

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	2.41	<p>FTTSGH0341 329238 330104 [+3 L= 867 r=-1.179] (FTT0314 329238 330104 +) ==>ref YP_123996.1 Elongation factor Ts (EF-Ts) [Legionella pneumophila str. Paris]emb CAH12830.1 Elongation factor Ts (EF-Ts) [Legionella pneumophila str. Paris] Score = 342 bits (876), Expect = 1e-92==>ref YP_169363.1 protein chain elongation factor EF-Ts [Francisella tularensissubsp. tularensis Schu 4] Score = 543 bits (1398), Expect = e-153</p> <p>FTTSGH0473 452620 453273 [+1 L= 654 r=-1.229] (FTT0439 452620 453273 +) ==>emb CAG76519.1 probable tRNA/rRNA methyltransferase [Erwinia carotovora subsp.atroseptica SCRI1043] Score = 174 bits (440), Expect = 2e-42==>ref YP_169479.1 tRNA/rRNA methyltransferase [Francisella tularensis subsp.tularensis Schu 4] Score = 428 bits (1101), Expect = e-119</p> <p>FTTSGH0610 575725 576333 [+1 L= 609 r=-1.203] (FTT0558 575725 576333 +) ==>emb CAD17119.1 CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum]ref NP_521450.1 hypothetical protein RSc3331 [Ralstonia solanacearum GMI1000] Score = 183 bits (464), Expect = 3e-45==>ref YP_169584.1 hypothetical protein FTT0558 [Francisella tularensis subsp.tularensis Schu 4] Score = 392 bits (1006), Expect = e-108</p> <p>FTTSGH2004 1848001 1847591 [-2 L= 411 r=-1.271] [DelayedBy _2056 L=72] (FTT1759 1848091 1847591 -) ==>ref NP_229142.1 oxidase-related protein [Thermotoga maritima MSB8]gb AAD36412.1 oxidase-related protein [Thermotoga maritima MSB8] Score = 66.2 bits (160), Expect = 3e-10</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</p>	25	5.6	30.97	
2	1.7e-010	-		16	7.8	23.67	
3	1.4e-010	-		17	6.3	21.69	
4	1.2e-010	-		23	9.6	16.58	
5	9.5e-011	-		6	6.1	38.89	

			(197), Expect = 8e-14====>ref YP_169534.1 hypothetical protein FTT0499 [Francisella tularensis subsp.tularensis Schu 4] Score = 194 bits (492), Expect = 5e-48 FTTSGH0612 578057 577008 [-3 L=1050 r=-1.236] (FTT0560c 578057 577008 -) ====>ref YP_204282.1 phosphoserine aminotransferase [Vibrio fischeri ES114]gb AAW85394.1 phosphoserine aminotransferase [Vibrio fischeri ES114] Score = 288 bits (736), Expect = 3e-76====>ref YP_169586.1 phosphoserine aminotransferase [Francisella tularensis subsp.tularensis Schu 4] Score = 694 bits (1791), Expect = 0.0 FTTSGH1755 1613174 1613998 [+2 L= 825 r=-1.277] (FTT1552 1613174 1613998 +) ====>ref YP_046295.1 delta 9 acyl-lipid fatty acid desaturase [Acinetobacter sp. ADP1]emb CAG68473.1 delta 9 acyl-lipid fatty acid desaturase [Acinetobacter sp. ADP1] Score = 271 bits (694), Expect = 1e-71====>ref YP_170476.1 Delta 9 acyl-lipid fatty acid desaturase [Francisella tularensissubsp. tularensis Schu 4] Score = 584 bits (1505), Expect = e-165 FTTSGH0460 442076 442213 [+2 L= 138 r=-1.199] (FTT0426 442076 442213 +) ====>emb CAH02099.1 unnamed protein product [Kluyveromyces lactis NRRL Y-1140]ref XP_451706.1 unnamed protein product [Kluyveromyces lactis] Score = 63.5 bits (153), Expect = 2e-09 FTTSGH0502 481750 481935 [+1 L= 186 r=-1.353] [Vote] (FTT0465 481750 481935 +) ====>ref YP_169503.1 hypothetical protein FTT0465 [Francisella tularensis subsp.tularensis Schu 4] Score = 124 bits (311), Expect = 9e-28 FTTSGH0905 833724 833479 [-1 L= 246 r=-1.183] (FTT0815 833724 833479 -) ====>ref YP_169822.1 hypothetical protein FTT0815c [Francisella tularensis subsp.tularensis Schu 4] Score = 167 bits (423), Expect = 9e-41				
6	9.2e-011	-		8	6.0	39.25	
7	3.7e-012	-		11	9.4	31.92	
8	1.5e-012	-		30	4.9	4.85	
9	1.4e-012	-		27	8.1	6.18	
10	9.8e-013	-		17	5.6	9.29	

NOTE:

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

Input Summary

Search id 20060404160959-1F0C-192168001107
Sequences 2059
Date & Time Tue Apr 04 21:09:59 2006 UTC (Search Time: 0.16 sec.)
Sample ID Schu4 255
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) 747.867 928.525 975.375 1302.743 1387.722 1468.874 1519.828
1575.831 1593.848 1690.941 1835.819 1994.005 2118.134
2246.232 2474.351
Tolerance (mon) 50.00 ppm
Number of 15
Peptides

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