

**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	0.89	<b>FTTSGH0150</b> 150045 151226 [+3 L=1182 r=-1.259] (FTT0137 150045 151226 +) ====>gb AAM35853.1  elongation factor Tu [Xanthomonas axonopodis pv. citri str. 306]gb AAM35841.1  elongation factor Tu [Xanthomonas axonopodis pv. citri str. 306] Score = 673 bits (1737), Expect = 0.0====>ref YP_169203.1  elongation factor Tu (EF-Tu) [Francisella tularensis subsp.tularensis Schu 4] Score = 788 bits (2034), Expect = 0.0	16	5.1	43.39	
2	1.3e-002	0.28	<b>FTTSGH1816</b> 1672528 1673349 [+1 L= 822 r=-1.210] (FTT1606 1672528 1673349 +) ====>gb AAN33522.1  septum site-determining protein MinD [Brucella suis 1330]ref NP_699517.1  septum site-determining protein MinD [Brucella suis 1330] Score = 330 bits (845), Expect = 4e-89====>ref YP_170522.1  septum site-determining protein MinD [Francisella tularensis subsp.tularensis Schu 4] Score = 528 bits (1360), Expect = e-149	24	6.9	30.10	
3	7.7e-004	-	<b>FTTSGH1667</b> 1530857 1530108 [-3 L= 750 r=-1.213] (FTT1478c 1530857 1530108 -) ====>gb AAO90028.1  3-deoxy-D-manno-octulosonate cytidyltransferase [Coxiellaburnetii RSA 493] Score = 250 bits (638), Expect = 3e-65====>ref YP_170414.1  3-deoxy-D-manno-octulosonate cytidyltransferase [Francisellatularensis subsp. tularensis Schu 4] Score = 485 bits (1249), Expect = e-136	15	5.9	28.17	
4	6.0e-005	-	<b>FTTSGH0681</b> 637131 636151 [-1 L= 981 r=-1.242] (FTT0617c 637131 636151 -) ====>ref YP_237414.1  PhoH-like protein [Pseudomonas syringae pv. syringae B728a]gb AAY39376.1  PhoH-like protein [Pseudomonas syringae pv. syringae B728a] Score = 342 bits (877), Expect = 1e-92====>ref YP_169638.1  phoH-like protein [Francisella tularensis subsp. tularensis Schu 4]gb AAV29526.1  NT02FT0778 [synthetic construct] Score = 640 bits (1650), Expect = 0.0	13	6.6	36.61	
5	3.7e-005	-	<b>FTTSGH0998</b> 901330 902370 [+1 L=1041 r=-1.211] (FTT0893 901330 902370 +) ====>ref YP_123967.1  Phosphoribosylformylglycinamide cyclo ligase [Legionellapneumophila str. Paris] Score = 361 bits (927), Expect = 2e-98====>ref YP_169890.1  Phosphoribosylaminoimidazol (AIR) synthetase [Francisella tularensissubsp. tularensis Schu 4]	13	5.2	37.76	

			Score = 693 bits (1788), Expect = 0.0 <a href="#">FTTSGH0635</a> 594822 596192 [+3 L=1371 r=-1.223] (FTT0577 594822 596192 +) ====>ref YP_094826.1  L-serine dehydratase (iron, sulfur-dependent) [Legionella pneumophilasubsp. pneumophila str. Philadelphia 1]	10	5.1	49.99	
6	1.9e-005	-	Score = 437 bits (1123), Expect = e-121====>ref YP_169601.1  L-serine dehydratase 1 [Francisella tularensis subsp. tularensis Schu4] Score = 916 bits (2367), Expect = 0.0 <a href="#">FTTSGH0494</a> 475520 476149 [+2 L= 630 r=-1.226] (FTT0458 475520 476149 +) ====>ref ZP_00122375.1  COG0625: Glutathione S-transferase [Haemophilus somnus 129PT]Length = 212 Score = 112 bits (280), Expect = 8e-24====>ref YP_169496.1  stringent starvation protein A, regulator of transcription[Francisella tularensis subsp. tularensis Schu 4] Score = 414 bits (1065), Expect = e-115 <a href="#">FTTSGH0425</a> 394694 395539 [+2 L= 846 r=-1.198] (FTT0394 394694 395539 +) ====>gb AAP56682.1  conserved hypothetical [Mycoplasma gallisepticum R]ref NP_853114.1  hypothetical protein MGA_1224 [Mycoplasma gallisepticum R] Score = 56.2 bits (134), Expect = 1e-06====>ref YP_169439.1  hypothetical protein FTT0394 [Francisella tularensis subsp.tularensis Schu 4] Score = 544 bits (1401), Expect = e-153 <a href="#">FTTSGH1622</a> 1484850 1484362 [-1 L= 489 r=-1.245] (FTT1437 1484399 1484046 -) (FTT1437 1484823 1484401 -) ====>gb AAF40870.1  conserved hypothetical protein [Neisseria meningitidis MC58]pir  B81200 conserved hypothetical protein NMB0432 [imported] - Neisseria Score = 97.1 bits (240), Expect = 2e-19 <a href="#">FTTSGH0738</a> 685953 687125 [+3 L=1173 r=-1.240] (FTT0669 685953 687125 +) ====>dbj BAC24142.1  MagA protein [Magnetospirillum magnetotacticum]Length = 432 Score = 229 bits (583), Expect = 2e-58====>ref YP_169686.1  Sodium/hydrogen exchanger family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 734 bits (1896), Expect = 0.0	17	9.0	24.03	
7	1.1e-005	-		11	9.1	32.97	
8	6.9e-006	-		16	9.1	17.84	
9	1.8e-006	-		8	9.1	42.77	
10	1.6e-006	-					

## NOTE:

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

## Input Summary

Search id 20060330150330-1C90-192168001107

Sequences 1985

**Date & Time** Thu Mar 30 21:03:31 2006 UTC (Search Time: 0.30 sec.)

**Sample ID** Schu4 168

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

**Taxonomy** -

**Mass Range** 0 - 50 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)** 856.529 868.528 893.580 1158.663 1199.677 1233.649 1234.693  
1277.731 1337.803 1375.635 1417.897 1457.777 1621.886 1638.859  
1685.859 1696.884 1707.787 1800.810 1834.261 1834.872 2009.085  
2163.090 2206.352 2315.172 2483.123

**Tolerance (mon)** 100.00 ppm

**Number of** 25

**Peptides**

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