAEWDDMMKVIVGNMAWHADSTYMPVM
 118

+FG +E V S+ + G V+ + SP + ++ +WH D+T+
 Sbjct: 80 KFGELE----DHPVVGSHPEHPGLVQIYKTPDSPLDRNEN-----SWHTDATWREQP
 127

Query: 119 AQQAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA
 178

G V P VGG T + +M AY+ L + + + ARHS+ S + +++
 Sbjct: 128 PMGCVLRVCECPPVGGDTMWNMVMAYENLPDDIKVKIEHLRARHSIEASFGAIMPIEKR
 187

Query: 179 GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIIPGMDAAE-S
 226

+ Y P+V++HPETG L + A+ G+D + S
 Sbjct: 188 LALKAQY-----PDAEHPVVRHPETGEKILFVNSSFTTHTNYNTPANVRFGLDKSPGS
 242

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ L L A +W+ V WDNR H A
 Sbjct: 243 SQLLNYLTSQAMIPEYQVRFKWSKNSVAFWDNRSTQHAYA 281

>ref|ZP_06511502.1| dioxygenase [Mycobacterium tuberculosis T92]
 gb|EFD60140.1| dioxygenase [Mycobacterium tuberculosis T92]
 Length = 252

Score = 83.6 bits (205), Expect = 2e-14, Method: Compositional matrix
 adjust.

Identities = 65/223 (29%), Positives = 95/223 (42%), Gaps = 13/223 (5%)

Query: 44 LLIFPGQH-LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVI
 102

Sbjct: 1 ++ F GQH L + +Q+ FA G IG +A+++ D + +E+ +
 MVFFRGQHQLDDAEQLAFAGLLGT--PIGHPAAIALAD---DAPIITPINSEFGKANR-- 53

Query: 103 VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSAR
 162

Sbjct: 54 -----WHTDVTFAANYPAASVLRVSLPSYGGSTLWANTAAAYAELPEPLKCLTENLWAL
 108
 WH D T+ +V A +P+ GG T +A+ AAY L E + L A

Query: 163 HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMD
 222

Sbjct: 109 HTNRYDYVTTKPLTAAQRAFRQVFEKPDFRTEHPVVRVHPETGERTLLAGDFVRSFVGLD
 168
 H+ Y + A A+ P+V+VHPETG +LL G + G+D

Query: 223 AAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

Sbjct: 169 SHESRVLFVQLQRRITMPENTIRWNWAPGDVAIWDNRATQHRA 211
 + ES E L WA GDV +WDNR HRA

>ref|YP_703743.1| taurine dioxygenase [Rhodococcus jostii RHA1]
 gb|ABG95585.1| taurine dioxygenase [Rhodococcus jostii RHA1]
 Length = 304

Score = 83.6 bits (205), Expect = 2e-14, Method: Compositional matrix
 adjust.

Identities = 75/278 (26%), Positives = 118/278 (42%), Gaps = 34/278 (12%)

Query: 5 TLQITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
 + ++ P +LGA + V+L A+ DDA FA L L++ +L Q +S + + A+

Sbjct: 22 SFRLAPMTCSLGAELFDVNLGDASRDDALFAELRELLLEYKVLFLRDQDISRAEHVALAE 81

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQH----SPAEWDDMMKVIVGNMAWHADSTYMPVM
 118

Sbjct: 82 RFGPLE----DHPVAGSDPDHPGLVQIYKDLDSPAEHYEN-----AFHCDATWREN
 129
 RFG +E VA S+ G V+ + SPAE + A+H D+T+

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQA
 178

Sbjct: 130 PMGCVLRVCVATPPVGGDTIWNMAEAYAKLPDAVKKQIDGLRARHSI---EASFGAAQPT
 186
 G V P VGG T + +M AY L +A + + ARHS+ ++ G Q

Query: 179 GSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LE
 231

Sbjct: 187 EQRHALHQRFDAE--HPVVRTHPETGEKILFVNAFATHFVNYHTPENIRYGIDYAPGSS
 244
 + + A P+V+ HPETG L + A E+ R+

Query: 232 GLVDWACQAPRVHAHQ----WAAGDVVVWDNRCLLHRA 265

Sbjct: 245 NLLNYLISQAAIPEYQVRWRWTPNSVAIWDNRSTQHYA 282
 L+++ + +Q W V +WDNR H A

>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 = 2e-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-RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG ++ G I + T+ + +P E M++ WH+D T+ G
Sbjct: 62 FGPLQTHPAYGTIEGFPEI----TILESTP-EKPTMIE-----CWHSDMTFKKHPPMGT
110

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

+ + ++P GG T ++ M AAYD L + + +A H + K + G
Sbjct: 111 ILRSRIIPKGGDTLWSSMTAAYDGLSSGMQNFLSSLTAVHDFAFG-FKESLAEAGGRER
169

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDDAESERFLEGLVDWACQAP
241

+ + P++ HPE+G+ + + I GM A ES L L +
Sbjct: 170 LAQAVADNPPVEHPVICHTHPESGKKVIFVNELFTTHIVGMTAKESRALLGFLYEHI VTPE
229

Query: 242 RVHAHQWAAGDVVVWDNRCLLHR 264

W + +WDNR H+
Sbjct: 230 FTCTFRFSWQPNSIALWDNRSTQHK 252

>emb|CAY27288.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 119

Score = 83.6 bits (205), Expect = 2e-14, Method: Compositional matrix
adjust.

Identities = 50/125 (40%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
195

T FADMRAAYDALDE + + HS +YS+ KLG + P+R
Sbjct: 1 TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLGGLADFTEEERRVF-----KPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDDAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

LV+ H TGR SL + HA I GM E+ L L ++A + P V++H W D V

Sbjct: 55 QRLVRRHSVTGRKSLFLSAHAGEIEGMSIPEARMLLLDLTEFATRDPFVYSHVWRLNDFV
114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>ref|ZP_05068539.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate

dioxygenase, putative [Octadecabacter antarcticus 238]

gb|EDY88076.1| alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate
dioxygenase, 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 MGARIEGLDLSKPVSAEDHRVVVQALGENGMICIPDQHISAGELKAFAQRFGTLEINVAN 60

Query: 73 G-----DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
125

+++ +SN+K DG S A D WH D +Y +A V

Sbjct: 61 SFMDEDHPEVMILSNIKKDGKPIGLSDAGQD-----WHTDMSYSKDIAFANVLY
109

Query: 126 AEVVPVAVGGR----TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
181

+P G T FA+M AYD L E + + R+A H K+ + +

Sbjct: 110 GLEIPTRDGEPLGCTEFANMHQAYDDLPEELKTKLAGRTATHDFNKFWEKMRSEKGS SRP
169

Query: 182 YIGYGMDTTATP-LRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQ
239

+ P L+P+ HP TGR L + I GMD ES+ L L Q

Sbjct: 170 ALTPEQRAKKPPVLQPVFLTHPITGRTVLYANPGYTMQIDGMDTQESDEILAFLEFKHQLQ
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 = 3e-14, Method: Compositional matrix
adjust.

Identities = 51/125 (40%), Positives = 66/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F+DMR AYD LD+AT+ HS +YS+S LG I + P++
Sbjct: 1 TEFSDMRTAYDRLLDDATKQECGLICEHSQIYSRSLGLGFSDFTDEDLIRF-----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 QRLVRTHPSTGRKSLYLASHAGAIVGWPIPEARAFRLDLNEHATQRALVYAHVVKQWDLV
114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>gb|EEU36693.1| hypothetical protein NECHADRAFT_97202 [Nectria
haematococca mpVI
77-13-4]
Length = 366

Score = 83.2 bits (204), Expect = 3e-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---VGTEVHGLQLSSLSKQKDELALLVAERGVLVFRGQDFADIGFDRQKEFGAH
140

Query: 64 FGAIE-RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG + GG + + R + D+ +K V ++ WH D +Y
Sbjct: 141 FGKLVHGHGHHVKDYPELLP--VYRDFTAGAVDNEIKNNVSSIKWHTDMSYEINGMGT
198

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

+F A P GG T + AAY+AL R +H A HS + Q++ V Y
Sbjct: 199 IFLALDAPPSGGDTLYLSTVAAYNALSPLYREKLGLEATHS-GFEQAR---VADHKERY
254

Query: 183 IGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-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---WTPGTVVVVDNRITQHS 335

>ref|YP_003209304.1| Alpha-ketoglutarate-dependent taurine dioxygenase
[Cronobacter

turicensis z3032]

emb|CBA28475.1| Alpha-ketoglutarate-dependent taurine dioxygenase

[Cronobacter

turicensis z3032]

Length = 283

Score = 83.2 bits (204), Expect = 3e-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 ITITPLGPYIGALVSDINLARPLSDSQFEQLYHALIRHQVLFVRDQPITPQQORALAMRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
118

G + G + + + D +P + D+ WH D T++

Sbjct: 65 GDLHIHPVYPHAEGVEEIIIVLDTHND-----NPPDNDN-----WHTDVTFIDTP
108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ-Q
177

GA+ +A+ +P GG T + AA++AL + L+ A H S + H + +

Sbjct: 109 PAGAILAAKALPPTGGDTLWTSGIAAFEALSAPFQQLLSGLRAEHDFRKSFPPEWKHTKTE
168

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW
236

++ L P+V+ HP +G+ +L + I + ES+ L L

Sbjct: 169 EEHQRWLTAVEKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSPKESDALLSFLFAH
228

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ +W DV +WNR H A RVM + + G

Sbjct: 229 ITKPEFQVRWRWQENDVALWDRVTVQHYANADYLPARRVMHRATILG 275

>ref|ZP_02487377.1| dioxygenase TauD/TfdA family protein [Burkholderia
pseudomallei

7894]

Length = 282

Score = 83.2 bits (204), Expect = 3e-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 MRIEPLTCAIGAELVGVCLADAHDDGLFAEIRAALLAHRVLFRLDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

Sbjct: 61 FG +E VA S+ G VR + E + AWH D+T+ G V
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--HPVVRTHPETGKVLVFNFTTHTNYHTPARVRVGDANPGAALLGY
227

Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

+ P +W V +WDNR H A
Sbjct: 228 LLSQAYIPEYQVRWRWRKNSVAIWDNRSTQHYA 260

>ref|ZP_04026341.1| Probable taurine catabolism dioxygenase [Tsukamurella
paurometabola

DSM 20162]

gb|EEK01743.1| Probable taurine catabolism dioxygenase [Tsukamurella
paurometabola

DSM 20162]

Length = 297

Score = 83.2 bits (204), Expect = 3e-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 GEHIGSRIDGIRLGGDLAEDEDIAFIRATLLERKVVFFRDQHDLDAAHQEFGRRLGDL-- 67

Query: 70 IGGGDIVAIISNVKADGTVRQHSPAEWDDMMKVIVGNMA--WHADSTYMPVMAQGAVFSAE
127

G V + P+ + G A WH D T+ GA+ A
Sbjct: 68 -----GAVHLNDPSAHVAAIDSEHGGKANWWHTDITFSERPPAGAILRAV
112

Query: 128 VVPAVGGRTCFADMRAAYDALDEATRAL-----VHQRSA-RHSLVYSQSKLGHVQQAGS
180

+P GG T +A+ AAY L R L VH SA R L Q++ +
Sbjct: 113 QLPDFGGTTIWANTAAAYAQLPAELRRLADALWAVHDNSAFRDDLSPQARAARDHPDTA
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 PELTVRWDWQPGDVVVIWDNRATQHYA 257

>gb|ABL97678.1| taurine dioxygenase [uncultured marine bacterium
EB0_39H12]
Length = 288

Score = 83.2 bits (204), Expect = 3e-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 FKNRSLPTIGGEIHGVDLSSPLDTTTKELIYEALLVYKVIFFRDQDISTEEHINFSKSF 75

Query: 65 GAIE-----RIGGGDIVAIS-NVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP
116
G +E + +++ I+ N K+ G WH+D T+
Sbjct: 76 GELEIHPFAPKKQDFPEVLVITHNEKSKGQEN-----VWHS DVTWRQ
117

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ
176
+ G+V P GG T F+DM AAY+ L + + + A H +++L
Sbjct: 118 EP SLG SVLRMIEKPQHGGDTLFS DMNAAYNNLSDEVKDRLEGAI AVHDFANFRNRLIKEG
177

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVD
235
++ + + P P+++ HP+T + + + I G D ES+ L L
Sbjct: 178 KSKEEITAFN-EQYPMPEHPVIRTHPDTKNKVIYVNKAFTQYIKGWDKEESDDMLNYLYS
236

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
A W + WDNR H A
Sbjct: 237 RASVPEFQCRFAWQDNSIAFWDNRACQHYA 266

>emb|CAY27518.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 83.2 bits (204), Expect = 3e-14, Method: Compositional matrix
adjust.
Identities = 53/125 (42%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195
T F DMRAAYDALDE T+A HS ++S+S LG + P+R
Sbjct: 1 TEFWDMRAAYDALDEETKAECENLICEHSQ LFSRSILGFTDFTDDERRKFA-----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 QRLVRRHPVTGRRSLYLASHAGAILGWPVPEARAFRLRDLTEHATQRSFVYAHVWRQWDPV
114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>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 = 4e-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 LTKNKITAVSNGSGVCADIVGFDFNDYDAQDVAEVRKIWLQYGVVRFRDIDITDEQHIKF 61

Query: 61 AKRFGAI----ERIGGG-----DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNM--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 HTDTSWFYERPPAGALLRSIALPPTGGDTYVWSMYQAYETLPSYLLDAVKGRQIFFQSVYD
169

Query: 169 QSKLGHVQQAGSAYIGYGMTTATP--LRPLVKVHPETGRPSLLIG----RHAHAIPGM
221

+ + + + D P + PLV+VH ++GR +L +G I G+
Sbjct: 170 AAGGLRLNKQ----VPKSDDIREWP GIVHPLVRVHGDSDGRQALYLGAKGVREQDSWIVGL
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 = 4e-14, Method: Compositional matrix adjust.

Identities = 51/125 (40%), Positives = 65/125 (52%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDALDE T+ HS ++S+S LG + P+R
Sbjct: 1 TEFGDMRAAYDALDEETKTECENLVCEHSQLF SRSILGFTDFTEDEHRHFA-----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 QRLVRRHPVTGRRSLYLASHAGAILGWPGPEARAFRLDLNEHATQPEFVYVHKWTLHDLV
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 = 4e-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 TEFGDMRAAYDALDDETQAEIVGLISEHSLIYSRESLGFNDPTEAER-----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| 2-oxoglutarate-dependent 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

NTUH-K2044]

Length = 283

Score = 82.8 bits (203), Expect = 4e-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 LSITPLGPYIGAQVSGADLTRPLSDNQFEQLYHAVLRHQVVFLREQNITPAQQORDLALRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
118

G + G + + + D +P + D+ WH D T++

Sbjct: 65 GDLHIHPVYPHAPGVVEEIIIVLDTHND-----NPPDNDN-----WHTDVTFIDTP
108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
178

GA+ +A+ +P GG T + AA++AL E R L+ A H S + + +

Sbjct: 109 PAGAILAAKELPTTGGDTLWTSGIAAWEALSEPFRQLLSGLHAEHDFRKSFQEYKYNKTE
168

Query: 179 GSAYIGYGMDTTATP-LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW
236

P L P+V+ HP TG+ +L + I + ES L L

Sbjct: 169 AEHRRWQEAVAKHPPLLHPVVRTHPVTGKQALFVNEGFTTRIVEVSEKESAALLNFLFAH
228

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ +W DV +WNR H A R+M + + G

Sbjct: 229 VTKPEFQVRWRWQPNDVAIWDNRVTQHYANADYLPQRRIMHRATILG 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 = 4e-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 MRIEPLTCAIGAELVGMCLADAAHDDDLFAEIRAALLAHRVLFRLDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
 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-----AHAI PGMDAAESERFLEGL
 233
 A P+V+ HPETG L + A G DA L G
 Sbjct: 170 LKAQFPDAE--HPVVRTHPETGEKVLVNAFTTHTFTNYHTPARVRVGDANPGAALLLGY
 227

Query: 234 VDWACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
 + P +W V +WDNR H A
 Sbjct: 228 LLSQAYIPEYQVRWRWRKNSVAIWDNRSTQHYA 260

>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 = 4e-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 LSITPLGPYIGALISGADLSRPLSDNQFEQLYHAVLRHQVVFLREQVITPQQQRALALRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
118
G + G + + + D +P + D+ WH D T++
Sbjct: 65 GDLHIHPVYPHAEGVEEIIIVLDTHND-----NPPDNDN-----WHTDVTFIETP
108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
178
GA+ +A+ +P+ GG T + AAY+AL R L+ A H + +S H +A
Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGIAAYEALSAPFRQLLSGLRAEHD--FRKSFPEHKYRA
166

Query: 179 GSAYIGYGMDTTATP---LRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLV
234
+ A L P+V+ HP +GR +L + I + ES+ L L
Sbjct: 167 TEEEHQRWREAVAKHPPLLHPVVRTHPVSGRQALFVNEGFTTRIVDVTEKESDALLSFLF
226

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
+ +W DV VWDNR H A R+M + + G
Sbjct: 227 AHITRPEFQVRWRWQPNDVAVWDNRVTQHYANADYLPQRRIMHRATILG 275

>emb|CAY27446.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY27557.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 82.4 bits (202), Expect = 6e-14, Method: Compositional matrix adjust.

Identities = 48/125 (38%), Positives = 63/125 (50%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAAGSAYIGYGMDTTATPLR
195
T FADMRAAYDALD+ T+A HSL+YS+ LG + + P+R
Sbjct: 1 TEFADMRAAYDALDDETKAETEDLICEHSLMYSRGSGLGFTDYSEEEKQMFK-----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 = 6e-14, Method: Compositional matrix
adjust.

Identities = 67/219 (30%), Positives = 98/219 (44%), Gaps = 39/219 (17%)

Query: 56 QQITFAKRFGAI-----ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGN
105

QQI FAKR+G I + G +IV K D TV GN
Sbjct: 1 QQIAFAKRWGEIHLHPMPCLPDNPGIIEIVK----KEDDTV-----AFGGN 43

Query: 106 MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSL
165

WH D A+ + A+ VPA GG T +A++ AYD+L + +A++
Sbjct: 44 --WHTDQMLTDTPARVTMLYAKQVPAAGGDTLYANLYQAYDSLSDGMKAMIED----- 94

Query: 166 VYSQSKLGHVQQAGSAYIGYGMTTATPLR-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 EAESRPILSYLLNHAIRPEFTCRFRWQVGSLLVVWDNRCV 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 = 6e-14, Method: Compositional matrix
adjust.

Identities = 70/271 (25%), Positives = 114/271 (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 LSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFLRDQAITPQQQRALAQRF 64

Query: 65 GAIE-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
118

G + G D + + + D +P + D+ WH D T++
Sbjct: 65 GELHIHPVYPHAEGVDEIIVLDTHND-----NPPDND-----WHTDVTFIETP
108

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQA
178

GA+ +A+ +P+ GG T + AY+AL R L+ A H S + + ++

Sbjct: 109 PAGAILAAKELPSTGGDTLWTSGITAYEALSVPFRQLLSGLRAEHDFRKSFPPEYKY-RKT
167

Query: 179 GSAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD
235

 + + P L P+V+ HP +G+ +L + I + ESE L G +
Sbjct: 168 EEEHQRWREAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALL-GFLF
226

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

 P +W D+ +WDN H A
Sbjct: 227 AHITKPEFQVRWRWQPNDIAIWDNCVTQHVA 257

>ref|NP_767577.1| putative dioxygenase [Bradyrhizobium japonicum USDA 110]
dbj|BAC46202.1| blr0937 [Bradyrhizobium japonicum USDA 110]
Length = 309

Score = 82.0 bits (201), Expect = 6e-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 TIAVEKLTPIIGAEISGVDIGRLVSDDVRSNQMDIHRALAENLVIFFRDQHISPPQHL 94

Query: 59 TFAKRFGAIERIGGG----DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTY
114

F ++FG + + A+ + AD ++SP WH+D +
Sbjct: 95 AFGKRFGEHLHFHPAAPHEDDEPALMKIYAD----KNSPR-----ANGEGWHSVSDVSC
141

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
174

G++ + P GG T FA+M AAY+AL + +A + +A H G
Sbjct: 142 DLEPPMGSILYIKQCPPRGGDTLAFANMYAAYEALS DRMKAYLDGLTALHD-----GE
193

Query: 175 VQQAGSAYIGYGM-DTTATP--LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL
230

G Y YG+ D + P P+++ HP TGR +L + R I G+ ES+ L
Sbjct: 194 PIYRG-LYANYGVADRPSYPNAEHPVLRTHPVGTGRKALYVNRGFTRHINGIPRDESDAML
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 = 6e-14, Method: Compositional matrix adjust.

Identities = 46/128 (35%), Positives = 70/128 (54%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDAL + T+ + A HS+ +S+S++G + + D A L
Sbjct: 1 TEFADMRAAYDALPDETKRQIEGLIAEHSIFHSRSRIG-----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 = 7e-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 LTIRPLAPGFGAEIVGLDLNRPIDAATEAAIRA AWIEHGILLFRGEDQDDAAQMRLSAIF 70

Query: 65 GAIERIGGGDI-----VAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTY
114

G +E D+ +A +QH D G + WH D ++
Sbjct: 71 GEMEPAAATADMNDPNDNRFMMTLAYDPDDKAPRFQQHYNVGGIDR----AGWLGWHWDQSF
126

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGH
174

MP + +GAV E+ G T F D A+D L + +A R +VY +
Sbjct: 127 MPTIVRGAVLRMEMPSPEMGETGFIDAVGAWDRLPDDLKA----RIEGLVYVYLFNP---
179

Query: 175 VQQAGSAYIGYGMDDTTATP-----LRPLVKVHPETGRPSL-LIGRHAHA I
218

S G+ D A P + P+V ETGR L L HA I
Sbjct: 180 --DFVSGQYGFPEDIRALPRERPSKEPSYDFPPVHVMVITQVETGRKVLKLSMPHARYI
237

Score = 81.6 bits (200), Expect = 9e-14, Method: Compositional matrix adjust.

Identities = 48/124 (38%), Positives = 66/124 (53%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
195

T F DMRAAYDALD T+AL+ HS ++S+ LG ++ + A +
Sbjct: 1 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 RLVTRHPKTGRKSLYLSSHAGRIVGWPVPEAMLLLRDLNEHATQPEFVYVHKWTLHDLVM
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 NSIQVEPVTCTIGAELSNVNLGAAAEEDEQLMAEIRALLLRHRVLFVRDQDITRAQHVAFA 78

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQH----SPAEWDDMMKVIVGNMAWHADSTYMPV
117

+RFG +E V S+ G V+ + SP + ++ +WH D+T+
Sbjct: 79 RRFGELE----DHPVVGSHPDYPGLVQIYKTPDSPDRNEN-----SWHTDATWREK
126

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQ
177

G V P VGG T + +M AY+ L E + + ARH + S +++
Sbjct: 127 PPLGCVLRICIECPPVGGDTMWNMVEAYNQLPEDIKTKIATLRARHGIEASFGAAMPIEK
186

Query: 178 AGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-----AHAIP-----GMDAAE-
225

+ Y P+V+ HPETG L + + +P G+D A
Sbjct: 187 RLALKAQY-----PDAEHPVVRTHPETGKVLVFNVSFTTHTNYNVPANVRFGIDKAPG
241

Query: 226 SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 + L LV A +W V WDNR H A
 Sbjct: 242 AANLLSYLVSQATIPEYQVRFRWKKNSVAFWDNRSTQHYA 281

>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 MRIEPLTCAIGAELVGMCLADAAHDDDLFAEIRAALLAHRVLFRLDQDITRAEHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVI VGNMAWHADSTYMPVMAQGA
 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 GYGMDDTATPLRPLVKVHPETGRPSLLIGRH-----AHAI PGMDAAESERFLEGL
 233
 A P+++ HPETG L + A G DA L G
 Sbjct: 170 LKAQFPDAE--HPVMRTHPETGEKVLVNAFTTHTFTNYHTPARVRVGDANPGAALLLGY
 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---LGAIVDDVDLSNATDALRDDIRAAALAHHQVLFVRGQRLSAAHRHRDFAAGFGD 59

Query: 67 I-----ERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMA
 119

+ +I+ + N D + N WH D T+
 Sbjct: 60 LHVHPIYPSHPDAREIMVLDNAVFD-----LQDNAIWHTDVTFTETPP
 102

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLV--YSQSKLGHVQQ
 177

+ ++ +A +P GG T + AAYDAL +A + +A+H + + G V
 Sbjct: 103 RASILAAHTLPETGGDTLWGSFGFAAYDALSGRVKAQLDGLTAQHDFTKSFPLKRFG-VTA
 161

Query: 178 AGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGR----HAHAIPGMDAAESERFL---
 230

A T + P+V+ HPETGR +L + +P + A RFL
 Sbjct: 162 EDRARWEKTRATHPSVAHPVVRTHPETGRKTLFVNEGFTTEIDELPEEEGAALLRFLFAH
 221

Query: 231 ----EGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP
 285

E + W +W GDV WDNR +H A K RVM + + G RP
 Sbjct: 222 QSRPEFTLRW-----RWQPGDVAFWDNRSTIHYAVNDYGKAHRVMHRATIVGDRP
 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 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLG--HVQQAGSAYIGYMDTTATP
 193

T FADMRAA+D LD T+ V HS +YS+ LG ++ A+ A
 Sbjct: 1 TEFADMRAAWDMLDARTKEQVKDLVVEHSRIYSKGVLPFTEEEKRAF-----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 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

V P VGG T +A+M AY+ L + + + ARHS+ S V + +

Sbjct: 112 VLRCIEGPPVGGDTMWANMVLAYERLPDHVKQQIADLRARHSIEASFGAAMPVDKRLALK
171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----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 YLISQAYIPEYQVRWRWKKNSVAIWDNRSTQHAYA 260

>gb|ADC33936.1| TfdA-like protein [uncultured bacterium]

Length = 124

Score = 81.3 bits (199), Expect = 1e-13, Method: Compositional matrix
adjust.

Identities = 48/128 (37%), Positives = 70/128 (54%), Gaps = 6/128 (4%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATP--
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 ERPLVDVHRPTGRRCLMLGANIASVGALDEIESVAFLDELTD RATAPAFVYSHRWSAGDL
116

Query: 254 VVWDNRCL 261
++WDNRC+

Sbjct: 117 LLWDNRCV 124

>ref|ZP_04028685.1| Probable taurine catabolism dioxygenase [Tsukamurella
paurometabola

DSM 20162]

gb|EEJ99292.1| Probable taurine catabolism dioxygenase [Tsukamurella
paurometabola

DSM 20162]

Length = 305

Score = 81.3 bits (199), Expect = 1e-13, Method: Compositional matrix
adjust.

Identities = 69/265 (26%), Positives = 109/265 (41%), Gaps = 23/265 (8%)

Query: 2 AQTTLQITPTGATLGATVTGVHLA-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 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG
179

+ ++ +P GG T +A AYD L E + L A H+ Y + Q

Sbjct: 112 KASILRPVTLPPHGGNTTWASTTRAYDRLPEPLKVLAEENLRAIHTNDYDYAGHNSTYQRA
171

Query: 180 SAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ
239

+ + + P+V++HPETGR SLL+G G+ + +S L L+ +

Sbjct: 172 EYHQEF-IRNIFEAEHPVVRMHPETGRRSLLLGHFVSKFAGLSSQDSAPIL-ALLQRRIE
229

Query: 240 APRVHAH-QWAAGDVVWDNRCLLH 263
P W GDV +WDNR H

Sbjct: 230 NPDNTVRWAWQPGDVAIWDRNSTQH 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 = 1e-13, Method: Compositional matrix
adjust.

Identities = 68/266 (25%), Positives = 112/266 (42%), Gaps = 27/266 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKR 63
 ++ G +GA + GVHL+ L + A++ A H ++ F GQ HL + Q FA
 Sbjct: 22 ITVHKVGELIGARIDGVHLSGDLSEETAYAINYALAAHKVVFQGGQHLDDTSQYEFAGT 81

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
 123

G VK+ G D ++ + +WH D T++ + + ++
 Sbjct: 82 LGT-----QTPHPTVKSKG-----DKLLVLDRAANSWHTDVTFVDRIPKASI
 124

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS---
 180

A +P GG T +A AAY+ L + + V A H+ Y +++ V QA
 Sbjct: 125 LRATTIPEYGGATTWASTTAAEQLPASLKVFFVENLRAVHTNAYDYAEV--VNQANPVDA
 182

Query: 181 ---AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA
 237

AY P+V++HP TG +LL+G G+ +ES + L
 Sbjct: 183 QRLAYYAEFTREIYETEHPVVRHPATGEKTLLLGHFFKEFVGLKPSESVALYQLLQARI
 242

Query: 238 CQAPRVHAHQWAAGDVVVDNRCLLH 263

+ W+AGD+ +WDN+ H
 Sbjct: 243 IKLENTVRWNWSAGDLAIWDNQATQH 268

>ref|YP_002650372.1| Taurine dioxygenase, 2-oxoglutarate-dependent

[*Erwinia pyrifoliae*

Ep1/96]

emb|CAX57170.1| Taurine dioxygenase, 2-oxoglutarate-dependent [*Erwinia*
pyrifoliae

Ep1/96]

emb|CAY76028.1| taurine dioxygenase, 2-oxoglutarate-dependent [*Erwinia*
pyrifoliae

DSM 12163]

Length = 279

Score = 81.3 bits (199), Expect = 1e-13, Method: Compositional matrix
 adjust.

Identities = 75/290 (25%), Positives = 122/290 (42%), Gaps = 31/290 (10%)

Query: 6 LQITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 ++I G +GA V+ ++L+ L DA F L+ A ++H +L Q L+ QQ A RF
 Sbjct: 5 IRIQTLGPHIGALVSDINLSRPLSDAQFEQLYHALIRHQVLFRLDQPLTPPQQRQLAARF 64

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIV-----GNMAWHADSTYM
 115

G + V H+P D+ ++IV N WH D T++
 Sbjct: 65 GDLHI-----HPVYPHAP----DVEEIIIVLDTHDDNPPDNDNWHTDVTFI
 105

LV+ HP TGR SL + HA AI G E+ FL L + A Q V+AH W D+V
 Sbjct: 55 QRLVRRHPVTGRRSLYLASHAGAILGWPVPEARAFRLRDLNEHATQRRFVYAHVWRQWDLV
 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 = 1e-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 ITVEPASRNCGAFVDGVDLTKPVTSIAICREIHTALMRHQVVFVRDQDVTTPVEQTTFARNF 66

Query: 65 GAIERIGGGDIVAISNVKADGTV----RQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
 120

G + RI + + ++ +V R+H P + D +HAD +
 Sbjct: 67 GPL-RIKHRSAFELHDDTSEVSVIVNNREHPP--YID-----HYHADGMFRMEPEF
 114

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGS
 180

++ AE P +GG T F ++AA++ L +A RA + + A VY KL +
 Sbjct: 115 ASMLKAEAPPKMGGDITFVSLKAAWNGLSDALRATLDDKIA----VYDFMKLHSTPEKAR
 170

Query: 181 AYIG---YGM----DTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEG
 232

+ G GM D PLV HP +G L AI G++ ESE +
 Sbjct: 171 NWTGPSRQGMIKSRDENPPVQHPLVPKHPVSGERCLYFSESFTAAAILGLNKYESEA-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

>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 TCFADMRAAYDALDEATRVLVHQRSAHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
 195

T F DMR A++ L +A + + +A HS+ +S++ G + GY P R
 Sbjct: 1 TEFCDMRRRAWELLSPEEQAELEELTANHSIAHSRALAGFTEWPA----GYDEFLQRVP-R 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
 255

PLV VHP+TGR +LL H + G + E+ + L+ A +AH+W+ GD ++
 Sbjct: 56 PLVGVHPDTGRKALLTASHIETLTGKNKEETTELVAELIQRATVPENCYAHRWSKGFILM
 115

Query: 256 WDNRCL 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---FCAEIRDIKLNQPLNKDIIKTIESDLEEHEVLVFPDQDITSEDLMRIGR 64

Query: 63 RFGAI-----ERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP
 116

FG + E + + + K+ P D WH+D TY
 Sbjct: 65 YFGQLTVHPFAENSEKNPELIVFDYKSGN-----PPVLT-----RWHSDETYKL
 109

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSAHSLVYSQSKLGHVQ
 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 TEEGKLLQKKELEYPPIAHPVRIHPKTRKKTLEFVNPYTRYIKNMDQRDSALLAQLF
227

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ + H W +V+WDNR + H A
Sbjct: 228 NTTSVLEYQYRHHWKPNMLVMWDNRSVQHAA 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 MQIEQLTCNIGAELSGVKLSDAIYDDGLFAEIRTQLLKHVFLFLRDQHLTRQDHVAFER 60

Query: 64 FGAIERIGGGDIVAI-SNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG +E D A+ S+ G V+ + E V AWH+D+++ G
Sbjct: 61 FGQLE-----DHPAVGSDPDHPGLVQIYKHPE----SPVNRyenAWHSDASWRKAPPMGC
111

Query: 123 VFSAEVVPVAVGGRTCFADMRAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

V P VGG T + +M AY++L + + + A HS+ ++ G +
Sbjct: 112 VLHCVECPPVGGDTMWTNMVMAYESLPDDIKNKIADLRAYHSI---EASFG-----AAMP
163

Query: 183 IGYGMDDTTAT---PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----
229

+ +D A P+V+ HPETG L + E RF
Sbjct: 164 LEKRLDLKAKFPDAEHPVVRTHPETGEKILYVNAFTTTHFSNYHTKERVRFQDANPGSAE
223

Query: 230 -LEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

L L+ A P +W + +WDNR H A
Sbjct: 224 LRLYLISQA-YIPEFQVRWRWKPNISIAIWDNRSTQHAYA 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 SITVDRVSANIGAVIGGVRIGGDLDATTVSEIKRALVEHKVVFLRGQQHADDATQRAFAS 78

Query: 63 RFGAIE----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
 118

G + G D + A+G +WH D T++ +
 Sbjct: 79 LLGTPTLPHTVTGADNSVLPIDAAEGKAN-----SWHTDVTFVDRI
 120

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY-----SQSKL
 172

+V A +P GG T +A+ AY L+ A +AL + A HS +Y ++ +
 Sbjct: 121 PSASVLRVAVTLPPYGGTTWANTAHAYSTLNPALQALADRLWAVHSNLYDYAAERTEKAI
 180

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG
 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 LQRHVIRLEHTVQWSWRDGDIAIWDNRATQHAYAIADYDDQPRRLHRITLAG 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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
 195

T FADMR AYD LD+ TRALV H+ +YS+ +G + P+R
 Sbjct: 1 TEFADMRIAYDLLDDETRALVEDLVCEHTQLYSRGSMTGFSDWTEERAMFK-----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 QRLVRTHPVTGRKSLYLSSHAGTIIGWQMPEARDLLRDLNEHATRPELVYIHRWRQYDLV
 114

Query: 255 VWDNR 259
 +WDNR

Sbjct: 115 MWDNR 119

>ref|ZP_06239906.1| Taurine dioxygenase [Frankia sp. Eu11c]
 gb|EFA58810.1| 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 TLDVRPMSGHIGAEIFGVDLSEPLAPAVTAEIRAALLAWKVIFFRDQRLTPDQHIAFGRL 79

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
 115

FG + G +I+A+ + +A + D +++ WH D T++
 Sbjct: 80 FGEVGPGHPTLPTLEGHPEILAL-DTRAYAGLDSSGDRRGDGGIRI---KSLWHTDVTFL
 135

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHV
 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--ASSPLEAVHPVVRVHPETGERALFVNPTFTTRIVELTNTESAHVLN
 247

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH 263

L +W GD+ WDNR H
 Sbjct: 248 LLYQHMTNLEFTCRFRWQPGDLAFWDNRATAH 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----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
 118

FG + + GD + V+A+ R WH D T
 Sbjct: 81 LFGPLRALPVDSIDGDDPELVVVRANAQSR-----FAAGELWHTDGTADLEP
 127

Query: 119 AQGAVFSAEVVPAV--GGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
 176

+ G++ + PA+ GG T FA+M A + L A + + +A H G +

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 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM
115
 QQI FAK+FGA V +K +P + + G + WH+D+TY+
Sbjct: 1 QQIAFAKKFGAP-----VEYPQLKGLAECYPVTPVVKLEHERNNFGGI-WHSDTTYL 51

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATR----ALVHQRSARHSLVYSQSK
171
 + G++ A VP GG T FA+ AY+AL + + L+ S+ + V ++++
Sbjct: 52 EIPPMGSMLLAREVPPYGGDTMFANQYLAYEALS DGLKQTL DGLIGVSSSAKADV-TKTR
110

Query: 172 LGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFL
230
 ++QAG ++ PLV+ HPETGR +L H I G ES L
Sbjct: 111 EDALKQAGERATPKVLEAE----HPLVRTHPETGRKALYTSVAHTARIKGWTEQESLPLL
166

Query: 231 EGLVDWACQA-PRVHAH-QWAAGDVVVDNRCL 261
 E L WA Q P QW G + WDNRC+
Sbjct: 167 EFL--WAQQVRPEFTCRFQWLVGSLAFWDNR CV 197

>ref|ZP_06235283.1| Taurine dioxygenase [Frankia sp. Eu1lc]
gb|EFA63399.1| Taurine dioxygenase [Frankia sp. Eu1lc]
 Length = 324

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: 41 RLTPR---IGARLDGLDLRTLPRSGRAEELRTALVAHKVLFVPGQDL DADDHVALGRALG 97

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
125
 V S+ G +H D ++ WH D T+MP ++
Sbjct: 98 D-----VTTSHPVVPGADERHPEIYELDSHDGGTSDV-WHTDVTFMPRPPMASILR
147

Query: 126 AEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
185
 A +P +GG T + D+ AY++L A RAL A H + G + G
Sbjct: 148 AVRLPDLGGATNWDLEQAYESLSPAVRALADGLEAIHD---GNREFG--EYLAHRRGGE
202

Query: 186 GMDTTATPLRPL-----VKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA
237
 G D T +R L V+VHPETGR SL + I G+ AES L+

Sbjct: 203 GNDWDGTRVRALVPVRHPVVRVHPETGRRSLFVNPGFTVRIAGVSDAESRGLLDIFFAHL
262

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAG 283
+ + H W GDVV+WDNR H A+ R+M L G

Sbjct: 263 TRPEHLVRHHWRPGDVVLWDNRSTAHYADHDYGDYQFQIMHRITLRG 308

>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 EVSDV D L C N P M T D D M K R S L R E L V N R H E L V F F R D Q A I T P A Q Q R D L A A L F 60

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF
124

G ++ D V + V + +P + + WH+D T+ V

Sbjct: 61 GPLQSHPAYDTVPD---LPEVMVLESTPEKPSKIE-----VWHS D M T F R Q H P P S I T V L
110

Query: 125 SAEVVPVAVGGRTCFADMR AAYDALDEATR ALVHQRSARHSLVYSQS-KLGHVQQAGSAYI
183

+P+VGG T +A M AAY+AL + + +A H +SQ K ++ G +

Sbjct: 111 RGVEIPSVGGDTLWASMTAA YEALSPGMQRYLQDLTAVHD--FSQGFKESLSEEGGRERL
168

Query: 184 GYGMDDTATPLRPLVKVHPETGRPSLLIG----RHAHAI PGMDAAESERFL---EGLVDW
236

+ P+++ HPETGR ++ + H I +++AE +FL ++

Sbjct: 169 ADALANNPPVRHPVIQTHPETGRKAIFVNALFTTHIEGISPLESAEVLQFLYKHSTTPEF
228

Query: 237 ACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
C+ +WA VV+WDNR H+

Sbjct: 229 TCRL-----RWAKDTVVIWDNRSTQHK 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-SPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
 122

FG +E VA S+ + G VR + SP + +D + AWH+D+++ G
 Sbjct: 61 FGELE----DHPVAGSDPEHPGLVRIYKSPDQPNDRYE-----NAWHS DASWRVAPPFGC
 111

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAY
 182

V P VGG T +A+M AY+ L + + + ARHS+ S + + +
 Sbjct: 112 VLRCIDGPPVGGDTMWANMVLAYENLPDHVKQIADLRARHSIEASFGAAMPIDKRLALK
 171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGM DAAE-SERFLE
 231

Y P+V+ HPETG L + A G DA + + L
 Sbjct: 172 AQY-----PDAEHPVVRTHPETGEKVLVNAFTTHFTNFHTPARVRVGQDANPGAGQLLH
 226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

L+ A +W V +WDNR H A
 Sbjct: 227 YLIGQAAIPEYQVRWRWKKNSVAIWDNRATQHYA 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-----IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTY
 114

+G + + G V ++ K+ + P D+ WH D T+
 Sbjct: 108 YGPLHQHPTMGYPKGTGPEFHVVYADEKSGNLRKLLGPRTTYDL-----WHVDQTF
 158

Query: 115 MPVMAQGAVFSAEVVPAVGG-RTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLG
 173

P + + F +P+ GG T F + AAY+AL A R Q L ++ + G
 Sbjct: 159 TPNVPSTSFFWVLEIPSSGGGDTAFTSLTAAYEALSPA FR----QTLTLNKLHHTSASEG
 214

Query: 174 HVQQAGSAY-IGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGM DAAEESERFLE
 231

Sbjct: 1 T FADMRAAYDALD+ T+A + RHS +YS+ KLG + +
TEFADMRAAYDALDDRTKAEIEDLVCRHSNMYSRGLGLAEFTNEERAVFKPVRQRL--- 57

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

Sbjct: 58 --VRRQRVSGRKSFLSAHAGEIEGMPTPQARMLLLDLTEFATREPFVYSHVWRVNDLVM
115
V+ +GR SL + HA I GM ++ L L ++A + P V++H W D+V+

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 = 2e-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 IGTEIVGLQLKDLTNQQRDELALLIAERSVVFFRDQDLSPQQQKALGEHFGEIEVHPQVG
155

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVG
133

+ + V Q E + + G WH+D + A + +P+VG

Sbjct: 156 QVPGVPGVTVLWPALQ--AVEREPNFRKTGGASTWHSDLVHESQPAGITHLHNDTIPSVG
213

Query: 134 GRTC FADMRAAYDALDEATR LVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATP
193

G T +A +AY+ L + R + ++A + +S G+ QAG ++

Sbjct: 214 GDTLWASGYSAYEKLSPSFRKFIDGKTAIYRSAHSYLDGRN-PQAGPQFVERE-----
265

Query: 194 LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAG
251

PLV+ HP TG +L + R I G+D AES+ L L D ++P + +W+

Sbjct: 266 -HPLVRTHPATGWKALWVNRSMTRIVGLDKAESDLILGYLYDVYERSPDIQVRFKWSPK
324

Query: 252 DVVVWDNRCLLHRAEPWDFK 271

+WDNR +H A WD++

Sbjct: 325 SSALWDNRITIHNAS-WDYE 343

>gb|EEU37137.1| hypothetical protein NECHADRAFT_86763 [Nectria
haematococca mpVI
77-13-4]
Length = 363

Score = 80.5 bits (197), Expect = 2e-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 LLKEGVKISEITKSIGAEVTGVQLSQLDNKAKDELALLVAQKKVVVFHDQDFNTIPIQQA
137

Query: 58 ITFAKRFGA--IERIGGGDIVAISNVKADGTV-RQHSPAEWDDMMKVIVGNMAWHADSTY
114
+ FA FG + + G A+ V R D ++ +++WH+D +Y
Sbjct: 138 VDFASYFGKLVHPVSG----AVPGFPQLHMVHRGLDDVGHDKFLETRTTSVSWHSDVSY
193

Query: 115 MPVMAQGAVFSAEV-VPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLG
173
+ G F + VP GG T F + AY+ L A R + HS
Sbjct: 194 E-LQPPGTTFLYAIDVPEAGGDTLFVNQVKAYERLSPAQRLEGLKVVHS-----A
244

Query: 174 HVQ-QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLE
231
H Q QA G T + PLV+ HP TG +L I + A +I G ES+ L
Sbjct: 245 HEQAQAALKNDGQLRRDPITSVHPLVRTHPATGEKALYIQPFARSIVGYKKEESDSLNN
304

Query: 232 GLV-----DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR
284
L D C+ +W+ VVVWDNR H D++ PR + +RLA +
Sbjct: 305 FLYHHIAFSQDLQCRV-----KWSPRSVVVWDNRVTAHSGL-VDWEGPRFRYIARLAAQ
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 = 2e-13, Method: Compositional matrix
adjust.

Identities = 48/126 (38%), Positives = 65/126 (51%), Gaps = 10/126 (7%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLG--HVQQAGSAYIGYGMDTTATP
193
T F DMRAA+D LD T+ V HS +YS+ LG ++ A+ A
Sbjct: 1 TEFGDMRAAWDMLDARTKEQVKDLVVEHSRIYSKGVLPFTEEEKRAF-----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|ACG80552.1| TfdA [uncultured bacterium]
Length = 119

Score = 80.1 bits (196), Expect = 2e-13, Method: Compositional matrix
adjust.

Identities = 46/128 (35%), Positives = 69/128 (53%), Gaps = 13/128 (10%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDAL T+ + A HS+ +S+S++G + + D A L
Sbjct: 1 TEFADMRAAYDALPNDTKRELEGLVAEHSIFHSRSRIG-----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 PVQQVVVRTHPGSGRKTLYLASHASHVIGWPIERGRKLIEDLLDFATQPFVYQHRWQV
111

Query: 252 DVVVDNR 259

D+V+WDNR
Sbjct: 112 DLVVDNR 119

>gb|ADC33937.1| TfdA-like protein [uncultured bacterium]
Length = 124

Score = 80.1 bits (196), Expect = 2e-13, Method: Compositional matrix
adjust.

Identities = 47/128 (36%), Positives = 71/128 (55%), Gaps = 6/128 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL-
194

T F DMR A++AL +A + ARHSL S+ K G + ++ D P
Sbjct: 1 TEFCDMRLAWEALPPDEQAALPLIARHSLWLSRRKYG----SDKSFSFNEDDVRRYPPV 56

Query: 195 -RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV
253

RPLV VH TGR L++G + ++ +D +S FL+ L D A +++H+W AGD+
Sbjct: 57 GRPLVDVHRPTGRRCLMLGANIASV GALDEVDSVAFLDELTD RATAPDFIYSHRWTAGDL
116

Query: 254 VVWDNRCL 261

++WDNRC+
Sbjct: 117 LLWDNRCI 124

>emb|CAY27245.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 80.1 bits (196), Expect = 2e-13, Method: Compositional matrix
adjust.

Identities = 49/125 (39%), Positives = 64/125 (51%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
195

T FADMRAAYDALDE + + HS +YS+ KLG + P+R
Sbjct: 1 TEFADMRAAYDALDERLKHQIEDLVCLHSNMYSRGKLGADFTTEERRVF-----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 = 2e-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 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 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

V P VGG T +A+M AY+ L E + + ARHS+ S + + +
Sbjct: 112 VLRCIDGPPVGGDTMWANMVLAYERLPEHVKQQIDGLRARHSIEASFGAAMPIDKRLALK
171

Query: 183 IGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGMDAAE-SERFLE
231

Y P+V+ HPETG L + A G DA + + L

Sbjct: 172 AQY-----PDAEHPVVRTHPETGEKVLVNAFTTHTNFHTPARVVRVGDANPGAGQLLH
226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
L+ A +W V +WDNR H A

Sbjct: 227 YLISQAAIPEYQVRWRWKKNSVAIWDNRATQHYA 260

>gb|EAZ63084.2| alpha-ketoglutarate catabolism dioxygenase [Pichia
stipitis CBS
6054]
Length = 386

Score = 80.1 bits (196), Expect = 2e-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---FGSSVTGVQLSQLDSAGKDELALLVAQRGVVIFREQDFADKGPFAVEYQKH
142

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

FG + I ++ + T R+ E++ + N+ WH+D +Y

Sbjct: 143 FGRL-HIHPTSGAPRNHPELHITYRRPDKGEFERVFSNRTNNVWHSVSYELQPPGTTF
201

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
183

FS P GG T FAD AY+ L + + + H L S+ + + + G

Sbjct: 202 FSVIEGPESGGDTIFADTVEAYNRLSPEFQKRL---AGLHVLHTSKDQASNSRGQG----
254

Query: 184 GYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPR
242

G + + PL++ HP TG ++ + + A I + ESE L+ L D +

Sbjct: 255 GIERRKPVSNIHPLIRTHPVTGEKAIFLNKPFARKIVELKEESEYLLKFLFDHIESSHD
314

Query: 243 VHAH-QWAAGDVVVWDNRCLLHRA 265
+ W VV+WDNR +H A

Sbjct: 315 LQLRANWEPNSVVLWDRRTVHSA 338

>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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

Sbjct: 1 T FADMRAA+D LD T+A HS ++S++++G G D T R
TEFADMRAAWDTLDRETQAECLPLVCEHSQVLFSAQIGF-----GDFTEQERRDFTPVQQR 56

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

Sbjct: 57 LV+ HP TGR SL + HA I G E+ FL L + A Q V++H+W D+V+
-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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLG--HVQQAGSAYIGYGMDDTTATP
193

Sbjct: 1 T FADMRAA+D LD T+ V HS +YS+ LG ++ A+ A
TEFADMRAAWDMLDARTKEQVKDLVVEHSRIYSKGVLPFTEEEKRAF-----APV 52

Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV
253

Sbjct: 53 +PLV+ H TGR SL + HA + G +E L L++ A Q V+ H+W GD+
TQPLVRTHQRTGRHSLFLSSHAGRMVGPVSEGMLLLLRELMEHATQREFVYRHRWRVGD
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 ITPTGATLGATVTGVHLLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66
+TPT +GA ++G+ L L DA A L A L+ +L F Q L + FA+R+G

Sbjct: 46 VTPT---IGAEISGIRLGGDLSDAVIAELRRALLEWKVLFVRVQDLGRAEHRAFAERWGD
102

Query: 67 IERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
126

+E+ D T D M+ + N WH D T+ + AV A
 Sbjct: 103 LEQHPFFKYTQPGQTDVDVTTLAK-----DAMVGGVENN--WHNDVTWHEFPSFAAVLRA
 155

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG
 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 KFAVQ--HPVVRVIPESGRRVLFVNMTFTQIRILGVSEEEESNELLTMLYRHNVRPEFQVR
 270

Query: 246 HQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP 285

+W V WDNR H A F RVM + G RP
 Sbjct: 271 LKWEPTVAFWDNRTCQHYAASDYFPARRVMDRISIVGDRP 311

>gb|ACG80577.1| 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 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
 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 PVQQVVVRTHPGSGRKTLYLASHASHVIGWPIERGRKLIEDLLDFATQPQFVYQHRWQV
 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 = 3e-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

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG--HVQQAGSAYIGYGMDDTTATP
193

T F DMRAA+D LD T+ V HS +YS+ LG ++ A+ A
Sbjct: 1 TEFGDMRAAWDMLDARTKEQVKDLVVEHSRIYSKGVLPFTEEEKRAF-----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 = 3e-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 TEFGDMRAAYDALDEEIKTECENLICEHSQLFSRSILGSTDFTDERRRFA-----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 = 3e-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 SEVGLDVRPMSGYIGAEIFGIDLTGPIEPEVVAEVRAALLKWKVVFRRDQHITPAQQIAF 78

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 FSVAPCTPAIGAEIDGVNLARLDDTTYRALRQALLKYKVLFFRDQDITPAQHVAAARRFG 78

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVG-----NMAWHADSTYMPV
 117
 +E V P + V+ G +H+D ++ V
 Sbjct: 79 ELE-----VHPMI PHHPEHPELVVFGRGDKRGRENLYHSDVSWREV
 120

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--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 RMAEMDLMQYLFRQAAPEYQVRLRWRANTVALWDNRATQHYA 275

>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 = 3e-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 QRSIHVEPLTCSIGAELSHVNLGAASRDPLVAEIRALLLRHRVLFRRDQDISRAEHVAF 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 FGCVLRICIECPPVGGDTMWANMVLAYERLPEHVKTQIAGLRARHSI---EASFGAAMPID
 189

Query: 180 SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER-----
228

A P+V+ HPETG L + A++ R
Sbjct: 190 KRLALKAQFPDAE--HPVVRTHPETGEKILFVNAFTTTHFSNFHTADNVRVVGQDYTHAGPQ
247

Query: 229 FLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

L+ L+ A Q P +W + +WDNR H A
Sbjct: 248 LLQYLIGQA-QIPEYQVRWRWRPNSMAMWDNRSTQHYA 284

>ref|XP_001482071.1| hypothetical protein PGUG_05834 [Pichia guilliermondii ATCC 6260]

gb|EDK41736.1| hypothetical protein PGUG_05834 [Pichia guilliermondii ATCC 6260]

Length = 382

Score = 79.7 bits (195), Expect = 3e-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---LGTEVTGIQLSQLDDKKGDELALYVAQRGVVIFREQDFAK-HGPQFAVEYG-
136

Query: 67 IERIGGGDIVAISNVKADG-----TVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
121

G I S D T R+ E+D + + WH+D +Y
Sbjct: 137 -RHFGRHLIHPTSGAPKDHPEIHVTYRRADKNEFDRLFAQRTNAVGWHSVSYELQPPGT
195

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
181

FS P GG T FAD+R AY L + + H+ QA A
Sbjct: 196 TFFSVLEGPDAGGDTIFADVREAYRRLSPEFQKRLEGLHVLHT-----SADQARDA
246

Query: 182 YIGYGMDDTTATP---LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWA
237

+G G P + PL++VHP TG + + R + I + ES L L D
Sbjct: 247 -VGLGGIERRKPVSSIHLIRVHPGTGEKFIYLNRPFSRKIVELKEQESNYLLNFLYDHI
305

Query: 238 CQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

+A + +W VVVWDNR ++H A
Sbjct: 306 EKAHDLQLRAKWEPNVSVVVWDNRLLVVHSA 334

>emb|CAY27408.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 121

Score = 79.7 bits (195), Expect = 3e-13, Method: Compositional matrix adjust.

Identities = 49/127 (38%), Positives = 67/127 (52%), Gaps = 9/127 (7%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT--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 = 3e-13, Method: Compositional matrix
adjust.

Identities = 51/124 (41%), Positives = 66/124 (53%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR
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_05536663.1| taurine catabolic dioxygenase protein [Streptomyces
griseoflavus

Tu4000]

Length = 227

Score = 79.7 bits (195), Expect = 3e-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: 3 LSLRPLDKSGFGAVVDTNLAT--DAEHLAPHLAAALHQHRLIVPRQHLTHADLLTVASC 60

Query: 64 FGAIER-----IGG-GDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM
115

FG ++ +GG + ISN+ DG R + D+ + WHAD+++
Sbjct: 61 FGTVDTSVDRRYAVGGFPGLTVISNIVEDG--RHIGVYDGDNEEE-----WHADNSFK
111

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHV
175

P + + + P GG T FAD AY L +A R + ARHSL +
Sbjct: 112 PQLTSATMLYSVITPQRGGETRFADATRAYSDLPDAVRQRIGPMRARHSLAQLGALQSQA
171

Query: 176 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG 212

S + + + + PLV HP TG SLL+G
Sbjct: 172 SGGQSSIVAGSLAASPEAVHPLVLPHPVTGAR SLLLG 208

>ref|ZP_06226313.1| taurine dioxygenase [Burkholderia sp. CCGE1002]
gb|EFA54606.1| taurine dioxygenase [Burkholderia sp. CCGE1002]
Length = 327

Score = 79.7 bits (195), Expect = 4e-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 NLRIRRVAGLIGGEVQDFKLSPALDESVIDTLHRALVKYKVLFFRDQGHLLDDVSHQAFGA 74

Query: 63 RFG-----AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
116

RFG + G + + K G +WH D T++
Sbjct: 75 RFGQTVAHPTVPSPEGTALFELDASKGGGRAD-----SWHTDVTTFVD
116

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVY---SQSKLG
173

+ ++ +PA GG T +A+ AY+ L + + L A H+ Y ++ G
Sbjct: 117 AFPKISILRGVKIPAYGGDTVWANTAVAYERLPDDLKRLADSLWAVHTNDYDYGAERIAG
176

Query: 174 HVQQAGSAYIGYGMDDTTATPL----RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF
229

Q+ +A + + + + + P+V VHP +G +LL+G I G+ ++ES R
Sbjct: 177 TDTQSAAARLAHHQNVFVSAVYEAEHPIVHVHPVSGERALLLGHFIKRIVGLSSSESARI
236

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

E L + + QW DV +WDNR H A
Sbjct: 237 FEILQNRVIRLENTVRWQWRQNDVAIWDNRATQHAYA 272

>gb|ADC34038.1| TfdA-like protein [uncultured bacterium]
Length = 200

Score = 79.7 bits (195), Expect = 4e-13, Method: Compositional matrix adjust.

Identities = 65/211 (30%), Positives = 93/211 (44%), Gaps = 16/211 (7%)

Query: 56 QQITFAKRFGAIE--RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
113

QQI FA+R+ IE R ++ VR+ + K +G WH D +
Sbjct: 1 QQIAFARRWAPIEINRF----FTPVAGHPEIAEVRK-----EKAQKTNIGG-GWHTDHS 49

Query: 114 YMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
173

Y A G++ A +P GG T FA M AAYDAL E + + A HS + G
Sbjct: 50 YDEAPAMGSILVARELPEDGGDTLFASMYAAYDALSEGLQRTLDGLRAIHSDEHVFQAKG
109

Query: 174 HVQQAG--SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFL
230

+ ++AG S IG + P+V HPE+ R +L + G A+S+ L
Sbjct: 110 YHKKAGETSDRIGNAGAVRGEVVHPVIRHPESKRKALYVNPFAFTLRFEGWSEADSKPLL
169

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

E L A + +WA G + WDNRC+
Sbjct: 170 EHLYRHATRPEFTCRFRWAPGSIAFWDNRVCV 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 = 4e-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 FTITPLDAPLGAQVRGFDGARAASGPQILALKQALRDHHLIFKDDQQLDDAAFSRLASWF 73

Query: 65 GAI-----ERIGG-----GDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW--H
109

G++ +G DIV +SNV DG ++GN+ H
Sbjct: 74 GSVYVPPADAPVLGSHDDGTVPDIVLVSND-DG-----VLGNIELPAH
116

Query: 110 ADSTYMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ
169

+D + P + G++ A VP GG T + ++ AAY+ L RA + L+
Sbjct: 117 SDHHWTPQPSSGSLLYALEVPEHGGDTTWYNLAAAYEDLSADLRAQIDDLR----LITYN
172

Query: 170 SKLGHVQQAGSAYIGYGMTTATPLRP-----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 SAGARLIEALRTHILSPRYAYRHRWSVGDIVFWDNQATLHGRDDFDSGERRVLKRISLAG
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 = 4e-13, Method: Compositional matrix
adjust.

Identities = 73/270 (27%), Positives = 115/270 (42%), Gaps = 33/270 (12%)

Query: 15 LGATVTGVH-LATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAI----ER 69

 LGA V V L LD G + + A H +++ GQ+LS +Q+ F + G +
Sbjct: 51 LGAIVDVVDDLTELDSGASKILDVRAHGMIVIKQNLSRAEQVEFTSKLGEVIVLPSS
110

Query: 70 IGGGD-----IVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYM--PVMAQ
120

 G D I I+N ADGT + S WH D + P
Sbjct: 111 FEGKDPEPFHPAIQRITNFWADGTWKGPSAKL-----GAYWHQDQGQFVWPPKHN
160

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGS
180

 ++ A+ P GG T FAD+R A L + + +R++R S+ S + +
Sbjct: 161 LSILHAQATPPKGGETGFADLRGARATLSQP----LLERASRASIQVSVRDIADFAKGSE
216

Query: 181 AYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER-FLEGLVDWACQ
239

 + D + +++ H G P L +G + G+++AE+ + LE L+ A
Sbjct: 217 EDLAQFPDAS----HAILQSHLLDGGPLLYVGSPhMKVQGLESAEAGKALLEMLLAHATS
272

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRAEPWD 269

 + H W GDV+VWDN LH A P++
Sbjct: 273 PAFTYFHAWDVGDVIVWDNTQTLHHAMPYN 302

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKL----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 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 LDAHINSTDFQVRAQHRGTSGATVIAWDNRIVLHTA 350

>ref|XP_001386601.1| hypothetical protein PICST_33987 [Pichia stipitis CBS
6054]

gb|ABN68572.1| predicted protein [Pichia stipitis CBS 6054]
Length = 432

Score = 79.3 bits (194), Expect = 4e-13, Method: Compositional matrix
adjust.

Identities = 76/273 (27%), Positives = 111/273 (40%), Gaps = 25/273 (9%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
T+ ++P G + G+ L+ LDDAG L L +F Q D+ FAK+F

Sbjct: 89 TVDLSPN---YGTEIDGIQLSELDDAGKNDLALYLETRGLAVFRNQDFR-DKGPFAFAKQF
144

Query: 65 GAIERIGGGDI--VAISNVKADGTVRQHSPEAWDDMMKVIVGNM----AWHADSTYMPVM
118

G E G I V+ + + + PA + V N WH+D ++
Sbjct: 145 G--EYFGPLHIHPVSFAAENYPELLVITYRPAGGAERYPVQFANSTNTAGWHSDISFEEYF
202

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQA
178

+ + F A P GG T F D+R AY L + + H+ Y Q++ ++
Sbjct: 203 SSFSFFVALEAPESGGDTVFLDLREAYKRLSPQIQKFFETLTIHTNYY-QNQFAKLKNY
261

Query: 179 GSAYIG-YGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW
236

+ G Y + PLV+ HP TG SL R A I G+ ES+ L L
Sbjct: 262 EARVKGDYFTE-----HPLVRTHPVTGEKSLFFSRGFALRIKGLKQQESDSILSFLESH
315

Query: 237 ACQAPRVH---AHQWAAGDVVV-WDNRCLLHRA 265

P + +HQ V+ WDNR LH A
Sbjct: 316 VLNNPEIQVRASHQGTESRTVIAWDNRISLHTA 348

>ref|XP_001387107.1| alpha-ketoglutarate catabolism dioxygenase [Pichia stipitis CBS

6054]
Length = 386

Score = 79.3 bits (194), Expect = 5e-13, Method: Compositional matrix adjust.

Identities = 69/264 (26%), Positives = 112/264 (42%), Gaps = 16/264 (6%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQ---ITFAKR 63
++TP G+ VTGV L+ LD AG L Q ++IF Q ++ + + K
Sbjct: 86 KVTPK---FGSLVTGVQLSQLDSAGKDELALLVAQRGVVIFREQDFADKGPFAVEYKGH
142

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

FG + I ++ + T R+ E++ + N+ WH+D +Y

Sbjct: 143 FGRL-HIHPTSGAPRNHPELHITYRRPDKGEFERVFSNRNTNNVGVHSDVSYELQPPGTTF
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 GIERRKPVSNIHPLIRTHPVTGEKAIFLNKPFARKIVELKEESEYLLKFLFDHIESSHD
314

Query: 243 VHAH-QWAAGDVVVWDNRCLLHRA 265

+ W VV+WDNR +H A

Sbjct: 315 LQLRANWEPNSVVLWDNRRTVHSA 338

>ref|YP_369080.1| taurine dioxygenase [Burkholderia sp. 383]

gb|ABB08436.1| Taurine dioxygenase [Burkholderia sp. 383]

Length = 282

Score = 79.3 bits (194), Expect = 5e-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 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

V P VGG T +A+M AY+ L + + ARHS+ S + + +
Sbjct: 112 VLRCIDGPPVGGDTMWANMVLAYERLPAHVKQOIDDLRARHSIEASFGAAMPIDKRLALK
171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIP-----GMDAAE-SERFLE
231

Y P+V+ HPETG L + A G DA + + L+
Sbjct: 172 AQY-----PDAEHPVVRTHPETGEKVLVNAFATHFTNFHTPARVRVGQDANPGAGQLLQ
226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265

L+ A +W V +WDNR H A
Sbjct: 227 YLISQAYIPEYQVRWRWKKNSVAIWDNRSTQHYA 260

>gb|ACG80566.1| TfdA [uncultured bacterium]
Length = 119

Score = 79.0 bits (193), Expect = 5e-13, Method: Compositional matrix
adjust.

Identities = 45/126 (35%), Positives = 68/126 (53%), Gaps = 13/126 (10%)

Query: 138 FADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPL
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 QQVVVRTHPGSGRKTLYLASHASHVIGWPIERGRKLIEDLLDFATQPQFVYQHRWQVGD
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 = 5e-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 EMTLNIEIIKSSIGAI IHDVDLNTVDENTTQQIQQALLDHHVIFFRNQQLAPQAQAE LAR 69

Query: 63 RFGA-----IERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
 113

FG+ +E + +I+ + + K D + N WH D T
 Sbjct: 70 FFGSLHIHPIFPTVENVP--EIIVLDSWKQD-----LRDNELWHTDVT
 110

Query: 114 YMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--VYSQSK
 171

+ G V A +P VGG T ++ AA+ LD++ + + +A H + + +
 Sbjct: 111 FSKNPPLGCVLQAIKIPVGGDTLWSSGVAAAFAGLDQSLQQKLGKLTATHDIRQSFPIER
 170

Query: 172 LGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL
 230

H + + P+V+ HP TG+P L + I ++ +ES L
 Sbjct: 171 FAH-NDVERKKLEETFKRNPVHPVVRTHPVTGPILFVSEGFTTRINELEESESAELL
 229

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ L A QW GDV +WDRNC H+A
 Sbjct: 230 QYLFHAATHEQFHLRWQWQEGDVAIWDNRCTQHKA 264

>gb|ADC33972.1| TfdA-like protein [uncultured bacterium]
 Length = 121

Score = 79.0 bits (193), Expect = 5e-13, Method: Compositional matrix
 adjust.

