

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	1.56	<p>FTTSGH0609 575198 575719 [+2 L= 522 r=-1.197] (FTT0557 575198 575719 +) ==>ref ZP_00621608.1 Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Malallergen [Silicibacter sp. TM1040] Score = 255 bits (651), Expect = 5e-67 ==>ref YP_169583.1 AhpC/TSA family protein [Francisella tularensis subsp. tularensisSchu 4] Score = 358 bits (920), Expect = 3e-98</p>	26	5.1	19.68	
2	1.4e-006	-	<p>FTTSGH0709 661868 662008 [+2 L= 141 r=-1.231] (FTT0643 661868 661978 +) ==>emb CAH09234.1 putative reductoisomerase [Bacteroides fragilis NCTC 9343]ref YP_213148.1 putative reductoisomerase [Bacteroides fragilis NCTC 9343] Score = 55.5 bits (132), Expect = 5e-07</p>	28	4.8	5.15	
3	1.3e-006	-	<p>FTTSGH0148 147668 148162 [+2 L= 495 r=-1.242] (FTT0135 147668 148165 +) ==>ref NP_778009.1 putative membrane protein [Buchnera aphidicola str. Bp (Baizongiapistaciae)] Score = 95.5 bits (236), Expect = 5e-19</p>	5	8.6	17.80	
4	1.2e-006	-	<p>FTTSGH1003 907323 906973 [-1 L= 351 r=-1.266] (FTT0898 907323 906973 -) ==>ref YP_237182.1 Protein of unknown function UPF0102 [Pseudomonas syringae pv.syringae B728a] Score = 92.0 bits (227), Expect = 5e-18 ==>ref YP_169895.1 hypothetical protein FTT0898c [Francisella tularensis subsp.tularensis Schu 4] Score = 236 bits (602), Expect = 2e-61</p>	13	6.3	13.54	
5	7.7e-007	-	<p>FTTSGH0810 754791 755135 [+3 L= 345 r=-1.224] (FTT0732 754791 755135 +) ==>ref YP_169745.1 hypothetical protein FTT0732 [Francisella tularensis subsp.tularensis Schu 4] Score = 231 bits (589), Expect = 5e-60</p>	9	9.3	13.24	
6	7.1e-007	-	<p>FTTSGH0707 661111 661515 [+1 L= 405 r=-1.258] (FTT0641 661078 661518 +) ==>gb AAO61969.1 acetohydroxy acid synthase II [Aster yellows phytoplasma]Length = 117 Score = 134 bits</p>	10	4.8	15.30	

			(338), Expect = 7e-31				
7	7.0e-007	-	FTTSGH0859 792806 792387 [-3 L= 420 r=-1.250] (FTT0771c 792806 792399 -) ====>ref ZP_00133479.2 COG1929: Glycerate kinase [Haemophilus somnus 2336]Length = 380 Score = 134 bits (338), Expect = 7e-31	7	6.3	15.37	
8	6.8e-007	-	FTTSGH1989 1837331 1837750 [+2 L= 420 r=-1.176] (FTT1748 1837331 1837750 +) ====>ref YP_154626.1 Rhodanese-related sulfurtransferase [Idiomarina loihiensis L2TR]gb AAV81077.1 Rhodanese-related sulfurtransferase [Idiomarina loihiensis L2TR] Score = 83.6 bits (205), Expect = 2e-15====>ref YP_170642.1 thiosulfate sulfurtransferase [Francisella tularensis subsp.tularensis Schu 4] Score = 277 bits (709), Expect = 6e-74	11	9.2	15.86	
9	6.6e-007	-	FTTSGH0051 47244 47405 [+3 L= 162 r=-1.173] (FTT0046 47241 47405 +) ====>ref NP_799436.1 ComM-related protein [Vibrio parahaemolyticus RIMD 2210633]dbj BAC61320.1 ComM-related protein [Vibrio parahaemolyticus RIMD 2210633] Score = 61.6 bits (148), Expect = 7e-09	24	9.6	6.12	
10	5.8e-007	-	FTTSGH0034 30951 30532 [-1 L= 420 r=-1.258] (FTT0030c 30951 30532 -) ====>gb AAW90398.1 ferric uptake regulation protein [Neisseria gonorrhoeae FA 1090]sp Q51008 FUR_NEIGO Ferric uptake regulation protein (Ferric uptake regulator) Score = 143 bits (360), Expect = 2e-33====>ref YP_169106.1 ferric uptake regulation protein [Francisella tularensis subsp.tularensis Schu 4] Score = 284 bits (727), Expect = 5e-76	7	6.9	16.13	

NOTE:

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

Input Summary

Search id 20060330154356-184C-192168001107

Sequences 2058

Date & Time Thu Mar 30 21:43:56 2006 UTC (Search Time: 0.06 sec.)

Sample ID Schu4 181

Database schu2K [..\databases\schu2k]

Taxonomy -

Mass Range 0 - 20 kDa

Peptides