





ProFound - Search Result SummaryVersion 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	1.89	<p>FTTSGH1933 1779919 1781658 [+1 L=1740 r=-1.219] (FTT1703 1779931 1781658 +) =====>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 =====>ref YP_170608.1 conserved hypothetical protein. [Francisella tularensis subsp.tularensis Schu 4] Score = 1123 bits (2905), Expect = 0.0 =====>gb AAP58971.1 unknown [Francisella tularensis subsp. novicida]Length = 251 Score = 483 bits (1244), Expect = e-135</p> <p>FTTSGH1517 1386575 1388314 [+2 L=1740 r=-1.219] (FTT1348 1386587 1388314 +) =====>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 =====>ref YP_170608.1 conserved hypothetical protein. [Francisella tularensis subsp.tularensis Schu 4] Score = 1123 bits (2905), Expect = 0.0 =====>gb AAP58971.1 unknown [Francisella tularensis subsp. novicida]Length = 251 Score = 483 bits (1244), Expect = e-135</p> <p>FTTSGH1672 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</p> <p>FTTSGH1495 1356774 1354075 [-1 L=2700 r=-1.241] [DelayedBy _1534 L=117] (FTT1328 1356834 1354072 -) =====>ref ZP_00514536.1 FAD linked oxidase, C-terminal:FAD linked oxidase, N-terminal[Crocospaera watsonii WH 8501]</p>	7	8.9	68.07	
-	-	-		7	8.9	68.07	
-	-	-		4	4.8	67.23	
-	-	-		5	9.0	102.28	

		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=====>ref YP_169125.1 translation initiation factor IF-2 [Francisella tularensis subsp.tularensis Schu 4] Score = 1607 bits (4161), Expect = 0.0	
-	-		6 6.4 92.39
		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=====>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	
-	-		4 9.4 56.27
		FTTSGH1930 1775771 1779049 [+2 L=3279 r=-1.197] (FTT1700 1775771 1779049 +) =====>gb EAA17514.1 hypothetical protein [Plasmodium yoelii yoelii]Length = 2835 Score = 87.4 bits (215), Expect = 3e-15=====>ref YP_170605.1 hypothetical protein FTT1700 [Francisella tularensis subsp.tularensis Schu 4] Score = 2172 bits (5627), Expect = 0.0=====>gb AAP58967.1 PdpB [Francisella tularensis subsp. novicida]Length = 1093 Score = 2122 bits (5497), Expect = 0.0	
-	-		3 9.1 127.56
		FTTSGH1514 1382427 1385705 [+3 L=3279 r=-1.197] (FTT1345 1382427 1385705 +) =====>gb EAA17514.1 hypothetical protein [Plasmodium yoelii yoelii]Length = 2835 Score = 87.4 bits (215), Expect = 3e-15=====>ref YP_170605.1 hypothetical protein FTT1700 [Francisella tularensis subsp.tularensis Schu 4] Score = 2172 bits (5627), Expect = 0.0=====>gb AAP58967.1 PdpB [Francisella tularensis subsp. novicida]Length = 1093 Score = 2122 bits (5497), Expect = 0.0	
-	-		3 9.1 127.56
		FTTSGH1804 1660712 1662166 [+2 L=1455 r=-1.217] (FTT1597 1660712 1662166 +) =====>ref YP_170513.1 hypothetical	
-	-		6 4.6 55.09

		protein FTT1597 [Francisella tularensis subsp. tularensis Schu 4] Score = 971 bits (2511), Expect = 0.0			
		FTTSGH0757 706529 705165 [-3 L=1365 r=-1.217] (FTT0687c 706529 705165 -) ==>ref ZP_00419169.1 Heat shock protein HslU [Azotobacter vinelandii AvOP]gb EAM04539.1 Heat shock protein HslU [Azotobacter vinelandii AvOP] Score = 587 bits (1513), Expect = e-166 ==>ref YP_169703.1 ATP-dependent protease, ATP-binding subunit [Francisella tularensis subsp. tularensis Schu 4] Score = 872 bits (2254), Expect = 0.0			
-	-	FTTSGH1303 1170587 1168803 [-3 L=1785 r=-1.247] (FTT1156c 1170584 1168803 -) ==>ref ZP_00472994.1 type II and III secretion system	9	5.9	51.22
-	-	protein: NolW-like: NolW-like [Chromohalobacter salexigens DSM 3043] Score = 314 bits (805), Expect = 5e-84 ==>ref YP_170123.1 Type IV pilin multimeric outer membrane protein [Francisella tularensis subsp. tularensis Schu 4] Score = 1149 bits (2972), Expect = 0.0	4	5.2	65.06

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 20060404123620-0F3C-192168001107
Sequences 2056
Date & Time Tue Apr 04 17:36:20 2006 UTC (Search Time: 0.13 sec.)
Sample ID Schu4 236 [Pass: 1]
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) 882.518 982.552 1172.678 1276.716 1374.713 1418.719 1470.866
1619.849 1631.851 1746.869 1794.835 1797.859 1811.891
1826.835 1940.954 2230.212
Tolerance (mon) 50.00 ppm

**Number of 16
Peptides**

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