

**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	1.55	<p><a href="#">FTTSGH1166</a> 1056578 1056150 [-3 L= 429 r=-1.182] (FTT1045 1056578 1056150 -)            =====&gt;ref YP_170028.1  hypothetical protein FTT1045c [Francisella tularensis subsp.tularensis Schu 4] Score = 280 bits (715), Expect = 1e-74</p> <p><a href="#">FTTSGH1183</a> 1070682 1070323 [-1 L= 360 r=-1.295] (FTT1062c 1070655 1070323 -)            =====&gt;ref NP_935777.1  ribosomal protein S6 [Vibrio vulnificus YJ016]dbj BAC95748.1  ribosomal protein S6 [Vibrio vulnificus YJ016] Score = 149 bits (376), Expect = 3e-35</p> <p><a href="#">FTTSGH1506</a> 1368817 1368440 [-2 L= 378 r=-1.214] (FTT1338 1368817 1368440 -)            =====&gt;ref YP_254429.1  translation initiation inhibitor [Staphylococcus haemolyticusJCSC1435] Score = 145 bits (365), Expect = 5e-34</p> <p><a href="#">FTTSGH0621</a> 584188 583796 [-2 L= 393 r=-1.204] [DelayedBy _642 L=24] (FTT0567 584224 583793 -)            =====&gt;ref YP_095562.1  peptide transport protein, POT family [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] Score = 65.1 bits (157), Expect = 6e-10</p> <p><a href="#">FTTSGH169702</a> 169702 169702 [-1 L= 360 r=-1.295] (FTT1062c 1070655 1070323 -)            =====&gt;ref YP_169702.1  Proton-dependent oligopeptide transport (POT) family protein[Francisella tularensis subsp. tularensis Schu 4] Score = 61.2 bits (147), Expect = 9e-09</p> <p><a href="#">FTTSGH169991</a> 169991 169991 [-1 L= 360 r=-1.295] (FTT1062c 1070655 1070323 -)            =====&gt;ref YP_169991.1  Proton-dependent oligopeptide transporter (POT) family protein[Francisella tularensis subsp. tularensis Schu 4] Score = 51.2 bits (121), Expect = 9e-06</p>	13	6.8	16.12	
2	4.8e-005	0.13	<p><a href="#">FTTSGH1183</a> 1070682 1070323 [-1 L= 360 r=-1.295] (FTT1062c 1070655 1070323 -)            =====&gt;ref NP_935777.1  ribosomal protein S6 [Vibrio vulnificus YJ016]dbj BAC95748.1  ribosomal protein S6 [Vibrio vulnificus YJ016] Score = 149 bits (376), Expect = 3e-35</p> <p><a href="#">FTTSGH1506</a> 1368817 1368440 [-2 L= 378 r=-1.214] (FTT1338 1368817 1368440 -)            =====&gt;ref YP_254429.1  translation initiation inhibitor [Staphylococcus haemolyticusJCSC1435] Score = 145 bits (365), Expect = 5e-34</p> <p><a href="#">FTTSGH0621</a> 584188 583796 [-2 L= 393 r=-1.204] [DelayedBy _642 L=24] (FTT0567 584224 583793 -)            =====&gt;ref YP_095562.1  peptide transport protein, POT family [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] Score = 65.1 bits (157), Expect = 6e-10</p> <p><a href="#">FTTSGH169702</a> 169702 169702 [-1 L= 360 r=-1.295] (FTT1062c 1070655 1070323 -)            =====&gt;ref YP_169702.1  Proton-dependent oligopeptide transport (POT) family protein[Francisella tularensis subsp. tularensis Schu 4] Score = 61.2 bits (147), Expect = 9e-09</p> <p><a href="#">FTTSGH169991</a> 169991 169991 [-1 L= 360 r=-1.295] (FTT1062c 1070655 1070323 -)            =====&gt;ref YP_169991.1  Proton-dependent oligopeptide transporter (POT) family protein[Francisella tularensis subsp. tularensis Schu 4] Score = 51.2 bits (121), Expect = 9e-06</p>	12	6.5	14.20	
