

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	9.7e-001	0.65	<p>FTTSGH1543 1415025 1413970 [-1 L=1056 r=-1.250] (FTT1368c 1415013 1413970 -) =====>dbj BAB81010.1 glyceraldehyde-3-phosphate dehydrogenas [Clostridium perfringens str.13] Score = 463 bits (1192), Expect = e-129=====>ref YP_170317.1 Glyceraldehyde-3-phosphate dehydrogenase [Francisella tularensissubsp. tularensis Schu 4] Score = 674 bits (1739), Expect = 0.0</p> <p>FTTSGH0928 850799 851158 [+2 L= 360 r=-1.252] (FTT0834 850799 851158 +) =====>emb CAD75895.1 chorismate mutase [Rhodopirellula baltica SH 1]ref NP_868518.1 chorismate mutase [Rhodopirellula baltica SH 1] Score = 119 bits (299), Expect = 2e-26=====>ref YP_169839.1 chorismate mutase [Francisella tularensis subsp. tularensis Schu 4]gb AAV29324.1 NT02FT0715 [synthetic construct] Score = 236 bits (602), Expect = 2e-61</p> <p>FTTSGH1775 1633098 1632085 [-1 L=1014 r=-1.208] (FTT1571c 1633095 1632085 -) =====>gb AAO90157.1 UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Coxiellaburnetii RSA 493] Score = 310 bits (794), Expect = 5e-83=====>ref YP_170493.1 UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase[Francisella tularensis subsp. tularensis Schu 4] Score = 662 bits (1708), Expect = 0.0</p> <p>FTTSGH0871 801268 800558 [-2 L= 711 r=-1.236] (FTT0781 801268 800558 -) =====>gb AAQ58454.1 conserved hypothetical protein [Chromobacterium violaceum ATCC12472] Score = 246 bits (628), Expect = 4e-64=====>ref YP_169788.1 hypothetical protein FTT0781c [Francisella tularensis subsp.tularensis Schu 4] Score = 476 bits (1224), Expect = e-133</p>	8	6.4	37.72	
2	4.8e-003	-		16	9.0	13.51	
3	3.4e-003	-		9	5.8	35.54	
4	2.7e-003	-		5	6.5	26.45	

5	2.3e-003	-	<p>FTTSGH0587 558346 558978 [+1 L= 633 r=-1.231] (FTT0537 558346 558978 +) ====>ref NP_635869.1 ubiquinone biosynthesis protein [Xanthomonas campestris pv.campestris str. ATCC 33913] Score = 211 bits (536), Expect = 2e-53====>ref YP_169566.1 ubiquinone biosynthesis protein [Francisella tularensis subsp.tularensis Schu 4] Score = 424 bits (1089), Expect = e-117</p> <p>FTTSGH1414 1277343 1276498 [-1 L= 846 r=-1.283] (FTT1255 1277343 1276498 -) ====>gb AAQ59499.1 probable transcriptional regulator, AraC family [Chromobacterium violaceum ATCC 12472] Score = 278 bits (710), Expect = 2e-73====>ref YP_170213.1 transcriptional regulator araC family protein [Francisella tularensis subsp. tularensis Schu 4] Score = 573 bits (1476), Expect = e-162</p> <p>FTTSGH0093 91678 92703 [+1 L=1026 r=-1.255] (FTT0088 91678 92703 +) ====>ref ZP_00146697.1 COG2805: Tfp pilus assembly protein, pilus retraction ATPase PilT[Psychrobacter sp. 273-4] Score = 369 bits (948), Expect = e-101====>ref YP_169162.1 Type IV pili nucleotide-binding protein [Francisella tularensis subsp. tularensis Schu 4] Score = 660 bits (1704), Expect = 0.0</p> <p>FTTSGH1033 937121 938092 [+2 L= 972 r=-1.220] (FTT0926 937121 938092 +) ====>emb CAA25826.1 unnamed protein product [Escherichia coli]gb AAC75984.1 glutathione synthetase [Escherichia coli K12] Score = 320 bits (820), Expect = 4e-86====>ref YP_169922.1 glutathione synthetase [Francisella tularensis subsp. tularensis Schu 4] Score = 647 bits (1668), Expect = 0.0</p> <p>FTTSGH0919 845068 844466 [-2 L= 603 r=-1.246] (FTT0828 845068 844475 -) ====>ref ZP_00168540.2 COG0436: Aspartate/tyrosine/aromatic aminotransferase [Ralstonia eutropha JMP134] Score = 217 bits (552), Expect = 2e-55</p> <p>FTTSGH1687 1550643 1549633 [-1 L=1011 r=-1.235] (FTT1496 1550643 1549633 -) ====>ref YP_170431.1 hypothetical membrane protein [Francisella tularensis</p>	11	8.9	23.74	
6	2.1e-003	-		11	9.5	31.89	
7	1.8e-003	-		8	6.4	38.01	
8	1.7e-003	-		5	9.0	37.14	
9	1.5e-003	-		11	5.2	23.02	
10	1.4e-003	-		6	6.5	37.74	

subsp.tularensis Schu 4] Score = 663 bits
(1710), Expect =
0.0====>ref|YP_170535.1| hypothetical
membrane protein [Francisella tularensis
subsp.tularensis Schu 4] Score = 150 bits
(380), Expect = 5e-35

NOTE:

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

Input Summary

Search id 20060404160057-1D68-192168001107
Sequences 1986
Date & Time Tue Apr 04 21:00:57 2006 UTC (Search Time: 0.16 sec.)
Sample ID Schu4 252
Database schu2K [..\databases\schu2k]
Taxonomy -
Mass Range 0 - 40 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) 861.474 862.482 882.530 1180.679 1356.766 1387.749 1505.848
1583.896 1660.968 1687.873 1703.412 1794.801 1817.883
1892.101 1920.117
Tolerance (mon) 50.00 ppm
Number of
Peptides 15

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