

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	2.27	<p>FTTSGH1181 1070076 1069615 [-1 L= 462 r=-1.186] (FTT1060c 1070067 1069615 -) =====>ref NP_253619.1 50S ribosomal protein L9 [Pseudomonas aeruginosa PAO1]gb AAG08317.1 50S ribosomal protein L9 [Pseudomonas aeruginosa PAO1] Score = 157 bits (396), Expect = 1e-37=====>ref YP_170041.1 50S ribosomal protein L9 [Francisella tularensis subsp. tularensisSchu 4] Score = 287 bits (734), Expect = 8e-77</p> <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>FTTSGH0438 413780 414853 [+2 L=1074 r=-1.219] (FTT0407 413780 414853 +) =====>ref YP_156475.1 Glycine cleavage system T protein [Idiomarina loihiensis L2TR]gb AAV82926.1 Glycine cleavage system T protein [Idiomarina loihiensis L2TR] Score = 382 bits (982), Expect = e-105=====>ref YP_169452.1 glycine cleavage complex protein T (aminomethyltransferase)[Francisella tularensis subsp. tularensis Schu 4] Score = 719 bits (1855), Expect = 0.0</p> <p>FTTSGH1664 1527544 1528566 [+1 L=1023 r=-1.229] (FTT1475 1527544 1528566 +) =====>gb AAK03120.1 GalT [Pasteurella multocida subsp. multocida str. Pm70]ref NP_245973.1 GalT [Pasteurella multocida subsp. multocida str. Pm70] Score = 389 bits (999), Expect = e-107=====>ref YP_170411.1 Galactose-1-phosphate uridylyltransferase [Francisella tularensissubsp. tularensis Schu</p>	55	5.6	16.38	
2	9.3e-016	-		15	5.3	38.13	
3	4.5e-018	-		16	5.7	39.57	
4	9.5e-019	-		16	6.6	39.57	

			4] Score = 706 bits (1821), Expect = 0.0 FTTSGH2047 1882631 1883056 [+2 L= 426 r=-1.197] (FTT1794 1882631 1883056 +) ====>ref YP_247020.1 Small heat shock protein [Rickettsia felis URRWXCal2]gb AAY61855.1 Small heat shock protein [Rickettsia felis URRWXCal2] 30 5.6 16.69
5	7.4e-019	-	Score = 116 bits (291), Expect = 2e-25====>ref YP_170678.1 heat shock protein [Francisella tularensis subsp. tularensis Schu4] Score = 287 bits (734), Expect = 8e-77 FTTSGH0022 16728 17798 [+3 L=1071 r=-1.246] (FTT0018 16728 17798 +) ====>ref YP_094279.1 RND efflux membrane fusion protein [Legionella pneumophila subsp.pneumophila str. Philadelphia 1] Score = 305 bits (781), Expect = 2e-81====>ref YP_169094.1 15 9.2 40.02
6	2.1e-019	-	Secretion protein [Francisella tularensis subsp. tularensis Schu 4]emb CAG44651.1 Secretion protein [Francisella tularensis subsp. tularensis SCHU S4] Score = 703 bits (1814), Expect = 0.0 FTTSGH1253 1124717 1123776 [-3 L= 942 r=-1.216] (FTT1114c 1124717 1123776 -) ====>gb AAO90654.1 protein-export membrane protein SecF [Coxiella burnetii RSA 493]ref NP_820140.1 protein-export membrane protein SecF [Coxiella burnetii RSA 493] Score = 311 bits (796), Expect = 2e-83====>ref YP_170088.1 preprotein translocase, subunit F, membrane protein [Francisellatularensis subsp. tularensis Schu 4] Score = 597 bits (1540), Expect = e-169 19 6.0 34.47
7	1.2e-019	-	FTTSGH0354 339314 340135 [+2 L= 822 r=-1.265] (FTT0328 339314 340135 +) ====>ref NP_715874.1 ribosomal protein L2 [Shewanella oneidensis MR-1]gb AAN53319.1 ribosomal protein L2 [Shewanella oneidensis MR-1] Score = 413 14 11.1 30.37
8	1.1e-019	-	bits (1062), Expect = e-114====>ref YP_169377.1 50S ribosomal protein L2 [Francisella tularensis subsp. tularensisSchu 4] Score = 555 bits (1430), Expect = e-157 FTTSGH1393 1252948 1254090 [+1 L=1143 r=-1.227] (FTT1234 1252948 1254090 +) ====>ref YP_222152.1 choloylglycine 17 8.9 42.52
9	7.8e-020	-	hydrolase family protein [Brucella abortus biovar 1str. 9-941] Score = 166 bits (420),

			Expect = 1e-39====>ref YP_170192.1 chologylglycine hydrolase family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 765 bits (1976), Expect = 0.0			
+10	9.0e-021	-	FTTSGH0380 352919 353911 [+2 L= 993 r=-1.186] (FTT0354 352919 353911 +) ====>ref YP_170220.1 hypothetical protein FTT1263c [Francisella tularensis subsp.tularensis Schu 4] Score = 684 bits (1766), Expect = 0.0	12	9.1	39.15
		-	FTTSGH1426 1286067 1285075 [-1 L= 993 r=-1.186] (FTT1263 1286067 1285075 -) ====>ref YP_170220.1 hypothetical protein FTT1263c [Francisella tularensis subsp.tularensis Schu 4] Score = 684 bits (1766), Expect = 0.0	12	9.1	39.15
		-	FTTSGH0409 380978 379986 [-3 L= 993 r=-1.186] (FTT0378 380978 379986 -) ====>ref YP_170220.1 hypothetical protein FTT1263c [Francisella tularensis subsp.tularensis Schu 4] Score = 684 bits (1766), Expect = 0.0	12	9.1	39.15

NOTE:

1. To search again using [unmatched masses](#), click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id 20060404155246-1E00-192168001107

Sequences 1977

Date & Time Tue Apr 04 20:52:47 2006 UTC (Search Time: 0.48 sec.)

Sample ID Schu4 250

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) 817.431 882.494 903.437 910.462 935.504 962.433 973.538
 1012.556 1030.597 1057.563 1082.605 1087.594 1108.583
 1125.618 1140.612 1158.668 1194.662 1204.679 1263.699
 1302.724 1304.703 1323.664 1357.717 1405.707 1431.819
 1447.784 1490.863 1493.769 1523.825 1533.796 1621.904
 1638.877 1657.849 1674.926 1716.880 1758.905 1838.956
 1950.979 1993.998 2013.115 2025.041 2079.059 2240.150

2270.257 2383.953 2501.218

Tolerance (mon) 100.00 ppm**Number of** 46
Peptides

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