3	1.4e-005	-	<p><a href="#">FTTSGH1183</a> 1070682 1070323 [-1 L= 360 r=-1.295] (FTT1062c 1070655 1070323 -)            =====&gt;ref NP_935777.1  ribosomal protein S6 [Vibrio vulnificus YJ016]dbj BAC95748.1  ribosomal protein S6 [Vibrio vulnificus YJ016] Score = 149 bits (376), Expect = 3e-35</p> <p><a href="#">FTTSGH1506</a> 1368817 1368440 [-2 L= 378 r=-1.214] (FTT1338 1368817 1368440 -)            =====&gt;ref YP_254429.1  translation initiation inhibitor [Staphylococcus haemolyticusJCSC1435] Score = 145 bits (365), Expect = 5e-34</p> <p><a href="#">FTTSGH0621</a> 584188 583796 [-2 L= 393 r=-1.204] [DelayedBy _642 L=24] (FTT0567 584224 583793 -)            =====&gt;ref YP_095562.1  peptide transport protein, POT family [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] Score = 65.1 bits (157), Expect = 6e-10</p> <p><a href="#">FTTSGH169702</a> 169702 169702 [-1 L= 360 r=-1.295] (FTT1062c 1070655 1070323 -)            =====&gt;ref YP_169702.1  Proton-dependent oligopeptide transport (POT) family protein[Francisella tularensis subsp. tularensis Schu 4] Score = 61.2 bits (147), Expect = 9e-09</p> <p><a href="#">FTTSGH169991</a> 169991 169991 [-1 L= 360 r=-1.295] (FTT1062c 1070655 1070323 -)            =====&gt;ref YP_169991.1  Proton-dependent oligopeptide transporter (POT) family protein[Francisella tularensis subsp. tularensis Schu 4] Score = 51.2 bits (121), Expect = 9e-06</p>	25	5.5	13.73	
4	9.4e-008	-	<p><a href="#">FTTSGH1183</a> 1070682 1070323 [-1 L= 360 r=-1.295] (FTT1062c 1070655 1070323 -)            =====&gt;ref NP_935777.1  ribosomal protein S6 [Vibrio vulnificus YJ016]dbj BAC95748.1  ribosomal protein S6 [Vibrio vulnificus YJ016] Score = 149 bits (376), Expect = 3e-35</p> <p><a href="#">FTTSGH1506</a> 1368817 1368440 [-2 L= 378 r=-1.214] (FTT1338 1368817 1368440 -)            =====&gt;ref YP_254429.1  translation initiation inhibitor [Staphylococcus haemolyticusJCSC1435] Score = 145 bits (365), Expect = 5e-34</p> <p><a href="#">FTTSGH0621</a> 584188 583796 [-2 L= 393 r=-1.204] [DelayedBy _642 L=24] (FTT0567 584224 583793 -)            =====&gt;ref YP_095562.1  peptide transport protein, POT family [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] Score = 65.1 bits (157), Expect = 6e-10</p> <p><a href="#">FTTSGH169702</a> 169702 169702 [-1 L= 360 r=-1.295] (FTT1062c 1070655 1070323 -)            =====&gt;ref YP_169702.1  Proton-dependent oligopeptide transport (POT) family protein[Francisella tularensis subsp. tularensis Schu 4] Score = 61.2 bits (147), Expect = 9e-09</p> <p><a href="#">FTTSGH169991</a> 169991 169991 [-1 L= 360 r=-1.295] (FTT1062c 1070655 1070323 -)            =====&gt;ref YP_169991.1  Proton-dependent oligopeptide transporter (POT) family protein[Francisella tularensis subsp. tularensis Schu 4] Score = 51.2 bits (121), Expect = 9e-06</p>	5	8.8	14.16	

