

**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	9.4e-001	0.53	<p><a href="#">FTTSGH1994</a> 1840524 1841675 [+3 L=1152 r=-1.228] (FTT1753 1840524 1841675 +) =====&gt;emb CAA06175.1  acetate kinase [Thermoanaerobacterium thermosaccharolyticum] Length = 400 Score = 364 bits (934), Expect = 3e-99=====&gt;ref YP_170647.1  propionate kinase [Francisella tularensis subsp. tularensis Schu 4]gb AAV28949.1  NT02FT0350 [synthetic construct] Score = 762 bits (1967), Expect = 0.0</p> <p><a href="#">FTTSGH0590</a> 561874 560387 [-2 L=1488 r=-1.214] (FTT0540 561874 560387 -) =====&gt;ref YP_123426.1  hypothetical protein lpp1102 [Legionella pneumophila str. Paris]emb CAH12253.1  hypothetical protein [Legionella pneumophila str. Paris] Score = 63.5 bits (153), Expect = 2e-08=====&gt;ref YP_169568.1  hypothetical protein FTT0540c [Francisella tularensis subsp. tularensis Schu 4] Score = 1011 bits (2614), Expect = 0.0</p> <p><a href="#">FTTSGH0316</a> 304822 305730 [+1 L= 909 r=-1.213] (FTT0291 304822 305730 +) =====&gt;ref YP_125218.1  hypothetical protein lpp2916 [Legionella pneumophila str. Paris]emb CAH14069.1  hypothetical protein [Legionella pneumophila str. Paris] Score = 171 bits (433), Expect = 3e-41=====&gt;ref YP_169341.1  hypothetical protein FTT0291 [Francisella tularensis subsp. tularensis Schu 4] Score = 602 bits (1553), Expect = e-171</p> <p><a href="#">FTTSGH0200</a> 200211 198490 [-1 L=1722 r=-1.227] (FTT0183c 200157 198490 -) =====&gt;ref YP_113870.1  ribosomal protein S1 [Methylococcus capsulatus str. Bath]gb AAU92309.1  ribosomal protein S1 [Methylococcus capsulatus str. Bath] Score = 655 bits (1691), Expect = 0.0=====&gt;ref YP_169244.1  30S ribosomal protein S1 [Francisella tularensis subsp. tularensis Schu 4] Score = 1089 bits (2817), Expect = 0.0</p>	11	7.9	42.17	
2	1.4e-002	-	<p><a href="#">FTTSGH0590</a> 561874 560387 [-2 L=1488 r=-1.214] (FTT0540 561874 560387 -) =====&gt;ref YP_123426.1  hypothetical protein lpp1102 [Legionella pneumophila str. Paris]emb CAH12253.1  hypothetical protein [Legionella pneumophila str. Paris] Score = 63.5 bits (153), Expect = 2e-08=====&gt;ref YP_169568.1  hypothetical protein FTT0540c [Francisella tularensis subsp. tularensis Schu 4] Score = 1011 bits (2614), Expect = 0.0</p> <p><a href="#">FTTSGH0316</a> 304822 305730 [+1 L= 909 r=-1.213] (FTT0291 304822 305730 +) =====&gt;ref YP_125218.1  hypothetical protein lpp2916 [Legionella pneumophila str. Paris]emb CAH14069.1  hypothetical protein [Legionella pneumophila str. Paris] Score = 171 bits (433), Expect = 3e-41=====&gt;ref YP_169341.1  hypothetical protein FTT0291 [Francisella tularensis subsp. tularensis Schu 4] Score = 602 bits (1553), Expect = e-171</p> <p><a href="#">FTTSGH0200</a> 200211 198490 [-1 L=1722 r=-1.227] (FTT0183c 200157 198490 -) =====&gt;ref YP_113870.1  ribosomal protein S1 [Methylococcus capsulatus str. Bath]gb AAU92309.1  ribosomal protein S1 [Methylococcus capsulatus str. Bath] Score = 655 bits (1691), Expect = 0.0=====&gt;ref YP_169244.1  30S ribosomal protein S1 [Francisella tularensis subsp. tularensis Schu 4] Score = 1089 bits (2817), Expect = 0.0</p>	12	5.9	55.96	
3	8.2e-003	-	<p><a href="#">FTTSGH0316</a> 304822 305730 [+1 L= 909 r=-1.213] (FTT0291 304822 305730 +) =====&gt;ref YP_125218.1  hypothetical protein lpp2916 [Legionella pneumophila str. Paris]emb CAH14069.1  hypothetical protein [Legionella pneumophila str. Paris] Score = 171 bits (433), Expect = 3e-41=====&gt;ref YP_169341.1  hypothetical protein FTT0291 [Francisella tularensis subsp. tularensis Schu 4] Score = 602 bits (1553), Expect = e-171</p> <p><a href="#">FTTSGH0200</a> 200211 198490 [-1 L=1722 r=-1.227] (FTT0183c 200157 198490 -) =====&gt;ref YP_113870.1  ribosomal protein S1 [Methylococcus capsulatus str. Bath]gb AAU92309.1  ribosomal protein S1 [Methylococcus capsulatus str. Bath] Score = 655 bits (1691), Expect = 0.0=====&gt;ref YP_169244.1  30S ribosomal protein S1 [Francisella tularensis subsp. tularensis Schu 4] Score = 1089 bits (2817), Expect = 0.0</p>	14	9.5	34.46	
4	7.7e-003	-	<p><a href="#">FTTSGH0200</a> 200211 198490 [-1 L=1722 r=-1.227] (FTT0183c 200157 198490 -) =====&gt;ref YP_113870.1  ribosomal protein S1 [Methylococcus capsulatus str. Bath]gb AAU92309.1  ribosomal protein S1 [Methylococcus capsulatus str. Bath] Score = 655 bits (1691), Expect = 0.0=====&gt;ref YP_169244.1  30S ribosomal protein S1 [Francisella tularensis subsp. tularensis Schu 4] Score = 1089 bits (2817), Expect = 0.0</p>	9	5.2	63.43	

