ProFound - Search Result Summary

Protein Candidates

Rank	Probability	Est'd Z	Protein Information and Sequence Analyse Tools (T)	%	*pI*	kDa	R
1	9.8e-001	0.67	FTTSGH1393 1252948 1254090 [+1 L=1143 r=-1.227] (FTT1234 1252948 1254090 +) =====>ref|YP_222152.1| choloylglycine hydrolase family protein [Brucella abortus biovar 1str. 9-941] Score = 166 bits (420), Expect = 1e-39====>ref|YP_170192.1| choloylglycine hydrolase family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 765 bits (1976), Expect = 0.0	13	8.9	42.52	
2	4.6e-003	-	FTTSGH1220 1097865 1095853 [-1 L=2013 r=-1.237] (FTT1087c 1097865 1095853 -) =====>gb|AAU37020.1| UvrD protein [Mannheimia succiniciproducens MBEL55E]ref|YP_087605.1| UvrD protein [Mannheimia succiniciproducens MBEL55E] Score = 622 bits (1603), Expect = e-176====>ref|YP_170066.1| ATP-dependent DNA helicase [Francisella tularensis subsp. tularensisSchu 4] Score = 1326 bits (3431), Expect = 0.0	3	6.2	78.20	
3	2.6e-003	-	FTTSGH2015 1860351 1857775 [-1 L=2577 r=-1.240] (FTT1769c 1860351 1857775 -) =====>ref|YP_127052.1| endopeptidase Clp ATP-binding chain B (ClpB) [Legionella pneumophilastr. Lens] Score = 1098 bits (2841), Expect = 0.0====>ref|YP_170660.1| ClpB protein [Francisella tularensis subsp. tularensis Schu 4]emb|CAG46402.1| ClpB protein [Francisella tularensis subsp. tularensis SCHU S4] Score = 1655 bits (4285), Expect = 0.0	4	5.5	95.91	
4	2.1e-003	-	FTTSGH1781 1640746 1641828 [+1 L=1083 r=-1.220] (FTT1577 1640746 1641828 +) =====>ref|YP_204773.1| carbohydrate binding domain protein [Vibrio fischeri ES114]gb|AAW85885.1| carbohydrate binding domain protein [Vibrio fischeri ES114] Score = 54.7 bits (130), Expect = 5e-06====>ref|YP_170499.1| hypothetical protein FTT1577 [Francisella tularensis subsp.tularensis Schu 4] Score = 764 bits (1973), Expect = 0.0	9	5.1	41.25	
5	2.0e-003	-	FTTSGH1169 1058317 1057958 [-2 L= 360 r=-1.234] (FTT1047 1058317 1057958 -) =====>ref|YP_170030.1| hypothetical	22	9.5	13.51	

			protein FTT1047c [Francisella tularensis subsp.tularensis Schu 4] Score = 229 bits (583), Expect = 3e-59				
6	1.9e-003	-	FTTSGH1358 1220376 1219657 [-1 L= 720 r=-1.229] (FTT1201 1220376 1219657 -) =====>gb|AAF96951.1| oxidoreductase, short-chain dehydrogenase/reductase family [Vibriocholerae O1 biovar eltor str. N16961] Score = 337 bits (864), Expect = 2e-91====>ref|YP_170160.1| Oxidoreductase, short-chain dehydrogenase family protein[Francisella tularensis subsp. tularensis Schu 4] Score = 463 bits (1192), Expect = e-129	15	6.1	25.97	
7	8.3e-004	-	FTTSGH1058 961036 959975 [-2 L=1062 r=-1.246] (FTT0947 960009 959497 -) (FTT0948 961036 959975 -) =====>emb|CAC45719.1| PUTATIVE OXIDOREDUCTASE PROTEIN [Sinorhizobium meliloti]ref|NP_385246.1| PUTATIVE OXIDOREDUCTASE PROTEIN [Sinorhizobium meliloti 1021] Score = 328 bits (840), Expect = 2e-88====>ref|YP_169940.1| Aldo/keto reductase [Francisella tularensis subsp. tularensis Schu 4]emb|CAG45581.1| Aldo/keto reductase [Francisella tularensis subsp. tularensis SCHU Score = 729 bits (1882), Expect = 0.0	8	7.8	40.77	
8	6.1e-004	-	FTTSGH0803 750029 748998 [-3 L=1032 r=-1.215] (FTT0726 750029 748998 -) =====>ref|NP_773224.1| putative glycerophosphoryl diester phosphodiesterase [Bradyrhizobiumjaponicum USDA 110] Score = 215 bits (547), Expect = 2e-54====>ref|YP_169739.1| glycerophosphoryl diester phosphodiesterase family protein[Francisella tularensis subsp. tularensis Schu 4] Score = 707 bits (1824), Expect = 0.0	9	5.4	39.02	
9	5.9e-004	-	FTTSGH1064 964146 965468 [+3 L=1323 r=-1.224] (FTT0952 964146 965468 +) =====>ref|NP_799900.1| ATP-dependent RNA helicase RhlE [Vibrio parahaemolyticus RIMD2210633] Score = 462 bits (1188), Expect = e-128====>ref|YP_169942.1| ATP-dependent RNA helicase RhlE [Francisella tularensis subsp.tularensis Schu 4] Score = 852 bits (2200), Expect = 0.0	8	9.9	48.66	
10	5.1e-004	-	FTTSGH1585 1458131 1457049 [-3 L=1083 r=-1.209] (FTT1407 1458131 1457049 -) (FTT1408c 1458846 1458100 -)	7	8.9	40.00	

=====>ref|XP_635612.1| hypothetical protein DDB0188916 [Dictyostelium discoideum]gb|EAL62112.1| hypothetical protein DDB0188916 [Dictyostelium discoideum] Score = 53.1 bits (126), Expect = 1e-05=====>ref|YP_170351.1| hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 677 bits (1747), Expect = 0.0

NOTE:

1. To search again using unmatched masses, click the symbol .

Input Summary

Search id	20060404123243-1E9C-192168001107
Sequences	1984
Date & Time	Tue Apr 04 17:32:44 2006 UTC (Search Time: 0.27 sec.)
Sample ID	Schu4 235 [Pass: 1]
Database	SCHU2K [..\databases\schu2k]
Taxonomy	-
Mass Range	0 - 150 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)	935.478 962.444 1109.620 1140.661 1158.685 1302.768 1323.717 1340.757 1357.777 1424.789 1434.802 1493.779 1621.954 1638.911 1674.971 1838.957 1940.935 1994.033 2501.236
Tolerance (mon)	50.00 ppm
Number of Peptides	19