


**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	1.02	<p><a href="#">FTTSGH0212</a> 213991 212453 [-2 L=1539 r=-1.235] (FTT0195 213991 212453 -)  =====&gt;ref XP_392523.2  PREDICTED: similar to ENSANGP00000014913 [Apis mellifera]Length = 626 Score = 440 bits (1132), Expect = e-122=====&gt;ref YP_169256.1  L-glutaminase [Francisella tularensis subsp. tularensis Schu 4]emb CAG44828.1  L-glutaminase [Francisella tularensis subsp. tularensis SCHU S4] Score = 1042 bits (2695), Expect = 0.0</p> <p><a href="#">FTTSGH0070</a> 66188 66622 [+2 L= 435 r=-1.227] (FTT0065 66188 66622 +)  =====&gt;ref ZP_00459476.1  H+-transporting two-sector ATPase, delta/epsilon subunit[Burkholderia cenocepacia HI2424] Score = 96.3 bits (238), Expect = 3e-19=====&gt;ref YP_169140.1  ATP synthase epsilon chain [Francisella tularensis subsp.tularensis Schu 4] Score = 281 bits (719), Expect = 4e-75</p> <p><a href="#">FTTSGH0790</a> 737241 737498 [+3 L= 258 r=-1.224] (FTT0717 737241 737483 +)  =====&gt;emb CAE10530.1  FORMYLTETRAHYDROFOLATE DEFORMYLASE [Wolinella succinogenes]ref NP_907630.1  FORMYLTETRAHYDROFOLATE DEFORMYLASE [Wolinella succinogenes DSM Score = 80.5 bits (197), Expect = 1e-14</p> <p><a href="#">FTTSGH2020</a> 1863777 1862590 [-1 L=1188 r=-1.244] (FTT1773c 1863777 1862590 -)  =====&gt;ref YP_204411.1  tryptophan synthase beta chain [Vibrio fischeri ES114]gb AAW85523.1  tryptophan synthase beta chain [Vibrio fischeri ES114] Score = 692 bits (1787), Expect = 0.0=====&gt;ref YP_170663.1  tryptophan synthase beta chain [Francisella tularensis subsp.tularensis Schu 4] Score = 788 bits (2036), Expect = 0.0</p> <p><a href="#">FTTSGH0695</a> 652799 651612 [-3 L=1188 r=-1.213] (FTT0632 652799 651612 -)  =====&gt;ref NP_215089.1  POSSIBLE</p>	11	5.6	57.19	
2	7.9e-004	-		21	6.1	15.75	
3	2.0e-004	-		37	9.0	10.13	
4	4.9e-005	-		9	6.9	43.06	
5	4.3e-005	-		8	5.7	45.00	

			OXIDOREDUCTASE [Mycobacterium tuberculosis H37Rv]emb CAA17446.1  POSSIBLE OXIDOREDUCTASE [Mycobacterium tuberculosis H37Rv] Score = 239 bits (610), Expect = 1e-61====>ref YP_169653.1  monooxygenase family protein [Francisella tularensis subsp.tularensis Schu 4] Score = 793 bits (2048), Expect = 0.0			
			<a href="#">FTTSGH0958</a> 872090 871500 [-3 L= 591 r=-1.268] (FTT0861 872090 871500 -)====>emb CAA36654.1  unnamed protein product [Dichelobacter nodosus]sp P17824 FMA2_BACNO Fimbrial protein precursor (Pilin) (Serogroup C2) Score = 50.1 bits (118), Expect = 4e-05====>ref YP_169863.1  Type IV pili fiber building block protein [Francisella tularensissubsp. tularensis Schu 4] Score = 382 bits (982), Expect = e-105====>ref YP_169885.1  Type IV pili fiber building block protein [Francisella tularensissubsp. tularensis Schu 4] Score = 50.4 bits (119), Expect = 3e-05			
6	2.6e-005	-	<a href="#">FTTSGH0397</a> 369734 368193 [-3 L=1542 r=-1.226] (FTT0368c 369734 368193 -)====>gb AAY89950.1  predicted virulence factor MviN [uncultured bacterium BAC13K9BAC]Length = 523 Score = 253 bits (645), Expect = 2e-65====>ref YP_169415.1  virulence factor MviN [Francisella tularensis subsp. tularensis Schu4] Score = 978 bits (2528), Expect = 0.0	10	9.8	21.93
7	1.9e-005	-	<a href="#">FTTSGH1690</a> 1552228 1554798 [+1 L=2571 r=-1.219] (FTT1499 1552228 1554798 +)====>gb AAO90571.1  DNA mismatch repair protein MutS [Coxiella burnetii RSA 493]ref NP_820057.1  DNA mismatch repair protein MutS [Coxiella burnetii RSA 493] Score = 751 bits (1938), Expect = 0.0====>ref YP_170434.1  DNA mismatch repair protein MutS [Francisella tularensis subsp.tularensis Schu 4] Score = 1665 bits (4311), Expect = 0.0	7	9.7	57.54
8	1.8e-005	-	<a href="#">FTTSGH0506</a> 487872 488657 [+3 L= 786 r=-1.251] (FTT0469 487872 488657 +)====>gb AAQ57800.1  dimethyladenosine transferase [Chromobacterium violaceum ATCC12472] Score = 211 bits (537), Expect =	6	6.6	97.15
9	1.3e-005	-		8	9.5	29.74

2e-53====>ref|YP\_169507.1|  
 dimethyladenosine transferase , kasugamycin  
 resistance [Francisellatularensis subsp.  
 tularensis Schu 4] Score = 512 bits (1318),  
 Expect = e-144  
[FTTSGH0907](#) 835101 837002 [+3 L=1902  
 r=-1.241] (FTT0817 835101 837002 +)  
 ====>ref|ZP\_00283967.1| COG0441:  
 Threonyl-tRNA synthetase [Burkholderia  
 fungorum LB400]Length = 648 Score = 767 6 5.7 72.37   
 bits (1981), Expect =  
 0.0====>ref|YP\_169824.1| Threonyl-tRNA  
 synthetase [Francisella tularensis subsp.  
 tularensisSchu 4] Score = 1290 bits (3339),  
 Expect = 0.0

## NOTE:

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

**Input Summary**

**Search id** 20060330140252-1CBC-192168001107  
**Sequences** 1983  
**Date & Time** Thu Mar 30 20:02:52 2006 UTC (Search Time: 0.13 sec.)  
**Sample ID** Schu4 151  
**Database** schu2K [.\databases\schu2k]  
**Taxonomy** -  
**Mass Range** 0 - 150 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)** 1192.221 1208.600 1395.844 1417.934 1470.102 1619.088  
 1634.896 1666.747 1702.350 1794.828 2180.023 2297.162  
 2313.220 2314.213  
**Tolerance (mon)** 50.00 ppm  
**Number of**  
**Peptides** 14

Profound is provided under exclusive licence by Genomic Solutions Ltd.