

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	0.91	FTTSGH1092 988868 988578 [-3 L= 291 r=-1.247] (FTT0977 988868 988578 -) =====>ref ZP_00511438.1 conserved hypothetical protein [Chlorobium limicola DSM 245]gb EAM43972.1 conserved hypothetical protein [Chlorobium limicola DSM 245] Score = 73.2 bits (178), Expect = 2e-12=====>ref YP_169965.1 hypothetical protein FTT0977c [Francisella tularensis subsp.tularensis Schu 4] Score = 196 bits (498), Expect = 2e-49	34	9.6	11.15	
2	1.1e-003	-	FTTSGH1506 1368817 1368440 [-2 L= 378 r=-1.214] (FTT1338 1368817 1368440 -) =====>ref YP_254429.1 translation initiation inhibitor [Staphylococcus haemolyticusJCS1435] Score = 145 bits (365), Expect = 5e-34=====>ref YP_170290.1 translation initiation inhibitor [Francisella tularensis subsp.tularensis Schu 4] Score = 246 bits (629), Expect = 1e-64	23	5.5	13.73	
3	1.0e-003	-	FTTSGH0364 344037 344432 [+3 L= 396 r=-1.254] (FTT0339 344037 344432 +) =====>ref ZP_00133685.1 COG0096: Ribosomal protein S8 [Haemophilus somnus 2336]Length = 130 Score = 154 bits (388), Expect = 1e-36=====>ref YP_169388.1 30S ribosomal protein S8 [Francisella tularensis subsp. tularensisSchu 4] Score = 261 bits (668), Expect = 4e-69	21	9.4	14.38	
4	8.4e-004	-	FTTSGH0423 393795 393469 [-1 L= 327 r=-1.216] (FTT0392 393795 393469 -) =====>ref NP_142079.1 hypothetical protein PHS001 [Pyrococcus horikoshii OT3]dbj BAA29130.1 78aa long hypothetical protein [Pyrococcus horikoshii OT3] Score = 49.7 bits (117), Expect = 3e-05=====>ref YP_169437.1 hypothetical protein FTT0392c [Francisella tularensis subsp.tularensis Schu 4] Score = 211 bits (536), Expect = 7e-54	25	5.1	12.64	
5	1.3e-005	-	FTTSGH0028 22790 22888 [+2 L= 99 r=-1.274] (None identical in .gff) =====>ref YP_169100.1 hypothetical protein FTT0024c [Francisella tularensis	48	6.0	3.57	

			subsp.tularensis Schu 4] Score = 67.4 bits (163), Expect = 1e-10				
6	8.8e-006	-	FTTSGH1974 1823623 1823715 [+1 L= 93 r=-1.236] (None identical in .gff) =====>Hypothetical ORF FTTSGH1974	52	9.2	3.27	
7	8.3e-006	-	FTTSGH0905 833724 833479 [-1 L= 246 r=-1.183] (FTT0815 833724 833479 -) =====>ref YP_169822.1 hypothetical protein FTT0815c [Francisella tularensis subsp.tularensis Schu 4] Score = 167 bits (423), Expect = 9e-41	22	5.6	9.29	
8	6.9e-006	-	FTTSGH1011 913674 913579 [-1 L= 96 r=-1.228] [ShorterThan _1037 L=79 S=74] (None identical in .gff) =====>ref YP_169902.1 Type IV pili glycosylation protein [Francisella tularensis subsp.tularensis Schu 4] Score = 55.8 bits (133), Expect = 4e-07	41	9.5	3.47	
9	6.9e-006	-	FTTSGH0329 317157 317489 [+3 L= 333 r=-1.232] (FTT0302 317157 317489 +) =====>ref YP_169351.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 219 bits (559), Expect = 2e-56	10	9.0	12.60	
10	6.0e-006	-	FTTSGH1208 1087105 1087329 [+1 L= 225 r=-1.255] (FTT1075 1087105 1087329 +) =====>gb AAB91769.1 Y4mF [Rhizobium sp. NGR234]ref NP_443972.1 Y4mF [Rhizobium sp. NGR234] Score = 65.5 bits (158), Expect = 5e-10=====>ref YP_170054.1 transcriptional regulator [Francisella tularensis subsp. tularensisSchu 4] Score = 150 bits (379), Expect = 1e-35	24	9.4	8.07	

NOTE:

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

Input Summary**Search id** 20060330160606-1CD4-192168001107**Sequences** 2059**Date & Time** Thu Mar 30 22:06:06 2006 UTC (Search Time: 0.09 sec.)**Sample ID** Schu4 189**Database** schu2K [..\databases\schu2k]**Taxonomy** -**Mass Range** 0 - 15 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)	856.497	868.520	925.565	969.554	1126.587	1172.625	1229.613
	1374.079	1395.953	1400.795	1424.799	1451.751	1470.225	
	1487.030	1524.812	1531.006	1547.897	1555.019	1561.849	
	1656.910	1666.857	1702.472	1801.944	1816.883	1863.943	
	1926.318	1940.942	1945.921	1983.220	1986.053	1998.044	
	2021.055	2045.040	2180.064	2527.697	2538.695	2823.210	

Tolerance (mon) 50.00 ppm

Number of 37
Peptides

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