5	4.6e-008	-	<p><a href="#">FTTSGH1171</a> 1059821 1059363 [-3 L= 459 r=-1.210] (FTT1049c 1059917 1059360 -) ====&gt;gb AAK78088.1  Adenylylsulfate kinase [Clostridium acetobutylicum ATCC 824]sp Q97MT8 CYSC_CLOAB Adenylyl-sulfate kinase (APS kinase) (Adenosine-5'phosphosulfate Score = 190 bits (482), Expect = 1e-47</p>	13	6.0	17.53	
6	4.4e-008	-	<p><a href="#">FTTSGH0493</a> 475434 475123 [-1 L= 312 r=-1.278] (FTT0457c 475434 475123 -) ====&gt;gb AAK02485.1  unknown [Pasteurella multocida subsp. multocida str. Pm70]ref NP_245338.1  hypothetical protein PM0401 [Pasteurella multocida subsp. multocida Score = 117 bits (292), Expect = 1e-25====&gt;ref YP_169495.1  anaerobic sulfite reductase subunit [Francisella tularensis subsp.tularensis Schu 4] Score = 212 bits (540), Expect = 2e-54</p>	7	6.3	11.83	
7	4.1e-008	-	<p><a href="#">FTTSGH0677</a> 633099 632683 [-1 L= 417 r=-1.206] (FTT0613 633099 632683 -) ====&gt;ref YP_095858.1  hypothetical protein lpg1832 [Legionella pneumophila subsp.pneumophila str. Philadelphia 1] Score = 54.3 bits (129), Expect = 1e-06====&gt;ref YP_169634.1  hypothetical protein FTT0613c [Francisella tularensis subsp.tularensis Schu 4] Score = 279 bits (714), Expect = 2e-74</p>	9	6.8	15.68	
8	3.9e-008	-	<p><a href="#">FTTSGH1289</a> 1155426 1155923 [+3 L= 498 r=-1.217] (FTT1144 1155453 1155907 +) ====&gt;ref NP_388300.1  hypothetical protein BSU04190 [Bacillus subtilis subsp. subtilisstr. 168] Score = 128 bits (321), Expect = 8e-29</p>	12	8.4	19.13	
9	3.0e-008	-	<p><a href="#">FTTSGH1298</a> 1166122 1165838 [-2 L= 285 r=-1.190] (FTT1151 1166122 1165838 -) ====&gt;ref YP_047696.1  hypothetical protein ACIAD3189 [Acinetobacter sp. ADP1]emb CAG69874.1  conserved hypothetical protein [Acinetobacter sp. ADP1] Score = 60.5 bits (145), Expect = 2e-08====&gt;ref YP_170118.1  hypothetical protein FTT1151c [Francisella tularensis subsp.tularensis Schu 4] Score = 194 bits (493), Expect = 7e-49</p>	14	9.0	11.30	
10	3.0e-008	-	<p><a href="#">FTTSGH0984</a> 890650 890922 [+1 L= 273 r=-1.310] [LowScoreBy _1011 L=56 S=0] (FTT0883 890885 890962 +) (FTT0883 890650 890886 +) ====&gt;ref ZP_00318408.1  COG1062:</p>	9	6.1	9.60	

Zn-dependent alcohol dehydrogenases, class  
III[Microbulbifer degradans 2-40] Score =  
108 bits (271), Expect = 4e-23

## NOTE:

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

**Input Summary**

**Search id** 20060404165147-1DBC-192168001107

**Sequences** 2059

**Date & Time** Tue Apr 04 21:51:47 2006 UTC (Search Time: 0.08 sec.)

**Sample ID** Schu4 270

**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)** 745.775 800.540 803.466 807.412 841.356 864.455 876.451  
961.516 963.423 1045.570 1492.787 1510.823 1606.894 1667.900  
1945.929 1993.979 2047.006 2144.104 2176.082 2272.178  
3093.592

**Tolerance (mon)** 20.00 ppm

**Number of** 21

**Peptides**

Profound is provided under exclusive licence by Genomic Solutions Ltd.