Identities = 43/126 (34%), Positives = 67/126 (53%), Gaps = 5/126 (3%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLR
 195

T F DMR A++ + A +A + +A HS+ +S++ G + GY P R
 Sbjct: 1 TEFCDMRQAWEQVPPAEQAELEALTAHHSIAHSRALCGFTEWPE----GYDLLQKIP-R 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
 255

PLV VHP+TGR +LL H + G + E+ F+ L+ A ++H+W GD ++
 Sbjct: 56 PLVGVHPDPTGRKALLTASHIETLTGKNKDETTEFVAELIQRATVPENCYSHRWTKGDFLM
 115

Query: 256 WDRNCL 261

WDRNC+

Sbjct: 116 WDRNCV 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 = 5e-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 RRGVVFVKQELSADEQKFVTDRLGHLTGKPATSGLHIHPVYNAERVGKDQVVDEKGTQN
 153

Query: 95 WDDMMKVIVGNM-----AWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADM
 141
 D+ + VI N+ WH+D + PV A +P GG T +A
 Sbjct: 154 KDNEISVISSNLHRS LDVEPRSGADEWHS DIAFEVPADY TSLKVHTLPQTGGDTMWASG
 213

Query: 142 RAAVDALDEATR ALVHQRSARH---SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLV
 198
 YD L + R + + + + S ++ G+ G +DT T PL+
 Sbjct: 214 YEVYD LLSQPF RNMFEKLG FYYPPEFINS AARHG YALYPGPRGAAENV DTHLTA EHPLI
 273

Query: 199 KVHPETGRPSLL-IGRHAHAIPGM DAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVW
 256
 + +P TG S+ IG H + I G+ ES+ + D Q ++W D+ +W
 Sbjct: 274 RTNPVTGWKSVF GIGHHFN RILGVSLDES DMLKRYIRDLVTQNHSTQLR YRWGKNDLAIW
 333

Query: 257 DNRCLLHRAEPWDFKL-PR 274
 DNR H A P F L PR
 Sbjct: 334 DNRSTYHAATPDYFDLGPR 352

>gb|ADC33957.1| TfdA-like protein [uncultured bacterium]
 Length = 121

Score = 79.0 bits (193), Expect = 6e-13, Method: Compositional matrix adjust.

Identities = 47/126 (37%), Positives = 67/126 (53%), Gaps = 5/126 (3%)

Query: 136 TCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
 195
 T F DMRAAYDAL E +A + A+H + +S+ ++G + Y +P R
 Sbjct: 1 TEFCDMRAAYDALPETMKA EIDGLVAQH DIFWSRGQIGFTEFP PGEREKY----PPSPQR 56

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
 255
 LV++HP + R +L + HA I G AE L L A Q V++H+W GD V+
 Sbjct: 57 -LVRLHPGSR RKTLYLSA HASHILGW PVAEGRLLLWDLTAHATQNR FVYSHRWRVGD AVI
 115

Query: 256 WDNRCL 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 = 6e-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 VFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
 182
 V P VGG T +A+M AY+ L + + + ARHS+ S + + +
 Sbjct: 112 VLRCIDGPPVGGDTMWANMVLAYENLPDHVKQQIADLRARHSIEASFGAAMPIDKRLALK
 171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAI PGMDAAE-SERFLE
 231
 Y P+V+ HPETG L + A G DA + + L
 Sbjct: 172 AQY-----PDAEHPVVRTHPETGEKVLVNAFTTHTNFHTPARVVRVGDANPGAGQLLH
 226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 L+ A +W V +WDNR H A
 Sbjct: 227 YLISQAAIPEYQVRWRWKKNSVAIWDNRATQHAYA 260

>gb|ADD78810.1| TauD [Pantoea ananatis LMG 20103]
 Length = 279

Score = 79.0 bits (193), Expect = 6e-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 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
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-QWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAG-RP 285

P +W D+ +WDNR H A + RVM + + G RP
Sbjct: 226 FAHVTRPEFQVRWRWPNDLAIWDNRVTQHYANADYYPARRVMQRATVLGDRP 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 = 6e-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 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGA
122

RFG++E VA S+ G VR + +D N ++H D ++ A GA
Sbjct: 78 RFGSLE----DHPVAPSDPDHPGLVRIYKS---EDSAPEHYEN-SYHCDGSWRREPAMGA
129

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY
182

V P+VGG T + +M AAY+ L + + + ARHS+ + V +
Sbjct: 130 VLRCVQTPSVGGDTIWWNMAAAYEGLPDHVKERIAGLRARHSIEATFGARLPVAERHRLK
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 YLIGRAAIPEYQVRWRWSADSF AIWDNRATQHYA 278

Sbjct: 81 LFGPLRALPVDSIDGDDPELVVVRANAQSR-----FAAGELWHTDGTADLEP
127

Query: 119 AQGAVFSAEVVPAV--GGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
176

+ G++ + PA+ GG T FA+M A + L A + + +A H G +
Sbjct: 128 SMGSMLYVKETPAIGTGGDTLAFANMHLAIEMLS PAMQQFLGGLTAIHD-----GEI-
178

Query: 177 QAGSAYIGY----GMDTTATPLRPLVKVHPETGRPSLLI--GRHAHAIPGMDAAESERFL
230

+ GY G+ + P+V HPETGR SL + G +H + + ES L
Sbjct: 179 ----PWKGYQPPPGLPKSE---HPVVVRHPETGRRSLFVNSGFTSHIV-QLSPGESRTVL
230

Query: 231 EGLVDWACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSR---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 = 7e-13, Method: Compositional matrix
adjust.

Identities = 46/125 (36%), Positives = 64/125 (51%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
195

T F DMRAAY+ALD+ + + HS +YS+ +LG + + P+R
Sbjct: 1 TEFGDMRAAYEALDDRLKHQIEDLVCLHSNMYSRGRGLTEFTEEERRVF-----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 QRLVRRHPVTGRKSLFLSAHAGEIEGMSIPEARMLLLLDLTELATREQFVYSHAWRVNDFV
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 = 7e-13, Method: Compositional matrix
adjust.

Identities = 61/219 (27%), Positives = 88/219 (40%), Gaps = 29/219 (13%)

Query: 56 QQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW
108

Sbjct: 16 VTPLAGRVGAIVSNIRLSGDLDPSTIARLEQLLRLHKVLFRRDQSHLDDAEQERFGARFG 75

Query: 66 A-IERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMA--WHADSTYMPVMAQGA
122

G + ++V T R P + G A WH D T++ +
Sbjct: 76 EPFAHPTQGALSGTASVLDLDRRDREPKEG-----AGGARADQWHTDITFVEAYPRIT
130

Query: 123 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALL-----VHQRSARHSLVYSQSKLGHVQ
176

+ + V PA GG T F++ AAY++L E +AL VH + ++ V + +
Sbjct: 131 ILRSVVAPASGGDTVFSNTVAAYESLPEPLKALADRLWAVHSNAYDYAAVRPHATADEQK
190

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW
236

Q + +T P+V+V P +G +LL+G G+ A+ ++ D
Sbjct: 191 QFARQFTSTVFETE-----HPVVRVLP-SGERTLLLGNFVQRFRTGIARADFQKLFALFQDH
245

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRA 265

+W AGDV +WDN H A
Sbjct: 246 IQAQENTVRWRWQAGDVALWDNTATQHYA 274

>ref|XP_001834704.1| hypothetical protein CC1G_05841 [Coprinosia cinerea
okayama7#130]

gb|EAU87152.1| hypothetical protein CC1G_05841 [Coprinosia cinerea
okayama7#130]

Length = 369

Score = 78.6 bits (192), Expect = 8e-13, 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 LGTELRNVQISQLSPEGLNELALYTAERKVLIFRDQDFKDLTPERQIEIANHFGPIQRHP
151

Query: 71 GGGDIVAISNV---KADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
126

G++ + G R + +D+ + + +WH+D TY F
Sbjct: 152 TSGNVKGFPEFHVVYRDPGFDRNLNRYRGFDNKINL----TSWHSVDVTEKQTPGTTFE
207

Query: 127 EVVPAVGGRTCFADMRAAYDAL-DEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
185

P VGG T F AY+ L DE + LV R A HS V + H + G
Sbjct: 208 LDQPEVGGDTLFTSQVEAYNRLSDEFKRLVGLR-AIHSV---PQAEHSRSIGGPVRE
263

Query: 186 GMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAP--R
242

>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 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGH
 174

G V P VGG T + +M AY+ L + + ARHS+ +
 Sbjct: 121 RVNPPMGCVLRVETPPVGGDTIWNMALAYENLPARVKEQIKDLRARHSIESTFGARMP
 180

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----
 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|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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
 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 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTA--TP
193

T F DMR AYD LD+ TRALV + H+ +YS+ +G + G+ + A P
Sbjct: 1 TEFGDMRIAYDLLDDDDTRALVEELVCEHTQLYSRGSMSG-----FSGWTEEELAMFKP 52

Query: 194 LRP-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD
252

+R LV+ HP TGR SL + HA I G E+ L + A + V+ H+W D
Sbjct: 53 VRQRLVRTHPVTGRKSLYLSSHAGTIIGWQMPEARLDLPRDLNEHATRPELVYVHRWRLHD
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 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALDE + HS ++S+S LG + + A +
Sbjct: 1 TAFADMRAAYDALDEEIKTECENLICEHSQSFERSILG-----STDFTDERRRRFAPVTQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

LV+ HP TGR SL + HA AI G E+ L L + A Q V+AH W D+V+
Sbjct: 56 RLVRRHVPVTGRRSLYLASHAGAILGWLVPPEARASLRDLNEHATQRQFVYAHVWRQWDLVM
115

Query: 256 WDNR 259
WDNR

Sbjct: 116 WDNR 119

>ref|YP_498356.1| taurine catabolism dioxygenase TauD/TfdA
[Novosphingobium]

Query: 256 WDNRCL 261
WDNRC+
Sbjct: 116 WDNRCV 121

>gb|ADC33967.1| TfdA-like protein [uncultured bacterium]
Length = 124

Score = 77.8 bits (190), Expect = 1e-12, Method: Compositional matrix
adjust.

Identities = 46/128 (35%), Positives = 70/128 (54%), Gaps = 6/128 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSAHSLVYSQSKLGHVQQAGSAYIGYGMDDTATP--
193

T F DMR A++AL +A + ARH L S+ K G ++ D P
Sbjct: 1 TEFCDMRLAWEALPAEEQAKLEPLIARHPLWLSRRKYGD----DKSFSFSEEDVRRYPPV 56

Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV
253

RPLV +H TGR +L++G + ++ +D +S FL+ L D A V++H+W AGD+
Sbjct: 57 ERPLVDIHRPTGRRALMLGANIASVGELDEIDSVAFLELTDTRATAPEFVYSHRWTAGDL
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 = 1e-12, Method: Compositional matrix
adjust.

Identities = 46/128 (35%), Positives = 70/128 (54%), Gaps = 6/128 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSAHSLVYSQSKLGHVQQAGSAYIGYGMDDTATP--
193

T F DMR A++AL +A + ARHSL S+ K G ++ D P
Sbjct: 1 TEFCDMRLAWEALPADAQAELEPLVARHSLWLSRRKYGD----DKSFKFNEDVRRYPPV 56

Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV
253

RPLV H TGR +L++G + ++ +D ES FL+ L + A +++H+W AGD+
Sbjct: 57 ERPLVDTHRPTGRRALMLGANIASVGDLDEIESVAFLELTERATAPAFIYSHRWTAGDL
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

>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 FADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPL
197

F DMR A++ L +A + + +A HS+ +S++ G + GY P RPL
Sbjct: 3 FCDMRRRAWELLSPEEQAELEELTANHSIAHSRALCGFTEWPE----GYDDLQKIP-RPL 57

Query: 198 VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWD
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

>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 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGH-VQQAGSAYIGYGMDDTTATPL
194

T F DMRAA+D LD+ T+ + HSL+YS+ LG V A P+
Sbjct: 1 TEFGDMRAAWMLDDETKRICEPLICEHSLLYSRGLLGFVDVTDEERAIF-----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|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 TLAVRGLTPVIGAEVSGLDLSRELTGDQLAELRTVFLDHHVLFVFRDQDLTPEDHQRLAAH 81

Query: 64 FGAIERI-----GGGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV
 117
 FG + + G I+ ++ TV GN WHAD T
 Sbjct: 82 FGELRPVNPPPEHGNPYILEVATSPEAATV-----FGN-GWHADGTADAE
 125

Query: 118 MAQGAVFSAE VVPA--VGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV
 175
 + G++ +PA GG T FA+M AYD L + L+ + L +
 Sbjct: 126 PSLGSM LHITE MPAPGSGGDTL FANMHLAYDMLSPK LKELL-----TGLTAI
 172

Query: 176 QQAGSAYIGYGM DTTATPL---RPLVKVHPETGRPSLLIGR-HAHAI PGMDAAE SERFLE
 231
 A+ G+ + P P+V HPET RP L + + IP + A ES L+
 Sbjct: 173 HDGAHAFRGHKI PEGYEPPVSEHPVVVRHPETDRPLLYVNPAYTSRI PQLSADESRAVL D
 232

Query: 232 GLVDWACQAPRVHAH-QWAAGDVVVWDNRCL LHRAEPWDFKLP RVMWHSRLAGRPETE GA
 290
 L P + +W +V WDNRC+ H A +D+ H+R R G
 Sbjct: 233 LLFSVVPNRPMLACRVRWEPNTLVFWDNRCVQH HAV-YDY-----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 LPKDKAQVDHLTPTIGSEIRGVQLS QLTKEGKDQLALYVAQRKVVAFRDQDFAHLPIDQA
 150

Query: 58 ITFAKRFGA--IERIGGGDI----VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHAD
 111
 + F FG I + G + + + AD T D + + WH+D

Sbjct: 151 LDFGSYFGRHHIHQTSYGAPKGYPEIHLVHRGADDT-----SGADFLATRTNTITWHS
203

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK
171

T+ P GG T FADM AY L R +H A HS + +
Sbjct: 204 VTFEKQPPGTTFLYLLDGPDTGGDTLFADMAQAYKRLSPEFRKRLHGLKAAHSGI---EQ
260

Query: 172 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFL
230

+ + G G T P+V+ HP TG +L + + I G ES+ L
Sbjct: 261 INNSLNRG---GIARREGITSEHPIVIRTHPVTGEKALFVNPQFTRYIVGYKKEESDMLL
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 [Pichia stipitis CBS
6054]

gb|ABN64776.1| predicted protein [Pichia stipitis CBS 6054]
Length = 420

Score = 77.0 bits (188), Expect = 2e-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-EKGPFAKRF
145

Query: 65 GAIERIGGGDI---VAISNVKADGTVRQHSPA----EWDDMMKVIVGNMAWHADSTYMPV
117

G + G I V+ S ++ + + PA ++ WH+D ++
Sbjct: 146 G--QHFGLPHIHPSVSYSAEESPELLVTYRPAGGPERYNAQFAGTTTTTGWHSVDFEY
203

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
177

A + F A P GG T F D+R AY L + + H+ Y L + +
Sbjct: 204 PASFSFFVALEAPETGGDTVFLDLREAYRRLSPPIQKFFESLTIIHTNYY----LNQLAK
259

Query: 178 AGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDW
236

D+ A PLV+ HP TG SL + A + G+ ES+ L L D
Sbjct: 260 LKDLDRVNAADSFAE--HPLVIRTHPVTGEKSLFYKGFALRVKGLKQESDAILSFLEDH
317

Query: 237 ACQAPRVH---AHQWA-AGDVVVWDNRCLLHRA 265

P + +H+ +G ++ WDNR +H A

Sbjct: 318 INNNPEIQVRASHRGTNSGTIIAWDNRISIHTA 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 = 2e-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 GAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGAVF
124

G ++ + V + T+ + +P + + WH D T+ +

Sbjct: 62 GPVQTHPAYETV---EGFPEITILESTPEKPTKIE-----TWHTDMTFNQHPMATML
111

Query: 125 SAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIG
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 DAVANPPVRHPVIRTHPETGKKAIFVNELFTTHIDGLRRDES DALLGFLYKHVTTDEFT
230

Query: 244 HAHQWAAGDVVVWDNRCLLHR 264

W A +V+WDNRC H+

Sbjct: 231 CRFHWQANSLVIWDNRCTQHK 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 = 2e-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 TIEVRQLGPTVGAIEIGVDLAKDVSEAQFAEIHRLDENLAIVFRDQDISKEDHKRFARR 85

Query: 64 FG-AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG ++ R +A + + DG + D WH D + P +
Sbjct: 86 FGKSLHR----HELAATRFRHDGPFDFEFLSWKTDANSRFTAGDGHWPDVSCDPSPPIAVS
141

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARH--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-----PQSEHPVVVTHPRTGRKFLYVNASFTSHIVQLTRRES DALLQLLFRHVES
252

Query: 240 APRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLA 282

+ QW ++VWDN H A WD+ P W R++
Sbjct: 253 QLALQTRVQWRPNSSLVWDN WASQHHAV-WDY-YPEERWGERVS 294

>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 = 2e-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 FDLEPVT PRLGARLTGIDLKRPIDDALADALRAALAERLVLFLPGQFLDGAALKRATEVF 64

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVF
124

G + R+ +A S D D ++ WH+D +++ G++
Sbjct: 65 GPLFRV---PYIAPSAEDPDVVAVLKEA----DEHRISTFGGDWHSDFSFLERPPGGSL
117

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHS-LVYSQSKLGHVQQAGSAYI
183

Sbjct: 55 QRLVRTHPVAGRKSLYLSSHIGTIVDWPMPPEARAFIRDLTEHATQPRYTYSHKWRQFDLV
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 = 2e-12, Method: Compositional matrix
adjust.

Identities = 46/125 (36%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL-
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 QTLLRRHPGSGRMGLFLASHAGRIFGMPEDGKALLQRLIEHATQQQFVYTHRWRLYDLV
114

Query: 255 VWDNR 259
+WDNR

Sbjct: 115 MWDNR 119

>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 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
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 RLVKTHPRSGRKTFLFIATHACRIVGWPVPEALDLLRELLFATKPEFIYTHSWTVRDLVM
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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
195

T F DMRAAYDAL ++ + A H + S+ LG + + P+
Sbjct: 1 TEFCDMRAAYDALPRDLQSELEGLRAEHYALNSRFLGLGDTDYSEA-----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 = 3e-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 LTDEQAAEVKRAFLRHHVLFVFRDQVIDGEQHKRFARHFGELHPVALAPEGSDPHILEISA 61

Query: 84 DGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAV--GGRTCFADM
141

D R V WHAD T + G++ P + GG T F++M
Sbjct: 62 DKDSRN-----VAGHGWHADGTADLKPSLGSMLYVTRTPPEIGSGGDTMFSNM
108

Query: 142 RAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVH
201

AY+ L A + L+ +A H+ + + + + Y + + P+V H
Sbjct: 109 HLAYEMLSPAMKELLDPMTAVHNGLLA-----WEGATPPPEYDVPVN---VHPVVARH
158

Query: 202 PETGRPSLLI-GRHAHAIPGMDAAESERFLEGLV----DWACQAPRVHAHQWAAGDVVVW
256

P+TGR L I G + I + ES ++ LV + A + RV +W +V W
Sbjct: 159 PDTGRKLLFINGIYVSHIEQLSKGESRAIIDMLVKQITNTALLSCRV---RWTPTNLVFW
215

Query: 257 DNRCLLHRAEPWDFKLPVMMWHSRLAGR 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 = 3e-12, Method: Compositional matrix
adjust.

Identities = 46/125 (36%), Positives = 69/125 (55%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPL-
194

T FADMRAAYDAL E + + A H++++S+ KLG + + T P+
Sbjct: 1 TEFADMRAAYDALPEDMKQRLRGLVAEHAIMHSRRKLGFDDEFSDEE-----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 QTLLRRHPGSGRMGLFLASHAGRIFGMPEDGKALLQRLIEHATQQQFVYTHRWRLHDLV
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 = 3e-12, Method: Compositional matrix
adjust.

Identities = 45/128 (35%), Positives = 70/128 (54%), Gaps = 6/128 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATP--
193

T F DMR A++ L +A + ARHSL S+ K G ++ D P
Sbjct: 1 TEFCDMRLAWEELSAEEQASLEPLIARHSLWLSRRKYGD----DKSFKFNEEDVRRYPPV 56

Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV
253

RPLV +H TGR +L++G + ++ +D +S FL+ L + A V++H+W AGD+
Sbjct: 57 ERPLVDLHRPTGRRALMLGANIASVGDLEIDSVAFLDELTERATAPAFVYSHRWTAGDL
116

Query: 254 VVWDNRCL 261
++WDNRC+

Sbjct: 117 LLWDNRCV 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 = 3e-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-GTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVM
118

K FG ++ I A+ + + VR+ D+ K + G WH D + V
Sbjct: 61 VGKYFGELQ-----IHALKGLSEEHPVVRK---LHADENSKHVAGE-EWHTDMSCAAVP
110

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
178

G++ +P +GG T FA M AAYDAL + + + +A H + G
Sbjct: 111 PLGSILYLHTLPTLGGDTMFASMYAAYDALSDRMKTYLEGLTATHD---GKLAFGFRDPT
167

Query: 179 GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWA
237

G+ + P+++ HP TG+ L + R I + ESE L L
Sbjct: 168 GNFPVA-----THPVIRTHPVGTGKLLLFVNRGFTSHINEISKEESESILAYLFR-H
217

Query: 238 CQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDF 270

C+ P +W V WDNRC H A WD+
Sbjct: 218 CENPLFQLRFRWEPHSVAFWDNRCTQHILA-IWDY 250

>ref|XP_001487814.1| hypothetical protein PGUG_01191 [Pichia guilliermondii ATCC 6260]

Length = 430

Score = 76.6 bits (187), Expect = 3e-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---RYFGPLHIHPVAYSIDGYPELLVTFRKEGGPERYEGEFASRTTLVGWHS DISFEEY
204

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKL----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 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 = 3e-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 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
 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 TQY-----PDAEHPVVRTHPETGEKVLVNAFTTHFTNFHTPARVVRVGDANPGAGQLLH
 226

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

 L+ A +W V +WDNR H A
 Sbjct: 227 YLISQATIPEYQVRWRWKKNSVAIWDNRATQHYA 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 = 3e-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 IGTEIVGLQLKDLTNQQRDELALLIAERSVFFRDQDLSPQQQKELGEHFGEVEVHPQVG
155

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVG
133

+ + V Q E + + G AWH D + A + +P+VG
Sbjct: 156 QVPGVPGVTVLWPALQA--VEREPNFRKTGGASAWHTDLVHENQPAGITHLHNDTIPSVG
213

Query: 134 GRTCFADMRAAYDALDEATRVLVHQRSA--RHSLVYSQSKLGHVQQAGSAYIGYGMTTA
191

G T +A +AY+ L + R + ++A R + Y K +AG YI
Sbjct: 214 GDTLWASGYSAYEKLSPSFRKFIDGKTAIYRSAHTYLDRK---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 PRTSALWDNRITIHNAS-WDYE 343

>ref|YP_002007367.1| Taurine dioxygenase; TauD/TfdA taurine catabolism
dioxygenases

family [Cupriavidus taiwanensis]
emb|CAQ71309.1| Taurine dioxygenase; TauD/TfdA taurine catabolism
dioxygenases

family [Cupriavidus taiwanensis]
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 QHSIKVELCTPAIGAELSNISLADAAQDPDLIAEIRALWLKHKVLFRRDQDITPLEQQAF 87

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTV---RQHSPA EWDDMMKVIVGNMAWHADSTYMPV
117

A +FG +E +A S+ A+ + R P + + + K+ N+ WH+D TY
Sbjct: 88 AAQFGELE----AHPLAPSHPDANKLLMLYRNLDPNKQNFVEKISRENI-WHSDV TYKKA
142

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS---LVYSQSKLGH
174

+GAV E+ P GG T +++M AY+ L EA + + A+HS + +Q
Sbjct: 143 PPRGAVLRREMGPENGGDTIWSNMVMAYERLPEAVKQRIDGLYAKHSAEHVFLAQY PKDE
202

Query: 175 VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-----RHAHAIPGMDAAESERF
229

A + G P+V +HPET L + + D + F
Sbjct: 203 RHAAAANKPNPNE-----HPVLIHPETQEKVLFVNSAFTTHFVNYFNFTDIRYGQDF
254

Query: 230 LEG---LVDWACQAPRVHAHQ---WAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLA
282

+ L+ + C + +Q W V +WDN H A PR M + L
Sbjct: 255 MPESHHLMYYLCSQAAIPEYQVRLKWRDNTVAMWDNLLCQHYAVADYGNAPRKM LRATLT
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-----DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM
115

FG I G +I + D T + + ++AWH+D TY
Sbjct: 155 YFGRPHIHPTSGAPLNHPEIHLVHRAAGDKTA-----ESFFEARTNSVAWHSDV TYE
206

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV
175

VP GG T FA+ AY+ L +A + +H SA HS G

Sbjct: 207 KQPPGTTFLYVLDVPETGGDTLFFANGVEAYNRLSDAFKERLHGLSATHS-----GIE
258

Query: 176 QQAGSAY-IGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGL
233

Q S Y G + P+V+ HP TG +L + R I G+ ES+ L L
Sbjct: 259 QVNASRYRNGIARREPVVNVHPVIRVTHPVVTGEKALYVNRQFTRKIVGLKQEEESDVLNLF
318

Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
D H +WA VVVWDNR H A

Sbjct: 319 YDHIALGADFHVVRVWAPKTVVVWDNRVATHTA 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 = 4e-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 AHIGTEVVGLQLKDLTDQQKDELGLLIAERSVVFFRDQDLSPQQKKGGEWYGEIEVHPQ
154

Query: 69 --RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
126

+ G + ++ + D + +P+ + G WH D + A

Sbjct: 155 VPFVPG--VPGVTVLWPDQLQATEVTPS-----FRKTGGASRWHTDLVHERQPAGVTHLHN
207

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG
186

+ +P +GG T ++ AAY+ L A R ++ R A + + + AG YI

Sbjct: 208 DTIPKIGGDTLWSSGYAAYEKLSPAFRKIIDGREAVYRSAHPYLDRDNT-SAGPKYIER-
265

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD-WACQAPRVH
244

+ P+V+VHP TG SL + R I G+D AES+ L L D +

Sbjct: 266 -----VHPVIRVHPATGWKSLWVNRAFTDRIVGLDKAESDVILNYLFDVYENNVDTQV
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 = 4e-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 TIGTELEGIKLGLTDQQKDELALLVAERGVVFFRQDDWTIEEQALALGRYWGPLHKHAT
 162

Query: 73 GDIVAIISNVKADGTVRQHSPAEWDDMMKVIVGNMA-----WHADSTYMPVMAQGAVFSA
 126
 + A ++ V H + D K+ G + WH+D TY F
 Sbjct: 163 TGVPARGLDEVHVVYAHPTS--DPQEKIYRGPVKHSRSDLWHSVITYEVNPPSYTSFKL
 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 NTVRRDPVETEHPVLRVHPVTNHKALFFNPGFVRYIPGVPKAESDYLVQFLTNHVSTASD
 330

Query: 243 VHAH-QWAAGDVVVWDNRCLLHRA 265
 +W AGDV +WDNR +H A
 Sbjct: 331 FSVRFKWNAGDVAIWDNRTNIHSA 354

>ref|XP_001396406.1| hypothetical protein An13g02700 [Aspergillus niger]
 emb|CAK41667.1| unnamed protein product [Aspergillus niger]
 Length = 385

Score = 75.9 bits (185), Expect = 5e-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 GGDIVAIISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVPA
 131
 VA V SPA + + G WH D + A + +P+
 Sbjct: 153 QVPGVAGVTVIWPALQATESPANF----RRPGGASRWHTDLVHERQPAGVTHLHNDTIPS
 208

+WA G VVVWDNR H A

Sbjct: 323 GQDFQVRIKWAPGTVVVWDNRVTAHSA 349

>ref|ZP_05006078.1| taurine dioxygenase [Streptomyces clavuligerus ATCC 27064]

gb|EDY50377.1| taurine dioxygenase [Streptomyces clavuligerus ATCC 27064]
Length = 324

Score = 75.9 bits (185), Expect = 5e-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 IGAEIPGVDLAAPLSAAVLAAIRAALLRHKVVFFRGQRLSHPAHIAFGRRLLGPLTRRPGP 79

Query: 74 D-----IVAISNVKADGT-VRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
125

I V D R E K + + WH D +V

Sbjct: 80 KHGVHPEGYPEILTVDPDAEDTRYGRRFEERLRPKELRPDSGWHVDLAAAVNPPAISVLR
139

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
185

AE VP GG T + + AA+ L R L A H+L ++ +L + A I

Sbjct: 140 AETVPDHGGDTQWTSLVAAHQGLSAPLRELAAGLRAEHTL-FAGCELLLSDEEDVAVIRR
198

Query: 186 GMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVH
244

+ T + P+V+VHPETG +L + + + I G+ ES LE +

Sbjct: 199 LTEDTLLSVHPVVRVHPETGERALFVPPASVSRIAGLLPWESRLLLLLHFGHIGRPEHTV
258

Query: 245 AHQWAAGDVVVWDNRCLLH 263

+WAAGDV VWDNR + H

Sbjct: 259 RWRWAAGDVAVVWDNRVAH 277

>gb|ADC34002.1| TfdA-like protein [uncultured bacterium]

Length = 206

Score = 75.9 bits (185), Expect = 5e-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 + +

Score = 75.5 bits (184), Expect = 6e-12, Method: Compositional matrix adjust.

Identities = 44/128 (34%), Positives = 70/128 (54%), Gaps = 6/128 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATP--
193

T F DMR A++A +A + ARHSL S+ K G + ++ D P
Sbjct: 1 TEFCDMRLAWEAFPPDEQAALPLIARHSLWLSRRKYG----SDKSFSFNEDVRRYPPV 56

Query: 194 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV
253

RPLV +H TGR +L++G + ++ +D +S FL+ L + A +++H W AGD+
Sbjct: 57 ERPLVDIHRPTGRRALMLGANIASVGELDEIDSVAFLDALTERATALAFIYSHCWTAGDL
116

Query: 254 VVWDNRCL 261

++WDNRC+
Sbjct: 117 LLWDNRCV 124

>ref|ZP_00990204.1| Probable taurine catabolism dioxygenase [Vibrio splendidus 12B01]

gb|EAP94904.1| Probable taurine catabolism dioxygenase [Vibrio splendidus 12B01]

Length = 180

Score = 75.5 bits (184), Expect = 6e-12, Method: Compositional matrix adjust.

Identities = 51/168 (30%), Positives = 82/168 (48%), Gaps = 23/168 (13%)

Query: 6 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65

L+I P +GA + GV+LAT ++ A L + ++ Q LS++Q + A+RF 61
Sbjct: 2 LKIEPITPHIGARIHGVNLATCSATELDEVYQALLTNQVIFLDDQTLSSSQHLMIAERF 61

Query: 66 AIE-----RIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM
118

+E R+ V++ T R ++P E WH D T+ +
Sbjct: 62 QLEPAHPFFPRVEHAPQVSVIE-----TTRGNAPME-----SYWHTDLTWRELP
105

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLV 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

>ref|YP_438996.2| taurine dioxygenase [Burkholderia thailandensis E264]
 Length = 277

Score = 75.5 bits (184), Expect = 7e-12, Method: Compositional matrix
 adjust.

Identities = 70/277 (25%), Positives = 111/277 (40%), Gaps = 38/277 (13%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
 T L++T +GA V V L+ + AA +H +L F Q LS + FA
 Sbjct: 2 TRCLKLTRLTPAIGAIVDNVDSLNSATGDLRDGIRAALARHQVLFVRDQRLSAVRHRDFAAG 61

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP
 116

FG + +I+ + N D + N WH D T+
 Sbjct: 62 FGDLVHVPYPSHPDAREIMVLDNAVFD-----LKDNAIWHTDVTFAE
 104

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLV--YSQSKLGH
 174

+ ++ +A +P GG T + AAYDAL + +A + +A+H + + G
 Sbjct: 105 TPPRASILAARTLPETGGDTLWGSFAAYDALSDRVKAQLDGLTAQHDFTKSFPLKRFGL
 164

Query: 175 VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR----HAHAIPGMDAAESERFL
 230

+ + + P+V+ HPETGR +L + + +P + A RFL
 Sbjct: 165 TADDRARWEDTRIKHPPV-THPVVRTHPETGRRALFVNEGFTTEINELPEEEGAALLRFL
 223

Query: 231 EGLVDWACQA-PRVHAH-QWAAGDVVVWDNRCLLHRA 265

+A Q+ P +W GDV WDNR +H A
 Sbjct: 224 -----FAHQSRPEFTLRWRWQPGDVAFWDNRSTIHYA 255

>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 = 7e-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 TRCLKLTRLTPAIGAIVDNVDSLNSATGDLRDGIRAALARHQVLFVRDQRLSAVRHRDFAAG 94

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP
 116

FG + +I+ + N D + N WH D T+
 Sbjct: 95 FGDLVHVPYPSHPDAREIMVLDNAVFD-----LKDNAIWHTDVTFAE
 137

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLV--YSQSKLGH
 174

Query: 64 FGA--IERIGGGDI-----VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV
117

FG I + G + + + AD T Q D + ++ WH+D T+
Sbjct: 157 FGRHHIHQTS GAPKGFPEIHLVHRGADDTSGQ-----DFLATRTNSITWHS DVTFEKQ
209

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQ
177

P+ GG T F DM AY L R +H A HS + ++ +
Sbjct: 210 PPGTTFLYLLDGPSSGGDTLFCDMAQAYRRLSPEFRRLHGLRAVHSGI---EQINNSLN
266

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDW
236

G G+ T P+V+ HP TG +L + + I G ES+ L+ L D
Sbjct: 267 KGGIARREGIMTE----HPIVRTHPVTGEKALFVNPQFTRYIVGYKKEESDFLLKFLYDH
322

Query: 237 ACQAPRVHAH-QWAAGDVVWDNRCLLHRA 265

+ + +W G VVWDNR + H A
Sbjct: 323 IALSQDIQTRVRWRPGTVVWDNRVVAHSA 352

>gb|ABC34147.1| alpha-ketoglutarate-dependent taurine dioxygenase

[Burkholderia

thailandensis E264]

Length = 335

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: 60 TRCLKLRLTPAIGAIVDNVDLSNATGDLRDGIRAALARHQVLFVRDQRLSAVRHRDFAAG
119

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
116

FG + +I+ + N D + N WH D T+
Sbjct: 120 FGDLVHVPYPSHPDAREIMVLDNAVFD-----LKDNAIWHHTDVTFAE
162

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLV--YSQSKLGH
174

+ ++ +A +P GG T + AAYDAL + +A + +A+H + + G
Sbjct: 163 TPTRASILAARTLPETGGDTLWGSFGAAYDALSDRVKAQLDGLTAQHDFTKSFPLKRFGL
222

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR----HAHAIPGMDAAESERFL
230

+ + + P+V+ HPETGR +L + + +P + A RFL
Sbjct: 223 TADDRARWEDTRIKHPPV-THPVVRTHPETGRRALFVNEGFTTEINELPEEEGAALLRFL
281

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62
 T L++T +GA V LA +DD +A+ A +H +L F Q LS Q FA
 Sbjct: 2 TRCLKLTRLTPAIGAIVDNADLANAVDDDDVRSAIRDALARHQVLFVRDQRLSAVQHRDFAA 61

Query: 63 RFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
 115
 FG + +I+ + N D + N WH D T+
 Sbjct: 62 GFGDLHVHPIYSPHPDAREIMVLDNEVFD-----LKDNAIWHTDVTF
 104

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLV--YSQSKLG
 173
 ++ +A +P GG T + AAYDAL + + + +A+H + + G
 Sbjct: 105 ETPPCASILAACLTLPDTGGDTLWGSFGFAAYDALSDRVKTQLEGLTAQHDFTKSFPLKRF
 164

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEG
 232
 + + + P+V+ HPE+GR +L + I + ES L
 Sbjct: 165 LTADDRARWEETRIKHPPV-THPVVRTHPESGRRALFVNDGFTTEINELPEEESAALLRF
 223

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 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]

Length = 389

Score = 74.7 bits (182), Expect = 1e-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---MGTILTGVKLEELSDEGKDELALLITERKIVVLREQSDFLHSGPQFQQDFMSY
 143

Query: 64 FG--AIERIGGGDIVAISNVKADGTV----RQHSPAEWDDMMKVIVGNMAWHADSTYMPV
 117
 FG +I+ + G +VK R H+ E + + + + WH D +Y
 Sbjct: 144 FGPLSIQPVSG-----SVKGFPHFVHVRDHNEEEIANFFQKLTSTLWHHDVSYEK-
 195

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQ
 177
 G + P VGG T FAD AY L RA++ A HS SQ +G+ +
 Sbjct: 196 QPPGYIMLG-TCPDVGGDTVFADTVEAYKRLSPTFRAMIQDLKATHS---SQKMIGYARA
 251

Score = 74.7 bits (182), Expect = 1e-11, Method: Compositional matrix adjust.

Identities = 65/215 (30%), Positives = 93/215 (43%), Gaps = 37/215 (17%)

Query: 56 QQITFAKRFGAIERIGGGDIVA-----ISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHAD
111

 QQI FA +FG + D+ + I V AD T + V WH+D
Sbjct: 1 QQIAFAAQFGKLYIHPVADMASRHPEILPVYADETTTK-----VFGEDWHSD 47

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSK
171

 ++ G++ + +P VGG T F+ M AAYDAL E + L+ +A H
Sbjct: 48 ASCDTEPPMGSILQLQEIPDVGGDTMFSSMYAAYDALSEPLKQLLEGLTAVHD-----
100

Query: 172 LGHVQQAGSAYIGYGMDDTT---ATPLRPLVKVHPETGRPSLLIG-RHAHAIPGM DAAESE
227

 GHV + D T T +P+V HPE+GR +L + ++ I + ES+
Sbjct: 101 GGHV-----FRHRFDKTRFYPTTEQPVVTRHPESGRKALYVNAQYTTTHIVQLKPRESD
153

Query: 228 RFLEGLVDWACQAPRVHAH-QWAAGDVVVW DNRCL 261

 L L + P H W G VV WDNRC+
Sbjct: 154 ALLAFLYR-HVETPEFHCRFSWRQGSVVFWDNR CV 187

>gb|ADC33944.1| TfdA-like protein [uncultured bacterium]
Length = 121

Score = 74.3 bits (181), Expect = 1e-11, Method: Compositional matrix adjust.

Identities = 45/127 (35%), Positives = 69/127 (54%), Gaps = 7/127 (5%)

Query: 136 TCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL-
194

 T F DMR A++AL A +A + +A HS+++S++ G + + + P+
Sbjct: 1 TEFCDMRLAWEALPLADQARLEGLTAYHSIMHSRATYGFDEWSREEQKRF-----PPIP 54

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

 RPLV +H E+GR SLL+ H I GM ES + L A +AH+W GD++
Sbjct: 55 RPLVGLHEESGRKSLLLASHVADIAGMARDESAALVREL TARATVTEHCYHRWTQGDLL
114

Query: 255 VWDNRCL 261

 +WDNRC+
Sbjct: 115 LWDNR CV 121

>ref|XP_001836817.1| hypothetical protein CC1G_04130 [Coprinopsis cinerea
okayama7#130]

 gb|EAU85034.1| hypothetical protein CC1G_04130 [Coprinopsis cinerea
okayama7#130]

Length = 366

Score = 74.3 bits (181), Expect = 1e-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: 90 LGTEVRGVQLSLSNEGLDELALFVAERKVVVFREQDLKDQPPEKQLKFSSYFGRSHVHP
 149

Query: 69 -RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
 127

+ D ++ + D +P D+++K + + WH+D +Y F
 Sbjct: 150 LSVNVKDYPELAVIYRD----PENPGFLDELVKPRINHTNWHSDVSYEKQPPGTTAFYIL
 205

Query: 128 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
 187

P VGG T F AY+ L A R + A H+ G Q G+ G+
 Sbjct: 206 DGPDVGGDTLFLSQVEAYNRLSPAFRERLIGLKAVHT-----GIPQAEQAK--KRGV
 255

Query: 188 DTTATPLR---PLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQAPRV
 243

P+ P+V+VHP T +L + I G ES+ L L D +
 Sbjct: 256 HVRREPVESEHPVVRVHPVTKEKALYVNPFGFTTRIVGFKKEESDALLGFLFDHITKGADF
 315

Query: 244 HAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAA 291

H + G VV+WDNR +H A P DF H RL + E AA
 Sbjct: 316 HVRASYEPGTVVIWDNRVTVHSAIP-DFDRSLRRHHIRLTPQAEVPIAA 363

>ref|XP_001799620.1| hypothetical protein SNOG_09325 [Phaeosphaeria nodorum SN15]

gb|EAT83517.2| hypothetical protein SNOG_09325 [Phaeosphaeria nodorum SN15]

Length = 328

Score = 74.3 bits (181), Expect = 1e-11, Method: Compositional matrix adjust.

Identities = 72/288 (25%), Positives = 122/288 (42%), Gaps = 45/288 (15%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 T+ + GA + G D F + +A ++ +L+F LS+ + + F+ R
 Sbjct: 13 TITFKELHPSYGAEIIGADFENATDEQFQEIKSAMAKYGVLVFRNTGLSDAKHVEFSSRI 72

Query: 65 GAIERI----GGG-----DIVAISNVKADGT-VRQHSP-AEWDDMMKVIVGNMAWHA
 110

GA++ + GG ++ NV +G + SP A ++ GN +H
 Sbjct: 73 GALDNVRRYLGTGGRKLRHYELFDAGNVDEEGNAIDPDSRAHYNK-----GNALFHV
 126

Query: 111 DSTYMPVMAQGAVFSAEVV--PAVGGRTCFADMRAAYDALDEATRA--LVHQRSARHSLV
166

DS++ P A ++ A + P +GG T FAD R A+D LDE + L H+L+
Sbjct: 127 DSSFNPRRASWSLLRAVKLPPPGMGGETEFADSRTAWDDLDEDFKIELLLDCDLVGAHTLL
186

Query: 167 YSQSKLGHVQQAGSAYIGYGMDDTATPL--RPLVKVHPETGRPSLLIGRHAHAIPGMDAA
224

H ++ GS + + P+ +V+ H +G H +P +
Sbjct: 187 -----HSRKLGSPEFFADLVPESEPMRHKIVQTHEPSG-----HCKPLP---ES
228

Query: 225 ESERFLEGLVDWACQAPRVHAHQW-AAGDVVVWDNRCLLHRAEPWDFK 271

ES E L+ Q + + W GD+V WDN ++HRA F+
Sbjct: 229 ESAALFERLLKHVTQPKYILSVDWLNEGDMVAWDNTAVMHRATGGGSFE 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 = 1e-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 AAQPVDVIPLSAHIGAEIRGVDLTQPLTTPQIAAIRAALLKWRVIFRFREQFLTHEQHVAF 67

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
120

+ +FG +G + A ++ +H A + V WH D T
Sbjct: 68 SAQFGE-PTVGHPVFGHVDGHPAVYSIAKHRKATRFEGEPVRRPWTGWHTDVTA AVNPPW
126

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS
180

++ +P GG T + ++ AY+ L R V H +A
Sbjct: 127 ASILRGVTIPPYGGDTHWTNLV RAYETLSAPLRGFVDTLRGIHRFTPPPGA-----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 PEFTIRFKWEPRSI AFWDNRATAHLAPVDIFDLDFDRQLYRTTLIG 287

>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 ASFPLTISPLQPTIGAEIAGVDLREPLTPALRDEIKAAILKYKVVFFRDQHITREQQAAF 70

Query: 61 AKRFGAI-----ERIGGGDIVAISNVKA-DGTVRQHSPA--EWDDMMKVIVGNMAWHAD
111

A++FG + ++ G +I + A D + + A D++ + +H D
Sbjct: 71 ARQFGPLYTHPTTKQTDGTVDASIHRIA AVDFQLYEKEAAVRKDEIQEF-----YHTD
124

Query: 112 STYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK
171

+++ V GAV A +P VGG T + D AY L + R + H
Sbjct: 125 TSWRLVPTWGAVLRAVTLDPVGGDTIWVDAGLAYRNLPDDIRERLEGLHVTHDF-----
178

Query: 172 LGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAH-AIPGMDAAESERFL
230

+A + G D + +V+ H ETG L + H I G+D AES L
Sbjct: 179 -----RNALLCAGHDYPIVAHK-IVRTHRETGEKILWVNFSQHPTIIGLDRAESRALL
230

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM 276

E + + W G + WDNR +H A PR++
Sbjct: 231 EEVAAYRPEHQVRFVSWRPGSIAFWDNRASVHYAVRNYGDFPRL 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 LSDNQFEQLYHAVLRHQVVFRLDQAITPQQQRALAQRFGE LHIHPVYPHAEGVDEIIVLD
145

Query: 81 VKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFAD
140

Sbjct: 146 THND-----NPPDNDN-----WHTDVTFIETPPAGAILAAKELPSTGGDTLWTS
189

Query: 141 MRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP--LRPLV
198

AAY+AL R L+ A H S + + ++ + + P L P+V
Sbjct: 190 GIAAYEALSVPPFRQLLSGLRAEHDFRKSFPPEYKY-RKTEEEHQRWREAVAKNPPLLHPVV
248

Query: 199 KVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWD
257

+ HP +G+ +L + I + ESE L L + +W D+ +WD
Sbjct: 249 RTHPVSGKQALFVNEGFTTRIVDVSEKESALLSFLFAHITKPEFQVRWRWQPNDIAIWD
308

Query: 258 NRCLLHRA 265

NR H A
Sbjct: 309 NRVTQHYA 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 MQIKKITPTIGAELSGVDFTKDLTTAQQDEIYQALLDHQVIFVRGCDISPANHVAFQAQTF 60

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF
124

G ++ N G + ++ K +WH D T+ + ++
Sbjct: 61 GDLDE-----PNPMYPGVDGFKNIMLLENDAKRPPDTNSWHTDLTFKVEQSFASIL
111

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQ--AGSAY
182

+ VVP GG T ++ AAYDAL E +A + SA H L ++ + +G
Sbjct: 112 VSRVVPDCGGDTLWSSNYAAYDALSEGKADLEGLSAVHDLGDFRNNFAQPKDGLSGEER
171

Query: 183 IGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQAP
241

+ + ++P++ HP T R L I G ES L + Q
Sbjct: 172 LNAAVGRMGHAIKPIIDEHPVTKRKFLLNFNEAFITHIVGKTPNESNALRIWLANHMQPE
231

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

R LV H E+GR +LL+ H AI G D AE+ + L+ A + H+W+ GD++
Sbjct: 55 RALVARHEESGRKALLLASHIEAIDGCDDAETAAMVRDLMARATSRENCYVHRWSEGDLL
114

Query: 255 VWDNRCL 261
+WDNRC+

Sbjct: 115 LWDNRV 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 TRCLKLTRLTPAIGAIVDNVDSLNTGDLRDGIRAAALRHQVLFVRDQRLSAVRHRDFAAG 94

Query: 64 FGAI-----ERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP
116

FG + +I+ + N D + N WH D T+
Sbjct: 95 FGDLHVHPIYPSHPDAREIMVLDNAVFD-----LKDNAIWHHTDVTFAE
137

Query: 117 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV--YSQSKLGH
174

+ ++ +A +PA GG T + AAYDAL + +A + +A+H + + G
Sbjct: 138 TPPRASILAARTLPATGGDTLWGSFGAAYDALSDRVKAQLDGLTAQHDFTKSFPLKRFGL
197

Query: 175 VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL
233

+ + + P+V+ HPETGR +L + I + E L L
Sbjct: 198 TADDRARWEDTRIKHPPV-THPVVRTHPETGRRALFVNEGF'TTEINELPEEEGAALLCFL
256

Query: 234 VDWACQAPRVHAHQWAAGDVVWDNRCLLHRA 265

+ +W GDV WDNR +H A
Sbjct: 257 FAHQSRPEFTLRWRWQPGDVAFWDNRSTIHYA 288

>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.

ES L L D A Q +WA G V +WDNR W + + H+R
 Sbjct: 132 REESVPLLRELYDHAMQPAHQCRVEWAPGTVAIWDNRRT-----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 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
 195

T FADMRAAYD L E + + A H + S+ LG + S P+
 Sbjct: 1 TEFADMRAAYDDLPEDFKKEQLGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAESERFLEGLVDWACQAPRVHAHQWAAGDVV
 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 = 2e-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--IERIGGGDIVAISNVKADGTVRQHSPPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
 120

FG I + G +N + T R+ E+ + + WH D +Y
 Sbjct: 159 HFGKLIHQTSQH---PQNNPELHITFRRPDAEEFARVFDDSTSSGGWHTDVSYELQPPS
 215

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGS
 180

FS P GG T FAD A+D L + + + S H + S+ + + Q+ G

Sbjct: 216 YTFFSVVEGPDGGGDTLAFADTIEAFDRLSKPLQDFL---STLHVIIHSSKEQAENSQRQG-
271

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQ
239

G T + PLV+VHP + L + R + I + ESE L L +
Sbjct: 272 ---GIKRRAPVTHIHPLVRVHPVLKKKCLYVNRASF SRKIVELKRQESSELLNFLYNLVES
328

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ + +W VV+WDNR + H A

Sbjct: 329 SHDLQLRAKWEPHSVVIWDNRRVQHSA 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 = 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 AAQPVDVIPLSAHIGAEIRGVDLTQPLTTPQIAAIRAALLKWRVVFREQFLTHEQHVAF 67

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ
120

+ +FG +G + A ++ +H A + V WH D T
Sbjct: 68 SAQFGE-PTVGHPVFGHVDGHPAVYSIAKHRKATRFEGEPVRRPWTGWHTDVTA AVNPPW
126

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGS
180

++ +P GG T + ++ AY+ L R V H +A
Sbjct: 127 ASILRGVTIPPYGGDTHWTLNLRVAYETLSAPLRGFVDTLRGIHRFTPPPGA-----RATG
181

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAI PGMDAAESERFLEGLVDWACQ
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 PEFTIRFKWEPRSI AFWDNRATAHLAPVDIFDLDFDRQLYRTTLIG 287

>ref|YP_837646.1| taurine dioxygenase [Burkholderia cenocepacia HI2424]
gb|ABK10753.1| Taurine dioxygenase [Burkholderia cenocepacia HI2424]

Length = 315

Sbjct: 219 DTPDTGGDTLAFANTVEAYERLSPAFQKLLHGLKATHSGI-----EQVNASVKKGS
268

Query: 188 DTTATPL---RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRV
243

P+ P+V+ HP TG SL + + I G+ ES+ L L +
Sbjct: 269 IKRREPVVNEHPIVRTHPVTGEKSLFVNPQFTRDIVGLKKEESDAILNFLYEHIWAGADF
328

Query: 244 HAH-QWAAGDVVVWDNRCLLHRA 265
HA +W VVVWDNR + H A

Sbjct: 329 HARVKWQEKTVVVWDNRSVQHTA 351

>ref|NP_013043.1| 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]

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]

Length = 412

Score = 73.6 bits (179), Expect = 2e-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 LKVKKITPKLGLLEINGIQLTDLSDAAKDELALLVAQKGVVFRNQNFADDEGPDYVTEYGR
172

Query: 63 RFGA--IERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
120

FG I + G +N + T R+ E+ + + WH D +Y

Sbjct: 173 HFGKLIHQTSQH---PQNNPELHITFRRPDAEEFARVFDDSTSSGGWHTDVSYELQPPS
229

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGS
180

FS P GG T FAD A+D L + + + S H + S+ + + Q+ G

Sbjct: 230 YTFFSVVEGPDGGGDTLAFADTIEAFDRLSKPLQDFL---STLHVIIHSSKEQAENSQRQG-
285

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQ
239

G T + PLV+VHP + L + R + I + ESE L L +
Sbjct: 286 ---GIKRRAPVTHIHPLVRVHPVLKKKCLYVNRASF SRKIVELKRQESSELLNFLYNLVES
342

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
+ + +W VV+WDNR + H A

Sbjct: 343 SHDLQLRAKWEPHSVVIWDNRRVQHSA 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 = 2e-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 KRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVI--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 PYTMLHGIDVPGTSGHTLYANAADVYDRLPEEWKERIEGRIAVHTVAKRQRISAEHAGLS
181

Query: 180 SAYIGYGMDDTTATPLR-PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWA
237

A ++ P++ PLVK P TGR + + + G DA E+E F L++
Sbjct: 182 IAEFKALVEEQYPPVQHPLVKTDPTTGRRYVYGAPEYMERVIGFDANENEEFF-ALLNRL
240

Query: 238 CQAPR-VHAHQWAAGDVVVWDNRCLLHRA 265
Q P V+ H+W D+VVW H A

Sbjct: 241 IQDPEHVYTHRWTPRDLVVKCELTYHAA 269

>gb|AAS64584.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
Length = 119

Score = 73.6 bits (179), Expect = 2e-11, Method: Compositional matrix adjust.

Identities = 48/125 (38%), Positives = 61/125 (48%), Gaps = 7/125 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
195

T FADMRAAYD L E + + A H + S+ LG + S P+
Sbjct: 1 TEFADMRAAYDDLPEDFKKEQLGLRAEHYALSSRFILGDTDYSES-----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

>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 = 2e-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 AAQPVDVIPLSAHIGAEIRGVDLTQPLTTPQIAAIRAALLKWRVIFRFREQFLTHEQHVAF 81

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
120

+ +FG +G + A ++ +H A + V WH D T
Sbjct: 82 SAQFGE-PTVGHPVFGHVDGHPAVYSIAKHRKATRFEGEPVRRPWTGWHTDVTA AVNPPW
140

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGS
180

++ +P GG T + ++ AY+ L R V H +A
Sbjct: 141 ASILRGVTIPPYGGDTHWTLV RAYETLSAPLRGFVDTLRGIHRFTPPPGA-----RATG
195

Query: 181 AYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQ
239

A+ PLV+VHPETG +L + I G+ ES+ LE L + +
Sbjct: 196 AFDDAVERRPLVTEHPLVRVHPETGERALYVSPSFLKTIVGLTPRESQALLELLWEHVTR
255

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA--EPWDFKLPRVMWHSRLAG 283

+W + WDNR H A + +D R ++ + L G
Sbjct: 256 PEFTIRFKWEPRSI AFWDNRATAHLAPVDIFDLDFDRQLYRTTLIG 301

>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 = 2e-11, Method: Compositional matrix adjust.

Identities = 81/299 (27%), Positives = 117/299 (39%), Gaps = 39/299 (13%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITF 60
T ++TPT G+ +TG+ L++L D L Q +L+F Q ++ DQ + F
Sbjct: 76 TVKRLTPT---TGSEITGIQLSSLTDKAKDQLALFAAQRKVLVFRDQDFADLPIDQAVAF
132

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA---WHADSTYMPV
117

FG R + + V + D + G + WH+D TY
Sbjct: 133 GGYFG---RHHVHTTAGVPEGYPEVHVYMMDTKNGDFATFLAGKNSTVLWHS DVTYDEQ
189

Query: 118 MAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
177

+ A +P VGG T FA+ AY L A R +H H V SQ++
Sbjct: 190 PPGMTILYALELPEVGGDTAFANQVEAYKRLSPALRERLHGLKGVHDGV-SQAE-----
242

Query: 178 AGSAYIGYGMDTTATPL---RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
234

Y G P+ PLV+ HP TG +L + I GM ES+ L L+
Sbjct: 243 ---PYRAGRLVRREP VIVEHPLVRTHPVTGEKALFVNALTRIVGMKKEESDMLLGF L M
299

Query: 235 DWA--CQAPRVHAHQWAAGDVVVWDNRCLLHRA-----EPWDFKLPRVMWHSR 280

+ C +V +W VV+WDNR + R W LPR+ H R
Sbjct: 300 NHIGHCLEHQVRV-RWEPKTVVIWDNRTVSLRTLRSSTGELVSVGTWHASLPRLSVHLR 357

>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 LKVKKITPKLGLLEINGIQLTDLSDAAKDELALLVAQKGVVFRNQNFADGEPDYVTEYGR
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 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGS
180

FS P GG T FAD A+D L + + + S H + S+ + + Q+ G
Sbjct: 230 YTFFSVVEGPDGGGDTL FADTIEAFDRLSKPLQDFL---STLHV IHS SKEQAENSQRQG-
285

Query: 181 AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQ
239

G T + PLV+VHP + L + R + I + ESE L L +
Sbjct: 286 ---GIKRRAPVTHIHPLVRVHPVLKKKCLYVNR AF SRKIVELKRQES ELLNFLYNLVES
342

Query: 240 APRVHAH-QWAAGDVVVDNRCLLHRA 265

+ + +W VV+WDNR + H A
Sbjct: 343 SHDLQLRAKWEPHSVVIWDNR RVQHS A 369

>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 QITPTGATLGATVTGVHLATLDDAGFAALHA AWLQHALLIFPGQHLSNDQQITFAKRFGA 66

+ITP LG VTG+ L+ LDD G L Q +++F Q + + FA +G+
Sbjct: 85 RITPK---LGTEVTGIQLS QLDDK GKDELALFVAQRGVVVFREQDFAT-KGPKFATEYGS
140

Query: 67 IERIGGGDIVAISNVKADG-----TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQG
121

G I S D T R+ E+ + + ++ WH+D +Y
Sbjct: 141 --HFGRLHIHPTSGAPKDHPELHITYRRAD EGEFSRVFSNRLNSIGWHS DVS YELQPPGT
198

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSA
181

F+ P GG T FAD+ AY+ L + + + H L S+ + + + G
Sbjct: 199 TFFT VLQGPDAGGDTNFADVVEAYNRLSPEFQKRL---ANLHVLHTSEDQASNSRTQG--
253

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQA
240

G + + PL++ HP TG + + R + I + ES+ L L A
Sbjct: 254 --GIERRKPVSNIHPLIRQHPATGDKFIYLNRPFSRRIVELKEDES DYLLNFLFQHIESA
311

Query: 241 PRVHAH-QWAAGDVVVWDNRCLLHRA 265
 + +W VVVWDNR ++H A
 Sbjct: 312 HDLQLRARWEPNSVVVWDNRVHSA 337

>ref|XP_457814.1| hypothetical protein DEHA0C03553g [Debaryomyces hansenii CBS767]

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---LGTEVTGIQLSQLDDKKGKDELALFVAQRGVVVFREQDFAT-KGPKFATEYGS
 140

Query: 67 IERIGGGDIVAISNVKADG-----TVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
 121

G I S D T R+ E+ + + ++ WH+D +Y

Sbjct: 141 --HFGRLLHIHPTSGAPKDHPELHITYRRADGEFESRVFNSRLNSIGWHSVSYELQPPGT
 198

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
 181

F+ P GG T FAD+ AY+ L + + + H L S+ + + + G

Sbjct: 199 TFFTVLQGPDAGGDTNFADVVEAYNRLSPEFQKRL---ANLHVLHTSEDQASNSRTQG--
 253

Query: 182 YIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQA
 240

G + + PL++ HP TG + + R + I + ES+ L L A

Sbjct: 254 --GIERRKPVSNIHPLIRQHPATGDKFIYLNRPFSRRIVELKEDESDYLLNFLFQHIESA
 311

Query: 241 PRVHAH-QWAAGDVVVWDNRCLLHRA 265
 + +W VVVWDNR ++H A

Sbjct: 312 HDLQLRARWEPNSVVVWDNRVHSA 337

>ref|XP_001834709.1| hypothetical protein CC1G_05846 [Coprinopsis cinerea okayama7#130]

gb|EAU87157.1| hypothetical protein CC1G_05846 [Coprinopsis cinerea okayama7#130]

Length = 368

Score = 73.6 bits (179), Expect = 3e-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

Query: 173 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIP-GMD--AAESERF
229

 Q D + PLV H TG+ L +G AIP GM+ E++++
Sbjct: 187 WFWQ-----NLDWDNVPKVKHPLVSTHKVTGKKGLYLGSWNTAIPLGMEDKQEEAQQY
239

Query: 230 LEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWD 269

 + L + + V++H W GD+V WDN ++HR +D
Sbjct: 240 WQDLWNMVLERTPVYSHVWEPGDIVFWDNSQVMHRGTFYD 279

>ref|ZP_05016256.1| 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 = 3e-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-DGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAV
132

 A NV A DGT + A + K WH D T++ Q + V
Sbjct: 66 -TTAHPNVPATDGTT--NVLAVDSETSKA----NEWHTDVTFVINPPQLTTLRSIVTTPY
118

Query: 133 GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTAT
192

 GG T A+ AAY L RAL H+ Y ++ Y + T
Sbjct: 119 GGETLIANAAAAYRDLPAPLRALADTLRVVHTNQYDYARPASTTAQRQEYDRAFVSTPYE
178

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD
252

 P+V+VHP TG L IG A I G+ +++S L L + + + W+
Sbjct: 179 AEHPVVRVHPLTGERGLFIGGFAKRIVGLPSSDSADLLRILQSYVTRPENILSWTWSPNQ
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]
Length = 118

Score = 73.2 bits (178), Expect = 3e-11, Method: Compositional matrix
adjust.

Identities = 45/123 (36%), Positives = 61/123 (49%), Gaps = 7/123 (5%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-P
196

F DMRAAYD L E + + A H ++S+ LG + + S P+ P
Sbjct: 2 FCDMRAAYDDLPEDFKKEQLGLRAEHYALHSRFLGDTEYSES-----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 LIRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQPKFVYRHSWKVGDLMVMW
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 = 3e-11, Method: Compositional matrix
adjust.

Identities = 40/127 (31%), Positives = 65/127 (51%), Gaps = 6/127 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL-
194

T F DM AY+ L A + + A H+L +S+++ + G + P+
Sbjct: 1 TEFCDMYGAYERLSPAWNRIATLRAMHNLDIFSRTTR-----RHGEEPMTAQORDAVPPVD 55

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

P+V+ HP+TGR L +G HA + GM+ + +E L A A + H+W G+++
Sbjct: 56 HPIVRTHPDTGRKCLFLGDHAQYVVGMMNYEDGRALIEELNALAIHADLTYEHRWTPGELL
115

Query: 255 VWDNRCL 261

VWDNRC+

Sbjct: 116 VWDNRCL 122

>gb|ACB30159.1| 2,4-D/alpha-ketoglutarate dioxygenase [Rhodococcus sp.
HDN3]

Length = 118

Score = 73.2 bits (178), Expect = 3e-11, Method: Compositional matrix
adjust.

