

**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	9.0e-001	0.52	<a href="#">FTTSGH0272</a> 260394 260891 [+3 L= 498 r=-1.199] (FTT0248 260523 260891 +) =====>ref YP_169300.1  hypothetical protein FTT0248 [Francisella tularensis subsp.tularensis Schu 4] Score = 252 bits (644), Expect = 3e-66	8	9.2	19.10	
2	1.1e-002	-	<a href="#">FTTSGH0218</a> 218746 218952 [+1 L= 207 r=-1.257] (FTT0201 218746 218919 +) =====>ref YP_204026.1  serine transporter [Vibrio fischeri ES114]gb AAW85138.1  serine transporter [Vibrio fischeri ES114] Score = 73.6 bits (179), Expect = 2e-12	12	9.9	7.46	
3	1.0e-002	-	<a href="#">FTTSGH0405</a> 376849 377244 [+1 L= 396 r=-1.244] (FTT0375 376732 377244 +) =====>ref ZP_00587395.1  C4-dicarboxylate anaerobic carrier [Shewanella amazonensis SB2B]gb EAN38169.1  C4-dicarboxylate anaerobic carrier [Shewanella amazonensis SB2B] Score = 125 bits (314), Expect = 4e-28	9	9.2	14.36	
4	8.4e-003	-	<a href="#">FTTSGH1213</a> 1090715 1090870 [+2 L= 156 r=-1.185] [ShadowedBy _1245] (None identical in .gff) =====>ref YP_170059.1  hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 97.8 bits (242), Expect = 9e-20	21	9.7	5.86	
5	8.3e-003	-	<a href="#">FTTSGH0823</a> 761109 761002 [-1 L= 108 r=-1.247] (None identical in .gff) =====>ref YP_169505.1  organic solvent tolerance protein [Francisella tularensis subsp.tularensis Schu 4] Score = 55.8 bits (133), Expect = 4e-07	19	8.3	4.02	
6	6.2e-003	-	<a href="#">FTTSGH1102</a> 996325 996519 [+1 L= 195 r=-1.255] (FTT0987 996325 996519 +) =====>ref YP_169975.1  hypothetical protein FTT0987 [Francisella tularensis subsp.tularensis Schu 4] Score = 128 bits (321), Expect = 6e-29	11	9.1	7.58	
7	4.7e-003	-	<a href="#">FTTSGH1813</a> 1671349 1671582 [+1 L= 234 r=-1.272] (FTT1603 1671349 1671582 +) =====>ref ZP_00316346.1  COG0227: Ribosomal protein L28 [Microbulbifer	14	11.1	8.92	

			degradans 2-40]Length = 78 Score = 135 bits (339), Expect = 5e-31====>ref YP_170519.1  50S ribosomal protein L28 [Francisella tularensis subsp. tularensisSchu 4] Score = 160 bits (406), Expect = 9e-39 <a href="#">FTTSGH0447</a> 427438 427575 [+1 L= 138 r=-1.139] (FTT0415 427438 427575 +) ====>ref ZP_00279281.1  COG0448:				
8	4.4e-003	-	ADP-glucose pyrophosphorylase [Burkholderia fungorumLB400] Score = 61.2 bits (147), Expect = 9e-09 <a href="#">FTTSGH1854</a> 1703207 1703007 [-3 L= 201 r=-1.218] (FTT1637 1703207 1703007 -) ====>ref YP_170550.1  hypothetical protein FTT1637c [Francisella tularensis subsp.tularensis Schu 4] Score = 135 bits (341), Expect = 3e-31	15	4.9	5.10	
9	4.4e-003	-	<a href="#">FTTSGH1379</a> 1239528 1239791 [+3 L= 264 r=-1.255] (FTT1221 1239528 1239791 +) ====>ref ZP_00620357.1  BolA-like protein [Silicibacter sp. TM1040]gb EAN57639.1  BolA-like protein [Silicibacter sp. TM1040] Score = 52.8 bits (125), Expect = 3e-06====>ref YP_170179.1  hypothetical protein FTT1221 [Francisella tularensis subsp.tularensis Schu 4] Score = 176 bits (446), Expect = 2e-43	15	9.6	7.97	
10	4.3e-003	-		13	9.4	10.10	

## NOTE:

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

**Input Summary****Search id** 20060404164912-1BE4-192168001107**Sequences** 2059**Date & Time** Tue Apr 04 21:49:12 2006 UTC (Search Time: 0.09 sec.)**Sample ID** Schu4 269 [Pass: 1]**Database** SCHU2K [..\databases\schu2k]**Taxonomy** -**Mass Range** 0 - 20 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)** 882.484 912.473 943.488 962.449 996.547 1216.706 1239.699  
1240.683 1338.813 1524.902 1636.828 1641.915 1660.933  
1703.527 2110.161 2166.694 2439.117 2660.630

**Tolerance (mon)** 40.00 ppm

**Number of** 18  
**Peptides**

Profound is provided under exclusive licence by Genomic Solutions Ltd.