

**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	1.0e+000	1.45	<p><a href="#">FTTSGH1760</a> 1619463 1618780 [-1 L= 684 r=-1.196] (FTT1557 1619463 1618780 -) ====&gt;ref YP_123579.1  hypothetical protein lpp1255 [Legionella pneumophila str. Paris]ref YP_126605.1  hypothetical protein lpl1254 [Legionella pneumophila str. Lens] Score = 208 bits (530), Expect = 1e-52====&gt;ref YP_170481.1  Two-component response regulator [Francisella tularensis subsp.tularensis Schu 4] Score = 439 bits (1130), Expect = e-122</p> <p><a href="#">FTTSGH1074</a> 973599 974258 [+3 L= 660 r=-1.191] (FTT0962 973599 974258 +) ====&gt;ref YP_130934.1  putative ThiJ/PfpI family protein [Photobacterium profundum SS9]emb CAG21132.1  putative ThiJ/PfpI family protein [Photobacterium profundum SS9] Score = 181 bits (459), Expect = 2e-44====&gt;ref YP_169952.1  ThiJ/PfpI family protein [Francisella tularensis subsp. tularensisSchu 4] Score = 444 bits (1141), Expect = e-123</p> <p><a href="#">FTTSGH1626</a> 1487705 1488187 [+2 L= 483 r=-1.208] (FTT1441 1487705 1488187 +) ====&gt;ref YP_096401.1  bacterioferritin (cytochrome b1) [Legionella pneumophila subsp.pneumophila str. Philadelphia 1] Score = 173 bits (439), Expect = 1e-42====&gt;ref YP_170379.1  hypothetical protein FTT1441 [Francisella tularensis subsp.tularensis Schu 4] Score = 317 bits (811), Expect = 1e-85====&gt;gb AAT77116.1  bacterioferritin [Francisella tularensis subsp. tularensis]Length = 146 Score = 288 bits (736), Expect = 5e-77</p> <p><a href="#">FTTSGH1267</a> 1137666 1138421 [+3 L= 756 r=-1.232] (FTT1127 1137666 1138421 +) ====&gt;ref ZP_00521456.1  Rhodanese-like [Solibacter usitatus Ellin6076]gb EAM59572.1  Rhodanese-like [Solibacter usitatus Ellin6076] Score = 140 bits (352), Expect = 5e-32====&gt;ref YP_170100.1  Rhodanese-like family protein [Francisella</p>	19	6.0	25.49	
2	5.7e-006	-		8	4.7	24.22	
3	4.0e-006	-		23	5.3	18.49	
4	2.2e-006	-		12	6.6	28.19	

			tularensis subsp.tularensis Schu 4] Score = 509 bits (1310), Expect = e-143			
			<a href="#">FTTSGH1085</a> 984281 985027 [+2 L= 747 r=-1.204] (FTT0972 984281 985027 +) =====>ref ZP_00316715.1  COG0396: ABC-type transport system involved in Fe-S clusterassembly, ATPase component			
5	1.7e-006	-	[Microbulbifer degradans Score = 337 bits (863), Expect = 3e-91=====>ref YP_169961.1  ABC transporter, ATP-binding protein [Francisella tularensis subsp.tularensis Schu 4] Score = 484 bits (1247), Expect = e-136	13	5.8	27.43
			<a href="#">FTTSGH0346</a> 333070 333513 [+1 L= 444 r=-1.242] (FTT0319 333070 333513 +) =====>ref ZP_00281220.1  COG0756: dUTPase [Burkholderia fungorum LB400]Length = 148 Score = 181 bits (458), Expect = 8e-45=====>ref YP_169368.1  dUTP pyrophosphatase (Deoxyuridine 5'-triphosphatenucleotidohydrolase) [Francisella tularensis subsp. Score = 291 bits (745), Expect = 4e-78			
6	1.0e-006	-	<a href="#">FTTSGH1271</a> 1143578 1144318 [+2 L= 741 r=-1.235] (FTT1131 1143578 1144321 +) =====>ref YP_127901.1  hypothetical protein lpl2573 [Legionella pneumophila str. Lens]emb CAH16814.1  hypothetical protein [Legionella pneumophila str. Lens] Score = 120 bits (300), Expect = 5e-26	28	5.4	15.92
7	7.4e-007	-	<a href="#">FTTSGH0218</a> 218746 218952 [+1 L= 207 r=-1.257] (FTT0201 218746 218919 +) =====>ref YP_204026.1  serine transporter [Vibrio fischeri ES114]gb AAW85138.1  serine transporter [Vibrio fischeri ES114] Score = 73.6 bits (179), Expect = 2e-12	7	6.3	28.38
8	8.4e-009	-	<a href="#">FTTSGH0537</a> 517523 517407 [-3 L= 117 r=-1.255] [OlapWith _555 L=53 S=99] (FTT0497 517523 517413 -) =====>Hypothetical ORF FTTSGH537	12	9.9	7.46
9	8.2e-009	-	<a href="#">FTTSGH0023</a> 17884 18162 [+1 L= 279 r=-1.218] (FTT0019 17884 18162 +) =====>emb CAF19949.1  GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE (SUBUNIT C) [Corynebacteriumglutamicum ATCC 13032] Score = 60.5 bits (145), Expect = 2e-08=====>ref YP_169095.1  Glu-tRNAGln amidotransferase C subunit [Francisella tularensissubsp. tularensis Schu	46	9.4	4.36
10	6.7e-009	-		27	4.9	10.83

4] Score = 191 bits (486), Expect = 4e-48

NOTE:

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

### Input Summary

**Search id** 20060404162256-1BE4-192168001107

**Sequences** 1652

**Date & Time** Tue Apr 04 21:22:56 2006 UTC (Search Time: 0.16 sec.)

**Sample ID** Schu4 260

**Database** schu2K [..\databases\schu2k]

**Taxonomy** -

**Mass Range** 0 - 30 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)** 714.100 768.610 826.470 828.476 850.511 882.514 927.538  
995.648 1051.607 1144.599 1182.589 1241.697 1263.728  
1279.733 1328.805 1456.900 1462.827 1464.750 1480.909  
1604.872 1630.781 1703.486 1917.042 1994.050 2762.478  
2763.307 2774.392 2780.337

**Tolerance (mon)** 30.00 ppm

**Number of** 28

**Peptides**

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