

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	2.10	<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> <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>FTTSGH1074 973599 974258 [+3 L= 660 r=-1.191] (FTT0962 973599 974258 +) =====>ref YP_130934.1 putative ThiJ/Pfpl family protein [Photobacterium profundum SS9]emb CAG21132.1 putative ThiJ/Pfpl family protein [Photobacterium profundum SS9] Score = 181 bits (459), Expect = 2e-44=====>ref YP_169952.1 ThiJ/Pfpl family protein [Francisella tularensis subsp. tularensisSchu 4] Score = 444 bits (1141), Expect = e-123</p> <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 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>	23	6.6	28.19	
2	1.0e-008	0.17		19	5.6	16.38	
3	1.8e-012	-		10	4.7	24.22	
4	1.5e-012	-		11	10.1	31.65	

5	1.1e-012	-	<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>	14	5.3	18.49	
6	5.2e-013	-	<p>FTTSGH0080 76456 77154 [+1 L= 699 r=-1.279] (FTT0075 76456 77154 +) =====>ref YP_155891.1 Succinate dehydrogenase/fumarate reductase Fe-S protein [Idiomarina loihiensis L2TR] Score = 357 bits (917), Expect = 1e-97=====>ref YP_169150.1 succinate dehydrogenase iron-sulfur protein [Francisella tularensis subsp. tularensis Schu 4] Score = 484 bits (1247), Expect = e-136</p>	10	8.4	26.58	
7	3.1e-013	-	<p>FTTSGH0065 61304 61771 [+2 L= 468 r=-1.202] (FTT0060 61304 61771 +) =====>emb CAA34177.1 unnamed protein product [Vibrio alginolyticus]pir S06078 H+-transporting two-sector ATPase (EC 3.6.3.14) chain b - Vibrio Score = 149 bits (376), Expect = 3e-35=====>ref YP_169135.1 ATP synthase B chain [Francisella tularensis subsp. tularensis Schu4] Score = 290 bits (741), Expect = 1e-77</p>	7	6.7	17.35	
8	2.9e-013	-	<p>FTTSGH1692 1555510 1556538 [+1 L=1029 r=-1.234](FTT1501 1555510 1556538 +) =====>gb AAO36241.1 putative carbamoyl-phosphate synthase large chain [Clostridium tetani 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>	10	6.1	38.89	
9	2.7e-013	-	<p>FTTSGH1431 1288617 1289510 [+3 L= 894 r=-1.231] (FTT1267 1288617 1289510 +) =====>ref ZP_00640820.1 regulatory protein, LysR:LysR, substrate-binding [Shewanella frigidimarina NCIMB 400] Score = 169 bits (429), Expect =</p>	6	9.4	34.18	

			8e-41====>ref YP_170223.1 LysR transcriptional regulator family protein [Francisellatularensis subsp. tularensis Schu 4] Score = 580 bits (1496), Expect = e-164====>ref YP_169530.1 transcriptional regulator, LysR family [Francisella tularensissubsp. tularensis Schu 4] Score = 143 bits (360), Expect = 8e-33						
			FTTSGH1313 1178800 1177910 [-2 L= 891 r=-1.204] (FTT1164c 1178800 1177910 -)						
			====>gb AAN67056.1 GTP-binding protein Era [Pseudomonas putida KT2440]sp Q88MY4 ERA_PSEPK						
10	2.6e-013	-	GTP-binding protein era homolog Score = 316 bits (809), Expect = 7e-85====>ref YP_170130.1 GTP-binding protein [Francisella tularensis subsp. tularensis Schu4] Score = 580 bits (1496), Expect = e-164	9	9.0	33.96			

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

Input Summary

Search id

20060404161937-1E00-192168001107

Sequences

1986

Date & Time

Tue Apr 04 21:19:37 2006 UTC (Search Time: 0.16 sec.)

Sample ID

Schu4 259

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)

896.398 935.505 962.459 972.578 1144.613 1174.750 1178.641
1182.539 1216.543 1479.785 1604.863 1638.919 1667.925
1703.527 1994.028 2013.129 2270.265 2482.170

Tolerance (mon)

50.00 ppm

Number of Peptides

18

Profound is provided under exclusive licence by Genomic Solutions Ltd.