

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	9.9e-001	0.70	<p>FTTSGH2025 1867604 1867197 [-3 L= 408 r=-1.211] (FTT1777 1867604 1867197 -) =====>ref YP_170666.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 261 bits (667), Expect = 5e-69=====>ref YP_170667.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 150 bits (380), Expect = 9e-36</p> <p>FTTSGH0621 584188 583796 [-2 L= 393 r=-1.204] [DelayedBy _642 L=24] (FTT0567 584224 583793 -) =====>ref YP_095562.1 peptide transport protein, POT family [Legionella pneumophilasubsp. pneumophila str. Philadelphia 1] Score = 65.1 bits (157), Expect = 6e-10=====>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=====>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> <p>FTTSGH1031 935773 936168 [+1 L= 396 r=-1.245] (FTT0924 935773 936168 +) =====>ref YP_169920.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 270 bits (689), Expect = 1e-71</p> <p>FTTSGH1224 1100421 1100906 [+3 L= 486 r=-1.206] (FTT1091 1100421 1100906 +) =====>ref ZP_00106217.2 COG1335: Amidases related to nicotinamidase [Nostoc punctiforme PCC73102] Score = 92.8 bits (229), Expect = 3e-18=====>ref YP_170070.1 isochorismatase hydrolase family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 335 bits (860), Expect = 2e-91=====>ref YP_170068.1 isochorismatase hydrolase family protein</p>	17	6.5	14.52	
2	3.4e-003	-	<p>FTTSGH0621 584188 583796 [-2 L= 393 r=-1.204] [DelayedBy _642 L=24] (FTT0567 584224 583793 -) =====>ref YP_095562.1 peptide transport protein, POT family [Legionella pneumophilasubsp. pneumophila str. Philadelphia 1] Score = 65.1 bits (157), Expect = 6e-10=====>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=====>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> <p>FTTSGH1031 935773 936168 [+1 L= 396 r=-1.245] (FTT0924 935773 936168 +) =====>ref YP_169920.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 270 bits (689), Expect = 1e-71</p> <p>FTTSGH1224 1100421 1100906 [+3 L= 486 r=-1.206] (FTT1091 1100421 1100906 +) =====>ref ZP_00106217.2 COG1335: Amidases related to nicotinamidase [Nostoc punctiforme PCC73102] Score = 92.8 bits (229), Expect = 3e-18=====>ref YP_170070.1 isochorismatase hydrolase family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 335 bits (860), Expect = 2e-91=====>ref YP_170068.1 isochorismatase hydrolase family protein</p>	5	8.8	14.16	
3	2.4e-003	-	<p>FTTSGH1031 935773 936168 [+1 L= 396 r=-1.245] (FTT0924 935773 936168 +) =====>ref YP_169920.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 270 bits (689), Expect = 1e-71</p> <p>FTTSGH1224 1100421 1100906 [+3 L= 486 r=-1.206] (FTT1091 1100421 1100906 +) =====>ref ZP_00106217.2 COG1335: Amidases related to nicotinamidase [Nostoc punctiforme PCC73102] Score = 92.8 bits (229), Expect = 3e-18=====>ref YP_170070.1 isochorismatase hydrolase family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 335 bits (860), Expect = 2e-91=====>ref YP_170068.1 isochorismatase hydrolase family protein</p>	8	6.8	15.04	
4	1.9e-003	-	<p>FTTSGH1224 1100421 1100906 [+3 L= 486 r=-1.206] (FTT1091 1100421 1100906 +) =====>ref ZP_00106217.2 COG1335: Amidases related to nicotinamidase [Nostoc punctiforme PCC73102] Score = 92.8 bits (229), Expect = 3e-18=====>ref YP_170070.1 isochorismatase hydrolase family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 335 bits (860), Expect = 2e-91=====>ref YP_170068.1 isochorismatase hydrolase family protein</p>	14	6.3	19.02	

			[Francisella tularensissubsp. tularensis Schu 4] Score = 69.7 bits (169), Expect = 3e-11 FTTSGH1446 1301460 1301296 [-1 L= 165 r=-1.193] [LowScoreBy _1484 L=38 S=38] (None identical in .gff)				
5	1.4e-003	-	=====>ref YP_170238.1 hypothetical protein FTT1282 [Francisella tularensis subsp.tularensis Schu 4] Score = 90.9 bits (224), Expect = 1e-17 FTTSGH0039 33957 34442 [+3 L= 486 r=-1.269] (FTT0035 33957 34442 +)=====>ref YP_096782.1 NADH dehydrogenase I, E subunit [Legionella pneumophila subsp.pneumophila str. Philadelphia 1] Score = 168 bits (426), Expect = 5e-41=====>ref YP_169111.1 NADH dehydrogenase I, E subunit [Francisella tularensis subsp.tularensis Schu 4] Score = 326 bits (836), Expect = 1e-88 FTTSGH0163 167609 167854 [+2 L= 246 r=-1.211] (FTT0150 167609 167854 +)=====>ref ZP_00134830.1 COG0228: Ribosomal protein S16 [Actinobacillus pleuropneumoniaes serovar 1 str. 4074] Score = 132 bits (333), Expect = 2e-30=====>ref YP_169216.1 30S ribosomal protein S16 [Francisella tularensis subsp. tularensis Schu 4] Score = 162 bits (410), Expect = 3e-39 FTTSGH1728 1593509 1593994 [+2 L= 486 r=-1.277] (FTT1532 1593509 1593994 +)=====>gb AAO75306.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] Score = 71.2 bits (173), Expect = 1e-11=====>ref YP_170462.1 hypothetical protein FTT1532 [Francisella tularensis subsp.tularensis Schu 4] Score = 345 bits (885), Expect = 3e-94 FTTSGH1596 1466068 1466547 [+1 L= 480 r=-1.240] (FTT1414 1466068 1466547 +)=====>ref YP_170357.1 hypothetical protein FTT1414 [Francisella tularensis subsp.tularensis Schu 4] Score = 328 bits (842), Expect = 3e-89 FTTSGH0589 560380 559838 [-2 L= 543 r=-1.236] (FTT0539 560380 559637 -)=====>emb CAJ04249.1 ubiquitin-activating enzyme, putative [Leishmania major] Length = 276 Score =	13	10.0	6.36	
6	8.3e-004	-		4	5.0	18.15	
7	7.9e-004	-		9	10.6	9.06	
8	7.5e-004	-		4	8.5	18.65	
9	6.9e-004	-		9	9.6	18.44	
10	6.6e-004	-		4	8.7	19.60	

174 bits (440), Expect = 2e-42

NOTE:

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

Input Summary

Search id 20060404165440-1E5C-192168001107

Sequences 2059

Date & Time Tue Apr 04 21:54:40 2006 UTC (Search Time: 0.05 sec.)

Sample ID Schu4 271 [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) 864.455 889.460 1104.945 1174.650 1338.869 1448.721 1510.856
1667.995 1703.595 1835.631 1945.855 2129.377 2249.173
2577.369 2593.343 2684.454

Tolerance (mon) 20.00 ppm

Number of 16

Peptides

Profound is provided under exclusive licence by Genomic Solutions Ltd.