Identities = 45/123 (36%), Positives = 60/123 (48%), Gaps = 7/123 (5%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-P
196

F DMRAAYD L E + + A H ++S+ LG + S P+ P
Sbjct: 2 FCDMRAAYDDLPEDFKKELQGLRAEHYALHSRFLGDTEYCES-----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 LIRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQPKFVYRHSWKVGDLMW
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 = 3e-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----VAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVF
124

+ G + + + AD T D + ++ WH+D T+ V G F
Sbjct: 167 QASGAPRGYPEIHLVHRGADDT-----SGADFLAQHTNSITWHSVDVTFE-VQPPGTTF
218

Query: 125 SAEVV-PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
183

+ P GG T FADM AY L R +H A HS V+Q ++ +
Sbjct: 219 LYLLDGPTTGGDTLFDADMAQAYKRLSPEFRKRLHGLKAVHS-----GVEQVNNS-L
268

Query: 184 GYGMDDTTATPL---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 SQDIQTRVRWRPQTVVVWDNRVACHSA 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 = 4e-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 ITETKLEFAKLGSRIGAEIRGLDLGGDLAETVAQIRAALNEHKALVFREANILTDEAQV 63

Query: 59 TFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMA---WHADSTYM
 115

FA FG + KA TV E ++ V N + WH D T++
 Sbjct: 64 KFAGHFGPL-----TKAHTVASVEGKE--SVLPVDSSENGSANNWHTDVTFV
 108

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS---KL
 172

Q + + +PA GG T A AY L E R A H+ Y S L
 Sbjct: 109 VNPPQASTLRSIDLPAYGGETLIASSAGAYRDLPEELRNFAATLWAIHTNDYDYSVPKNL
 168

Query: 173 GH--VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH--AIPGMDAAESER
 228

H ++ + +T P+V+VHP TG L IG A I G+ ES+
 Sbjct: 169 EHENAEEERRKEFTRLKFETA----HPVVRVHPLTGERGLFIGGFAQRLRIVGLSNTESKD
 224

Query: 229 FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

+ L + + V W +V++DNR H A PR + +AG
 Sbjct: 225 IIRLLQAYVTRPENVVRVNWEPNQLVLFDNRITQHYAPDNYDGQPRKLN RVTIAG 279

>ref|XP_001834272.1| hypothetical protein CC1G_12351 [Coprinopsis cinerea
 okayama7#130]

gb|EAU87552.1| hypothetical protein CC1G_12351 [Coprinopsis cinerea
 okayama7#130]
 Length = 364

Score = 72.8 bits (177), Expect = 4e-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

Score = 72.8 bits (177), Expect = 4e-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 RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
 122

FG E G T+ D +K N WH D + P +
 Sbjct: 111 LFGHSEYTGTPYTPVAEESNVNTI-----DSKVKKTRMNFIIWHIDQAFRPEPPRF
 162

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAY
 182

V + VP GG T F + AAY+ LD L Q S+ +G + A
 Sbjct: 163 VLFGKKVPPFGGDTVFTNATAAYELLD----PLFAQYLETLSVAQDVETMGFLTAYREE
 218

Query: 183 IGYGMDTTATP-LR-PLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQ
 239

P +R PL++VHP+TG+ + + + I G+ S+ L L D
 Sbjct: 219 EELARQKARFPWIRTP LIRVHPDTGKKQIYVNELYTQRILGLSRIASQNILGILFDLIKS
 278

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHR 264

+ ++W G V++WDNR + HR
 Sbjct: 279 PEVLTRYRWEEG SVLIWDNRVVQHR 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 = 4e-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 QSAFTLTRISPALGAEVGNIDLNVPLDDDTIAALRRALVEHKVLFVFRDQDITPSQHVSLA 82

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVG-----NMAWHADST
 113

+RFG +E V P + V++G +H+D +
 Sbjct: 83 RRFGELE-----VHPAFPHHEEFPELVLLGGDDKKPAMENGYHSDVS
 124

Query: 114 YMPVMAQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLG
 173

+ + + ++ P +GG T + +M AY+ L E + + A H ++ +

Sbjct: 125 WREIPSMASMLRCVQCPEIGGDTVWVNMALAYEKLPEHRKQQIEGLFAAHDILPA-----
179

Query: 174 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-----RHAHAIPGMDA
223

G + P+V+ HPE+G L + R +A+ G
Sbjct: 180 ----FGDKMTPEQRKQFPPAIHPVVRTHPESGEKILYVNGAFVTHFLNFRSRNAVVGAFE
235

Query: 224 AESERFLEGLVDWACQAPRVHAHQ----WAAGDVVVWDNRCLLHRAEPWDFKLPVVMWHS
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 = 4e-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---IGSEIHGVQLSQLSDKGDQLALYVAQRRVVAFRDQDFASRPIQEVDYAGY
155

Query: 64 FGA--IERIGGG-----DIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMP
116

FG I + G +I + D T + +K + WH+D T+
Sbjct: 156 FGRHHIHQTSGAPKGFPEIHLVFRGADDRT-----GETFLKERTNTITWHSVTFEK
207

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
176

P+ GG T FADM AY L R +H A HS ++
Sbjct: 208 QPPGTTFLYVLDGPSTGGDTLFDADMVQAYKRLSPGFRERLHGLKAVHS-----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 VDWACQAPRVHAHQ--QWAAGDVVVWDNRCLLHRA 265
D + + A +W AG VVVWDNR H A

Sbjct: 319 YDHIALSQDLQARIRWKAGTVVVWDNRLACHSA 351

>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 = 5e-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 MKVEQLTCSIGAEVSDIHLGDASRDKGLAEEIRALLLQHKVLFRRDQDITRAEHVGFARH 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVI VGNMAWHADSTYMPVMAQGAV
 123

FG +E VA S+ + G V+ + + ++ +H+D + G V
 Sbjct: 61 FGDLE----DHPVAGSDPEHPGLVQIYRSEKRENYENT-----YHSDGQWRENPTMGCV
 110

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQAGSAYI
 183

PAVGG T + +M AY L E + + A+ S+ + G V
 Sbjct: 111 LRCIEGPAVGGDTIWWNMAEAYRNLPEDIKQKIDGLKAKSSIEHG---FGAVMPEDKR--
 165

Query: 184 GYGMDDTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LE
 231

+ P+ P+V+ HPETG L + E+ R+ L
 Sbjct: 166 -LELGRQHPPVEHPVVRTHPETGEKVLVCSFTTHFANYHTPENVRYGQDKTPGASMLLN
 224

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

L+ A +W G V +WDNRC H A
 Sbjct: 225 YLISQAAIPEYQVRFWRKPGSVAMWDNRCTQHYA 258

>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 = 5e-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 ISIRPYKPLIGAVIENIDLTRPLSDQNKQDLNRRALVQHGVIFFRKQALSFAQHVDLARIF 78

Query: 65 G-----AIERIGGGDIVA-ISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
113

G ++E +++A N K GT WH D +
Sbjct: 79 GNPIRKNIYLP SVEGFPEIEVIAHDENTKTGGTDN-----WHVDVS
119

Query: 114 YMPVMAQGAVFSAE VVPAVGG-RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
172

+ + V + +P GG T +A A YD LD + +A ++ S K
Sbjct: 120 WQRQPPKATV LHIKQLPPDGGGDTIWASSTAVYDLLDPDLARYFEKLTAVNTFFASPKK-
178

Query: 173 GHVQQAGSAYIGY--GMDTTAT-----PLR-PLVKVHPETGRPSLLIGR-H
214

+ GY G + TA P+ P+VK HPETGR + + H
Sbjct: 179 ---EALSDLLTG YAEGREETAE EGLARVQDATVKFPPIEVPVKTHPETGRKLI FVNEAH
235

Query: 215 AHAI PGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

+ G+ S+ L L D + P V A W GDV +W DNR + H A
Sbjct: 236 TSHLLGVSKTASQ SLLNYLYDL-VKTPEVQARFAWQEGDVAIWDNRQVQH YA 286

>gb|ADC33960.1| TfdA-like protein [uncultured bacterium]
Length = 121

Score = 72.0 bits (175), Expect = 7e-11, Method: Compositional matrix
adjust.

Identities = 44/127 (34%), Positives = 68/127 (53%), Gaps = 7/127 (5%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY GMDTTATPL-
194

T F DMR A++AL A +A + +A HS+++S++ G + + + P+
Sbjct: 1 TEFCDMRLAWEALPPADQARLEGLTAYHSIMHSRATYGFDEWSREEQKRF-----PPIP 54

Query: 195 RPLVKVHPETGRPSLLIGRHAHAI PGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

RPLV +H E+GR SLL+ H I GM ES + L A +A +W GD++
Sbjct: 55 RPLVGLHEESGRK SLLLASHVADIAGMARDESAALVREL TARATVTEHCYARRWTQGDLL
114

Query: 255 VWDNRCL 261

+W DNR C+

Sbjct: 115 LWDNR CV 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 = 7e-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 TFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA---WHADSTYM
 115

FA FG + +N + PA ++ V N + WH D T++
 Sbjct: 64 RFASHFGPL-----TNAHPTVASVEGKPA----VLPVDSSENGSANNWHTDVTFV
 108

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHV
 175

Q + + +P GG T A AY L + R A H+ Y S+ ++
 Sbjct: 109 VNPPQASTLRSITLPEYGGETLIASSAGAYRDLPELRFADTLWAIHTNDYDYSRPNL
 168

Query: 176 QQAGS-----AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH--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 ILRILQAYITRPENVVRVNWEPNQLVLFDNRITQHYAPDNYDGQPRKLN 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 = 7e-11, Method: Compositional matrix
 adjust.

Identities = 71/267 (26%), Positives = 113/267 (42%), Gaps = 20/267 (7%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
 T ++TP LG+ + G+ L+ LDD L + +++F Q ND+ FA
 Sbjct: 89 TVKRLTPK---LGSEIDGIQLSQLDDKAKLDLAKFVAERGVVVFKNQDF-NDKGPQFAID
 144

Query: 64 FGAIERIGGGDIVAISNVKADG-----TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
 118

F + G I S + T R S E D +++WH+D +Y
 Sbjct: 145 F--MNYFGPLHIHPTSGSPENFPQM HITFRGASQDEIDTAFKNTNSISWHSDCSYSLNA
 202

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQA
 178

Q +FS +P GG T FA+ AY+ L A + + HS V Q++ ++A

Sbjct: 203 LQLTLFSCQLPESGGDTLFAANTVEAYNRLSPAMQERLEGLHLHSSV-EQAETN--KKA
259

Query: 179 GSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWA
237

G G T + P+V+V+P TG+ L + + I + ES+ L+ L D
Sbjct: 260 G----GITRREPETNIHPIVRVNPLTGKKHLYVNKEFGRRRIELKKEESDYLLKFLYDHI
315

Query: 238 CQAPRVHAH-QWAAGDVVVWDNRCLLH 263

A + W VV+W+N +H
Sbjct: 316 EGAQDLQIRVSWQPNTVVLWNNATTVH 342

>gb|EEU47182.1| predicted protein [Nectria haematococca mpVI 77-13-4]
Length = 331

Score = 72.0 bits (175), Expect = 8e-11, Method: Compositional matrix
adjust.

Identities = 72/289 (24%), Positives = 120/289 (41%), Gaps = 48/289 (16%)

Query: 4 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITF 60
T ITP +G + GV ++ L G + + +++F Q ++ D+Q

Sbjct: 48 TVTDITPR---IGTEIRGVQISKLSSEGLDEIALLAERG VVFRDQDFADVGFDRQREI
104

Query: 61 AKRFGAIE-----RIGGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHAD
111

K +G + + G + + + G +R P D+ WH D
Sbjct: 105 VKHYGPLHLHPTMGYPKGTGPEFHVVYADEKSGNLRSLGPRTTYDL-----WHID
155

Query: 112 STYMPVMAQGAVF-SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS
170

T+ P + F E+ + GG T F + AY+AL A R + +H+ +
Sbjct: 156 QTFTPNVPSTTFFWVLEIPQSGGGDTAFTSLTHAYEALS PAFRETLTSLKLQHT----SA
211

Query: 171 KLGHVQQAGSAY-IGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESER
228

G V++ G+ + ++TT PLV HP TG+P+L + A + G ES+
Sbjct: 212 SEGEVRRVGTTERALAEAINTT----HPLVIKHPVTGKPALFVNPTIARQVEGFLPEESQH
267

Query: 229 FLEGL-----VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFK 271

L L +D++C+ +W G VV+WD R H A P DF+
Sbjct: 268 LLSFLHNHIRSLDFSCRV-----KWEKGTVVIWDQRSAGHS AVP-DFQ 309

>gb|ADC33951.1| TfdA-like protein [uncultured bacterium]
Length = 122

Score = 71.6 bits (174), Expect = 8e-11, Method: Compositional matrix
adjust.

Identities = 40/127 (31%), Positives = 64/127 (50%), Gaps = 6/127 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL-
194

T F DM AY+ L A + + A H+L +S+++ + G + P+
Sbjct: 1 TEFCDMYGAYERLSPAWKGRIAGLRVHNLDFSRTTR-----RHGEDPMTEAQRERPPVD 55

Query: 195 RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDVV
254

P+V+ HPETGR + +G HA +I GMD +E L A + H+W+ G ++
Sbjct: 56 HPIVRTHPETGRKCIFLGDHAESIQQMDYEAGRALIEELNALAVHPDLTYRHRWSPGQLI
115

Query: 255 VWDNRCL 261

+WDRNC+
Sbjct: 116 LWDNRV 122

>dbj|BAG68904.1| hypothetical protein [Schizosaccharomyces pombe]
Length = 391

Score = 71.6 bits (174), Expect = 9e-11, 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 LGTVLYGIQLSKLNDAQKNE LARYIAERGVVYFPDQEQTLEEFQELGQYYGHSHKHGSNS
170

Query: 75 IVAISNVKADGTVRQHSPA EWDDMMKVIVGN--MAWHADSTYMPVMAQGAVFSAEVVPAV
132

V + +D K N WH+D ++ + F A VP
Sbjct: 171 RPFEDKFAEFQVVYSDRFSPYDQHAK---NNSLRYWHS DVSFEKQPSAQTFFKALTVPEQ
227

Query: 133 GGRTCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT
192

GG T F AAY+AL + + ++V+S + + ++ DT A
Sbjct: 228 GGDTLFISGYAAEALSTPLKKYLEGL----TVVHSGKEQSEYHRRSGQHVRLDGD TNA-
282

Query: 193 PLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAA
250

P+V+ HP TG SL I IPG+ ES+ L+ L + +W +
Sbjct: 283 --HPIVRTHPVTGWKSLFISPGFTRYIPGIPRGESDAILYQHIANLSQSTVRIKWTS
340

Query: 251 GDVVVWDRNRCLLHRAEPWDFKLPRVMWHSRLAGRPE 286

V WDRN ++HRA +D LP+ R+A + E
Sbjct: 341 NGVAAWDRNRIVIHRA-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 = 9e-11, 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 FTITRSTPTIGAEVGGIDLAETLDDATVAALRQALVRHKVLFVRDQDITPAQHVQLARRF 84

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVG-----NMAWHADSTYMP
116

G +E V P D V++G +H+D ++
Sbjct: 85 GELE-----VHPVFPHHEDHPELVLLGGSKDMRGRENIYHSDVSWRE
126

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
176

V + ++ P GG T + DM AY AL +A + + A H ++ G
Sbjct: 127 VPSMASMLRCVECPDGTGGDTIWVDMARAYAALPDAVKERIDGLYAVHDIM---PGFGARM
183

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI-----GRHAHAIPGMDAAE
225

+ T P+V+ HPE+G L + G A G D
Sbjct: 184 TPEEREVNRKKFPAVT--HPVVRTHPESGEKILYVNEGFVTHLANFGEKAQFRVGFDFRY
241

Query: 226 SERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

E L + P +W + WDNR H A F R M + + G
Sbjct: 242 GELDLLQYLFRQAAVPEYQVRLKWRPNTIAFWDNRSTQHYAVQDYFPAVRRMMRATIIG 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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD-----T
189

T FADM AAY AL + +A R A V++ SKL + + S G D +
Sbjct: 1 TEFADMTAAYQALPDTVKA----RIATLKGVHAVSKLKNTRVTVSPRRPDGKDFYERQKS 56

Query: 190 TATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQW
248

+ PLV+ HP TG+ SL + R I G+ E++ L+GL +A V+ H+W
Sbjct: 57 LPDQVWPLVRTHPVVTGKKSLSYLSRFTIGIEGLSEVEADEILDGLFAHQIRAEFVYRHRW
116

Query: 249 AAGDVVVWDNRCL 261

GD+V+WDNRC+

Sbjct: 117 QDGLVMWDNRCV 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 FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR-P
196

F DMRAAYD L E + + A H + S+ LG + S P+ P
Sbjct: 1 FGDMRAAYDDLPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----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 LVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDLMW
114

Query: 257 DNR 259
DNR

Sbjct: 115 DNR 117

>ref|ZP_06234112.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp.
Eu11c]

gb|EFA64571.1| 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 VDRVADDT-LAALDAG----GVVIFREANVDDAELVAFSRLLEGEVVPKYGKVKGHPEV 79

Query: 82 KADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA-EVVPVAVGGRTCFAD
140

+A R S + +M WH D + + + +A EV G T FA+
Sbjct: 80 QA--ITRDASKS---NMAAYREATFWWHFDGSTDTLDPKYTLTAREVSGDDDGDETFAN
134

Query: 141 MRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKV
200

AAYD+L + +A + HS SQ +V S D + PLV
Sbjct: 135 TYAAYDSLTDDEKAELAGLRVVSFENSQR---NVYPNPSPEEKAVWDRIPSREHPLV-W
190

Query: 201 HPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRC
260

H +GR SLL+G A + G+ E+ L+ L++ A V H+W GD+V+WDN
 Sbjct: 191 HRRSGRRSLLLGATAGEVVGVPAGEARPLLDRLLERATAPEFVVRHKWQRGDLVIWDNTG
 250

Query: 261 LLHRAEPWDFKLPVMMWHSRLAG 283
 +LHRA P+ R+M + + G

Sbjct: 251 MLHRAMPYGEGSSRLMHRYSIVG 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 TIGAEIRGVDLRDLDDETYAALRRALLKFKVLFVRDQDITPAQHVAVAKRFGGELE---- 85

Query: 73 GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVG-----NMAWHADSTYMPVMAQGA VF
 124

+ P + VI+G +H+D ++ + + G++
 Sbjct: 86 -----IHPAFPHHPEHPELVILGRNDTKRGRENLYHSDVSWREIPSMGSML
 131

Query: 125 SAEVVPVAVGGRTCFADMR AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG
 184

P VGG T + +M AAYD L +A + +A H + Q +
 Sbjct: 132 RCVQCPEVGGDTMWINMVAAYDNLP GDVKARIAGLNAVHDFLPLFGIAVPKDQHAT----
 187

Query: 185 YGMDTTATPLR-PLVKVHPETGRPSLLIGR-----HAHAIPGMDAAESERFL
 230

M P+ P+V++HPETG L + G D +E L
 Sbjct: 188 --MRAKFPVVEHPVVRIPHETGEKILYVNEAFTTHLSNYGQLTATEYRVGFDYKLAELDL
 245

Query: 231 EGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAG-RP 285
 + QAP +W + WDNR H A F PR M + + G RP

Sbjct: 246 LQYLFRQAQAPYQVRLKWRPNTIAFWDNRSQHYAVQDYFPAPRHMMRATVIGDRP 302

>ref|XP_001903417.1| unnamed protein product [Podospora anserina]
 emb|CAP61192.1| unnamed protein product [Podospora anserina]
 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%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH---LSNDQQITFAKRF 64
 +T T+G V G+ L+TL DAG L + ++ F Q LS +Q + F F

Sbjct: 94 VTHLTPTIGTEVKG IQLSTLS DAGKDELARFVAERKVVAFRDQDFRDL SIEQALEFGGYF
153

Query: 65 GA--IERIGGG-----DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV
117

G I G +I + D +V D ++AWH+D +Y

Sbjct: 154 GRHHIHPTSGAPEGYPEIHLVHRGAGDNSV-----DKFFANRTSSVAVHSDVSYEAQ
205

Query: 118 MAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
177

P GG T F + AY+ L A + +H A HS H Q

Sbjct: 206 PPGTTFLYIFDKPESGGDTL FVNAAEAYNRLSPAFQERLHGLKATHS-----AHEQA
257

Query: 178 AGSAYIGYGMDTTATPL---RPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGL
233

SA G G+ P+ P+++ HP TG ++ + + I G+ ES+ L+ L

Sbjct: 258 NASALRG-GI-VRREPVIHEHP IIRTHPVTGEKAIYVNPQFTRDIVGLKKEESDVLLKFL
315

Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

D A +W G VVVWDNR H A

Sbjct: 316 YDHLAYGADFQARVKWEEGT VVVWDNRVTQHSA 348

>ref|XP_001387108.1| Fe(II)-dependent sulfonate/alpha-ketoglutarate
dioxygenase-like

protein [Pichia 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%)

Query: 3 QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQ---IT 59
Q ++TP LG+ V GV L+ LD AG L Q ++IF Q + +

Sbjct: 81 QIVKKVTPK---LGSEVRGVQLS QLDSAGKDELALFVAQRGVVIFRDQDFAAKGPAFAVE
137

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMA
119

+ K FG + I ++ + T R+ P E++ + + +H D +Y A

Sbjct: 138 YGKHFGRLH-IHPTSGAPRNHP ELHITYRRADPGEFERVFSNSTNAVQYHTDVSYELQPA
196

Query: 120 QGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG
179

FS P GG T FAD AY+ L A + + + H L S+ + + + G

Sbjct: 197 GITFFSVLEGPESGGDTIFADSVEAYNRLSPAFQKRL---AGLHVLHTSEDQASNSRGQG
253

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWAC
238

G + + PLV++HP TG SL + R A I + ESE L+ L D
Sbjct: 254 ----GIERRKPVSNIHPLVRIHPVTGAKSLFVNRSFARRIVELKEEESESLKFLYDHI
309

Query: 239 QAPRVHAH-QWAAGDVVVDNRCLLHRA 265

Q+ + W VV+WDNR + H A
Sbjct: 310 QSHDLQLRANWEPNTVVIWDNRRVHSA 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 TEFCDMRLAYEALSSEEQARLAPLKHARHPTLHRSRKLGTGFTDWSEEALSRLGWVD----- 54

Query: 195 RPLVKVHPETGRPSLLIGRHAHAI PGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
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|ADC34042.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 71.2 bits (173), Expect = 1e-10, Method: Compositional matrix
adjust.

Identities = 53/210 (25%), Positives = 94/210 (44%), Gaps = 19/210 (9%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYM
115

QQI FA+RFG + +A +K +P + +V G + WH+D+TY+
Sbjct: 1 QQIAFAQRFG-----EPMAYPQLKGLPECPLITPVIKLEHERVNFQGV-WHSDTTYL 51

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV---YSQSKL
172

++ A +P+ GG T FA+ A++ L E + ++ + ++ S+++
Sbjct: 52 ERPPTASMLYALEIPSYGDDTLFANQYLAFETLSEGLKRVLASLAGVNTSTKAEVSKTRE
111

Query: 173 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLE
231

+++AG+ + P+V+ HPETGR +L + H G ES L+
Sbjct: 112 DRLREAGAE-----RKALAGIHPVVRTHPETGRRALYVNTGHTARFDGWTEEEESAPLLD
165

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

L + +W G + WDNRC+
Sbjct: 166 YLFRHQVRPEFTCRFRWERGSLAFWDNRCV 195

>gb|EEY19626.1| alpha-ketoglutarate-dependent sulfonate dioxygenase
[Verticillium
albo-atrum VaMs.102]
Length = 384

Score = 71.2 bits (173), Expect = 1e-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 SIGTVLEGVQLSTLSLEQLDELAALVTERGVVFFRNQDLTTDGQVKLFEHYGVLDKHPAQ
129

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW-----HADSTYMPVMAQGAVFSAEV
128

+ +V G+ H + I+ W HAD+++ ++ E
Sbjct: 130 K--DVKHVVIKGSTEDH-----REILNYTPWPSGDFHADTSFEINPPSYSLLRMEE
178

Query: 129 VPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
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 AVRWKWEVGSVAMWDNRATIHRVIPGTYDAPR 320

>ref|YP_587951.1| taurine catabolism dioxygenase TauD/TfdA [Ralstonia
metallidurans

CH34]

gb|ABF12682.1| taurine dioxygenase, 2-oxoglutarate-dependent [Cupriavidus
metallidurans CH34]

Length = 295

Score = 71.2 bits (173), Expect = 1e-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 FSITPVPVIGAEIGDIDLRETLDDPTYQALRQALVRHKVLFVRDQDITPAQHVALARRF 75

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVG-----NMAWHADSTYMP
116

G +E V P D V++G +H+D ++
Sbjct: 76 GELE-----VHPVFPHPDHPELVLLGGNKDTKGRENIYHSDVSWRA
117

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
176

V + G++ P +GG T + +M AY L + +A + A H L+ G
Sbjct: 118 VPSMGMLRCVECPMGGDTIWNMAQAYAGLPDDVKARIEGLEAVHDLM---PGFGARM
174

Query: 177 QAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLI-----GRHAHAIPGMDAE
225

A + AT P+V+ HPE+G L + G H G D
Sbjct: 175 SAEERLVNREKFPPAT--HPVVRTHPESGEKILYVNEGFVTHLANYGAHIQYRVGADFRL
232

Query: 226 SERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAG-
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 = 1e-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---IGTEFPQLTSLIEDDTLIRDLAVEVSRRGVVFFRNQDITDDQQQFLGQ 83

Query: 63 RFGAI-----ERIGGGDIVAI-SNVKADGTVRQHSPAEWDDMMKVIVG
104

RFG + R G +I+ I K+ + AE D ++ +

Sbjct: 84 RFGELTGKPAESTLHVHPAKDLSRPAGKEILEILPEGKSAKELVTRFDAE-DAVVPTVRA
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-AYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HA
215

S +V + + Q G+ A +G + TT P+++ +P TG SL +
Sbjct: 203 SGQFFHQVVNKRGEVYDQPRGNPANVGNKLFITT----HPVIRTNPVTGWKSLFVNPGFT
258

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDF 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]

gb|ACY34513.1| Taurine catabolism dioxygenase TauD/TfdA [Comamonas
testosteroni

CNB-2]

Length = 280

Score = 71.2 bits (173), Expect = 1e-10, Method: Compositional matrix
adjust.

Identities = 67/274 (24%), Positives = 108/274 (39%), Gaps = 30/274 (10%)

Query: 6 LQITPTGATLGATVTGVHL--ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKR 63
+++ ++GA V+ +HL A+ D + A LQH +L F Q ++ + + FA+

Sbjct: 1 MKVEQLTCSIGAEVSDIHLGDASRDKGLAEEIRALLLQHKVLFRRDQDITRAEHVGFARH 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
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 LRCIEGPAVGGDTIWNMAEAYRNLPEDIKKIDGLKAKSSIEHG---FGAVMPEEKR--
165

Query: 184 GYGMDDTATPLR-PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LE
231

+ P+ P+V+ HPETG L + E+ R+ L
Sbjct: 166 -LELGRQHPPVEHPVVRTHPETGEKILYVCSFTTTFANYHTPENVRYGQDKTPGASMLLN
224

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

PLV+ H +GR L IG HA I G AE L L++ A + V+ H W GD+V
Sbjct: 55 WPLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATRRKFVYRHSWKVGDV
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 = 1e-10, Method: Compositional matrix
adjust.

Identities = 42/127 (33%), Positives = 63/127 (49%), Gaps = 7/127 (5%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMR+AY AL E + L+ A HS+ +S+S + + + P+R
Sbjct: 1 TEFCDMRSAYAAPERLKMIEDLQAEHSIAHSRSLVD-----PTVLSEAQKAESPVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

LV+++P GR +L IG HA I G + L L + + +H W GD++
Sbjct: 55 QRLVRINPINGRKALYIGAHASHIVGWPLEKGRALLAELAEELGKPEFRLSHAWREGDLI
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 FADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP-
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 PHRLVSDPVNGRKSLEYLSSHIGGIRDWPVPEARAFIRDILIXHATQRQFVYVAHEWQVNDL
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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL-
194

T F DM AY+ L +A + A H+L +S+++ + G + P+
Sbjct: 1 TEFCDMYGAYERLSPEWKARIAPLRVHNLDFSRTTR-----RHGEDPMTEAQRREVPPVD 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 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ---HLSNDQQ 57
+ Q +Q+ T+G+ V GV L+ L G L Q ++ F Q HL ++

Sbjct: 91 LPQGVQVDNLTPTIGSEVRGVQLSQTKEGKDQLALYVAQRKVVAFRDQDFAHLPIEKA
150

Query: 58 ITFAKRFGA--IERIGGGDI----VAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHAD
111

+ F FG I + G + + + AD S AE+ + + WH+D
Sbjct: 151 LEFGGYFGRHHIHQTS GAPKGYPEIHLVHRGAD----DRSGAEF---LATRTNTVTWHS
203

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSK
171

T+ P GG T FADM AY L R +H A HS + +
Sbjct: 204 VTFEKQPPGTTFLYLLDGPTSGGDTLFADMAQAYRRLSPEFRKRLHGLKAVHSGI---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 KFLYDHIALSQDLQTRVWRWLPGTVVVWDNRVVAHSA 352

>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 LGSVITGIQLSQLSDAAKNDLSRFVAERGVVVFRDQDFNQGGPQAAVEFAQYFGPLYKHA
150

Query: 71 GGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVP
130

G + R S E D + +++WH+D +Y Q +FS +P
Sbjct: 151 TSGSPEGFPELHV--CFRGASQDEIDSVFSDRTNSISWHSDCSYSLNALQLTLFSCQLQLP
208

Query: 131 AVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDT
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 REPEANIHPLVRVNPVTKQKHLYLNKEFGRRIVELKEDESDYLLSFLYDHIEKAQDLQIR
318

Query: 247 -QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLA 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 GGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVP
 130

G + R S E D + +++WH+D +Y Q +FS +P
 Sbjct: 151 TSGSPEGFPELHV--CFRGASQDEIDSVFSDRTNSISWHSDCSYSLNALQLTLFSLQLP
 208

Query: 131 AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDT
 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 REPEANIHPLVRVNPVTKQKHLNKEFGRRIVELKEDESDYLLSFLYDHIEKAQDLQIR
 318

Query: 247 -QWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLA 282

W VV+W+N +H + DF P + R++
 Sbjct: 319 VTWEENTVVLWNNSTTIH-SPCVDFDEPEIRHAYRIS 354

>emb|CAY81185.1| Jlp1p [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--IERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQ
 120

FG I + G +N + T R+ E+ + + WH D +Y

Sbjct: 173 HFGKLIHQTSUGH---PQNNPELHITFRRPDAEEFARVFDSTSSGGWHTDVSYELQPPS
229

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGS
180

FS P GG T FAD A+D L + + + S H + S+ + + Q+ G
Sbjct: 230 YTFFSVVEGPDGGGDTLFDADIEAFDRLSKPLQDFL---STLHVIHSSKEQAENSQRQG-
285

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQ
239

G T + PLV+VHP + L + R + I + ESE L L +
Sbjct: 286 ---GIKRRAPVTHIHPLVRVHPVLKKKCLYVNRASF SRKIVELKRQESLNLNFLYNLVES
342

Query: 240 APRVHAH-QWAAGDVVVDNRCLLHRA 265
+ + +W VV+WDNR + H A

Sbjct: 343 SHDLQLRAKWEPHSVVIWDNRRVQHS 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 = 2e-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 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYM
115

+++ A+ + +I + K + TVR+H W + + N WH D T
Sbjct: 134 RKLEMARYYVQPRPPTSTEISVVYQDKVN-TVRKHW---WPNRLT----NAIWHIDQT-Q
184

Query: 116 PVMAQGAVFSAEV---VPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKL
172

G F + P+ GG T + AY+ L + V A HS +K
Sbjct: 185 ERQPPGITFFCCMQHDAPS-GGDTLVGSLVEAYNRLSPKMKEFVCGLKAVHSSAVMSAKA
243

Query: 173 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAI PGMDAAESERFLE
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]
emb|CAQ71436.1| Alpha-ketoglutarate-dependent taurine dioxygenase,
2-aminoethanesulfonate dioxygenase [Cupriavidus
taiwanensis]
Length = 280

Score = 70.5 bits (171), Expect = 2e-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 MRVQQLTCSIGAELSGVSLADAARDAALFAEIRSLLEHKVLFRLGQEISRADHVAFARR 60

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123
FG +E VA S+ G V+ + + ++ ++H D ++ G V
Sbjct: 61 FGELE----DHPVAGSDPDHPGLVQIYRSDKRENYEN-----SYHTDGSWRECPMGCV
110

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
183
P VGG T + +M AAY+ L E + + A+H + +S +
Sbjct: 111 LRCIESPPVGGDTIWNMGAAYEHLPEEIKQRIAGLRAKHGIEHSFGAAMSPENRAKLAA
170

Query: 184 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF-----LEG
232
Y P+V+ HPETG L + + E+ R+ L
Sbjct: 171 QYPAVE----HPVVRTHPETGKVLVYVCGFSTHFVNFHTPENVRVYQDKTPGASHLLNY
225

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283
L+ A +W V +WDNRC H A + PR M + + G
Sbjct: 226 LISQAAIPEYQVRFRWQPNSVAIWDNRCTQHYAVQDYWPAPRKMERAAIIG 276

>gb|ADC33948.1| TfdA-like protein [uncultured bacterium]
Length = 123

Score = 70.5 bits (171), Expect = 2e-10, Method: Compositional matrix
adjust.

Identities = 47/128 (36%), Positives = 61/128 (47%), Gaps = 11/128 (8%)

Query: 138 FADMRAAYDALDEATRALVHQRSARHSLVYSQSK---LGHVQQAGSAYIGYGMDTTATPL
194

Sbjct: 3 F DM AAYDAL +A + + + +H Y ++ LG +G G P
 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 HPIVSTHPDTGCNSLFLGRRPRHYINGCTPEESAALLDKLWAHATQPCFRITHHTWRQGDV
 115

Query: 254 VVWDNRCL 261

V+WDNRC+

Sbjct: 116 VMWDNRCV 123

>gb|ADC34021.1| TfdA-like protein [uncultured bacterium]
 Length = 195

Score = 70.5 bits (171), Expect = 2e-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 AEPPMGSMMLLAREVPPHGGDTMFANQYLAYDGLSDGLKKALDGLIGVSSSAKADV-TKTR
 110

Query: 172 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL
 230

++ AG+ T P+V+ HPETGR +L H I G ES L
 Sbjct: 111 EDRMKAAGAEL-----KVLTAEHPIVRTHPETGRKALYTSDAHTAHIKGWTEKESLPLL
 164

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

L D + +W G + WDNRC+

Sbjct: 165 RFLWDHQTRPEFTCRFRWQVGSALFWDNRCV 195

>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 = 2e-10, Method: Compositional matrix
 adjust.

Identities = 45/123 (36%), Positives = 61/123 (49%), Gaps = 7/123 (5%)

Query: 138 FADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR-P
196

F DMRAAYDAL ++ + A H + S+ LG + + P+ P
Sbjct: 2 FCDMRAAYDALPRDLQSELEGLRAEHYALNSRFLGDTDYSEA-----QRNAMPPVSWP 55

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDDAESERFLEGLVDWACQAPRVHAHQWAAGDVVVW
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_05480798.1| 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 AKFGVVVEGFDATTATSEEFALKRQVYENKIAVLKDQKLSPEDEFVEMGKRMGEPSSYYE 68

Query: 71 -----GGGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVF
124

I SNV DG + V WHAD +M +
Sbjct: 69 PVYHHPDNPLIFVSSNVPKDGK-----QIGVPKTGKFWHADYQFMDKPYGLTLI
117

Query: 125 SAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHS--LVYSQSKLGHVQQAGSAY
182

+VVP T F DM AAY+ L E+ + V A HS + + G
Sbjct: 118 YPQVVPQKNRGTYFIDMGAAEGLPESLKQEVADAVAVHSPRRFFKIRPSDVYRPVGEGL
177

Query: 183 IGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAESE-----RFLE--G
232

T R +VK HP TG L + G++ A+ E R L+ G
Sbjct: 178 AEIEERTPEVRHRAVVK-HPVTGESVLYVSEGFTT--GLEDAKGEEIRGDLLSRLLDVAVG
234

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 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-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA--WH
109

FA++ G + ++ SNV DG KV V WH
Sbjct: 61 FARKIGRPQVYFQHNYHHPQHPELFSNVLEDGK-----KVG VAGTGRYWH
107

Query: 110 ADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVH-QRSARHSLVYS
168

D + + +V+P T F DM+ Y+A+ RA V R+ +
Sbjct: 108 TDYQFFQEPLPLVMVYPQVLPKAKRETYFIDMQRVYEAMPAELRAYVEGHRAIQEGKWRY
167

Query: 169 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESE
227

+ V +A + P V HP TGR SL + I G+ E+
Sbjct: 168 KITPEDVDKALVDILAAVEKQVPAITHPAVIEHPLTGRKSLYLSSGFTTGIEGLTHEENR
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 = 3e-10, Method: Compositional matrix adjust.

Identities = 45/123 (36%), Positives = 61/123 (49%), Gaps = 7/123 (5%)

Query: 138 FADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-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 I G AE L L++ A Q V+ H+W GD+V+W
Sbjct: 56 LVRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQRQFVYRHRWQVGDLMW
115

Query: 257 DNR 259

DNR
Sbjct: 116 DNR 118

>gb|ADC34029.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 70.1 bits (170), Expect = 3e-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

GG+ A VP GG T FA+ AY+ L + + LV S+ + V ++++
Sbjct: 52 AEPPMGSMMLLAREVPPFGGDTMFANQYLAYEGLSDGLKKTLDGLVGVSSSAKADV-TKTR
110

Query: 172 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL
230

++ AG+ T P+V+ HPETGR +L H I G ES L
Sbjct: 111 EDRMKAAGAEL-----KMLTAEHPIVRTHPETGRKALYTSDAHTAHIKGWTEKESLPLL
164

Query: 231 EGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

L + + +W G + WDNRC+
Sbjct: 165 RFLWEHQTRPEFTCRFRWQVGS LAFWDNR CV 195

>gb|ADC33947.1| TfdA-like protein [uncultured bacterium]
Length = 121

Score = 70.1 bits (170), Expect = 3e-10, Method: Compositional matrix
adjust.

Identities = 42/127 (33%), Positives = 61/127 (48%), Gaps = 7/127 (5%)

Query: 136 TCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMR+AY AL E + L+ A HS+V+S+ + + P+R
Sbjct: 1 TEFCDMRSAYAALPERLKVLI EDLQAEHSIVHSRGLVD-----PTVLTEAQKAETPPVR 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 VWDNR CV 121

>gb|EEY23151.1| alpha-ketoglutarate-dependent sulfonate dioxygenase
 [Verticillium
 albo-atrum VaMs.102]
 Length = 378

Score = 70.1 bits (170), Expect = 3e-10, Method: Compositional matrix
 adjust.

Identities = 75/273 (27%), Positives = 110/273 (40%), Gaps = 25/273 (9%)

Query: 4 T T L Q I T P T G A T L G A T V T G V H L A T L D D A G F A A L H A A W L Q H A L L I F P G Q H L S N D Q Q I T F A K R 63
 T Q+ T+G+ V G+ L++L A G L Q ++ F Q + D I A
 Sbjct: 91 T G T Q V N H L T P T I G S E V K G I Q L S S L T P A G R D E L A L F V A Q R K V V A F R A Q D F A - D L P I G E A L D
 149

Query: 64 F G A I E R I G G G D I V A I S N V K A D G T V R Q H - - - - - S P A E W D D M M K V I V G N M A W H A D S T Y M P V
 117
 F G G + ++ +G H + + ++AWH+D +Y
 Sbjct: 150 F G G Y - - - F G R H H I H P T S G S P E G F P E V H L V H R G A N D R S A E S F F A T R T S S V A W H S D V S Y E Q Q
 206

Query: 118 M A Q G A V F S A E V V P A V G G R T C F A D M R A A Y D A L D E A T R A L V H Q R S A R H S L V Y S Q S K L G H V Q Q
 177
 V P A V G G T F A D A Y L R +H A H S G Q
 Sbjct: 207 P P G T T F L Y I L D V P A V G G D T L F A D G V E A Y R R L S P L F R E R L H G L K A V H S - - - - - G F E Q V
 258

Query: 178 A G S A Y I G Y G M D T T A T P L - - - R P L V K V H P E T G R P S L L I G - R H A H A I P G M D A A E S E R F L E G L
 233
 S + G P+ P+V+ H P T G ++ + + I G+ E S+ L+ L
 Sbjct: 259 E A S - - V R K G S I K R R E P V A N E H P I V R T H P A T G E K A I Y V N P Q F T R D I V G L K K E E S D A L L K F L
 316

Query: 234 V D W A C Q A P R V H A H - Q W A A G D V V V W D N R C L L H R A 265
 + + + A +W A G V V V W D N R H A
 Sbjct: 317 Y E H I A W S A D I Q A R V K W E A G T V V V W D N R V T Q H S A 349

>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 = 3e-10, Method: Compositional matrix
 adjust.

Identities = 66/274 (24%), Positives = 113/274 (41%), Gaps = 16/274 (5%)

Query: 15 L G A T V T G V H L A T L D D A G F A A L H A A W L Q H A L L I F P G Q H L S N - - - D Q Q I T F A K R F G A I E R - I 70
 L G + + T G + L + L D A L + + + + F Q + + F A + F G + +

Sbjct: 91 LGSVITGIQLSQLSDAAKNLDRFVAERGVVVFRNQDFNQGGPQAAVDFARYFGPLYKHA
150

Query: 71 GGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVP
130

G + R S E D + +++WH+D +Y Q +FS +P
Sbjct: 151 TSGSPEGFPELHV--CFRGASQEEIDSVFADRTNSISWHSDCSYSLNALQLTLFSLQLP
208

Query: 131 AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDT
190

GG T FA+ AY+ L A + + HS + + + AG G
Sbjct: 209 DAGDTLFANTVEAYNRLSPAMKERLEGLHILHSSI---EQAANNKSAG----GIIRREP
261

Query: 191 ATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW
248

+ PLV+V+P T + L + + I + ES+ L L D +A + W
Sbjct: 262 EANIHPVLRVNPLTKQKHLNKEFGRRIVELKEDESDYLLAFLYDHIEKAQDLQIRVTW
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 = 3e-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 TVEEITPF---IGVKVTGLDLASLDKAGQDLALLAARKGIVFFASNDKVKQTYRDTSM
133

Query: 56 QQITFAKRFGAIE-----RIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWH
109

+++ A+ +G + R +++ TVR+H W + + N WH
Sbjct: 134 RKLEMARYYGQLHQHSVQPRPPTSTEISVVYQDKVNTVRKHW---WPNRLT----NAIWH
186

Query: 110 ADSTYMPVMAQGAVFSAEV---VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
166

D T G F + P+ GG T + AY+ L + V A HS
Sbjct: 187 IDQT-QERQPPGITFFCCMQHDAPS-GGDTLVGLSVEAYNRLSPKMKEFVCGLKAVHSSA
244

Query: 167 YSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAE
225

+K V G L PLV VHP TG SL I I G+ E
Sbjct: 245 VMSAKAARVG-----GASRRNEIESLHPLVTVHPATGSKSLYINPERMTYIEGLRNEE
297

Query: 226 SERFLEGLVDWACQAPRVHA-HQWAAGDVVVWDNRCLLHRA 265

S+ L+ L D HA ++W+ GDV VWD R ++H A
Sbjct: 298 SDNMLKFLSDHVKLGADFHARYKWSEGDVVCVWDQRVIIHSA 338

>ref|XP_002372616.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Aspergillus
flavus NRRL3357]
gb|EED57004.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Aspergillus
flavus NRRL3357]
Length = 375

Score = 69.7 bits (169), Expect = 3e-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 KVTEIQPKIGTIIIEGVQLSLSDAAKDELALLVSEKVVAFPAQDLIDAGPEAQEQFMRH
145

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQH-----SPAEWDDMMKVIVGNMAWHADST
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 YEIQPPSYVMLGLLEGPEVGGDTVFAATDMAYKRLSPTFCSWLDTLRVHS---SAKMIN
251

Query: 174 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEG
232

H + S +DT + PLV+VHP TG L I G I G+ E E
Sbjct: 252 HARLTNSLVRKDPVDT----VHPLVRVHPVTGEKCLFINGEFITKIQGLKEPEQRWLTEF
307

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

L++ A +W +V++DNRC LH A
Sbjct: 308 LMNHIITGHDFQARVRWQPKTIVIFDNRCTLHSA 341

>gb|ADC34046.1| TfdA-like protein [uncultured bacterium]
Length = 187

Score = 69.7 bits (169), Expect = 3e-10, Method: Compositional matrix adjust.

Identities = 60/211 (28%), Positives = 88/211 (41%), Gaps = 29/211 (13%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM
115
 QQI FA +FG + I +++++ A + P D+ G WH+D++
Sbjct: 1 QQIAFAAQFGKLY-----IHPVADMSAKHP--EILPVYADEKSTRAFGE-EWHS DASC D 51

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHV
175
 G++ +VVP VGG T + M AAYDAL E + L + H
Sbjct: 52 LEPPLGSILQLQVVPEVGGDTMLSSMYAAYDALSEPLK KLCESLTVVHD-----
100

Query: 176 QQAGSAYIGYGMDTTAT---PLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAE SERFLE
231
 G D T P+V HPE+GR L + ++ IP + ES+ L+
Sbjct: 101 ---GQHVFRRRFDPTKYPANEHPVCKHPESGRKLLFVNAQYTTHIPQLKPRESDAVLQ
157

Query: 232 GLVDWACQAPRVHAH-QWAAGDVVVWDNRCL 261
 L + P H +W VV WDNRC+
Sbjct: 158 MLYR-HIETPEFH YRFKWRPNSVVFWDNR CV 187

>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 = 4e-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---LGTEVTGVQLS QLDSK GKDELALLVAQRGVVIFRDQDFATHGPGFAVEY G
139

Query: 62 KREGAIERIGGGDIVAISNVKADG-----TVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
116
 K FG + I S D T R+ +PAE++ + + WH+D +Y
Sbjct: 140 KHFGRLH-----IHPTSGAPKDHP ELHITYRRANPAEFERVF SERTH AVGWHS DVS YEL
193

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ
176
 FS P GG T FAD AY L + + H L S + + +
Sbjct: 194 QPPGITFFSVLDGPEAGGDTIFADTVEAYKRLSPEFQKRL---EGLHVLHTSGDQAANAR
250

Query: 177 QAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV-
234

+ G G + + PL++ HP T + + R + I + ES+ + L
Sbjct: 251 RQG----GVERRKPVSHIHPLIRTHPVTKKIIYLNRPFSRRIVELKEQESDYLMNFLYT
306

Query: 235 -----DWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

D+ +A +W VVVWDNR ++H A
Sbjct: 307 HIESGHDFQLRA-----KWEPRSVVVWDNRVHSA 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 = 4e-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 KVTEIQPQIGSVVEGVQLSLSNAAKDELALLVAERKVVAFPNQDLIDAGPEAQESFMRY
146

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPA-----EWDDMMKVIVGNMAWHADS
112

FG + GTVR H PA E ++ WH D
Sbjct: 147 FGKP-----NYQPVSGTVRNH-PAFHIIHRDGNREEISRFLEQRTTTTLWHQDV
194

Query: 113 TYMPVMAQGAVFSAEVV-PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK
171

+Y + G V + P VGG T FA AY L R+ + HS S
Sbjct: 195 SYE-IQPPGYVMLGLLEGPEVGGDTVFAATDMAYKRLSPTLRSWLDTLRVTHS---SAKM
250

Query: 172 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLI-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 = 4e-10, Method: Compositional matrix
adjust.

Identities = 47/131 (35%), Positives = 64/131 (48%), Gaps = 13/131 (9%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY----IGYGMDDTA
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 -PGHPIVSTHPDTGCNSLFLGRRPRHYVNGYTLLEESAALLDALWAHATQLRFRI SHAWRQ
112

Query: 251 GDVVVWDNRCL 261

GDVV+WDNRC+
Sbjct: 113 GDVVMWDNRCV 123

>ref|XP_505767.1| YALI0F22825p [Yarrowia lipolytica]
emb|CAG78578.1| YALI0F22825p [Yarrowia lipolytica]
Length = 385

Score = 69.3 bits (168), Expect = 4e-10, Method: Compositional matrix
adjust.

Identities = 65/260 (25%), Positives = 100/260 (38%), Gaps = 21/260 (8%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQ---HLSNDQQITFAKRFGAIE-RI 70
G+ V GV L+ L D L + +++F Q L + +A+ FG

Sbjct: 106 FGSEVRGVQLSKLSKAKDELAYFVAERGVVVFQDFRELPIKDALKYAEHFGRQHIHP
165

Query: 71 GGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVP
130

G A V R+ + + + ++AWH+D TY +P
Sbjct: 166 TSGSPQAYPEVHL--IFREEGDDIYKEYFSSNLSSVAWHSDVTYEKQPPGTTFLGILEMP
223

Query: 131 AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDT
190

GG T F+D AY+ L + + A HS + A I G
Sbjct: 224 RTGGDTLFSDNTEAYNRLSPEFQKRLEGLKAVHS-----AHEQADASIRRGVVR
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 -QWAAGDVVVWDNRCLLHRA 265

+W G VVVWDNR H A
Sbjct: 334 ARWEDGSVVVWDNRRTSHTA 353

>ref|XP_002502918.1| predicted protein [Micromonas sp. RCC299]
 gb|ACO64176.1| predicted protein [Micromonas sp. RCC299]
 Length = 326

Score = 69.3 bits (168), Expect = 4e-10, Method: Compositional matrix
 adjust.

Identities = 62/199 (31%), Positives = 86/199 (43%), Gaps = 25/199 (12%)

Query: 108 WHADSTYMP----VMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL----DEATRALVHQR
 159

 WH D +++P +A A + +P GG T FA AA++AL E R L
 Sbjct: 125 WHTDGSFLPNPKVAIALYAPQLDDALPPEGGETRFASCTAAFEALAREEQEKLRLGLCSVH
 184

Query: 160 SARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA--
 217

 S + +S+ Q+ + I L P+V+ HP T SL I A
 Sbjct: 185 SWEKFMRLLESRDPRQKVTAEQIA----EKPPQLWPFVVRTHPVTKAESLYINPKNTAAV
 240

Query: 218 -----IPGMDAAE-SERFLEGLV-DWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEP
 267

 IP DA +R E +V D +V+AH W GD V+WDNR LLH A P
 Sbjct: 241 VNKATGEPPIPEEDARRLVDRLEAVVGDGLPGNSKVYAHTWKRGFVIWDNRVLLHAASP
 300

Query: 268 WDF-KLPRVMWHSRLAGRP 285

 +D K R+++ G P
 Sbjct: 301 FDAEKYQRLLEFRMEFKGEP 319

>gb|EDP53557.1| alpha-ketoglutarate-dependent taurine dioxygenase
 [Aspergillus
 fumigatus A1163]
 Length = 388

Score = 69.3 bits (168), Expect = 4e-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 IGTEIVGLQLKDLNDKQKDELGLLIAERSVVFFRDQDISPQQQKELGEWFGEVEVHPQVP
 152

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVG
 133

 + + V Q AE + G WH D + A + VP++G
 Sbjct: 153 QVPGVPGVTVLWPALQA--AETPAAFRRPFGASRWHTDLVHERQPAGVTHLHNDTVPSIG
 210

Query: 134 GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP
 193

 G T +A AAY+ L + R + ++A + + H ++ G Y+

Sbjct: 211 GDTLWASGYAAYEKLSPSFRQFIDGKTAIYRSAHPYLDRKHPEK-GPVYVERE-----
262

Query: 194 LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAG
251

PLV+VHP TG +L + R I G+D AES+ L L D + + +W
Sbjct: 263 -HPLVRVHPATGWKTLWVNRAMTVRIVGLDKAESDVILGYLCDVYEKNIDIQVRFKWT
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 = 4e-10, Method: Compositional matrix
adjust.

Identities = 40/127 (31%), Positives = 63/127 (49%), Gaps = 6/127 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL-
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 HPIVRTHPETGRKCVFLGDHAEDIVGMAYAAGRALIEELNALIVHPDLTYEHHWSAGQLI
115

Query: 255 VWDNRCL 261

+WDNRC+
Sbjct: 116 LWDNRCV 122

>emb|CAY27490.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 69.3 bits (168), Expect = 5e-10, Method: Compositional matrix
adjust.

Identities = 52/127 (40%), Positives = 68/127 (53%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT---
192

T FADMRAAYDALD+ +A + HSL+YS+ LG ++ Y + A
Sbjct: 1 TEFADMRAAYDALDDDAKAEIEDMICEHSLMYSRGS LG-----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 VLQRLVRTHPVHRRKSLYLSSHAGAIAKGMVPEARLLLLRDLNEHATQREFVHIHKWTVHD
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 = 5e-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-----MEY PQLKGLPECPMITPVV KLEHERDNFGGV-WHS DTTYL 51

Query: 116 PVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRA----LVHQRSARHSLVYSQSK
171

G++ A VP GG T FA+ AY++L + +A LV ++ + S+++
Sbjct: 52 ERPPMGSM LYALEVPPQGGDTMFANQYLAYESLS DGLQAVLGGLVGVNTSTKAAA-SKTR
110

Query: 172 LGHVQQAGSAYIGYGM DTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFL
230

++ AG + P+V+ HPETGR +L + H G AES L
Sbjct: 111 EDRMRAAGEELKVLAGE-----HPVVRTHPETGRRALYVNVGH TERFKGWSEAESRPLL
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 = 5e-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 QVTEITPYIGSEVRGVQLS QLT DAKDQLALFVAQRKVVAFRDQDFAKLPIEKALEFGGY
158

Query: 64 FGA--IERIGGG-----DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
116

FG I G +I + D + Q + ++ WH+D +Y
 Sbjct: 159 FGRHHIHPTSGAPKGFPEIHLVHRGADDNSFLQ-----TFLHEHTNSVTWHSDDVSYE-
 210

Query: 117 VMAQGAVFSAEVV-PAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHV
 175

G F + P GG T FA++ AY L R +H A HS
 Sbjct: 211 AQPPTTFLYLLDGPTSGGDTLFANLAKAYQRLSPEFRKRLHGLKAVHS-----GF
 261

Query: 176 QQAGSAYIGYGMDDTA--TPLR---PLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERF
 229

+QA SA D+T P++ P+V+ HP TG +L + + I G ES+
 Sbjct: 262 EQAQSAL---ARDSTVRRDPVKHEHPVIRTHPVTGEKALYVNPQFTRYIVGYKKEESDHL
 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|EDO87370.1| dioxygenase TauD/TfdA family [Burkholderia pseudomallei
 406e]

Length = 191

Score = 69.3 bits (168), Expect = 5e-10, Method: Compositional matrix
 adjust.

Identities = 50/148 (33%), Positives = 68/148 (45%), Gaps = 5/148 (3%)

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVY----SQSKLGHVQQ
 177

+V A +P GG T +A+ AAY L + + LV + A H + S+ +L H
 Sbjct: 11 SVLRALALPDAGGDTVWANTVAAYQHLPSLQDLVDKLWAVHGNDFDYAASRVELLHDPV 70

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA
 237

A Y T P+V++HPETG SLL+G +A D +S R E L
 Sbjct: 71 AKEYRKKYAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRFVQYDTHDSNRLYEILQAH
 129

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ WAAGDV +WDNR H A
 Sbjct: 130 TRLENTVRWHWAAGDVVAIWDNRSTQHVA 157

>emb|CAY27357.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 119

Score = 69.3 bits (168), Expect = 5e-10, Method: Compositional matrix
 adjust.

Identities = 44/124 (35%), Positives = 66/124 (53%), Gaps = 5/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
195

T F DM AA+DAL EA + + S+ +S++KLG Y + +
Sbjct: 1 TVFPDMPAAWDALPEAKKKKLAGLKVFPSIFHSRAKLGMTD-----YTEKERASLPGAEQ 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

LV+ P++GR +L + HA I GM ESE L L+++A + V+AH+W D+V+
Sbjct: 56 GLVRTIPQSGRKALYLASHAVRIQGMPDGESESLLAELMEFATERRFVYHRWRVHDLVM
115

Query: 256 WDNR 259

WDNR

Sbjct: 116 WDNR 119

>emb|CAY27420.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 68.9 bits (167), Expect = 5e-10, Method: Compositional matrix
adjust.

Identities = 44/124 (35%), Positives = 58/124 (46%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
195

T F DMRAA+DALD RA + HS+ YS+ LG A +
Sbjct: 1 TEFGDMRAAHDALDAERRASLEGLCVHHSIAYSRETGFEFSAAET-----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

>ref|ZP_06281011.1| Taurine catabolism dioxygenase TauD/TfdA [Streptomyces
sp. ACT-1]

gb|EFB79936.1| Taurine catabolism dioxygenase TauD/TfdA [Streptomyces sp.
ACT-1]

Length = 299

Score = 68.9 bits (167), Expect = 6e-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 V TG L D A + L + L++ ++ +QQI A
Sbjct: 14 TGIRIGELTPFIGAEVVTGATFEDLRDPALWEQLTLLHERELVVVRSLDITPEQQIDLAG 73

Score = 68.9 bits (167), Expect = 6e-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---IGTEIRGVQLSQLSTDGLDQLALLAAQRGVLVFRDQDFADIGTGRQORDIAAHY
112

Query: 65 GAIER-----IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA----WHADSTYM
115

G + + G V AD V ++ ++G WH D T+
Sbjct: 113 GPLHQHPTMGYPQGTSPPEFQVYADEKVGN-----LRTLLGTRTSYDLWHIDQFTT
163

Query: 116 PVMAQGAVFSAEVPVAVGG-RTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGH
174

P F PA GG T F + AAY AL R +H R L+++ + +G
Sbjct: 164 PNTPGVTFFWVLETPASGGGDTAFTSLTAAAYQALSPTFREGLH----RLKLLHTSASVGE
219

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGL
233

V + G + PLV HP T P L + A + G ESE L L
Sbjct: 220 VARIGQER---ALKDAVQTEHPLVIGHPVTHDPVLFVNPAIARQVVGYPKEESENLLSFL
276

Query: 234 -----VDWACQAPRVHAHQWAAGDVVVVDNRCLLHRAEPWDFK 271

+D++C+ W G VVVWD R + H A P DF+
Sbjct: 277 HNHIRSLDFSCRV-----SWEKGTVVVWDQRAVAHSAVP-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 = 6e-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 TGIRIGELTPFIGAEVTGATFEDLRDPALWEQLTLLHERELVVVRSLDITPEQQIDLAG 73

Query: 63 RFG-----AIERIGGGDIVAISNVKAD----GTVRQHSPAEWDDMMKVIVGNMAWHA
110

R G +I+ SN K + G R VGN WH
Sbjct: 74 RLGRPVPFLMAKYRHPDHEEIMISSNAKKNLAIGVAR-----VGNF-WHQ
118

Query: 111 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRNLVHQRSARHSLVYSQS
170

DS+Y + VP G T +A+ YD L + + V R+A H++ Q
Sbjct: 119 DSSYQRSAPPYTMLHGIDVPGTSGHTLYANAADVDRPLKWKLVKVEGRTAVHTVAKRQR
178

Query: 171 KLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESER
228

A ++ P+ PL+K P TGR + + + G DA E+E
Sbjct: 179 ISPEHAGLSIAEFKALVEEQHPPEHPLIKTDPTTGRRYVYGAPEYMERVIGFDANENEE
238

Query: 229 FLEGLVDWACQAP-RVHAHQWAAGDVVVWDNRCLLHRA 265

F L+D Q P RV+ H+W D+V+W H A
Sbjct: 239 FF-ALLDRLIQDPARVYHRWTPRDLVIWKCELTYHAA 275

>emb|CAY27378.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 113

Score = 68.9 bits (167), Expect = 6e-10, Method: Compositional matrix
adjust.

Identities = 47/119 (39%), Positives = 59/119 (49%), Gaps = 7/119 (5%)

Query: 136 TCFADMRAAYDALDEATRNLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALDE + HS ++S+S LG + P+R
Sbjct: 1 TEFADMRAAYDALDEEIKTECENLICEHSQLF SRSILGFTDFDERRRFA-----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 QRLVRRHPVTGRRSLYLASHAGAILGWLVPPEARAFRLDLNEHATQRQFVYAHVWRQWDL 113

>gb|AAR38315.1| alpha-ketoglutarate-dependent taurine dioxygenase
[uncultured
marine bacterium 581]
Length = 275

Score = 68.6 bits (166), Expect = 7e-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 MYFRPLTTRIGAEVQGIDLGAQLPNDALDALYDGLIRYQVLFREQKLNPPQHLALAESF 60

Query: 65 GAIER-----IGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP
116

G ++ G IV + N + DD WH D T+
Sbjct: 61 GEVDPGHPVYPHVDGYQSIVELRN-----EDDKAPDTDD-----WHKDLTFRA
103

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQ
176

A ++ VP VGG T +A M A YD+L ++ + A H + + +++
Sbjct: 104 EPAFASILRGVEVPQVGGDTLWASMSAVYDSLSSGWKSDLEGLYAIHDM--GTFRNDYLR
161

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD
235

+ G I + + + P++ HP TG L + + I + S+ L+ L
Sbjct: 162 KGGVTAIDEALTEVGSVHPVIATHPVTGLKYLNVNQSFTRNIVDLTQGASDEVLYQYLYQ
221

Query: 236 WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ +W V +WDNR H A
Sbjct: 222 HVRRPEFQVRFRWENDSVAIWDNRITQHYA 251

>gb|ADC33982.1| TfdA-like protein [uncultured bacterium]
Length = 122

Score = 68.6 bits (166), Expect = 7e-10, Method: Compositional matrix
adjust.

Identities = 42/132 (31%), Positives = 64/132 (48%), Gaps = 16/132 (12%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSK-----LGHVQQAGSAYIGYGMDDT
189

T F DM AY+ LD +A + A H+L +S+++ L Q+ + +
Sbjct: 1 TEFCDMYGAYERLDARWKARIAGLRVHNLDFSRTTRRHAEDPLTEAQLAKPPVDH---- 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 = 7e-10, Method: Compositional matrix
adjust.

Identities = 46/126 (36%), Positives = 60/126 (47%), Gaps = 9/126 (7%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP--
193

T F DMRAAYD L ++ + A H + S+ LG + + A P
Sbjct: 1 TEFGDMRAAYDELPADLKSELEGLHAEHYALNSRFVLGDTDYSEA-----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 TWPLVRTHAGSGRKFLFIGAHAGRIEGRPLAEGRMLLAELLEHATQRRFVYRHSWKVGD
113

Query: 254 VVWDNR 259

V+WDNR

Sbjct: 114 VMWDNR 119

>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 = 7e-10, Method: Compositional matrix
adjust.

Identities = 62/254 (24%), Positives = 100/254 (39%), Gaps = 34/254 (13%)

Query: 41 QHALLIFPGQH-LSNDQQITFAKRFQAI-----ERIGGGDIVAISNV 81

Q ++ F Q L+ND Q A+R G + R+GGGD IS +

Sbjct: 78 QRGVVFRAQDDLNDLQKELAQRLGELSGKPATSKLHIHPVINSGRRLGGGD-NEISVI
136

Query: 82 KADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
141

++ +S D K WH+D T+ P+ + A+ +P GG T +A

Sbjct: 137 SSEQAKEIYSKRLLDLSAKKQSAKSGWHS DITFEPIPSDYALLRRLTELPKTGGDTLWASG
196

Query: 142 RAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYI-----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 HPVIRTNPVTGWKSIFAVGHVQQINGLTKEESRTALDWFVSLITDNHDLQVRHRWQNVN
312

Query: 252 DVVWDNRCLLHRA 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

Query: 172 LGHVQQAGSAY---IGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESE
227

+++AG+ + IG P+V+ HPETGR +L + H G A ES
Sbjct: 111 EDRLREAGAEHKVLI GE-----HPVVRTHPETGRKALYVNAGHTT NFKGFTAEE SA
161

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL 261

L L + + W G + WDNRC+
Sbjct: 162 PLLSYLFNHQVRPEFTCRFYWEPGSLAFWDNRCV 195

>ref|XP_001387045.1| hypothetical protein PICST_53191 [Pichia stipitis CBS
6054]

gb|EAZ63022.1| predicted protein [Pichia stipitis CBS 6054]
Length = 378

Score = 68.6 bits (166), Expect = 8e-10, Method: Compositional matrix
adjust.

Identities = 77/273 (28%), Positives = 112/273 (41%), Gaps = 33/273 (12%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQ---QITFA 61

T ITP LG V GV L+ LD AG L + L++F Q L++ Q
Sbjct: 83 TKNITPK---LGTEVFGVQLSQLDSAGKDELALFVAKRGLVVFRDQDLASKGPAFQTELG
139

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQ--HSPAEWDDMMKVIVGNMAWHADSTYMPVMA
119

+ FG + I S D + + D+ + + +H+D TY +
Sbjct: 140 RHFGPLH-----IHPTSGAPKDHPELHVYRPPDKDLFEHRNNLVGFHSDVTYE-LQP
192

Query: 120 QGAVFSAEVV-PAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLV----YSQSKLGH
174

G F A V P GG T FAD AY+ L + + HS V +S+ G
Sbjct: 193 PGTTFLAVVEGPESGGDTLFADTVEAYNRLSPEFQKRLEGLHVLHSAVEQANFSRKNNGV
252

Query: 175 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGL
233

V++ I PLV+ HP TG +L I + I + ES+ L L
Sbjct: 253 VKRDPVQNI-----HPLVRTHPVTGEKALFINSGF SRKIVELKEEESDYLLTFL
301

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

++ + + A +W A VVVWDNR ++H A
Sbjct: 302 LNHINNSHDLQARAKWEANTVVVWDNRRVVHSA 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 = 9e-10, Method: Compositional matrix adjust.

Identities = 54/200 (27%), Positives = 86/200 (43%), Gaps = 11/200 (5%)

Query: 72 GGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVPA
131

G +I ISN Q S D ++K GN WH+D T+ P + A +P

Sbjct: 130 GDEISVISNQFVFDKNFQKSD---DTVLKRPFPGNTLWHS DITFEPHPSDYATLQIRTLPE
186

Query: 132 VGGRTCFADMRAAYDALDEATRALVHQRSA----RHSLVYSQSKLGHVQQAGSAYIGYGM
187

VGG T +A AYD L A R + +A +H + ++ +++ A G

Sbjct: 187 VGGDTLWASSYEAYDRLSPAYRTFLEGLTATHVQHFIDMARKTNATLREPRGAPENVGQ
246

Query: 188 DTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH
246

+A + P+++ +P TG L + R I + ES+R L L + +

Sbjct: 247 HLSA--VHPVIRTNPVTGWKGLFVNRVFTKKINELTPHESDRLLGFLYEHIDGNHDLQVR
304

Query: 247 -QWAAGDVVVWDNRCLLHRA 265

+W ++ +WDNRC H A

Sbjct: 305 FRWEENNLAIWDNRCTFHSA 324

>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 = 9e-10, 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 AHIGTEIVGLQLKDLTAQQKDELGLLIAERSVVFFRDQDISPQQQKALGEWYGEIEVHPN
155

Query: 70 IGGDIVAI SNVKADGTVRQHSPA-EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV
128

I + ++ V + A E + G WH D + A +

Sbjct: 156 IEKPQVPSVPGVVGTTVIWPALQATERAASFRQTGGASRWHTDLVHERQPAGVTHLHNDT
215

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
188

+P +GG T +A AAY+ L R ++ R A + + AG Y+

Sbjct: 216 IPKIGGDTLWASGYAAEKLSPGFRKIIDGREAVYRSAHPYLDRND-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 QWAAGDVVVWDNRCLLHRAEPWDFK 271

+W G +WDNR +H A WD++

Sbjct: 327 KWTPGTSALWDNRITIHNAS-WDYE 350

>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 = 9e-10, 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----IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP
116

FG I + G + + + AD S AE+ + + WH+D T+

Sbjct: 156 YFGRHHIHQTSGAPRGYPEIHLVHRGAD----DRSGAEF---LATRTNTVTWHS DVTFEK
208

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQ
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----GIARREGITSEHPIVRTHPVTGEEKALFVNPQFTRYIVGYKKEESDMLLKFLYD
 321

Query: 236 WACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265

 + + +W G VVVDNR + H A
 Sbjct: 322 HIALSQDLQTRVRWLPGTVVVDNRVVAHSA 352

>gb|AAS64598.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
 Length = 119

Score = 68.2 bits (165), Expect = 9e-10, Method: Compositional matrix
 adjust.

