ProFound - Search Result Summary

Protein Candidates

Rank	Probability	Est'd Z	Protein Information and Sequence Analyse Tools (T)	%	*pI*	kDa	R
1	1.0e+000	1.90	FTTSGH1776 1633617 1633117 [-1 L= 501 r=-1.187] (FTT1572c 1633617 1633117 -) ======>dbj|BAC24529.1| hlpA [Wigglesworthia glossinidia endosymbiont of Glossinabrevipalpis] Score = 90.9 bits (224), Expect = 1e-17=====>ref|YP_170494.1| outer membrane protein OmpH [Francisella tularensis subsp.tularensis Schu 4] Score = 318 bits (816), Expect = 3e-86	34	7.7	18.75	
2	4.1e-006	0.12	FTTSGH0402 373851 373432 [-1 L= 420 r=-1.195] (FTT0373c 373851 373432 -) ======>gb|AAO90766.1| nucleoside diphosphate kinase [Coxiella burnetii RSA 493]ref|NP_820252.1| nucleoside diphosphate kinase [Coxiella burnetii RSA 493] Score = 214 bits (546), Expect = 5e-55=====>ref|YP_169420.1| nucleoside diphosphate kinase [Francisella tularensis subsp.tularensis Schu 4] Score = 273 bits (699), Expect = 9e-73	34	5.9	15.51	
3	9.6e-007	-	FTTSGH1688 1551127 1550627 [-2 L= 501 r=-1.227] (FTT1497 1551127 1550627 -) ======>ref|YP_170432.1| hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 318 bits (814), Expect = 5e-86=====>ref|YP_170537.1| hypothetical protein FTT1624c [Francisella tularensis subsp.tularensis Schu 4] Score = 55.8 bits (133), Expect = 5e-07	15	5.2	18.61	
4	2.9e-009	-	FTTSGH1973 1823516 1823328 [-3 L= 189 r=-1.246] (FTT1735c 1823663 1823328 -) ======>gb|EAM76051.1| Response regulator receiver:Transcriptional regulatory protein,C-terminal [Kineococcus radiotolerans SRS30216] Score = 67.4 bits (163), Expect = 1e-10	35	9.5	7.01	
5	1.2e-009	-	FTTSGH1993 1839942 1840415 [+3 L= 474 r=-1.213] (FTT1752 1839942 1840415 +) ======>ref|ZP_00134369.1| COG0629: Single-stranded DNA-binding protein [Actinobacilluspleuropneumoniae serovar 1 str. 4074] Score = 137 bits (344), Expect = 1e-31=====>ref|YP_170646.1| Single-strand binding protein [Francisella	11	5.6	17.51	

			tularensis subsp.tularensis Schu 4] Score = 327 bits (839), Expect = 6e-89			
6	1.1e-010	-	FTTSGH1437 1295900 1296352 [+2 L= 453 r=-1.216] (FTT1273 1295900 1296352 +) ======>ref|ZP_00473773.1| Ribosomal protein L13, bacterial and organelle form[Chromohalobacter salexigens DSM 3043] Score = 214 bits (544), Expect = 9e-55=====>ref|YP_170229.1| 50S ribosomal subunit protein L13 [Francisella tularensis subsp.tularensis Schu 4] Score = 307 bits (786), Expect = 7e-83	17	10.1	16.90
7	3.5e-012	-	FTTSGH1091 988429 988575 [+1 L= 147 r=-1.276] (None identical in .gff) ======>Hypothetical ORF FTTSGH1091	16	4.2	5.67
8	1.7e-012	-	FTTSGH1946 1798614 1798522 [-1 L= 93 r=-1.236] (FTT1716 1798650 1798522 -) ======>Hypothetical ORF FTTSGH1946	26	9.7	3.35
9	1.7e-012	-	FTTSGH1530 1405270 1405178 [-2 L= 93 r=-1.236] (FTT1361 1405306 1405178 -) ======>Hypothetical ORF FTTSGH1530	26	9.7	3.35
10	1.6e-012	-	FTTSGH0464 444629 444402 [-3 L= 228 r=-1.223] (FTT0429c 444629 444399 -) ======>gb|AAN47234.1| beta-galactosidase I [Leptospira interrogans serovar lai str.56601] Score = 80.1 bits (196), Expect = 2e-14	16	4.5	8.99

NOTE:

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

Input Summary

Search id 20060404164229-1E5C-192168001107
Sequences 2058
Date & Time Tue Apr 04 21:42:29 2006 UTC (Search Time: 0.09 sec.)
Sample ID Schu4 267
Database schu2K [..\databases\schu2k]
Taxonomy -
Mass Range 0 - 20 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)	848.475 882.526 962.427 970.517 1006.545 1050.585 1224.654 1313.784 1509.834 1535.913 1577.731 1631.885 1703.587 1729.816 1732.265 1746.871 1874.962 2001.997 2013.144 2202.145 2299.145 2667.097 2679.152 2689.195 2721.199
Tolerance (mon)	30.00 ppm
Number of Peptides	25