

**ProFound - Search Result Summary**

Version 2002.03.01

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**Protein Candidates**

Rank	Probability	Est'd Z	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	1.0e+000	1.85	<a href="#">FTTSGH1506</a> 1368817 1368440 [-2 L= 378 r=-1.214] (FTT1338 1368817 1368440 -) ====>ref YP_254429.1  translation initiation inhibitor [Staphylococcus haemolyticusJCS1435] Score = 145 bits (365), Expect = 5e-34====>ref YP_170290.1  translation initiation inhibitor [Francisella tularensis subsp.tularensis Schu 4] Score = 246 bits (629), Expect = 1e-64 <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 = 3e-05====>ref YP_169437.1  hypothetical protein FTT0392c [Francisella tularensis subsp.tularensis Schu 4] Score = 211 bits (536), Expect = 7e-54 <a href="#">FTTSGH1169</a> 1058317 1057958 [-2 L= 360 r=-1.234] (FTT1047 1058317 1057958 -) ====>ref YP_170030.1  hypothetical protein FTT1047c [Francisella tularensis subsp.tularensis Schu 4] Score = 229 bits (583), Expect = 3e-59 <a href="#">FTTSGH1613</a> 1478126 1477863 [-3 L= 264 r=-1.208] (FTT1429 1478126 1477872 -) ====>Hypothetical ORF FTTSGH1613 <a href="#">FTTSGH1561</a> 1430003 1429737 [-3 L= 267 r=-1.232] (FTT1385 1430003 1429737 -) ====>ref YP_170330.1  hypothetical protein FTT1385c [Francisella tularensis subsp.tularensis Schu 4] Score = 187 bits (474), Expect = 1e-46 <a href="#">FTTSGH0455</a> 437733 437909 [+3 L= 177 r=-1.253] (FTT0423 437733 437909 +) ====>ref YP_169466.1  hypothetical protein FTT0423 [Francisella tularensis subsp.tularensis Schu 4] Score = 125 bits (315), Expect = 3e-28 <a href="#">FTTSGH0990</a> 895824 895931 [+3 L= 108 r=-1.349] (None identical in .gff)	48	5.5	13.73	
2	7.1e-007	-		27	5.1	12.64	
3	1.1e-007	-		19	9.5	13.51	
4	1.0e-007	-		11	8.8	10.24	
5	8.0e-009	-		20	6.2	10.34	
6	6.4e-009	-		31	8.1	6.66	
7	3.0e-009	-		31	8.5	3.72	

			=====>Hypothetical ORF FTTSGH990					
8	3.0e-009	-	<a href="#">FTTSGH1062</a> 963421 963146 [-2 L= 276 r=-1.257] (FTT0950 963385 963149 -) =====>Hypothetical ORF FTTSGH1062	20	9.2	10.02		
			<a href="#">FTTSGH0481</a> 460514 460693 [+2 L= 180 r=-1.200] (FTT0445 460499 460696 +) =====>emb CAD78259.1  ABC transporter ATP-binding protein uup-1 [Rhodopirellula balticaSH 1] Score = 50.1 bits (118), Expect = 2e-05	17	4.4	7.21		
10	2.2e-009	-	<a href="#">FTTSGH0453</a> 435656 435886 [+2 L= 231 r=-1.268] (FTT0421 435656 435886 +) =====>ref YP_094900.1  cytochrome c type biogenesis protein CycH [Legionella pneumophilasubsp. pneumophila str. Philadelphia 1] Score = 75.5 bits (184), Expect = 5e-13	17	8.1	8.24		

## NOTE:

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

**Input Summary****Search id** 20060330160002-1B78-192168001107**Sequences** 2059**Date & Time** Thu Mar 30 22:00:02 2006 UTC (Search Time: 0.09 sec.)**Sample ID** Schu4 187**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)** 1127.545 1139.975 1158.670 1174.649 1373.801 1469.957  
 1492.802 1510.840 1561.586 1618.901 1622.007 1634.727  
 1638.894 1666.646 1694.333 1702.164 1707.864 1733.993  
 1838.959 1918.980 1945.920 2008.163 2047.456 2113.044  
 2129.635 2184.075 2384.020

**Tolerance (mon)** 100.00 ppm

**Number of** 27  
**Peptides**

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