

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	2.33	<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> <p>FTTSGH1181 1070076 1069615 [-1 L= 462 r=-1.186] (FTT1060c 1070067 1069615 -) =====>ref NP_253619.1 50S ribosomal protein L9 [Pseudomonas aeruginosa PAO1]gb AAG08317.1 50S ribosomal protein L9 [Pseudomonas aeruginosa PAO1] Score = 157 bits (396), Expect = 1e-37=====>ref YP_170041.1 50S ribosomal protein L9 [Francisella tularensis subsp. tularensisSchu 4] Score = 287 bits (734), Expect = 8e-77</p> <p>FTTSGH1057 960009 959497 [-1 L= 513 r=-1.289] (FTT0947 960009 959497 -) (FTT0948 961036 959975 -) =====>ref YP_095910.1 major facilitator family transporter [Legionella pneumophila subsp.pneumophila str. Philadelphia 1] Score = 67.8 bits (164), Expect = 1e-10=====>ref YP_169174.1 major facilitator superfamily (MFS) transport protein [Francisellatularensis subsp. tularensis Schu 4] Score = 65.5 bits (158), Expect = 7e-10=====>ref YP_169194.1 major facilitator superfamily (MFS) transport protein [Francisellatularensis subsp. tularensis Schu 4] Score = 64.7 bits (156), Expect = 1e-09</p> <p>FTTSGH1692 1555510 1556538 [+1 L=1029 r=-1.234] (FTT1501 1555510 1556538 +) =====>gb AAO36241.1 putative carbamoyl-phosphate synthase large chain [Clostridiumtetani E88] Score = 80.5 bits (197),</p>	24	5.1	59.27	
2	6.2e-016	-		19	5.6	16.38	
3	2.4e-017	-		16	10.2	19.49	
4	2.2e-017	-		10	6.1	38.89	

			Expect = 8e-14====>ref YP_169534.1 hypothetical protein FTT0499 [Francisella tularensis subsp.tularensis Schu 4] Score = 194 bits (492), Expect = 5e-48			
5	4.9e-018	-	FTTSGH0803 750029 748998 [-3 L=1032 r=-1.215] (FTT0726 750029 748998 -) ====>ref NP_773224.1 putative glycerophosphoryl diester phosphodiesterase [Bradyrhizobiumjaponicum USDA 110] Score = 215 bits (547), Expect = 2e-54====>ref YP_169739.1 glycerophosphoryl diester phosphodiesterase family protein[Francisella tularensis subsp. tularensis Schu 4] Score = 707 bits (1824), Expect = 0.0	9	5.4	39.02
6	2.1e-018	-	FTTSGH1985 1835112 1833418 [-1 L=1695 r=-1.250] (FTT1744c 1835112 1833418 -) ====>emb CAG37059.1 related to indole-3-pyruvate decarboxylase [Desulfotalea psychrophilaLSv54] Score = 412 bits (1058), Expect = e-113====>ref YP_170639.1 indolepyruvate decarboxylase [Francisella tularensis subsp.tularensis Schu 4] Score = 1122 bits (2902), Expect = 0.0	6	5.3	62.21
7	1.8e-018	-	FTTSGH1036 941728 941132 [-2 L= 597 r=-1.203] (FTT0929 941911 941132 -) ====>ref ZP_00465325.1 3-hydroxybutyrate dehydrogenase [Burkholderia cenocepacia HI2424]ref ZP_00458064.1 3-hydroxybutyrate dehydrogenase [Burkholderia cenocepacia AU 1054] Score = 244 bits (624), Expect = 9e-64	14	6.3	21.44
8	1.3e-018	-	FTTSGH1504 1365397 1367043 [+1 L=1647 r=-1.228] (FTT1336 1365397 1367043 +) ====>ref NP_797628.1 transport ATP-binding protein CydC [Vibrio parahaemolyticus RIMD2210633] Score = 400 bits (1027), Expect = e-110====>ref YP_170288.1 ABC transporter, ATP-binding and membrane protein [Francisellatularensis subsp. tularensis Schu 4] Score = 1061 bits (2745), Expect = 0.0	5	8.6	62.04
9	9.6e-019	-	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	7	4.8	67.23

tularensis subsp.tularensis Schu 4] Score = 1204 bits (3116), Expect = 0.0
[FTTSGH0452](#) 434120 435571 [+2 L=1452 r=-1.207] (FTT0420 434135 435571 +)
 =====>ref|NP_439291.1|
 UDP-N-acetylmuramyl-tripeptide synthetase [Haemophilus influenzae RdKW20] Score = 317 bits (812), Expect = 6e-85 =====>ref|YP_169464.1|
 UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase[Francisella tularensis subsp. tularensis Schu 4] Score = 960 bits (2482), Expect = 0.0

10 9.5e-019 - 8 6.6 55.53 

NOTE:

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

Input Summary

Search id 20060404145732-1AE4-192168001107
Sequences 1982
Date & Time Tue Apr 04 19:57:32 2006 UTC (Search Time: 0.30 sec.)
Sample ID Schu4 240
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 (avg) 1.00 ppm
Masses (mon) 769.555 897.546 935.534 962.434 1047.548 1064.572 1183.723
 1338.575 1470.900 1581.924 1595.775 1619.870 1638.927
 1703.258 1767.036 1901.851 1993.989 2008.969 2013.110
 2148.061 2270.245
Tolerance (mon) 100.00 ppm
Number of Peptides 21

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