

**ProFound - Search Result Summary**Version 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	9.8e-001	0.67	<a href="#">FTTSGH1626</a> 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	12	5.3	18.49	
2	3.3e-003	-	<a href="#">FTTSGH0921</a> 846588 846722 [+3 L= 135 r=-1.216] [ShadowedBy _948] (None identical in .gff) =====>ref YP_169835.1  Aspartate:alanine antiporter [Francisella tularensis subsp.tularensis Schu 4] Score = 87.0 bits (214), Expect = 2e-16	18	7.9	5.04	
3	2.8e-003	-	<a href="#">FTTSGH1077</a> 977198 976935 [-3 L= 264 r=-1.175] (None identical in .gff) =====>ref NP_621799.1  hypothetical protein TTE0099 [Thermoanaerobacter tengcongensis MB4]gb AAM23403.1  conserved hypothetical protein [Thermoanaerobacter tengcongensis Score = 48.9 bits (115), Expect = 5e-05	10	9.6	9.96	
4	2.6e-003	-	<a href="#">FTTSGH0809</a> 754694 754251 [-3 L= 444 r=-1.227] (FTT0731 754694 754251 -) =====>ref YP_169744.1  hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 296 bits (759), Expect = 1e-79	4	9.2	17.38	
5	2.2e-003	-	<a href="#">FTTSGH0693</a> 649910 650236 [+2 L= 327 r=-1.257] (FTT0630 649910 650236 +) =====>gb AAK02990.1  Hfq [Pasteurella multocida subsp. multocida str. Pm70]ref NP_245843.1  Hfq [Pasteurella multocida subsp. multocida str. Pm70] Score = 120 bits (302), Expect = 1e-26 =====>ref YP_169651.1  host factor I for bacteriophage Q beta replication [Francisellatularensis subsp. tularensis Schu 4] Score = 220 bits (560), Expect = 1e-56	11	4.9	12.51	

			<a href="#">FTTSGH1581</a> 1454226 1454005 [-1 L= 222 r=-1.229] (FTT1403c 1454226 1454005 -) =====>ref NP_756049.1  Ferrous iron transport protein A [Escherichia coli CFT073]gb AAN82623.1  Ferrous iron transport protein A [Escherichia coli CFT073]	20	9.6	8.28	
6	1.8e-003	-	Score = 48.5 bits (114), Expect = 6e-05=====>ref YP_170347.1  ferrous iron transport protein A [Francisella tularensis subsp.tularensis Schu 4] Score = 153 bits (386), Expect = 2e-36  <a href="#">FTTSGH1298</a> 1166122 1165838 [-2 L= 285 r=-1.190] (FTT1151 1166122 1165838 -) =====>ref YP_047696.1  hypothetical protein ACIAD3189 [Acinetobacter sp. ADP1]emb CAG69874.1  conserved hypothetical protein [Acinetobacter sp. ADP1] Score = 60.5 bits (145), Expect = 2e-08=====>ref YP_170118.1  hypothetical protein FTT1151c [Francisella tularensis subsp.tularensis Schu 4] Score = 194 bits (493), Expect = 7e-49	11	9.0	11.30	
7	1.6e-003	-	 <a href="#">FTTSGH1916</a> 1759255 1759097 [-2 L= 159 r=-1.246] (None identical in .gff) =====>Hypothetical ORF FTTSGH1916  <a href="#">FTTSGH1993</a> 1839942 1840415 [+3 L= 474 r=-1.213] (FTT1752 1839942 1840415 +) =====>ref ZP_00134369.1  COG0629: Single-stranded DNA-binding protein [Actinobacilluspleuropneumoniae serovar 1 str. 4074] Score = 137 bits (344), Expect = 1e-31=====>ref YP_170646.1  Single-strand binding protein [Francisella tularensis subsp.tularensis Schu 4] Score = 327 bits (839), Expect = 6e-89	28	10.1	6.27	
8	1.5e-003	-	 <a href="#">FTTSGH1175</a> 1064878 1064393 [-2 L= 486 r=-1.193] (FTT1054c 1064878 1064393 -) =====>ref YP_045607.1  ribosomal-protein-alanine acetyltransferase (Acetylating enzyme forN-terminal of ribosomal protein S18) [Acinetobacter sp. Score = 81.6 bits (200), Expect = 8e-15=====>ref YP_170035.1  Ribosomal-protein-alanine acetyltransferase [Francisella tularensissubsp. tularensis Schu 4] Score = 317 bits (813), Expect = 6e-86	8	5.6	17.51	
9	1.4e-003	-		7	8.5	18.75	
10	1.1e-003	-					

## NOTE:

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

## Input Summary

**Search id** 20060330155524-1B78-192168001107

**Sequences** 2059

**Date & Time** Thu Mar 30 21:55:24 2006 UTC (Search Time: 0.08 sec.)

**Sample ID** Schu4 185

**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)** 763.474 1093.621 1261.727 1277.768 1337.768 1373.874  
1395.794 1417.860 1470.015 1621.912 1638.913 1702.282  
1707.829 1838.916

**Tolerance (mon)** 50.00 ppm

**Number of** 14

**Peptides**

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