

**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	1.56	<p><a href="#">FTTSGH0162</a> 167315 166158 [-3 L=1158 r=-1.213] (FTT0149c 167315 166158 -)            =====&gt;ref ZP_00315922.1  COG0192: S-adenosylmethionine synthetase [Microbulbifer degradans2-40] Score = 552 bits (1423), Expect = e-156=====&gt;ref YP_169215.1  S-adenosylmethionine synthetase [Francisella tularensis subsp.tularensis Schu 4] Score = 766 bits (1978), Expect = 0.0</p>	13	6.1	42.12	
2	6.5e-006	-	<p><a href="#">FTTSGH0530</a> 512981 512058 [-3 L= 924 r=-1.237] (FTT0492c 512981 512058 -)            =====&gt;ref NP_799897.1  transcriptional regulator, LysR family [Vibrio parahaemolyticusRIMD 2210633] Score = 195 bits (496), Expect = 1e-48=====&gt;ref YP_169530.1  transcriptional regulator, LysR family [Francisella tularensissubsp. tularensis Schu 4] Score = 617 bits (1592), Expect = e-175</p>	9	8.6	35.74	
3	1.3e-006	-	<p><a href="#">FTTSGH1628</a> 1490754 1489855 [-1 L= 900 r=-1.239] (FTT1443 1490754 1489855 -)            =====&gt;ref NP_251303.1  hypothetical protein PA2613 [Pseudomonas aeruginosa PAO1]gb AAG06001.1  conserved hypothetical protein [Pseudomonas aeruginosa PAO1] Score = 253 bits (647), Expect = 4e-66=====&gt;ref YP_170381.1  ATPase, AAA family [Francisella tularensis subsp. tularensis Schu4] Score = 600 bits (1547), Expect = e-170</p>	6	7.2	33.99	
4	1.0e-006	-	<p><a href="#">FTTSGH1757</a> 1617223 1616318 [-2 L= 906 r=-1.227] (FTT1554c 1617223 1616318 -)            =====&gt;ref ZP_00474242.1  tRNA pseudouridine synthase B [Chromohalobacter salexigens DSM3043] Score = 245 bits (626), Expect = 1e-63=====&gt;ref YP_170478.1  tRNA pseudouridine synthetase B [Francisella tularensis subsp.tularensis Schu 4] Score = 589 bits (1519), Expect = e-167</p>	7	8.6	33.94	
5	1.7e-007	-	<p><a href="#">FTTSGH0630</a> 591568 592419 [+1 L= 852 r=-1.235] (FTT0574 591568 592419 +)            =====&gt;gb AAO91289.1  amino acid permease family protein [Coxiella burnetii]</p>	3	8.8	30.61	

			RSA 493]ref NP_820775.1  amino acid permease family protein [Coxiella burnetii RSA 493] Score = 252 bits (644), Expect = 9e-66====>ref YP_170116.1  amino acid transporter family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 180 bits (457), Expect = 4e-44====>ref YP_170005.1  amino acid permease [Francisella tularensis subsp. tularensis Schu4] Score = 171 bits (432), Expect = 3e-41				
6	8.2e-008	-	FTTSGH0493 475434 475123 [-1 L= 312 r=-1.278] (FTT0457c 475434 475123 -)====>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====>ref YP_169495.1  anaerobic sulfite reductase subunit [Francisella tularensis subsp.tularensis Schu 4] Score = 212 bits (540), Expect = 2e-54	8	6.3	11.83	🔴
7	7.8e-008	-	FTTSGH0111 106707 106832 [+3 L= 126 r=-1.204] (FTT0102 106599 106817 +)====>Hypothetical ORF FTTSGH111	24	9.9	4.68	🔴
8	6.5e-008	-	FTTSGH1043 946558 945884 [-2 L= 675 r=-1.253] (FTT0934c 946558 945884 -)====>ref ZP_00317647.1  COG0132: Dethiobiotin synthetase [Microbulbifer degradans 2-40]Length = 230 Score = 150 bits (380), Expect = 2e-35====>ref YP_169927.1  dethiobiotin synthetase [Francisella tularensis subsp. tularensisSchu 4] Score = 447 bits (1149), Expect = e-124	7	5.2	25.17	🔴
9	6.1e-008	-	FTTSGH0715 668997 668569 [-1 L= 429 r=-1.254] (FTT0647 668997 668569 -)====>ref YP_128144.1  hypothetical protein lpl2817 [Legionella pneumophila str. Lens]emb CAH17060.1  hypothetical protein [Legionella pneumophila str. Lens] Score = 129 bits (323), Expect = 4e-29====>ref YP_169665.1  hypothetical protein FTT0647c [Francisella tularensis subsp.tularensis Schu 4] Score = 294 bits (753), Expect = 5e-79	10	5.6	17.08	🔴
10	5.7e-008	-	FTTSGH0595 564751 565080 [+1 L= 330 r=-1.257] (FTT0544 564751 565080 +)====>ref NP_709833.1  hypothetical protein SF4115 [Shigella flexneri 2a str. 301]gb AAN45540.1  orf, conserved	9	5.3	12.14	🔴

hypothetical protein [Shigella flexneri 2a str.  
301] Score = 158 bits (400), Expect =  
4e-38====>ref|YP\_169571.1|  
phosphonoacetate hydrolase [Francisella  
tularensis subsp.tularensis Schu 4] Score =  
223 bits (568), Expect = 1e-57

## NOTE:

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

**Input Summary**

**Search id** 20060404154930-1E00-192168001107  
**Sequences** 2057  
**Date & Time** Tue Apr 04 20:49:30 2006 UTC (Search Time: 0.09 sec.)  
**Sample ID** Schu4 249  
**Database** schu2K [..\databases\schu2k]  
**Taxonomy** -  
**Mass Range** 0 - 50 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)** 883.479 1038.492 1061.637 1338.699 1348.832 1471.002  
1628.005 1667.820 1703.396 1835.391 1914.939  
**Tolerance (mon)** 40.00 ppm  
**Number of**  
**Peptides** 11

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