

ProFound - Search Result Summary

Version 2002.03.01

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Protein Candidates

Rank	Probability	Est'd Z	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	1.0e+000	1.55	FTTSGH0585 557718 556711 [-1 L=1008 r=-1.220] (FTT0535c 557667 556711 -) ====>ref ZP_00054189.1 COG0039: Malate/lactate dehydrogenases [Magnetospirillum magnetotacticum MS-1] Score = 411 bits (1056), Expect = e-113====>ref YP_169564.1 lactate dehydrogenase [Francisella tularensis subsp. tularensis Schu4] Score = 620 bits (1598), Expect = e-176====>gb AAN37808.1 malate dehydrogenase [Francisella tularensis subsp. holarctica]gb AAN37807.1 malate dehydrogenase [Francisella tularensis subsp. holarctica] Score = 619 bits (1597), Expect = e-176	19	6.4	36.05	
2	4.9e-006	-	FTTSGH1866 1713251 1712496 [-3 L= 756 r=-1.233] (FTT1647c 1713239 1712496 -) ====>ref NP_439554.1 dihydroorotate dehydrogenase [Haemophilus influenzae Rd KW20]gb AAC23047.1 dihydroorotate dehydrogenase (pyrD) [Haemophilus influenzae Rd Score = 57.8 bits (138), Expect = 3e-07====>ref YP_170556.1 dihydroorotate dehydrogenase [Francisella tularensis subsp.tularensis Schu 4] Score = 506 bits (1303), Expect = e-142	11	9.8	28.26	
3	2.3e-006	-	FTTSGH1735 1598011 1597493 [-2 L= 519 r=-1.243] (FTT1535 1597587 1597146 -) (FTT1535 1598086 1597587 -) ====>emb CAA82966.1 ornithine cyclodeaminase [Agrobacterium tumefaciens]emb CAA30316.1 unnamed protein product [Agrobacterium tumefaciens] Score = 164 bits (415), Expect = 1e-39	18	9.2	19.13	
4	7.8e-007	-	FTTSGH0343 330889 331443 [+1 L= 555 r=-1.190] (FTT0316 330889 331443 +) ====>ref YP_123994.1 Ribosome recycling factor [Legionella pneumophila str. Paris]emb CAH12828.1 Ribosome recycling factor [Legionella pneumophila str. Paris] Score = 230 bits (586), Expect = 2e-59====>ref YP_169365.1 ribosome recycling factor [Francisella tularensis subsp. tularensisSchu 4] Score = 355 bits (910), Expect = 5e-97	10	5.4	20.53	

5	2.4e-007	-	FTTSGH1561 1430003 1429737 [-3 L= 267 r=-1.232] (FTT1385 1430003 1429737 -) ====>ref YP_170330.1 hypothetical protein FTT1385c [Francisella tularensis subsp.tularensis Schu 4] Score = 187 bits (474), Expect = 1e-46	20	6.2	10.34	
6	2.2e-007	-	FTTSGH0819 758671 758847 [+1 L= 177 r=-1.193] (None identical in .gff) ====>Hypothetical ORF FTTSGH819	24	4.7	6.99	
7	8.0e-008	-	FTTSGH0218 218746 218952 [+1 L= 207 r=-1.257] (FTT0201 218746 218919 +) ====>ref YP_204026.1 serine transporter [Vibrio fischeri ES114]gb AAW85138.1 serine transporter [Vibrio fischeri ES114] Score = 73.6 bits (179), Expect = 2e-12	12	9.9	7.46	
8	7.3e-008	-	FTTSGH0815 756842 757093 [+2 L= 252 r=-1.236] [OlapWith _838 L=87 S=99] (FTT0735 756842 757912 +) ====>ref YP_078587.1 putative muconate cycloisomerase [Bacillus licheniformis ATCC14580] Score = 67.0 bits (162), Expect = 2e-10	10	5.6	8.94	
9	6.1e-008	-	FTTSGH1052 954987 954637 [-1 L= 351 r=-1.232] (FTT0943c 954987 954637 -) ====>ref ZP_00373446.1 dihydroneopterin aldolase [Wolbachia endosymbiont of Drosophilaananassae] Score = 62.0 bits (149), Expect = 5e-09====>ref YP_169936.1 dihydroneopterin aldolase [Francisella tularensis subsp. tularensisSchu 4] Score = 237 bits (605), Expect = 7e-62	16	5.4	13.73	
10	5.2e-008	-	FTTSGH1923 1763730 1763299 [-1 L= 432 r=-1.218] (FTT1694 1763730 1763299 -) ====>ref YP_133086.1 hypothetical membrane protein [Photobacterium profundum SS9]emb CAG23286.1 hypothetical membrane protein [Photobacterium profundum SS9] Score = 122 bits (305), Expect = 4e-27====>ref YP_170599.1 conserved hypothetical membrane protein [Francisella tularensissubsp. tularensis Schu 4] Score = 284 bits (727), Expect = 5e-76	5	8.2	16.94	

NOTE:

1. To search again using [unmatched masses](#), click the symbol .

Input Summary

Search id 20060404160345-1D0C-192168001107

Sequences 1653

Date & Time Tue Apr 04 21:03:45 2006 UTC (Search Time: 0.16 sec.)

Sample ID Schu4 253

Database schu2K [..\databases\schu2k]

Taxonomy -

Mass Range 0 - 40 kDa

pI Range 0.0 -14.0

Digestion Trypsin

Missed Cuts 1

Modifications +O@M(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 714.079 768.572 850.497 862.456 882.497 902.460 939.506
1204.650 1356.782 1367.847 1387.772 1660.998 1794.864
1835.521 1918.951 2163.016 2362.232

Tolerance (mon) 30.00 ppm

Number of 17

Peptides

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