Identities = 46/126 (36%), Positives = 60/126 (47%), Gaps = 9/126 (7%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSAHSLVYSQSKLGHVQQAGSAYIGYGMDDTATP--
 193

 T F DMRAAYD L ++ + A H + S+ LG + + A P
 Sbjct: 1 TEFCDMRAAYDELPADLKSELEGLHAEHYALNSRFVLGDTDYSEA-----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 TWPLVRTHAGSGRKFLFIGAHAGRIEGRPLAEGRMLLAELLEHATQRRFVYRHSWKVGD
 113

Query: 254 VVVDNR 259

 V+VDNR
 Sbjct: 114 VMVDNR 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 = 9e-10, 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+ DQQI F +++G + +
 Sbjct: 37 LGHTINDVDVNNLTTKQFEDIKDALWTHGVICIKNQKLTMDQQIAFTQKWGKLMILPIQQ 96

Query: 71 -----GGGDIVAISNVKADGTVRQH-SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
 122

 IV + N+ DG+++++ S E+ WH D +
 Sbjct: 97 AYTKRDPNQPAIVRVGNINIDGSIKENCSDTEY-----WHKDGDFKK--PGEN
 142

Sbjct: 198 ITHLHNDTVPSVGGDTLWASGYAAAYEKLSPEFRKIIDGRSAVYRSAHPYLDRDD-PEAGP
256

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQ
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-----WDYSGKEPR 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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP--
193

T F DMRAAYD L ++ + A H + S+ LG + + A P
Sbjct: 1 TEFCDMRAAYDELPADLKSELEGLHAEHYALNSRFVLGDTDYSEA-----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 TWPLVRTHAGSGRKFLFIGAHAGRIEGRPLAEGRMLLAELLEHATQRRFVYRHSWEVGD
113

Query: 254 VVWDNR 259

V+WDNR

Sbjct: 114 VMWDNR 119

>ref|YP_002799362.1| Taurine catabolism dioxygenase TauD/TfdA family
[Azotobacter

vinelandii DJ]

gb|ACO78387.1| Taurine catabolism dioxygenase TauD/TfdA family

[Azotobacter

vinelandii DJ]

Length = 317

Score = 68.2 bits (165), Expect = 1e-09, Method: Compositional matrix
adjust.

Identities = 60/243 (24%), Positives = 94/243 (38%), Gaps = 18/243 (7%)

Query: 27 LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIER---IGGGDIVAISNVKA 83

LD+ L A +L Q L+ +Q + A FG + + D V A
Sbjct: 44 LDEPVREELRQALRDFEVLFLTPQELTPEQHLELASVFGPVAQGAYFPRKDSHPQIEVLA
103

Query: 84 DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVPAVGGRTCFADMRA
143

+ R PA D WH+D T++ G +PA GG T +A M
Sbjct: 104 NDARR---PASVDH-----WHSDLTWLE EPPAGVAIQ LVEIPANGGNTAWASMSK
150

Query: 144 AYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM DTTATPLRPLVKVHPE
203

A+ AL + + A H+ SQ + ++ G + + P+V+ HP+
Sbjct: 151 AFAALSPGLQEYLRGLRATHTWEISQWR-NYLANLGEEVLLNSIRRFKPVSHPVVQKHPQ
209

Query: 204 TGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL
262

+G+ L + I + ES L L +W Q VH+H+W + +WDN
Sbjct: 210 SGKEILYVNETFTRNIDDVPPQESREILRFLCEWLKQPEFVHSHRWQRNGIAIWDNLATQ
269

Query: 263 HRA 265

H A

Sbjct: 270 HYA 272

>gb|ADC34026.1| TfdA-like protein [uncultured bacterium]
Length = 201

Score = 68.2 bits (165), Expect = 1e-09, Method: Compositional matrix
adjust.

Identities = 57/207 (27%), Positives = 85/207 (41%), Gaps = 7/207 (3%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM
115

QQI FA++ G IG I + +V + A+ + + WH D T
Sbjct: 1 QQIAFARQMGQ-PTIGHAVFGHIEDFPEIYSVAKFRTAQTNRGARPQRPWTGWHTDITAA 59

Query: 116 PVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHV
175

+ ++ +P GG T + ++ AY E R +V H Q+ G
Sbjct: 60 LNPPKASILRGVTIPPYGGDTFWTNLAVAYQGPSETMRGIVDGLRGVHRF---QAPAGTA
116

Query: 176 QQAGSAYIGYGM DTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLV
234

+ AY P+V+VHPETG L + AI G+ A ESE LE L
Sbjct: 117 K--SQAYDESVRREMETEHPIVRVHPETGERVLYVSPSFLKAIVGLTARESEMMLLELLW
174

Query: 235 DWACQAPRVHAHQWAAGDVVVWDNRCL 261

+ + +W AGD+ +WDNRC+

Sbjct: 175 EHVVRPEYTVRFKWEAGDIAMWDNRCV 201

>ref|XP_002152850.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Penicillium

marneffeii ATCC 18224]
gb|EAA19913.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Penicillium
marneffeii ATCC 18224]
Length = 374

Score = 68.2 bits (165), Expect = 1e-09, Method: Compositional matrix
adjust.

Identities = 70/274 (25%), Positives = 106/274 (38%), Gaps = 21/274 (7%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQ 57
+ +T +I+ +G+ V GV L L DA L + ++ FP Q L + ++Q
Sbjct: 72 LLSSTARISHIQPCIGSIVEGVQLNKLSDAAKDELALLIAERKVVAFPDQDLIDAGPEEQ
131

Query: 58 ITFAKRFGA--IERIGGG--DIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADST
113
+ F + FG + I G + DG V E + ++ WH D +
Sbjct: 132 YSFMRFHGKPNYQPISGSMKGYPGFHIIHRDGNV-----DEINRFLEQRTTTTLWHQDVS
186

Query: 114 YMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
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 LMQHLITGHDFQARVRWQPRTVVMFMDNRSTIHS 333

>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 = 1e-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 IGTEIVGLQLKDLNDKQKDELGLLIAERSVVFRRDQDISPQQQKELGEWFGEVEVHPQVP
152

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVG
133

+ + V Q AE + G WH D + A + VP++G
Sbjct: 153 QVPGVPGVTVLWPALQA--AETPAAFRRPPGGASRWHTDLVHERQPAGVTHLHNDTVPSIG
210

Query: 134 GRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP
193

G T +A AAY+ L + R + ++A + + H ++ G Y+
Sbjct: 211 GDTLWASGYAAYEKLSPSFRQFIDGKTAIYRSAHPYLDRKHPEK-GPVYVERE-----
262

Query: 194 LRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAG
251

PLV+VHP TG +L + R I G+D AES+ L L D + + +W
Sbjct: 263 -HPLVRVHPATGWKTLWVNRAMTVRIVGLDKAESDVILGYLCDVYEKNIDIQVRFKWT
321

Query: 252 DVVVWDNRCLLHRAEPWDFK 271

+WDNR +H WD++
Sbjct: 322 TSALWDNRITIHNVS-WDYE 340

>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 = 1e-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---IGSEVTGVQLSSLSAAGKQLALLVAQRKVVAFRDQDFA-DLPIADALKFGS
145

Query: 67 IERIGGGDIVAISNVKADGTV-----RQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
120

G + ++ + +G R S E D +AWH+D TY
Sbjct: 146 Y---FGRHHIHPTSGQPEGYPEIHLVHRHSSKGELDAFFADRNSTVAWHS DVTYEAQPPG
202

Query: 121 GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGS
180

P VGG T F D AY L A + +H A HS + Q++ +Q G
Sbjct: 203 TTFLYILDTPVGGDTAFVDQVEAYRRLSPAIKERLHGLKAVHS-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 = 1e-09, Method: Compositional matrix
adjust.

Identities = 40/122 (32%), Positives = 60/122 (49%), Gaps = 3/122 (2%)

Query: 138 FADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPL
197

 F DMRAA++AL +A + HS++ S+ + G + A + + PL
Sbjct: 2 FGDMPRAAWNALPPERQAQLEHLQVVHSILRSREQTGFTVEKFDAQT---LKDHPPAVHPL 58

Query: 198 VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWD
257

 V+ HP GR SL + HA I G +E L+ +A Q V++H W D+V+WD
Sbjct: 59 VRTHPCNGRKSLSYLASHASHIVGWPLERGRALIEELIAFATQPRFVYSHSWQLHDLVMWD
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 = 1e-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 VKVTEIQPQIGSIVEGVQLSLSNAAKDELALLVSEKRVVAFPAQDLI-DAGPEHLERF-
143

Query: 66 AIERIGGGDIVAISNVKADGTVRQH-----SPAEWDDMMKVIVGNMAWHADSTYM
115

+ G + +S GTVR H + E ++ WH D +Y

Sbjct: 144 -MSHFGKPNYQPVS-----GTVRNHPGFHIIHRDGNKQEIARFLEQRTTTTTLWHQDVSYE
197

Query: 116 PVMAQGAVFSAEVV-PAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGH
174

+ G V + P VGG T FA AY L + + A HS S + H
Sbjct: 198 -IQPPGYVMLGLLEGPEVGGDTVFAATDMAYKRLSPTFTSFLDGLRAVHS---SAKMINH
253

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGL
233

+ G +DT + PLV+VHP TG L I G I G+ E + L
Sbjct: 254 TRLMGGLVRKDPVDT----VHPLVRVHPVTGEKCLFINGEFITRIQGLKEPEQRYLTDL
309

Query: 234 VDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

+ A +W +V++DNRC +H A
Sbjct: 310 MQHIVTGHDFQARVRWQPKTIVIFDNRCTIHS 342

>ref|XP_001483210.1| hypothetical protein PGUG_05165 [Pichia
guilliermondii ATCC 6260]
gb|EDK41067.1| hypothetical protein PGUG_05165 [Pichia guilliermondii
ATCC 6260]

Length = 403

Score = 67.8 bits (164), Expect = 1e-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---VGTELVGIQLEKLNKQLDELALLIAERVVVIRNQLDLSPOKQLAIGKYYGE
167

Query: 67 IE-----RIGG--GDIVAINVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM
118

+E + G G S G + + + N WH D +
Sbjct: 168 VEVHPLVAHVPGYPGITTVWSKFNRRGGLISYQKG-----IHN-GWHQDMDHERSP
217

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQA
178

A + VP VGG T FA AAYD L + + + +R+A H +S K +V A
Sbjct: 218 AGITHLHLDSPVEVGGDTGFASGYAAYDKLSKTLQEFLEKRTALHRSYKRDNLAA
277

Query: 179 GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL----
233

+ PLV HP TG SL + R H I G++ +ES LE L
Sbjct: 278 PEPVIRE-----HPLVITHPATGWKSLFVNRAHTFKIVGLEDSSEAVLLEYLFSVY
328

Query: 234 -----VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEP 267

V W P G V+WDNR H A P
 Sbjct: 329 ERNLDVQTRVTWQPTEP-----GLGTSVLWDNRISQHIAIP 364

>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 = 1e-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 THDAPELEEIRQAIYRNKLIVIKGQNMGDNPAEYVEFTRKLGTPQVYFQENYHHPDFPEV 89

Query: 76 VAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGR
 135

SN+ +G + + V WH D + + V+P
 Sbjct: 90 FVSSNINKEG-----EKVGVAGTGKYWHTDCQFEQKPLSFTSITPVVIPNTVRA
 138

Query: 136 TCFADMRAAYDALDEATRALV-----HQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT
 189

T + DM Y+ L +ALV H + R+ + + + ++ I Y M+
 Sbjct: 139 TYYIDMHKVYENLPADLKALVEGATMIHGNNRYKV-----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 IVPPVEHPAVIEHPVNGDKILYMSSGFTMKIKGLTYEENEKAMKALFDFIEQEKHIHHTS
 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 IGSVVEGVQLSQLS DAAKDELALLV SERKVVAFPAQDLIDAGPEKLEQFMRHFGKP-----
150

Query: 72 GGDIVAI SNVKADGTVRQH-----SPA EWDDMMKVIVGNMAWHADSTYMPVMAQG
121

+ GTVR H + E ++ WH D +Y + G
Sbjct: 151 -----NYQPVS GTVR DHPGFHIIHRDGNRQEIARFLEQR TTTTLWHQDVSYE-IQPPG
202

Query: 122 AVFSAE VV-PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS
180

V + P VGG T FA AY L + + A HS S + H + G
Sbjct: 203 YVMLGLLEGPEVGGDTVFAATDMAYKRLSPTFTSFLDGLRAVHS---SAKMINHTRLIGG
259

Query: 181 AYIGYGM DTTATPLRPLVKVHPETGRPSLLI-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 GHDFQARVRWQPKTIVIFDNRCTI HSA 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 LPDAGGDTVWANTVAAYQHLPSLQDLVDKLVAVHGNDFDYAASRVELLHDPVAKEYRKK 62

Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH
244

Y T P+V++HPETG SLL+G +A D +S R E L +
Sbjct: 63 YAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQR FVQYDTHDSNRLYEILQAHITRLENTV
121

Query: 245 AHQWAAGDVVVWDNRCLLHRA 265

WAAGDV +WDNR H A
Sbjct: 122 RWHWAAGDVVAIWDNRSTQH YA 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 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMM-----KVIVGNMAWHADSTYM
 115

A+RFG +E V H P + ++ KV +H D ++
 Sbjct: 79 ARRFGELEL-----HPVFPHPDHAELVLLGGNSKVPGTENVYHTDVS
 123

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYS-QSKLGH
 174

+ +V P VGG T + +M AY+ L E + + A H ++ S +++
 Sbjct: 124 ETPSMASVLRVCECPEVGGDTVWINMEQAYEQLPETRKQIAGLYAVHDILPSFGARMT
 183

Query: 175 VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-----HAHAIPGMDAEESERF
 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 IHAQQQDLMDYLLRQPAILEYQMLRHWEPTIAMWDNRSTQHYAIQDYFPVVRMRHRATV
 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 VPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY----SQSKLGHVQQAGSAYIG
 184

+P GG T +A+ AAY L + + LV + A H + S+ +L H A
 Sbjct: 3 LPDAGGDTVWANTVAAAYQHLPSLQDLVDKLVAVHGNDFDYAASRVELLHDPVAKEYRKK 62

Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH
244

Y T P+V++HPETG SLL+G +A D +S R E L +
Sbjct: 63 YAAQVIKTE-HPVVQIHPETGEKSLLLGHYAQRVQYDTHDSNRLYEILQAHITRLENTV
121

Query: 245 AHQWAAGDVVVWDNRCLLHRA 265
WAAGDV +WDNR H A

Sbjct: 122 RWHWAAGDVVAIWDNRSTQHYA 142

>ref|XP_001389970.1| hypothetical protein An03g00660 [Aspergillus niger]
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 VQVTHLTPTIGTEIRGIQLSQLSAAGKDQLARYVAERKVVAFRAQDFASLPIDKAVDFAR
145

Query: 63 RFGAI-----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
115

FG + G ++ + D + + + ++ ++AWH+D +Y
Sbjct: 146 YFGPLHIHPTSGSPEGFPVHVLVHRAAGDRSAQAY-----LQTRTTSVAWHSVSYE
197

Query: 116 PVMAQGAVFSAEVEVPAVGGRTCFADMRAAYDALDEATRNLVHQRSARHSLVYSQSKLGHV
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 EQANTSLSRGGILRRDPVVSTHPIVRTHPVTGEKALFVNPQSGREVVGLKQEESMLLKF
308

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
L D +W VVVWDNR H A

Sbjct: 309 LYDHIASGADFQVRVRWEENSVVVWDNRVTQHTA 342

>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 ADIEAGMDKYAVLLFPGQDVTDDQQLAFALNFGEREQVHGGNVTRKEDYRLTSGLNDSVN 73

Query: 81 VKADGTVRQHSPAEDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
 + DG P DD + +GN WH+DS++ P+ A+ ++ SA VV
 Sbjct: 74 LGKDG-----KPLPRDDRTHLFLNLSLWHSDDSSFRPIPAPKFSLLSARVV 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 LTILPLSPRFGAEVGGIDLRDTPERRALLRLLFEHGVLFVFRDQALDTAGHVAFAEAF 71

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVI-VGNMAWHADSTYMPVMAQGAVF
 124
 G I +V S V + PA + +V G++ WH D++ +P V
 Sbjct: 72 GQI-----LVFTSVVDPE-----PAR-PGVHEVHGGSVGWHFDASSLPAPPVATVL
 116

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIG
 184
 A VPA G T +A AAY AL RAL R H G +
 Sbjct: 117 RAVRVP AEGNDTLWASGVAAAYQALTPELRALATGRYVTH-----GRGVVR
 161

Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIGR---HAHAIPGMDAAESERFLEGLVDWACQAP
 241
 D LV+ HP TG L I + I GM +S+ + L +
 Sbjct: 162 GPDDERPVVAHRLVRRHPHTGEHYLYINLPDWDSPILIGMSPDDSDALVAELRAAYLRPE
 221

Query: 242 RVHAHQWAAGDVVVWDNRCLLH 263
 W G +V+WDN +LH
 Sbjct: 222 HQIRLHWTPGTIVLWDNLAVLH 243

>ref|YP_728585.1| taurine catabolism dioxygenase [Ralstonia eutropha H16]
 emb|CAJ95220.1| taurine catabolism dioxygenase [Ralstonia eutropha H16]
 Length = 301

Score = 67.0 bits (162), Expect = 2e-09, Method: Compositional matrix
 adjust.

Identities = 74/300 (24%), Positives = 123/300 (41%), Gaps = 44/300 (14%)

Query: 4 TTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAK 62

Sbjct: 27 T +I+P LGA V + LA LDD +AL A ++H +L+F Q ++ Q + A+
TVSRISPA---LGAEVGSIDLAAPLDDDTISALRRALVEHKVLFVFRDQDITPAQHVALAR 83

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPAEW---DDMMKVIVGNMAWHADSTYMPVMA
119

Sbjct: 84 RFG +E V + P D K + N +H+D ++ + +
RFGELE-----VHPAFPHHEQFPPELVLLGGDERKPAMEN-GYHSDVSWRELPS
130

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYS-QSKLGHVQQA
178

Sbjct: 131 G++ P +GG T + +M AY+ L + + + A H + + K+ QQ
MGSMRLRCAQCPEIGGDTVWVNMALAYERLPDHRKQQIEGLLAVHDIGPAFGDKMTPEQQR
190

Query: 179 GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-----RHAHAIPGMDAAESERFL
230

Sbjct: 191 + + P+V+ HPE+G L + P A ES+
QFPPVAH-----PVVRTHPESGEKILYVNSGFVTHFANFKSRNPLRGAFESQSEK
240

Query: 231 EGLVDWACQAPRVHAHQ----WAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG-RP
285

Sbjct: 241 + L+D+ + P + +Q W + WDNR H A F R M + + G RP
QDLLDYLFQPAILEYQMRLRWRPNTIAFWDNRSTQHYAIQDYFPAVRRMMRATIIGDRP
300

>emb|CAY27450.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 67.0 bits (162), Expect = 2e-09, Method: Compositional matrix
adjust.

Identities = 51/127 (40%), Positives = 68/127 (53%), Gaps = 11/127 (8%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTAT---
192

Sbjct: 1 T FADMRAAYDALD+ +A + HSL+YS+ LG ++ Y + A
TEFADMRAAYDALDDDAKAEIEDMICEHSLMYSRGS LG-----FLDYTDEEKAMFKP 52

Query: 193 PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAAGD
252

Sbjct: 53 L+ LV+ HP R SL + HA AI GM E+ L L + A Q V+ H+W D
VLQRLVRTHPVHRRKSLYLSSHAGAILGMSPEARLLLLRDLTEHATQREFVYVHKWTLHD
112

Query: 253 VVVWDNR 259
+V+WDNR

Sbjct: 113 LVMWDNR 119

>gb|ADC34009.1| TfdA-like protein [uncultured bacterium]
Length = 195

Score = 67.0 bits (162), Expect = 2e-09, Method: Compositional matrix adjust.

Identities = 57/214 (26%), Positives = 92/214 (42%), Gaps = 27/214 (12%)

Query: 56 QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYM
115
 QQI FA++FG + +K +P + +V G + WH+D++Y+
Sbjct: 1 QQIAFAQQFG-----QPMEYPQLKGLPECPLVTFVIKLEHERVNFGGV-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---IGYMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDDAAESE
227
 +++AG+ + IG P+V+ HPETGR +L + H G A ES
Sbjct: 111 EDRLREAGAETHKVLIGE-----HPVVRTHPETGRKALYVNAGHTTTFKGFTEESA
161

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCL 261
 L L + + W G + W+NRC+
Sbjct: 162 PLLSYLFNHQVRPEFTCRFYWEPGSLAFWENRCV 195

>ref|XP_001483830.1| hypothetical protein PGUG_04559 [Pichia guilliermondii ATCC 6260]
 Length = 423

Score = 67.0 bits (162), Expect = 2e-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 VGTEIVGLQLSELNDKQKDELALLIAERVVFFRDQDLSPQKQLELKGKYGQVEVHAQVP
187

Query: 69 ----RIGGGDIVAISNVKADGTVRQHS-PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123
 + G D+ IS + D + P + I GN WH D + A
Sbjct: 188 RVPNGVDGKDLNGISVIWQDYAREYYGLPLTFKSS---IGGNSQWHTDLVHEFQPAGITH
244

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA----RHSLVYSQSKLG---HVQ
176
 + +P+VGG T +A AYD L A + + ++A HS + ++ L H++
Sbjct: 245 LHNDAIPSVGGDTLWASGYGAYDKLSPALQQFLDGKTAIYRSAHSYINRENPLNGPRHIE
304

Query: 177 QAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDDAESERFLEGLVD
235
 + P+++ HP TG SL + R I G++ ES LE L

Sbjct: 305 RE-----HPIIRTHPATGWKSLFVNRSM TVRIVGLNPEESRILLEYLFG
348

Query: 236 WACQAPRVHAH-QWAA----GDVVVWDNRCLLHRAEPWD 269
+ + W + G +WDNR H A WD

Sbjct: 349 VFEKNLDIQVRFNWKSKPGLGTSALWDNRISQHNA-VWD 386

>gb|EDK40461.2| hypothetical protein PGUG_04559 [Pichia guilliermondii
ATCC 6260]

Length = 423

Score = 67.0 bits (162), Expect = 2e-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-PAEWDDMMKVI VGNMAWHADSTYMPVMAQGAV
123

+ G D+ IS + D + P + I GN WH D + A

Sbjct: 188 RVPNGVDGKDLNGISVIWQDYAREYYGLPLTFKSS---IGGNSQWHTDLVHEFQFAGITH
244

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA-----RHSLVYSQSKLG---HVQ
176

+ +P+VGG T +A AYD L A + + ++A HS + ++ L H++

Sbjct: 245 LHNDAIPSVGGDTLWASGYGAYDKLSPALQQFLDGKTAIYRSAHSYINRENPLNGPRHIE
304

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVD
235

+ P+++ HP TG SL + R I G++ ES LE L

Sbjct: 305 RE-----HPIIRTHPATGWKSLFVNRSM TVRIVGLNPEESRILLEYLFG
348

Query: 236 WACQAPRVHAH-QWAA----GDVVVWDNRCLLHRAEPWD 269
+ + W + G +WDNR H A WD

Sbjct: 349 VFEKNLDIQVRFNWKSKPGLGTSALWDNRISQHNA-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 = 2e-09, Method: Compositional matrix
adjust.

Identities = 68/272 (25%), Positives = 102/272 (37%), Gaps = 32/272 (11%)

Query: 12 GATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAI----- 67

Sbjct: 7 G LGA VTG+ LD + +H L++ G H + +Q I + G I
 GEGLGAQVTGIDPGNLDGITTEEIRELVYRHKLVLKGVHPTPEQFIELGRLIGEIVPYY 66

Query: 68 -----ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
 123

Sbjct: 67 +I S + G R WH D +MP ++
 EPVYHHQDHPEIFVSSTEEGQVPR-----GAFWHVDYMFMPKPFASF
 111

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATR-ALVHQRSARHSLVYSQSKLGHVQQAGSAY
 182

Sbjct: 112 VP T F D+ +++L T+ A + S Y + + V +
 VLPLAVPGHDRGTYFIDLKSVWESLPAKTKDAALGTFSTHTPRRYIKIRPSDVYRPIGEI
 171

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPG-----MDAAESERFLE--GLV
 234

Sbjct: 172 + TT P V HP+TG L I DAA ++ LE G +
 LAEIERTTPPQKWPTVIKHPKTGEEILYICEAGTETIEDGAGRIQDAALLQQLLEASGQL
 231

Query: 235 DWACQAPRVHAHQWAAGDVVVDNRCLLHRAE 266
 D +P +HA + GD+V+WDNR L+HRA+

Sbjct: 232 DPDYASPFIAHQHYEVGDIVLWDNRSLVHRAK 263

>ref|XP_001830759.1| hypothetical protein CC1G_03296 [Coprinosia cinerea
 okayama7#130]
 gb|EAU91128.1| hypothetical protein CC1G_03296 [Coprinosia cinerea
 okayama7#130]
 Length = 352

Score = 67.0 bits (162), Expect = 2e-09, Method: Compositional matrix
 adjust.

Identities = 68/268 (25%), Positives = 110/268 (41%), Gaps = 32/268 (11%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRFG----- 65
 +G ++G+ L+ L G L Q L+IF Q + ++Q+ A FG

Sbjct: 78 IGTELSGIQLSQTKEGLDELGLFVAQRKLVIFREQDFQDLPPEKQVAIAAHFGVPHLHA
 137

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDD-MMKVIVGNMAWHADSTYMPVMAQGAVF
 124

Sbjct: 138 + I G A N+ +RQ +D + + WH+D +Y P F
 TLPNIEGHP--AYVNL-----LRQPGKRNINDYFIDTFLSYAFWHSVSYEPQPPSTTF
 190

Query: 125 SAEVPAVGGRTCFADMRAAYDALDEATR-ALVHQRSARHSLVYSQSKLGHVQQAGSAYIG
 184

Sbjct: 191 P VGG T F AY+ L + + A HS V +++ +++G A
 WPLDQPTVGGDTLFLSTTEAYNRLSPEFQKRLVGLKALHSGV---AQVEESRRSGGAVRK
 247

Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIG-----RHAHAIPGMDAAESERFLEGLVDWACQA
240

++ + P+++VHP TG S+ + RH I G+ ES+ L+ L D +
Sbjct: 248 EPVEA----VHPVIRVHPVTGEKSIFVNPAFTRH---IVGLKKEESDALLKFLYDHIAKG
300

Query: 241 PRVHAH-QWAAGDVVVWDNRCLLHRAEP 267

+ G V++WDNR H A P
Sbjct: 301 ADFQVRARHEPGSVIWDNRVTNHSAPV 328

>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 = 2e-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 TIGADVEGIDFREPLDDDTYLSLRRALLKYKVLFFRKQAITPAQHVAVARRFGELEVHPM 91

Query: 69 RIGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV
128

+ + DGT R N+ +H+D ++ + + G++
Sbjct: 92 FTNHPEHPELVVFGRDGTTREGRE-----NL-YHSDVSWREIPSMGSMRLRCVE
137

Query: 129 VPAVGGRTCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYGMD
188

P VGG T + +M AAY+ L + +A + A H + + + ++ Y
Sbjct: 138 CPEVGGDTMWINMAAAYENLPQDMKARIANLKAVHDAMPTFGSALNEEKYAEMRAKY---
194

Query: 189 TTATPLRPLVKVHPETGRPSLLIG-----RHAHAIPGMDAAESERFLEGLVDWA
237

+ P+V+ HPETG L + + A G D +E L +
Sbjct: 195 --PPMVHPVVRTHPETGEKILFVNEAFTTHFANFVKEAPYRIGSDYRPAELDLLQYLYRQ
252

Query: 238 CQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

AP +W + +WDNR H A
Sbjct: 253 AAPEYQVRLRWQPDTIALWDNRSTQHAYA 281

>ref|XP_384843.1| hypothetical protein FG04667.1 [Gibberella zeae PH-1]
Length = 378

Score = 67.0 bits (162), Expect = 2e-09, Method: Compositional matrix
adjust.

Identities = 70/269 (26%), Positives = 108/269 (40%), Gaps = 24/269 (8%)

Query: 7 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA 66

Score = 66.6 bits (161), Expect = 3e-09, Method: Compositional matrix adjust.

Identities = 73/278 (26%), Positives = 113/278 (40%), Gaps = 40/278 (14%)

Query: 7 QITPTGATLGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
 ++TP +GA ++ + L + D L +A Q+ +L F Q +S++ T K +G
 Sbjct: 17 RLTPY---MGAELSDIDLEQAIGDEAAEELRSALTQYQVLGFRNQEISHEAHKTMGKIYG 73

Query: 66 --AIERIGGG-----DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
 118

AI G +IVAI H+ A+ K + G WHAD +
 Sbjct: 74 PLAIHFAVPGIEEHPEIVAI-----HADAD----SKYVAGE-NWHADLSASDEP
 117

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLHQRSARHSLVYSQSKLGHVQQA
 178

G++ VP GG TCF M AYDAL + + + A H +L
 Sbjct: 118 PLGSILYLHTVPETGGDTCFCSMTKAYDALSDKMKDYLDGLYAMHDSNPVYHRL-----
 171

Query: 179 GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-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 KNPNFQMRFTWEPHSIVMWDNLAVQHHLA-VWDY-FPNV 263

>gb|AAS64595.1| alpha-KG-dependent dioxygenase [uncultured soil bacterium]
 Length = 119

Score = 66.6 bits (161), Expect = 3e-09, Method: Compositional matrix adjust.

Identities = 45/126 (35%), Positives = 59/126 (46%), Gaps = 9/126 (7%)

Query: 136 TCFADMRAAYDALDEATRVLHQRSARHSLVYSQSKLGHVQQAAGSAYIGYGMDTTATP--
 193

T F DMRAAYD L ++ + A H + + LG + + A P
 Sbjct: 1 TEFADMRAAYDELPADLKSELEGLHAEHYALNPRFVLGDTDYSEA-----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 TWPLVRTHAGSRKFLFIGAHAGRIEGRPLAEGRMLLAELLEHATQRRFVYRHSWKVGD
 113

Query: 254 VVWDNR 259

V+WDNR

Sbjct: 114 VMWDNR 119

>gb|EEY17009.1| alpha-ketoglutarate-dependent sulfonate dioxygenase
 [Verticillium
 albo-atrum VaMs.102]
 Length = 383

Score = 66.6 bits (161), Expect = 3e-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 KVTDLTTHIGTEIEGIQLKDLTNVQRDELALLIAERSVVFVRDQDITPQQQKELGEHFQ
 144

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQ
 120
 +E ++ G + V + T E+ + G WH+D + A
 Sbjct: 145 VEVHPQVPQVPGVEGVTVIWPDLQAT-----EFPASFRPPGGASRWHSDLVHELQPAG
 197

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGS
 180
 + VP GG T +A +AY+ L R ++ R A + + AG
 Sbjct: 198 ITHLHNDTVPPTGGDTLWASGYSAYEKLSPFRKIIDGRKAVYRSAHPYLDLDRK-PNAGP
 256

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQ
 239
 ++ PLV+VHP TG +L + R I G+D AES+ L L D +
 Sbjct: 257 KHVER-----THPLVRVHPATGWKALWVNRAMTDRIVGLDRAESDVILNYLYDVYEK
 308

Query: 240 APRVHAH-QWAAGDVVVDNRCLLHRAEPWDF--KLPR 274
 + +W G +WDR +H A WD+ K PR
 Sbjct: 309 NVDIQLRFKWTPGTSALWDRITIHNAS-WDYAGKHPR 345

>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 = 3e-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 QVTEITPYIGSEVRGVQLSRLTNTGKDQLALFVAQRKVVAFRDQDFASLPIDKALEFGGY
 158

Query: 64 FGA--IERIGGG-----DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
116

FG I G +I + D + Q + ++ WH+D +Y
Sbjct: 159 FGRHHIHPTSGAPKGFPEIHLVHRGADDNSFLQ-----TFLHEHTNSVTWHS DVSYER
211

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ
176

P GG T FA++ AYD L + +H A HS +
Sbjct: 212 QPPGTTFLYL LDGPTSGGDTLFANLAKAYDRLSPEFKKRLHGLKAVHS-----GFE
262

Query: 177 QAGSAYIGYGM DTTATPLR---PLVKVHPETGRPSLLIG-RHAHAIPGM DAAESERFLEG
232

QA SA + P++ P+V+ HP TG ++ + + I G ES+ L+
Sbjct: 263 QAQSA-LARESTVRRDPVKHEHPVVRTHPVTGEKAIYVNPQFTRYIVGYKKEESDYLLKF
321

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCL LHRA 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 = 3e-09, Method: Compositional matrix
adjust.

Identities = 44/131 (33%), Positives = 65/131 (49%), Gaps = 5/131 (3%)

Query: 136 TCFADMRAAYDALDEATR ALVHQRSARHSLVYSQS---KLGHVQQAGSAYIGYGM DTTAT
192

T F DM AYDAL + + V R A H + +++ + + Y T
Sbjct: 1 TEFCDMYQAYDALPDDLKRAVEGRLAIHHISKTKNPRVTISPDRPGAKEYYEARAKETQE 60

Query: 193 PLRPLVKVHPETGRPSLLIG-RHAHAIPGM DAAESERFLEGLVDWACQAPRV-HAHQWAA
250

L+PLV+ HPETGR +L I R I M AE++ L+ L + + + H+W
Sbjct: 61 ILQPLVRTHPETGRQALYISPRFTIGIADMPDAEAQSLLDRLFASFVKNRGIQYRHKWRD
120

Query: 251 GDVVVWDNRCL 261

GD+V+WDNRC+
Sbjct: 121 GDLVMWDNRCV 131

>gb|EDP48989.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Aspergillus

fumigatus A1163]
Length = 396

Score = 66.6 bits (161), Expect = 3e-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 TIGSEVTGVQLSSLSAAGKDQLALLVAQRVVVFRDQDFA-DLPIADALEFGS--HFGRH
150

Query: 74 DIVAISNVKADGTV-----RQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
127

I S + +G R +S E D +AWH+D TY

Sbjct: 151 HIHPTSG-QPEGYPEIHLVHRHNSQGELDAFFADRNSTVAWHSDVTYEAQPPGTTFLYIIL
209

Query: 128 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
187

P VGG T F D AY L A + +H A HS + Q++ +Q G

Sbjct: 210 DSPEVGGDTVFDVQVEAYRRLSPAIKERLHGLRAVHS-GFEQAEFS--RQRGGV-----
260

Query: 188 DTTATPLR---PLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVDWACQAPRV
243

P++ P+V+ HP TG +L + G +I G+ ES+ L L++ +

Sbjct: 261 -VRRDPVKHEHPIVIRTHPVTGEKALFVNGGFTRSIVGLKKEESDALLGFLLNHVGRGIDY
319

Query: 244 HAH-QWAAGDVVVWD 257

A +WA VVVWD

Sbjct: 320 QARIKWAPKTVVVWD 334

>gb|ADC33976.1| TfdA-like protein [uncultured bacterium]

Length = 122

Score = 66.2 bits (160), Expect = 4e-09, Method: Compositional matrix
adjust.

Identities = 37/127 (29%), Positives = 63/127 (49%), Gaps = 6/127 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL-
194

T F DM AY+ LD+ + + A H+L +S+++ + G + P+

Sbjct: 1 TEFCDMYGAYERLDDGWKRRRIAGLRAVHNLDFSRTTR-----RHGEDPMTEAQKRDTPPVD 55

Query: 195 RPLVKVHPETGRPSLLIQRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

P+V+ H ETGR + +G HA ++ GM E +E L + H+W+ G ++

Sbjct: 56 HPIVIRTHSETGRKCVFLGDHAESVVGMPYDEGRALIEELNAAIIHDDLTYRHRWSPGQLI
115

Query: 255 VWDNRCL 261

+WDRNC+

Sbjct: 116 LWDNRV 122

>ref|XP_459245.1| hypothetical protein DEHA0D18953g [Debaryomyces hansenii CBS767]

emb|CAG87418.1| DEHA2D17446p [Debaryomyces hansenii]
Length = 380

Score = 66.2 bits (160), Expect = 4e-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---LGTEITGIQLSQLDDRGKDELALLVAKRGLVIFRDQDFGAKGPQFVSDYGKY
140

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIV-----GNMAWHADSTYMPVM
118

FG + + + G H +D + + + WH+D +Y
Sbjct: 141 FGPLH-----IHPTTGSPKGHSEIHVVYRRNDYNEALTFANRTNLVQWHSADVSYELQP
193

Query: 119 AQQAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
178

FS P GG T FAD AY+ L + L+ H L S+ + ++
Sbjct: 194 PGTTFFSVIEGPESGGDTLFDADNVEAYNRLSPRLKELI---EGLHVLHSSEEQAKFSRKE
250

Query: 179 GSAYIGYGMDDTTATPLR---PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV
234

G A P+R PLV+VHP TG L + + I ES+ L L
Sbjct: 251 GGA-----ERRDPVRNIHPLVRVHPVTGDKILYVNPFGFSRKIVEFKQEESDALLNFLY
303

Query: 235 DWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

+ + + A W VVVWDNR + H A
Sbjct: 304 NHIGNSHDLQARVNWEPNSVVVWDNRRVSHTA 335

>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 = 4e-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 IDLIPSIGTELIGVITYEDLQKDDVLDEFVDTLH----QRELVIIRGIELTPGQQVGLAAR 59

Query: 64 FG-----AIERIGGGDIVAI-----SNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHAD
111

G +E+ ++ I N K+ G R VGN WH D

Sbjct: 60 IGKPIPFVLEQYRYPELPEIMISSNEVRNNSIGVAR-----VGNF-WHQD
104

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS-QS
170

S+++ A+ + VP G T FA YD L + + R A H++V +
Sbjct: 105 SSFVAKPAEYTMLHGVNVPQTSGHITLFAVAVDRLPGDWKKKIDRRRAWHTTVVKRLRI
164

Query: 171 KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG--RHAHAIPGMDAAESER
228

+ HV + + Y + + PLV+ P + R + L G + ++ G DA E+
Sbjct: 165 RSEHVGLSTAHEYKAWIEEKHPKVEHPLVRQDPFSKR-TYLYGAPEYLDVQGF DANENAA
223

Query: 229 FLEGLVDWACQAPR-VHAHQWAAGDVVVWDNRCLLHRA 265
F L+D Q P V+ H+W D+VVW LH A

Sbjct: 224 FF-ALLDSLIQDPEHVYTHRWTPKDLVVWKTATTLHAA 260

>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 = 5e-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 LLSSTAKVSHIQPCIGSIVEGVQLNKLSDAAKDELALLIAERKVVAFDPDQDLIDAGPEEQ
129

Query: 58 ITFAKRFGA--IERIGGG--DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
113

+F + FG + I G + DG V E + ++ WH D +
Sbjct: 130 YSFMRYFGKPNYQPISGSMKGYPGFHIIHRDGNV-----DEINRFLEQRTTTTLWHQDVS
184

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
173

Y + P VGG T FA AAY L ++ + A H+ S +
Sbjct: 185 YEIQPPAYVMLGLLQGPVGGDTVFAATDAAYKRLSPTFQSFIDNLKAVHT---SAKMIA
241

Query: 174 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEG
232

H + GS ++ + PLV+VHP TG L I G + G+ E +
Sbjct: 242 HARLTGSLVRKDPVEN----VHPLVRVHPVTGERCLFINGEFITRVEGLKEPEFRVLQDF
297

Identities = 71/255 (27%), Positives = 102/255 (40%), Gaps = 28/255 (10%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERIGGG 73
+G V GV LATL +A L ++ F QH DQQ K F ++

Sbjct: 95 IGTEVHGVDLATLTNAQKNDLARLIATRQVFFRNQHNFDIDQQRELKGFWRRTTQVWK-
153

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM---PVMAQGAVFSAEVVP
130

+++S A G SP D+ + WH+D TY P V S
Sbjct: 154 --MSMSYSLAKG-----SP----DLRALFTPTFLWHS DVTYEIQPPSYTSLKVLSGPPR-
201

Query: 131 AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM-D
189

GG T ++ AAYD L + + +A HS +Q GS +G +
Sbjct: 202 GGGGDTLWSSQYAAAYDMLSPHMQRYLESLTALHS-----AELQAQGSRD LGRTVRE
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 WEEGDVAFWDRATV 328

>gb|EEU46770.1| hypothetical protein NECHADRAFT_77499 [Nectria
haematococca mpVI

77-13-4]
Length = 356

Score = 65.9 bits (159), Expect = 6e-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 GWHS DITFEKVPDYAMLKIHTLPATGGDTLWASGYEIDRLSPPMKQFLEGLTATHDAS
217

Query: 167 Y---SQSKLGHVQQAGSAYIGYGM DTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMD
222

+ ++LG+ + G + + PLV+ +P TG S+ + + I G+
Sbjct: 218 FFHDEAARLGNPLRKGIRGSPLNQENLSAVHPLVRTNPVTGWKSVYVNGFTKRINGLS
277

Query: 223 AAESERFLEGLVDWACQAPRVHA-HQWAAGDVVVWDNRCLLHRAEPWDFKLPR 274

ES+ L L + Q ++W+ D +WDNR LH A +D+ R
Sbjct: 278 KDES DTLLSYLFNLVTONHDAQVRYRWSKNDCAIWDNRSTLHCAT-YDYDAAR 329

>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 = 6e-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 SQLGFVINGVDLSNLTQDEFENIQQALWTHGVICIKNQLTAQQQIAFTERWGKLVILPS 65

Query: 73 -----GDIVAISNVKADGTVRQHSP-AEWDDMMKVIVGNMAWHADSTYMPVMAQ
120

IV + NV+ D TV+ +S AE+ WH D +

Sbjct: 66 FYAFDNREPEYPAIVRVGNVRLDDTVKPNKDAEY-----WHKDGDFRQPGEN
113

Query: 121 G--AVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
178

++ + + + VGG+T + D + L++ L + S++ SQ+ +

Sbjct: 114 FILSILTPKEIAQVGGQTYVD---SEQILNDMPADLREKLEGAKSIIRSQN----ISDF
166

Query: 179 GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWA
237

SA + P + HP +G+ L I + + + D ++

Sbjct: 167 SSA---KPEEHYPEAHHPAIATHPISGKKILNITYNNLNDVVLKDGITLNS--RDI IPEI
221

Query: 238 CQAPRVHAHQWAAGDVVVDNRCLLHRA 265

Q ++++H+W GDVV+WDN ++HR+

Sbjct: 222 EQVYKIYSHRWEMGDVVIWDNIRVIHRS 249

>ref|XP_001820787.1| hypothetical protein [Aspergillus oryzae RIB40]

dbj|BAE58785.1| unnamed protein product [Aspergillus oryzae]

Length = 333

Score = 65.5 bits (158), Expect = 6e-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---IGTEIRGVQLSQLSTDGLDQLALLAAQRGVLVFRDQDFADIGTGRQDIAAHY
112

Query: 65 GAIER-----IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMA----WHADSTYM
115

G + + G V A D V ++ ++G WH D T+
Sbjct: 113 GPLHQHPTMGYPQGTSPPEFQVYADEKVGNI-----LRTLLGTRTSYDLWHIDQFT
163

Query: 116 PVMAQGAVFSAEVVPAVGG-RTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGH
174

P F PA GG T F + AAY AL R +H R L+++ + +G
Sbjct: 164 PNTPGVTFFWVLETPASGGGDTAFTSLTAAYQALSPTFREGH----RLKLLHTSASVGE
219

Query: 175 VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGL
233

V + G + PLV HP T P L + A + G ESE L L
Sbjct: 220 VARIGQE---RALKDAVQTEHPLVIGHPVTHDPLVFNPAIARQVVGYPKEESENLLSFL
276

Query: 234 -----VDWACQAPRVHAHQWAAGDVVVWDNRCLL 262

+D++C+ W G VVVWD CL+
Sbjct: 277 HNHIRSLDFSCRV-----SWEKGTVVVWDQVCLV 305

>gb|EDP48444.1| alpha-ketoglutarate-dependent taurine dioxygenase

[Aspergillus

fumigatus A1163]

Length = 371

Score = 65.5 bits (158), 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 AVFSAEVV-PAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGS
180

V + P VGG T FA AY L + + A HS S + H + G
Sbjct: 203 YVMLGLLEGPEVGGDTVFAATDMAYKRLSPTFTSFLDGLRAVHS---SAKMINHTRLLGG
259

Query: 181 AYIGYGMDDTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVDWACQ
239

+DT + PLV++HP TG L I G I G+ E L+ L+
Sbjct: 260 LVRKDPVDT----VHPLVRIHPVTGKCLFINGEFITRIQGLKEPEQRYLLDFLMQHIMT
315

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDALD+A +A + HSL+YS+ LG + Y L+
Sbjct: 1 TEFGDMRAAYDALDDAAKAEIEDMICEHSLMYSRGALGFLD-----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 RLVTRHPVHGRKSLYLSSHAGGIVGMTPEARVLLRDLNEHATQPEFVYVHKWKLHDLVM
115

Query: 256 WDNR 259

WDNR

Sbjct: 116 WDNR 119

>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 = 7e-09, Method: Compositional matrix
adjust.

Identities = 47/174 (27%), Positives = 73/174 (41%), Gaps = 14/174 (8%)

Query: 104 GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARH
163

G WH+D T+ P+ + A+ +P GG T +A YD + R + +A
Sbjct: 191 GKNQWHS DITFEPIPSDYALLRLTQLPKTGGDTLWASGYELYDRISPTLRHFLDTLTA--
248

Query: 164 SLVYSQSKLGHVQQAGSAYIGYG-----MDTTATPLRPLVKVHPETG-RPSLLIGRHA
215

Y+Q + + + G T + P+V+ +P TG R +G H
Sbjct: 249 --TYAQPLFNEAARRNFTLYSGARGAPENTGDTLDAVHPVVRTNPVTGWRVFAVGHVH
306

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW-AAGDVVVWDNRCLLHRAEP 267

I G+ ES+ FLE V + + +W A DV +WDNR + H A P
Sbjct: 307 QRIHGLSDEESKHFLEWFVRLVVENHDLQVRLRWKAVNDVAIWDNRSVYHAATP 360

>emb|CAG85382.2| DEHA2B09768p [Debaryomyces hansenii]

Length = 383

Score = 65.5 bits (158), Expect = 7e-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: 252 ---GIERRKPVSSIHP LIRQHPATGDKFIYLNRPFSRRIVELKQDESDYLINFLFHIES
308

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
A + W VVVWDNR ++H A

Sbjct: 309 AHDLQLRANWEPNTVVVWDNRVHSA 335

>ref|XP_001482070.1| hypothetical protein PGUG_05833 [Pichia
guilliermondii ATCC 6260]
>gb|EDK41735.1| hypothetical protein PGUG_05833 [Pichia guilliermondii
ATCC 6260]

Length = 384

Score = 65.1 bits (157), Expect = 8e-09, 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---MGTEIRGVQLSQLDDKAKDELALYVAQRGVVVFRDQDFAAKGPKFVTEYGRH
140

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123

FG + I + T R+ E+D + + WH+D +Y + G

Sbjct: 141 FGRLH-IHPTSGAPRGFPPELHITYRRPDEKEFDRI FSETTTAVQWHS DISYE-LQPSGLT
198

Query: 124 FSAEVV-PAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAY
182

F A + P GG T FAD++ AY L R + HS +QA ++

Sbjct: 199 FFAVLEGPESGGDTIFADVKEAYRRLSPEFRKRLEGLHVLHS-----SNEQAQNSR
249

Query: 183 IGYGMDTTA--TPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQ
239

G++ A + + PL++ HP T + + R + I + ES+ L L D +

Sbjct: 250 GQGGVERRAPVSNIHPLIRQHPATKEKYIYLNRPFSRRIVELKQEESDYLLNFLYDHIK
309

Query: 240 APRVHAH-QWAAGDVVVWDNRCLLHRA 265
A + W VVVWDNR + H A

Sbjct: 310 AHDLQLRASWEPNTVVVWDNRVVEHSA 336

>gb|ADC33950.1| TfdA-like protein [uncultured bacterium]
Length = 121

Score = 65.1 bits (157), Expect = 8e-09, 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 TEFCDMGSAYAALPERLKVLIEDLQAEHSIVHSRGLVDPTVLTQAQA-----ET 50

Query: 191 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
250

+ LV+++P GR +L IG HA I G + L L + + +H W
Sbjct: 51 PPDRQRLVRINPINGRRALYIGAHASHIVGWPLEKGRALLAELTELTRPEFRLSHAWRE
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 = 8e-09, 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 IGTEIVGLQLKDLNDKQKDELGLLIAERSVVFFRDQDLSPQQQKELGEWYGEIEVHPQVP
152

Query: 70 ----IGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
125

+ G ++ + A+ + P G WH+D +
Sbjct: 153 QVPGVPGVTVLWPALAAAERSAAFRRPG-----GAAHWHSDLVHERQPPGVTHLH
202

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
185

+ VP++GG T +A AAY+ L A R ++ ++A + ++ H ++ G ++
Sbjct: 203 NDTVPSIGGDTLWASGYAAAYEKLSPAFRQIIDGKTAIYRSAHAYLDRDHPEE-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 LRFKWTPTRSALWDNRITIHNAS-WDYE 340

>gb|ACG80583.1| TfdA [uncultured bacterium]
Length = 118

Score = 65.1 bits (157), Expect = 8e-09, Method: Compositional matrix
adjust.

Identities = 40/124 (32%), Positives = 58/124 (46%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYDAL +A + HS+ +S+ LG + + +
Sbjct: 1 TEFGDMRAAYDALPTDMKAQLEGLRVHHSIAHSRQILGF-----EFSQQEQENLKGAIH 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

PL++ P + R SL + HA I E L L++ A Q V+ H+W D+V+
Sbjct: 55 PLIRTLPRSQRKSLYVAahasRILDWPIPEGRLLLRDLMEHATQPQFVYRHEWRDHDLMV
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 = 9e-09, 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---LGSEINGIQLSQLSLSAKNDLARFVAERGVVVFKNQDFNQGKQPFAVDFAKY
146

Query: 64 FGAIER-IGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGA
122

FG + + G + R + E + + +++WH+D +Y Q
Sbjct: 147 FGTLYKHATSGSPEGFPELVH--CFRGATQDEINSVFANRTNSISWHSDCSYALNALQLT
204

Query: 123 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAY
182

+FS +P GG T FA AY+ L A + + HS S + + ++ G
Sbjct: 205 LFSLQIPEAGGDTLFASTVEAYNRLSPAMKERLEGLHVLHS---SIEQARNNKEVG---
258

Score = 65.1 bits (157), Expect = 9e-09, Method: Compositional matrix adjust.

Identities = 41/111 (36%), Positives = 56/111 (50%), Gaps = 5/111 (4%)

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHP
202

AAYDALD+ TR + HSL+YS+ LG + Y + L+ LV+ HP
Sbjct: 1 AAYDALDDETRREIEDMVCEHSLMYSRGA LGFLD-----YSEEEKEMFRPVLQRLVVRTHP 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 = 9e-09, 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-----RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYM
115

FG +E + D+ +SNV+++G VG WH D ++
Sbjct: 64 WFGELESTFYKHPKSPHPDVFRVSNVESEGCRG-----VGR TGWHIDGSFQ
109

Query: 116 PVMAQGA VFSAE VVP AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV
175

P +++ VVP G T FA L+E L + A+ +Y S
Sbjct: 110 PAFNYSLYYMHVVPKEGD-TVFA-----PLNEIEGLSEDQQA KWDKLYMMS-----
156

Query: 176 QQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHA-----HAIPGM---DAAE
225

D + + PLV HP TG+ +L + PG D +E
Sbjct: 157 -----DRRGS LVHPLVYSHPR TGKKTLCFHLGMTDAFTWDYGTGPGQRM TDPSE
204

Query: 226 SERFLEGLV-----DWACQAPRVHAHQWAAGDVVVDNRCLLHRAEP 267

+++ L + D A Q ++H+W GD ++ DN + H A P
Sbjct: 205 TQQILNEIRHEFVKDDGAIQ----YSHKWQVGFIIISDNLAVGHEATP 248

>ref|XP_002497214.1| ZYR00F00286p [Zygosaccharomyces rouxii]

emb|CAR28281.1| ZYR00F00286p [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---LGTEVKGIQLSLSPEGKDELALLVAQRGIVVFRNQDFAKHGPEFAVEYG
175

Query: 62 KRFGA--IERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
119

K FG I + G A + T R+ AE++ + + ++ WH D +Y

Sbjct: 176 KYFGKLHIHQTSGHPETA---PELHVITYRRPDHAEFERVFEDESHTSIGWHTDVSVELQPP
232

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAG
179

FS P GG T FAD AY+ L + + HS V+QA

Sbjct: 233 SYTFFSVLQGPPEGGDTLAFADSVEAYERLSPTLKQFLEGLHVIHS-----SVEQAQ
283

Query: 180 SAYIGYGMDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESE---RFLEGL
233

++ + G+ + PL++ HP R SL + + + I + ES+ FL L

Sbjct: 284 NSKLQGGIQRREPTGHIHPLIRWHPVLKRKSLYVNKAFSRRIVELKKPESDLLLNFLYSL
343

Query: 234 VDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+ A ++ A+ W V +WDNR +H A

Sbjct: 344 FNNALDL-QLRAY-WEPDTVAIWDNRRTIHS 373

>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 TAKVSHIQPSLGTIVENVQLSDL SAAGRDELALLISERKVVAFPDQDLIDAGPDAQESFM
137

Query: 62 KRFGA--IERIGGG--DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
117

+ FG + + G D A + DG E ++ WH D +Y +

Sbjct: 138 RHFQKPNYQPVSGSMTDHPAFHIIHRDGNR-----DEIARFLQQRRTTTTLWHQDVSYE-I
191

Query: 118 MAQGAVFSAEVLV-PAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQ
176

Sbjct: 192 QPPGYVMLGLLQGPEVGGDTVFAATDLAYKRLSPAVTAFDGLKVTHS---SAKMIAHAR
248

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVD
235

Sbjct: 249 MTGGLVRKDPVDT----VHPLIRVHPVTGEKCMFLNGEFITRIDGLKDSETKWVLDFLMN
304

Query: 236 WACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

Sbjct: 305 HLVTGHDFQVRVRWQPRTIVMFDNRSTIHS 335

>ref|XP_001391238.1| hypothetical protein An07g01510 [Aspergillus niger]
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

Sbjct: 87 KVTEIQPRIGSIVEGVQLNQLTDAQKDELALLVAERKVVAFPDQDLIDDGPEAQEAFMRH
146

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVI---VGNMAWHADSTYMPVMAQ
120

Sbjct: 147 FGK----PNYQPVSGSMRGHPGFHIIHRDGNREEITRFLSQRTTTTLWHQDVSYE-IQPP
201

Query: 121 GAVFSAEVV-PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG
179

Sbjct: 202 GYVMLGLLLEGPEVGGDTVFSATDMAYKRLSPTLTSWLDTLRATHS---SAKMIQHARLTG
258

Query: 180 SAYIGYGMDTTATPLRPLVKVHPETGRPSLLI-GRHAHAIPGMDAAESERFLEGLVDWAC
238

Sbjct: 259 GLVRKEAVDT----VHPLVRVHPVTGEKCLFVNGEFITKIQGLKEPEQRWLLDFLMQHII
314

Query: 239 QAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

Sbjct: 315 TGHDFQARVRWQPRTIVIFDNRCTTHSA 342

>emb|CAY25793.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 64.7 bits (156), Expect = 1e-08, Method: Compositional matrix adjust.

Identities = 36/110 (32%), Positives = 61/110 (55%), Gaps = 18/110 (16%)

Query: 33 AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISN 80
A + A ++A+L+FPGQ +++DQQ+ FA FG E++ GG++ +SN

Sbjct: 14 AYIEAGMDKYAVLLFPGQDVTDDQQLAFALNFGEREQVHGGNVTRKEDYRLTSGLNDSVN 73

Query: 81 VKADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
+ DG +P D + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 74 LGKDG-----NPLPRDHRTHLFLNLGNCLWHS DSSFRPIPAKFSLLSARVV 118

>gb|EEU35175.1| hypothetical protein NECHADRAFT_97607 [Nectria
haematococca mpVI
77-13-4]
Length = 355

Score = 64.7 bits (156), Expect = 1e-08, Method: Compositional matrix adjust.

