


**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	2.11	<p><a href="#">FTTSGH0411</a> 383364 382018 [-1 L=1347 r=-1.217] (FTT0380c 383364 382018 -) =====&gt;emb CAA77805.1  Glutamate Dehydrogenase [Clostridium symbiosum]pir  S22403 glutamate dehydrogenase (EC 1.4.1.2) - Clostridium symbiosum Score = 578 bits (1489), Expect = e-163=====&gt;ref YP_169425.1  NAD(P)-specific glutamate dehydrogenase [Francisella tularensissubsp. tularensis Schu 4] Score = 905 bits (2338), Expect = 0.0</p> <p><a href="#">FTTSGH0150</a> 150045 151226 [+3 L=1182 r=-1.259] (FTT0137 150045 151226 +) =====&gt;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=====&gt;ref YP_169203.1  elongation factor Tu (EF-Tu) [Francisella tularensis subsp.tularensis Schu 4] Score = 788 bits (2034), Expect = 0.0</p> <p><a href="#">FTTSGH1828</a> 1679490 1680881 [+3 L=1392 r=-1.207] (FTT1616 1679490 1680881 +) =====&gt;ref ZP_00415193.1  Cysteinyl-tRNA synthetase, class Ia [Azotobacter vinelandii AvOP]gb EAM07047.1  Cysteinyl-tRNA synthetase, class Ia [Azotobacter vinelandii AvOP] Score = 539 bits (1389), Expect = e-152=====&gt;ref YP_170531.1  Cysteinyl-tRNA synthetase [Francisella tularensis subsp. tularensisSchu 4] Score = 941 bits (2431), Expect = 0.0</p> <p><a href="#">FTTSGH0601</a> 567978 569411 [+3 L=1434 r=-1.226] [DelayedBy _620 L=18] (FTT0550 567978 569411 +) (FTT0549 567545 568015 +) =====&gt;ref ZP_00586126.1  TPR repeat [Shewanella amazonensis SB2B]gb EAN39373.1  TPR repeat [Shewanella amazonensis SB2B] Score = 88.2 bits (217), Expect = 6e-16=====&gt;ref YP_169577.1  hypothetical protein FTT0550 [Francisella tularensis subsp.tularensis Schu 4] Score = 933 bits</p>	41	6.5	49.09	
2	1.3e-017	0.13		30	5.1	43.39	
3	1.6e-024	-		12	5.3	53.12	
4	1.2e-024	-		18	7.6	54.31	

			(2412), Expect = 0.0====>ref YP_170465.1  hypothetical protein FTT1537c [Francisella tularensis subsp.tularensis Schu 4] Score = 179 bits (454), Expect = 2e-43 <a href="#">FTTSGH1733</a> 1597072 1595660 [-2 L=1413 r=-1.214] (FTT1534 1597072 1595660 -) ====>ref YP_202586.1  pre-B cell enhancing factor related protein [Xanthomonas oryzae pv.oryzae KACC10331] Score = 434 bits (1115), Expect = e-120====>ref YP_170463.1  hypothetical protein FTT1534c [Francisella tularensis subsp.tularensis Schu 4] Score = 947 bits (2449), 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] 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="#">FTTSGH1400</a> 1260817 1262067 [+1 L=1251 r=-1.224] (FTT1241 1260817 1262067 +) ====>ref YP_149642.1  serine hydroxymethyltransferase [Salmonella enterica subsp. entericaserovar Paratyphi A str. ATCC 9150] Score = 574 bits (1479), Expect = e-162====>ref YP_170199.1  serine hydroxymethyltransferase [Francisella tularensis subsp.tularensis Schu 4] Score = 833 bits (2151), Expect = 0.0 <a href="#">FTTSGH1492</a> 1352533 1351925 [-2 L= 609 r=-1.244] (FTT1325c 1352533 1351925 -) ====>ref ZP_00415189.1  tRNA--hydroxylase [Azotobacter vinelandii AvOP]gb EAM07043.1  tRNA--hydroxylase [Azotobacter vinelandii AvOP] Score = 216 bits (550), Expect = 4e-55====>ref YP_170278.1  tRNA-(ms(2)io(6)a)-hydroxylase [Francisella tularensis subsp.tularensis Schu 4] Score = 404 bits (1039), Expect = e-112 <a href="#">FTTSGH0895</a> 824838 826052 [+3 L=1215 r=-1.212] (FTT0805 824838 826052 +) ====>emb CAD71904.1  capsule biosynthesis protein CapB [Rhodopirellula baltica SH 1]ref NP_864227.1  capsule				
5	3.1e-026	-		11	6.0	53.19	🔴
6	2.6e-028	-		12	5.1	49.99	🔴
7	2.1e-028	-		9	6.6	45.30	🔴
8	1.0e-028	-		15	7.1	23.70	🔴
9	2.4e-029	-		12	7.2	44.84	🔴

biosynthesis protein CapB [Rhodopirellula  
 baltica SH 1] Score = 345 bits (885), Expect  
 = 2e-93====>ref|YP\_169812.1| capsule  
 biosynthesis protein capB [Francisella  
 tularensis subsp.tularensis Schu 4] Score =  
 803 bits (2075), Expect = 0.0  
[FTTSGH0865](#) 796770 795679 [-1 L=1092  
 r=-1.196] (FTT0776c 796770 795679 -)  
 ====>ref|YP\_033771.1| Ribonuclease D  
 [Bartonella henselae str.  
 Houston-1]emb|CAF27773.1| Ribonuclease D  
 [Bartonella henselae str. Houston-1] Score = **10** 7.7 42.88   
 10 1.4e-029 - 156 bits (394), Expect =  
 1e-36====>ref|YP\_169783.1| Ribonuclease  
 D [Francisella tularensis subsp. tularensis  
 Schu 4]emb|CAG45409.1| Ribonuclease D  
 [Francisella tularensis subsp. tularensis SCHU  
 S4] Score = 719 bits (1856), Expect = 0.0

## NOTE:

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

**Input Summary**

**Search id** 20060404153533-1E94-192168001107  
**Sequences** 1980  
**Date & Time** Tue Apr 04 20:35:33 2006 UTC (Search Time: 0.33 sec.)  
**Sample ID** Schu4 246  
**Database** schu2K [..\databases\schu2k]  
**Taxonomy** -  
**Mass Range** 0 - 55 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)** 882.520 963.562 975.069 1114.608 1118.581 1120.634 1199.706  
 1233.662 1241.666 1243.624 1247.710 1281.655 1295.610  
 1309.634 1311.640 1420.818 1652.918 1696.957 1709.949  
 1716.907 1816.871 1905.905 1913.965 1920.532 1940.934  
 1975.000 1993.976 2009.131 2024.025 2111.994 2163.170  
 2288.176 2482.184  
**Tolerance (mon)** 50.00 ppm  
**Number of** 33  
**Peptides**

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