

ProFound - Search Result Summary

Version 2002.03.01

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Protein Candidates

Rank	Probability	Est'd Z	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	1.0e+000	2.41	<p>FTTSGH1925 1764261 1765937 [+3 L=1677 r=-1.212] (FTT1696 1764306 1765937 +) ====>ref YP_047391.1 chaperone Hsp60, peptide-dependent ATPase, heat shock protein[Acinetobacter sp. ADP1] Score = 797 bits (2059), Expect = 0.0====>gb AAT77113.1 GroEL [Francisella tularensis subsp. tularensis]ref YP_170601.1 Chaperone protein, groEL [Francisella tularensis subsp. tularensis Score = 1037 bits (2682), Expect = 0.0====>emb CAA67358.1 groEL [Francisella tularensis]sp P94798 CH60_FRATU 60 kDa chaperonin (Protein Cpn60) (groEL protein) Score = 1030 bits (2664), Expect = 0.0</p>	22	5.1	59.27	
2	1.4e-013	-	<p>FTTSGH1376 1238031 1236823 [-1 L=1209 r=-1.243] (FTT1218c 1238031 1236823 -) ====>ref YP_115166.1 2-octaprenyl-6-methoxyphenol hydroxylase [Methylococcus capsulatusstr. Bath] Score = 205 bits (521), Expect = 3e-51====>ref YP_170176.1 2-octaprenyl-6-methoxyphenyl hydroxylase [Francisella tularensissubsp. tularensis Schu 4] Score = 788 bits (2035), Expect = 0.0</p>	12	9.5	45.04	
3	1.2e-013	-	<p>FTTSGH1867 1713885 1713244 [-1 L= 642 r=-1.259] (FTT1648c 1713885 1713244 -) ====>ref YP_192625.1 Orotidine 5'-phosphate decarboxylase [Gluconobacter oxydans 621H]gb AAW61969.1 Orotidine 5'-phosphate decarboxylase [Gluconobacter oxydans 621H] Score = 91.3 bits (225), Expect = 2e-17====>ref YP_170557.1 Orotidine 5'-phosphate decarboxylase [Francisella tularensis subsp.tularensis Schu 4] Score = 426 bits (1096), Expect = e-118</p>	10	6.2	23.82	
4	9.7e-014	-	<p>FTTSGH0658 614621 614007 [-3 L= 615 r=-1.263] (FTT0596 614621 614007 -) ====>ref YP_169619.1 hypothetical protein FTT0596c [Francisella tularensis subsp.tularensis Schu 4] Score = 421 bits (1083), Expect = e-117</p>	18	8.5	24.05	
5	8.7e-014	-	<p>FTTSGH0417 387934 388974 [+1 L=1041 r=-1.247] (FTT0386 387934 388974 +) ====>ref NP_924606.1 hypothetical protein glr1660 [Gloeobacter violaceus PCC 7421]dbj BAC89601.1 glr1660 [Gloeobacter violaceus PCC 7421] Score = 238 bits (608), Expect = 2e-61====>ref YP_169431.1 Nicotinamide-nucleotide adenylyltransferase [Francisella tularensissubsp. tularensis Schu 4] Score = 717 bits (1850), Expect = 0.0</p>	12	6.2	40.39	
6	7.8e-014	-	<p>FTTSGH1956 1807479 1805992 [-1 L=1488 r=-1.240] (FTT1721c 1807479 1805992 -) ====>ref YP_149816.1 amidophosphoribosyltransferase [Salmonella enterica subsp. entericaserovar Paratyphi A str. ATCC 9150] Score</p>	10	6.7	55.33	

			= 555 bits (1431), Expect = e-156====>ref YP_170623.1 Amidophosphoribosyltransferase [Francisella tularensis subsp.tularensis Schu 4] Score = 995 bits (2573), Expect = 0.0			
7	3.4e-014	-	FTTSGH1843 1691809 1690502 [-2 L=1308 r=-1.229] (FTT1628 1691809 1690502 -) =====>ref YP_126009.1 hypothetical protein lpl0646 [Legionella pneumophila str. Lens]emb CAH14879.1 hypothetical protein [Legionella pneumophila str. Lens] Score = 359 bits (921), Expect = 1e-97====>ref YP_170541.1 metal ion transporter [Francisella tularensis subsp. tularensis Schu4] Score = 858 bits (2216), Expect = 0.0	9	7.7 50.13	
8	2.7e-014	-	FTTSGH1313 1178800 1177910 [-2 L= 891 r=-1.204] (FTT1164c 1178800 1177910 -) =====>gb AAN67056.1 GTP-binding protein Era [Pseudomonas putida KT2440]sp Q88MY4 ERA_PSEPK GTP-binding protein era homolog Score = 316 bits (809), Expect = 7e-85====>ref YP_170130.1 GTP-binding protein [Francisella tularensis subsp. tularensis Schu4] Score = 580 bits (1496), Expect = e-164	13	9.0 33.96	
9	1.1e-014	-	FTTSGH1894 1740630 1741694 [+3 L=1065 r=-1.271] (FTT1671 1740630 1741694 +) =====>ref YP_148150.1 riboflavin-specific deaminase(diaminohydroxyphosphoribosylaminopyrimidine deaminase ; Score = 273 bits (697), Expect = 9e-72====>ref YP_170577.1 riboflavin biosynthesis protein ribD [Francisella tularensis subsp.tularensis Schu 4] Score = 718 bits (1853), Expect = 0.0	9	9.5 39.56	
10	9.9e-015	-	FTTSGH0212 213991 212453 [-2 L=1539 r=-1.235] (FTT0195 213991 212453 -) =====>ref XP_392523.2 PREDICTED: similar to ENSANGP00000014913 [Apis mellifera]Length = 626 Score = 440 bits (1132), Expect = e-122====>ref YP_169256.1 L-glutaminase [Francisella tularensis subsp. tularensis Schu 4]emb CAG44828.1 L-glutaminase [Francisella tularensis subsp. tularensis SCHU S4] Score = 1042 bits (2695), Expect = 0.0	6	5.6 57.19	

NOTE:

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

Input Summary

Search id 20060330142321-1B50-192168001107

Sequences 2056

Date & Time Thu Mar 30 20:23:22 2006 UTC (Search Time: 0.28 sec.)

Sample ID Schu4 159

Database schu2K [..\databases\schu2k]

Taxonomy -

Mass Range 0 - 80 kDa

pI Range 0.0 -14.0

Digestion Trypsin

Missed Cuts 1

Modifications +O@M(Partial);

Charge State MH+

Masses (avg)

Tolerance 1.00 ppm

(avg)

Masses (mon) 875.421 897.531 925.520 974.446 1047.547 1064.559
1184.670 1288.087 1337.821 1395.833 1417.898 1470.078
1581.947 1595.807 1618.992 1634.897 1666.781 1702.345
1767.061 1834.310 1847.746 1901.877 2148.079 2276.362
2888.841

Tolerance 100.00 ppm

(mon)

Number of 25

Peptides

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