Identities = 63/276 (22%), Positives = 108/276 (39%), Gaps = 27/276 (9%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQI 58
+ Q++ +G + G+ L+ L+D L + +++F Q + +Q

Sbjct: 59 GNSDFQVSKITPVIIGTEIRGLQSQLNDLQKDELALLIAERGVVVFREQDFKDIGIQKQK
118

Query: 59 TFAKRFGAIERIGGG----DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY
114

F + FG + G D + N+ + ++ D + + +H+D +Y
Sbjct: 119 EFGRYFGPLHIHPTGAHIKDHLEFHNIYLGPDNEYRNEKLDKL-----STIGYHSDVSY
173

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
174

+ + VP GG T +A AAY L + L+ A HS Y Q++
Sbjct: 174 EHQPPIGITILTLLSVPPSGGDTI WASQTAAAYARLSTPIKTLLEGLRAEHS-GYPQAEKAR
232

Query: 175 VQQAGSAYIGYGMDDTTATPLR---PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFL
230

G P++ P+V++HP TG+ +L I I G+ ES+ L
Sbjct: 233 RD-----GRHVRREPVKSEHPVRIHPATGQKALFIQPGFTKRIIGLKQEESDGLL
283

Query: 231 EGLVDWACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
+ L Q A +W G V +WDNR H A

Sbjct: 284 KILFKHIAQGQDFQARVRWEEGTVALWDNRVTAHTA 319

>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 = 1e-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 TIGSEVTGVQLSSLSAAGKQDLALLVAQRRVVVFRDQDFAG-LPIADALEFGS--HFGRH
 150

Query: 74 DIVAISNVKADGTV-----RQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
 127

 I S + +G R +S E D +AWH+D TY
 Sbjct: 151 HIHPTSG-QPEGYPEIHLVHRHNSQGELDAFFADRNSTVAWHS DVTYEAQPPGTTFLYIIL
 209

Query: 128 VVPAVGGRTCFADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYGM
 187

 P VGG T F D AY L A + +H A HS + Q++ +Q G
 Sbjct: 210 DSPEVGGDTVFVDQVEAYRRLSPAIKERLHGLKAVHS-GFEQAEFS--RQRGGV-----
 260

Query: 188 DTTATPLR---PLVKVHPETGRPSLLI-GRHAHAIPGM DAAESERFLEGLVDWACQAPRV
 243

 P++ P+V+ HP TG +L + G +I G+ ES+ L L++ +
 Sbjct: 261 -VRRDPVKHEHPIVRTHPVTGEKALFVNGGFTRSIVGLKKEESDALLGFLLNHVGRGIDY
 319

Query: 244 HAH-QWAAGDVVVWD 257
 A +WA VVVWD

Sbjct: 320 QARIKWAPKTVVVWD 334

>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---LGSEVRGVQLSLSQKDDLALYVAQRGVVVVFRDQDL-RDKNLQEVK
 156

Query: 63 RFGAIERIGGGDIVAISNVKADG-----TVRQHSPAEWDDMMKVIVGNMAWHADSTYMP
 116

 FG + G I S +G T R+ P++ + ++AWH+D TY

Sbjct: 157 EFG--QYFGPLHIHQTSQA-PEGFPEFHITYRRAGPSK---PFINKIASIAWHS DITYEL
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 KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFL
230

K G +Q+ T+ + PLV+ HP G+ S+ I G+ ES+ L
Sbjct: 269 K-GSIQRK-----KFTSETVHPLVRYHPVLGKKSIIYAKAFGTRIIGLQKQEESDLVL
318

Query: 231 EGLVDWACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265

+ ++ A + + G VV WDNR + H A
Sbjct: 319 NFIQNFIAATAQDLQLRASIEPGTVVAWDNRVVFHSA 354

>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-LSNDQQITFAKRFGAI-----ERIGGGDIVAISNVK 82
Q ++ F Q+ L+ND Q R G + ER GGD + +S +

Sbjct: 71 QRGVVFRAQNNLTNDLQKKLILRLGELTGRPASSTLHHIPLLN SERELGGDDLEVSTIS
130

Query: 83 ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR
142

+ + + + N WH+D + P A +P+ GG T +A
Sbjct: 131 SKQHAKFYRKTQDNGVVVTKRNNEMWHS DIAFEPA PADYTS LRLVELPSTGGDTLWASGY
190

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM-----DTTATPLR--
195

YD L A + + +A + Q V + S + Y D LR
Sbjct: 191 DVYDHLSPAYQKFLEGLTA----TFEQPNFAKVAER-SGFELYDKPRGSPDNV GRELRAI
245

Query: 196 -PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWA-AG
251

P+V+ +P TG S+ IG H I + A ES+ L+ D + + +W
Sbjct: 246 HPVVRTNPVTGWKSVFPIGAHVGHINDVTAEESDNLKWFYDLVAKDHSIQVRLRWENPN
305

Query: 252 DVVVWDNRCLLHRA 265

D+ +WDNR + H A

Sbjct: 306 DIAIWDNRSVFHSA 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 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQS---KLGHVQQAGSAYIGYGMDDTAT
192

T F DM AY+AL + + V R A H + +++ + + Y T
Sbjct: 1 TEFCDMYLAYEALPDDLKRAVAGRRRAIHHISKTRNPRVTISPDRPGAKEYYEARARETRE 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 GDLVMWDNRCV 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-DGEALPGITVIWQDYAREFFGLPLTFKNSIGGNSQWHTDLVHEFQPAGITH
238

Query: 124 FSAEVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSA----RHSLVYSQSKLG---HVQ
176

+ +P VGG T +A AAYD L A + + ++A HS + ++ L H++
Sbjct: 239 LYNDTIPEVGGDTVWASGYAAYDKLSPAFQKFLDGKTAIYRSAHSYLDRENPLNGPKHIE
298

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSELLIGRHAHA-IPGMDAAESERFLEGLVD
235

+ PLV+ HP TG L + R I G+ ESE LE L
Sbjct: 299 RE-----HPLVRTHPATGWKYL FVNRSMTVRIVGLQPKSESEVILEYLF
342

Query: 236 WACQAPRVHAH-QWAA----GDVVVWDNRCLLHRAEPWD 269

+ + W + G +WDNR H A WD
Sbjct: 343 LFERNLDIQVRWNWKS KPGYGTSAIWDNRISQHNAV-WD 380

>ref|XP_001906307.1| unnamed protein product [Podospora anserina]
emb|CAP66973.1| unnamed protein product [Podospora anserina]
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-LSNDQOI 58
+ +TP +G + V L L D L Q ++ F Q L++D Q
Sbjct: 108 SFDVTPV---IGREYSNVDLVKLLRAPNSDELLRDLAITISQRGVVFFRKQEGLTDDLQK
164

Query: 59 TFAKRFG-----AIERIGGGD--IVAISNVKADGTVRQHSPAEWDDM 98
+R G A GG D I IS+ +A + W+
Sbjct: 165 ELVQRLGQLSGKPETSGLHIHPISNAAREHGGKDD EISVISSEQAKKLYADRFASAWNGG
224

Query: 99 MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ
158
G WH+D T+ P+ + A+ +P GG T +A YD + R +
Sbjct: 225 RHRQSGKGQWHS DITFEPIPSDYALLKLTQLPKTGGDTLWASGYELYDRISP KLRGFLDT
284

Query: 159 RSARHS---LVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSELL-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-LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMM 99
 Q ++ F Q L ND Q +R G + + I V G R+HS DD +
 Sbjct: 79 QRGVFFFRKQDSLNDLQKELVQRLGELSGKPKSTSLGLHIHPVANS--REHSVK--DDEI
 134

Query: 100 KVI-----VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR
 142
 VI WH+D T+ P+ + + +P GG T +A
 Sbjct: 135 SVISSASREKLYKDRNTRKQTSRREWHSDITFEPIPSDYTLRLTELPKTGGDTLWASGY
 194

Query: 143 AAYDALDEATR LVHQRSARHSLVYSQSKLGHVQAGSAYIGYG----MDTTATPLR---
 195
 YD + + + + +A Y+Q V + I G + LR
 Sbjct: 195 EVYDRISQPYQKFLEGLTA----TYAQP GFNEVAKRNDFTIHPGPRGAPENVGEEELRAEH
 250

Query: 196 PLVKVHPETGRPSLL-IGRHAIIPGMDAAESERFLEGLVDWACQAPRVHA-HQWA-AGD
 252
 P+++ +P TG S+ +G H + G+ ES R L+ V + + ++W D
 Sbjct: 251 PVIRTNPVTGWKSVFAVGTHVQKVN GVSEEE SRRLLDW FVSLIVENHDLQVRNRWQNPND
 310

Query: 253 VVVWDRCLLHRAEPWDF 270
 + +WDR + H A WD+
 Sbjct: 311 LAIWDNRSVYH-AATWDY 327

>ref|XP_001816593.1| hypothetical protein [Aspergillus oryzae RIB40]
 dbj|BAE54591.1| unnamed protein product [Aspergillus oryzae]
 Length = 420

Score = 63.9 bits (154), Expect = 2e-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 IGTEIVGLQLKDLTDQQKDELGLLIAERSVVFFRDQDLSPQQQKALGEYFGEVEVHPQVP
 177

Query: 69 RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV
 128
 ++ G V++ T R S + G WH D + A +
 Sbjct: 178 QVPLPGVSVLWPALQATERAAS-----YRRPGGASRWHTDLVHERQPAGVTHLHND
 230

Query: 129 VPAVGGRTCFADMRAAYDALDEATR LVHQRSA--RHS LVYSQSKLGHVQAGSAYIGYG
 186
 VP +GG T +A AAY+ L R ++ R+A R + Y K +AG YI
 Sbjct: 231 VPTIGGDTLWASGYAAAYEKLSPEFRKIIDGRTAIYRSAHPYLDK---DPEAGPKYIERE
 287

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHA
245

 P+V+VHP TG +L + R I G+D AES+ L L D + +
Sbjct: 288 -----HPIVVRVHPATGWKALWVNRAMTDRIVGLDKAESDVILGYLFDVYEKNIDIQV
339

Query: 246 H-QWAAGDVVVWDNRCL 261

 +W +WDNR +
Sbjct: 340 RFKWTPRTSALWDNRCLV 356

>ref|XP_002383506.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Aspergillus

flavus NRRL3357]

gb|EED47326.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Aspergillus

flavus NRRL3357]

Length = 395

Score = 63.9 bits (154), Expect = 2e-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: 93 IGTEIVGLQLKDLTDQQKDELGLLIAERSVVFVRDQDLSPQQKALGEYFGEVEVHPQVP
152

Query: 69 RIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV
128

++ G V++ T R S + G WH D + A +

Sbjct: 153 QVPGLPGVSVLWPALQATERAAS-----YRRPGGASRWHTDLVHERQPAGVTHLHND
205

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSA--RHSLVYSQSKLGHVQQAGSAYIGYG
186

VP +GG T +A AAY+ L R ++ R+A R + Y K +AG YI

Sbjct: 206 VPTIGGDTLWASGYAAAYEKLSPFRKIIDGRTAIYRSAHPYLDRK---DPEAGPKYIERE
262

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHA
245

 P+V+VHP TG +L + R I G+D AES+ L L D + +
Sbjct: 263 -----HPIVVRVHPATGWKALWVNRAMTDRIVGLDKAESDVILGYLFDVYEKNIDIQV
314

Query: 246 H-QWAAGDVVVWDNRCL 261

 +W +WDNR +
Sbjct: 315 RFKWTPRTSALWDNRCLV 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 = 2e-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 SIRIRPLQPTIGAEVEGVVLSRPLAPAQRDAIRAAVLRHKVVFFRDQALDNESQAAFAAQ 73

Query: 57 -----QITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAW
 108

T R I R I 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 HSDTSWRLVPTWGAVLRAVTLPEVGGDTIWVDANLAYEGLSAELKERLEGLHVTHDFREA
 177

Query: 169 QSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESE
 227

+ GH Y + P+V+ H ETG+ L + I G++ AES
 Sbjct: 178 LAASGH-----DYPIVA-----HPVVRAHRETGQKILWVNLTKPQILGVELAESR
 223

Query: 228 RFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPET
 287

L+ ++ + W G V WDNR +H A PR + +A P
 Sbjct: 224 ALLDEVLRQYKRPEFQVRFVSWRPGSVAFWDNRAAVHYAVRNYGDFPRHLERVLIADDEPLY
 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 = 2e-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 ATFFHDEARRLGNPLREGIRGSPLNSGPSLTTVHPVIRTNPVTGWKSVFVNKGFTKRING
272

Query: 221 MDAAESERFLEGLVDWACQAPRVHA-HQWAAGDVVVWDNRCLLHRAEPWDFKLPRV 275
+ ES+ L+ L + Q ++W DV +WDNR H A +D+ R+

Sbjct: 273 VTKDESDILLQYLFNLVLTQNHDAQVRYKWNKNDVAIWDNRSNWHCAT-YDYDETRI 327

>ref|XP_001593138.1| hypothetical protein SS1G_06060 [Sclerotinia
sclerotiorum 1980]

gb|EDO03579.1| hypothetical protein SS1G_06060 [Sclerotinia sclerotiorum
1980]

Length = 389

Score = 63.5 bits (153), Expect = 2e-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 GASRWHSDLVHELHPAGLTHLHNDTVPEVGGDTLWASGYAAYSKLSPEFRKFINGKQAIY
254

Query: 164 SLVYSQSKLGHVQ-QAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGM
221

V + + L AG +I + P+V+VHP TG +L + R +I G+

Sbjct: 255 --VSTHTYLDRDDPSAGPKHIER-----VHPIVRVHPVTGWKTLWVNRSMTKSIVGL
304

Query: 222 DAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFK 271
D AES+ L L D + + +W AG +WDNR +H A WD++

Sbjct: 305 DKAESDLILGYLYDVFEKNVDIQVRFRTAGTSAIWDNRSTIHNAS-WDYE 354

>ref|XP_001593310.1| hypothetical protein SS1G_06232 [Sclerotinia
sclerotiorum 1980]

gb|EDO03751.1| hypothetical protein SS1G_06232 [Sclerotinia sclerotiorum
1980]

Length = 393

Score = 63.5 bits (153), Expect = 2e-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 SIGTELVGIQLTSLDDTQKNELARLVAERGVVFLRDQKMDVHEQIEFGSYFGELH-----
179

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF-SAEVVPA-
131

I + + + D + P D+ K + WH+D +Y + G F + +P
Sbjct: 180 -IHQMAGIIPD--LPWVHPIHKDETAKNGRSHQIWHSDVSYE-IQPPGLTFLRMDTLPKA
235

Query: 132 -----VGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
185

GG T +A Y++L + ++ A+HS ++QA A G
Sbjct: 236 GPDGYEAGGDTIWASGYGIYESLSP TLKGILETLEAKHS-----GLEQA EKALKGN
286

Query: 186 GM--DTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAPR
242

G + P+V+ HP TG+ +L + + I G++ SE L+ L +A
Sbjct: 287 GCLRRNPIETIHPVVRTHPVTGQKTLVYVNFNFTKEIVGVEKRFSESLDFLNRTVAEAYE
346

Query: 243 VHAH-QWAAGDVVVW DNRCLLH 263

+W+ V +W DNR 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 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

PLV+ H +GR L IG HA + G+ AE L L++ A Q V+ H+W GD+V+
Sbjct: 32 PLVRTHAGSGRKFLFIGAHASHVEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGD LVM 91

Query: 256 W DNRCL 261

W DNR C+
Sbjct: 92 W DNR CV 97

>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 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM DTTATPLR
195

T F DM AYD L E + + A H S++ G +++ T A
Sbjct: 1 TEFCDMYDAYDRLPEELKQIRIGMRAVHD--DSRTAAGGLRKGKGDVTDVRHVVTGAR--H 56

Query: 196 PLVKVHPETGRPSLLIGRHAHA-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---IGTEVKGIQLSALTSAGKDELARFIAERKVVAFRQQDFADLPIEEALKV
152

Query: 61 AKRFGA--IERIGGG-----DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADST
113

+ FG I G +I + D +V D ++AWH+D +
Sbjct: 153 GEYFGRHHIHPTSGSPEGFPEIHLVHRSAGDNSV-----DLFFANRTSSVAWHS
204

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
173

Y P GG T F D AY+ L + +H A HS
Sbjct: 205 YEQQPPGTTFLYILEKPEPETGGDTLFVDAVEAYNRLSPLFQERLHGLKATHS-----
255

Query: 174 HVQQAGSAYIGYGMDDTATPLR--PLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFL
230

++Q SA G+ + P+++ HP TG ++ + + I G+ ES+ L
Sbjct: 256 GIEQVNSAAARGGIKRREPVVNEHPIIRTHPATGEKAIYVNPQFTREIVGLKKEESDTLL
315

Query: 231 EGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

+ L D A +W VVVDNR H A
Sbjct: 316 KFLYDHLAYGADFQARIKWEEDTVVVVDNRVTQHSA 351

>ref|XP_001803696.1| hypothetical protein SNOG_13485 [Phaeosphaeria
nodorum SN15]

gb|EAT78932.2| hypothetical protein SNOG_13485 [Phaeosphaeria nodorum
SN15]

Length = 294

Query: 227 ERFL----EGLVDWACQAPRVHAHQ----WAAGDVVVWDNRCLLHRAEPWDFKLPVMMWH
278

+ + L+++ + P + +Q W + + +WDNR H A F R M
Sbjct: 235 ANEIHAAQQODLMNYLLRQPAILEYQMRLHWESNTIAMWDNRSTQHYAIQDYFFAVRRMHR
294

Query: 279 SRLAG 283

+ + G
Sbjct: 295 ATVVG 299

>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 = 4e-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 KITRITPKFGTEVDGIQLSQLNDAGKDELALLLAQRKVLFFNDQDFASHGPGFAVEFGKY
140

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
123
FG + I + + T R+ E + + + N WH+D TY ++ V
Sbjct: 141 FGPLH-IHPSSGSPKGGHPELHITYRRPEKGELERIFRERTTNTGWHSDVTYELTPSRFTV
199

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
183
F + GG T FAD AY L + A+ + H L S+ Q A S +
Sbjct: 200 FQV-LESGDGGDTV FADTAEAYRRL---SPAMQQRLEGLHVLHTSED-----QAANSTFQ
250

Query: 184 GYGMD--TTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVD 235
G G++ + + PL+++ P TG S+ + R I + ESE L L D
Sbjct: 251 G-GIERRKAVSNIHPLIRLDPVTGEKSIYVNRAFGRRIVELKKEESEYLLNFLYD 304

>emb|CAY27234.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 118

Score = 62.8 bits (151), Expect = 4e-08, Method: Compositional matrix
adjust.

Identities = 46/124 (37%), Positives = 60/124 (48%), Gaps = 6/124 (4%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
195

Sbjct: 1 T FADMRAAYDAL + +A + A HS+ +S+ LG + D +
TEFADMRAAYDALSDDEMKAIEDGLYAHHSIAHSRQTLGF-----EFSRDEEDRLKGAVH 54

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

Sbjct: 55 PLV+ P +G SL I HA I +S L L D A Q + H W GD+V+
PLVRTIPGSGWKSLEYIASHASRIVDQPIPDSSRLLLLDLRDHATQPRFRYRHSWRVGDLMV
114

Query: 256 WDNR 259

WDNR

Sbjct: 115 WDNR 118

>ref|XP_001836179.1| hypothetical protein CC1G_06264 [Coprinosia cinerea
okayama7#130]

gb|EAU85551.1| hypothetical protein CC1G_06264 [Coprinosia cinerea
okayama7#130]

Length = 405

Score = 62.8 bits (151), Expect = 4e-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 IGTEIEGIDLRQLTDEQKDELALLVAERGVVFFRDQEIDIYQLELAKHWGPLHRHATTP
153

Query: 70 IGGGDIVAIISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVS
129

Sbjct: 154 I + + V D + R+ P+ + + WH+D TY
ITKNGLEHVHVYNDAS-RRPDPSAFSKLE-----LWHSVTVYELQPPGPTSLKVITN
205

Query: 130 PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDT
189

Sbjct: 206 P VGG T ++ A Y +L + + SA HS V Q G+ G+
PEVGGDTIWSSGYALYSSLSPLGKYLEGLSAVHSAV-----AQADGNR--AAGLPV
255

Query: 190 TATPLR---PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHA
245

Sbjct: 256 P+ PLV+VHP TG S+ + I G+ AES+ L L + P
RREPIETVHPLVRVHPATGWKSVFVNPFGFTRRIIGIPKAESDAILTFLFRQISENPDFQV
315

Query: 246 H-QWAAGDVVVWDNRCLLHRAEPWDF 270

+W + +WDNR + H A +DF

Sbjct: 316 RFRWETNSIAIWDNRVVTHSAT-FDF 340

>ref|ZP_02189793.1| putative alpha-ketoglutarate-dependent taurine
dioxxygenase

oxidoreductase protein [alpha proteobacterium BAL199]

gb|EDP63398.1| putative alpha-ketoglutarate-dependent taurine dioxxygenase

oxidoreductase protein [alpha proteobacterium BAL199]

Length = 338

Score = 62.4 bits (150), Expect = 5e-08, Method: Compositional matrix
adjust.

Identities = 73/284 (25%), Positives = 111/284 (39%), Gaps = 51/284 (17%)

Query: 42 HALLIFPGQHLSNDQQ---ITFAKRFGAIERIGGGDIVAISNVKADGTV----- 87
H LLI G H +DQ + ++ FG + + +N+ AD

Sbjct: 52 HGLLILKGMHAISDQPELLVRLSRLFGPEVEDYRQTVTSRNNIHADVPEILVVSINVPPAT
111

Query: 88 -----RQHSPAEWDDMMKV-IVGNMAWHADSTYMPVMAQGAVFSAEV-VPAVGGRTCFAD
140

R P D + V WH D +Y ++F A++ P G+T +AD

Sbjct: 112 PRVPERPDPLTADGKLPVQFPHRRGWHTDQSYRRPPDISLFYADLPTPKGQGQTLYAD
171

Query: 141 MRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPL-----
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 AYAHDWDRGDLVIYDNRSTIHSATWFDADTHRRRMWRTTVHGPN 324

>emb|CBI56031.1| unnamed protein product [Sordaria macrospora]
Length = 380

Score = 62.4 bits (150), Expect = 5e-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---LGREYVNVLDSELLRAPNSDELLRDLAITISQRGVVFFRKQDNLTDLQK
118

Query: 59 TFAKRFGAI---ERIGGGDIVAISNVKADGTVRQHSPAED-DMMKVIVGNMA----WHA
110

R G + G I ISN R+H + + + V G + WH+

>gb|ABD39112.1| alpha-ketoglutarate dioxygenase [uncultured bacterium]
Length = 119

Score = 62.4 bits (150), Expect = 6e-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 PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDLMV
112

Query: 256 WDNRCV 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 = 6e-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 LSSVPFEISYPAQSFQVEIENLKLHKNLSFDTIAAIKKCLAYRGFVLFVFNQNLTRREQIA 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 IWDEKDNHTKGGTSCWHTGDSEAINVETINCLY-AELAAAQGGATLFCDTVAAAYNDLED
183

Query: 151 ATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLL
210

+ + + H V Q T +PLVK +P T + L
Sbjct: 184 SLKKRIDNLRVVHYFVDPQR-----TEPVSQPLVKTNPITRQKYL
224

Query: 211 IGRHA-HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264

+ + + G+ +ES R L+ L D + V+ H W D ++W+ +H+
Sbjct: 225 LNYNTMERVEGLSKSESYRLLKFLFDHQIKDQYVYEHFWKQDDFLIWCNGTMMHK 279

>gb|ABD39116.1| alpha-ketoglutarate dioxygenase [uncultured bacterium]
Length = 107

Score = 62.4 bits (150), Expect = 6e-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 PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDLMV
100

Query: 256 WDNRC 260

WDNRC

Sbjct: 101 WDNRC 105

>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 = 7e-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 LSSVPFEISYPAQSFQVEIENLKLHKNLSFDTIAAIKKCLAYRGFVLFNRNQLTRREQVA 64

Query: 60 FAKRFG-----AIERIGGGDIVAISN-----VKADGTVRQHS 91
+ G IE GD I N D T +H+

Sbjct: 65 VTRLLGNPNLKSHSWAPQIETTTFGDDEVIPNGLPLINHGEILYFVNGPDFCDKTQDEHA
124

Query: 92 PAEWDDMMKVIVGNMAWHA-DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDE
150

+ D G WH DS + V ++ AE+ A GG T F D AAY+ L++
Sbjct: 125 IWDEKDNHTKGGTSCWHTGDSEAINVETINCLY-AELAAAQGGATLFCDTVAAYNDLED
183

Query: 151 ATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLL
210

+ + + H V Q T +PLVK +P T + L
Sbjct: 184 SLKKRIDNLRVLHYFVDPQR-----TEPVNQPLVKTNPITRQKYL
224

Query: 211 IGRHA-HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR 264
+ + + G+ +ES R L+ L D + V+ H W D ++W+ +H+

Sbjct: 225 LNYNTMERVEGLSKSESYRLLKFLFDHQIKDQYVYEHFWKQDDFLIWNCGTMMHK 279

>ref|XP_001409620.1| hypothetical protein MGG_12505 [Magnaporthe grisea 70-15]

gb|EDK01381.1| hypothetical protein MGG_12505 [Magnaporthe grisea 70-15]
Length = 371

Score = 62.0 bits (149), Expect = 7e-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 QRGVVFRAQDNLTNDLQKKLILRLGELTGRPKTSLGLHIHPLLNAERETYGGDDNEISTI
140

Query: 79 SNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCF
138

S+ + D ++ + + D++ WH+D + PV A +P GG T +

Sbjct: 141 SSAQNDKLYKK-TWTQPDELSPPKQSTAQWHSDIAPFVPADYTSRLRLTELPKTGGDTLW
199

Query: 139 ADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM-----DTT
190

A YD + + + S+ ++Q + + A G+ + +

Sbjct: 200 ASGYEYDKISAPYQKFLETL----SVTFAQKRFNEIADAN----GFSLYSQPRGAPENV
251

Query: 191 ATPLR---PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH
246

T LR PLV+ +P TG S+ +G H + G+ ES+ L+ +D + +

Sbjct: 252 GTDLRAVHPLVRTNPVTGWKSIFPVGGHVQHVNGLTDEESDGLLKWYLDLVYRNHELQTR
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 = 7e-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 IGTEIVGLQLKDLTDQQKDELGLLIAERSVVFRRDQDISPQEQQKLGWEYGEIEVHPQAA
 152

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVG
 133

+ + V Q + E + G WH D + A + VP++G
 Sbjct: 153 QVPGVPGVTVMWPALQAT--EIPASFRPPGGASRWHTDLVHERQPAGVTHLHNDTVPSIG
 210

Query: 134 GRTCFAADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATP
 193

G T +A AAY+ L A R ++ R+A + + +AG Y+
 Sbjct: 211 GDTLWASGYAAYEKLSPAFRKIIDGRTAVYRSAHPYLDRND-PEAGPKYVERE-----
 262

Query: 194 LRPLVKVHPETGRPSELLIGRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAG
 251

PLV+VHP TG +L + R I G+D AES+ L L D + + +W
 Sbjct: 263 -HPLVRVHPATGWKALWVNRAMTVRIVGLDKAESDLILGYLYDVFEKNVDIQVRFKWT
 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 = 7e-08, Method: Compositional matrix
 adjust.

Identities = 30/65 (46%), Positives = 37/65 (56%)

Query: 196 PLVKVHPETGRPSELLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
 255

PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+
 Sbjct: 40 PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGD
 LVM 99

Query: 256 WDNRC 260

WDNRC
 Sbjct: 100 WDNRC 104

>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 = 8e-08, 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 IGTEIVGLQLADLNDKQKDELALLIAERVVFFRDQDLSPQKQLELGKYWGQVEV--HAQ
 179

Query: 75 IVAISNVKADGTVRQHSPAEWDDMMK-----VIVGNMAWHADSTYMPVMAQGAV
 123
 + + + K DG W D + I G WH D + A
 Sbjct: 180 VPRVPDTK-DGEALPGITVIWQDYAREFYGIPLTYKNSIGGTAQWHTDLVHEFQFAGITH
 238

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA----RHSLVYSQSKLG---HVQ
 176
 + +P VGG T +A AAYD L A + + ++A HS + ++ L H++
 Sbjct: 239 LHNDTIPEVGGDTVWASGYAAYDKLSPAFQKFLDGKTAIYRSAHSYLDRENPLNGPKHIE
 298

Query: 177 QAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVD
 235
 + PLV+ HP TG L + R I G+ ESE LE L
 Sbjct: 299 RE-----HPLVRTHPATGWKYL FVN RAMTVRIVGLQPKESELILEYLF
 342

Query: 236 WACQAPRVHAH-QWAA----GDVVVWDNRCLLHRAEPWD 269
 + + W + G +WDNR H A WD
 Sbjct: 343 LFERNLDIQVRWNWKS KPGYGTSAIWDNRISQHNAV-WD 380

>gb|ABD39115.1| alpha-ketoglutarate dioxygenase [uncultured bacterium]
 Length = 91

Score = 62.0 bits (149), 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: 25 PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDVLM 84

Query: 256 WDNRC 260
 WDNRC
 Sbjct: 85 WDNRC 89

>ref|XP_001397508.1| hypothetical protein An16g01950 [Aspergillus niger]
 emb|CAK42812.1| unnamed protein product [Aspergillus niger]
 Length = 376

Score = 62.0 bits (149), Expect = 8e-08, 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---IGTEVRGVQLSLSKEGKDQLALYVAQRKVVAFRDQDFAHLPIEKALEFGGYF
 159

Query: 65 GA--IERIGGGDI-----VAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
 118

G I + G + + + AD S AE+ + + WH+D T+
 Sbjct: 160 GRHHIHQTSGAPKGFPEIHLVHRGAD----DRSGAEF---LSQRTNTITWHS DVTFEKQP
 212

Query: 119 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQA
 178

P+ GG T FADM AY L R +H A HS + ++ +
 Sbjct: 213 PGTTFLYILDGPSSGGDTLFADMAQAYRRLSPEFRKRLHGLKAVHSGI---EQVNNSLNK
 269

Query: 179 GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWAC
 238

G G T P+V+ HP L I G ES+ L+ L D
 Sbjct: 270 G----GIARRDPITSEHPIVRTHP-----TLTETVTRYIVGYKKEESDYLLKFLYDHIA
 319

Query: 239 QAPRVHAH-QWAAGDVVWDNRCLLHRA 265

+ + +W G VVWDNR + H A
 Sbjct: 320 LSQDLQTRVRWRPQTVVWDNRVVTHSA 347

>gb|ABD39111.1| alpha-ketoglutarate dioxygenase [uncultured bacterium]
 Length = 104

Score = 61.6 bits (148), Expect = 9e-08, Method: Compositional matrix
 adjust.

Identities = 30/65 (46%), Positives = 37/65 (56%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
 255

PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+
 Sbjct: 39 PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGD LVM 98

Query: 256 WDNRC 260

WDNRC
 Sbjct: 99 WDNRC 103

>ref|XP_454600.1| unnamed protein product [Kluyveromyces lactis]

emb|CAG99687.1| KLLA0E14433p [Kluyveromyces lactis]

Length = 382

Score = 61.6 bits (148), Expect = 9e-08, 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 VEISPITPKLGEIRGLQLSELNAGKDELALLTAERGVLI FRDQDFVD-----RGPG
132

Query: 66 AIERIGG--GDI-----VAISNVKADGTVRQHSPAEDDMMKVIVGNMA
107

IE G G++ V NVK + ++D + + ++
Sbjct: 133 YIEEYGYKFGELHVHASPAPGHPYIHVVYKVNKTE-----DYDKFFEQTLSVY
183

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL--
165

+H D T+ + F+ P GG T F D +D L + + + A H+L
Sbjct: 184 FHTDITFELQPSGYTFFAVLDAPQSGGDTLFGDAIEIFDRLSPSLQEYLSGLHAVHALPP
243

Query: 166 ---VYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGM
221

+S + S + Y + + P+V+VHP + L I + I +
Sbjct: 244 NGDAFSPDPTKRI----SRHEIYDV-----IHPVVRVHPVLKKKVLNINKVFTRKIVEL
293

Query: 222 DAAESE---RFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLLHRAEPWDFKLPRVMWH
278

ES+ FL ++D A A +V A+ W G VVWDNR L H A +DF H
Sbjct: 294 KKPESDALLAFLYQVIDNAHDA-QVRAN-WKPGTVVWDNRRLYH-AGVYDFDASESTRH
350

Query: 279 ----SRLAGRP 285
+ LA RP

Sbjct: 351 HVRVTPLAERP 361

>ref|XP_001584962.1| hypothetical protein SS1G_14059 [Sclerotinia sclerotiorum 1980]
gb|EDN99199.1| hypothetical protein SS1G_14059 [Sclerotinia sclerotiorum 1980]

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 -----GDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
127

GD+ + V D + D + WH+D TY + + S +
Sbjct: 160 SVPKRGDLDDVHVYTDENSK-----DQRALFTPTFLWHSVDTYE--IQPPSYTSLK
209

Query: 121 GAVFSAEVVPAVGGR---TCFADMRAAYDALDEATRALVHQRSARHS-LVYSQSKLGHVQ
176

 FS + A+ G T F D+ +++L A + V + HS Y + + V
Sbjct: 106 PFAFSMTLPLAMPGHDRGTHFIDLSQVWESLPNAMKDSVRGTYSNHSPRRYIKIRPSDVY
165

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPG-----MDAAESERFL
230

 + + + T P V HP+TG+ L I A +D + L
Sbjct: 166 RPVGEVLAEIEEVTPFPQKWPTVIKHPKTGQEILYICEAATVSVEDKNGNLLDPMVLQELL
225

Query: 231 --EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE 266

 G +D C++ +H + GDVV+WDNR L+HRA+
Sbjct: 226 TASGQLDPCKSLLIHTQHVEYGDVVLWDNRALVHRAK 263

>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 = 1e-07, Method: Compositional matrix
adjust.

Identities = 62/218 (28%), Positives = 89/218 (40%), Gaps = 48/218 (22%)

Query: 7 QITPTGATLGATVTGVHLAT-LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65

 ++ LGA + GV LA +DDA AL + ++ +L+ QHLS D + + F
Sbjct: 10 EVRQASPVLGAEIVGVDLANGVDDATAEALRDDFWKYKVLVLRDQHLSPDAHVEAVRIFD 69

Query: 66 A-----IERIGGGDIVAISNV-KADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
117

 + R +V + N+ KA G R H W + P
Sbjct: 70 EPFDHPKWLYRHEDNRLVYVFNLEKAGGAARWHIGGIWRNP-----PF
112

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
177

 + + +VVP +GGRT +AD++AAVD L E R L+ SA VYS
Sbjct: 113 TIESLTY--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| hypothetical protein An11g00600 [Aspergillus niger]
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 IGTEVHGVNLAKLNDAQKDDLARLVAVRGVVFVRGQDDLIDIDAQRELGRHFGKLGKHA--
152

Query: 74 DIVAISNVKADGTVRQHSAPAEWD---DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVP
130

S K +G H D D + + WH+D TY P
Sbjct: 153 ---TTSVPKREGLEDVHVVTGDNSTDQRAMFTPSFLWHSVITYEVQPPSYTSLKVLTP
209

Query: 131 AVGG--RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
188

GG T + AAYDAL + + +A HS +Q + S +G +
Sbjct: 210 PRGGGGDTLWTSQYAAAYDALSPHMQTYLKGLTALHS-----ADMQASDSHALGRPVR
261

Query: 189 -TTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH
246

T PL++ +P TG SL I G+ ES+ + L + +HA
Sbjct: 262 RDPVTTEHPLIRTNPVTGWNLSFFNPGFVTKIVGIPKTESDAIIRYLTEVIATTQEMHAR
321

Query: 247 -QWAAGDVVVWDNRCLLHRA 265

QW DV +WDNR H A
Sbjct: 322 FQWNKNDVAIWDNRRTTNHSA 341

>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 VGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTA
191

GG T FA+M A + L A + + Q +A H G + G
Sbjct: 1 TGGDTLAFANMHLAIEMLSPAMQQFLGQLTAIHD-----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 APNTLVFWDNRCTQHHAHV-WDY-FPHSRYGERTVILGGRP 145

>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 IEWHS DITFEPIPSDY TSLRLTVLPKTGGDTLWASGYEVYDRISPPYQKFLEGLTA----
213

Query: 166 VYSQSKLGHVQQAGSAYIGYG----MDTTATPLR---PLVKVHPETGRPSLL-IGRHAHA
217

Y+Q K V + + + G + LR P+++ +P TG S+ +G H
Sbjct: 214 TYAQPKEEVARDKNFELHPGPRGAPENVGNILRAVHPVIRTNPVTGWKSVFAVGTHCQK
273

Query: 218 IPGMDAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVWDNRCLLHRAEPWDF 270

+ G+ ES L+ VD + + +W D+ +WDNR + H A WD
Sbjct: 274 VNGLSQEESHLLKWFVDLIVENHDLQVRFRWQNPNDIAIWDNRSVYH-AATWDI 327

>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 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLR-PLVKVHPE
203

YD L E + + A H ++S+ LG + + S P+ PLV+ H
Sbjct: 9 YDDLPEDFKKELAGMRAEHYALHSR FILGDTEYSES-----QRNAMPPVSWPLVRTHAG 62

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNR 259

+GR L IG HA I G AE L L++ A Q V+ H W GD+V+WDNR
Sbjct: 63 SGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQPKFVYRHSWNVGDLMWDNR 118

>ref|XP_459311.1| hypothetical protein DEHA0D20493g [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 GWHSDITFEPVTSYAVLKVIVESTPTGGDTLWASGYALYEKLTPTFRSYLETTLTG----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 GLSDSESALIKDYLSSELLYGSHDIQVRFWRWKNKDVAIWDNRSVYHTA 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 = 2e-07, Method: Compositional matrix adjust.

Identities = 62/253 (24%), Positives = 98/253 (38%), Gaps = 36/253 (14%)

Query: 41 QHALLIFPGQH-LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMM 99

 Q ++ F Q L ND Q +R G + + I V G R+H DD +
Sbjct: 81 QRGVVFVRKQDDLDNDSQKELIQRLGQLAGKPATSGLHIHPVTNAG--REHGGK--DDEI
136

Query: 100 KVIVGNM-----AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR
142

 VI WH+D T+ PV + AV +P GG T +A
Sbjct: 137 SVISSEQRKKLYKGRYVSGQSLKGGWHSITFEPVPSDYAVLRLTKLPKTGGDTLWASGY
196

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG----MDTTATPLR---
195

 +D + E + + +A Y+Q + + + G + T LR
Sbjct: 197 EVFDRISEPYQRFLESLAA----TYAQPFGFNQSAKDNNFELYSGPRGAPENVGTELRAEH
252

gb|EAU91105.1| hypothetical protein CC1G_03273 [Coprinopsis cinerea
okayama7#130]

Length = 358

Score = 60.5 bits (145), Expect = 2e-07, Method: Compositional matrix
adjust.

Identities = 68/271 (25%), Positives = 100/271 (36%), Gaps = 32/271 (11%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFAKRFGAIER-- 69
+G ++GV L+ L G L Q +LI Q + ++ I FG I
Sbjct: 82 IGTELSGVQLSOLSKEGLDELALLAAQRKVLILRDQDFQDLPAEKLIELTSFHGPIHSH
141

Query: 70 -----IGGGDIVAISNVKADGTVRQHSPAEDMMKVIVGNMAWHADSTYMPVMAQGA
124
G + V I ++ G ++ + + WH+D +Y F
Sbjct: 142 TAPNVKGFTEFVNI--LREPGYTSKYFASRTASSTNYVY----WHSVSYERQPPSTTF
195

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSAHSLVYSQSKLGHVQQAGSAYIG
184
P VGG T F AY+ L + + +A HS V + Y G
Sbjct: 196 WLLDKPDVGGDTLFLSTVEAYNRLSPEFKRLEGLTALHSGVAQADE-----SRKYGG
248

Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIG----RHAHAIPGMDAAESERFLEGLVDWACQA
240
+ P+V+VHP TG +L + RH I G ES+ L+ L D +
Sbjct: 249 VVRRDPVESIHPVVRVHPVTGEKALFVNPEFTRH---IVGFKKEESDALLKFLYDHIAG
305

Query: 241 PRVHAH-QWAAGDVVWDNRCLLHRAEPWDF 270
+ G VV+WDNR H A P DF
Sbjct: 306 ADFQVRANYLPGTVVIWDNRVTNHSAPV-DF 335

>ref|NP_983695.1| ACR293Cp [Ashbya gossypii ATCC 10895]
gb|AAS51519.1| ACR293Cp [Ashbya gossypii ATCC 10895]
Length = 386

Score = 60.5 bits (145), Expect = 2e-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 NVQISKITPRFGSEVRGLQLSSSLDAAGKDELALLASQRGVLFVFRDQDFASKGPGYF-EQY
141

Query: 65 GAIERIGGGDIVAISNVKADG-----TVRQHSPAEDMMKVIVGNMAWHADSTYMPVMA
119
G+ G + S A T R+ E++ + + ++ +H+D +Y
Sbjct: 142 GS--HFGKLVHQTSGAPAGHPYLHVTFRRPDRKEFERVFRDHHSSIRFHSVSYELQPP
199

+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 FAQTRLP-VTAAEKGFKLYSEPRGSPNNIGTSLSAVHPVVRTNPVTGWKSLFAVGNHVVK
 269

Query: 218 IPGMDAAESER----FLEGLVDWACQAPRVHAHQWAAG-DVVVWDNRCLLHRA 265

 I + A ES R FL+ +V+ R H+W D+ +WDR + H A
 Sbjct: 270 INEVTADESRRLHDWFLQMIVEEHDTQLR---HRWQNPYDIAIWDNRVYHSA 319

>ref|ZP_03156695.1| Taurine catabolism dioxygenase TauD/TfdA [Cyanotheca
 sp. PCC 7822]

gb|EDX95434.1| Taurine catabolism dioxygenase TauD/TfdA [Cyanotheca sp.
 PCC 7822]

Length = 283

Score = 60.5 bits (145), Expect = 2e-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 LTQEVVVGKFAVWVHHDKDHLPKTEGLDMNALYVVMPLYGVEIPAEGIDGEPHTTFLDMME
 154

Query: 144 AYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPE
 203

 AY L+ R + ++S H S + L P+V H
 Sbjct: 155 AYQNLERQHRQOLEKQSMYHL-----SPITPPPGEDI PRKLHPIVSTHKI
 199

Query: 204 TGRPSLLIGRHAHAIPGMD--AAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL
 261

 TGR L +G + G++ E++ + L V+AH W GD+V WDN +
 Sbjct: 200 TGRKGLYLGSSTSILQGLEDKPQEAQLYWNDFATILDCTPVYAHIQPGDIVFWDNSQV
 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 = 2e-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 KVTDLTTHIGTEIEGLQLKDLTPEQRDELALLIAERSVVFVRNQQDITPQQQKELGEWFG
 144

Query: 67 IE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
 117

+E + G ++ D P G +WH D +
 Sbjct: 145 VEIHPQVPQVPGVAGVTVIWPDLFAQDNAASFRKPG-----GASSWHTDLVHERQ
 194

Query: 118 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
 177

A + VP VGG T +A AY+ L R L+ + A + +S +
 Sbjct: 195 PAGVTHLHNDTVPPVGGDTLWASGYGAYEKLSPEFRKLIDGKQAVYRSAHSYLDREN-PT
 253

Query: 178 AGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDW
 236

AG +I PLV+VHP TG +L + R I G+D AES+ L L D
 Sbjct: 254 AGPKHIER-----THPLVRVHPATGWKALWVNRAMTVRIVGLDKAESDLILNYLYDV
 305

Query: 237 ACQAPRVHAH-QWAAGDVVVDNRC 260

++ + +W G +WDNR
 Sbjct: 306 FERSVDIQVRFKWTGTSALWDNRS 330

>emb|CAY25737.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 60.1 bits (144), Expect = 2e-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 IEAGMDKYAVLLFRDQDVSDQQLVFNFRNFRGERENARGGTVTKKEDYRLTSGLNDSVNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPV 129

DG PA +GN WH+DS++ P+ A+ ++ SA VV
 Sbjct: 76 KDG NPLPRDPA----THLFLNGLGNCLWHS DSSFRPIPAKFSLLSARVV 118

>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 IEASMDKYAVLLFRDQDVSDQQLVFNARNGERENARGGTVTKKEDYRLTSGLNVDVSNLD 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
 DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
 Sbjct: 76 KDG-----NPLPRDPRTHLFLNGLNCLWHSDDSSFRPIPAKFSLLSARVV 118

>ref|XP_001943646.1| PREDICTED: hypothetical protein [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 LGCEVRGVLDKTENRPEIIKQIQEDVTKHRILIFKDQGI VSGDRHVEISRWFGELESTFY 67

Query: 69 ---RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
 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 MESVPK-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--APRVHAHQWAAGDVVVDNRCLLHRA 265
 Q ++ H+W GD ++ DN + H A
 Sbjct: 209 KINQDNGKYIYVHKWEPGDFIISDNLAVGHFA 240

>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 = 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 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 INEVTADESRRLHDWFLQMIVEEHDTQLR---HRWQNPYDIAIWDNRTVYHSA 319

>dbj|BAD15034.1| hypothetical protein [Bradyrhizobium elkanii USDA 94]
Length = 102

Score = 60.1 bits (144), Expect = 3e-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 ALDDETKAIELEDMICEHSLMYSRGS LGFLD-----YTDEEKQMFKPVLRQRLVTRTHPAHGR 55

Query: 207 PSLLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

SL + HA AI GM E+ L L + A Q V+ H+W D+

Sbjct: 56 KSLYLSSHAGAIRGMSPEARLLLLRDLTEHATQPEFVYVHKWTVHDL 102

>gb|EEY15355.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Verticillium

albo-atrum VaMs.102]

Length = 257

Score = 59.7 bits (143), Expect = 3e-07, Method: Compositional matrix
adjust.

Identities = 44/173 (25%), Positives = 73/173 (42%), Gaps = 6/173 (3%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
166

WH+D T+ PV + A+ +PA GG T +A YD L A + + +A H

Sbjct: 59 GWHSDITFEPVPSDYAMLKIHTLPATGGDTMWASGYEYDRLSPAMQVFLEGLTATHDAK
118

Query: 167 Y---SQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMD
222

+ +LG+ + G + P+++ +P TG S+ + R I G+

Query: 6 LQITPTGATLGATVTGVHLLA-TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 64
 +++ P +GA +TGV LA LDD A+ AA L+ ++ F GQ L + + FA+RF
 Sbjct: 33 IEVNPVAGHIGAEITGVDLAGDLDDRVRVGAIRAAVLRWKVVFFRQKLDHAGHVAFARRF 92

Query: 65 G---AIERIGGGDIVAISNVKAD-----GTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
 115

G + + G V+ G EW + + WH D
 Sbjct: 93 GEPVVLKRGASASPAQFPEVETTADRLELGEKFGMEHEEWLQRRRHTL-LRGWHCDHGAR
 151

Query: 116 PVMAQGAVFSAEYVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSL 165

+ AE VP GG T ++++ AAY L RA V H L
 Sbjct: 152 VDPPAATILRAETVPPYGGDTTWSNLAAAYAGLSAPVRAFDGLRVEHRL 201

>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]
 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]

Length = 289

Score = 59.7 bits (143), Expect = 4e-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 GEGLGAQVTGVDPKNLDDITDEIRDIVYTNKLVVLKDVHPSREFIKLGRIIGQI---- 62

Query: 72 GGDIVAI SNVKADGTVRQHSPA-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++ +

+ P+V+ +P TG S+ IG I G+ ES L+ D + +W +
 Sbjct: 176 -VHPVVRTNPITGWKSIFPIGSFPTQIDGLTRRESASMLQWFHDMITHGHDLQVRFKWN
 234

Query: 250 AGDVVVWDNRCLLHRA 265
 D+ +WDNR + H A

Sbjct: 235 PNDIAIWDNRSVFHTA 250

>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 = 4e-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 NVKVTDIQPRIGSVLEGVQLSQAALKDELALLVSEKRVVAFPNQDLIDAGPAAQAAFM
 144

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQ-----HSPAEWDDMMKVI---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 KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL-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 LDFLMQHIVSGHDFQARVRWQPKTIVIFDNRSTIHTSA 342

>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 = 4e-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 IGTEIHGVNLAKLDEAQKDDLARLVAVRGVVFVRDQKDLDDIDAQRELGRHFGRLHKHATT
 154

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVG
 133
 + ++ V +S D + + WH+D TY + P G
 Sbjct: 155 SVPRKQGLEDVHVV--YSGDNSGDQRALFTPSFLWHSVITYEVQPPSYTMLKVLTPGPPRG
 212

Query: 134 G--RTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD-TT
 190
 G T + AAYDAL + + +A HS +Q + S +G +
 Sbjct: 213 GGGDTLWTSQYAAAYDALSSHMQTYLKGLTAIHS-----ADMQASDSRALGRPVRREP
 264

Query: 191 ATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW
 248
 T PL++ +P TG SL I G+ ES+ ++ L D +HA QW
 Sbjct: 265 VTTEHPLIRTNPVTGWNSLFFNPGFVTKIVGIPKTESDAIKYLTDVIATTQEMHARFQW
 324

Query: 249 AAGDVVVWDNRCLLHRA 265
 D+ +WDNR H A
 Sbjct: 325 NKDDLAIWDNRRTTNHTA 341

>ref|YP_003039151.1| taurine dioxygenase, 2-oxoglutarate-dependent
 (taurine dioxygenase)
 [Photorhabdus asymbiotica]
 emb|CAR67294.1| taurine dioxygenase, 2-oxoglutarate-dependent (taurine
 dioxygenase)
 [Photorhabdus asymbiotica subsp. asymbiotica ATCC 43949]
 emb|CAQ82406.1| taurine dioxygenase, 2-oxoglutarate-dependent (taurine
 dioxygenase)
 [Photorhabdus asymbiotica]
 Length = 179

Score = 59.3 bits (142), Expect = 5e-07, Method: Compositional matrix
 adjust.

Identities = 51/179 (28%), Positives = 78/179 (43%), Gaps = 10/179 (5%)

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGS
 180

Sbjct: 2 GA+ +A+ VP GG T + AA++AL E + L+ A H V S + H + +
 GAILAAKKVPPFGGDTLWCSGIAAFEALSEPFFKKLLIGLEAEHDFVKSFPPEHRH-RGSEE 60

Query: 181 AYIGYGMDDTTATP--LRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWA
 237

Sbjct: 61 Y + + P L P+V+ HP + R +L + I G+ ESE L L
 EYQRWLVGKEKNPPLLHPVVRTHPVSDRLALFVNEGFTTRIVGLSDKESEAILNFLFVHI
 120

Query: 238 CQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAG-RP-----ETEGA 290
 + +W D+ +WDNR H A R+M + + G +P E EGA

Sbjct: 121 TKPEFQVRWRWQENDIAIWDNRVTQHYANADYLPQRRIMHRATILGDKPRYFGKENEGA 179

>ref|XP_001820775.1| hypothetical protein [Aspergillus oryzae RIB40]
 dbj|BAE58773.1| unnamed protein product [Aspergillus oryzae]
 Length = 396

Score = 59.3 bits (142), Expect = 5e-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 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVG
 133

Sbjct: 155 + ++ V +S D + + WH+D TY + P G
 SVPRKQGLEDVHVV--YSGDNSGDQRALFTPSFLWHS DVTYEVQPPSYTMLKVLGTGPPRG
 212

Query: 134 G--RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDD-TT
 190

Sbjct: 213 G T + AAYDAL + + +A HS +Q + S +G +
 GGGDTLWTSQYAAAYDALSSHMQTYLKGLTAIHS-----ADMQASDSRALGRPVRREP
 264

Query: 191 ATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQAPRVHAH-QW
 248

Sbjct: 265 T PL++ +P TG SL I G+ ES+ ++ L D +HA QW
 VTTEHPLIRTNPVGTGWSLFFNPGFVTKIVGIPKTESDAIKYLTVDVIATTQEMHARFQW
 324

Query: 249 AAGDVVVWDNRCLLHRA 265

Sbjct: 325 D+ +WDNR H A
 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 = 5e-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 IGTEIEGLQLKDLTPQQRDELALLIAERSVFFRNQDLTPQQQKELGEWFGEVEVHPQTP
152

Query: 69 RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV
128

++ G + ++ + D + PA + + G WH+D + A +
Sbjct: 153 QVPG--VPGVTVIWPDLEFTLER-PANF----RRPGGASNWHSDLVHERQPAGITHLHNDT
205

Query: 129 VPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
188

VP GG T +A +AY+ L R ++ + A VY + +Q +A Y
Sbjct: 206 VPPTGGDTLWASGYSAYEKLSPEFRKIIDGKYA----VYRSAHPYLDRQDPNAGPKYIER
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|CAY27326.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 59.3 bits (142), Expect = 5e-07, Method: Compositional matrix adjust.

Identities = 45/122 (36%), Positives = 56/122 (45%), Gaps = 15/122 (12%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T FADMRAAYDALDE + HS ++S+S LG + P+R
Sbjct: 1 TEFADMRAAYDALDEEIKTECENLICEHSQSFERSILGFTDFTDDERRRFA-----PVR 54

Query: 196 P-LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
254

LV+ HP TGR SL + HA AI G ++ FL L D HA V+
Sbjct: 55 QRLVRRHPVTGRRSLYLASHAGAILGCLEPKARAFLSYLND-----HATHRQFFFVI
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 = 5e-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 GDIVAISNVKADGTVRQH-----SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
126

I S +G +H D + ++ WH+D TY
Sbjct: 156 HHIHPTSGA-PEGYPQVHLVHRGTDDTSARDFFEERTNSITWHS DVTYEKQPPGTTFLYL
214

Query: 127 EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV----YSQSKLGHVQQAGSAY
182

PA GG T FA+ AAY+ L R +H HS V S+++ G V++
Sbjct: 215 LDGPAAGGDTL FANQAAAYNRLSPEFRKRLHGLKVVHSAVEQADNSKNRGGIVRR-----
269

Query: 183 IGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAP
241

T + PLV+ HP TG +L + + + I G ES+ L L D +
Sbjct: 270 -----DPVTSIHPLVRTHPATGEKALFVNPQFSRRIVGYKKEESDFLLNFLYDHIAKGQ
323

Query: 242 RVHAH-QWAAGDVV 254

A +WA G VV
Sbjct: 324 DFQARVKWAPGTVV 337

>emb|CAY25785.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 59.3 bits (142), Expect = 5e-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 IEAGMDKYAVLLFRDQDVSDQQLVFNARNGERENARGGTVTKKEDYRLTSGLN DVS NLD 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAE VV 129

DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLFNLGNCLWHS DSSFRPIPAKFSLLSARVV 118

>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 = 6e-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--DGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFAD
 140
 + H+ + D + WH+D + PV A +P GG T +A
 Sbjct: 144 SIQHRKFYNHTSEDDDDQLSPKKQYTAQWHSDI AFEPVPADYTSRLRVQLPKTGGDTLWAS
 203

Query: 141 MRAAYDALDEATR ALVHQRSA---RHSLVYSQSKLGH--VQQAGSAYIGYGMTTATPLR
 195
 YD + E + + + + + ++G ++ A G + A +
 Sbjct: 204 GYEIYDRISEPYQKFLEGLTVTFQQPGFNRTAERIGFKIYEKPRGAPENVGSELKA--VH
 261

Query: 196 PLVKVHPETGRPSLL-IGRHAHAI PGMDAAESERFLEGLVDWACQAPRVHAH-QWAA-GD
 252
 P+V+ +P TG S+ +G H + G+ ES+R LE ++ + + +W D
 Sbjct: 262 PVVRTNPVTGWKSVFPVGGHVQVNGVTKEESDRLLEWFLELLQKNHDLQVRFRWTGEND
 321

Query: 253 VVVWDNRCLLHRA 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 = 6e-07, Method: Compositional matrix
 adjust.

Identities = 50/170 (29%), Positives = 69/170 (40%), Gaps = 29/170 (17%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVY
 167
 WHAD TY P GG T + A YD+L E + + +A HS
 Sbjct: 176 WHADVTYEKQPPSYTSLKVLNPPPTGGDTLWTSNYAVYDSLSEPMQKYLESLTAIHS---
 232

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLR-----PLVKVHPETGRPSLLIGR-HAHAI
 218
 G Q A SA +G PLR P+++ HP TG S+ + A+

Sbjct: 233 -----GVAQAADSARVG-----QPLRRDPIETEHPVIRTHPVTGWKSVFLNPGFVTAL
280

Query: 219 PGMDAAESE---RFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
G+ +ES+ ++ LV A Q +W + DV WDNR H A

Sbjct: 281 RGIPTSESQAIMTYINSLV--ATQQEDTVRFKWN SQDVAFWDRNRTTSHA 328

>ref|XP_001383149.1| taurine catabolism dioxygenase [Pichia stipitis CBS
6054]
gb|ABN65120.1| taurine catabolism dioxygenase [Pichia stipitis CBS 6054]
Length = 414

Score = 58.9 bits (141), Expect = 6e-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 LGTEIVGLQLSDLNDQQDELALLVAERVVFFRDQDLSPQKQLELGHYWGQVEVHPQVP
182

Query: 69 RIGGGDIVAISNVKADGTVRQHSPAEDW---DMMKVIVGNMAWHADSTYMPVMAQGAVFS
125

RI + +S + D + A++ K I GN WH D + A

Sbjct: 183 RISE-EFNGVSVIWQD-----YRAKYGLHLSFKKAIGGNAQWHTDLVHELQOPAGITHLH
236

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSA----RHSLVYSQSKLGHVQQAGSA
181

+ +P+VGG T +A AAYD L A + + ++A H V ++ L G

Sbjct: 237 NDAIPSVGGDTLWASGYAAYDKLSPAFQKFLDGKTAIYRSAHQYVDPENPL-----KGPK
291

Query: 182 YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAEESERFLEGLVDWACQA
240

Y+ P+V+ HP TG L + R I G++ ES+ LE L +

Sbjct: 292 YV-----EREHPVIRTHPATGWKFLFVNRSMTVRIVGLEPEESKILEYLFVSVYEKN
343

Query: 241 PRVHAH-QW-----AAGDVVVDNRCLLHRAEPWD 269

+ W G +WDNR H A WD

Sbjct: 344 LDIQVRFNWRPTKEGLGTSIWDNRASQHFV-VWD 377

>ref|XP_001905437.1| unnamed protein product [Podospora anserina]
emb|CAP65678.1| unnamed protein product [Podospora anserina]
Length = 375

Score = 58.9 bits (141), Expect = 7e-07, Method: Compositional matrix
adjust.

Identities = 67/278 (24%), Positives = 110/278 (39%), Gaps = 34/278 (12%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQI 58

A + +TP +G + G+ L+ L+D L + +++F Q + ++Q
 Sbjct: 80 ALKVINLTPG---IGTEIRGLQLSQLNDIQKDELALLIAERGVVFRDQDFKDIGIEKQK
 136

Query: 59 TFAKRFGA--IERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGN----MAWHADS
 112

F + FG I +G + + + S E+ + + GN +H+D
 Sbjct: 137 EFGRYFGPLHIHPVGA----HVKESQELHNIYLGSDNEYRNRRR---GNRLTTTGYHSDV
 189

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKL
 172

+Y + + VP GG T + AAY L +AL+ A HS
 Sbjct: 190 SYERQPPGITILTLLSVPPPTGGDTAWESQTAAYARLSPPIQALLENLRAEHS-----
 241

Query: 173 GHVQQAGSAYIGYGMDDTATPLR---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 +WDNR H A
 Sbjct: 300 LLKLLFHHITFGQDFQVRVKEEGTVALWDNRVTSHTA 337

>emb|CAY25764.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 58.9 bits (141), Expect = 7e-07, Method: Compositional matrix
 adjust.

Identities = 34/102 (33%), Positives = 55/102 (53%), Gaps = 18/102 (17%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGA IERIGGGDIVA-----ISNVKADGTVR 88
 ++A+LIF GQ ++++QQ+ FA FG E+ GG + +SN+ DGT

Sbjct: 22 KYAVLIFHGQDITDEQQQLAFALNFGEREKARGGTVTKKEDYRLTTGLNDVSNLKGKDGTT-- 79

Query: 89 QHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

P D + +GN WH+DS++ P+ A+ ++ SA VV
 Sbjct: 80 ---PLSRDHRTHLFLNGLNCLWHS DSSFRPIPAKFSLLSARVV 118

>ref|XP_001014128.1| hypothetical protein TTHERM_00405520 [Tetrahymena
 thermophila]

gb|EAR93883.1| hypothetical protein TTHERM_00405520 [Tetrahymena
 thermophila

SB210]

Length = 323

Score = 58.9 bits (141), Expect = 7e-07, Method: Compositional matrix
 adjust.

Identities = 51/269 (18%), Positives = 103/269 (38%), Gaps = 38/269 (14%)

Query: 11 TGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERI 70
 +G+ LG V + + AA +H + Q+L QQ+ FA++FG+I
 Sbjct: 57 SGSQGLGFIVENIDCNKATPEDIEKIKAAALWEHG TICLKNQNL DAGOQVEFAQKFGSI---
 113

Query: 71 GGGDIVAISNVKAD-----GTVRQHS PAEWDDMMKVI VGNMAWHADSTYMPVMAQG--
 121
 IV D +R + ++ WH D ++
 Sbjct: 114 ----IVRPPYYAPDFREPGHPAII RVGNVGVGGVPLQKPQDAELWHKDG SFEQPGKNFLL
 169

Query: 122 AVFSAEVVPAVGGRTCFADMRAAYDALDEATR-----ALVHQRSARHSLVYSQSKLGHVQ
 176
 + +++ +GG+T F D Y+ L + A V + S +S + + H +
 Sbjct: 170 SFLHPKIIITQIGGQTGFVDCEDTYNKL PSEIKEQLEGATVLET SKTNSFFNNIMEEQHFE
 229

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDW
 236
 + + ++HP + RP + + I + + + VD
 Sbjct: 230 DSHHK-----IFQIHPISKRPIHFLTHR NYEITLKNGEKVDS--TPFVDE
 272

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRA 265
 + +++H+W+ GD+V+WDN ++H++
 Sbjct: 273 FEKYNIYSHKWSPGDLVIWDNYRVIHKS 301

>ref|XP_001941451.1| taurine dioxygenase [Pyrenophora tritici-repentis Pt-1C-BFP]
 gb|EDU44170.1| taurine dioxygenase [Pyrenophora tritici-repentis Pt-1C-BFP]

Length = 378

Score = 58.5 bits (140), Expect = 7e-07, Method: Compositional matrix adjust.

Identities = 46/174 (26%), Positives = 72/174 (41%), Gaps = 12/174 (6%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVY
 167
 WH D + + VVP GG T FA YD L + + + V
 Sbjct: 181 WHHDIGFENNTSDY TSLIMRVVPEYGGDTVFASAYEVYDRLS APYQKFLEGLTCTFRPVG
 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-QWAAGDVVVDNRCLLHRAEPWDFKLP R 274
 AES++ L+ L D + + +W D+ VWDNR + H A +D+ PR
 Sbjct: 297 TEAESQKLLKWLSDLITENHDLQLRMKGVNDLAVWDNR AVYHTAT-YDYDGPR 349

>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 = 7e-07, Method: Compositional matrix
adjust.

Identities = 64/257 (24%), Positives = 98/257 (38%), Gaps = 16/257 (6%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERIGGG 73
+G + GV+LA L+DA L ++ F Q D Q K FG + R
Sbjct: 95 IGTEIHGVNLARLNDAQRDDLARLIAVRGVFFRNQKDFDIDAQRELKGYFGTLHRHATT
154

Query: 74 DIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVG
133
+ ++ V ++ D + + WH+D TY P G
Sbjct: 155 AVPKKKGLEDVHVV--YTGDNSSDQRALFSPSFLWHSVDTYEVQPPSYTSLKVLTPGPPRG
212

Query: 134 G--RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTA
191
G T ++ AAYDAL + + +A H+ ++Q + S +G +
Sbjct: 213 GGGDTLWSSQYAAAYDALSSHMQNYLKGLTALHT-----ANMQASDSRALGRTIRREP
264

Query: 192 -TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-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

>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 = 8e-07, Method: Compositional matrix
adjust.

Identities = 42/166 (25%), Positives = 75/166 (45%), Gaps = 9/166 (5%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
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 FFHDEARRLGNPLRKGIRGSPLNHGEELTA--VHPVIRTNPVTGWKSVYVVKGFTKRING
289

Query: 221 MDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

+ ES+ L+ L + Q +W D+ +WDNR H A

Sbjct: 290 VTKDESDVLLQYLFNLTQNHDAQVRFKWRKNDMAIWDNRSTWHCA 335

>emb|CAY25795.1| alpha-KG-dehydrogenase [uncultured bacterium]
emb|CAY25800.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 58.5 bits (140), Expect = 8e-07, 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 IESGMDKYAVLIFHGQDITDEQQLAFALNFGERENPRGGSVVKPEDSRLQTGLNDVSNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

DG P D + + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 76 RDG-----KPLPRDSRINLFLGNCLWHSDDSSFRPIPAKFSLLSARVV 118

>ref|XP_002490893.1| Fe(II)-dependent sulfonate/alpha-ketoglutarate
dioxxygenase,

involved in sulfonate catabolism for use [Pichia
pastoris GS115]

emb|CAY68613.1| Fe(II)-dependent sulfonate/alpha-ketoglutarate
dioxxygenase,

involved in sulfonate catabolism for use [Pichia
pastoris GS115]

Length = 417

Score = 58.5 bits (140), Expect = 8e-07, 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---LGSKVEGVQLSQLTPDQKDDLALFVA--QRGVVFRDQDL-RDKDLG
151

Query: 60 FAKRFGAIERIGGGDIVAISNVKADG-----TVRQHSPAEWDDMMKVIVGNMAWHADST
113

K+FG + G I S +G T ++ P + + + WH+D T

Sbjct: 152 EVKKFG--QHFGPLHIHQTSGA-PEGYPEFHITFKRAGPP---NTFRNKISAPGWHSDVT
205

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL---VYSQS
170

Y A F P GG T FAD AY+ L + + + HS

Sbjct: 206 YELQPAGITFFGLIEGPEAGDTLFADAIEAYERLSPSFQKFLDGLRLIHSARAQAEDSL
265

Query: 171 KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAES----
226

K G +Q+ T+ + PL++ HP + S+ I G+ ES

Sbjct: 266 KKGSIQRK-----KFTSETVHPLIRYHPVLNKRISIFAKAFGTKIVGLKQEESDLIL
316

Query: 227 ---ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265

+RF+ +D +A + G VV WDNR + H A

Sbjct: 317 NFIQRFIATALDLQLRA-----SYEPGTVVAWDNRRVFHSA 352

>emb|CAY27301.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 106

Score = 58.5 bits (140), Expect = 9e-07, Method: Compositional matrix
adjust.

Identities = 44/124 (35%), Positives = 56/124 (45%), Gaps = 18/124 (14%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR
195

T FADMRAAYDALDE + + HS +YS+ KL + + R

Sbjct: 1 TEFADMRAAYDALDEQLKHQIEDLVCLHSNMYSRGKL-----ELADFTEEEERRVFKPVRR 55

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

LV+ HP T R SL + HA I GM E+ L L ++A P V+

Sbjct: 56 RLVRRHVPVTRKSLFLSAHAGEIEGMSIPEARMLLLDLTEFA-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 = 9e-07, Method: Compositional matrix
adjust.

Identities = 36/104 (34%), Positives = 49/104 (47%), Gaps = 5/104 (4%)

Query: 153 RALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG
212

RA + HSL+YS+ LG + Y L+ LV+ HP GR SL +

Sbjct: 6 RAEIDDMICEHSLMYSRGSGLGFLD-----YTEEEKQMFKPVLQRLVVRTHPVHGRKSLYLS 60

Query: 71 -GGGDIVAIISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVMAQGA VFSAEVV
129

G DI I GT+ + ++ +H+D ++ +
Sbjct: 116 YGRLDI-DIPLFSKTGTLTKSIH-----VIAFAEFHSDHSFEINPPSYTLLRMVKT
165

Query: 130 PAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT
189

P GG T + A +D L + HS + + + + G+ +
Sbjct: 166 PEYGGDTIWTSQTALFDKLSPTFQKTFEGLHGVHS--SEHTYINTINRGGTTF-----
216

Query: 190 TATPLR---PLVKVHPETGRPSLLIGR----HAHAIPGMDAAESERFLEGLVDWACQAPR
242

P+R PLV+ HP T + +L H + G +A + FL R
Sbjct: 217 -RLPVRREHPLVRTHPVTKQKALFYNP AFVIHIAELKGFEALHTLNFL-----R
264

Query: 243 VH AH-----QWAAGDVVVW DNRCLLHRAEP 267

H H QW AG + +W DNR +HRA P
Sbjct: 265 EHLHSADDLTVRWQWEAGSIALW DNRVAVHRAVP 298

>gb|AAO39411.1| TfdA alpha-like protein [uncultured bacterium]
Length = 119

Score = 58.2 bits (139), Expect = 9e-07, 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 IEAGMDKYAVLVFHGQDISDDQQMAFAPNFGKRENARGGTVTKKEDYRLSSGLNDVSNLG 75

Query: 83 ADGTVRQHS PAEWDDMMKVI-VGNMAWHADSTYMPVMAQGA VFSAEVV 129

DG P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----KPLPKDHRTHLFNLGNCLWSDSSFRPIPAKFSLLSARVV 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 PLIRTHAGSRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQPKFVYRHSWKVGD LVM 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 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSK---LGHVQQAGSAYIGYGMDDTAT
192

T F DM YDAL + R A H + + + + + + Y T
Sbjct: 1 TEFCDMSMVDYDALPAELKRAAEGRYAIHHVSKTRNRRVTISPDRPGAKDYERRATETHE 60

Query: 193 PLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRV-HAHQWAA
250

+PLV+ HPETGR +L I R I M E++ L+ L + + + H W
Sbjct: 61 VRQPLVRTHPETGRQALYISPRFTIGIADMPDEEAQALLDKLFATFVRERKQYRHTWRD
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-----IGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMP
116

+ FG + + I + + V D + R+ P+ + + WH+D +Y
Sbjct: 98 RYFGPLHKHATTPIPRNGLEEVHVYNDAS-RRPDPSAFSKL-----ELWHSVDVSYE-
148

Query: 117 VMAQGAVFSAEVV--PAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGH
174

+ ++ S +++ P VGG T ++ A Y +L + + +A HS V ++
Sbjct: 149 -LQPPSITSLKLITGPEVGGDTLWSSGYALYSSLSPGLQTYLEGLTAVHSV---AQADG
204

Query: 175 VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGL
233

+ AG ++T + PLV+VHP T S+ + I G+ AES+ L L

Sbjct: 205 NRAAGLPVRRQEIET----IHPLVRVHPATQWKSIVYVNPGFTRRIVGVPKAESDAVLTFL
260

Query: 234 VDWACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDF 270
+ P +W + WDNR + H A +DF

Sbjct: 261 FRQINENPDHQVRFWRPNSIAFWDNRIVTHSAT-FDF 297

>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 IEAGMDKYAVLLFRDQDVSDQQLVFNARFGERENARGGTVTKKEDYRLTSGLNVDVNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVL 129
DG +P D ++ +GN WH+D+++ P+ A+ ++ SA VV

Sbjct: 76 KDG-----NPPRPDPHTRLFNLGNCLWSDNSFRPIPAKFSLLSARVV 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 IEAGMGKYAVLLFRDQDVSDQQLVFNARFGERENARGGTVTKKEDYRLTSGLNVDVSNL 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVL 129
DG +P D + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 76 KDG-----NPLPRDHRTHLNLGNCLWSDSSFRPIPAKFSLLSARVV 118

>ref|XP_001909009.1| unnamed protein product [Podospora anserina]
emb|CAP70141.1| unnamed protein product [Podospora anserina]
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 QRGVVFRAQDELTNELQKKLILRLGELTGRPATSGLHIHPLLNSERELGGDDPEISTIS
138

Query: 83 ADGTVRQHSP-AEWDDMMKVI VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
141

+ + ++ A D++ WH+D + PV A +P GG T +A
Sbjct: 139 SIQNKKFYARGAIADELSPPKQSTGQWHS DIAFEFVPADY TSLRLVELPTTGGDTLWASG
198

Query: 142 RAAVDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYI-----GYGMDTTATPL
194

YD L E + + ++ + Q V +A + + T +
Sbjct: 199 YELYDRLSEPYQKFLESL----TVTFQQPGFNKVAEAAAGFKLYDKPRGAPENIGTELKAV
254

Query: 195 RPLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWA-AG
251

P+++ +P TG SL +G H I G+ ES+ L +D + + QW
Sbjct: 255 HPVIRTNPVTGWKSLFPVGGHVKHINGVTEEEESKALLTWFLDLVYKNHDLTVRLQWKNKN
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 IEAGMDKYAVLLFRGQDITDEQQALAFALNFGEREHARGGTVTKKEDYRLTSGLNDSVNLG 75

Query: 83 ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

DG +P D +++ +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTRLLNLGNCLWHS DSSFRPIPAKFSLLSARVV 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 = 1e-06, Method: Compositional matrix
adjust.

