

ProFound - Search Result Summary

Version 2002.03.01

© 1997-2002 Proteometrics LLC

Protein Candidates

Rank	Probability	Est'd Z	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	1.0e+000	1.08	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 FTTSGH1637 1501521 1500640 [-1 L= 882 r=-1.239] (FTT1451c 1501521 1500640 -) ====>gb AAL26874.1 glucose-1-phosphate thymidyltransferase [Acinetobacter calcoaceticus] Score = 409 bits (1050), Expect = e-113====>ref YP_170388.1 Glucose-1-phosphate thymidyltransferase [Francisella tularensissubsp. tularensis Schu 4] Score = 586 bits (1511), Expect = e-166 FTTSGH0367 345394 345891 [+1 L= 498 r=-1.229] (FTT0342 345394 345891 +) ====>ref ZP_00473502.1 Ribosomal protein S5, bacterial and organelle form[Chromohalobacter salexigens DSM 3043] Score = 228 bits (582), Expect = 4e-59====>ref YP_169391.1 30S ribosomal protein S5 [Francisella tularensis subsp. tularensisSchu 4] Score = 322 bits (826), Expect = 2e-87 FTTSGH1908 1753817 1754716 [+2 L= 900 r=-1.245] (FTT1684 1753817 1754716 +) ====>ref YP_122688.1 hypothetical protein lpp0348 [Legionella pneumophila str. Paris]emb CAH11496.1 hypothetical protein [Legionella pneumophila str. Paris] Score = 176 bits (445), Expect = 1e-42====>ref YP_170589.1 transcription regulator [Francisella tularensis subsp. tularensisSchu 4] Score = 592 bits (1527), Expect = e-168 FTTSGH1028 932218 932739 [+1 L= 522 r=-1.255] (FTT0921 932218 932688 +) ====>ref YP_132231.1 hypothetical	18	5.6	30.97	
2	6.3e-004	0.03		14	5.5	32.38	
3	7.0e-005	-		23	10.0	17.54	
4	3.6e-005	-		14	9.3	34.13	
5	2.3e-005	-		17	10.0	20.38	

			protein PBPRB0558 [Photobacterium profundum SS9]emb CAG22431.1 hypothetical protein [Photobacterium profundum SS9] Score = 97.4 bits (241), Expect = 2e-19			
6	4.4e-006	-	FTTSGH1276 1149242 1148598 [-3 L= 645 r=-1.269] (FTT1135 1149409 1148598 -) ==>ref ZP_00262873.1 COG4637: Predicted ATPase [Pseudomonas fluorescens PfO-1]Length = 386 Score = 275 bits (702), Expect = 1e-72	8	5.3	24.14
7	4.1e-006	-	FTTSGH2003 1847606 1847016 [-3 L= 591 r=-1.260] [Contains _2053] (FTT1758 1847606 1847016 -) ==>ref ZP_00210411.1 COG3038: Cytochrome B561 [Ehrlichia canis str. Jake]Length = 173 Score = 110 bits (276), Expect = 2e-23==>ref YP_170650.1 B-type cytochrome [Francisella tularensis subsp. tularensis Schu 4]emb CAG46391.1 B-type cytochrome [Francisella tularensis subsp. tularensis SCHU Score = 391 bits (1005), Expect = e-108	12	9.8	22.62
8	1.8e-006	-	FTTSGH0529 512014 511343 [-2 L= 672 r=-1.217] (FTT0491c 512014 511343 -) ==>ref NP_886288.1 putative phosphoglycolate phosphatase [Bordetella parapertussis12822] Score = 138 bits (347), Expect = 2e-31==>ref YP_169529.1 phosphoglycolate phosphatase [Francisella tularensis subsp.tularensis Schu 4] Score = 443 bits (1140), Expect = e-123	12	5.0	24.88
9	1.7e-006	-	FTTSGH0351 337708 338340 [+1 L= 633 r=-1.241] (FTT0325 337708 338340 +) ==>gb AAK03499.1 RpL3 [Pasteurella multocida subsp. multocida str. Pm70]ref NP_246354.1 RpL3 [Pasteurella multocida subsp. multocida str. Pm70] Score = 299 bits (766), Expect = 4e-80==>ref YP_169374.1 50S ribosomal protein L3 [Francisella tularensis subsp. tularensisSchu 4] Score = 425 bits (1093), Expect = e-118	18	9.6	22.48
10	1.3e-006	-	FTTSGH1036 941728 941132 [-2 L= 597 r=-1.203] (FTT0929 941911 941132 -) ==>ref ZP_00465325.1 3-hydroxybutyrate dehydrogenase [Burkholderia cenocepacia HI2424]ref ZP_00458064.1 3-hydroxybutyrate dehydrogenase [Burkholderia cenocepacia AU 1054] Score =	19	6.3	21.44

244 bits (624), Expect = 9e-64

NOTE:

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

Input Summary

Search id 20060330151530-16EC-192168001107
Sequences 1984
Date & Time Thu Mar 30 21:15:30 2006 UTC (Search Time: 0.20 sec.)
Sample ID Schu4 171
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) 747.628 856.541 928.558 1087.600 1139.957 1171.072 1191.321
1287.969 1316.284 1337.711 1344.839 1373.808 1395.698
1417.761 1469.929 1519.843 1561.531 1621.974 1638.913
1690.940 1702.161 1834.128 2083.119 2112.036 2113.111
2149.288 2178.057 2179.710
Tolerance (mon) 100.00 ppm
Number of 28
Peptides

Profound is provided under exclusive licence by Genomic Solutions Ltd.