

**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	9.9e-001	0.82	<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 <a href="#">FTTSGH0257</a> 249475 249125 [-2 L= 351 r=-1.276] [DelayedBy _265 L=48] (FTT0235c 249523 249125 -) ====>gb AAF93184.1  ribonuclease P protein component [Vibrio cholerae O1 biovar eltorstr. N16961] Score = 60.5 bits (145), Expect = 2e-08====>ref YP_169288.1  Ribonuclease P protein component [Francisella tularensis subsp. tularensis Schu 4] Score = 235 bits (599), Expect = 4e-61 <a href="#">FTTSGH0790</a> 737241 737498 [+3 L= 258 r=-1.224] (FTT0717 737241 737483 +) ====>emb CAE10530.1  FORMYLTETRAHYDROFOLATE DEFORMYLASE [Wolinella succinogenes]ref NP_907630.1  FORMYLTETRAHYDROFOLATE DEFORMYLASE [Wolinella succinogenes DSM Score = 80.5 bits (197), Expect = 1e-14 <a href="#">FTTSGH2002</a> 1847287 1847433 [+1 L= 147 r=-1.218] [ShadowedBy _2054] (None identical in .gff) ====>ref YP_170650.1  B-type cytochrome [Francisella tularensis subsp. tularensis Schu 4]emb CAG46391.1  B-type cytochrome [Francisella tularensis subsp. tularensis SCHU Score = 101 bits (251), Expect = 8e-21 <a href="#">FTTSGH0423</a> 393795 393469 [-1 L= 327 r=-1.216] (FTT0392 393795 393469 -) ====>ref NP_142079.1  hypothetical protein PHS001 [Pyrococcus horikoshii OT3]dbj BAA29130.1  78aa long hypothetical protein [Pyrococcus horikoshii OT3] Score = 49.7 bits (117), Expect =	23	4.9	12.51	
2	9.3e-004	-		13	10.1	13.67	
3	7.7e-004	-		16	9.0	10.13	
4	6.3e-004	-		18	10.5	5.24	
5	5.8e-004	-		6	5.1	12.64	

			3e-05====>ref YP_169437.1  hypothetical protein FTT0392c [Francisella tularensis subsp.tularensis Schu 4] Score = 211 bits (536), Expect = 7e-54				
6	5.8e-004	-	<a href="#">FTTSGH0916</a> 841603 841271 [-2 L= 333 r=-1.266] (FTT0825 841603 841271 -) ====>ref YP_169832.1  hypothetical protein FTT0825c [Francisella tularensis subsp.tularensis Schu 4] Score = 213 bits (541), Expect = 2e-54 <a href="#">FTTSGH0952</a> 868518 868162 [-1 L= 357 r=-1.250] (FTT0855 868518 868162 -) ====>ref NP_967856.1  hypothetical protein Bd0906 [Bdellovibrio bacteriovorus HD100]emb CAE78849.1  conserved hypothetical protein [Bdellovibrio bacteriovorus HD100] Score = 77.0 bits (188), Expect = 2e-13====>ref YP_169857.1  hypothetical protein FTT0855c [Francisella tularensis subsp.tularensis Schu 4] Score = 249 bits (637), Expect = 1e-65 <a href="#">FTTSGH0049</a> 45721 45912 [+1 L= 192 r=-1.211] (FTT0045 45721 45912 +) ====>ref ZP_00584875.1  Protein of unknown function DUF526 [Shewanella amazonensis SB2B]gb EAN40902.1  Protein of unknown function DUF526 [Shewanella amazonensis SB2B] Score = 53.9 bits (128), Expect = 1e-06====>ref YP_169121.1  hypothetical protein FTT0045 [Francisella tularensis subsp.tularensis Schu 4] Score = 122 bits (306), Expect = 3e-27 <a href="#">FTTSGH1702</a> 1564367 1564014 [-3 L= 354 r=-1.232] (FTT1509 1564367 1564014 -) ====>ref YP_170443.1  hypothetical protein FTT1509c [Francisella tularensis subsp.tularensis Schu 4] Score = 239 bits (609), Expect = 2e-62 <a href="#">FTTSGH0956</a> 871078 870758 [-2 L= 321 r=-1.231] (FTT0859 871078 870758 -) ====>ref YP_169861.1  hypothetical protein FTT0859c [Francisella tularensis subsp.tularensis Schu 4] Score = 207 bits (528), Expect = 6e-53	9	4.9	12.21	
7	3.6e-004	-		5	9.8	14.02	
8	3.6e-004	-		14	9.6	7.44	
9	3.6e-004	-		8	5.6	13.99	
10	3.5e-004	-		8	9.8	12.68	

## NOTE:

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

## Input Summary

Search id 20060330155828-184C-192168001107

**Sequences** 2059**Date & Time** Thu Mar 30 21:58:28 2006 UTC (Search Time: 0.05 sec.)**Sample ID** Schu4 186**Database** schu2K [..\databases\schu2k]**Taxonomy** -**Mass Range** 0 - 15 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)** 856.517 1045.598 1087.695 1234.717 1277.771 1337.831  
1395.810 1470.080 1473.881 1634.920 1666.778 1702.356  
1800.044 1816.742**Tolerance (mon)** 60.00 ppm**Number of** 14  
**Peptides**

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