Identities = 49/199 (24%), Positives = 79/199 (39%), Gaps = 34/199 (17%)

Query: 109 HADSTYMPVMAQGAVFSAEVV--AVGGRTCFADMRAAY-DALDEATR ALVHQRSARHSL
165

H D Y P + + +F P + GGRT F D DA D+ + ++
Sbjct: 102 HWDGMYKPTIPEFQIFHCVSAPEASQGGRTTFVDTEQLIADASDDERHEWKNT-----TI
156

Query: 166 VYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPE-----TGRPSLLIGR
213

Y S++ H YG + + PL+ +HP+ TG+
Sbjct: 157 TYRTSRVTH-----YGGEVVS----PLICLHPDGKKWVMRYNEPMTGKDDKYADH
202

Query: 214 HAHAI PGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLP
273

H I G+ + + F + L + + +AHQW +GD+V+ DN LLH E + P
Sbjct: 203 HLLTIHGLSIEQQKEFEKNLNFNRLYDSRYFYAHQWQSGDLVISDNFTLLHGREAIFITHSP
262

Query: 274 RVMWHSRLAGRPETEGAAL 292

R + + G P E +
Sbjct: 263 RHLQRVHVHGTPVCENLSF 281

>gb|AAO39410.1| TfdA alpha-like protein [uncultured bacterium]
Length = 119

Score = 58.2 bits (139), Expect = 1e-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 ADIEAGMDKYAVLLFRDQDITDDQQLIFARNFGERENARGGTVTKKEDYRLTSGLNDSVN 73

Query: 81 VKADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

+ DG P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 74 LGKDG-----KPLPRDHRTHLFLNGLNCLWHS DSSFRPIPAKFSLLSARVV 118

>ref|XP_001828620.1| hypothetical protein CC1G_10291 [Coprinopsis cinerea
okayama7#130]

gb|EAU93223.1| hypothetical protein CC1G_10291 [Coprinopsis cinerea
okayama7#130]

Length = 382

Score = 57.8 bits (138), Expect = 1e-06, Method: Compositional matrix
adjust.

Identities = 74/283 (26%), Positives = 115/283 (40%), Gaps = 26/283 (9%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAAL----HA-AWLQHALLIFPGQHLSNDQ 56

A + +ITP LG V+GV+LA LD G L H+ + L++F Q D+
Sbjct: 84 ATSVFEITPY---LGTEVSGVNLADLSDGRDQLALEVHSLTQSRRLMVFRDQQDFIDR
140

Query: 57 QITFAKRFGAIERIGGGDIVAISNVKADG-----TVRQHSPA EWDDMMKVI VGNMAWHA
110

F ++G R G V ++ +G R H ++ + + + WH+
Sbjct: 141 GPEFYLQWG---RHFGRLHVHPTSGHPEGYPEFHLVYRDHK-TTFNFEIDESISSTIWS
196

Query: 111 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQS
170

D +Y F P GG T F +A L A + A HS + Q+
Sbjct: 197 DVSYELQPPGLTTFLLSAPPSGGDTLFTSQVSALRKLSPQFVAFLKTLKAVHS-GFEQA
255

Query: 171 KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERF
229

+ G+ ++ + P+V+ HP TG +L + R I G+ ESE
Sbjct: 256 DFSRSGKRGATVRREPVEH----IHPVVRKHPVTGEEALYVNRQFTRRIVGLKKEESEAT
311

Query: 230 LEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFK 271

L+ L D ++ A +W +V+WDNR H A DFK
Sbjct: 312 LKLLYDHIDKSADNQARVRWTPNTIVLWDRITAHSAT-VDFK 353

>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 = 1e-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 PVVQIHPETGEKSLLLGHYAQRFVQYDTHDSNRLYEILQAHITRLENTVRWHWAAGDVAI
103

Query: 256 WDNRCLLHRA 265

WDNR H A
Sbjct: 104 WDNRSTQHYA 113

>gb|ADC33943.1| TfdA-like protein [uncultured bacterium]

Length = 131

Score = 57.8 bits (138), Expect = 1e-06, Method: Compositional matrix
adjust.

Identities = 40/131 (30%), Positives = 60/131 (45%), Gaps = 5/131 (3%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSK---LGHVQQAGSAYIGYGMDDTAT
192

T F DM YDAL + R A H + +++ + + Y T
Sbjct: 1 TEFCDMSMVYDALPAELKRAAEGRYAIHHVSKTRNRRVTISPDRPDAKDYERRATETHE 60

Query: 193 PLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDWACQAPRV-HAHQWAA
250

+PLV+ HPETGR +L I R I M E++ L+ L + + + H W

Sbjct: 61 VRQPLVRTHPETGRQALYISPRFTIGIADMPDEEAQALLDKLFATFVRERKRFQYRHTWRD
120

Query: 251 GDVVVWDNRCL 261
GD+V+WDNRC+

Sbjct: 121 GDLVMWDNRCV 131

>ref|XP_001522837.1| hypothetical protein MGCH7_ch7g935 [Magnaporthe
grisea 70-15]
gb|EAQ71528.1| hypothetical protein MGCH7_ch7g935 [Magnaporthe grisea 70-
15]

Length = 437

Score = 57.8 bits (138), Expect = 1e-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 QRGVVFRAQDNLTNDLQKKLILRLGELTGRPKTSLGLHIHPLLNAERETYGGDDNEISTI
140

Query: 79 SNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCF
138
S+ + D ++ + + D++ WH+D + PV A +P GG T +
Sbjct: 141 SSAQNDKLYKK-TWTQPDELSPKKQSTAQWHSDI AFEPVPADYTSRLRLTELPKTGGDTLW
199

Query: 139 ADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM-----DTT
190
A YD + + + S+ ++Q + + A G+ + +
Sbjct: 200 ASGYEIIDKISAPYQKFLETL----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 = 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 IEAGMDKYAVLLFRDQDVSDQQLVFARNFGEREDARGGTVTKKEDYRLTSGLNVDVSNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
 DG +P D + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 76 KDG-----NPLPRDHRTHLFLNLGNCLWHS 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 = 1e-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 ADIEAGMDKYAVLLFRDQDITDDQQLIFARNFGERENARGGTVTKKEDYRLTSGLNVDVSN 73

Query: 81 VKADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
 + DG P D + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 74 LGKDG-----KPLPKDHRTHLFLNLGNCLWHS DSSFRPIPAKFSLLSARVV 118

>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 = 1e-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 TITVKELHPTFGAEVLGIQWGDNGVISDEQLQELRDTYGFII LRATPLTDSTHVSFSRLF 76

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSP-----AEWDDMMKVIV-----GN
 105

+ G + IS G V ++ P + D + I+ N
 Sbjct: 77 AS-----GPLDDISRFLPPGRVPRYYPHLELFDASNLSDDGRAILD PSSSPRAMLLRAN
 130

Query: 106 MAWHADSTYMPVMAQGAVFSAEVVPA-----VGGRTCFADMRAAYDALD-EATRALV
 156

+WH+D Y P + ++ A +P+ + G T FAD R A++ L E R L+
 Sbjct: 131 SSWHSDLAYNPRRSSYSLLRAVELPSREPGEMGEIEGNTEFADSRTAWEELAAEKKRELL
 190

Query: 157 HQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL--RPLVKVHPETGRPSLLIGRH
214

+ + VY+ + H ++ G+ ++ P+ +V+ H E+GR +L +G +
Sbjct: 191 ---TKDWTGVYNAA---HSRKLGAPEYFKDVNPEEGPIARHKVVQEHVESGRMNLCVGAY
244

Query: 215 -----AHAIIPGMDAAESERFLEGLVDWACQAPRVHAHQWA-AGDVVVWDNRCLLHRA
265

+PG SE ++ L + V + +W GD+V+WDNR +LHRA
Sbjct: 245 LWRLEDGEGKTVPG-----SEGIKFLNEHVANKSFVASVRWERPGDLVIWDNRRAVLHRA
299

>gb|AA039408.1| TfdA alpha-like protein [uncultured bacterium]
Length = 119

Score = 57.8 bits (138), 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 IEAGMDKYAVLVFHGQDISDDQQMAFALNFGKRENARGGTVTKKEDHRLSSGLSDVSNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG P D + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 76 KDG-----KPLPKDHRTHLFLNCLWHSDDSSFRPIPAKFSLLSARVV 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 = 1e-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 SVETLREGLGFGKQVVGLARQDIDREAVRAELRDHWIRDGLVVFRGSEVTPEFQIALSRV 63

Query: 64 FGAIE-----RIGGGD----IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY
114

FG +E + D I +S+ +G E D + V + WH+D +
Sbjct: 64 FGELEVHPIPELRSADHPELITLVSDKDKLEGLF-----EVDGVESVAF--LPWHSDLIF
115

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQ--SKL
172

+ + G + +A+ + + GG+T F D AY+ L E +A + + L + S+

Sbjct: 116 VDSINHGGLLTAKTIASWGGQTGFIDQVQAYELLPETLKAEIEGLEIVYQLCVNPGGSRY
175

Query: 173 GHVQQAGSAYIGYGMDTTATPL-----RPLVKVHPETGRPSLLIGRH-AHAIPGMDA
223

G + + G + L P+V V P+TGR L + A I G D
Sbjct: 176 GTRSRVRTILTGDFEKSVGPRLDADYPPVVHPVVFVQPDGTGRKVLNVSPFGALHILGHDD
235

Query: 224 AESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH 263

L LVD P + HQW ++++WDN + H
Sbjct: 236 EAGHALLGRLVDHLTACP-AYFHQWQPSEMLLWDNRMAH 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 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDPRTHLFLNCLWHS DSSFRPIPAKFSLLSARVV 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 DAIIRDLAITISQRGVCVFPQKLNLTVDQKLLCHRLGQLTTRPYTSGLNHPLNQTELP
129

Query: 84 DGTVRQHSPAEWDDMMKVIVGNMA-----WHADSTYMPVMAQGAVFSAEVVP
130

DGT+ D K +V WH D +Y + A + +V P
Sbjct: 130 DGTIDAELTTLARDPKKKLVQAGFGKKEKKQSHSDGWHTDCSYENIPADYTMLHMKVTP
189

Query: 131 AVGGRTCFAFMRAAYDALDEATRVLVHQRSAR-----HSLVYSQSKLGHVQQAGSAYIGY
185

A GG T FA AYD L + ++ + A H ++ + +G

Query: 119 AQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
178

A + VP VGG T +A AY+ L R + + A V ++
Sbjct: 196 AGITHLHNDTVPPVGGDTLWASGYGAYEKLSPEFRKFIDGKQA-----VYRS
242

Query: 179 GSAYIGYGMDTTATP-----LRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG
232

AY+ + +A P + PLV+VHP TG +L + R I G+D AES+ L
Sbjct: 243 AHAYLDR-ENPSAGPKFVERVHPLVRVHPATGWKALWVNRAMTTRIVGLDKAESDLILNY
301

Query: 233 LVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFK 271

L D + + +W AG +WDN WD++
Sbjct: 302 LHDVYEKNADIQVRFRWTAGTSALWDNSA-----SWDYE 335

>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 VAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGR
135

+ V + A WH D ++ + VP GG
Sbjct: 155 -HVPGVPEASVIWSQFFASHIRKPTFRTPFQGWHTDIVHLKQNFGITHLHYDTVPPYGGD
213

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAAGSAYIGYGMDTTATP--
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---IGREFPDVQLTDLNNDQTLRDLAITVSRGVVFFRNQDINSQQKVLGQ 103

Query: 63 RFGAIERIGGGDIV---AISNVKADGTVRQHSPAEWDDMMKVIVGNM----- 106

+ G + + A++N K + TV + + DD + VI +

Sbjct: 104 KLGELTGKPATSKLHRHAVNNSKRNITVNE---GKLDDEISVISSEINRKLYGDRFKSSS 160

Query: 107 -----AWHADSTYMPVMAQGAVFSAEVVPA--VGGRTCFADMRAAYDALDEATRALVHQ 158

WHAD T+ V + A+ P GG T +A YD L + L

Sbjct: 161 HHLASEGWHADITFENVPSDYAILKITDSPEDNPGGDTLWASGYEVYDRLSSPIQQQLADT 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 HQVEHGWIEGVTPRESEILKQYFNQLIAENHDLQVRFKWNNTNDVAIWDNRSVFHTATN-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 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGR
206

ALD+ T+A + HSL+YS+ LG + Y + L+ LV+ HP GR
Sbjct: 1 ALDDETKAEIEDMICEHSLMYSRGSLGFLD-----YSDEEKEMFKPVLQRLVLRTHPVHGR 55

Query: 207 PSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

SL + HA AI M E L L + A Q V+ H+W D+
Sbjct: 56 KSLYLSSHAGAIRDMSMPEGRVLLRDLTEHATQGEFVYVHKWTLHDL 102

>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 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
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 AQPLFNAAKRNNFSIYSGERGAPENVGEILEAIHPVIRTNPVTGWRSVYAVDHHHCQRIH
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 = 2e-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 ADIEAGMDKYAVLLFRDQDITDDQQLIFARNFGERENARGGTVTKKEDYRLTSGLNDVSN 73

Query: 81 VKADGT--VRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV 129

+ DG + H ++ +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 74 LGKDGKPLPKDHRTHPFN-----LGNCLWHS DSSFRPIPAKFSLLSARVV 118

>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 = 2e-06, Method: Compositional matrix
adjust.

Identities = 36/107 (33%), Positives = 50/107 (46%), Gaps = 5/107 (4%)

Query: 147 ALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGR
206

ALD+ T+A + HSL+YS+ LG + Y L+ LV+ HP GR
Sbjct: 1 ALDDETKAEIADMICEHSLMYSRGSGLGFLD-----YTDEEKQMFKPVLRQRLVVRTHPVHGR 55

Query: 207 PSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

SL + HA AI GM E+ L L + A V+ H+W D+
Sbjct: 56 KSLYLSSHAGAIRGMSMPEARLLLLRDLTEHATSPEFVYVHKWTVHDL 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 = 2e-06, Method: Compositional matrix
adjust.

Identities = 54/207 (26%), Positives = 82/207 (39%), Gaps = 23/207 (11%)

Query: 108 WHADSTYM-PVMAQGAVFSAEVVPA-VGGRTCFADMRAAYDALDEATRVLVHQRSARHSL
165

WH D + P ++ + PA GG T FADM AA +ALD R + + A S
Sbjct: 171 WHTDQAFRDPPPFASLLYCVKSPAGAGGDTAFADMTAACNALDNRREELRKLRAVCSY
230

Query: 166 VYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSL-----LIGRHAH
216

+ +K+ + +++ P+T SL +I
Sbjct: 231 AHHNAKVNRRTPPTYPLLTPTQRAAHPPVAQRIIRADPDTNTESLYGFSSAVCAVIDEKDE
290

Query: 217 AIPG-----MDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
266

P DA+ + L+ +A A + H W GD+VVWDN +H A
Sbjct: 291 VTPEDLDRLYDGLGEEEDASVRALMYDELLPFATGAEFTYRHSWTEGDLVVWDNLRRTIHTAT
350

Query: 267 PWDFKLPRVMWHSRLAGRPETEGAALV 293

P+D + R MW + +A ET G A +
Sbjct: 351 PFDERYDREMWRRTTVAH--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 = 2e-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 KYAVLIFHGQDITDEQQQLAFALNFGEREKARGGTVTKKEDYRLTTGLNDVSNLGKDG--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

P D + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 79 --KPLSRDHRTHLFLNCLWHSDFRPIPAKFSLLSARVV 118

>dbj|BAD15035.1| hypothetical protein [Bradyrhizobium sp. jwc91-2]
Length = 102

Score = 57.0 bits (136), Expect = 2e-06, Method: Compositional matrix
adjust.

Identities = 37/110 (33%), Positives = 53/110 (48%), Gaps = 11/110 (10%)

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTAT---PLRPLVKVHPE
203

ALD+ +A + HSL+YS+ LG ++ Y + A L+ LV+ HP

Sbjct: 1 ALDDEXKAEIEDMICEHSLMYSRGSLG-----FLDYTNEEKAMFKPVLQRLVLRTHPV 52

Query: 204 TGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

GR SL + HA AI M E+ L L + A Q V+ H+W A D+

Sbjct: 53 HGRKSLYLSSHAGAIRDMSPEARLLLLRDLTEHATQGEVPYXHKWTAHDL 102

>dbj|BAD15037.1| hypothetical protein [Bradyrhizobium sp. DesT1]
Length = 102

Score = 57.0 bits (136), Expect = 2e-06, Method: Compositional matrix
adjust.

Identities = 37/110 (33%), Positives = 53/110 (48%), Gaps = 11/110 (10%)

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTAT---PLRPLVKVHPE
203

ALD+ T+A + HSL+YS+ LG ++ Y + A L+ LV+ HP

Sbjct: 1 ALDDETKAEIEDMICEHSLMYSRGSLG-----FLDYTDEEKAMFKPVLQRLVLRTHPV 52

Query: 204 TGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

GR SL + HA AI M E+ L L + A Q V+ H+W D+

Sbjct: 53 HGRKSLSLSSHAGAIRDMSPEARLLLLRDLTEHATQGEVCYVHKWTVHDL 102

>gb|EFE34370.1| alpha-ketoglutarate-dependent taurine dioxygenase
[Arthroderma

benhamiae CBS 112371]

Length = 358

Score = 57.0 bits (136), Expect = 2e-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 WHSDVAFEPiPAEYTTLRRLTQVPKTGGDTLWASGYELYDRISKPYQRFLETLTATCAQPG
212

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLL-IGRHAHAIP
219

 + KL Q+ IG + + P+V+ +P TG S+ G H I
Sbjct: 213 YNKVAATGKFKLFDGQRGAPENIGSNFSS----VHPVVRTNPVTGWKSIYSAGFHVQKIN
268

Query: 220 GMDAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVDNRCLLHRA 265

 + AES+ L+ + + + +W A D+ +WDNRC+ H A
Sbjct: 269 DVTEAESKALLDWFLRLINENNDLQVRFKWKNNANDMAIWDNRCVFHTA 316

>emb|CAY25752.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 57.0 bits (136), Expect = 2e-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 IEAGMDKYAVLLFRNQDITDEQQALAFALNFGERENPRGGSVVKPEDSRLQTGLNDVSNL 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

 DG P D + + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 RDG-----KPLPRDSRVNLFNLGNCLWHSDDSSFRPIPAKFSLLSARVV 118

>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 WHSDVAFEPiPAEYTTLRRLTQVPKTGGDTLWASGYELYDRISKPYQRFLETLTATCAQPG
212

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLL-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 DVTEAESKALLDWFLRLINENNDLQVRFKWKNDMAIWDNRCVFHTA 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 SVGWHSDFERVPDYAMLKIHTLPPTGGDTLWASAYEVYDRLSPAMATFLEGLTATHD
208

Query: 165 Lvy---SQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPG
220

+ +LG+ + G + + P+++ +P TG S+ + R I G
Sbjct: 209 ASFFHDEARRLGNPLRKGVRGSPLNVEELQAVHPVIRTNPVTGWKSVYVNRGFTKRING
268

Query: 221 MDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

+ ES+ L+ L + Q +W D+ +WDNR H A
Sbjct: 269 VTKDES DVLLQYLFNLVLTQNHDAQVRFKWKNDLAIWDNRSTWHCA 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 KYAVLIFHGQDITDEQQALAFALNFGEREKARGGTVTKKEDYRLTTGLNDVSNLKGKD--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

P D ++ +GN WH+D ++ P+ A+ ++ SA VV
Sbjct: 79 --KPLSRDHRTRLFNLGNCLWHS DGSFRPIPAKFSLLSARVV 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 IEAGMDKYAVLLFRDQDVSDDRQLVFNRFGERENARGGTVTKKEDYRLTSGLNDSVNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLFLNLGNCLWHS 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 ADIEAGMDKYAVLLFRDQDIADDQQLIFARNFGERENAHGGTVTKKGDYRLTSGLNDSV 73

Query: 81 VKADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
+ DG P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 74 LGKDG-----KPLPKDHRTHLFLNLGNCLWHS 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 DISFERVPSDYAMLKIHTLPPTGGDTLWASAYEVYDR LSPAMATFLEGLTATHD
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 VTKDESDVLLQYLFNLVLTQNHDAQVRFWRWNKNDLAIWDNRSTWHCA 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 = 3e-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 HWDGMYKPTLPEFQLFHCVHAPAVDEGGRTTFINTRQLLTELDTG-----ERLARWERV
159

Query: 167 YSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSL-----LIGRHA
215

+ ++ V + YG + PL+ HP +G L + +HA
Sbjct: 160 HITYRIKQV-----VHYGGQVRS----PLLVPHPVSGETVRLRYNEPPREGVRFNLQHA
208

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE 266

I G+ AE F++ L +AHQW GDVV+ DN LLH E
Sbjct: 209 LEIEGVAPAEQAAFVQDLHQRLYDPRYFYAHQWGGDVVIADNLGLLHGHE 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 = 3e-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-----LVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGR
 206

RA + +ARHS G ++ + + G + T+ P+V+ +P TG
 Sbjct: 195 YRAFLETLTARHSGDGFHRAAQAGGFGLYEKPRGSPLNVGSELTS--HPVVRTNPITGW
 252

Query: 207 PSL-----IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW-AAGDVVV
 255

S+ G + G+ ESE L+ D + +W D+ +
 Sbjct: 253 KSIFPVGTELIAATGTFPKVNGLSTRESENLLKYFHDLITYGHDLQVRFKWNPNDAI
 312

Query: 256 WDNRCLLHRA 265

WDNR + H A

Sbjct: 313 WDNRSVFHTA 322

>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 = 3e-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 IGTENVGIQLKDLTAQQRDELGLLIAERSVVFFRDQDISPQQQKELGEWYGEIEVHPQVP
 152

Query: 69 RIGG--GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
 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 DTVPTVGGDTLWASGYAAYEKLSPLMREFIDGKTAIYRSRHPYLDNRNP-----EDGLKY
 258

Query: 183 IGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAP
 241

+ PLV+VHP TG +L + R I G+D AES+ L L D + P

Sbjct: 259 VERE-----HPLVRVHPATGWKALWVNRAMTVRIVGLDKAESDVLGLLCDVYKPNP
 310

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 = 3e-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 IEAGMDKYAVLLFRDQDVSDQQLVFNARFGERENARGGTVTKKEDYRLTSGLN DVSNLG 75

Query: 83 ADGTVRQHSPA EWDDMMKVIV-GNMAWHADSTYMPVMAQGAVFSAEVV 129
DG P D + GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----RPLARDGRTHL FNPGNCLWHS DSSFRPIPAKFSLLSARVV 118

>emb|CAY25786.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 56.6 bits (135), 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 KYAVLIFHGQDITDEQQ LAFALNFGEGEKARGGTVTKKEDYRLTTGLN DVSNLGKDG--- 78

Query: 89 QHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 79 --KPLSRDHRTHL FN LGNCLWHS DSSFRPIPAKFSLLSARVV 118

>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 TCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195
T F DMRAAYD L E + + A H + S+ LG + S P+
Sbjct: 1 TEFCDMRAAYDDLPEDFKKE LQGLRAEHYALNSRFILGDTDYSES-----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 WPLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVG 111

>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 KYAVLIFHGQDIADQQQLAFALNFGEREKARGGTVTKKEDYRLTTGLNDVSNLGKDG--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 79 --KPLSRDHRTHLFLNCLWHSDFRPIPAKLSLLSARVV 118

>emb|CAY25740.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 56.2 bits (134), Expect = 4e-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 KYAVLVFHGQDITDEQQQLAFALNFGEREKARGGTVTKKEDYRLTTGLNDVSNLGKDG--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 79 --KPLSRDHRTHLFLNCLWHSDFRPIPAKFSLLSARVV 118

>emb|CAY25757.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 56.2 bits (134), Expect = 4e-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 IEAGMDKYAVLLFRGQDITDEQQQLAFALNFGEREHARGGTVTKKEDYRLTSGLNDSNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG +P D ++ +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLLNCLWHSDFRPIPAKFSLLSARVV 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 = 4e-06, Method: Compositional matrix
 adjust.

Identities = 67/296 (22%), Positives = 110/296 (37%), Gaps = 57/296 (19%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
 A+ + +TP +G + G+ LA LDD L + ++ F Q LS +Q+
 Sbjct: 125 AKDVINLTPY---VGTEIVGLQLADLDDKQKDELALLIAERVVFFKDQDLSPKQLELG
 181

Query: 62 KRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
 115
 K +G +E RIG D I+ + D + + G WH D ++
 Sbjct: 182 KYWGQVEVHPQANRIGP-DYDGITVIWQDYFNEKGGGLGL--SFQRSRQGTSRWHGDL SHE
 238

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHV
 175
 A + +P GG T ++ AYD L A + + ++A +
 Sbjct: 239 FQTAGITHLHQDSIPDAGGETIWSSTYGAYDKLSPAFKEFLDGKTA-----I
 285

Query: 176 QQAGSAYIGYGMDTTATPLR-----PLVKVHPETGRPSLLIGR-HAHAIPGMDAAE
 225
 ++ Y+ + PL+ P+V+ HP TG L + R + I G+ E
 Sbjct: 286 FKSAHVYL-----SRENPLKGPKHVEREHPIVRTHPATGWKYL FVNRSYTTTRIVGLLPEE
 340

Query: 226 SERFLEGL-----VDWACQAPRVH----AHQWAAGDVVVWDNRCLLHR 264
 S+ L L W + P + AH+ G +WDNR H
 Sbjct: 341 SDAILNYLFSVIENNRDIQVTFWSWQKLPGLKSPSDAHKTYRGTSALWDNR IANHN 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 = 4e-06, Method: Compositional matrix
 adjust.

Identities = 39/117 (33%), Positives = 55/117 (47%), Gaps = 7/117 (5%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
 195
 T F DMRAAYDAL ++ + A H + S+ LG + + P+
 Sbjct: 1 TEFCDMRAAYDALPRDLQSELEGLRAEHYALNSRFL LGD TDYSEA-----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| hypothetical protein [Aspergillus oryzae RIB40]
 dbj|BAE59069.1| unnamed protein product [Aspergillus oryzae]
 Length = 355

Score = 56.2 bits (134), Expect = 4e-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 ATFFHDEARRLGNPLRKGVRGSPLNHGEELTA--VHPVVRTNPVTGWKSVYVNGGFTRRI
 271

Query: 219 PGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVDNRCLLHRA 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 = 4e-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 ATFFHDEARRLGNPLRKGVRGSPLNHGEELTA--VHPVVRTNPVTGWKSVYVNGGFTRRI
 271

Query: 219 PGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
 G+ ES+ L+ L + Q +W D+ +WDNR H A
 Sbjct: 272 NGVTKDESDMLLQYLFNLVLTQNHDAQVRFKWNKNDMAIWDNRSTWHCA 319

>ref|XP_001818415.1| hypothetical protein [Aspergillus oryzae RIB40]
 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 = 4e-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---IGSEVHGIQLSQLTDKGKDLALYVAQRKVVAFRDQDFAQLPIEKALEFGGY
 156

Query: 64 FGA--IERIGGGDI----VAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
 117
 FG I + G + + + AD S AE+ ++ ++ WH+D T+
 Sbjct: 157 FGRHHIHQSSGAPKGFPEIHLVHRGAD----DRSGAEF---LEHTNSLTWHSDVTFEKQ
 209

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQ
 177
 P GG T F +M AY L R +H A HS V ++ +
 Sbjct: 210 PPGTTFLYLLDGPTSGGDTLFCNMAQAYRRLSPEFRKRLHGLKAVHSGV---EQVNNSLN
 266

Query: 178 AGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESERFLEGLVDW
 236
 G G T P+V+ HP TG +L + + I G ES+ L+ L D
 Sbjct: 267 KG----GIARRDPITTEHPVVRTHPVTGEKALYVNPQFTRYIVGYKKEESDFLLKFLYDH
 322

Query: 237 ACQAPRVHAH-QWAAGDVVVWD 257
 + + +W VVVWD
 Sbjct: 323 IALSQDIQTRVRWRPNTVVVVWD 344

>ref|XP_500332.2| YALI0A21439p [Yarrowia lipolytica]
 emb|CAG84270.2| YALI0A21439p [Yarrowia lipolytica]
 Length = 372

Score = 56.2 bits (134), Expect = 4e-06, Method: Compositional matrix
 adjust.

Identities = 51/183 (27%), Positives = 78/183 (42%), Gaps = 11/183 (6%)

Sbjct: 22 NFASITDQQVEELKQSLWEHGVIVVRKQKLTASQLKDFAIQTFGDSTLGRRPKPLDPEIA 81

Query: 79 SNVKADGTVRQHSPA EWDDMMKVIVGNMAW--HADSTYMP-----VMAQGAVF
124

++++ G +P + +VG +AW H D ++P VM G
Sbjct: 82 PDLQSPGVSILGNPK---GLSGEVGKVAWQWHHDKDHLPKTQGLDMNALYVVMLYGVSI
138

Query: 125 SAEVVPVAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIG
184

E T F DM AY L A HQ+ + +Y S + Q G
Sbjct: 139 PDEGTDGHPHTTLFLDMVEAYHNL-----APQHQQQLKLLSMYHLSPIS--PQPGVE---
188

Query: 185 YGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAE--SERFLEGLVDWACQAPR
242

L P+V H TGR L +G + G++ +++ + L
Sbjct: 189 -----IPRKLHPIVSTHKVTGRYCLYLGS DTSILKLENKPEAAKQYWQELFQEILSCTP
243

Query: 243 VHAHQWAAGDVVVW DNRCLLHRAEPWD 269

V+AH W AGD+V WDN ++H P++
Sbjct: 244 VYAHIWQAGDIVFWDNSQVMHTGMPYN 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 = 5e-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 SIRFEKVTGNIGAIIVHGVDVHVAHGDEVA-SVLLRSLHEHGVLFFHSDTAISSEQFSGFS 74

Query: 62 KRFGA--IERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMA
119

FG + G G ++ AD V + WH D +
Sbjct: 75 SVFGEQYVYPYKGGPGQFVTEEGADA-----VRLRTSYWHTDGSPQEKPP
119

Query: 120 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAG
179

Q A+ A VPA GG T +A M AA+DAL + L A V+S + + A
Sbjct: 120 QAALLCAVEVPAFGGDTMWASMTAAFDALSSRYQRLFEGMEA----VHSTATVARYHDA-
174

Query: 180 SAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWAC
238

G G + P+V P T R +L + + + GM E+E L L +
Sbjct: 175 ---FGQG---ESHAPVVITDPVTRRKALYVNSVYTERLVGM SERENETLLRMLYE-HV
226

Score = 56.2 bits (134), Expect = 5e-06, Method: Compositional matrix adjust.

Identities = 43/164 (26%), Positives = 66/164 (40%), Gaps = 7/164 (4%)

Query: 106 MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSL
165

+ +H+D +Y + +P GG T +A YD L + +A+H
Sbjct: 137 LEYHSDGSGYEVCPDFMTLMRTEIPPTGGDTLWASGYELYDRLSTPYQKFFESLTAQHE-
195

Query: 166 VYSQSKLGHVQQA---GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGM
221

V S KL + G D P+V+ HP TG +L G H + +
Sbjct: 196 VPSLRKLAETEPGIYDGPARGAPANTDMQFKQSHPMVRTHPVTGWKTLFAGGLHCRRVNDV
255

Query: 222 DAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVWDNRCLLH 263

ESE+ L ++ + +W GDV +WDNRC+LH
Sbjct: 256 TDFESEQLLSKIISLVGDNHDLQVRFRWNNPGDVAIWDNRCVLH 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 = 5e-06, Method: Compositional matrix adjust.

Identities = 50/172 (29%), Positives = 71/172 (41%), Gaps = 18/172 (10%)

Query: 128 VVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAG-----
179

VV G T F D+ AYDALD T+ L+ + +S + + +V G
Sbjct: 2 VVAEEDGLTGFGDLAKAYDALDSETQDILLEKLEVAYSFSMQRRHMRYVNLEGEYEPGPHSP 61

Query: 180 --SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-----AHAIPGM DAAESERFLE
231

A +GY A + P V HP +GR L I G+ ES LE
Sbjct: 62 KKPADVGY--DFADAVYPVVTHPVSGRKVLEIVEQFLDRVITPQQFGLSNDESIELLE
119

Query: 232 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG 283

LV + + HQW GD+V+WDN +H A + RV+ + + G
Sbjct: 120 RLVAHTKKPEFTYFHQWRDGMVLWDNWRAMHCATGTRPGIKRVINRTTIEG 171

>ref|XP_002392556.1| hypothetical protein MPER_07845 [Moniliophthora
perniciosa FA553]

gb|EEB93486.1| hypothetical protein MPER_07845 [Moniliophthora perniciosa
FA553]

>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 = 5e-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---DPAQVHDHADALRRLLAERQVIFFRDQTLDPAAQQVRV 57

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ
 120

A+ FG +E + + + + Q + G WHAD T+
 Sbjct: 58 AQVFGKVEPVSSSTFPSPDDPHVELLISQGT-----RTGTDIWHADLTWQTKPPA
 107

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYS--QSKLGHVQQA
 178

GA A VP GG T +A M A+ +L +A + + A H+ + L +
 Sbjct: 108 GACLYAVDVPPTGGDTMWASMTTAFASLAP ELQAYLRKLRATHNWEAPALRQSLMRRDPS
 167

Query: 179 GSAYIGYGMDDTTATPL-RPLVKVHPETGRPSLLIGR-HAHAIPGM DAAESERFLEGLVDW
 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 AKVPEWQVRFRWRKGSVAIWDNLATQH YA 254

>emb|CAY25753.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 55.8 bits (133), Expect = 5e-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 IEAGMDKYAVLLFRGQDITDEQQ LAFALNFGGREHARGGTVTKKEDYRLTSGLN NVSNLG 75

Query: 83 ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQ GAVFSAEVV 129

DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
 Sbjct: 76 KDG-----NPLPRDHRTHL FNLGNCLWHS DSSFRPIPAKFSLLSARVV 118

>ref|YP_002007989.1| taurine dioxygenase, 2-oxoglutarate-dependent
 [Cupriavidus

taiwanensis]
 emb|CAQ71933.1| taurine dioxygenase, 2-oxoglutarate-dependent
 [Cupriavidus
 taiwanensis]
 Length = 303

Score = 55.8 bits (133), Expect = 5e-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 TVRRCPT---IGAEVEGIDFREAFDHDHTYLSLRRALLKYKVLFFRKQAITPAQHVAVAR 81

Query: 63 RFGAIE-----RIGGGDIVAI-SNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY
 114

RFG +E ++V N K G +H+D ++
 Sbjct: 82 RFGELVHPMFTNHPEHPELVVFGGRNDKTRGR-----ENLYHSDVSW
 123

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLV-----YS
 168

+ + G++ P VGG T + +M AAY+ L + + + A H + S
 Sbjct: 124 REIPSMGSMRLRCLECEVGGDTIWINMAAAYENLPQEMKDRIASLKAVHDAMPAPGAALS
 183

Query: 169 QSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-----HAHAIP-
 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 RFGSDFRPAELDLMQYLYRQAAPEYQVRLRWQPDIALWDNRSTQHYA 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 = 5e-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---TGSEVRGVQLSKLSAAGKDQLALLVAQRKVVAFRDQDLADLPIEEALEFGGY
 149

Query: 270 --FKL-PRVMWHSRLAGRPETE 288
K+ P V + S + GR E
Sbjct: 228 KALKIYPDVHYQSEIPGREIKE 249

>ref|ZP_03525650.1| putative taurine dioxygenase protein [Rhizobium etli
CIAT 894]
Length = 169

Score = 55.8 bits (133), Expect = 5e-06, Method: Compositional matrix
adjust.

Identities = 43/162 (26%), Positives = 70/162 (43%), Gaps = 27/162 (16%)

Query: 15 LGATVTGVHLA-TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGAI----- 67
+GA + G+ L L D AA++ L+H ++ F Q HL + +Q FA+R G +
Sbjct: 23 VGAEIKGIRLGGELSDDTTVAAINQLLLKHKVIFFRDQGHLLDSEQEAFARRLGLVPHPT 82

Query: 68 --ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
125

G I+ + + + G Q WH D T++ + +V
Sbjct: 83 QGPVDGTASILNLDSSRGGGRADQ-----WHTDVTFVDAYPKFSVLR
124

Query: 126 AEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY 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 = 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 IEAGMDKYAVLLFRGQDITDEQQLAFALNFGEREHARGGTVTKKEDYRLTSGLNDVSNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLFSLGNCLWHSDFRPIPAKFSLLSARVV 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 = 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 IEAGMDKYAVLLFRGQDITDEQQALAFALNFGEREHARGGTVTKKEDYRLTSGLNVDVSNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-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 = 6e-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 KYAVLIFHGQDITDEQQALAFALNFGEREKARGGTVTKKEDYRLTAGLNVDVSNLGKDG--- 78

Query: 89 QHSPAEWDDMMKVIV-GNMAWHADSTYMPVMAQGAVFSAEVV 129
 P D + GN WH+DS++ P+ A+ ++ SA VV
 Sbjct: 79 --KPLSRDHRTHLFLNPGNCLWHS DSSFRPIPAKFSLLSARVV 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 = 6e-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 AWHTDTGYERNPADYSILKLVKLPETGGDTIWGSSCEIYDKISPAYRSFLEGLTA----T
 206

Query: 167 YSQSKLGHVQQAGSAYIGYGM-----DTTATPLR---PLVKVHPETGRPSLL-IGRHAHA
 217
 ++Q++L + A + Y + T LR P+V+ +P TG SL +G H
 Sbjct: 207 FAQTRLP-ISAAEKGFELYAEPRGSPNNVGTSLRAVHPVVRTNPVTGWKSLFAVGNHVER
 265

Query: 218 IPGMDAAESER----FLEGLVDWACQAPRVHAHQWAAG-DVVVWDNRCLLHRA 265
 I + ES R FL+ +V+ R H+W D+ +WDNR + H A
 Sbjct: 266 INELTPDESRLHDWFLQMIVEEHDTQLR---HRWENQYDIAIWDNRTVYHSA 315

>ref|YP_003270385.1| Taurine catabolism dioxygenase TauD/TfdA [Haliangium
 ochraceum DSM

Sbjct: 223 ASFFHDEARRLGNPLRKGIRGSPLNQGEDLKA--VHPVVRTNPVTGWKSVYVVKGFTRKI
280

Query: 219 PGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
G+ ES+ L+ L + Q +W D+ +WDNR H A

Sbjct: 281 NGVTKDESDMLLQYLFNLVLTQNHDAQVRFWRWNKNDMAIWDNRSTWHCA 328

>ref|XP_001031480.1| hypothetical protein TTHERM_00823780 [Tetrahymena thermophila]

gb|EAR83817.1| hypothetical protein TTHERM_00823780 [Tetrahymena thermophila

SB210]
Length = 250

Score = 55.5 bits (132), Expect = 7e-06, Method: Compositional matrix adjust.

Identities = 59/266 (22%), Positives = 109/266 (40%), Gaps = 44/266 (16%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQH----ALLIFPGQHLSNDQQITFAKR 63
++ + LG T+TGV L L + F + A H L+I P + +++ +

Sbjct: 1 MSEVKSQGLGYTITGVLDLNNLTEEQFKNIQEALWTHEKWGKLVILPPYYAFDNRD----PQ 56

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSP-AEWDDMMKVIVGNMAWHADSTYMPVMAQG-
121

+ AI R+G NV+ DG+V+ +S AE+ WH D +

Sbjct: 57 YPAIVRVG-----NVRLDGSVKPNSKDAEY-----WHKDGNGFRQPGENFI 96

Query: 122 -AVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGS
180

++ + + VGG+T +A + L + + + +V +Q+ + + A

Sbjct: 97 ISILVPKEIAQVGGQTGYA---CSEQVLKDLPENIKEKLEGAQIIIVRTQT-ISDFKDAKP
152

Query: 181 AYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ-
239

+ P+ HP TGR I + + + R ++ +

Sbjct: 153 E-----EHLPEAHHPVFAPHPITGRKVFNITQKNQN--DVILKDGNRIDSKDINPEIEN
204

Query: 240 APRVHAHQWAAGDVVVWDNRCLLHRA 265
+ ++H HQW GDVV+WDN ++HR+

Sbjct: 205 SYKIHGHQWEMGDVVIWDNIRVIHRS 230

>emb|CAY25783.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 55.5 bits (132), Expect = 7e-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 KYAVLIFHGQDITDEQRLAFALNFGEREKARGGTVTKKEDYRLTTGPNDVSNLKGKDG--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
 P D + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 79 --KPLSRDHRTHLFLNCLGNCLWHSOSSFRPIPAKFSLLSARVV 118

>emb|CBI55832.1| unnamed protein product [Sordaria macrospora]
 Length = 381

Score = 55.5 bits (132), Expect = 7e-06, Method: Compositional matrix
 adjust.

Identities = 59/254 (23%), Positives = 101/254 (39%), Gaps = 31/254 (12%)

Query: 41 QHALLIFPGQH-LSNDQQITFAKRFGAI-----ERIGGGD--IVAIS 79
 + ++ F Q+ L+ND Q R G + +GG D I IS

Sbjct: 88 RRGVVFRAQNNLTNDLQKQLILRLGELTGRPSTSGLHIHPILNSDRELGGNDPEISTIS
 147

Query: 80 NVKADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFA
 139

+V+ R S + +++ WH+D + PV A +P GG T +
 Sbjct: 148 SVQNRKLYRDWSGEKAEELSTKKQYTSQWHS DIAFEFVPADYTSRLVQLPKTGGDTLWG
 207

Query: 140 DMRAAYDALDEATR ALVHQRSARHSL--VYSQSKLGHVQ---QAGSAYIGYGMDDTTATPL
 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 HPVVRTNPVTGWKSVYPVGGHVKHVNGVTKEESQKLLGWFVELLERNHDLQVRFKWSNEN
 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 = 7e-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 IEAGVDKYAVLLFRDQDVSDQQQLVFARNFGERENARGGTVTKKEDYRLTSGLNDSVNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

DG +P D + +G+ WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLFLNLSCLWHS DSSFRPIPAKFSLLSARVV 118

>emb|CAY25749.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 55.5 bits (132), Expect = 7e-06, Method: Compositional matrix
adjust.

Identities = 33/108 (30%), Positives = 56/108 (51%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGDIVA-----ISNVK 82
 + A ++A+L+F GQ +++QQ+ FA FG E GG + +SN+

Sbjct: 16 IEAGMDKYAVLLFRGQDITDEQQLAFALNFGEREHARGGTVTRKEDYRLTSGLN DVSNLG 75

Query: 83 ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
 DG +P D + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 76 KDG-----NPLPRDHRTHLFLNLSCLWHS DSSFRPIPAKFSLLSARVV 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 = 7e-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 IGTEIHGVNLRNLNDAQRDDLARLI AVRGVVFVRN QKDFDIDAQRELKGYFGTLHKHATT
154

Query: 74 DIVAISNVKADGTVRQHSPA EWDDMMKVI VGNMAWHADSTYMPVMAQGAVFSAEVVPAV-
132

 + ++ V ++ D + + WH+D TY + + S +V+

Sbjct: 155 AVPKKKGLEDVHVV--YTGDNSSDQRALFSPSFLWHS DVTYE--IQPPSYTSLKVL TGPP
210

Query: 133 ---GGRTC FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT
189

 GG T ++ AAYDAL + + +A H+ ++Q + S +G +

Sbjct: 211 RGGGGDTLWSSQY AAYDALSSHM QNYLKGLTALHT-----ANMQASDSRALGRTVRR
262

Query: 190 TA-TPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQAPRVHAH-
246

T PL++ +P TG SL I G+ ES+ + L + H
 Sbjct: 263 EPITTEHPLIRTNPVGTGWSLFFNPGFVTKIVGIPKTESDAIIRYLTEVVATTQEAVRF
 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 = 7e-06, Method: Compositional matrix
 adjust.

Identities = 40/117 (34%), Positives = 54/117 (46%), Gaps = 7/117 (5%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
 195

T F DMRAAYDAL ++ + A H + S+ LG + + P+
 Sbjct: 1 TEFCDMRAAYDALPRDLQSELEGLRAEHYALNSRFLGDTDYSEA-----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 = 7e-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 AAIGREFSTLQLSEILHDDAKIRDGLIIVSQRGVVFLRNQNLISIADQKNLAIKIGQLTGR
 106

Query: 69 -----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVG-----NMAWHA
 110

G + + K D V S + M + G + WH+
 Sbjct: 107 PEASYLHKHPLSNGKRGLAVDKDGKLDDEVTIMSSEQNKKMYRGRCGPGTKRLASEGWH
 166

Query: 111 DSTYMPVMAQGAVFSAEVVPA-VGRTCFADMRAAYDALDEATRALLVHQRSARH
 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--HPVVVRTNPVTGWKSLFAAGFQIRAGWIDN
283

Query: 221 MDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFKLPRV 275
+ ESE + + + +W+ DV +WDNRC+ H A +D+ RV

Sbjct: 284 VTDYESEMLKSYFLKLISENHDLQVRFWSENDVAIWDNRCVFHTAT-YDYNGARV 338

>ref|XP_501183.1| YALI0B21472p [Yarrowia lipolytica]
emb|CAG83436.1| YALI0B21472p [Yarrowia lipolytica]
Length = 345

Score = 55.5 bits (132), Expect = 7e-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 GWHTDITFEKVPDYLKILSPPTGGGGDTLWASGYHAYEKLTPAYRAFLETTLTAHHS
197

Query: 166 VYSQ-----SKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIP
219

Y + S G V++ + G A PL++ +P TG S+ + +I
Sbjct: 198 EYFKTVAAASGHGIVERPRGHPLNQG DYLOAD--HPLIRTNPVTGWKSVYVNPIFTKSIN
255

Query: 220 GMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

G+ ES+ LE L + H +W DV +WDNR H A
Sbjct: 256 GLSWDESKSILEFLNQNLENHDTVFRFRWPNPDVAIWDNRSTYHTA 302

>emb|CAY25726.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 55.5 bits (132), Expect = 7e-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 IEAGMDKYAVLLFRDQDVSDQQQLVFARNFGERGNARGGTVTKKEDYRLTSGLNDSVNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLFLNLGNCLWHS DSSFRPIPAKFSLLSARVV 118

>emb|CAY25722.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 119

Score = 55.5 bits (132), Expect = 8e-06, Method: Compositional matrix adjust.

Identities = 32/102 (31%), Positives = 53/102 (51%), Gaps = 18/102 (17%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----ISNVKADGTVR 88
 ++A+LIF GQ ++++QQ+ FA FG E+ GG + +SN+ DG
 Sbjct: 22 KYAVLIFHGQDITDEQQQLAFALNFGEREKARGGTVTKKEDYRLTTGLNDVSNLGKDG--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
 P D + +GN WH+DS++ P+ + ++ SA VV
 Sbjct: 79 --KPLSRDHRTHLFLNGLNRLWHSDFRPIPVKFSLLSARVV 118

>emb|CAY25787.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 55.5 bits (132), Expect = 8e-06, 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 KYAVLIFHGQDITDEQQQLAFALNFGEREKARGGTVTKKEDYRLTTGLNDVSNLGKDGKPL 81

Query: 87 VRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
 R H ++ +GN WH+DS++ P+ A+ ++ SA VV
 Sbjct: 82 FRDHRTHLFLN-----LGNCLWHSDFRPIPAKFSLLSARVV 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 = 8e-06, Method: Compositional matrix adjust.

Identities = 38/115 (33%), Positives = 54/115 (46%), Gaps = 7/115 (6%)

Query: 142 RAAVDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR-PLVKV
200

RAAYD L E + + A H ++S+ LG + + S P+ PL++
Sbjct: 1 RAAVDDLPEDFKKELQGLRAEHYALHSRFLGDTEYSES-----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 HAGSRKFLFIGAHASHIEGRPVAEGRMLLAELEHATQPKFVYRHSWKVGDLMV 109

>ref|XP_001387032.1| hypothetical protein PICST_28893 [Pichia stipitis CBS
6054]

gb|EAZ63009.1| predicted protein [Pichia stipitis CBS 6054]
Length = 412

Score = 55.1 bits (131), Expect = 8e-06, 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 IGTEIVGLQLSELTDQQRDELALLIAERVVFFRDQDLSPQKQFELGEYFGKVEVHPQQV
182

Query: 71 GGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVP
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 -----HPIIRTHPVGTGWSLYVNRAMTSRIVGLEPGESKVILEYLFDFVEKNLDIQVRF
348

Query: 247 -----QWAAGDVVVWDNRCLLHRA 265

Q G +WDNR H A
Sbjct: 349 NWKPSQPGLGTSALWDNRISQHFA 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 = 8e-06, Method: Compositional matrix adjust.

Identities = 35/86 (40%), Positives = 47/86 (54%), Gaps = 8/86 (9%)

Query: 196 PLVKVHPETGRPSL-----LIGRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAG
251

P+V VHPETGR L L+ RH I G++ ES L L D + V ++W G
Sbjct: 26 PVVAVHPETGRKDLFVNPLLTRH---IKGLEPVESAALLALLYDRGARLENVIQYRWRRG 82

Query: 252 DVVVWDNRCLLH-RAEPWDFKLPRVM 276

D+V+WDNR + H R E D PR++
Sbjct: 83 DLVLWDNRAVRHRRVEDNDPAAPRIV 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 = 8e-06, 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 KHGVVVIKNQNLTRNQEVFTARLGKTIILPSSFQGNNSYLGHPAIAVVSNYWLNQSWKG
142

Query: 89 -QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS---AEVVPVAV--GGRTCFADMR
142

QHS ++ WH D Y P +FS + + A GG T F D
Sbjct: 143 PQHSFGQY-----WHKDGDFPY-PNNFIFSIYLGDEISAFLEGGDTGFID--
187

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP
202

A + A ++++ ++ +V K+ + + + ++ AT + HP
Sbjct: 188 -GCLAAENAPQSILDVLNSTKIIV---KVSFIDDFRNLKDH-LELYATVKHNFISKHP
241

Query: 203 ETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL
262

R + + + A + E R + + + Q + H+W+ D+++WDN +
Sbjct: 242 LNKRDVCFMFKVAKEQELLYTQEELRAFDEMWKYMLQDKFFYFHKWSQSDILIWDNMAVF
301

Query: 263 HRAEP 267

HRA P
Sbjct: 302 HRAMP 306

>ref|YP_003040556.1| similar to pyoverdine biosynthesis protein pvcb of pseudomona

aeruginosa [Photobacterium aeruginosa]

emb|CAQ83812.1| similar to pyoverdine biosynthesis protein pvcb of
pseudomona

aeruginosa [Photorhabdus asymbiotica]
Length = 281

Score = 55.1 bits (131), Expect = 8e-06, 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 TEEIFPFGLKITPQYSDQHIDTLSVEQLKELTK---KHNLLILRGFKSNLSDHEKYEEYA 65

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGN--MAWHADSTYMPVMA
119
+ +G I G I+ VR+H D + N M H D Y P +
Sbjct: 66 RNWGEIMMWPFGAIL-----DVREHQ-----DATDHVFDNSYMPHLHWGDMYKPTIP
111

Query: 120 QGAVFSAEVPVAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
177
+ +F P GGRT F + R + AT+ + Q S+ Y +K+ H
Sbjct: 112 EFIMFHCAHAPESDQGGRTTFVNTRRV---IANATQQQLSQWKNI-SVTYRINKITH---
164

Query: 178 AGSAYIGYMDTTATPLRPLVKVHPE-----TGRPSL-----LIGRHAHAIPGMDAAES
226
YG + + PL++ HP+ P++ + +HA + +
Sbjct: 165 -----YGGEVHS-----PLLEEHPDNGYVIRYNEPAIDGKFLNKHAIEYHNISPDQV
213

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPE
286
F + ++ ++AH W GD+V+ DN LLH E + K R + + P
Sbjct: 214 AEFQQDFINILYDKRHLIAHSWQKGDLVIVDNFSLHGREGFTSKSERHLQRIHIQSNPV
273

Query: 287 TEGAAL 292
AL
Sbjct: 274 FNNQAL 279

>ref|XP_001903801.1| unnamed protein product [Podospora anserina]
emb|CAP61577.1| unnamed protein product [Podospora anserina]
Length = 377

Score = 55.1 bits (131), Expect = 8e-06, Method: Compositional matrix
adjust.

Identities = 46/194 (23%), Positives = 76/194 (39%), Gaps = 27/194 (13%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
166
AWH+D T+ PV + A+ +P GG T +A YD L E R ++ + +A H

Sbjct: 157 AWHSDITFEPVPSDYAMLKIHTLPVTGGDTLWASGYEVYDRLSEPMREMLKKL TATHDAK
216

Query: 167 Y---SQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPE-----
203

+ LG+ + + P+++ + E

Sbjct: 217 FFLDEARNLGNPLRECEGRSPLNKGAELAAVHPVIRTNREFPHLCLCTSLRVKLT F MVIA
276

Query: 204 -TGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNR
260

TG S+ + + I G+ ES+ L+ L + Q +W+ DV +WDNR

Sbjct: 277 VTGWNSVYVKNKGFTKRINGVTKDESDILLKYL FNMV TQNHDAQVRFRWSKNDVAIWDNRS
336

Query: 261 LLHRAEPWDFKLPR 274

H A +D+ PR

Sbjct: 337 TWHCAT-YDYNDPR 349

>gb|EEY60349.1| alpha-ketoglutarate-dependent sulfonate dioxygenase,
putative

[Phytophthora infestans T30-4]
Length = 355

Score = 55.1 bits (131), Expect = 9e-06, 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-----GGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTY
114

+G + + +G +V S ++G +++ ++ AWH+D +

Sbjct: 130 YGPLHAHQNLGHPKDHHEVVVVENSVETSEGFLKRQMYDPFN-----AWHSDVSN
179

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGH
174

F P VGG T +A AYD L R + +A H+ G

Sbjct: 180 ERQPPSYTSFKVLTNPPVGGDTLWASASEAYDRLTPPMREFISGLTAIHT-----GI
231

Query: 175 VQQAGSAYIGYMDTTATPLR-PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEG
232

Q +A G + P+V+ HP TGR L + I + AES+ L+

Sbjct: 232 PQATAAAARGQTIRRPVVEFEHPVVRTHPVTGRQGLYVNP AFTTRIVQLSKAESDAVLKL
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 = 9e-06, 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 IGTVVEGDVKLEDLGEAEKDDLALLVAQRGVVFFRNQQSMTIEQQRELKHKHFGPLHKHAT
181

Query: 73 -----GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
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 LTTPEVGNDTLWSSGYSVYSSLSKPFQYLESLSAIHS-----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

>dbj|BAD15043.1| hypothetical protein [Bradyrhizobium sp. BDV5680]
Length = 102

Score = 55.1 bits (131), Expect = 9e-06, Method: Compositional matrix
adjust.

Identities = 35/107 (32%), Positives = 50/107 (46%), Gaps = 5/107 (4%)

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGR
206

ALD+ T+A + HSL+YS+ LG + Y + L+ LV+ HP R
Sbjct: 1 ALDDETKAEIEDFVCEHSLMYSRGSLGFAE-----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 marneffe* ATCC 18224]

gb|EEA23373.1| alpha-ketoglutarate-dependent sulfonate dioxygenase,
putative

[*Penicillium marneffe* ATCC 18224]

Length = 419

Score = 55.1 bits (131), Expect = 9e-06, 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 GTEIQGVQISELTPEGLDEMALLCAERGCLVFRDQEFGNIGFEKQKEIARHFGLPHKHGW
187

Query: 72 -GGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA--EV
128

A+ + + + V + E + +H D + V G F E
Sbjct: 188 MPHRAAVHSSETEEFVIVYDSKEKSPIQ-----FHVDQS-PEVQPPGMTFFCMLLES
238

Query: 129 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMD
188

P GG T + M A++ L + R + A H+ S+ ++ G +
Sbjct: 239 PPGAGGDTLISSMTRAFERLSPSFRKRLEGLQALHTTAGPVSR--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--IHPVVTVHPVTGQKALFVNSSYTERIIGWDDEESEYLLRFLFDHVNVRGQDFCCRV
354

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFK 271

++ G VVVWD R H ++ D+K
Sbjct: 355 -----RYEPGTVVVWDQRVTQH-SQTLDYK 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 ADIEAGMDKCAVLLFRDQDITDDQQLIFARNFGERENARGGTVTKKEDYRLTSGLNDSVN 73

Query: 81 VKADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 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---FGTEVDGIQLSQLDDKKGKDELALFLAQRKVLLFNDQDFADKGPFGFAVEF
 138

Query: 61 AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
 120

K FG + I + T R+ E + ++ +H+D +Y ++

Sbjct: 139 GKYFGR LH-IHPSSGAPRGYPELHITYRRPEKGELQRFANRTTSIGFHSDVSYELTPSR
 197

Query: 121 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGS
 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-GVERRKPVSNIHPLVRLDPVTGEKSLYVNRAFGRRIVELKKEESDALLDFL 303

>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 KYAVLIFHGQDITDEQQALAFALNFGEREKARGSTITKKEDYRLTTGLNDVSNLGKDG--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
 P D + +GN WH+DS++ P+ A+ ++ SA VV
 Sbjct: 79 --KPLSRDHRTHLFLNLCNCPWHSDSSFPIPAKFSLLSARVV 118

>ref|XP_459377.1| hypothetical protein DEHA0E01606g [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 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGD 74
 +G + G+ L L+D L + ++ F Q LS +Q+ +G +E+
 Sbjct: 125 IGTEIIGLQLKDLNDQQKDELALLIAERVVFFRDQDLSPQKQLELGSYWGTVVEK--HAQ
 182

Query: 75 IVAISNVKADGTVRQHSPAEWDDMMK-----VIVGNMAWHADSTYMPVMAQGAV
 123
 V + + + W D+ + + G WH D T+
 Sbjct: 183 QVHVPGLHGITVI-----WQDLFRRNGLDINFKNAIGQGTSIWHTDLTHELQPPGITH
 235

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
 183
 + +P VGG T ++ AAYD L A + + ++A V + + Y+
 Sbjct: 236 LHNDIAPGVGGDTVWSSGYAAYDKLSPAFQKFLGKNA-----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-----GDVVVWDNRCLLHRAEPWD 269
 + + + W G +WDNR H A WD
 Sbjct: 338 FEVFEKNLDIQVRFNWKPTIDGLGTSALWDNRVSOHFA-IWD 378

>ref|NP_930051.1| hypothetical protein plu2817 [Photorhabdus luminescens subsp.

laumondii TTO1]

emb|CAE15191.1| unnamed protein product [Photorhabdus luminescens subsp. laumondii

TTO1]

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 TEEITPFGKIPQYSDQHIDTL---PVEQLKELARKHLLILRGFKSDLSDHEKYEKYA 65

Query: 62 KRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGN--MAWHADSTYMPVMA
119

+ +G I G I+ VR+H D + N M H D Y P +
Sbjct: 66 RNWGEIMMWPFGAIL-----DVREHQ-----DATDHVFDNSYMPPLHWDGMYKPTIP
111

Query: 120 QGAVFSAEVPVAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
177

+ +F P GGRT F + R + AT+ + Q S+ Y +K+ H
Sbjct: 112 EFIMFHCAHAPESDQGGRTTFVNTRRV---VANATQQQLEQWKNI-SITYRINKVTH---
164

Query: 178 AGSAYIGYGMDDTTATPLRPLVKVHPETG-----RPSL----LIGRHAHAIPGMDAAES
226

YG + + PLV+ HP+ P++ + +HA ++ +
Sbjct: 165 -----YGGEVHS----PLVEEHPDRNGFVIRYNEPAVDGEKFLNKHAIEYHNINPDQV
213

Query: 227 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPE
286

F + ++ ++AH W D+V+ DN LLH E + K R + + P
Sbjct: 214 AEFQQDFINILYDKRHLYAHAWKKSDDLVIVDNFSLLHGREGFTSKSERHLQRIHIQSNPA
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 KYTVLIFHGQDITDEQQALAFALNFGEREKARGGTVTKKEDYRLTTGLNDVSNLGKDG--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAE VV 129

P D + +GN WH+DS++ P A+ ++ SA VV
Sbjct: 79 --KPLSRDHRTHLFLNGLNCLWHS DSSFRPTPAEFSLLSARVV 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 IGTEIRGVNLGKLNDAQRDDLARLIAVRGVVFFRNQKDFDIQAQRELKGYFGTLHKHATT
155

Query: 74 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVG
133
+ ++ V ++ D + + WH+D TY P G
Sbjct: 156 AVPKKKGLEDVHV--YTKENAGDQRALFPPSFLWHSVDTYEVQPPSYTSLKVLTPGPPRG
213

Query: 134 G--RTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD-TT
190
G T ++ AAYDAL + + +A HS ++Q + S +G +
Sbjct: 214 GGGDTLWSSQYAAAYDALSSHMQNYLKGLTALHS-----ANMQASDSRALGRTVRRDP
265

Query: 191 ATPLRPLVKVHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQAPRVHAH-QW
248
T PL++ +P TG SL I G+ ES+ ++ L + H QW
Sbjct: 266 VTTEHPLIRTNPVTGWNSLFFNPGFVTKIVGIPKTESDAIKYLTEIIATTQEAHVRFQW
325

Query: 249 AAGDVVVWDNRCLLHRA 265
DV +WDNR H A
Sbjct: 326 GEDDVALWDNRRTTNHSA 342

>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 AVIGREFPKLQLSEILKDDTKLRDLAVLISQRGVVFFRNQDINIEDQKYLQORLG--ELT
117

Query: 71 GGGDIV-----AISNVKADGTVRQHSPAEWDDMMKVI-----VGNM
106

G + A+SN K V ++ + DD + VI +
Sbjct: 118 GKPETSKLHRHALSNSKRGIADVEND--GKLDDEVSVISSEQNRKFYSDRFSSLSRSLAGE
175

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPA-VGGRTCFADMRAAYDALDEATRVLVHQRSARH--
163

WHAD T+ + + A+ P VGG T +A YD L + L +A H
Sbjct: 176 GWHADITFENIPSDYAILKIIQPPEDVGGDTLWASGYELYDRLSPPIQKLAESLTATHHQ
235

Query: 164 -SLVYSQSKLGH--VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH---AHA
217

+ V +++ G + + + G+D A P+++ +P TG SL H A
Sbjct: 236 PNFVRVKNEFGQELIDENRGSPENGLDFKAE--HPVIRTNPVTGWKSLFAAGHQLTAGH
293

Query: 218 IPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVWDNRCLLHRA 265

I G+ ESE + + +W D+ +WDR + H A
Sbjct: 294 INGVTESEILKNYFRQLITENHDLQVRFRWGKNDLAIWDRSVFHTA 342

>emb|CAY25743.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 54.7 bits (130), Expect = 1e-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 ADIEAGMDKYAVLLFRNQDITDQQQLAFALNFGERESARGGTVTKKEDYRLTSGLNVDVN 73

Query: 81 VKADGTVRQHSPAEWDDMMKVI-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 = 1e-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 ADIEAGMDKYAVLLFRDQDITDQQQLIFARNFGERENARGGTVTKKEDYRLTSGLNVDVN 73

Query: 81 VKADGTVRQHSPAEWDDMMKVI-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 = 1e-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---IGTEIAGLQLTALTPAQKDDLALLVAERGVVFFRDQDMDVHEQIAFA
137

Query: 62 KRFGA--IERIGG--GDIVAISNVKADGTV---RQHSPAEWDDMMKVIVGNMAWHADSTY
114

FG I ++ G D+ + + D T R H WH+D +Y

Sbjct: 138 AYFGELHIHQMAGIIPDLPWVHPIYKDRtavNGRSHQ-----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-IHPVVRTHPVTKWKTLYVNENFTKEIIGIEK
292

Query: 224 AESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLH 263

S+ L+ L +A +W V +WDNR H

Sbjct: 293 RVSDALLDTLYRTIAEAYEYQVRWKWTPNAVAIWDNRVTFH 333

>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 ADIEAGMDKYAVLLFRNQDITDEQQLAFALNFGERESARGGTVTKKEDYRLTSGLNDSVN 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 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA-----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

>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 ADIEAGMDKYAVLLFRNQDISDEQQ LAFALNFGERESARGGTVTKKEDYRLTSG LNDASN 73

Query: 86 TVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
+ P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 74 LGK DGRPLARDSRTHL 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 RNASHVEGLPVAEGRMLLAELXEHATQREXVYRHRWNVGD XVMWDNRCVFHRGRRYDISA
100

Query: 273 PRVM 276
R +

Sbjct: 101 RREL 104

Query: 93 AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
152

VG WH D ++ P +++ VVP G T FA L+E
Sbjct: 95 -----VGRTGWHIDGSFQPAPFGYSLYHMVVVPKEGN-TVFA-----PLNELI
136

Query: 153 RALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLL--
210

L ++ R ++ S D P+ PL+ HP TG +L
Sbjct: 137 SGLTEEQRRRWEQLWMVS-----DRRGPPVHPLIYSHPLTGAKTLCFH
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 GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAY-----DA
147

G WH D +Y + VP G T F D A
Sbjct: 90 GGGYWHTDMSYKSANTVFSTLLSVQVPDQHGETQFIDCVAGLHQVRQWLVSFGPCQHLKG
149

Query: 148 LDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRP
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 SLYAPAATAMQIEGVTPALSHRILDSLVDLFLVQQAPR-YRHAYRPGDIVIWDNLSTLHKG
262

Query: 266 EP 267

P
Sbjct: 263 PP 264

>ref|ZP_05476507.1| putative taurine catabolism dioxygenase [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 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRF 65
 +++ +LG V+G L A + L++F Q L + A+R G

Sbjct: 1 MKVASLSRSLGLQVSGGALQDCSSGELAEALRLVERAGLVVFRQCLDDGDLHALARRIG 60

Query: 66 AIERIGGG-----DIVAISNVK-ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMP
 116

+E +I +SN++ DG A+ D WH+D +
 Sbjct: 61 PLEESSRKVCLSPHEPEISYLSNLRDEGQFIGFPGADTD-----YWHSDQQHRE
 110

Query: 117 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
 176

A AV V A GG T F LDEAT A + R A + ++ V+
 Sbjct: 111 RPATLAVLYCVVPAASGGATSFVSADVESAGLDEATVADLAGRRAYVEPAFNHDNAPRVR
 170

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW
 236

+ A + T+ T R V T +G G+ A ES + ++
 Sbjct: 171 VSHPLL-----TSRTGDRHYAYVSDNT-----LG-----FTGLAADESAALKQRVLSR
 214

Query: 237 ACQAPRVHAHQWAAGDVVVDNRCLLHRAEPW 268

+ R++AH+W AGD ++DN LLHR E +
 Sbjct: 215 LLEPSRIYHRWQAGDFALYDNTQLLHRRERF 246

>emb|CAY25741.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 119

Score = 53.9 bits (128), 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 ADIEAGMDKYAVLLFRDQDITDEQQLAFALNFGERESARGGTVTKKEDYRLTSGLNVDVSN 73

Query: 81 VKADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

+ DG P D + +GN WH+DS++ P+ A+ ++ SA VV
 Sbjct: 74 LGKDG-----RPLARDSRTHLFNLGNCLWHSDDSSFRPIPAKFSLLSARVV 118

>ref|ZP_06478274.1| taurine catabolism dioxygenase TauD/TfdA [Pseudomonas syringae pv.

aesculi str. 2250]
Length = 281

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 GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAY-----DA
147

G WH D +Y + VP G T F D A

Sbjct: 86 GGGYWHTDMSYKSANTVFTSLLSVQVPDQHGETQFIDCVAGLHQVRQWLVSFGCPQHLKG
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-APRVHAHQWAAGDVVVWDRCLLHRA
265

SL A I G+ A S R L+ LVD+ Q APR + H + GD+V+WDN LH+

Sbjct: 200 SLYAPAATAMQIEGVTPALSHRILDSLVDLFLVQQAPR-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 = 2e-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

>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 = 2e-05, Method: Compositional matrix adjust.

