

**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	9.9e-001	0.73	<p><a href="#">FTTSGH0001</a> 1558 2658 [+1 L=1101 r=-1.194] (FTT0002 1558 2658 +)            =====&gt;ref ZP_00318458.1  COG0592: DNA polymerase sliding clamp subunit (PCNA homolog)[Microbulbifer degradans 2-40]            Score = 286 bits (733), Expect = 6e-76=====&gt;ref YP_169085.1  DNA polymerase III, beta chain [Francisella tularensis subsp.tularensis Schu 4] Score = 720 bits (1858), Expect = 0.0</p>	15	5.3	41.66	
2	8.7e-003	0.05	<p><a href="#">FTTSGH0729</a> 678247 679656 [+1 L=1410 r=-1.200] (FTT0659 678247 679656 +)            =====&gt;ref ZP_00634898.1  Protein of unknown function DUF195 [Shewanella denitrificans OS-217]gb EAN70605.1  Protein of unknown function DUF195 [Shewanella denitrificans OS-217] Score = 364 bits (935), Expect = 3e-99=====&gt;ref YP_169676.1  DNA recombination protein RmuC family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 908 bits (2347), Expect = 0.0</p>	10	6.3	54.32	
3	3.4e-003	-	<p><a href="#">FTTSGH1880</a> 1726686 1725343 [-1 L=1344 r=-1.249] (FTT1660c 1726686 1725343 -)            =====&gt;ref NP_637612.1  dihydroorotase [Xanthomonas campestris pv. campestris str. ATCC33913] Score = 491 bits (1264), Expect = e-137=====&gt;ref YP_170568.1  Dihydroorotase [Francisella tularensis subsp. tularensis Schu 4]emb CAG46293.1  Dihydroorotase [Francisella tularensis subsp. tularensis SCHU S4] Score = 912 bits (2357), Expect = 0.0</p>	10	6.1	50.35	
4	6.2e-004	-	<p><a href="#">FTTSGH0430</a> 401042 399927 [-3 L=1116 r=-1.255] (FTT0399 401042 399927 -)            =====&gt;gb AAY93113.1  BNR/Asp-box repeat protein [Pseudomonas fluorescens Pf-5]ref YP_260949.1  BNR/Asp-box repeat protein [Pseudomonas fluorescens Pf-5] Score = 153 bits (387), Expect = 8e-36=====&gt;ref YP_169444.1  BNR/Asp-box repeat protein [Francisella tularensis subsp. tularensisSchu 4] Score = 751 bits (1939), Expect = 0.0</p>	8	9.5	42.50	

5	4.1e-004	-	<p><a href="#">FTTSGH0459</a> 440744 442054 [+2 L=1311 r=-1.224] (FTT0426 440744 442054 +) ====&gt;ref ZP_00204483.1  COG0527: Aspartokinases [Actinobacillus pleuropneumoniae serovar 1str. 4074] Score = 313 bits (803), Expect = 6e-84</p>	11	5.8	48.18	
6	3.2e-004	-	<p><a href="#">FTTSGH1401</a> 1262352 1263611 [+3 L=1260 r=-1.230] (FTT1242 1262352 1263611 +) ====&gt;ref YP_170200.1  hypothetical protein FTT1242 [Francisella tularensis subsp.tularensis Schu 4] Score = 826 bits (2133), Expect = 0.0====&gt;ref YP_170201.1  FAD binding family protein [Francisella tularensis subsp. tularensisSchu 4] Score = 90.5 bits (223), Expect = 1e-16</p>	9	7.1	45.93	
7	3.1e-004	-	<p><a href="#">FTTSGH0276</a> 267996 269366 [+3 L=1371 r=-1.209] (FTT0252 267996 269366 +) ====&gt;ref NP_773075.1  2-isopropylmalate synthase [Bradyrhizobium japonicum USDA 110]dbj BAC51700.1  2-isopropylmalate synthase [Bradyrhizobium japonicum USDA 110] Score = 217 bits (552), Expect = 8e-55====&gt;ref YP_169304.1  2-isopropylmalate synthase [Francisella tularensis subsp. tularensisSchu 4] Score = 924 bits (2388), Expect = 0.0</p>	7	5.9	50.75	
8	9.8e-005	-	<p><a href="#">FTTSGH1074</a> 973599 974258 [+3 L= 660 r=-1.191] (FTT0962 973599 974258 +) ====&gt;ref YP_130934.1  putative ThiJ/Pfpl family protein [Photobacterium profundum SS9]emb CAG21132.1  putative ThiJ/Pfpl family protein [Photobacterium profundum SS9] Score = 181 bits (459), Expect = 2e-44====&gt;ref YP_169952.1  ThiJ/Pfpl family protein [Francisella tularensis subsp. tularensisSchu 4] Score = 444 bits (1141), Expect = e-123</p>	14	4.7	24.22	
9	7.0e-005	-	<p><a href="#">FTTSGH0506</a> 487872 488657 [+3 L= 786 r=-1.251] (FTT0469 487872 488657 +) ====&gt;gb AAQ57800.1  dimethyladenosine transferase [Chromobacterium violaceum ATCC12472] Score = 211 bits (537), Expect = 2e-53====&gt;ref YP_169507.1  dimethyladenosine transferase , kasugamycin resistance [Francisellatularensis subsp. tularensis Schu 4] Score = 512 bits (1318), Expect = e-144</p>	12	9.5	29.74	

10 3.1e-005 - [FTTSGH1717](#) 1575294 1574413 [-1 L= 882  
 r=-1.223] (FTT1521c 1575294 1574413 -)  
 =====>emb|CAH08579.1| putative  
 diaminopimelate decarboxylase [Bacteroides  
 fragilis NCTC9343] Score = 249 bits (637),  
 Expect = 6e-65

11 5.8 33.73 

## NOTE:

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

**Input Summary**

**Search id** 20060404153133-1CAC-192168001107  
**Sequences** 2058  
**Date & Time** Tue Apr 04 20:31:34 2006 UTC (Search Time: 0.30 sec.)  
**Sample ID** Schu4 245  
**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)** 864.467 868.484 882.512 996.563 1051.614 1141.604 1183.696  
 1261.709 1314.696 1421.740 1450.783 1495.779 1547.806  
 1685.880 1748.991 1802.840 1940.966 2313.157 2412.177  
**Tolerance (mon)** 50.00 ppm  
**Number of**  
**Peptides** 19

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