

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	2.37	<p>FTTSGH1760 1619463 1618780 [-1 L= 684 r=-1.196] (FTT1557 1619463 1618780 -) =====>ref YP_123579.1 hypothetical protein lpp1255 [Legionella pneumophila str. Paris]ref YP_126605.1 hypothetical protein lpl1254 [Legionella pneumophila str. Lens] Score = 208 bits (530), Expect = 1e-52=====>ref YP_170481.1 Two-component response regulator [Francisella tularensis subsp.tularensis Schu 4] Score = 439 bits (1130), Expect = e-122</p> <p>FTTSGH0399 371311 370904 [-2 L= 408 r=-1.243] (FTT0370c 371311 370904 -) =====>ref NP_807997.1 hypothetical protein t4408 [Salmonella enterica subsp. entericaserovar Typhi Ty2] Score = 158 bits (399), Expect = 6e-38=====>ref YP_169417.1 Nucleotide-binding protein, yjeE [Francisella tularensis subsp.tularensis Schu 4] Score = 285 bits (730), Expect = 2e-76</p> <p>FTTSGH1626 1487705 1488187 [+2 L= 483 r=-1.208] (FTT1441 1487705 1488187 +) =====>ref YP_096401.1 bacterioferritin (cytochrome b1) [Legionella pneumophila subsp.pneumophila str. Philadelphia 1] Score = 173 bits (439), Expect = 1e-42=====>ref YP_170379.1 hypothetical protein FTT1441 [Francisella tularensis subsp.tularensis Schu 4] Score = 317 bits (811), Expect = 1e-85=====>gb AAT77116.1 bacterioferritin [Francisella tularensis subsp. tularensis]Length = 146 Score = 288 bits (736), Expect = 5e-77</p> <p>FTTSGH1374 1235573 1235115 [-3 L= 459 r=-1.155] (FTT1216 1235573 1235115 -) =====>ref YP_170174.1 hypothetical protein FTT1216c [Francisella tularensis subsp.tularensis Schu 4] Score = 303 bits (776), Expect = 1e-81</p> <p>FTTSGH1267 1137666 1138421 [+3 L= 756 r=-1.232] (FTT1127 1137666 1138421 +) =====>ref ZP_00521456.1 Rhodanese-like [Solibacter usitatus]</p>	24	6.0	25.49	
2	7.5e-013	-		24	5.2	15.87	
3	2.1e-013	-		29	5.3	18.49	
4	1.7e-013	-		21	4.6	17.88	
5	7.1e-014	-		12	6.6	28.19	

			Ellin6076]gb EAM59572.1 Rhodanese-like [Solibacter usitatus Ellin6076] Score = 140 bits (352), Expect = 5e-32====>ref YP_170100.1 Rhodanese-like family protein [Francisella tularensis subsp.tularensis Schu 4] Score = 509 bits (1310), Expect = e-143 FTTSGH0958 872090 871500 [-3 L= 591 r=-1.268] (FTT0861 872090 871500 -) ====>emb CAA36654.1 unnamed protein product [Dichelobacter nodosus]sp P17824 FMA2_BACNO Fimbrial protein precursor (Pilin) (Serogroup C2) Score = 50.1 bits (118), Expect = 4e-05====>ref YP_169863.1 Type IV pili fiber building block protein [Francisella tularensissubsp. tularensis Schu 4] Score = 382 bits (982), Expect = e-105====>ref YP_169885.1 Type IV pili fiber building block protein [Francisella tularensissubsp. tularensis Schu 4] Score = 50.4 bits (119), Expect = 3e-05 FTTSGH1793 1650199 1649921 [-2 L= 279 r=-1.203] (FTT1586 1650199 1649921 -) ====>ref YP_154709.1 Uncharacterized conserved membrane protein [Idiomarina loihiensisL2TR] Score = 69.3 bits (168), Expect = 3e-11====>ref YP_170506.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 184 bits (468), Expect = 5e-46 FTTSGH1708 1569496 1568900 [-2 L= 597 r=-1.242] (FTT1515 1569496 1568900 -) ====>ref YP_096113.1 predicted phosphatidoglycerophosphate synthase [Legionellapneumophila subsp. pneumophila str. Philadelphia 1] Score = 182 bits (462), Expect = 6e-45====>ref YP_170448.1 conserved hypothetical membrane protein [Francisella tularensissubsp. tularensis Schu 4] Score = 385 bits (988), Expect = e-106 FTTSGH0272 260394 260891 [+3 L= 498 r=-1.199] (FTT0248 260523 260891 +) ====>ref YP_169300.1 hypothetical protein FTT0248 [Francisella tularensis subsp.tularensis Schu 4] Score = 252 bits (644), Expect = 3e-66 FTTSGH1280 1151219 1151494 [+2 L= 276 r=-1.250] (FTT1139 1151219 1151485 +) ====>ref ZP_00592239.1 Deoxyribodipyrimidine photolyase			
6	9.4e-016	-	7 9.8 21.93			
7	7.9e-016	-	18 8.1 10.49			
8	4.6e-016	-	9 6.2 22.67			
9	3.9e-016	-	14 9.2 19.10			
10	3.7e-016	-	15 8.0 10.66			

[Prosthecochloris aestuarii DSM271] Score =
88.2 bits (217), Expect = 7e-17

NOTE:

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

Input Summary

Search id 20060404162506-1F0C-192168001107
Sequences 2059
Date & Time Tue Apr 04 21:25:06 2006 UTC (Search Time: 0.09 sec.)
Sample ID Schu4 261
Database schu2K [..\databases\schu2k]
Taxonomy -
Mass Range 0 - 30 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) 787.553 995.675 1263.713 1293.901 1328.813 1456.896 1480.938
1604.871 1609.018 1635.977 1667.858 1678.707 1896.008
1994.041 2763.271
Tolerance (mon) 50.00 ppm
Number of 15
Peptides

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