

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	1.52	<p>FTTSGH1548 1420127 1421044 [+2 L= 918 r=-1.243] (FTT1374 1420127 1421044 +) ==>gb AAU38480.1 FabD protein [Mannheimia succiniciproducens MBEL55E]ref YP_089065.1 FabD protein [Mannheimia succiniciproducens MBEL55E] Score = 302 bits (774), Expect = 8e-81 ==>gb AAT77114.1 probable S-malonyltransferase [Francisella tularensis subsp.tularensis] Score = 597 bits (1540), Expect = e-169</p> <p>FTTSGH1446 1301460 1301296 [-1 L= 165 r=-1.193] [LowScoreBy _1484 L=38 S=38] (None identical in .gff) ==>ref YP_170238.1 hypothetical protein FTT1282 [Francisella tularensis subsp.tularensis Schu 4] Score = 90.9 bits (224), Expect = 1e-17</p> <p>FTTSGH0175 176377 176898 [+1 L= 522 r=-1.234] (FTT0162 176377 176898 +) ==>ref ZP_00585791.1 N-acetylmuramoyl-L-alanine amidase, family 2 [Shewanellaamazonensis SB2B] Score = 189 bits (481), Expect = 2e-47 ==>ref YP_169228.1 N-acetylmuramoyl-L-alanine amidase [Francisella tularensis subsp.tularensis Schu 4] Score = 369 bits (947), Expect = e-101</p> <p>FTTSGH0556 533806 534351 [+1 L= 546 r=-1.229] (FTT0512 533806 534351 +) ==>sp Q5NHE5 PDXT_FRATT Glutamine amidotransferase subunit pdxT (Glutamine amidotransferaseglutaminase subunit pdxT) Score = 357 bits (917), Expect = 8e-98 ==>ref YP_169547.1 SNO glutamine amidotransferase family protein [Francisellatularensis subsp. tularensis Schu 4] Score = 361 bits (927), Expect = 5e-99</p> <p>FTTSGH0731 681159 680779 [-1 L= 381 r=-1.228] (FTT0662 681159 680779 -) ==>ref ZP_00376709.1 hypothetical protein ELI1950 [Erythrobacter litoralis HTCC2594]gb EAL75439.1 hypothetical protein ELI1950 [Erythrobacter litoralis HTCC2594] Score = 113 bits (282), Expect =</p>	12	5.1	33.48	
2	2.0e-006	-		15	10.0	6.36	
3	1.6e-006	-		10	7.0	19.78	
4	1.4e-006	-		8	7.1	20.28	
5	1.3e-006	-		10	5.2	14.53	

			2e-24====>ref YP_169679.1 hypothetical protein FTT0662c [Francisella tularensis subsp.tularensis Schu 4] Score = 265 bits (677), Expect = 3e-70				
6	1.3e-006	-	<p>FTTSGH1931 1779042 1779416 [+3 L= 375 r=-1.223] (FTT1701 1779042 1779416 +)====>ref YP_170606.1 hypothetical protein FTT1701 [Francisella tularensis subsp.tularensis Schu 4] Score = 254 bits (650), Expect = 4e-67</p> <p>FTTSGH0173 175200 175664 [+3 L= 465 r=-1.270] (FTT0160 175200 175664 +)====>ref ZP_00583903.1 NUDIX hydrolase [Shewanella baltica OS155]gb EAN41641.1 NUDIX hydrolase [Shewanella baltica OS155] Score = 196 bits (498), Expect = 2e-49====>ref YP_169226.1 (Di)nucleoside polyphosphate hydrolase [Francisella tularensissubsp. tularensis Schu 4] Score = 330 bits (846), Expect = 8e-90</p> <p>FTTSGH1515 1385698 1386072 [+1 L= 375 r=-1.223] (FTT1346 1385698 1386072 +)====>ref YP_170606.1 hypothetical protein FTT1701 [Francisella tularensis subsp.tularensis Schu 4] Score = 254 bits (650), Expect = 4e-67</p> <p>FTTSGH0639 598475 598960 [+2 L= 486 r=-1.221] (FTT0581 598475 598960 +)====>ref ZP_00535118.1 Coenzyme A biosynthesis protein:Cytidyltransferase-related[Geobacter metallireducens GS-15] Score = 155 bits (393), Expect = 3e-37====>ref YP_169605.1 phosphopantetheine adenylyltransferase [Francisella tularensissubsp. tularensis Schu 4] Score = 321 bits (822), Expect = 6e-87</p> <p>FTTSGH0656 613738 612869 [-2 L= 870 r=-1.211] (FTT0594 613738 612869 -)====>ref NP_798365.1 hypothetical protein VP1986 [Vibrio parahaemolyticus RIMD 2210633]dbj BAC60249.1 hypothetical protein [Vibrio parahaemolyticus RIMD 2210633] Score = 207 bits (528), Expect = 3e-52====>ref YP_169617.1 hypothetical protein FTT0594c [Francisella tularensis subsp.tularensis Schu 4] Score = 595 bits (1533), Expect = e-169</p>	8	8.6	14.48	
7	1.3e-006	-		6	8.9	18.54	
8	1.3e-006	-		8	8.6	14.48	
9	1.2e-006	-		11	7.8	18.50	
10	1.1e-006	-		6	9.2	33.46	

NOTE:

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

Input Summary

Search id 20060330151914-16EC-192168001107
Sequences 2058
Date & Time Thu Mar 30 21:19:14 2006 UTC (Search Time: 0.06 sec.)
Sample ID Schu4 172
Database schu2K [..\databases\schu2k]
Taxonomy -
Mass Range 0 - 35 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) 1002.563 1171.205 1218.646 1337.833 1373.972 1395.850
1584.732 1701.712 1887.692 1941.851 2009.075
Tolerance (mon) 20.00 ppm
Number of 11
Peptides

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