

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	2.32	<p>FTTSGH1816 1672528 1673349 [+1 L= 822 r=-1.210] (FTT1606 1672528 1673349 +) =====>gb AAN33522.1 septum site-determining protein MinD [Brucella suis 1330]ref NP_699517.1 septum site-determining protein MinD [Brucella suis 1330] Score = 330 bits (845), Expect = 4e-89=====>ref YP_170522.1 septum site-determining protein MinD [Francisella tularensis subsp.tularensis Schu 4] Score = 528 bits (1360), Expect = e-149</p> <p>FTTSGH1692 1555510 1556538 [+1 L=1029 r=-1.234] (FTT1501 1555510 1556538 +) =====>gb AAO36241.1 putative carbamoyl-phosphate synthase large chain [Clostridiumtetani E88] Score = 80.5 bits (197), Expect = 8e-14=====>ref YP_169534.1 hypothetical protein FTT0499 [Francisella tularensis subsp.tularensis Schu 4] Score = 194 bits (492), Expect = 5e-48</p> <p>FTTSGH1120 1016127 1015117 [-1 L=1011 r=-1.210] (FTT1003c 1016127 1015117 -) =====>ref NP_792198.1 phenylalanyl-tRNA synthetase, alpha subunit [Pseudomonas syringae pv.tomato str. DC3000] Score = 471 bits (1213), Expect = e-131=====>ref YP_169989.1 Phenylalanyl-tRNA synthetase, alpha subunit [Francisella tularensissubsp. tularensis Schu 4] Score = 684 bits (1765), Expect = 0.0</p> <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>FTTSGH1916 1759255 1759097 [-2 L= 159 r=-1.246] (None identical in .gff) =====>Hypothetical ORF FTTSGH1916</p>	26	6.9	30.10	
2	3.5e-011	-		14	6.1	38.89	
3	5.7e-012	-		12	6.1	38.46	
4	2.2e-012	-		14	5.6	16.38	
5	1.0e-012	-		53	10.1	6.27	

			<p>FTTSGH1078 978100 977198 [-2 L= 903 r=-1.207] (FTT0965 978100 977198 -) ====>ref XP_307366.2 ENSANGP00000001972 [Anopheles gambiae str. PEST]gb EAA03109.2 </p>				
6	3.2e-013	-	<p>ENSANGP00000001972 [Anopheles gambiae str. PEST] Score = 219 bits (559), Expect = 7e-56====>ref YP_169955.1 conserved hypothetical membrane protein [Francisella tularensissubsp. tularensis Schu 4] Score = 566 bits (1459), Expect = e-160</p> <p>FTTSGH0572 547051 547434 [+1 L= 384 r=-1.220] (FTT0524 547051 547434 +) ====>ref NP_662756.1 hypothetical protein CT1879 [Chlorobium tepidum TLS]gb AAM73098.1 conserved hypothetical protein [Chlorobium tepidum TLS] Score = 143 bits (361), Expect = 1e-33====>ref YP_169555.1 hypothetical protein FTT0524 [Francisella tularensis subsp.tularensis Schu 4] Score = 261 bits (666), Expect = 6e-69</p>	11	10.1	31.65	
7	2.8e-013	-	<p>FTTSGH1856 1705333 1704791 [-2 L= 543 r=-1.246] (FTT1639 1705333 1704791 -) ====>ref YP_170552.1 hypothetical protein FTT1639c [Francisella tularensis subsp.tularensis Schu 4] Score = 364 bits (935), Expect = e-100</p> <p>FTTSGH0468 447896 448879 [+2 L= 984 r=-1.240] (FTT0434 447896 448879 +) ====>ref YP_125384.1 hypothetical protein lpl0005 [Legionella pneumophila str. Lens]emb CAH14235.1 hypothetical protein [Legionella pneumophila str. Lens] Score = 247 bits (630), Expect = 5e-64====>ref YP_169474.1 hypothetical protein FTT0434 [Francisella tularensis subsp.tularensis Schu 4] Score = 677 bits (1747), Expect = 0.0</p> <p>FTTSGH1267 1137666 1138421 [+3 L= 756 r=-1.232] (FTT1127 1137666 1138421 +) ====>ref ZP_00521456.1 Rhodanese-like [Solibacter usitatus 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</p>	14	6.1	14.98	
8	2.5e-013	-	<p>FTTSGH1856 1705333 1704791 [-2 L= 543 r=-1.246] (FTT1639 1705333 1704791 -) ====>ref YP_170552.1 hypothetical protein FTT1639c [Francisella tularensis subsp.tularensis Schu 4] Score = 364 bits (935), Expect = e-100</p>	17	9.4	20.47	
9	2.1e-013	-	<p>FTTSGH0468 447896 448879 [+2 L= 984 r=-1.240] (FTT0434 447896 448879 +) ====>ref YP_125384.1 hypothetical protein lpl0005 [Legionella pneumophila str. Lens]emb CAH14235.1 hypothetical protein [Legionella pneumophila str. Lens] Score = 247 bits (630), Expect = 5e-64====>ref YP_169474.1 hypothetical protein FTT0434 [Francisella tularensis subsp.tularensis Schu 4] Score = 677 bits (1747), Expect = 0.0</p>	11	5.3	37.51	
10	1.4e-013	-	<p>FTTSGH1267 1137666 1138421 [+3 L= 756 r=-1.232] (FTT1127 1137666 1138421 +) ====>ref ZP_00521456.1 Rhodanese-like [Solibacter usitatus 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</p>	12	6.6	28.19	

NOTE:

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

Input Summary**Search id** 20060404161735-1E90-192168001107**Sequences** 1986**Date & Time** Tue Apr 04 21:17:36 2006 UTC (Search Time: 0.22 sec.)**Sample ID** Schu4 258**Database** schu2K [..\databases\schu2k]**Taxonomy** -**Mass Range** 0 - 40 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)** 882.473 956.478 962.476 1189.723 1233.721 1307.719 1338.739
1345.830 1493.786 1504.853 1559.779 1597.909 1604.867
1621.899 1638.906 1707.843 1838.931 1994.009 2013.104
2270.254 2300.199 2501.245 2705.219**Tolerance (mon)** 50.00 ppm**Number of** 23**Peptides**

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