Identities = 65/292 (22%), Positives = 109/292 (37%), Gaps = 32/292 (10%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG-QHLSNDQQI-TFAKRF 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 EISIWPFQKLVLEL-----VEQENPQ--DHIFDHSYVPMHW--DGMYPQVPEYQIFH
112

Query: 126 AEVVPVAVG--GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
183

P G GRT F++ A +A + + +Y + + + S I
Sbjct: 113 CVKAPLSGHGGRTTFSNTVLALKNASPELKAFWGKVTG----IYQREMEFYKSKTVSPII
168

Query: 184 GYGMDTTATPLRPLVKV---HPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQA
240

T P R + P + + G+ E E F +GL
Sbjct: 169 -----TKHPKRDFSVIRYNEPPSADKGFVNPPDLEFAGVPVGELEAFHQGLKSALYAP
222

Query: 241 PRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL 292

+AH+W GDVV+ DN LLH E + K PR + ++ P + L
Sbjct: 223 ENFYAHEWQDGDVVITDNFTLLHGREAFTSKSPRHLQRVQVQSSPPFDNPGL 274

>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 = 2e-05, Method: Compositional matrix adjust.

Identities = 63/275 (22%), Positives = 109/275 (39%), Gaps = 31/275 (11%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSN---DQQITFA 61
++ IT +G+ V G+ L+ L D L + +++F Q + +Q FA
Sbjct: 72 SVSITKLTTPRVGSEVRGLQLSLSVQKDELALLIAERGVVFRDQDFKDIDGPGKQKEFA
131

Query: 62 KRFGA--IERIGG--GDIVAISNVK--ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
115

FG + +G D + N+ AD R + + + +H+D +Y
Sbjct: 132 GYFGRLHVHPVGAHVKDHFHNIYLGADNLYRLQTRS-----TKLTTTGYHSDVSYE
184

Query: 116 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHV
175

 + + VP+ GG T + AAY+ L + + L+ A HS + Q++
Sbjct: 185 HQPPGVTLTLLSVPSSGGDTAWVSQVAAYERLSDPPIKKLLEGLRAEHS-GFPQAERARA
243

Query: 176 QQAGSAYIGYGMDTTATPLR---PLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLE
231

 G P++ P+V+VHP TG +L + I G+ ES+ L+
Sbjct: 244 D-----GKFFVRREPVKSEHPVVRVHPVTGEKALFVNSGF'TKRI IGLKDEESDAILQ
294

Query: 232 GLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 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 = 2e-05, Method: Compositional matrix
adjust.

Identities = 54/193 (27%), Positives = 80/193 (41%), Gaps = 43/193 (22%)

Query: 109 HADSTYMPVMAQGAVFSAEVVPAVG----GRTCFADMRAAYDALDEATRALVHQRSARHS
164

 H D Y+ + + VF + V AVG GRT F+ AA T+AL
Sbjct: 110 HWDGMYLKTVPPELQVF--QCVSAVGEGQGGR'TTFSSTTAALRLASPETKALW-----
159

Query: 165 LVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL-----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 PSTYHFSGIEPEEQEQLLSSLQD-ALYDPRVYYAHQWQSGDIAIADNYSLHGRESYTSQ
267

Query: 272 ----LPRVMWHSR 280

 L RV H++
Sbjct: 268 SGRHLRRVHIHAK 280

>ref|XP_001595570.1| hypothetical protein SS1G_03659 [Sclerotinia
sclerotiorum 1980]

 gb|EDO01185.1| hypothetical protein SS1G_03659 [Sclerotinia sclerotiorum
1980]

Length = 331

Score = 53.5 bits (127), Expect = 2e-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---MGTEIKGVQLSKLSNAGKDQLARFVAERKVVAFRDQDFADLPFAEAVEYG
 153

Query: 62 KRFGA--IERIGGG-----DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTY
 114
 + FG I G ++ + D T + + ++AWH+D TY
 Sbjct: 154 RYFGRPHIHPTSGAPAGHPEVHLVHRSAGDKTA-----ESFFETRNSVAWHSDVTY
 205

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGH
 174
 VP GG T FA+ AY+ L ++ + +H SA HS G
 Sbjct: 206 EKQPPGTTFLYVLDVPESGGDTLFANGVEAYNRLSDSFKERLHGLSATHS-----GI
 257

Query: 175 VQQAGSAY-IGYGMDTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDDAAESERFL 230
 Q S Y G + P+V+ HP TG +L + R + G ES+ L
 Sbjct: 258 EQVNASRYRNGIARREPVVNVHPIVIRTHPVTGEKALYVNRQFTRKVVGFKQEESDMLL 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 = 2e-05, Method: Compositional matrix adjust.

Identities = 37/115 (32%), Positives = 55/115 (47%), Gaps = 7/115 (6%)

Query: 142 RAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR-PLVKV
 200
 RAAYDAL ++ + A H + S+ LG + + P+ PLV+
 Sbjct: 1 RAAYDALPRDLQSELEGLRAEHYALNSRFLLGDTDYSEA-----QRNAMPPVNWPLVRT 54

Query: 201 HPETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
 H +GR L IG HA + G+ AE L L++ A Q V+ H+W GD+V+
 Sbjct: 55 HAGSGRKFLFIGAHASHVEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGDLM 109

>emb|CAY25735.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 53.5 bits (127), Expect = 2e-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 IEAGMDKYAVLLFRNQDITDEQQQLAFSLNFGEREKSRGGTVTKKEDYRLTSGLN DVSNLG 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 AAVHAGMDEFGVLFVFDQKIDDDQQLVFSRSLGPLEQATGDIAAPQDWRMSMDLNDISNL 73

Query: 82 KADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
+ + DD ++ +GN WH+DS++ V A+ ++ SA VV

Sbjct: 74 DKNNKILAR-----DDRRRLFGLGNQLWHS DSSFKDVPKYSLLSARVV 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 VEAGMDKYAVLLFRNQDISDDQQLAFALNFGEREHARGGTVTKKEDYRLTSGLN DVSSLG 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 GEGLGAQITGVDPKILDDITTDEIRDIVYANKLVILKDVNPSPEEFLKLGKIVGQIVPYY 66

Query: 68 -----ERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGAV
 123

+I S V+ G + + WH D +MP ++
 Sbjct: 67 EPMYHHEDHPEIFVSSSTVEGQGVPKTGA-----FWHIDYMFMPPEPFAFSM
 111

Query: 124 FSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQAGSAYI
 183

VP T F D+ + +L A +A AR +L + + Y
 Sbjct: 112 VLPLAVPGHDRGTYFIDLAKVWQSLPSAQQA-----PARGTLSTHDPRRHIKIRPSDVYR
 166

Query: 184 GYG-----MDTTATPLR-PLVKVHPETGRPSLLI-----GRHAHAIPGMDAAESER
 228

G + P++ P V HP+TG L I + + + D A
 Sbjct: 167 PIGEVWDEISRATPPIKWPTVIRHPKTGEEILYICATGTTKIEDKDGNLV---DPAVLAE
 223

Query: 229 FL--EGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE 266

L G +D +P +H + GD+++WDNR L+HRA+
 Sbjct: 224 LLAATGQLDPEYNSPFIHTQHIEVGDIIILWDNRVLMHRAK 263

>ref|XP_002472070.1| predicted protein [Postia placenta Mad-698-R]
 gb|EED82686.1| predicted protein [Postia placenta Mad-698-R]
 Length = 362

Score = 53.5 bits (127), Expect = 3e-05, Method: Compositional matrix
 adjust.

Identities = 42/180 (23%), Positives = 72/180 (40%), Gaps = 6/180 (3%)

Query: 90 HSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL
 148

H E ++ + V WH+D T+ PV + A+ +P GG T +A AYD L
 Sbjct: 135 HKQIELEEDLNVSQFATKEWHS DITFEPVPSDFAILKIHTLPETGGDTLWASGYEAYDRL
 194

Query: 149 DEATRALLVHQRSARHSLVYSQS---KLGHVQAGSAYIGYMDTTATPLRPLVKVHPETG
 205

A + +A H + +S + G G + T + P+++ +P TG
 Sbjct: 195 SPALAKHLEGLTAVHEATFFKSYVERQGQTLHEGPRGNPENVTDLRTVHPVIRTNPVTG
 254

Query: 206 RPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH
 263

+L + ++ I + ES+ L+ L + +W DV +W N H
 Sbjct: 255 WKALFVNKNFTRILELTKDES DATLDYLFRLVSDNHDLQVRFKWNKNDVAIWANSASFH
 314

>emb|CAY25769.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 53.5 bits (127), Expect = 3e-05, Method: Compositional matrix
 adjust.

Identities = 33/108 (30%), Positives = 55/108 (50%), Gaps = 18/108 (16%)

Query: 35 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGD-----IVAISNVK 82
 + A ++A+L+F GQ ++++QQ+ FA FG E GG + +SN+
 Sbjct: 16 IEAGMDKYAVLLFRGQDITDEQQALAFALNFGEREHARGGTATKKEDYRLTSGLN DVSNLG 75

Query: 83 ADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
 DG +P D + +GN WH DS++ P+ A+ ++ SA VV
 Sbjct: 76 KDG-----NPLPRDHRTHLFLNGLNCLWHPDSSFRPIPAKFSLLSARVV 118

>gb|EEU42983.1| hypothetical protein NECHADRAFT_46558 [Nectria
 haematococca mpVI
 77-13-4]
 Length = 333

Score = 53.5 bits (127), Expect = 3e-05, Method: Compositional matrix
 adjust.

Identities = 52/199 (26%), Positives = 80/199 (40%), Gaps = 29/199 (14%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
 167
 +HAD+++ ++ E P VGG T + YD L +A + V A H+
 Sbjct: 119 FHADTSFEINPPSYSLRMEEHPEVGGDTAWISGYGLYDTLSDAMKRFVEGLHAVHT---
 175

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPL---RPLVKVHPETG-----RPSLLIGRHAHAI
 218
 S+L Q + +G P+ P V+ HP TG P + G
 Sbjct: 176 --SRL----QYDTILDWGTGPNRPPIDTHHPAVRTHPVTGLKAVNVNPGFVTG-----F
 224

Query: 219 PGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVDNRCLLHRAEPWDFKLPRVMW
 277
 + ES++ L+ A + +W G V +WDRNC+LHR P + PR
 Sbjct: 225 AELKKVESDKLLDFFSYHLHSADDHYVRWKWTVGAVAMWDRNCVLRHVIPGTYDTPRRGI
 284

Query: 278 HSRLAGR-----PETEGAA 291
 + + G P +EG A
 Sbjct: 285 RTTVFGEKPYYPNSEGRA 303

>emb|CAY25766.1| alpha-KG-dehydrogenase [uncultured bacterium]
 Length = 119

Score = 53.5 bits (127), Expect = 3e-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 KYAVLIFHGQDITDEQQALAFALNFGEREKARGGTATKKEDYRPTTGLNDVSNLGKDG--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
 P D + +GN W++DS++ P+ A+ ++ SA VV
 Sbjct: 79 --KPLSRDHRTHLFLNGLNCLWYSDSSFRPIPAKFSLLSARVV 118

>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 = 3e-05, Method: Compositional matrix
 adjust.

Identities = 46/171 (26%), Positives = 77/171 (45%), Gaps = 21/171 (12%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH--SL
 165

WHAD T+ V + A+ +P GG T +A Y+ L + ++ +A H S
 Sbjct: 160 WHADITFERVPSDYAMKIHITLPETGGDTLWASGNEIYERLSPKMKEMLEGLTATHDASF
 219

Query: 166 VYSQS-KLGH--VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG----RHAHAI
 218

+ ++ +LG + + + G + +A + P+V+ +P TG+ SL I R H +
 Sbjct: 220 FHDEARRLGQDIREDMRGSPLNIGKELSA--VHPVVRTNPVTGKKSLEFINQGFTRRLHPL
 277

Query: 219 PGMDAAESERFLEGLVDWACQAPRVHAHQ----WAAGDVVVWDNRCLLHRA 265

++ +L+ LV P H Q W+ DV +WDNR H A
 Sbjct: 278 TKDESLLLLPWLKSLV-----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 = 3e-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 IEAGMDKYAVLLYRGQDITDEQQALAYALNFGEREHARGGTVTKKEDYRPTTGLNDVSNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

DG +P D + +GN WH+DS++ P+ A+ ++ SA VV
 Sbjct: 76 KDG-----NPLPRDHRTHLFLNGLNCLWHSDDSSFRPIPAKFSLLSARVV 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 = 3e-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---IGREFSDLQLTDILHDDQKLRDLAITVSRRGVVFRRNQSINSDEQKVLGQ
 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 RHLASEGWHADITFERVPSDYAILKITHSPEDQTGGDTLWASGYEVYDRLSPPIQALTD
 221

Query: 159 RSARH-----SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL--I
 211
 +A H + + + + +Q A G D A+ PL++ +P TG SL
 Sbjct: 222 LTAVHHQPSFNNAIKEHGIELIQGDRGAPENTGYDFRAS--HPLIRTNPVTGWKSLFGAA
 279

Query: 212 GRHAHA-IPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265
 G+ + I G+ ESE + + + +W D+ +WDNR + H A
 Sbjct: 280 GQVDNGWIEGVTKRESEILKKYFRQLIAENHDLQVRFKWTNDLAIWDNRSVFHTA 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 = 3e-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+FPGQ L+ QQI
 Sbjct: 1 MSTTALFSVTRLAPHLGAEITGLDLRPTVPKTLALIRYALVEHQLLVFPGQTLTPIQQI 60

Query: 59 TFAKRFGAIERIG----GGDIVAISNVKADGTVRQHSPAEWDDMMKVIIVGNMAWHADSTY
 114

++ FG +E D I V D R+ P VG WH D ++
 Sbjct: 61 ALSRAFGEVEIFSPHPATADFPEIFPVSNDP--RRGHPD-----VGRY-WHHDGSF
 108

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA-----LVHQRSARHSLVYS
 168

+ + F G F++ AY++LD + VH RH+
 Sbjct: 109 RKQATRLSFFYFREASEWVGDFLFSNSYLAYESLDRDVQQSFEPLITVHNSNGVRHA----
 164

Query: 169 QSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESE
 227

LV HP TGR L I A + GM A +
 Sbjct: 165 -----LVPTHPLTGRKLLYINLGLTAGVVGM-AKQDY
 195

Query: 228 RFLEGLVDWACQAPRVHA-HQWAAGDVVVWDNRCLLHRA 265

L G ++ P H+ GD+++ DN + H A
 Sbjct: 196 IKLAGFINRHLSRPEFTLRHKPRPGDLILCDNHSVAHNA 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 = 3e-05, Method: Compositional matrix
 adjust.

Identities = 39/115 (33%), Positives = 52/115 (45%), Gaps = 7/115 (6%)

Query: 142 RAAVDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR-PLVKV
 200

RAAYD L E + + A H + S+ LG + S P+ PLV+
 Sbjct: 1 RAAVDLDPEDFKKELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWPLVRT 54

Query: 201 HPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255

H +GR L IG HA I G AE L L++ A Q V+ H W GD+V+
 Sbjct: 55 HAGSRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDLM 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 = 3e-05, Method: Compositional matrix
 adjust.

Identities = 49/171 (28%), Positives = 69/171 (40%), Gaps = 31/171 (18%)

Query: 109 HADSTYMPVMAQGAVFSAEVVPAV--GGRTCFADMRAAYDALDEATRVLVHQRSARHSLV
166

H D Y P + + +F PA GGRT F + R LD A R R +
Sbjct: 107 HWDGMYKPTVPEFQLFHCVHAPAADEGGRTIFINTRQLLVLDLGERLA----RWERVVIT
162

Query: 167 YSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL-----LIGRHA
215

Y ++ H YG + ++ PL+ HP +G + + +HA
Sbjct: 163 YRIKQVVH-----YGGEVSS----PLLVPHPVSGETVMRYNEPPREGGRFLNQHA
208

Query: 216 HAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE 266

I G+ E FL+ L + +AHQW GDVV+ DN LLH E
Sbjct: 209 LQIEGIPPEEQGAFLQDLHERLYDPRYFYAHQWQPGDVVIADNFGLLHGRE 259

>emb|CAY25727.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 53.1 bits (126), Expect = 3e-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 KYAVLTFHGHGHDITDEQQALAFALNFGEREKARGGTVTKKEDYRLTTGLNDVSNLKGKDG--- 78

Query: 89 QHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129

P D + +GN WH+DS++ P+ A+ ++ SA VV
Sbjct: 79 --KPLSRDHRTHLFLNGLNCLWHS DSSFRPIPAKFSLLSARVV 118

>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;

dnaJ-like protein, putative [Candida dubliniensis CD36]

Length = 388

Score = 53.1 bits (126), Expect = 3e-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---LGTEIKGIQLSQLNDAKDEVALLAQRGVLFVFRDQDFI-DKGPEFVTK
138

Query: 64 FGAIERIGGGDIVAIS-----NVKADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTY
114

+ + G I S +V G +++ P E + V+ ++++ + T

Sbjct: 139 Y--VSHYGPLHIHPTSGAPKGHDPDIHVVLSGDTKEY-PFEKKTNLVVLHSDVSYELNPTA
195

Query: 115 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLV-----YSQS
170

+ +A + + + GG T F + AYD L + + A HS V ++
Sbjct: 196 LSFLA-----ATNIPQSGGGDTVVFVNTVEAYDRLSPLFKEKLEGLKAVHSAVEQANFAIF
250

Query: 171 KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERF
229

K GHV++ + P+V+ P G+ L + I G+ ES
Sbjct: 251 KKGHVKRH-----PVENVHPIVRTTP-LGQKVLVYVNNGFTRKIEGLKEEESYL
298

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 = 3e-05, Method: Compositional matrix
adjust.

Identities = 69/281 (24%), Positives = 113/281 (40%), Gaps = 42/281 (14%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGA-IER---- 69
+G + GV LA L++ L + ++ F Q L +Q+ + +G+ IE+

Sbjct: 111 IGTEIVGVQLADLNEQQLELALLIAERTVVFFRDQDLPPAKQLEIGQFWGSQIEKHPQV
170

Query: 70 --IGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
127

+ G I+ + D + + A + K G WH D + A +
Sbjct: 171 PHVPG--YPGITVLWPDHQILEGRKANF----KQPGGASGWHTDLVHEAQPAGLTHLHND
224

Query: 128 VVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
187

+P+VGG T ++ AYD L A + ++ ++A + ++ YI
Sbjct: 225 QIPSVGGDTAWSSGYGAYDKLSPAFQEFNGKTA-----IYRSAHTYIDRN-
270

Query: 188 DTTATPL-----RPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESERFLEGLVDWACQAP
241

D A P PLV+ HP TG +L + R I G++ ES+ L L D +
Sbjct: 271 DPLAGPKHIEREHPVLRTHPVTGWKTLWVNRAMTVRIVGLEPKESDAILSYLYDVYEKNQ
330

Query: 242 RVHAH-QWAA-----GDVVVWDNRCLLHRAEPWDF--KLPR 274

+ +W G +WDNR H A WD+ K PR
Sbjct: 331 DIQVFRWQPTKEGLGTSAIWDNRISQHNAI-WDYEGKEPR 370

>gb|ACG80575.1| TfdA [uncultured bacterium]
Length = 118

Score = 53.1 bits (126), Expect = 3e-05, Method: Compositional matrix
adjust.
Identities = 45/129 (34%), Positives = 58/129 (44%), Gaps = 20/129 (15%)

Query: 138 FADMRAAYDALDEATRVLVHQR SARHSLVYSQSKLGHVQQAGSAYIGYGM-----TTATP
193
FADMRAAYDAL E +A + A HS+ YS+ +LG A G T A
Sbjct: 3 FADMRAAYDALPEDMKARLEGLQAHHSIAYSRLGFEFSGDEAXAPEGRRASAGTHAAA 62

Query: 194 LRPLVKVHPETGRPS---LLIGRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAA
250
RP + + R S L+ R A P A ++R V+ H W A
Sbjct: 63 HRPQISL-SRLARESHTRLVRRRQAAAPRSHRAPTQRQF-----VYRHAWRA
109

Query: 251 GDVVVWDNR 259
GD+V+WDNR
Sbjct: 110 GDLVMWDNR 118

>emb|CAY25718.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 53.1 bits (126), Expect = 4e-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 IEAGMDKYAVLLFRGQDITDEQRLAFALNFGEREHARGGTVTKKEDYRLTSGLNDSVNLG 75

Query: 83 ADGTVRQHSAPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
DG +P D + +GN WH DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLFLNCLWHFDSFRPIPAKFSLLSARVV 118

>ref|XP_001826717.1| hypothetical protein [Aspergillus oryzae RIB40]
dbj|BAE65584.1| unnamed protein product [Aspergillus oryzae]
Length = 372

Score = 53.1 bits (126), Expect = 4e-05, Method: Compositional matrix
adjust.
Identities = 40/174 (22%), Positives = 72/174 (41%), Gaps = 15/174 (8%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQR SARHSLVY
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 AQPGFNRVAKENDFEIFTGPRGAPENVGDKLEAIHPVIRTNPVITGWKSVFAVGVHVAKVN
280

Query: 220 GMDAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVWDNRCLLHRAEPWDFK 271

+ ES+ L V + + +W D+ +WDNR + H A +D+K
Sbjct: 281 DLSEEDSDHLLRWVSLIVENHDLQVRLRWENPNDLAIWDNRSVYH-AATYDYK 333

>ref|ZP_06240159.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp.
Eu11c]

gb|EFA58494.1| Taurine catabolism dioxygenase TauD/TfdA [Frankia sp.
Eu11c]

Length = 316

Score = 52.8 bits (125), Expect = 4e-05, Method: Compositional matrix
adjust.

Identities = 70/317 (22%), Positives = 120/317 (37%), Gaps = 55/317 (17%)

Query: 1 MAQTTLQITPTGATLGATVTGVHLATL-DDAGFAALHAAWLQHALLIFPGQHLSNDQQIT 59

M+ T++ G GA ++G+ A L D A + + + +++F G S + Q+
Sbjct: 1 MSTITVKDLRDGLPFGARISGITSAAALADQAVRQEIADTFERRGVIVFEGVEPSTELQVQ 60

Query: 60 FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGN-----MAWHADST
113

+ FG ++ + + G + + DM V + WH D
Sbjct: 61 ISNVFGPLKDHPSKTTTRVDAERWPGVIAISATP---DMCIVEIDGKPRISWQPWHFDHC
117

Query: 114 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
173

Y + + V A V G T FAD ++ L +A+ +A +++Y+ L
Sbjct: 118 YNDELNRAGVLRVAVTVAPDDGLTGFADGIQIWNDLPAEAKAV----AADLNVIYTLDDL
173

Query: 174 HVQQAGSAYIGYGMDTTATPLRPLVK-----VHP-----ETGR-----PS
208

Q+ +G+ + LRP +HP ETG P
Sbjct: 174 PHQR-----FGLPASFKELRPYANAEQILRNAAALPRAIHPAVWTRETGEKVMHLS
226

Query: 209 LLIGRHAHAIPGMDAAESERFLEGLVDWA--CQAPRVHAHQWAAGDVVVWDNRCLLHRAE
266

+ +G P D E ++ WA + R + H W D+++WDN +LH A
Sbjct: 227 MAVGFEGQETP--DGEEKFHYV-----WAEVLKVIRPYWHSWKTTDMLIWDNWRMLHEAG
279

Query: 267 PWDFKLPRVMWHSRLAG 283

D L RVM + + G
Sbjct: 280 GCDPSLDRVMHRTTIK 296

>ref|XP_721596.1| potential taurine catabolic dioxygenase Tcd3 [Candida albicans

SC5314]

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 = 4e-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---LGTEIKGIQLSQLNDAAKDEVALLAAQRGVLVFRDQDFI-DKGPEFVTK
138

Query: 64 FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGN-----MAWHAD
111
+ + G I S +P + D+ V+ G+ +A H+D
Sbjct: 139 Y--VSHYGPLHIHPTSG-----APKDHPDIHVVLSGDTKEYPFKKTNLVALHSD
186

Query: 112 STYMPVMAQGAVFSAEVVP-AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV----
166
+Y + +A +P + GG T F D AY+ L + + A HS V
Sbjct: 187 VSYELNPTALSFLAATNIPQSGGGDTVFVDTVEAYNRLSPLFKEKLEGLKAVHSAVEQAN
246

Query: 167 YSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAE
225
++ K GHV++ + P+V+ P G+ L + I G+ E
Sbjct: 247 FAIFKKGHVKRHPVENV-----HPIVRTTP-LGQKVLYVNNGFTRRIEGLKEEE
294

Query: 226 SERFLEGLVD--WACQAPRVHAHQWAAGDVVVWDNRCLLHRA 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 = 5e-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 SFSDATVAAINQLLLKHKVIFFRDQDHLDDSEQEAFAARRLGDLPVPHPTQGPVVTGTASILN 73

Query: 78 ISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVPAVGGRTC
137

 + + + G Q WH D T++ + +V V+PA GG T
Sbjct: 74 LDSSRGGGRADQ-----WHTDVTTFV DAYPKFSVLRGVVIPAAGGDTI
115

Query: 138 FADMRAAYDALDEATR ALVHQRSARHSLVY 167

 +++ AAY++L + L A HS Y
Sbjct: 116 WSNTHAAYESLPAPL KLLADNLWAIHSNAY 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 = 5e-05, Method: Compositional matrix
adjust.

Identities = 40/174 (22%), Positives = 72/174 (41%), Gaps = 15/174 (8%)

Query: 108 WHADSTYMPVMAQGAVFSAE VVPAVGGRTC FADMRAAYDALDEATR ALVHQRSARHSLVY
167

 WH+D T+ P+ + V +P GG T +A YD + + + + +A Y
Sbjct: 165 WHSDITFEPIPSDYTVLRL TELPKTGGDTLWASGYELYDRISKPYQQFLEGLTA----TY
220

Query: 168 SQSKLGHVQQAGSAYIGYG-----MDTTATPLRPLVKVHPETGRPSLL-IGRHAHAIP
219

 +Q V + I G + + P+++ +P TG S+ +G H +
Sbjct: 221 AQPGFNRVAKENDFEIFTGPRGAPENVGDKLEAIHPVIRTNPVTGWKSVFAVGVHVAKVN
280

Query: 220 GMDAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVW DNRCLLHRAEPWDFK 271

 + ES+ L V + + +W D+ +WDNR + H A +D+K
Sbjct: 281 DLSEESDHLRWFVSLIVENHDLQVRLRWENPNDLAIW DNRSVYH-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 = 5e-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 ADIEAGMDKYAVLPFRNQDITDEQQ LAFALNFGERESARGGTVTKEEDYRLTSG LNDVSN 73

Query: 81 VKADGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAE VV 129

 + DG P D + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 74 LGKDG-----RPLARDSRTHLFNGLGNCLWHSDDSSFRPIPAPKFSLLSARVV 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 = 5e-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---IGTEIVGLQLSELTDKQKDELALLIAERVVFFKDQDLSPQKQLELG
166

Query: 62 KRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEDW---DMMKVIVGNMAWHADS
112

+G +E RIG + IS + ++ WD + GN WH+D

Sbjct: 167 HYWGQVEVHPQASRIGE-EFDGISVI-----WQEQQQRDRWDLNLTQKSKKNSQWHSDL
220

Query: 113 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSA----RHSLVYS
168

+ A + +P +GG T ++ AYD L A + + ++A H +

Sbjct: 221 VHEKQTAGITHLHLDALPGIGGETLWSSTYGAYDKLSPALQKFLDGKTAIYRSAHQYLDR
280

Query: 169 QSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAESE
227

+ L G Y+ P+V+ HP TG L + R I G+ ES+

Sbjct: 281 KDPL-----KGPKYVERE-----HPIVRTHPVTGWKYLNVNRSMTRIVGLLPEESD
327

Query: 228 RFLEGL-----VDWACQAP-----RVHAHQWAAGDVVVWDNRCLLH 263
L L V W+ Q + + G +WDNR H

Sbjct: 328 LILNYLYSVIETNRDIQVRWSWQKELGSVKNNKKEEPKQYRGVSALWDNRISNH 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 = 5e-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 IGTEIHGVDL SKLDDAQRDDLARLIAYRGVVFRRSQKNFDIESQRQLGQYWGKLRHATT
158

Query: 74 DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTY--MPVMAQGAVFSAEVVPA
131

+ ++ V ++ D + + WH+D TY P +
Sbjct: 159 SVPRKPGLEDVHV--YTGDNSGDNRALFTPSFLWHS DVTYEIQPPSYTSLKLLSGPPRG
216

Query: 132 VGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM 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

- >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 = 6e-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 PLVRTHAGSGRKFLFIGAHASHVEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGDLMV
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 = 6e-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 PLVRTHAGSGRKFLFIGAHASHVEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGDLMV
103

Query: 256 W 256
W
Sbjct: 104 W 104

>dbj|BAF81035.1| 2,4-D dioxygenase [Nocardioides sp. 116-VN10-1W]
Length = 104

Score = 52.4 bits (124), Expect = 6e-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 PLVRTHAGSGRKFLFIGAHASHVEGLPVAEGRMLLAELLEHATQREFVYRHRWNVGDLMV
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 = 6e-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 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 = 7e-05, Method: Compositional matrix
adjust.

Identities = 34/107 (31%), Positives = 47/107 (43%), Gaps = 5/107 (4%)

Query: 147 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGR
206

ALD+ T+A + HSL+YS+ LG + Y L+ LV+ HP R
Sbjct: 1 ALDDETKAEIEDLVCEHSLMYSRGS LGFTE-----YTDDEKQMFKPVLQRLVLRTHPVHRR 55

Query: 207 PSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

SL + HA I M E L L + A Q V+ H+W D+
Sbjct: 56 KSLYLSSHAGKIVSMSVPEGRLLLRDLNEHATQGEFVYVHKWKLHDL 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 = 7e-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---LGTEIRGIQLSELNDAGRQVALLASQRGVLFVFRDQDL-----
127

Query: 65 GAIERIGGGDIVAISNVKADGTVRQH----SPAEWDDMMKVIVGN-----MAW
108

I G + V GT H +P D+ V+ G+ + W
Sbjct: 128 -----IDKGPENLVEYVSHYGTPIHPTSGAPKGPDIHSVLTGDTKEDAFSTRNNLVVW
182

Query: 109 HADSTYMPVMAQGAVFSAEVVP-AVGGRTCFAADMRAAYDALDEATRALVHQRSARHSLVY
167

H+D +Y + + +P A GG T FAD R AY+ L + + A HS V
Sbjct: 183 HSDVSYELNPTAVSFLAVTNIPKAGGGDTVFADNREAYNRLSPLFKEKIDNLKAVHSAV-
241

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGR-HAHAIIPGMDAAES
226

Q+ L V+ G + ++ + P+V+ P +G+ L + I + ES
Sbjct: 242 DQANLAVVK--GGVVKRHPVEN----IHPVVRTTP-SGQKVLVNSGFTRRIVDLKGEES
294

Query: 227 ERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNRCLLHRA 265

+ L+ L+ + W G V ++DNR + H A
Sbjct: 295 DFLKFLLOHIASSQDFQVRVNWQPGTVAIFDNRIVSHSA 334

>ref|XP_001201468.1| PREDICTED: hypothetical protein, partial
[Strongylocentrotus
purpuratus]
Length = 176

Score = 52.0 bits (123), Expect = 7e-05, Method: Compositional matrix
adjust.

Identities = 50/186 (26%), Positives = 77/186 (41%), Gaps = 34/186 (18%)

Query: 5 TLQITPTGATLGATVTGVHLATLDDAG-FAALHAAWLQHALLIFPGQH-LSNDQQITFAK 62

T Q+ P+ LG V G+ LA G + QH L+IF Q +S D+ + +
Sbjct: 6 TYQLKPS--RLGVEVFGIDLAQQQPQGVIDQIKEDVTQHRLMIFRNQSPISGDRHVEISL 63

Query: 63 RFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
115

FG +E + D+ +SNV+++G VG WH D ++
Sbjct: 64 WFGELESTFYKHPKSPHPDVFRVSNVESEGCRG-----VGRTGWHIDGSFQ
109

Query: 116 PVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRA---LVHQRSAR-----HSLVY
167

P +++ VVP G T FA + + L E +A ++ S R H LVY
Sbjct: 110 PAFNYSLYMHVVPKEGD-TVFAPLNEIIIEGLSEDQQAQWKLMMSDRRGSLVHPLVY
168

Query: 168 SQSKLG 173

S + G
Sbjct: 169 SHPRTG 174

>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 = 7e-05, Method: Compositional matrix
adjust.

Identities = 61/257 (23%), Positives = 94/257 (36%), Gaps = 16/257 (6%)

Query: 15 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH-LSNDQQITFAKRFGAIERIGGG 73

+G V G++LA L+D L ++ F Q D Q + G + +

Length = 287

Score = 52.0 bits (123), Expect = 8e-05, Method: Compositional matrix adjust.

Identities = 77/300 (25%), Positives = 114/300 (38%), Gaps = 49/300 (16%)

Query: 9 TPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG--QHLSNDQQIT-FAKRF 65
 TP GA L G ++ L AAL A +H LL+ G ++ Q +T +A +G
 Sbjct: 14 TPFGAVLTPKYPGQPISELP---VAALRALAQRHLLVLRGFDGFTDPQVLTRYAGGW 70

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
 125

I G ++ V++H A+ D + + W D Y P + + +F
 Sbjct: 71 EIMMWPFQAVL-----DVKEHPDAK-DHIFDSSYVPLHW--DGMYPKPTIPEFQLFH
 118

Query: 126 AEVVPVAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
 183

P+ GGRT F D DE+ A + + S+ Y ++ H
 Sbjct: 119 CVAAPSQDEGGRTTFVDTRLLANADESLA----QWLKVSISYRIKQVVH-----
 165

Query: 184 GYGMDTTATPLRPLVKVHP-----ETGRP----SLLIGRHAHAIPGMDAAESERFLEG
 232

YG + + PLV HP P + +HA G+ E E F +
 Sbjct: 166 -YGGEVCS----PLVVTHPSGSGVIMRYNEPTEGKKFLNQHALEYHGVPEEQEETFHQ
 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 = 9e-05, 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 ALDDDTKAEIEDLVCEHSLMYRSGSLGFTE-----YTDDEKQMFKPVLRVLRTHPVHRR 55

Query: 207 PSELLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV 253

SL + HA I M E L L + A Q V+ H+W D+
 Sbjct: 56 KSLYLSSHAGKIVSMSVPEGRLLLLRDLNEHATQGEFVYVHKWKLHDL 102

>ref|XP_382474.1| hypothetical protein FG02298.1 [Gibberella zeae PH-1]
 Length = 346

Score = 51.6 bits (122), Expect = 9e-05, Method: Compositional matrix adjust.

Identities = 57/218 (26%), Positives = 90/218 (41%), Gaps = 45/218 (20%)

Query: 50 QHLSNDQQITFAKRFGAIERIGGGD-----IVAISNVKAD-----GTVRQHSPAEE- 94
 + L+N+ Q+ A R G R+ G + + N D T + +PAE
 Sbjct: 87 KDLTNELQMEADRLG---RLTGKPESTLHVHPLQNFNPDEEKHVNTITTDKAANPAED
 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----FSQRRLPKVAEKGFEELYTQPRGSPNNVGDLSLTTT----HPVVRTNP
 253

Query: 203 ETGRPSLL-IGRHAHAIPGMDDAAESERFLEGLVDWACQ 239

TG SL +G H +I + ES+R L+DW Q
 Sbjct: 254 VTGWKSLFAVGNHCESINDLTPDESKR----LLDWFLQ 287

>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 TCFADMRAAYDALDEATRSLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR
 195

T F DMRAAYD L E + + A H + S+ LG + + S P+
 Sbjct: 2 TEFCDMRAAYDDLPEDFKKELEGLRAEHYALNSRFILGDTEYSES-----QRNAMPPVS 55

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAH 246

PLV+ H +GR L IG HA I G AE L L++ A Q V+ H
 Sbjct: 56 WPLVRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQRKRVYRH 107

>ref|XP_001598964.1| hypothetical protein SS1G_01054 [Sclerotinia
 sclerotiorum 1980]

gb|EDN91650.1| hypothetical protein SS1G_01054 [Sclerotinia sclerotiorum
 1980]

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 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
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 FHDEARRLGQDIREDMRGSPLNIGKELSA--IHPVVRTNPVTGKKTFLVFNQGFTRKRLHPL
277

Query: 222 DAAESERFLEGLVDWACQAPRVHAHQ---WAAGDVVVWDNRCLLHRA 265

 ES+ L L + P H Q W+ DV +WDNR H A
Sbjct: 278 TKDESLLLLPWLKNL---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 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH-----
157

 WH+D + PV A +P GG T +A YD + +
Sbjct: 129 WHSDIQFEPVPADYTSRLRLTQLPKTGGDTLWASGYELYDRFSKPYQKFFEGLTATFIGSG
188

Query: 158 -----QRSARHSLVYSQSKLGHVQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLL-I
211

 +R + +Y++ + GS + G D + P+V+ +P TG S+ +
Sbjct: 189 FLQAAERDPDNVRIYTEPR-----GSP-LNVGKDLAT--VHPVVRTNPVTGWKSIFAV
238

Query: 212 GRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQ-QW-AAGDVVVWDNRCLLHRA 265

 G H I + ES+ L+ + + + +W D+ +WDNRC H A
Sbjct: 239 GPFPHKINELTQTESDELLKFKFYNTILENHDIQVRFKWRNKNDIAIWDNRCAFHTA 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 HWDGMYLKTVPPELQVF--QCVSAVGEQGGRTTFSSTTALRLASPETKALW-----
159

Query: 165 LVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL-----LIG
212

Q G Q+A Y ++T P+++ HP P + +
Sbjct: 160 ----QRATGQYQRAVELY-----SSTAQAPIIEQHPYRTHPVIRFCEPPIAGDKFLN
208

Query: 213 RHAHAIPGMDAAESERFLEGLVDWACQAPRV-HAHQWAAGDVVVDNRCLLHRAEPW 268
+ G++ E E+ L L A PRV +AHQW +GD+V+ DN LLH E +

Sbjct: 209 PSTYHFSGIEPEEQEQLLSSL-QHALYDPRVQYAHQWQSGDIVIADNYSLLHGRESY 264

>ref|ZP_02383058.1| pyoverdine biosynthesis protein PvcB [Burkholderia
ubonensis Bu]

Length = 280

Score = 51.2 bits (121), Expect = 1e-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 HWDGMYRKQVPEFQIFHCVSAPEVEQGGRTTFSNTKALLERAEPQARAL-----
146

Query: 167 YSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL-----LIGRH
214

K+ V + Y T A P+V HP G P + + R
Sbjct: 147 --WDKVTGVYHRKMEF--YDSKTIA----PIVTTHTPTQGFVVRVYNEPSIEGDDSFVNR
198

Query: 215 AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFKLPR
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 HLRRVHVLGNPPLDNPFLV 277

>emb|CAY25731.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 119

Score = 51.2 bits (121), Expect = 1e-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 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
 DG P D + +GN WH+DS++ P+ A+ ++ SA VV

Sbjct: 76 KDG-----KPLPKDHRTHLFNLGNCLWHS DSSFRPIPAKFSLLSARVV 118

>gb|EEQ91806.1| alpha-ketoglutarate-dependent taurine dioxygenase
 [Ajellomyces
 dermatitidis ER-3]
 Length = 391

Score = 51.2 bits (121), Expect = 1e-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 IGTEVHGVNLAKLTDNQRNALARLIAIRGVVFFRAQDDFDIEAQRDLGRYFGTLHRHATT
 149

Query: 74 DIVAISNVKADGTVRQHSPAEW---DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVP
 130
 + K G H D D + + WH+D TY P

Sbjct: 150 AVP-----KKAGLEDVHVVTGDYSVDQRALFSPSFLWHS DVTYEVQPPSYTSLKVLTP
 204

Query: 131 AVGG--RTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
 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 REPITTKHPLIRTNPVGTGWNLSFFNPGFITKIVGVPKLESDAIINYLSVVVTTQELHAR
 316

Query: 247 -QWAAGDVVVWDNRCLLHRA 265
 QW DV WDNR H A

Sbjct: 317 FQWGKNDVAFWDNRSTNHTA 336

>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 = 1e-04, Method: Compositional matrix adjust.

Identities = 58/277 (20%), Positives = 100/277 (36%), Gaps = 56/277 (20%)

Query: 41 QHALLIFPGQH-LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMM 99
 Q ++ F Q L++D Q +R G + + + V G R+HS DD +
 Sbjct: 78 QRGVVFFRKQDGLNDDLQKELVQRLGQLSGKPATSGLVHVPVANS--REHSVK--DDEI
 133

Query: 100 KVIVGNM-----AWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMR
 142

VI WH+D T+ P+ + + +P GG T +A
 Sbjct: 134 SVISSEQRKTLYRDRNNRKQSSRREWHSDITFEPIPSDYTLRLTQLPRTGGDTLWASGY
 193

Query: 143 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG-----MDTTATPLR
 195

YD + E + + +A Y+Q V + +I G + +
 Sbjct: 194 EVYDRISEPYQKFLESLTA----TYAQPGFNRVAKENDFHIHTGPRGAPENVGDELKAIH
 249

Query: 196 PLVKVHPETGRPSLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDV
 253

P+++ +P TG S+ +G H I G+ ES L+ V + + +W +
 Sbjct: 250 PVIRTNPVTGWKSVFAVGTHVEKINGLTHEESRHLLEDWFVTLIVENHDLQVRLRWQNPND
 309

Query: 254 V-----VWDNRCLLHRAEPWDF 270

+ +WDNR + H A WD+
 Sbjct: 310 LGELYRKRILRTLELISHASAIWDNRSVYH-AATWDY 345

>gb|ABD39113.1| alpha-ketoglutarate dioxygenase [uncultured bacterium]
 Length = 91

Score = 51.2 bits (121), Expect = 1e-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 PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGDVLM 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

Query: 196 PLVKVHPETGRPSELLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
255

PLV+ H +GR L IG HA I G AE L L++ A Q V+ H+W GD+V+
Sbjct: 43 PLVRTHAGSGRKFLFIGAHASHIEGRPVAEGRMLLAELLEHATQRQFVYRHRWQVGDLM
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 = 2e-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 VVSTNLDIRRVTGRIGAEIVGLDLRDALGD DTVIASIRAALVEHKALFFRQELDDAGQQ 62

Query: 59 TFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGN---MAWHADSTYM
115

FA RFGA+ A TV S A ++++V WH D T++

Sbjct: 63 RFAARFGAL-----TTAHTPV--PSLAGSPNVLRVDSTEGRANNWHTDVT FV
107

Query: 116 PVMAQGA VFSAEVVPVAVGGRTCFADMRAAYDAL 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 = 2e-04, Method: Compositional matrix
adjust.

Identities = 75/300 (25%), Positives = 114/300 (38%), Gaps = 49/300 (16%)

Query: 9 TPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG--QHLSNDQQIT-FAKRF 65
TP GA L G ++ + AAL + QH LL+ G ++ Q +T +A+ +G

Sbjct: 14 TPF GAVLTPQYPG---QSIRELPVAALRSLAQQHLLVLRGFDSGFTDPQLLTRYAEGWG 70

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
125

I G ++ V++H A+ D + + W D Y P + + +F
Sbjct: 71 EIMMWPFGAVL-----DVKEHPDAK--DHIFDSSYVPLHW--DGMYPKPTIPEFQLFH
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----PLVVDHPNGNGQIMRYNEPPTTEGKKFLNQHALEYHGVPOEQQEAHFQT
220

Query: 233 LVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL
292

L +AHQW GDVV+ DN LLH E + + R + + P AL
Sbjct: 221 LQQHLYDPRHYAHQWQQGDVVIADNFSLHGREGFTARSARHLQRVHIQSNPVCANQAL
280

>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%)

Query: 41 QHALLIFPGQH-LSNDQQITFAKRFGAI-----ERIGGGDIVAISNVK 82
Q ++ F Q L+N+ Q R G + ER GG+ IS +

Sbjct: 71 QRGVVFFRAQDGLTNELQKQLILRLGELVGRPATSGLHIHPILNSERELGGNDPEISTIS
130

Query: 83 ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR
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 PVVRTNPVTGWKSIFPVGGHVKHINGLTHEEESKLLSWFLDLVYKNHDLQVRLKWKPNPND
306

Query: 254 V-----VWDNRCLLHRA 265

+ +WDNR + H A
Sbjct: 307 IGESPWIGYRWQLLTCEAIWDNRSVFHTA 335

>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 WHTDQAFRDPPPYPASVLYCKTAPPPGAGGATIFADVTAAYAALPEDKRLELERYRAVCSY
176

Query: 166 VYSQSKLGHVQQAGSAYIGYGMDDTATPL-RPLVKVHPETGRPSLL-----
210

+ +K+ + P+ +PLV + TG S+
Sbjct: 177 AHNNAKVRKRGTSPYPLLTPEQRAEHPPVYQPLVLTNAATGEKSVYGFNSSVCAVVAEGE
236

Query: 211 -IGRHAHAIPGMDAAESERFLEGLVDWA---CQAPR-VHAHQWAAGDVVVWDNRCLLHRA
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 TPLEDGSHAREMWRRTTVAS 315

>gb|ACB21020.1| TfdA [uncultured bacterium]
Length = 64

Score = 50.1 bits (118), Expect = 3e-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 NQFWHSDSSFQQPAARYSMLSAVVVPPSGGDTEFCDMRAAYDALPRDLQSELEGLRAEH 59

>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 = 4e-04, Method: Compositional matrix adjust.

Identities = 46/188 (24%), Positives = 76/188 (40%), Gaps = 21/188 (11%)

Query: 90 HSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL
148

H E ++ + V WH+D T+ PV + A+ +P GG T +A + Y+A
Sbjct: 135 HKQIELEEDLNVSQFATKEWHS DITFEPVPSDFAILKIHTLPETGGDTLWA---SGYEAY
191

Query: 149 DEATRAL-----VHQRSARHSLVYSQSKLGHVQQAGS-AYIGYGMDDTTATPLRPLV
198

D +RAL VH+ + S V Q K H G+ +G + T + P++
Sbjct: 192 DRLSRALAKHLEGLTAVHEATFFKSYVERQKTLHEGPRGNPENVGTDLRT----VHPVI
247

Query: 199 KVHPETGR--PSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVV
255

+ +P TG + I + ES+ L+ L + +W+ DV +
Sbjct: 248 RTNPVTGMIATESCLYSFTRRILELTKDESDATLDYLFRLVSDNHDLQVRFKWSKNDVAI
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 = 4e-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 LGCEVRGVLDLKTENRPEI IKQIQEDVTKHRILIFKDQGIVSGDRHVEISRWFGELESTFY 67

Query: 69 ---RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVI VGNMAWHADSTYMPVMAQGAVFS
125

+ D+ +SN K +G VG WH D T+ P +++
Sbjct: 68 KHPKSPHPDVFRVSN DKNEGCTN-----VGRSGWHIDGTFQPAPFSYSLYH
113

Query: 126 AEVVPVAVGGRTCFADMRAAYDALDEATRA-----LVHQR--SARHSLVYSQSKLG 173
E VP G T F + ++LD+ T +V R S H L+YS + G

Sbjct: 114 MESVPK-EGHTLFIPLTELIESLDKDTYDTWNKAWMVSDRRSSLVHPLIYSHPQTG 168

>emb|CAY25780.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 118

Score = 49.7 bits (117), Expect = 4e-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 AAVHAGMDGFGVLFVFDQKIDDDHQLVFSRSLGPLEQATGDIAAPQDRRMSMDLNDISNL 73

Query: 82 KADGTVRQHSPEAWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVD 129
+ + DD ++ +GN WH+DS++ V A+ ++ SA VV
Sbjct: 74 DKNSKI-----LARDDRRRLFGLGNQLWHSDDSSFKDVPKYSLLSARVV 117

>ref|XP_001594485.1| hypothetical protein SS1G_04292 [Sclerotinia sclerotiorum 1980]
gb|EDO01817.1| hypothetical protein SS1G_04292 [Sclerotinia sclerotiorum 1980]

Length = 368

Score = 49.7 bits (117), Expect = 4e-04, Method: Compositional matrix adjust.

Identities = 42/181 (23%), Positives = 70/181 (38%), Gaps = 18/181 (9%)

Query: 97 DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVDPAVGGRTCFADMRAAYDALDEATRALV 156
D + + WHAD ++ P A + EV+P GG T +A YD + E + +
Sbjct: 157 DRANGLSNSSKWHADISFEPKPADYSSLKLEVLPKTGGDTLWASGYEIIDRISEPYQKFL 216

Query: 157 HQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP-----LRPLVKVHPETGRP 207
+L + + G ++ A + P + P+V+ +P TG
Sbjct: 217 -----ETLTVTFQQPGFIEAAANGGFELYDKPRGAPENIGKELKAVHPVVRTNPVTGWK 270

Query: 208 SLL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QWA-AGDVVVWDNRCLLHR 264
S+ +G H I + ES+ LE + +W D+ +WDNR H
Sbjct: 271 SVFPVGGHVSINDVTRWESQALLEWFKRLLVDNHDLQVRFKWKQNNDLAIWDNRSTFHT 330

Query: 265 A 265
A
Sbjct: 331 A 331

>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

Query: 218 IPGMDAAESER----FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA 265
 I + ESE F LVD +V D+ +WDNR + H A
 Sbjct: 282 INDVTQLESEALLGWFKRLLDV--NHDLQVRFKWKQNLDLAIWDNRSVFHTA 331

>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 = 5e-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 WHSDITFEPIPSDYALLRLTELPKTGGDTLWASGYEVYDRISKPVQKFLTELTA----TY 189

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATP-----LRPLVKVHPETGRPSLL-IGRHAHAI 218

+Q + I Y + A + P+V+ +P TG S+ +G H I
 Sbjct: 190 AQPEFNKAADKNGFKI-YSEERGAPENVGEKLEAVHPVVRTNPVTGWKSIFALGHHVSHI 248

Query: 219 PGMDAAESER----FLEGLVDWACQAPRVHAHQWA-AGDVVVWDNRCLLHRA 265

+ ES+ FL +VD R H+W D+ +WDNR H A
 Sbjct: 249 NDLTTIESDALLAWFLRLVVDNHDLQVR---HRWENVNDLAIWDNRSNYHVA 297

>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 = 5e-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 IGTEVHGVNLAKLTDNQRNALRLIAIRGVVFFRAQDDFDIEAQRDLGRYFGTLHRHATT 149

Query: 74 DIVAISNVKADGTVRQHSPAEDW---DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV 130

+ K G H D D + + WH+D TY P
 Sbjct: 150 AVP-----KKAGLEDVHVVTGDYSVDQRALFSPSFLWHSVITYEVQPPSYTSLKVLTP 204

Query: 131 AVGG--RTCFADMRAAYDALDEATR^LVHQ^SRSARHSLVYSQSKLGHVQQAGSAYIGYGM^D
188

GG T ++ AAYDAL + + +A HS +Q GS G +
Sbjct: 205 PRGGGGDTLWSSQYAA^YDALSPHM^QTYLKGLTALHS-----ADM^QADGSRAAGRPV^R
256

Query: 189 TTA-TPLRPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH
246

T PL++ +P TG SL I G+ ES+ + L +HA
Sbjct: 257 REPITTKHPLIRTNPVTGWN^SLFNPGFITKIVGVPKLESDAIINYLSSVVVTTQELHAR
316

Query: 247 -QWAAGDVVVWDNRC 260

QW DV WDNR
Sbjct: 317 FQWGKNDVAFWDNRS 331

>ref|XP_001727715.1| hypothetical protein [Aspergillus oryzae RIB40]
dbj|BAE60876.1| unnamed protein product [Aspergillus oryzae]
Length = 349

Score = 48.9 bits (115), Expect = 6e-04, Method: Compositional matrix
adjust.

Identities = 49/201 (24%), Positives = 86/201 (42%), Gaps = 21/201 (10%)

Query: 78 ISNVKADGTVRQHSPA^EWDDMMKVIVGNMAWHADSTYMPVMAQGA^VFSAEVVPVAVGGRTC
137

IS + ++G + +++ M V WH+D ++ A + +P GG T
Sbjct: 111 ISTINSEGRKTLTKGSDYTKMAAV-----WHSDISFEKAPAD^FSSLRLVQLPKTGGDTL
164

Query: 138 FADMRAAYDALDEATR^LVHQ^SRSARHSLV----YSQSKLGHV-QQAGSAYIGYGM^DTTAT
192

+A YD + + RA + SA H+ V +Q+ H+ ++ A + G D TA
Sbjct: 165 WASGYE^IYDRISKPYRAFLETLSATHAGVGFMR^LAQTGKFHLYEKERGAPVNVGGDLTA-
223

Query: 193 PLRPLVKVHPETGRPSLL-IGR--HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH---
246

+ P+V+ +P TG S+ IG+ I G+ ES L+ + + V +
Sbjct: 224 -VHPVVRTNPITGWKSIFPIGKAQSPCCIDGLTRRESASMLQSVSNGTALMTLVGVVYVPY
282

Query: 247 --QWAAGDVVVWDNRC^LLHRA 265

+ +WDNR + H A
Sbjct: 283 ILHCELTGLAIWDNRSVFHTA 303

>gb|EEY53775.1| taurine dioxygenase, putative [Phytophthora infestans T30-
4]

Length = 335

Score = 48.9 bits (115), Expect = 6e-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 IGTEILNLQLHELTDSQKDELALLVAQRGVVFFRDQKISIEDQLALGRYYGPLHVYQTV
144

Query: 71 ---GGGDIVAIISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
127

G + + N+ D R + A + WH+D +Y F
Sbjct: 145 HAKGTPQVHVVENLLEDSEKRIKTQA-----LEPVNLWHSVSYERQPPSYTSFKVL
196

Query: 128 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
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 -----PVVRTHPVTGRKALYVNAQFTTRINNLAAESGAFFSSILRFLHQHIAQGHE
282

Query: 246 HQ----WAAGDVVVWDNRCLLHRAEPWDF 270

Q W V +WDNR +H A +D+
Sbjct: 283 FQVRYRWTKDAVAIWDNRATVHYAT-YDY 310

>emb|CAY25739.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 119

Score = 48.9 bits (115), Expect = 7e-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 IEAGMDKYAVLLFRGQDITDEQQLAFALNSGEREHARGGTVTKKEDYRLTSGLNDSVNLG 75

Query: 83 ADGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAE VV 129

DG +P D + +G WH+DS++ P+ A+ ++ SA VV
Sbjct: 76 KDG-----NPLPRDHRTHLFLNLGYCLWHS DSSFRPIPAKFSLLSARVV 118

>gb|AAB08969.1| alpha ketoglutarate dioxygenase [Variovorax paradoxus]
Length = 106

Score = 48.5 bits (114), Expect = 8e-04, Method: Compositional matrix adjust.

Identities = 36/112 (32%), Positives = 49/112 (43%), Gaps = 7/112 (6%)

Query: 145 YDALDEATR^LVHQ^RSARH^SLVYSQ^SKLGHV^QQAGSAYIG^YGMDTTATPLR-PLVKVHPE
203

YD L E + + A H + S+ LG + S P+ PLV+ H
Sbjct: 1 YDDLPEDFK^KELQ^LGLRAE^HYALNS^RFILG^DTDYSES-----QRNAMPPVSWPLV^RTHAG 54

Query: 204 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255
+GR L IG HA I G AE L L++ A Q V+ H W GD+V+

Sbjct: 55 SGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGD^LV^M 106

>gb|AAX51275.1| TdfA [uncultured bacterium]
Length = 105

Score = 48.5 bits (114), Expect = 9e-04, Method: Compositional matrix
adjust.

Identities = 38/110 (34%), Positives = 49/110 (44%), Gaps = 7/110 (6%)

Query: 136 TCFADMRAAYDALDEATR^LVHQ^RSARH^SLVYSQ^SKLGHV^QQAGSAYIG^YGMDTTATPLR
195

T F DMRAAYD L E + + A H + S+ LG + S P+
Sbjct: 2 TEFCDMRAAYDDLPEDFK^KELQ^LGLRAE^HYALNS^RFILG^DTDYSES-----QRNAMPPV^S 55

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH 244

PLV+ H +GR L IG HA I G AE L L++ A Q V+
Sbjct: 56 WPLV^RTHAGSGR^KFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFV^Y 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 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR^LVHQ^RSARH 163

WH+DS++ A+ ++ SA VVP GG T F DMRAAYDAL ++ + A H
Sbjct: 3 WHSDSSFQ^QPAARYSMLSAVVVPPSGGDTEFC^DMRAAYDALPRDLQSELEGLRAEH 58

>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 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR^LVHQ^RSARH 163

WH+DS++ A+ ++ SA VVP GG T F DMRAAYDAL ++ + A H
Sbjct: 4 WHSDSSFQ^QPAARYSMLSAVVVPPSGGDTEFC^DMRAAYDALPRDLQSELEGLRAEH 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

>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 PLVKVHPETGRPSLLIGRHAHAIPGMDAE--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 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR_LVHQRSARH 163
WH+DS++ A+ ++ SA VVP GG T F DMRAAYDAL ++ + A H
Sbjct: 3 WHSDSSFQQPAARYSMLSAVVVPPSGGDTEFCDMRAAYDALPRDLQSELEGLRAEH 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 EVSGVDLSQPLQEAQLAEIRRAFL ENHVLVFRDQHMTVEQHKAFGR 80

Query: 63 RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
122

 FG + + DI DG + + + G + WH D T + G+
Sbjct: 81 LFGPLRALPVEDI-----DGDDAELVVVRANAQSRFVAGEL-WHTDGTADAEP SMGS
131

Query: 123 VFSAEVVPAV--GGRTCF 138
 + + PA+ GG T F

Sbjct: 132 MLYVKETPAIGTGGDTLF 149

>gb|ACB21028.1| TfdA [uncultured bacterium]
 Length = 62

Score = 48.1 bits (113), Expect = 0.001, 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: 3 WHSDSSFQQPAARYSMLSAVVVPPSGGDTEFCDMRAAYDAL 43

>gb|AAB18140.1| 2,4-dichlorophenoxyacetate dioxygenase [Halomonadaceae
gen. sp.

 strain I-18]
 Length = 105

Score = 48.1 bits (113), Expect = 0.001, 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 PLVRTHAGSGRKFLFIGAHAXHIEGRPVAEGRMLLAELLEHATQRKFVYRHSWKVGD LVM
105

>gb|AAX51279.1| TdfA [uncultured bacterium]
 Length = 102

Score = 47.8 bits (112), Expect = 0.001, Method: Compositional matrix
adjust.

Identities = 37/105 (35%), Positives = 47/105 (44%), Gaps = 7/105 (6%)

Query: 136 TCFADMRAAYDALDEATR LVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

 T F DMRAAYD L E + + A H + S+ LG + S P+
Sbjct: 1 TEFCDMRAAYDDLPEDFKKE LQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVS 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 = 0.001, Method: Compositional matrix
adjust.

Identities = 37/105 (35%), Positives = 47/105 (44%), Gaps = 7/105 (6%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYD L E + + A H + S+ LG + S P+
Sbjct: 1 TEFCDMRAAYDDLPEDFKKELOGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239

PLV+ H +GR L IG HA I G AE L L++ A Q
Sbjct: 55 WPLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQ 99

>gb|ACB21024.1| TfdA [uncultured bacterium]
Length = 61

Score = 47.8 bits (112), Expect = 0.001, 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 WHSDSSFQQPAARYSMLSAVVVPPSGGDTEFCMRAAYDAL 42

>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 = 0.001, 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 MPYKITSLDPFQVMEVQHSSTHVVELD---ISSLRHLFERHQLVLLRGFTVFEQAEDFA 57

Query: 59 TFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM
118

+ +++G + G ++ + +++ P D + M W D Y P +
Sbjct: 58 DYCEQWGEVSIWPFGRVLEL-----IQKEQPE--DHIFDSSYMPMHW--DGMYPQV
105

Query: 119 AQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
176

+ +F +P GGRT F A D E R+L + + GH Q
Sbjct: 106 PEYQIFQCVEAPLPGNGGRTTFCHTMLALDNASEQERSLWRKVT-----GHYQ
153

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESERF----LEG
232

+ Y + + P+V HP G ++ H + D + G
Sbjct: 154 RKMEFY-----HSKTVSPIVMPHPYKGY-DVIRYNEPHVVDNGDLLNPPDVTLSGISG
205

Query: 233 LVDWACQA-----PR-VHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG
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

>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--EVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARH
163

M H D Y P + + +F +P GGRT F++ + L H+ +
Sbjct: 93 MPLHWDGMYPQVPEYQIFHCVKAPLPGQGGRTTFSNTLLVLKNTSSEIKELWHKVT---
149

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGR-----PSLLIGRHA
215

G Q+ Y + + P++ HP+ G PS G
Sbjct: 150 -----GTYQRKMKFY-----NSKTISPIITDHPQKGYSVIRYNEPPSQDKGHFV
193

Query: 216 H----AIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFK
271

+ G+ E + F L +AH+W GD+V+ DN LLH E + K
Sbjct: 194 NPPELEFTGISHEELDVFHTSLAKALYSPDNFYAHEWQTGDIVDIADNFSLHGREEFSTK
253

Query: 272 LPRVMWHSRLAGRPETEGAAL 292

PR + + P + L
Sbjct: 254 SPRHIQRVHVLSNPPFDNPG 274

>gb|AAX51272.1| TfdA [uncultured bacterium]
 gb|AAX51286.1| 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 TEFCDMRAAYDDLPEDFKKELOGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239

PLV+ H +GR L IG HA I G AE L L++ A Q
 Sbjct: 55 WPLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQ 99

>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 SIGTELVGIQLTSLDDTQKNEALARLVAERGTVVFLRDQEMDVHEQIEFGSYFGELH-----
 160

Query: 74 DIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF-SAEVVPA-
 131

I ++ + D + P D+ K + WH+D +Y + G F + +P
 Sbjct: 161 -IHQMAGIIPD--LPWVHPIHKDETAKNGRSHQIWHSDVSYE-LQPPGLTFLRMDTLPKA
 216

Query: 132 -----VGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
 185

GG T +A Y++L + ++ A+HS ++QA A G
 Sbjct: 217 GPDGYEAGGDTIWASGYGIYESLSPTLKGILENLEAKHS-----GLEQAEKALKGN
 267

Query: 186 GM--DTTATPLRPLVKVHPETGRPSLLIGRH-AHAIPGMDAAESERFLEGLVDWACQA 240

G + P+V+ HP T + +L + + I G++ SE L+ L + +A
 Sbjct: 268 GCLRRNPIETIHPVVRTHPVTQQKTLYVNENFTKEIVGVEKRFSESLDFLNRYVAEA 325

>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 PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKVFYRHSWKVGDLMV
104

>ref|XP_001391648.1| hypothetical protein An07g05690 [Aspergillus niger]
emb|CAK48940.1| unnamed protein product [Aspergillus niger]
Length = 300

Score = 47.4 bits (111), Expect = 0.002, Method: Compositional matrix adjust.

