

**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	1.35	<p><a href="#">FTTSGH0066</a> 61794 62315 [+3 L= 522 r=-1.226] (FTT0061 61794 62315 +) ====&gt;ref YP_044976.1  membrane-bound ATP synthase , F1 sector, delta-subunit[Acinetobacter sp. ADP1] Score = 125 bits (314), Expect = 6e-28====&gt;ref YP_169136.1  ATP synthase delta chain [Francisella tularensis subsp. tularensisSchu 4] Score = 335 bits (858), Expect = 5e-91</p> <p><a href="#">FTTSGH0758</a> 707088 706540 [-1 L= 549 r=-1.189] (FTT0688c 707088 706540 -) ====&gt;ref YP_114446.1  ATP-dependent protease HsIV [Methylococcus capsulatus str. Bath]gb AAU91756.1  ATP-dependent protease HsIV [Methylococcus capsulatus str. Bath] Score = 221 bits (564), Expect = 7e-57====&gt;ref YP_169704.1  ATP-dependent protease, proteasome-related peptidase subunit[Francisella tularensis subsp. tularensis Schu 4] Score = 353 bits (906), Expect = 1e-96</p> <p><a href="#">FTTSGH0225</a> 224989 224510 [-2 L= 480 r=-1.212] (FTT0206 225061 224510 -) ====&gt;ref YP_125044.1  hypothetical protein lpp2739 [Legionella pneumophila str. Paris]emb CAH13892.1  hypothetical protein [Legionella pneumophila str. Paris] Score = 162 bits (410), Expect = 3e-39</p> <p><a href="#">FTTSGH0493</a> 475434 475123 [-1 L= 312 r=-1.278] (FTT0457c 475434 475123 -) ====&gt;gb AAK02485.1  unknown [Pasteurella multocida subsp. multocida str. Pm70]ref NP_245338.1  hypothetical protein PM0401 [Pasteurella multocida subsp. multocida Score = 117 bits (292), Expect = 1e-25====&gt;ref YP_169495.1  anaerobic sulfite reductase subunit [Francisella tularensis subsp.tularensis Schu 4] Score = 212 bits (540), Expect = 2e-54</p> <p><a href="#">FTTSGH2002</a> 1847287 1847433 [+1 L= 147 r=-1.218] [ShadowedBy _2054] (None identical in .gff) ====&gt;ref YP_170650.1  B-type cytochrome [Francisella tularensis</p>	28	5.8	19.18	
2	2.8e-004	0.18		13	6.2	19.78	
3	2.8e-005	-		18	9.1	18.41	
4	6.7e-007	-		13	6.3	11.83	
5	6.3e-007	-		37	10.5	5.24	

			subsp. tularensis Schu 4]emb CAG46391.1  B-type cytochrome [Francisella tularensis subsp. tularensis SCHU Score = 101 bits (251), Expect = 8e-21			
			<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			
6	5.7e-007	-		9	5.3	18.49
			<a href="#">FTTSGH0941</a> 858661 858897 [+1 L= 237 r=-1.240] (FTT0844 858178 858900 +) ====>gb AAT38610.1  predicted CsgA,Rossman fold oxidoreductase [uncultured gammaproteobacterium eBACHOT4E07] Score = 99.8 bits (247), Expect = 2e-20	14	5.2	8.59
7	5.6e-007	-				
8	4.5e-007	-	<a href="#">FTTSGH0645</a> 605728 605919 [+1 L= 192 r=-1.206] (None identical in .gff) ====>Hypothetical ORF FTTSGH645	25	5.5	7.58
			<a href="#">FTTSGH1596</a> 1466068 1466547 [+1 L= 480 r=-1.240] (FTT1414 1466068 1466547 +) ====>ref YP_170357.1  hypothetical protein FTT1414 [Francisella tularensis subsp.tularensis Schu 4] Score = 328 bits (842), Expect = 3e-89	9	9.6	18.44
9	4.4e-007	-				
10	4.4e-007	-	<a href="#">FTTSGH1383</a> 1242217 1241891 [-2 L= 327 r=-1.249] (FTT1225 1242217 1241891 -) ====>ref YP_170183.1  hypothetical protein FTT1225c [Francisella tularensis subsp.tularensis Schu 4] Score = 212 bits (539), Expect = 3e-54	17	5.4	12.59

## NOTE:

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

## Input Summary

**Search id** 20060404163403-1DDC-192168001107

**Sequences** 2059

**Date & Time** Tue Apr 04 21:34:04 2006 UTC (Search Time: 0.06 sec.)

**Sample ID** Schu4 264 [Pass: 1]

**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)** 815.653 962.459 975.262 1088.630 1268.669 1338.848 1434.835  
1471.177 1562.860 1636.092 1667.991 1796.898 1818.886  
1835.632 2255.257  
**Tolerance (mon)** 40.00 ppm  
**Number of** 15  
**Peptides**

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