

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	1.27	<p>FTTSGH0069 64799 66172 [+2 L=1374 r=-1.243] (FTT0064 64799 66172 +) ==>ref ZP_00565839.1 ATP synthase F1, beta subunit [Methylobacillus flagellatus KT]gb EAN02168.1 ATP synthase F1, beta subunit [Methylobacillus flagellatus KT] Score = 756 bits (1951), Expect = 0.0==>ref YP_169139.1 ATP synthase beta chain [Francisella tularensis subsp. tularensisSchu 4] Score = 894 bits (2309), Expect = 0.0</p>	13	5.1	49.78	
2	1.5e-004	0.01	<p>FTTSGH0758 707088 706540 [-1 L= 549 r=-1.189] (FTT0688c 707088 706540 -) ==>ref YP_114446.1 ATP-dependent protease HslV [Methylococcus capsulatus str. Bath]gb AAU91756.1 ATP-dependent protease HslV [Methylococcus capsulatus str. Bath] Score = 221 bits (564), Expect = 7e-57==>ref YP_169704.1 ATP-dependent protease, proteasome-related peptidase subunit[Francisella tularensis subsp. tularensis Schu 4] Score = 353 bits (906), Expect = 1e-96</p>	15	6.2	19.78	
3	4.5e-005	-	<p>FTTSGH1034 938085 939377 [+3 L=1293 r=-1.222] (FTT0927 938085 939377 +) ==>ref ZP_00133736.1 COG0001: Glutamate-1-semialdehyde aminotransferase [Actinobacilluspleuropneumoniae serovar 1 str. 4074] Score = 516 bits (1329), Expect = e-145==>ref YP_169923.1 Glutamate-1-semialdehyde-2,1-aminomutase [Francisella tularensissubsp. tularensis Schu 4] Score = 870 bits (2247), Expect = 0.0</p>	6	5.2	47.17	
4	3.5e-006	-	<p>FTTSGH1665 1528572 1529717 [+3 L=1146 r=-1.229] (FTT1476 1528572 1529717 +) ==>gb AAU37255.1 GalK protein [Mannheimia succiniciproducens MBEL55E]ref YP_087840.1 GalK protein [Mannheimia succiniciproducens MBEL55E] Score = 285 bits (730), Expect = 1e-75==>ref YP_170412.1 Galactokinase [Francisella tularensis subsp. tularensis Schu 4]emb CAG46109.1 Galactokinase [Francisella tularensis subsp. tularensis SCHU S4] Score = 776 bits (2003), Expect = 0.0</p>	8	6.1	43.42	

5	2.2e-006	-	FTTSGH0981 888910 889047 [+1 L= 138 r=-1.286] [ShadowedBy _1008] (None identical in .gff) =====>ref YP_169880.1 amino acid permease [Francisella tularensis subsp. tularensis Schu4] Score = 96.3 bits (238), Expect = 3e-19	33	5.3	5.19	
6	1.3e-006	-	FTTSGH1588 1459893 1459777 [-1 L= 117 r=-1.207] (None identical in .gff) =====>Hypothetical ORF FTTSGH1588	49	10.3	4.36	
7	1.2e-006	-	FTTSGH1691 1554873 1555313 [+3 L= 441 r=-1.220] (FTT1500 1554873 1555313 +) =====>ref ZP_00640679.1 protein export chaperone SecB [Shewanella frigidimarina NCIMB 400]gb EAN72554.1 protein export chaperone SecB [Shewanella frigidimarina NCIMB 400] Score = 147 bits (372), Expect = 8e-35=====>ref YP_170435.1 preprotein translocase, subunit B, chaperone protein [Francisellatularensis subsp. tularensis Schu 4] Score = 297 bits (760), Expect = 8e-80	10	4.7	16.68	
8	1.1e-006	-	FTTSGH1350 1210447 1209932 [-2 L= 516 r=-1.202] (FTT1193 1210447 1209932 -) =====>ref NP_248522.1 hypothetical protein MJ1515 [Methanocaldococcus jannaschii DSM2661] Score = 68.2 bits (165), Expect = 1e-10=====>ref YP_170153.1 hypothetical protein FTT1193c [Francisella tularensis subsp.tularensis Schu 4] Score = 358 bits (918), Expect = 5e-98	9	5.6	19.94	
9	9.8e-007	-	FTTSGH1206 1086581 1086465 [-3 L= 117 r=-1.319] [OlapWith _1236 L=59 S=98] (None identical in .gff) =====>Hypothetical ORF FTTSGH1206	36	6.2	4.43	
10	9.0e-007	-	FTTSGH1474 1331172 1330639 [-1 L= 534 r=-1.276] (FTT1307 1331172 1330639 -) =====>ref YP_170261.1 hypothetical protein FTT1307c [Francisella tularensis subsp.tularensis Schu 4] Score = 356 bits (913), Expect = 2e-97	9	6.0	19.13	

NOTE:

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

Input Summary

Search id 20060330144250-1D10-192168001107

Sequences 2059

Date & Time Thu Mar 30 20:42:50 2006 UTC (Search Time: 0.11 sec.)

Sample ID Schu4 163

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) 1191.443 1395.865 1417.953 1450.834 1464.372 1470.139
1494.789 1582.912 1586.001 1595.421 1605.152 1612.186
1619.024 1676.794 1689.928 1834.327 2149.564 2179.554
2189.172

Tolerance (mon) 70.00 ppm

Number of Peptides 19

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