

**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	1.66	<p><a href="#">FTTSGH0092</a> 88770 91580 [+3 L=2811 r=-1.220] (FTT0087 88770 91580 +) ==&gt;ref YP_004349.1  aconitate hydratase [Thermus thermophilus HB27]gb AAS80722.1  aconitate hydratase [Thermus thermophilus HB27] Score = 1062 bits (2746), Expect = 0.0==&gt;ref YP_169161.1  aconitate hydratase [Francisella tularensis subsp. tularensis Schu 4]emb CAG44720.1  aconitate hydratase [Francisella tularensis subsp. tularensis SCHU Score = 1862 bits (4824), Expect = 0.0</p> <p><a href="#">FTTSGH1517</a> 1386575 1388314 [+2 L=1740 r=-1.219] (FTT1348 1386587 1388314 +) ==&gt;emb CAA64574.1  rpoD [Plasmodium falciparum]pir  S72284 DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - Plasmodium Score = 64.3 bits (155), Expect = 1e-08==&gt;ref YP_170608.1  conserved hypothetical protein. [Francisella tularensis subsp.tularensis Schu 4] Score = 1123 bits (2905), Expect = 0.0==&gt;gb AAP58971.1  unknown [Francisella tularensis subsp. novicida]Length = 251 Score = 483 bits (1244), Expect = e-135</p> <p><a href="#">FTTSGH1933</a> 1779919 1781658 [+1 L=1740 r=-1.219] (FTT1703 1779931 1781658 +) ==&gt;emb CAA64574.1  rpoD [Plasmodium falciparum]pir  S72284 DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - Plasmodium Score = 64.3 bits (155), Expect = 1e-08==&gt;ref YP_170608.1  conserved hypothetical protein. [Francisella tularensis subsp.tularensis Schu 4] Score = 1123 bits (2905), Expect = 0.0==&gt;gb AAP58971.1  unknown [Francisella tularensis subsp. novicida]Length = 251 Score = 483 bits (1244), Expect = e-135</p>	8	5.4	102.60	
+2	7.4e-007	-		7	8.9	68.07	
		-		7	8.9	68.07	
3	6.5e-007	-	<p><a href="#">FTTSGH0601</a> 567978 569411 [+3 L=1434 r=-1.226] [DelayedBy _620 L=18]</p>	10	7.6	54.31	

			(FTT0550 567978 569411 +) (FTT0549 567545 568015 +) ====>ref ZP_00586126.1  TPR repeat [Shewanella amazonensis SB2B]gb EAN39373.1  TPR repeat [Shewanella amazonensis SB2B] Score = 88.2 bits (217), Expect = 6e-16====>ref YP_169577.1  hypothetical protein FTT0550 [Francisella tularensis subsp.tularensis Schu 4] Score = 933 bits (2412), Expect = 0.0====>ref YP_170465.1  hypothetical protein FTT1537c [Francisella tularensis subsp.tularensis Schu 4] Score = 179 bits (454), Expect = 2e-43				
4	4.2e-007	-	<a href="#">FTTSGH0907</a> 835101 837002 [+3 L=1902 r=-1.241] (FTT0817 835101 837002 +)====>ref ZP_00283967.1  COG0441: Threonyl-tRNA synthetase [Burkholderia fungorum LB400]Length = 648 Score = 767 bits (1981), Expect = 0.0====>ref YP_169824.1  Threonyl-tRNA synthetase [Francisella tularensis subsp. tularensisSchu 4] Score = 1290 bits (3339), Expect = 0.0	6	5.7	72.37	
5	2.5e-007	-	<a href="#">FTTSGH0729</a> 678247 679656 [+1 L=1410 r=-1.200] (FTT0659 678247 679656 +)====>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====>ref YP_169676.1  DNA recombination protein RmuC family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 908 bits (2347), Expect = 0.0	10	6.3	54.32	
6	2.1e-007	-	<a href="#">FTTSGH1672</a> 1536241 1534349 [-2 L=1893 r=-1.215] (FTT1484c 1536241 1534349 -)====>gb AAU37942.1  AceF protein [Mannheimia succiniciproducens MBEL55E]ref YP_088527.1  AceF protein [Mannheimia succiniciproducens MBEL55E] Score = 634 bits (1634), Expect = e-180====>ref YP_170419.1  pyruvate dehydrogenase, E2 component [Francisella tularensis subsp.tularensis Schu 4] Score = 1204 bits (3116), Expect = 0.0	4	4.8	67.23	
7	1.4e-007	-	<a href="#">FTTSGH1495</a> 1356774 1354075 [-1 L=2700 r=-1.241] [DelayedBy _1534 L=117] (FTT1328 1356834 1354072 -)	5	9.0	102.28	

			====>ref ZP_00514536.1  FAD linked oxidase, C-terminal:FAD linked oxidase, N-terminal[Crocospaera watsonii WH 8501] Score = 802 bits (2072), Expect = 0.0				
			FTTSGH0055 50700 53237 [+3 L=2538 r=-1.216] (FTT0050 50700 53237 +)				
			====>emb CAC92725.1  translation initiation factor IF2-2 [Yersinia pestis CO92]ref NP_406955.1  translation initiation factor IF2-2 [Yersinia pestis CO92] Score = 840 bits (2169), Expect = 0.0	6	6.4	92.39	
8	1.2e-007	-	====>ref YP_169125.1  translation initiation factor IF-2 [Francisella tularensis subsp.tularensis Schu 4] Score = 1607 bits (4161), Expect = 0.0				
			FTTSGH1640 1503886 1502402 [-2 L=1485 r=-1.277] [Contains _1678] (FTT1453c 1503886 1502402 -)				
			====>ref YP_236292.1  Polysaccharide biosynthesis protein [Pseudomonas syringae pv.syringae B728a] Score = 313 bits (801), Expect = 1e-83	4	9.4	56.27	
9	8.2e-008	-	====>ref YP_170390.1  O-antigen flippase [Francisella tularensis subsp. tularensis Schu 4]emb CAG46086.1  O-antigen flippase [Francisella tularensis subsp. tularensis SCHU S4] Score = 975 bits (2521), Expect = 0.0				
			FTTSGH0054 49192 50658 [+1 L=1467 r=-1.204] (FTT0049 49192 50658 +)				
			====>ref NP_253433.1  N utilization substance protein A [Pseudomonas aeruginosa PAO1]gb AAG08131.1  N utilization substance protein A [Pseudomonas aeruginosa PAO1] Score = 449 bits (1154), Expect = e-124	8	4.5	55.09	
10	8.0e-008	-	====>ref YP_169124.1  N utilization substance protein A [Francisella tularensis subsp.tularensis Schu 4] Score = 939 bits (2426), Expect = 0.0				

NOTE:

1. To search again using [unmatched masses](#), click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id 20060404123540-1E90-192168001107

Sequences 2055

Date & Time Tue Apr 04 17:35:40 2006 UTC (Search Time: 0.16 sec.)

Sample ID Schu4 236

Database schu2K [..\databases\schu2k]

**Taxonomy** -  
**Mass Range** 50 - 150 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)** 882.518 945.402 968.527 982.552 984.583 1037.543 1172.678  
1276.716 1318.719 1372.725 1374.713 1418.719 1470.866  
1619.849 1631.851 1746.869 1794.835 1797.859 1811.891  
1826.835 1940.954 1973.982 2230.212  
**Tolerance (mon)** 50.00 ppm  
**Number of** 23  
**Peptides**

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