



ProFound - Search Result SummaryVersion 2002.03.01
© 1997-2002 Proteometrics LLC**Protein Candidates**

Rank	Probability	Est'd Z	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	1.0e+000	2.21	FTTSGH0070 66188 66622 [+2 L= 435 r=-1.227] (FTT0065 66188 66622 +) ====>ref ZP_00459476.1 H+-transporting two-sector ATPase, delta/epsilon subunit[Burkholderia cenocepacia HI2424] Score = 96.3 bits (238), Expect = 3e-19====>ref YP_169140.1 ATP synthase epsilon chain [Francisella tularensis subsp.tularensis Schu 4] Score = 281 bits (719), Expect = 4e-75	54	6.1	15.75	
2	1.1e-013	-	FTTSGH1213 1090715 1090870 [+2 L= 156 r=-1.185] [ShadowedBy _1245] (None identical in .gff) ====>ref YP_170059.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 97.8 bits (242), Expect = 9e-20	38	9.7	5.86	
3	5.6e-015	-	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	8	9.2	19.10	
4	6.4e-017	-	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	
5	5.3e-017	-	FTTSGH0094 93225 92773 [-1 L= 453 r=-1.231] (FTT0089 93297 92773 -) ====>ref ZP_00376095.1 putative transmembrane protein [Erythrobacter litoralis HTCC2594]gb EAL75573.1 putative transmembrane protein [Erythrobacter litoralis HTCC2594] Score = 86.3 bits (212), Expect = 3e-16	15	6.0	17.46	
6	5.1e-017	-	FTTSGH0405 376849 377244 [+1 L= 396 r=-1.244] (FTT0375 376732 377244 +) ====>ref ZP_00587395.1 C4-dicarboxylate anaerobic carrier [Shewanella amazonensis SB2B]gb EAN38169.1 C4-dicarboxylate anaerobic carrier [Shewanella amazonensis	9	9.2	14.36	

			SB2B] Score = 125 bits (314), Expect = 4e-28			
			FTTSGH0823 761109 761002 [-1 L= 108 r=-1.247] (None identical in .gff)			
7	4.6e-017	-	====>ref YP_169505.1 organic solvent tolerance protein [Francisella tularensis subsp.tularensis Schu 4] Score = 55.8 bits (133), Expect = 4e-07	19	8.3	4.02 
			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			
8	4.2e-017	-	====>ref YP_170379.1 hypothetical protein FTT1441 [Francisella tularensis subsp.tularensis Schu 4] Score = 317 bits (811), Expect = 1e-85	14	5.3	18.49 
			====>gb AAT77116.1 bacterioferritin [Francisella tularensis subsp. tularensis]Length = 146 Score = 288 bits (736), Expect = 5e-77			
			FTTSGH1683 1545909 1546082 [+3 L= 174 r=-1.235] (None identical in .gff)			
9	3.7e-017	-	====>Hypothetical ORF FTTSGH1683	17	9.7	7.17 
			FTTSGH1102 996325 996519 [+1 L= 195 r=-1.255] (FTT0987 996325 996519 +)			
10	3.4e-017	-	====>ref YP_169975.1 hypothetical protein FTT0987 [Francisella tularensis subsp.tularensis Schu 4] Score = 128 bits (321), Expect = 6e-29	11	9.1	7.58 

NOTE:

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

Input Summary

Search id 20060404164807-1F10-192168001107
Sequences 2058
Date & Time Tue Apr 04 21:48:08 2006 UTC (Search Time: 0.09 sec.)
Sample ID Schu4 269
Database schu2K [..\databases\schu2k]
Taxonomy -
Mass Range 0 - 20 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)** 882.484 912.473 943.488 962.449 996.547 1029.544 1216.706
1239.699 1240.683 1246.717 1338.813 1524.902 1636.828
1641.915 1660.933 1703.527 2110.161 2166.694 2186.133
2221.159 2314.245 2439.117 2660.630 2715.371**Tolerance (mon)** 40.00 ppm**Number of** 24
Peptides

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