

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	0.89	FTTSGH1206 1086581 1086465 [-3 L= 117 r=-1.319] [OlapWith _1236 L=59 S=98] (None identical in .gff) =====>Hypothetical ORF FTTSGH1206	59	6.2	4.43	
2	3.6e-003	0.09	FTTSGH1393 1252948 1254090 [+1 L=1143 r=-1.227] (FTT1234 1252948 1254090 +) =====>ref YP_222152.1 choloylglycine hydrolase family protein [Brucella abortus biovar 1str. 9-941] Score = 166 bits (420), Expect = 1e-39=====>ref YP_170192.1 choloylglycine hydrolase family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 765 bits (1976), Expect = 0.0	14	8.9	42.52	
3	4.8e-004	-	FTTSGH1497 1357322 1358857 [+2 L=1536 r=-1.220] (FTT1329 1357322 1358857 +) =====>gb AAL22563.1 phosphoglyceromutase [Salmonella typhimurium LT2]sp Q8ZL56 GPMI_SALTY 2,3-bisphosphoglycerate-independent phosphoglycerate mutase Score = 603 bits (1554), Expect = e-171=====>ref YP_170281.1 2,3-bisphosphoglycerate-independent phosphoglycerate mutase[Francisella tularensis subsp. tularensis Schu 4] Score = 1044 bits (2699), Expect = 0.0	12	5.8	57.58	
4	3.1e-004	-	FTTSGH0895 824838 826052 [+3 L=1215 r=-1.212] (FTT0805 824838 826052 +) =====>emb CAD71904.1 capsule biosynthesis protein CapB [Rhodopirellula baltica SH 1]ref NP_864227.1 capsule biosynthesis protein CapB [Rhodopirellula baltica SH 1] Score = 345 bits (885), Expect = 2e-93=====>ref YP_169812.1 capsule biosynthesis protein capB [Francisella tularensis subsp.tularensis Schu 4] Score = 803 bits (2075), Expect = 0.0	14	7.2	44.84	
5	4.2e-005	-	FTTSGH0174 176303 175680 [-3 L= 624 r=-1.235] (FTT0161 176303 175680 -) =====>ref YP_222936.1 PAP2 family protein [Brucella abortus biovar 1 str. 9-941]gb AAX75575.1 PAP2 family protein [Brucella abortus biovar 1 str. 9-941] Score = 89.0 bits (219), Expect = 9e-17=====>ref YP_169227.1 PAP2 family	19	9.6	23.42	

			protein [Francisella tularensis subsp. tularensis Schu4] Score = 408 bits (1049), Expect = e-113====>ref YP_169888.1 conserved hypothetical membrane protein [Francisella tularensissubsp. tularensis Schu 4] Score = 53.5 bits (127), Expect = 4e-06 FTTSGH0216 216975 217805 [+3 L= 831 r=-1.257] (FTT0200 217756 218370 +) (FTT0199 216975 217805 +)				
6	2.5e-005	-	====>ref YP_169260.1 hypothetical protein FTT0199 [Francisella tularensis subsp.tularensis Schu 4] Score = 544 bits (1402), Expect = e-153 FTTSGH1443 1300415 1299675 [-3 L= 741 r=-1.266] (FTT1279c 1300415 1299675 -)====>ref YP_071368.1 putative SpoU-family rRNA methylase [Yersinia pseudotuberculosis IP32953] Score = 210 bits (534), Expect = 4e-53====>ref YP_170235.1 SpoU rRNA methylase family protein [Francisella tularensis subsp.tularensis Schu 4] Score = 482 bits (1240), Expect = e-135 FTTSGH1059 962049 961132 [-1 L= 918 r=-1.181] (FTT0949 962130 961129 -)====>ref YP_078191.1 hypothetical protein BL03168 [Bacillus licheniformis ATCC 14580]gb AAU22553.1 conserved hypothetical protein [Bacillus licheniformis ATCC 14580] Score = 106 bits (264), Expect = 1e-21 FTTSGH0883 811288 812967 [+1 L=1680 r=-1.215] (FTT0793 811288 812967 +)====>ref ZP_00532761.1 ABC transporter, transmembrane region:ABC transporter [Chlorobiumphaeobacteroides BS1] Score = 318 bits (816), Expect = 3e-85====>ref YP_169800.1 ABC transporter, ATP-binding and membrane protein [Francisellatularensis subsp. tularensis Schu 4] Score = 1080 bits (2794), Expect = 0.0 FTTSGH1169 1058317 1057958 [-2 L= 360 r=-1.234] (FTT1047 1058317 1057958 -)====>ref YP_170030.1 hypothetical protein FTT1047c [Francisella tularensis subsp.tularensis Schu 4] Score = 229 bits (583), Expect = 3e-59	8	5.6	29.89	
7	1.7e-005	-		13	6.1	27.69	
8	1.7e-005	-		12	6.9	34.21	
9	1.3e-005	-		10	9.2	63.80	
10	1.3e-005	-		22	9.5	13.51	

NOTE:

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

Input Summary

Search id 20060404145401-0F3C-192168001107
Sequences 1986
Date & Time Tue Apr 04 19:54:02 2006 UTC (Search Time: 0.25 sec.)
Sample ID Schu4 239
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) 962.445 1082.644 1434.779 1621.941 1638.865 1674.968
1687.886 1838.927 1886.955 1993.976 2013.116 2198.137
2271.255 2501.213 2567.291 2705.100
Tolerance (mon) 100.00 ppm
Number of 16
Peptides

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