Identities = 52/202 (25%), Positives = 78/202 (38%), Gaps = 29/202 (14%)

Query: 73 GDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMA---WHADSTYMPVMAQGAVFSAEYV
129
 GD + + + +H+ ++DD + A WHAD++Y + +
Sbjct: 110 GDDEVLRDPEIYAVSSEHNDRDKFDDYLNTKHKQFASRGWHADTSYENIPSDYIAIKMVKA
169

Query: 130 PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSAYIG
184
 P GG T FA AYD L E + + S L L GH Q G ++
Sbjct: 170 PMTGGDTLAFASCYGAYDRLEPWQRMADSLSYIMPLADKGINLWLGPRGHPQNFGGSF--
227

Query: 185 YGMDTTATPLRPLVKVHPETGRPSL-----LIGRHAHAIPGMDAEASE----RFLEGLVD
235
 AT PLV +P TG +L + R I G+ E E FL+ + D
Sbjct: 228 -----EAT--HPLVVVTNPVTGWKALWGFSPISMRANRINGVTDHEQELMKAYFLKLITD
280

Query: 236 WACQAPRVHAHQWAAGDVVVWD 257
 + H+W D+V+WD
Sbjct: 281 ---NHDLQYRHRWKPDDIVIWD 299

>ref|YP_125606.1| hypothetical protein lp10237 [Legionella pneumophila
str. Lens]
emb|CAH14466.1| hypothetical protein [Legionella pneumophila str. Lens]
Length = 278

Score = 47.0 bits (110), Expect = 0.002, Method: Compositional matrix adjust.

Identities = 46/201 (22%), Positives = 74/201 (36%), Gaps = 33/201 (16%)

Query: 106 MAWHADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARH
163

M H D Y P + + +F +P GGRT F++ A + L ++ S
Sbjct: 93 MPLHWDGMYRPQVPEYQIFHCVKAPLPGQGGRTTFSNTILALQFASSEIKELWNVKVS---
149

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE-----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 NPPDIEFTGIDQEELDSFHRSLNKALYSADNFYAHEWQNGDIVIADNFSLHGREGFVSR
253

Query: 272 LPRVMWHSRLAGRPETEGAAL 292

PR + + P + L
Sbjct: 254 SPRHIQRVHVLNPPFDNPG 274

>gb|ABI94568.1| TfdA [Burkholderia hospita]
Length = 99

Score = 47.0 bits (110), Expect = 0.002, Method: Compositional matrix
adjust.

Identities = 36/103 (34%), Positives = 46/103 (44%), Gaps = 7/103 (6%)

Query: 138 FADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-P
196

F DMRAAYD L E + + A H + S+ LG + S P+ P
Sbjct: 1 FCDMRAAYDDLPEDFKKEQLGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWP 54

Query: 197 LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239

LV+ H +GR L IG HA I G AE L L++ A Q
Sbjct: 55 LVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQ 97

>gb|AAX51288.1| TdfA [uncultured bacterium]
Length = 105

Score = 47.0 bits (110), Expect = 0.002, Method: Compositional matrix
adjust.

Identities = 37/110 (33%), Positives = 49/110 (44%), Gaps = 7/110 (6%)

Query: 136 TCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYD L E + + A H + S+ LG + S P+
Sbjct: 1 TEFCDMRAAYDDLPEDFKKEQLGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH 244

PLV+ H +GR L IG HA + G AE L L++ A Q V+

Sbjct: 55 WPLVRTHAGSGRKFLFIGAHAGHMEGRPVAEGRMLLAELLEHATQRKFVY 104

>gb|AAX51276.1| TdfA [uncultured bacterium]
Length = 99

Score = 47.0 bits (110), Expect = 0.002, Method: Compositional matrix adjust.

Identities = 36/103 (34%), Positives = 46/103 (44%), Gaps = 7/103 (6%)

Query: 138 FADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR-P
196

F DMRAAYD L E + + A H + S+ LG + S P+ P
Sbjct: 2 FCDMRAAYDDLPEDFKKEQLGLRAEHYALNSRFILGDTDYSES-----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---FGSEIDGVQLSQLNDKKGKDELALFLAQRKVLFFNEQDFADKGPFGFAVEFGKY
139

Query: 64 FGAIERIGGGDIVAISNVKADG-----TVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
117

FG + V S+ G T R+ E + ++ +H+D +Y
Sbjct: 140 FGRLH-----VHPSSGSPRGHQELHITYRRPEKGELQRFVFAHRTTSVGFHSDVSYEIT
192

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQ
177

++ +F + GG T F D AY+ L + A + H L S+ Q
Sbjct: 193 PSRFTLFQV-LESGDGGDTVFVDTVEAYNRL---SPAFQKRLEGLHVLHTSED-----QA
243

Query: 178 AGSAYIGYGMDD--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

>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%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
A+ + +TP +G + G+ L+ L + L + ++ F Q LS +Q+

Sbjct: 111 AEDIIHLTPY---IGTEIVGLQLSELTNKQKDELALLIAERVVFFKDQDLSPQKQLELG
167

Query: 62 KRFGAIE-----RIGGGDIVAISNVKADGTVRQHSPAEWDDM----MKVIVGNMAWHAD
111

+G +E RIG S + QH E + + GN WH+D

Sbjct: 168 HYWGQVEIHPQAARIG-----SEFDGVTVIWQHAYAKERRSINLTFKQSKKGNSTWHS
220

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA----RHSLVY
167

+ A + +P +GG T ++ AYD L + + + ++A H +

Sbjct: 221 LVHEKQTAGITHLHLDAIPNIGGETLWSSTYGAYDKLSPSLQQFLDGKTAIYRSAHQYLD
280

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAAES
226

L G YI P+++ HP TG L + R I G+ ES

Sbjct: 281 RNDPL-----KGPKYIERE-----HPIIRTHPVTGWKYL FVNRGMTVRIVGLLPEES
327

Query: 227 ERFLEGL-----VDWACQAP-----RVHAHQWAAGDVVVWDNRCLLH 263

+ L L V W+ Q + + G +WDNR H

Sbjct: 328 DLILNYLYSVIENNRDIQVRWSWQKELGSIKKNKSKEEDSKQYRGVSALWDNRISNH 384

>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 AVFSAEVVPAVGGRTCF A---DMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA
178

++ E P VGG T +A YDAL +A + + A H+ S+L Q
Sbjct: 149 SLLRMEEHPEVGGDTAWARKVSYGLYDALSDAYKKFLDGLHAVHT-----SRL-----QY
199

Query: 179 GSAYIGYGMDDTTATPL---RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLV
234

+ +G P+ P V+ HP TG +L + + AES++ L+ L
Sbjct: 200 DTILDWGTGPNRPPIDTHHPAVRTHPVTGLKALNVNPGFVTGFAELKKAESDKVLDFLA
259

Query: 235 DWACQAPRVHAH-QWAAGDVVVWDNRCLLHRAEPWDFK 271

A + +WA G V +WDNRC LHR P ++
Sbjct: 260 YHIHSADDHYVRWKWAVGVSAMWDNRCTLHRVIPGTYE 297

>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---FGSEIDGVQLSGLNDKKGKDELALFLAQRKVLFFNEQDFADKGGPFAVEFGKY
139

Query: 64 FGAIERIGGGDIVAISNVKADG-----TVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
117

FG + V S+ G T R+ E + ++ +H+D +Y
Sbjct: 140 FGRLH-----VHPSSGSPRGHQELHITYRRPEKGELQRVFAHRRTTSVGFHSDVSYEIT
192

Query: 118 MAQGAVFSAEVVPAVGGRTCFADMRAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA
177

++ +F + GG T F D AY+ L A + + H L S+ Q
Sbjct: 193 PSRFTLFQV-LESGDGGDTVFVDTVEAYNRLSPAFQKRL---EGLHVLHTSED-----QA
243

Query: 178 AGSAYIGYGMDD--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

>gb|AAX51287.1| TdfA [uncultured bacterium]
Length = 100

Score = 46.6 bits (109), Expect = 0.003, Method: Compositional matrix
adjust.

Identities = 36/103 (34%), Positives = 46/103 (44%), Gaps = 7/103 (6%)

Query: 138 FADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLR-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|EEQ44600.1| hypothetical protein CAWG_02874 [Candida albicans WO-1]
Length = 425

Score = 46.6 bits (109), Expect = 0.003, 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---IGTEIVGLQLSELTDKQKDELALLIAERVVVFFKDQDLSPQKQLELG
166

Query: 62 KRFGAIE-----RIGGGDIVAISNVKADGT--VRQHSPAEWDDM----MKVIVGNMAWH
109

+G +E R+G + DG + QH E + + GN WH
Sbjct: 167 HYWGQVEVHPQAARVGP-----EFDGVTVIWQHAKERSINLTFKQSKKGNVSWH
217

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSA----RHSL
165

+D + A + +P +GG+T ++ AYD L + + ++A H
Sbjct: 218 SDLVHEKQTAGITHLHLDAIPGIGGKTLWSSTYGAYDKLSPGLQRFLDGKTAIYRSAHQY
277

Query: 166 VYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAA
224

+ L G Y+ P+V+ HP TG L + R I G+
Sbjct: 278 LDRNDPL-----KGPKYVERE-----HPIVTRHPVTGWKYL FVNVRGMTVRIVGLLPE
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 = 0.003, Method: Compositional matrix
adjust.

Identities = 40/174 (22%), 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 GAAQWHSIDIQFEPVPADYTSRLRLTQLPKTGGDTLWASGYEMYDRFSTAYQKFFEGLTATF
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 HAHAIIPGMDAAESERFLEGLVDWACQAPRVHAH-QW-AAGDVVVWDNRCLLHRA 265

I ++ ES+ L+ + + +W A D+ +WDNR + H A
Sbjct: 262 FPKYINELNVEESDELLKRFRSVITENHDLQVRFKWRNANDLAIWDNRSVFHSA 315

>ref|ZP_02357712.1| pyoverdine biosynthesis protein PvcB [Burkholderia
oklahomensis

EO147]
Length = 303

Score = 46.6 bits (109), Expect = 0.003, 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 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLR--PLVK-VHPETGRPSLLIGRHAHAIPG
220

+YS + + + P R P+++ P S I ++A G
Sbjct: 170 VELYSNTVEAPIIEKH-----PRREFPILRFCEPPIANDSTFINPSSYAFGG
216

Query: 123 VFSAEVVPVAVG----GRTCFAADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQA
178

VF + V A+G GRT F+ A T+AL Q G Q+A
Sbjct: 124 VF--QCVAIGEGQGGRRTFSSTTTALRLASPETKALW-----QRATGQYQRA
169

Query: 179 GSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----LIGRHAHAIPGMDAAES
226

Y ++T L P+++ HP P + + + G++ E
Sbjct: 170 VELY-----SSTALAPIIEQHPYRTYPVIRFCEPPIAGDKEFLNPSTYHFSGIEPEEQ
222

Query: 227 ERFLEGLVDWACQAPRV-HAHQWAAGDVVVWDNRCLLHRAEPW 268

E L L PRV +AHQW +GD+V+ DN LLH E +
Sbjct: 223 ELLSSLQALYD-PRVQYAHQWQSGDIVIADNYSLHGRESY 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 = 0.005, 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---IGTEIVGLQLSELTEQQRDELALLIAERVVVFFKDQDLSPQKQLELG
166

Query: 62 KRFGAIE-----RIGGGDIVAISNVKADGTV---RQHSPAEDW---DMMKVIVGNMAWH
109

+G +E RIG + DG ++ W + GN WH
Sbjct: 167 HYWGQVEVHPQATRIGE-----EYDGISVIWQEQQQRDRWGLNLTFKQSKKGN SQWH
217

Query: 110 ADSTYMPVMAQGAVFSAEVVPVAVGGRTCFAADMRAAYDALDEATRVLVHQRSA----RHSL
165

+D + A + +P +GG T ++ AYD L A + + ++A H
Sbjct: 218 SDLVHEKQTAGITHLHLDAIPGIGGETLWSSTYGAYDKLSPALQKFLDGKTAIYRSAHQY
277

Query: 166 VYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAA
224

+ L G Y+ P+V+ HP TG L + R I G+
Sbjct: 278 LDRNDPL-----KGPKYVERE-----HPIVTRTHPVTGWKYL FVNRSMTVRIVGLLPE
324

Query: 225 ESERFLEGL-----VDWACQAP-----RVHAHQWAAGDVVVWDNRCLLH 263
 ES+ L L V W+ Q + + G +WDNR H
 Sbjct: 325 ESDLILNYLSVIETNRDIQVRWSWQKELGSVKNNKKDEPKQYRGVSALWDNRISNH 381

>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 = 0.005, Method: Compositional matrix adjust.

Identities = 45/201 (22%), Positives = 74/201 (36%), Gaps = 33/201 (16%)

Query: 106 MAWHADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARH 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-----NSKTVSPIITKHPQKDFSVIRYNEPPSVDKGHFV 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 SPRHIQRVHVLSNPPFDNPGL 274

>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 = 0.005, Method: Compositional matrix adjust.

Identities = 56/249 (22%), Positives = 93/249 (37%), Gaps = 42/249 (16%)

Query: 2 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFA 61
 A+ + +TP +G + G+ L+ L D L + ++ F Q LS +Q+

Sbjct: 110 AEDIIHLTPY---IGTEIVGLQLSELTDKQKDELALLIAERVVFFKQDQLSPQKQLELG 166

Query: 62 KRFGAIE-----RIGGGDIVAISNVKADGT--VRQHSPAEWDDM---MKVIVGNMAWH
109

+G +E R+G + DG + QH E + + GN WH
Sbjct: 167 HYWGQVEVHPQAARVGP-----EFDGVTVIWQH YAKERRSINLTFKQSKKGN SVWH
217

Query: 110 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSA----RHSL
165

+D + A + +P +GG T ++ AYD L + + ++A H
Sbjct: 218 SDLVHEKQTAGITHLHLDAIPGIGGETLWSSTYGAYDKLSPGLQRFLDGKTAIYRSAHQY
277

Query: 166 VYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHA-IPGMDAA
224

+ L G Y+ P+V+ HP TG L + R I G+
Sbjct: 278 LDRNDPL-----KGPKYVERE-----HPIVTRTHPVTGWKYL FVNRMGTVRIVGLLPE
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 = 0.006, Method: Compositional matrix
adjust.
Identities = 39/128 (30%), Positives = 52/128 (40%), Gaps = 20/128 (15%)

Query: 136 TCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATP--
193

T F DMRAAYDAL E +A + A HS+ YS+ +LG + D P
Sbjct: 1 TEFGDMRAAYDALPEDMKARLEGLQAHHSIAYS RQRLG-----FEFSGDEAE APEG 51

Query: 194 LRPLVKVHPETGRPSLLIGR-----HAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQW
248

R H RP + + R H + A + R Q V+ H W
Sbjct: 52 RRASAGTHAAHRPQISLSRLAESHTRLVRRRQAAA PRSHRA----PTQRQFVYRHAW
107

Query: 249 AAGDVVVW 256

AGD+V+W
Sbjct: 108 RAGDLVMW 115

>gb|EEY21481.1| alpha-ketoglutarate-dependent sulfonate dioxygenase
[Verticillium
albo-atrum VaMs.102]
Length = 386

Score = 45.4 bits (106), Expect = 0.006, Method: Compositional matrix
adjust.

Identities = 35/163 (21%), Positives = 66/163 (40%), Gaps = 7/163 (4%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQR SARHSLVY
167

WH+D T+ P+ + G + + A ++ A Q +

Sbjct: 178 WHSDITFEPIPSDYPCSDLPNTLWASGYEVYDRISATLQGFSLTATYAQPFGNEAADK
237

Query: 168 SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLL-IGRHAHAIPGM DAAES
226

+ K+ ++ +G ++ + P+++ +P TG S+ +G H I G+ ES

Sbjct: 238 NGFKIYSAERGAPENVGELLEA----IHPVIRTNPVGTGKSVFAVGHVQKINGLSDEES
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 [Legionella pneumophila str. Paris]
Length = 278

Score = 45.4 bits (106), Expect = 0.007, Method: Compositional matrix
adjust.

Identities = 46/201 (22%), Positives = 73/201 (36%), Gaps = 33/201 (16%)

Query: 106 MAWHADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRVLVHQR SARH
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-----NSKTVSPIITKHPQKDFSVIRYNEPPSADKGFV
193

Query: 216 H----AIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFK
271

+ G+D E + F L A +AH+W GD+V+ DN LLH E + +

Sbjct: 194 NPPDIEFTGIDQEELDFHRSLNKALYSADNFYAHEWQNGDIVIADNFSLHLHGREGFVSR
253

Query: 272 LPRVMWHSRLAGRPETEGAAL 292

PR + + P + L

Sbjct: 254 SPRHIQRVHVLNPPFDNPG 274

>gb|ADC33970.1| TfdA-like protein [uncultured bacterium]

Length = 128

Score = 45.4 bits (106), Expect = 0.007, Method: Compositional matrix adjust.

Identities = 34/128 (26%), Positives = 53/128 (41%), Gaps = 2/128 (1%)

Query: 136 TCFADMRAAYDALDEATR^LVHQ^SSAR^HSLV^SQSKLGHV^QQAGSAYIGY^GMDTTATPL-
194

T F DM AAYD L + + + ++A H + + + P+
Sbjct: 1 TEFCDMCAAYDDL^PDLKLELE^GKTALHDFN^RFWEM^MRSRPGSTRP^LSEAQRNAK^PPVS 60

Query: 195 RPLVKVHPETGRPSLLIGR-HAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV
253

P+V HP + R L + I + A+S+R L L D + + W GD
Sbjct: 61 HPVVLTHPISKRRVLYANPGYTVRINELPEADSDRTLALLFDHQTRDKYRYV^FHWQV^GDA
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 = 0.008, 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 GAASWHS^DIQFEEY^PADY^TSLRLTKLPSGGGDTLWASGYELYDRYSDPYQ^KFFEGLTAT^F
215

Query: 154 ---ALVHQ^SSAR--HSLV^SQSKLGHV^QQAGSAYIGY^GMDTTATPLRPLVKVHPETGRPS
208

+ R AR H +Y + + GH + G A + T+ P+V+ +P TG S
Sbjct: 216 SGD^GFLKARDAR^PDHF^KIYEE^PR-GHPENIGDA-----LKTS----HPVVRTNPVTG^WKS
265

Query: 209 LL-IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-QW-AAGDVVVWDNRCLLHRA
265

L +G I + A ES+ LE + + +W + D+ WDNR H A
Sbjct: 266 LFAVGNFPRRINELSA^RESKELLE^Sfykrieen^HDLQV^RFRWRSPNDIA^FWDNRSA^FHSA
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 = 0.008, 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 HWDGMYLETVPFQVVFQCVQAIGDAHGGRTTFSSTTEALRVATPETRALWHRAGRYRRT
169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----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-GSLTRALYDPRAHYHRWRTGDVVLTDNFTLLHGRRERFTS
266

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292

+ R + + G P L
Sbjct: 267 RSGRHLRRVHIHGDPPLRNPHL 288

>gb|AAX51278.1| TdfA [uncultured bacterium]
Length = 105

Score = 45.4 bits (106), Expect = 0.008, Method: Compositional matrix adjust.

Identities = 37/110 (33%), Positives = 48/110 (43%), Gaps = 7/110 (6%)

Query: 136 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
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|AAX51283.1| TdfA [uncultured bacterium]

gb|AAX51284.1| TdfA [uncultured bacterium]

gb|AAX51285.1| TdfA [uncultured bacterium]

Length = 96

Score = 45.4 bits (106), Expect = 0.008, 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 TEFCDMRAAYDDLPEDFKKELOGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVS 54

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD 235

PLV+ H +GR L IG HA I G AE L L++
Sbjct: 55 WPLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLE 95

>gb|ADC33968.1| TfdA-like protein [uncultured bacterium]
Length = 128

Score = 45.1 bits (105), Expect = 0.008, 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

>ref|ZP_04522600.1| PvcB [Burkholderia pseudomallei MSHR346]

gb|EEP51514.1| PvcB [Burkholderia pseudomallei MSHR346]
Length = 304

Score = 45.1 bits (105), Expect = 0.009, 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 HWDGMYLETVPFQVFQCVQAIGDAHGGRTTFSSTTEALRVATPETRALWQRAHGRYRRT
169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----LI
211

+YS + P+V+ HP P L I
Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDDPTFI
207

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 = 0.011, 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 HWDGMYLETVPFQVFQCVQAIGDAHGGRTTFSSTTEALRVATPETRALWHRAGRYRRT
169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----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-GSLTRALYDPAHYAHRWRTGDVVLTDNFTLLHGRRERFTS
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 = 0.012, 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 HWDGMYLETVPFQVFQVCVQAIGDAHGGRTTFSSTTEALRVATPETRALWQRAHGRYRRT
169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----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-GSLTRALYDPRAHYHRWRTGDVVLTDFNFTLLHGRRERFTS
266

Query: 271 KLPRVMWHSRLAGRP 285

+ R + + G P
Sbjct: 267 RSGRHLRRVHIHGDP 281

>ref|ZP_02405336.1| pyoverdine biosynthesis protein PvcB [Burkholderia
pseudomallei

DM98]
Length = 304

Score = 44.7 bits (104), Expect = 0.013, 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 HWDGMYLETVPFQVFQVCVQAIGDAHGGRTTFSSTTEALRVATPETRALWQRAHGRYRRT
169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----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-GSLTRALYDPRAHYAHRWRTGDVVLTDFNFTLLHGRRERFTS
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 = 0.013, 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 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL-----LI
211

+YS + P+V+ HP P L I
Sbjct: 156 VELYSNTVEA-----PIVERHPPREFPILRFCEPPIADDPFTFI
193

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDF
270

++A G+ +E + L G + A PR H AH+W GDVV+ DN LLH E +
Sbjct: 194 NPSSYAFGGIADSERDALL-GSLTRALYDPRAHYAHRWRTGDVVLTDFNFTLLHGRRERFTS
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 = 0.014, 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 HWDGMYLETVPFQVFQCVQAIGDAHGGRTTFSSTTEALRVATPETRALWVHRAHGRYRRT
 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----LI
 211

 +YS + P+V+ HP P L I
 Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPFI
 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--ADSERDALFGSLTRALYDPRAHYAHRWRTGDVVLTNDNFTLLHGRRERFT
 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 = 0.015, 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 HWDGMYLETVPFQVFQCVQAIGDAHGGRTTFSSTTEALRVATPETRALWQRAHGRYRRT
 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----LI
 211

+YS + P+V+ HP P L I
 Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPFI
 207

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDF
 270

++A G+ +E + L G + A PR H AH+W GDVV+ DN LLH E +
 Sbjct: 208 NPSSYAFGGIADSERDALL-GSLTRALYDPRAHYAHRWRTGDVVLTNDNFTLLHGRRERFTS
 266

Query: 271 KLPRVMWHSRLAGRP 285
 + R + + G P

Sbjct: 267 RSGRHLRRVHIHGDP 281

>ref|XP_001903241.1| unnamed protein product [Podospora anserina]
 emb|CAP61013.1| unnamed protein product [Podospora anserina]
 Length = 355

Score = 44.3 bits (103), Expect = 0.015, Method: Compositional matrix
 adjust.

Identities = 63/237 (26%), Positives = 93/237 (39%), Gaps = 45/237 (18%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV-----AISNVKADGTVRQHSPEAW 95
 Q ++ F Q LS D Q +R G E G + A++N K V ++ +

Sbjct: 112 QRGVVFFRNQDLSIDDQKLLGQRLG--ELTGKPEPESKLLKHALANSKRGIAVDEN--GKL
 167

Query: 96 DDMMKVI-----VGNMAWHADSTYMPVMAQGAVFSAEYVPA-VGGR
135

DD + VI + + WHAD T+ + + A+ P VGG
Sbjct: 168 DDEVSVISSEQNRKYYADRYGYTAKRLASEGWHADITFEHIPSDYAILKIVQPPEDVGGD
227

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARH---SLVYSQSKLGH--VQQAGSAYIGYGMDDT
190

T +A YD L A + L +A H + V + G + Q A G+D
Sbjct: 228 TLWASGYEVYDRLSPALQKLAESLTATHHQPNFVVRVKEAFGAELIDQFRGAPENGLDFK
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 = 0.015, Method: Compositional matrix
adjust.

Identities = 37/105 (35%), Positives = 48/105 (45%), Gaps = 8/105 (7%)

Query: 136 TCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
195

T F DMRAAYD ++ + L R A H + S+ LG + S P+
Sbjct: 1 TEFCDMRAAYDLPEDFKKELQGLR-AEHYALNSRFILGDDTDYSES-----QRNAMPPVS 53

Query: 196 -PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ 239

PLV+ H +GR L IG HA I G AE L L++ A Q
Sbjct: 54 WPLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQ 98

>gb|ABD39114.1| alpha-ketoglutarate dioxygenase [uncultured bacterium]
Length = 107

Score = 44.3 bits (103), Expect = 0.016, Method: Compositional matrix
adjust.

Identities = 28/96 (29%), Positives = 47/96 (48%), Gaps = 6/96 (6%)

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR-PLVKVHPETGRPSLLIGRHAHAIP
219

A H+L +S+++ + G + A P+ P+V++HPETGR + +G HA I
Sbjct: 10 AVHNLDIFSRTTR-----RHGIDLMTEEQKREAPPVEHPVVRHHPETGRCCIYLGDAEWIV 64

Query: 220 GMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV 255

GM E +E L A + H+W +++V
Sbjct: 65 GMPYEEGRALIEELNALAVHPDLSYHRWRPNELIV 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 = 0.017, Method: Compositional matrix
adjust.

Identities = 41/166 (24%), Positives = 63/166 (37%), Gaps = 9/166 (5%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVP--AVGGRTCFADMRAAYDALDEATR_LVHQ_RSARHS
164

 WH D ++ V + VP GG T FA AYD L + + SA
Sbjct: 170 GWHTDGSFENVPPDYTL_LHMVKVPVEGSGGDTMFASAYEAYD_LLLSPPMK_KFLEGISATF-
228

Query: 165 LVYSQSKLGHVQ_QAGSAYIGYGM_DTTATPLR---PLVKVHPETGRPS_LL-IGRHAHAIPG
220

 + + + G + LR P ++ +P TG SL G H G
Sbjct: 229 MPWDHKPENIIDHMWKGTRG-APENQGP_ELRASHPCIRTNPVTGWKSLFAFG_HHLEEFEG
287

Query: 221 MDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVW_DNRCLLHRA 265

 + E+ E + + ++ A +W D+V+W_DNR + H A
Sbjct: 288 LGDVENRMMKEFVQRLITENHQLQARVRWEQDD_LVIW_DNR_AVYHSA 333

>gb|AA_X51277.1| TdfA [uncultured bacterium]

Length = 97

Score = 44.3 bits (103), Expect = 0.017, Method: Compositional matrix
adjust.

Identities = 35/101 (34%), Positives = 45/101 (44%), Gaps = 7/101 (6%)

Query: 140 DMRAAYDALDEATR_LVHQ_RSARHSLVYSQSKLGHVQ_QAGSAYIGYGM_DTTATPLR-PLV
198

 DMRAAYD L E + + A H + S+ LG + S P+ PLV
Sbjct: 1 DMRAAYDDLPEDFK_KELQGLRAEHYALNSRFILGDTDYSES-----QRNAMPPVSWPLV 54

Query: 199 KVHPETGRPSLLIGRHAHAIPGM_DAAESERFLEGLVDWACQ 239

 + H +GR L IG HA I G AE L L++ A Q
Sbjct: 55 RTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLE_HATQ 95

>gb|ACB21022.1| TfdA [uncultured bacterium]

Length = 63

Score = 44.3 bits (103), Expect = 0.018, Method: Compositional matrix
adjust.

Identities = 24/56 (42%), Positives = 31/56 (55%)

Query: 108 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR_LVHQ_RSARH 163

 WH+D A+ ++ SA VVP GG T F DMRAAYDAL ++ + A H
Sbjct: 3 WHS_DXXXXXXXXAARYSMLSAVVVPPSGGDTEFCDMRAAYDALPRDLQSELEGLRAEH 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 = 0.018, 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 MPYKITALQPPFGVIVEPKHAPIHVNELD---IDELRELFREQLVLLRGFETFEHSEQFA 57

Query: 60 -FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVM
 118

+ +R+G + G ++ + + G D + M W D Y P +
 Sbjct: 58 DYCERWGEVSVWPFGRVLDLVQKEDPG-----DHIFDSSYMPMHW--DGMYPQV
 105

Query: 119 AQQAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
 176

+ +F +P GGRT F+ A Q + + L Q GH Q
 Sbjct: 106 PEYQIFQCVKAPLPGHGGRTTFSHTMLAL-----QHAPQPDLELWQQVTGHYQ
 153

Query: 177 QAGSAYIGYGMDDTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDDA
 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 QAIEFHKSLRRALYDPRNFYAHEWQTGDIVITDNFSLHGREAFNSHTPRHIRRVQVLSN
 266

Query: 285 PETEGAAL 292

P +L
 Sbjct: 267 PPYNNPSL 274

>gb|EEU35932.1| hypothetical protein NECHADRAFT_49706 [Nectria
 haematococca mpVI
 77-13-4]
 Length = 361

Score = 43.9 bits (102), Expect = 0.019, Method: Compositional matrix
 adjust.

Identities = 40/174 (22%), Positives = 69/174 (39%), Gaps = 16/174 (9%)

Query: 104 GNMAWHADSTYMPVMAQQAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARH
 163

G +WH+D + A +P+ GG T +A YD + + + +A

Sbjct: 154 GAASWHSDIQFEEFPADYTSRLRLTQLPSTGGDTLWASGYEIYDRFSDPWQKFLEGLTATF
213

Query: 164 S-----LVYSQSKLGHVQ-----QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLL-IGR
213

+ + ++ Q + A +G G+ T + P+V+ +P TG S+ IG
Sbjct: 214 KGEFGIKAADARPKFKQIYEEPRGNPANVGRGL-----TAVHPVVRTNPVTGWKSVFAIGN
269

Query: 214 HAHAIPGMDAAESERFLEGLVDWACQAPRVHAH-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 = 0.019, 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---IDELRELFREQLVLLRGFETFEHSEQFA 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 PEYQIFQCVKAPLPGHGGRTTFSHTMLAL-----QHAPQPDLELWQQVTGHYQ
158

Query: 177 QAGSAYIGYGMDTTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDAA
224

+ Y + + P+V HP P L+ ++ G+
Sbjct: 159 RKMEFY-----HSKTVSPIVMQHPYRDYQVIRYNEPHFEENGDLLNPPDVSLSGITPE
211

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR
284

++ F + L +AH+W GD+V+ DN LLH E ++ PR + ++
Sbjct: 212 QAIEFHKSLRRALYDPRNFYAHEWQTGDIVITDNFSLHGREAFNSHTPRHIRRVQVLSN
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 = 0.020, Method: Compositional matrix
adjust.

Identities = 32/114 (28%), Positives = 49/114 (42%), Gaps = 13/114 (11%)

Query: 144 AYDALDEATR~~AL~~VHQ~~RSARH~~SLVYSQSKLGHVQQAGSAYIGYGM~~DTTATPLRP~~----LVK
199

A++ LD+ + A HS +S+SK+ G L P +V
Sbjct: 2 AFERLDKDVAKRLENTFAWHSYAHRSR~~SKVA~~-----TGLATTEEVDALPPVCWRMVW 52

Query: 200 VHPETGRPSLLIGRHAHAIPGM~~DAAE~~SERFLEGLVDWACQAPRVHAHQWAAGDV 253
+P GR +L + HA+ + GMDA + +E L + A + HQW GDV

Sbjct: 53 RNPVNGRGALYLASHAYGVEGMDADAGKALIEQLTEAATALGV~~TYLHQW~~KQGDV 106

>ref|ZP_05476509.1| Alpha-ketoglutarate-dependent taurine dioxygenase
[Streptomyces sp.
AA4]
Length = 167

Score = 43.9 bits (102), Expect = 0.022, Method: Compositional matrix
adjust.

Identities = 31/74 (41%), Positives = 39/74 (52%), Gaps = 3/74 (4%)

Query: 194 LRPLVKVHPETGRPSLLIGRHA-HAIPGM~~DAAE~~SERFLEGLVDWACQAPR-VHAHQWAAG
251

L PLV HP TGR L + + G+ AE+ +E L APR V +WAAG
Sbjct: 59 LHPLVHTHPLTGRKGLYVSACPLTGVAGLADAEAAELIEQLFRQVV-APRFVSRVRWAAG
117

Query: 252 DVVVWDNRCLLHRA 265
VV+ DNRC+ H A

Sbjct: 118 LVVMIDNRCVQH~~YA~~ 131

>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 = 0.024, Method: Compositional matrix
adjust.

Identities = 34/128 (26%), Positives = 57/128 (44%), Gaps = 8/128 (6%)

Query: 144 AYDALDEATR~~AL~~VHQ~~RSARH~~SL----VYSQSKLGHVQQAGSAYIGYGM~~DTTATPLR~~PLVK
199

AYD L A + + +A H+ VY+Q+ +Q + G + TA + P+++

Sbjct: 7 AYDRLSPAFQRFLEGLTAVHNADFFNVYAQTHGLKIQDPRGSPENTGSNLTA--VHPVIR 64

Query: 200 VHPETGRPSLLIGR-HAHAI PGMDAAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWD
257

+P TG SL + + I + ES+ L+ L + + +W DV +WD
Sbjct: 65 TNPVTGFKSLFVNKTFTRILELTPDESDDVLDYLAKHISENHDLQVRFKWKNDVAIWD
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 = 0.024, Method: Compositional matrix
adjust.

Identities = 51/186 (27%), Positives = 75/186 (40%), Gaps = 23/186 (12%)

Query: 109 HADSTYMPVMAQGAVFSAE--VVPVAVGGRTCFADMRAAYDALDEATRAL---VHQRSARH
163

H D Y+ + + VF + A GGRT F+ A TRAL H R R
Sbjct: 110 HWDGMYLETVPEFQVFQCAQAIGDAHGGRTTFSSTTEALRVATPETRALWQRAHGRYRRT
169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR--PLVK-VHPETGRPSLLIGRHAHAIPG
220

+YS + + + P R P+++ P I ++A G
Sbjct: 170 VELYSNTVEASIVERH-----PRREFPILRFCEPPIADDPTFINSSYAFGG
216

Query: 221 MDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHS
279

+ +E + L G + A PR H AH+W GDVV+ DN LLH E + + R +
Sbjct: 217 IADSERDALL-GSLTRALYDPRAHYHRWRTGDVVLTDFNFTLLHGRERFTSRSGRHLRRV
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 = 0.025, Method: Compositional matrix adjust.

Identities = 41/185 (22%), Positives = 73/185 (39%), Gaps = 26/185 (14%)

Query: 105 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHS
164

++ WH D ++ V + A+ +P GG T +A YD L + +A H

Sbjct: 154 SVGWHTDISFERVPSDYAMLKIHTLPETGGDTLWASGYEYDRLSPQMAEFLEGLTATHD
213

Query: 165 LVY---SQSKLGHVQQAG--SAYIGYGMDDTTATPLRPLVKVHPE-----
203

+ +LG+ + G + + +G D A + P+++ + E

Sbjct: 214 ASFFHDEARRLGNPLRKGVRGSPLNHGEDLKA--VHPVIRTNREFSGLLSRAVSIKISA
271

Query: 204 -TGRPSLLIGR-HAHAIPGMDDAESERFLEGLVDWACQAPRVHAH-QWAAGDVVVWDNR
260

TG S+ + + I G+ ES+ L+ L + Q +W D+ +WDNR

Sbjct: 272 VTGWKSVYVNGFTKRINGVTKDESMLLQYLFNLVTQNHDAQVRFKWNKNDMAIWDNRS
331

Query: 261 LLHRA 265

H A

Sbjct: 332 TWHCA 336

>ref|YP_001249599.1| pyoverdine biosynthesis protein PvcB [Legionella pneumophila str.

Corby]

gb|ABQ54253.1| pyoverdine biosynthesis protein PvcB [Legionella pneumophila str.

Corby]

Length = 278

Score = 43.5 bits (101), Expect = 0.029, Method: Compositional matrix adjust.

Identities = 46/197 (23%), Positives = 70/197 (35%), Gaps = 25/197 (12%)

Query: 106 MAWHADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRALLVH
157

M H D Y P + + +F +P GGRT F++ A + L +

Sbjct: 93 MPLHWDGMYRPQVPEYQIFHCVKAPLPGQGGRTTFSNTILALQFASSEIKELWNKVCPTY
152

Query: 158 QRSAR--HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHA
215

QR +S S + H Q+ S I Y P + +

Sbjct: 153 QRKMEFYNSKTVSPIIMKHPQKDFSV-IRYN-----EPPSADKGFVNPPD
197

Query: 216 HAIPGMDDAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLP
275

G+D E + F L A +AH+W GD+V+ DN LLH E + + PR

Sbjct: 198 IEFTGIDQEELDFHRSLNKALYSADNFYAHEWQNGDIVIADNFSLLHGREGFVSRSPRH
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 = 0.032, 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 HWDGMYLETVPFQVFQVCVQAIGDAHGGRTTFSSTTEALRVATPETRALWHRAGRYRRT
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-GSLTRALYDPRAHYHRWRTGDVVLTDFNFTLLHGRRERFTS
266

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292
+ R + + G P L

Sbjct: 267 RSGRHLRRVHIHGDPPLRNPHL 288

>emb|CAY25794.1| alpha-KG-dehydrogenase [uncultured bacterium]

emb|CAY25798.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 118

Score = 43.1 bits (100), Expect = 0.033, 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 DGTVRQHSPAEWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAEVV 129
 Q DD ++ +GN WH DS++ + A+ ++ SA VV
 Sbjct: 71 SNLDEQSRVLAADDRRRMNGLGNRLWHTDSSFKAIPARYSLLSARVV 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 = 0.034, 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 HWDGMYLETVPEFQVFQCVQAIGDAHGGRTTFSSTTEALRVATPETRALWQRAHGRYRRT
 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----LI
 211
 +YS + P+V+ HP P L I
 Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPPIADDPFI
 207

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDF
 270
 ++ G+ +E + L G + A PR H AH+W GDVV+ DN LLH E +
 Sbjct: 208 NPSSYTFGGIADSERDALL-GSLTRALYDPRAHYHRWRTGDVVLTDFNFTLLHGRRERFTS
 266

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292
 + R + + G P L
 Sbjct: 267 RSGRHLRRVHIHGDPPLRNPHL 288

>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 = 0.038, Method: Compositional matrix
 adjust.

Identities = 60/301 (19%), Positives = 107/301 (35%), Gaps = 50/301 (16%)

Query: 8 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPG-QHLSNDQQIT-FAKRF 65
 + P G + +H+ LD L +L+ L++ G + + +Q + +R+G
 Sbjct: 13 LQPFQVIVEPKHAPIHVNELD---IDELRELFLREQLVLLRGFETFHSEQFADYCERWG 69

Query: 66 AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
125

+ G ++ + + G D + M W D Y P + + +F
Sbjct: 70 EVSVWPFGRVLDLVQKEDPG-----DHIFDSSYMPMHW--DGMYPQVPEYQIFQ
117

Query: 126 A--EVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYI
183

+P GGRT F+ A Q + + L Q GH Q+ Y
Sbjct: 118 CVKAPLPGHGGRTTFSHTMLAL-----QNAPQPDLELWQQVVTGHYQRKMEFY-
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 SLRRALYDPRNFYAHEWQTGDIVITDNFSL LHGREAF TSHTPRHIRRVQVLSNPPYNNPS
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 = 0.038, 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---IDELRELFRLREQLVLLRGFETFEHSEQFA 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--EVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ
176

+ +F +P GGRT F+ A Q + + L Q GH Q
Sbjct: 106 PEYQIFQCVKAPLPGHGGRTTFSHTMLAL-----QHAPQPDLELWQQVVTGHYQ
153

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDAA
224

+ Y + + P+V HP P L+ ++ G+
Sbjct: 154 RKMEFY-----HSKTVSPIVMQHPYRDYQVIRYNEPHFEENGDLLNPPDVSLSGITPE
206

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAGR
284

++ F + L ++AH+W GD+V+ DN LLH E + PR + ++
Sbjct: 207 QAIEFHKSLRRALYDPRNLYAHEWQTGDIVITDNFSLHGREFTSHTPRHIRRVQVLSN
266

Query: 285 PETEGAAL 292

P +L
Sbjct: 267 PPYNNPSL 274

>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 = 0.043, 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---IDELRELFREQLVLLRGFETFEHSEQFA 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 PEYQIFQCVKAPLPGHGGRTTFSHTMLAL-----QHAPQPDLELWQQVTGHYQ
153

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDAA
224

+ Y + + P+V HP P L+ ++ G+
Sbjct: 154 RKMEFY-----HSKTVSPIVMQHPYRDYQVIRYNEPHFEENGDLLNPPDVSLSGITPE
206

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAGR
284

++ F + L ++AH+W GD+V+ DN LLH E + PR + ++
Sbjct: 207 QAIEFHKSLRRALYDPRNFYAHEWQTGDIVITDNFSLHGREFTSHTPRHIRRVQVLSN
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 = 0.044, 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 MPYKITALQPFQVIVEPKHAPIHVNELD---IDELRELFREQLVLLRGFETFEHSEQFA 62

Query: 60 -FAKRFGAIERIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVM
118
+ +R+G + G ++ + + G D + M W D Y P +
Sbjct: 63 DYCERWGEVSVWPFGRVLDLVQKEDPG-----DHIFDSSYMPMHW--DGMYPQV
110

Query: 119 AQGAVFSAEVVPAVG--GRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
176
+ +F P +G GRT F+ A Q + + L Q GH Q
Sbjct: 111 PEYQIFQCVKAPLLGHGGRTTFSHTMLAL-----QHAPQPDLELWQQVTGHYQ
158

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDAA
224
+ Y + + P+V HP P L+ ++ G+
Sbjct: 159 RKMEFY-----HSKTVSPIVMQHPYRDYQVIRYNEPHFEENGDLLNPPDVSLSGITPE
211

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR
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

>emb|CAY67029.1| Alpha-ketoglutarate-dependent sulfonate dioxygenase
[Pichia
pastoris]
Length = 405

Score = 42.7 bits (99), Expect = 0.044, 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---FGSVVEGIQLSELSNDQKDDLALFVAQRGVVVFRDQNLK-DKSLSEVKKFGQ
 168

Query: 67 -----IERIGG---GDIVAINVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
 117
 I + G G + K G R + V M WH+D TY +
 Sbjct: 169 HFGPLHIHQTSGAPEGHPEFHISYKRSGRTRS-----FEKKVSAMTWHSDVTYE-L
 218

Query: 118 MAQGAVF-SAEVVPVAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
 176
 G F P VG L +R + AR G +Q
 Sbjct: 219 QPPGTTFLFVKAPRVG-----EIQLLQIPSRHMRDLSLAR-----GSIQ
 258

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDW
 236
 + T+ + PLV+ HP G+ S+ I G+ ES+ L+ + +
 Sbjct: 259 RK-----KFTSENVHPLVRYHPVLGKKSIFAKAFGTRIIGLKQEESDLILQFIENH
 309

Query: 237 ACQAPRVHAH-QWAAGDVVVDNRCLLHRA 265
 A + + G VV WDNR LH A
 Sbjct: 310 IATALDLQLRASYPEPGTVVAWDNRRLHSA 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 = 0.048, 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---IGTEVRGIQLSTLTAKGDELARFVAERKVVAFRDQDFADLPIDEAL
 129

Query: 59 TFAKRFGA--IERIGGG-----DIVAINVKADGTVRQHSPAEWDDMMKVIVGNMAWHAD
 111
 + FG I G +I + D + + ++AWH+D
 Sbjct: 130 EYGSYFGRHHIHPTSGAPEGYPEIHLVHRGAGD TSA-----EAFKARTSSVAWHS
 181

Query: 112 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSK
 171
 +Y PA GG T FAD AY L + +H A HS

Sbjct: 182 VSYEQQPPGTTFLYVLDRPATGGDTLFADAAEAYRRSLPLFQQLHGLRATHSA-----
235

Query: 172 LGHVQQAGSAYIGYGMTTATPLR--PLVKVHPETGRPSLLIG 212
V+QA ++ G+ + P+V+ HP TG ++ +

Sbjct: 236 ---VEQAAASLARGGVQRREPVINEHPIVRTHPVTGEKAIYVN 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]
gb|AAF95092.1| PvcB protein [Vibrio cholerae O1 biovar El Tor str.
N16961]
gb|EAY32805.1| PvcB protein [Vibrio cholerae 1587]
gb|EAZ73310.1| PvcB protein [Vibrio cholerae NCTC 8457]
gb|EAZ77190.1| PvcB protein [Vibrio cholerae B33]
gb|ACP06174.1| PvcB protein [Vibrio cholerae M66-2]
gb|EEO08604.1| PvcB protein [Vibrio cholerae RC9]
gb|EEO16708.1| PvcB protein [Vibrio cholerae B33]
gb|EEO20387.1| 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]

Length = 287

Score = 42.7 bits (99), Expect = 0.049, 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 -FAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM
118

+ +R+G + G ++ + + G D + M W D Y P +
Sbjct: 63 DYCERWGEVSVWPFGRVLDLVQKEDPG-----DHIFDSSYMPMHW--DGMYPQV
110

Query: 119 AQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
176

+ +F +P GGRT F+ A Q + + L Q GH Q
Sbjct: 111 PEYQIFQCVKAPLPGHGGRTTFSHTMLAL-----QHAPQPDLELWQQVTGHYQ
158

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDAA
224

+ Y + + P+V HP P L+ ++ G+
Sbjct: 159 RKMEFY-----HSKTVSPIVMQHPYRDYQVIRYNEPHFEENGDLLNPPDVSLSGITPE
211

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR
284

++ F + L +AH+W GD+V+ DN LLH E + PR + ++
Sbjct: 212 QAIEFHKSLRRALYDPRNFYAHEWQTGDIVITDNFSLHGREAFSHTPRHIRRVQVLSN
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 = 0.050, 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---IDELRELFLEQLVLLRGFETFEHSEQFA 62

Query: 60 -FAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVM
118

+ +R+G + G ++ + V++ P D + M W D Y P +
Sbjct: 63 DYCERWGEVSVWPFGRVLDL-----VQKEDPG--DHIFDSSYMPMHW--DGMYPQV
110

Query: 119 AQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
176

+ +F +P GGRT F+ A Q + + L Q GH Q
Sbjct: 111 PEYQIFQCVKAPLPGHGGRTTFSHTMLAL-----QNAPQPDLELWQQVTGHYQ
158

Query: 177 QAGSAYIGYGMDDTTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDAA
224

+ Y + + P+V HP P L+ ++ G+
Sbjct: 159 RKMEFY-----HSKTVSPIVMQHPYRDYQVIRYNEPHFEENGDLLNPPDVSLSGITPE
211

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR
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_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_04917913.1| PvcB protein [Vibrio cholerae RC385]
ref|ZP_04920074.1| PvcB protein [Vibrio cholerae V51]
gb|EAX58008.1| PvcB protein [Vibrio cholerae 2740-80]
gb|EAZ49344.1| PvcB protein [Vibrio cholerae V51]
gb|EDM54044.1| PvcB protein [Vibrio cholerae MZO-2]
gb|EDN11743.1| PvcB protein [Vibrio cholerae RC385]
gb|EDT88250.1| PvcB protein [Vibrio cholerae MZO-3]
gb|EE002561.1| PvcB protein [Vibrio cholerae bv. albensis VL426]
gb|EE005792.1| PvcB protein [Vibrio cholerae TM 11079-80]
gb|EE012992.1| PvcB protein [Vibrio cholerae TMA 21]
Length = 287

Score = 42.4 bits (98), 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: 6 MPYKITALQPFQVIVEPKHAPIHVNELD---IDELRELFREQLVLLRGFETFEHSEQFA 62

Query: 60 -FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVM
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 PEYQIFQCVKAPLPGHGGRTTFSHTMLAL-----QHAPQPDLELWQQVTGHYQ
158

Query: 177 QAGSAYIGYGMDDTATPLRPLVKVHP-----ETGRPSL-----LIGRHAHAIPGMDAA
224
+ Y + + P+V HP P L+ ++ G+
Sbjct: 159 RKMEFY-----HSKTVSPIVMQHPYRDYQVIRYNEPHFEENGDLLNPPDVSLSGITPE
211

Query: 225 ESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR
284
++ F + L +AH+W GD+V+ DN LLH E + PR + ++
Sbjct: 212 QAIEFHKSLRRALYDPRNFYAHEWQTGDIVITDNFSLHREGFTSHTPRHIRRVQVLSN
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 = 0.058, 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 HWDGMYLETVPFQVFQVCVQAIGDAHGGRTTFSSTTEALRVATPEARALWQRAHGRYRRT
 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 NPSSYAFGGIADSERDALL-GSLTRALYDPAHYAHRWRTGDVVLTDNFTLLHGRRERFTS
 266

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292
 + R + + G P L

Sbjct: 267 RSGRHLRRVHIHGDPPLRNPHL 288

>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 = 0.060, 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 HWDGMYLETVPPEFQVFQCVQAIGDAHGGRTTFSSTTEALRVATPEARALWQRAHGRYRRT
169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----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-GSLTRALYDPAHYAHRWRTGDVVLTDFNFTLLHGRRERFTS
266

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292

+ R + + G P L

Sbjct: 267 RSGRHLRRVHIHGDPPLRNPHL 288

>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

>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 = 0.072, Method: Compositional matrix
adjust.

Identities = 33/102 (32%), Positives = 44/102 (43%), Gaps = 22/102 (21%)

Query: 196 PLVKVHPETGRPSLLIGR-----HAHAIPGM DAAESERFL-----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 --RWQPGDVAFWDNRSTIHYAVNDYGKAHRVMHRATIVGDRP 102

>ref|XP_001389856.1| hypothetical protein An01g14680 [Aspergillus niger]
emb|CAK44165.1| unnamed protein product [Aspergillus niger]
Length = 369

Score = 42.0 bits (97), Expect = 0.080, 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 IDESKIQILPMVWKNPVTGKPALQIHPSAVRKIHRKDGTVIDDLGRVREIVYKLRPAIS
315

Query: 240 APRVHAHQWAAGDVVVWDNRCLLH 263

P V+AH W GD+V+++NR ++H

Sbjct: 316 PPHVYAHDWQEGDLVLFNNRGGVIH 339

>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 = 0.090, 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 YTVTYLTKKVVH-----YGGDFMAS----IIGEHPVTKERTLRYAEPVELLNPKV
162

Query: 216 HAIPGM DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH 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 = 0.094, Method: Compositional matrix adjust.

Identities = 51/195 (26%), Positives = 69/195 (35%), Gaps = 41/195 (21%)

Query: 109 HADSTYMPVMAQGAVFSA--EVVPAVGGRTCFADMRAAYDALDEATRAL---VHQRSARH
163

```
      H D Y+ + + VF      + A GGRT F+      A      TRAL      H R R
Sbjct: 110 HWDGMYLETVPPEFQVFQCVQAIGEADGGRTTFSSTAEALRIATPQTRALWQRAHGRYQRT
169
```

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----LI
211

```
      +YS +                      P+V+ HP      P L                      I
Sbjct: 170 VELYSNTVEA-----PIVERHPRREFPILRFCEPSIADDPFTFI
207
```

Query: 212 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDF
270

```
      + G+ E + L G + A PR H AH+W GDV DN LLH E +
Sbjct: 208 NPSRYTFGGIADGEQDALL-GSLKRALYDPAHYAHRWQTGDVAFTDNFTLLHGRRERFTS
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 = 0.097, Method: Compositional matrix adjust.

Identities = 20/57 (35%), Positives = 28/57 (49%)

Query: 107 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARH 163
WH+D T+ PV + A+ +PA GG T +A YD L A R + +A H
Sbjct: 161 GWHSDITFEPVPSDYAMLKIHTLPATGGDTLWASGYEYDRLSPAMRNFLQSLTATH 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 = 0.098, 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---IDTLRELAREYHLLVLRGFSSGFSDPETLTTEYAGHW 95

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGN--MAWHADSTYMPVMAQGA
122

G I G A+ +VK + H I N + H D Y P + +

Sbjct: 96 GEIMMWPFQ---AVLDVKEHADTKDH-----IFDNSYVPLHWGMYKPTIPEFQ
141

Query: 123 VFSAEVVPVAV--GGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGS
180

+F P GGRT F D D A + + R S+ Y + H

Sbjct: 142 LFHCVSAPGQDQGGRTTFVDTRLLAGAD----APLVEEWRRVSITYRIKAVVH-----
191

Query: 181 AYIGYGMDDTTATPLRPLVKVHPE-----TGRPSLLIGRHA----HAIPGMDAAE
225

YG + T+ PLV HP + + +HA H P

Sbjct: 192 ----YGGEVTS----PLVIPHPNGVGEIMRYNEPPTKGERFLNQHALEYHHIAPEAQNTF
243

Query: 226 SERFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGR
284

S+ + L D PR + AHQW GDVV+ DN LLH E + R + + G

Sbjct: 244 SQTLRQHLYD-----PRYYYAHQWLQGDVVIADNFSLLHGREAFTAHSARHLQRVHIQGT
298

Query: 285 P 285

P

Sbjct: 299 P 299

>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 = 0.14, 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 HWDGMYLETVPFQVFQVCVQAIGDAHGGRTTFSSTTEALRVATPEARALWQRAHGRYRRT
 169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----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-GSLTRALYDPRAHYHRWRTGDVVLTDFNFTLLHGRERFTS
 266

Query: 271 KLPRVMWHSRLAGRPETEGAAL 292

+ R + + G P L
 Sbjct: 267 RSGRHLRRVHIHGDPPLRNPHL 288

>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 = 0.17, 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 HWDGMYLETVPFQVVFQCVQAIGDAHGGRTTFSSTTEALRVATPEARALWQRAHGRYRRT
169

Query: 164 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL-----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-GSLTRALYDPRAHYHRWRTGDVVLTDNFTLLHGRRERFTS
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 = 0.17, 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---IDTLRELAREHLLLVLRGFSSGFSDPETLTEYAGHW 64

Query: 65 GAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF
124

G I G AI +VK + H +D+ + H D Y P + + +F
Sbjct: 65 GEIMMWPFQ---AILDVKEHAGTKDHI---FDN-----SYVPLHWDGMYKPTIPEFQLF
112

Query: 125 SAEVVPVAV--GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY
182

P GGRT F D L EA LV + R S+ Y + H
Sbjct: 113 HCVSAPGQDQGGRTTFVDTTRL---LAEADAQLVDEWR-RVSITYRIKAVVH-----
160

Query: 183 IGYGMDDTTATPLRPLVKVHPE-----TGRP-----SLLIGRHA-----HAIPGMDAAESE
227

YG + T+ PL+ HP P + +HA + P +A S+

Sbjct: 161 --YGGEVTS----PLIIPHPNGVGEIMRYNEPPTEGERFLNQHALEYHNVTPEAQSAFSQ
214

Query: 228 RFLEGLVDWACQAPRVH-AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP 285
+ L D PR + AH+W DVV+ DN LLH E + R + + G P

Sbjct: 215 TLRQHLYD-----PRYYYAHKWLQSDVVIADNFSLLHGREAFTAHSARHLQRVHIQGTP 268

>ref|ZP_02369596.1| pyoverdine biosynthesis protein PvcB [Burkholderia
thailandensis

TXDOH]

Length = 303

Score = 40.8 bits (94), Expect = 0.18, 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 HWDGMYLETVPEFQVFQCVQAIGEADGGRTTFSSTAEALRIATPQTRALWQRAHGRYQRT
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-GSLKRALYDPRAHYAHRWQTGDVAFTDNFTLLHGRRERFTSRTGRHLRRVHIH
278

Query: 283 GRP 285

G P

Sbjct: 279 GEP 281

>emb|CAY25744.1| alpha-KG-dehydrogenase [uncultured bacterium]

Length = 119

Score = 40.4 bits (93), Expect = 0.22, 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 ADGTVRQHSPAEWDDMMKVI-VGNMAWHAD 111

DG +P D + +GN WH+D

Sbjct: 76 KDG-----NPLPRDHRTHLFNLGNCLWHS 100

>gb|AAX51280.1| TdfA [uncultured bacterium]
Length = 105

Score = 40.4 bits (93), Expect = 0.22, 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 PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGRMLLAELLEHATQRKFVYRHSW 105

>emb|CAY25788.1| alpha-KG-dehydrogenase [uncultured bacterium]
Length = 115

Score = 40.0 bits (92), Expect = 0.27, 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 ATMAAIGEAADRYAVLVFHDQRITDEQQIAFSRGLGPLETTIKAYRPGHKPRLDLHISDV 70

Query: 84 DGTVRQHSPA EWDDMMKVI-VGNMAWHADSTYMPVMAQGAVFSAE 127
Q DD ++ +GN WH DS++ + A+ ++ SA
Sbjct: 71 SNLDEQSRVLAADDRRRMNGLGNRLWHTDSSFKAIPARYSLLSAR 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 = 0.30, 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 LAPLVRTDPRSGTKSLHSPVWASRPGVRPPIEVEGMTPEESREFLDRLEKHVLPQFRYD
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 = 0.31, Method: Compositional matrix adjust.

Identities = 51/243 (20%), Positives = 89/243 (36%), Gaps = 29/243 (11%)

Query: 41 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQH-----SPAEW 95
Q ++ F Q ++ D Q T KR G + S D T+ H S ++
Sbjct: 78 QRGVVFRAQDINVDDQKTLGKRLGEL-----SGKPGDSTLHIHPTTELSSSKG
126

Query: 96 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV--VPAVGGRTCFADMRAAYDALDEATR
153
D + + + + + PV + +V P GG T +A AY L
Sbjct: 127 DHISVITISSDTLISRLSLSPTTPSSKPPGQVHTAPPSGGDTIWASAYEAYSRLSPHFT
186

Query: 154 ALVHQRSARHSLVY---SQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLL
210
+ + A H + + + G + G + + + P+++V+P TG L
Sbjct: 187 KFLEGKEAFHEAAFFSKAAEQYGIELRTGERGSPLNEGPSLSAIHPVIRVNPVTGWKGLY
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

>ref|ZP_05225172.1| putative taurine dioxygenase [Mycobacterium intracellulare ATCC 13950]
Length = 153

Score = 40.0 bits (92), Expect = 0.32, 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 IHPVVRVHPETNERVVYVQNQFFTKEIVDLSPRESRHVLGLLFEQISRPEYSVRFKWEPGS 98

Query: 253 VVVWDNRCLLHRAEPWDFK 271
V WDNR LH A P DF+
Sbjct: 99 VAFWDNRATLHLA-PRDFE 116

>ref|ZP_05073584.1| taurine catabolism dioxygenase TauD/TfdA
[Rhodobacterales bacterium
HTCC2083]

gb|EDZ41244.1| taurine catabolism dioxygenase TauD/TfdA [Rhodobacterales
bacterium
HTCC2083]
Length = 155

Score = 40.0 bits (92), Expect = 0.33, 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 LPPFGGDALFASMTAAAYEGLSTGLKATLLNLNAINHSDGSFAESKVG-IDAETSAF----- 69

Query: 188 DTTATPLR-PLVKVHPETGRPSLLIG 212

P++ P+V HP+TG P L +
Sbjct: 70 ---RAPIKHPVVIAHPDTGAPCLYVN 92

>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 = 0.43, 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 LILGACAAAVPGIYTEPKAGFANISSQVTPAIGKRATAFAETQAENEALKKQVHAMVHRKT 73

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYGMDDT-----ATPLRPLVKV 200

Q L + + ++Y G+ +TP P+V +
Sbjct: 74 ISADTAV-QVALLNNKGLQASYANVGLSAAEAWQQSTPENPIVSI 117

>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 = 0.50, Method: Compositional matrix
adjust.

Identities = 29/105 (27%), Positives = 50/105 (47%), Gaps = 6/105 (5%)

Query: 101 VIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALLVHQRS
160
+I+G A Y A A S++V PA+G RT FA+ +A +AL + A+VH+++
Sbjct: 14 LILGACATAVPGIYTEPKAGFANISSQVTPAIGKRTAFAETQAENEALKKQVHAMVHRKT 73

Query: 161 ARHSLVYSQSKLGHVQQAGSAYIGYGMDDT-----ATPLRPLVKV 200
Q L + + ++Y G+ +TP P+V +
Sbjct: 74 ISADTAV-QVALLNNKGLQASYANVGLSAAEAWQQSTPENPIVAI 117

>emb|CAI47587.1| alpha-ketoglutarate dependent xanthine dioxygenase
[Emericella
nidulans]
Length = 370

Score = 39.3 bits (90), Expect = 0.52, 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 IDESAIQILPMVWKNPATGKPALQIHPSAVRKIHCGDGTVIDDLKQVRE--IAYKLQVPA
314

Query: 242 ----RVHAHQWAAGDVVVDNRCLLH 263
V+AH W GD+V++ NR +LH
Sbjct: 315 ISPQYVYAHDWEEGDLVLFHNRGVLH 340

>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 = 0.57, 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 IDESAIQILPMVWKNPATGKPALQIHPSAVRKIHCGDGTVIDDLKQVRE--IAYKLQVPA
298

Query: 242 ----RVHAHQWAAGDVVVDNRCLLH 263
V+AH W GD+V++ NR +LH
Sbjct: 299 ISPQYVYAHDWEEGDLVLFHNRGVLH 324

>ref|XP_658092.1| hypothetical protein AN0488.2 [Aspergillus nidulans FGSC
A4]
gb|EAA66587.1| hypothetical protein AN0488.2 [Aspergillus nidulans FGSC
A4]

Length = 689

Score = 38.9 bits (89), Expect = 0.61, Method: Compositional matrix adjust.

Identities = 27/86 (31%), Positives = 44/86 (51%), Gaps = 11/86 (12%)

Query: 187 MDTTATPLRPLVKVHPETGRPSLLIG----RHAHAIPGM DAAESERFLEGLVDWACQAP-
241

+D +A + P+V +P TG+P+L I R H G + ++ E + + Q P
Sbjct: 241 IDESAIQILPMVWKNPATGKPALQIHPSAVRKIHC GDGTVIDDLK KVRE--IAYKLQ RPA
298

Query: 242 ----RVHAHQWAAGDVVVWDNRCLLH 263

V+AH W GD+V++ NR +LH
Sbjct: 299 ISPQYVYAHDWEEGDLVLFHNRGVLH 324

>ref|XP_001214157.1| conserved hypothetical protein [Aspergillus terreus
NIH2624]

gb|EAU34048.1| conserved hypothetical protein [Aspergillus terreus
NIH2624]

Length = 368

Score = 38.9 bits (89), Expect = 0.75, 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 A+ + L A +
Sbjct: 255 IDESKIQILPMVWKNPVTGKPALQIHPSAVRKIHC KDGTVIDDLAKVREIVYKLQ RPAIR
314

Query: 240 APRVHAHQWAAGDVVVWDNRCLLH 263

V+ H W GD+V++ NR +LH
Sbjct: 315 PQYVYPHDWEEGDLVLFHNRGVLH 338

>gb|AAX51274.1| TdfA [uncultured bacterium]

Length = 58

Score = 38.5 bits (88), Expect = 0.93, Method: Compositional matrix adjust.

Identities = 22/53 (41%), Positives = 27/53 (50%)

Query: 196 PLVKVHPETGRPSLLIGRHAHAIPGM DAAESERFLEGLVDWACQAPRVHAHQW 248

PLV+ H +GR L IG HA I G AE L L++ A Q V+ H W
Sbjct: 6 PLVRTHAGSGRKFLFIGAHAGHIEGRPVAEGVMLLAELLEHATQRKFVYRHSW 58

Database: /usr/local/blast/db/blastlibs/nr
Posted date: Mar 22, 2010 2:54 AM
Number of letters in database: 3,615,943,919
Number of sequences in database: 10,606,545

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: 10606545

Number of Hits to DB: 2,170,962,368

Number of extensions: 90897354

Number of successful extensions: 195556

Number of sequences better than 1.0: 1588

Number of HSP's gapped: 192924

Number of HSP's successfully gapped: 1615

Length of query: 293

Length of database: 3,615,943,919

Length adjustment: 136

Effective length of query: 157

Effective length of database: 2,173,453,799

Effective search space: 341232246443

Effective search space used: 341232246443

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: 88 (38.5 bits)