

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	2.15	<p>FTTSGH1540 1411305 1410244 [-1 L=1062 r=-1.228] (FTT1365c 1411305 1410244 -) =====>emb CAA09871.1 fructose-1,6-bisphosphate aldolase [Pseudomonas stutzeri]sp O87796 ALF_PSEST Fructose-bisphosphate aldolase Score = 593 bits (1529), Expect = e-168=====>ref YP_170314.1 Fructose-1,6-bisphosphate aldolase [Francisella tularensis subsp.tularensis Schu 4] Score = 702 bits (1811), Expect = 0.0</p> <p>FTTSGH1351 1211390 1210467 [-3 L= 924 r=-1.229] (FTT1194 1211390 1210467 -) =====>ref ZP_00055100.1 COG2307: Uncharacterized protein conserved in bacteria[Magnetospirillum magnetotacticum MS-1] Score = 120 bits (301), Expect = 6e-26=====>ref YP_170154.1 conserved hypothetical lipoprotein [Francisella tularensis subsp.tularensis Schu 4] Score = 625 bits (1611), Expect = e-178</p> <p>FTTSGH0469 448884 449741 [+3 L= 858 r=-1.212] (FTT0435 448884 449741 +) =====>ref NP_798153.1 putative carbon-nitrogen hydrolase [Vibrio parahaemolyticus RIMD2210633] Score = 343 bits (881), Expect = 3e-93=====>ref YP_169475.1 Carbon-nitrogen hydrolase family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 588 bits (1515), Expect = e-167</p> <p>FTTSGH0167 170083 170958 [+1 L= 876 r=-1.257] (FTT0154 170083 170958 +) =====>ref NP_716579.1 integrase/recombinase XerD [Shewanella oneidensis MR-1]gb AAN54024.1 integrase/recombinase XerD [Shewanella oneidensis MR-1] Score = 315 bits (807), Expect = 1e-84=====>ref YP_169220.1 Integrase/recombinase [Francisella tularensis subsp. tularensisSchu 4] Score = 580 bits (1494), Expect = e-164</p>	14	5.3	38.13	
2	1.5e-008	-		13	5.4	36.14	
3	1.3e-008	-		16	5.7	32.41	
4	3.2e-009	-		12	9.4	33.33	

5	2.6e-009	-	FTTSGH0154 152943 153638 [+3 L= 696 r=-1.202] (FTT0141 152946 153638 +) =====>ref YP_068826.1 50S ribosomal protein L1 [Yersinia pseudotuberculosis IP 32953]ref NP_667819.1 50S ribosomal subunit protein L1 [Yersinia pestis KIM] Score 21 9.5 24.61
			= 320 bits (819), Expect = 3e-86=====>ref YP_169207.1 50S ribosomal protein L1 [Francisella tularensis subsp. tularensisSchu 4] Score = 441 bits (1135), Expect = e-123
6	6.4e-010	-	FTTSGH0865 796770 795679 [-1 L=1092 r=-1.196] (FTT0776c 796770 795679 -) =====>ref YP_033771.1 Ribonuclease D [Bartonella henselae str. Houston-1]emb CAF27773.1 Ribonuclease D [Bartonella henselae str. Houston-1] Score = 8 7.7 42.88
			= 156 bits (394), Expect = 1e-36=====>ref YP_169783.1 Ribonuclease D [Francisella tularensis subsp. tularensis Schu 4]emb CAG45409.1 Ribonuclease D [Francisella tularensis subsp. tularensis SCHU S4] Score = 719 bits (1856), Expect = 0.0
7	2.2e-010	-	FTTSGH0406 378540 377485 [-1 L=1056 r=-1.223] (FTT0376 378540 377485 -) =====>ref YP_169422.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 700 bits (1806), Expect = 0.0 11 5.5 40.56
			FTTSGH0843 777910 778350 [+1 L= 441 r=-1.256] (FTT0758 778311 779249 +) (FTT0758 777910 778308 +) =====>ref ZP_00619863.1
8	2.1e-010	-	AMP-dependent synthetase and ligase 13 9.1 17.30
			[Silicibacter sp. TM1040]gb EAN58298.1 AMP-dependent synthetase and ligase [Silicibacter sp. TM1040] Score = 152 bits (385), Expect = 2e-36
9	1.7e-010	-	FTTSGH0790 737241 737498 [+3 L= 258 r=-1.224] (FTT0717 737241 737483 +) =====>emb CAE10530.1 FORMYLTETRAHYDROFOLATE DEFORMYLASE 37 9.0 10.13
			[Wolinella succinogenes]ref NP_907630.1 FORMYLTETRAHYDROFOLATE DEFORMYLASE [Wolinella succinogenes DSM Score = 80.5 bits (197), Expect = 1e-14
10	9.8e-011	-	FTTSGH0410 381342 381818 [+3 L= 477 r=-0.991] (FTT0379 381348 381821 +) =====>ref YP_122434.1 hypothetical 21 9.4 18.12
			protein lpp0083 [Legionella pneumophila str. Paris]emb CAH11231.1 hypothetical protein

[Legionella pneumophila str. Paris] Score =
155 bits (392), Expect =
4e-37====>ref|YP_170453.1| Transposase
[Francisella tularensis subsp. tularensis Schu
4]ref|YP_170402.1| Transposase [Francisella
tularensis subsp. tularensis Schu 4] Score =
320 bits (819), Expect = 1e-86

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

Input Summary

Search id 20060330144942-16EC-192168001107

Sequences 1979

Date & Time Thu Mar 30 20:49:42 2006 UTC (Search Time: 0.28 sec.)

Sample ID Schu4 165

Database schu2K [..\databases\schu2k]

Taxonomy -

Mass Range 0 - 50 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) 1088.620 1101.617 1171.315 1191.566 1208.746 1288.194
1337.941 1368.821 1374.069 1405.752 1470.210 1487.076
1490.878 1500.467 1508.964 1523.389 1531.005 1533.843
1561.830 1619.201 1635.039 1666.925 1701.825 1702.484
1800.179 1816.863 1833.741 1834.461 1983.253 2047.857
2180.125 2189.296 2200.108 2206.577 2214.180 2216.948
2806.394

Tolerance (mon) 100.00 ppm

Number of 37

Peptides

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