

**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	9.7e-001	0.64	<p><a href="#">FTTSGH1383</a> 1242217 1241891 [-2 L= 327 r=-1.249] (FTT1225 1242217 1241891 -) =====&gt;ref YP_170183.1  hypothetical protein FTT1225c [Francisella tularensis subsp.tularensis Schu 4] Score = 212 bits (539), Expect = 3e-54</p> <p><a href="#">FTTSGH1668</a> 1531098 1530853 [-1 L= 246 r=-1.245] (FTT1479 1531038 1530853 -) =====&gt;ref YP_206384.1  conserved cytosolic protein [Vibrio fischeri ES114]gb AAW87496.1  conserved cytosolic protein [Vibrio fischeri ES114] Score = 80.9 bits (198), Expect = 1e-14=====&gt;ref YP_170415.1  hypothetical protein FTT1479c [Francisella tularensis subsp.tularensis Schu 4] Score = 129 bits (324), Expect = 3e-29</p> <p><a href="#">FTTSGH0343</a> 330889 331443 [+1 L= 555 r=-1.190] (FTT0316 330889 331443 +) =====&gt;ref YP_123994.1  Ribosome recycling factor [Legionella pneumophila str. Paris]emb CAH12828.1  Ribosome recycling factor [Legionella pneumophila str. Paris] Score = 230 bits (586), Expect = 2e-59=====&gt;ref YP_169365.1  ribosome recycling factor [Francisella tularensis subsp. tularensisSchu 4] Score = 355 bits (910), Expect = 5e-97</p> <p><a href="#">FTTSGH0778</a> 724463 725227 [+2 L= 765 r=-1.185] (FTT0706 724463 725224 +) =====&gt;gb AAO34878.1  transcriptional repressor [Clostridium tetani E88]ref NP_780941.1  transcriptional repressor [Clostridium tetani E88] Score = 153 bits (387), Expect = 5e-36</p> <p><a href="#">FTTSGH1036</a> 941728 941132 [-2 L= 597 r=-1.203] (FTT0929 941911 941132 -) =====&gt;ref ZP_00465325.1  3-hydroxybutyrate dehydrogenase [Burkholderia cenocepacia HI2424]ref ZP_00458064.1  3-hydroxybutyrate dehydrogenase [Burkholderia cenocepacia AU 1054] Score = 244 bits (624), Expect = 9e-64</p>	41	5.4	12.59	
2	4.3e-003	-		38	7.8	9.46	
3	3.5e-003	-		16	5.4	20.53	
4	3.4e-003	-		12	7.8	26.75	
5	3.0e-003	-		10	6.3	21.44	

			<p><a href="#">FTTSGH0085</a> 83407 84165 [+1 L= 759 r=-1.201] (FTT0080 83407 84165 +) ====&gt;gb AAX21646.1  Tpi [Wolbachia persica]Length = 150 Score = 273 bits (698), Expect = 4e-72====&gt;ref YP_169155.1  triosephosphate isomerase [Francisella tularensis subsp. tularensisSchu 4] Score =</p>	11	4.9	27.64	
6	2.1e-003	-	<p>490 bits (1262), Expect = e-137====&gt;gb AAB48822.1  triosephosphate isomerase [Francisella tularensis]sp P96763 TPIS_FRATU Triosephosphate isomerase (TIM) (Triose-phosphate isomerase) Score = 421 bits (1082), Expect = e-116</p> <p><a href="#">FTTSGH0104</a> 101596 102138 [+1 L= 543 r=-1.245] (FTT0097 101596 102138 +) ====&gt;gb AAU38873.1  unknown [Mannheimia succiniciproducens MBEL55E]gb AAU37842.1  unknown [Mannheimia succiniciproducens MBEL55E] Score = 59.7 bits (143), Expect = 4e-08====&gt;ref YP_169169.1  hypothetical protein FTT0097 [Francisella tularensis subsp.tularensis Schu 4] Score = 372 bits (956), Expect = e-102</p>	18	9.5	21.29	
7	1.8e-003	-	<p><a href="#">FTTSGH1592</a> 1461732 1462238 [+3 L= 507 r=-1.237] (FTT1411 1461732 1462226 +) ====&gt;ref YP_094854.1  ORF2 transposase [Legionella pneumophila subsp. pneumophila str.Philadelphia 1] Score = 127 bits (320), Expect = 1e-28</p>	13	9.8	19.62	
8	1.6e-003	-	<p><a href="#">FTTSGH1659</a> 1522381 1521812 [-2 L= 570 r=-1.220] (FTT1470c 1522381 1521812 -) ====&gt;ref NP_439887.1  guanylate kinase [Haemophilus influenzae Rd KW20]gb AAC23390.1  guanylate kinase (gmk) [Haemophilus influenzae Rd KW20] Score = 185 bits (470), Expect = 6e-46====&gt;ref YP_170406.1  guanylate kinase [Francisella tularensis subsp. tularensis Schu 4]emb CAG46103.1  guanylate kinase [Francisella tularensis subsp. tularensis SCHU S4] Score = 377 bits (969), Expect = e-104</p>	13	5.0	21.84	
9	1.4e-003	-	<p><a href="#">FTTSGH1782</a> 1642528 1641869 [-2 L= 660 r=-1.267] (FTT1578c 1642528 1641869 -) ====&gt;ref YP_071411.1  putative uracil-DNA glycosylase [Yersinia pseudotuberculosis IP32953] Score = 286 bits (733), Expect =</p>	13	8.9	25.28	
10	1.4e-003	-					

3e-76====>ref|YP\_170500.1| Uracil-DNA  
glycosylase [Francisella tularensis subsp.  
tularensisSchu 4] Score = 461 bits (1185),  
Expect = e-128

**NOTE:**

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

**Input Summary**

**Search id** 20060330153340-184C-192168001107  
**Sequences** 1985  
**Date & Time** Thu Mar 30 21:33:40 2006 UTC (Search Time: 0.22 sec.)  
**Sample ID** Schu4 177  
**Database** schu2K [..\databases\schu2k]  
**Taxonomy** -  
**Mass Range** 0 - 30 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)** 962.601 1139.712 1171.609 1191.822 1198.699 1277.726  
1417.515 1439.733 1469.647 1499.916 1522.850 1621.925  
1638.898 1701.895 1707.782 1838.950 1919.149 1964.085  
1970.088 1982.104 1994.044 2046.096 2112.421 2247.148  
**Tolerance (mon)** 100.00 ppm  
**Number of** 24  
**Peptides**

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