

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	2.06	<p>FTTSGH1924 1763981 1764265 [+2 L= 285 r=-1.205] (FTT1695 1763981 1764265 +) ==>ref NP_954379.1 chaperonin, 10 kDa [Geobacter sulfurreducens PCA]gb AAR36729.1 chaperonin, 10 kDa [Geobacter sulfurreducens PCA] Score = 130 bits (328), Expect = 1e-29==>ref YP_170600.1 Chaperonin protein, groES [Francisella tularensis subsp. tularensisSchu 4] Score = 186 bits (471), Expect = 3e-46==>emb CAA67359.1 groES [Francisella tularensis]sp P94797 CH10_FRATU 10 kDa chaperonin (Protein Cpn10) (groES protein) Score = 184 bits (468), Expect = 6e-46</p> <p>FTTSGH1447 1301423 1301557 [+2 L= 135 r=-1.168] [OlapWith _1483 L=38 S=61] [DelayedBy _1483 L=108] (FTT1282 1301315 1301557 +) ==>ref YP_170238.1 hypothetical protein FTT1282 [Francisella tularensis subsp.tularensis Schu 4] Score = 93.2 bits (230), Expect = 2e-18</p> <p>FTTSGH2025 1867604 1867197 [-3 L= 408 r=-1.211] (FTT1777 1867604 1867197 -) ==>ref YP_170666.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 261 bits (667), Expect = 5e-69==>ref YP_170667.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 150 bits (380), Expect = 9e-36</p> <p>FTTSGH0621 584188 583796 [-2 L= 393 r=-1.204] [DelayedBy _642 L=24] (FTT0567 584224 583793 -) ==>ref YP_095562.1 peptide transport protein, POT family [Legionella pneumophilasubsp. pneumophila str. Philadelphia 1] Score = 65.1 bits (157), Expect = 6e-10==>ref YP_169702.1 Proton-dependent oligopeptide transport (POT) family protein[Francisella tularensis subsp. tularensis Schu 4] Score = 61.2 bits (147), Expect =</p>	57	5.5	10.23	
2	9.0e-008	-		20	10.1	5.51	
3	6.9e-008	-		17	6.5	14.52	
4	2.4e-010	-		5	8.8	14.16	

			9e-09====>ref YP_169991.1 Proton-dependent oligopeptide transporter (POT) family protein[Francisella tularensis subsp. tularensis Schu 4] Score = 51.2 bits (121), Expect = 9e-06				
5	1.4e-010	-	FTTSGH1031 935773 936168 [+1 L= 396 r=-1.245] (FTT0924 935773 936168 +) ====>ref YP_169920.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 270 bits (689), Expect = 1e-71	8	6.8	15.04	
6	1.2e-010	-	FTTSGH1224 1100421 1100906 [+3 L= 486 r=-1.206] (FTT1091 1100421 1100906 +) ====>ref ZP_00106217.2 COG1335: Amidases related to nicotinamidase [Nostoc punctiforme PCC73102] Score = 92.8 bits (229), Expect = 3e-18====>ref YP_170070.1 isochorismatase hydrolase family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 335 bits (860), Expect = 2e-91====>ref YP_170068.1 isochorismatase hydrolase family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 69.7 bits (169), Expect = 3e-11	14	6.3	19.02	
7	9.5e-011	-	FTTSGH1446 1301460 1301296 [-1 L= 165 r=-1.193] [LowScoreBy _1484 L=38 S=38] (None identical in .gff) ====>ref YP_170238.1 hypothetical protein FTT1282 [Francisella tularensis subsp.tularensis Schu 4] Score = 90.9 bits (224), Expect = 1e-17	13	10.0	6.36	
8	6.0e-011	-	FTTSGH1596 1466068 1466547 [+1 L= 480 r=-1.240] (FTT1414 1466068 1466547 +) ====>ref YP_170357.1 hypothetical protein FTT1414 [Francisella tularensis subsp.tularensis Schu 4] Score = 328 bits (842), Expect = 3e-89	9	9.6	18.44	
9	5.7e-011	-	FTTSGH0039 33957 34442 [+3 L= 486 r=-1.269] (FTT0035 33957 34442 +) ====>ref YP_096782.1 NADH dehydrogenase I, E subunit [Legionella pneumophila subsp.pneumophila str. Philadelphia 1] Score = 168 bits (426), Expect = 5e-41====>ref YP_169111.1 NADH dehydrogenase I, E subunit [Francisella tularensis subsp.tularensis Schu 4] Score = 326 bits (836), Expect = 1e-88	4	5.0	18.15	
10	5.5e-011	-	FTTSGH0163 167609 167854 [+2 L= 246 r=-1.211] (FTT0150 167609 167854 +)	9	10.6	9.06	

====>ref|ZP_00134830.1| COG0228:
 Ribosomal protein S16 [Actinobacillus
 pleuropneumoniaesero var 1 str. 4074] Score
 = 132 bits (333), Expect =
 2e-30====>ref|YP_169216.1| 30S
 ribosomal protein S16 [Francisella tularensis
 subsp. tularensisSchu 4] Score = 162 bits
 (410), Expect = 3e-39

NOTE:

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

Input Summary

Search id 20060404165402-1DD4-192168001107
Sequences 2059
Date & Time Tue Apr 04 21:54:02 2006 UTC (Search Time: 0.06 sec.)
Sample ID Schu4 271
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) 864.455 889.460 1104.945 1142.612 1158.620 1174.650 1338.869
 1448.721 1510.856 1667.995 1703.595 1835.631 1945.855
 2129.377 2168.009 2183.994 2249.173 2554.337 2577.369
 2593.343 2684.454
Tolerance (mon) 20.00 ppm
Number of 21
Peptides

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