5	6.8e-003	-	<p><a href="#">FTTSGH1543</a> 1415025 1413970 [-1 L=1056 r=-1.250] (FTT1368c 1415013 1413970 -) ====&gt;dbj BAB81010.1  glyceraldehyde-3-phosphate dehydrogenas [Clostridium perfringens str.13] Score = 463 bits (1192), Expect = e-129====&gt;ref YP_170317.1  Glyceraldehyde-3-phosphate dehydrogenase [Francisella tularensissubsp. tularensis Schu 4] Score = 674 bits (1739), Expect = 0.0</p> <p><a href="#">FTTSGH1260</a> 1131189 1130089 [-1 L=1101 r=-1.241] (FTT1120c 1131189 1130089 -) ====&gt;ref YP_156586.1  tRNA-guanine transglycosylase [Idiomarina loihiensis L2TR]gb AAV83037.1  tRNA-guanine transglycosylase [Idiomarina loihiensis L2TR] Score = 550 bits (1418), Expect = e-155====&gt;ref YP_170094.1  queuine tRNA-ribosyltransferase. [Francisella tularensis subsp.tularensis Schu 4] Score = 752 bits (1941), Expect = 0.0</p> <p><a href="#">FTTSGH0054</a> 49192 50658 [+1 L=1467 r=-1.204] (FTT0049 49192 50658 +) ====&gt;ref NP_253433.1  N utilization substance protein A [Pseudomonas aeruginosa PAO1]gb AAG08131.1  N utilization substance protein A [Pseudomonas aeruginosa PAO1] Score = 449 bits (1154), Expect = e-124====&gt;ref YP_169124.1  N utilization substance protein A [Francisella tularensis subsp.tularensis Schu 4] Score = 939 bits (2426), Expect = 0.0</p> <p><a href="#">FTTSGH1480</a> 1339859 1339380 [-3 L= 480 r=-1.178] (FTT1313c 1339859 1339380 -) ====&gt;ref YP_155368.1  Transcription elongation factor GreA [Idiomarina loihiensis L2TR]gb AAV81819.1  Transcription elongation factor GreA [Idiomarina loihiensis L2TR] Score = 209 bits (533), Expect = 2e-53====&gt;ref YP_170266.1  transcriptional elongation factor [Francisella tularensis subsp.tularensis Schu 4] Score = 309 bits (792), Expect = 2e-83</p> <p><a href="#">FTTSGH1396</a> 1256424 1257311 [+3 L= 888 r=-1.241] (FTT1237 1256424 1257311 +) ====&gt;ref ZP_00589864.1  Glycosyl transferase, family 8 [Pelodictyon phaeoclathratiformeBU-1] Score = 103 bits (258), Expect = 5e-21====&gt;ref YP_170195.1  glycosyl</p>	13	6.4	37.72	
6	4.9e-003	-		10	8.9	41.48	
7	4.6e-003	-		10	4.5	55.09	
8	1.7e-003	-		16	4.8	17.69	
9	1.2e-003	-		19	9.3	35.24	

transferase family 8 protein [Francisella tularensissubsp. tularensis Schu 4] Score = 613 bits (1580), Expect = e-174  
[FTTSGH0092](#) 88770 91580 [+3 L=2811 r=-1.220] (FTT0087 88770 91580 +)  
 =====>ref|YP\_004349.1| aconitate hydratase [Thermus thermophilus HB27]gb|AAS80722.1| aconitate hydratase [Thermus thermophilus HB27] Score = 1062 bits (2746), Expect = 0.0  
 10 8.9e-004 - 5 5.4 102.60   
 =====>ref|YP\_169161.1| aconitate hydratase [Francisella tularensis subsp. tularensis Schu 4]emb|CAG44720.1| aconitate hydratase [Francisella tularensis subsp. tularensis SCHU Score = 1862 bits (4824), Expect = 0.0

## NOTE:

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

**Input Summary**

**Search id** 20060404122509-1EA4-192168001107

**Sequences** 1973

**Date & Time** Tue Apr 04 17:25:09 2006 UTC (Search Time: 0.38 sec.)

**Sample ID** Schu4 233

**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)** 832.490 897.405 963.449 973.501 982.485 1036.519 1057.582  
 1060.563 1140.644 1157.635 1323.710 1374.648 1383.696  
 1418.646 1470.849 1487.739 1619.874 1638.945 1657.888  
 1703.200 1837.959 1852.031 1942.071 1994.081 2185.204  
 2705.252

**Tolerance (mon)** 100.00 ppm

**Number of** 26

**Peptides**

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