

ProFound - Search Result SummaryVersion 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	0.87	<p>FTTSGH0495 476164 477180 [+1 L=1017 r=-1.206] (FTT0459 476164 477180 +) =====>ref ZP_00636494.1 Peptidase S49 [Shewanella denitrificans OS-217]gb EAN68982.1 Peptidase S49 [Shewanella denitrificans OS-217] Score = 302 bits (774), Expect = 1e-80=====>ref YP_169497.1 peptidase family S49 protein [Francisella tularensis subsp.tularensis Schu 4] Score = 658 bits (1697), Expect = 0.0</p> <p>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 = 244 bits (624), Expect = 9e-64</p> <p>FTTSGH1169 1058317 1057958 [-2 L= 360 r=-1.234] (FTT1047 1058317 1057958 -) =====>ref YP_170030.1 hypothetical protein FTT1047c [Francisella tularensis subsp.tularensis Schu 4] Score = 229 bits (583), Expect = 3e-59</p> <p>FTTSGH0432 403507 404226 [+1 L= 720 r=-1.207] (FTT0401 403507 404226 +) =====>ref ZP_00582277.1 conserved hypothetical protein [Shewanella baltica OS155]gb EAN43253.1 conserved hypothetical protein [Shewanella baltica OS155] Score = 85.5 bits (210), Expect = 1e-15=====>ref YP_169446.1 hypothetical protein FTT0401 [Francisella tularensis subsp.tularensis Schu 4] Score = 464 bits (1194), Expect = e-129</p> <p>FTTSGH2047 1882631 1883056 [+2 L= 426 r=-1.197] (FTT1794 1882631 1883056 +) =====>ref YP_247020.1 Small heat shock protein [Rickettsia felis URRWXCal2]gb AAY61855.1 Small heat shock protein [Rickettsia felis URRWXCal2] Score = 116 bits (291), Expect = 2e-25=====>ref YP_170678.1 heat shock</p>	7	9.1	38.10	
2	6.0e-004	-		15	6.3	21.44	
3	5.1e-004	-		22	9.5	13.51	
4	5.0e-004	-		6	8.9	27.35	
5	3.9e-004	-		12	5.6	16.69	

			protein [Francisella tularensis subsp. tularensis Schu4] Score = 287 bits (734), Expect = 8e-77			
6	1.1e-004	-	<p>FTTSGH1443 1300415 1299675 [-3 L= 741 r=-1.266] (FTT1279c 1300415 1299675 -) =====>ref YP_071368.1 putative SpoU-family rRNA methylase [Yersinia pseudotuberculosis IP32953] Score = 210 bits (534), Expect = 4e-53=====>ref YP_170235.1 SpoU rRNA methylase family protein [Francisella tularensis subsp.tularensis Schu 4] Score = 482 bits (1240), Expect = e-135</p> <p>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</p> <p>FTTSGH0523 504863 506662 [+2 L=1800 r=-1.241] (FTT0486 504863 506662 +) =====>ref ZP_00315672.1 COG0323: DNA mismatch repair enzyme (predicted ATPase) [Microbulbiferdegradans 2-40] Score = 523 bits (1346), Expect = e-146=====>ref YP_169524.1 DNA mismatch repair protein [Francisella tularensis subsp. tularensisSchu 4] Score = 1183 bits (3061), Expect = 0.0</p> <p>FTTSGH0492 475129 474839 [-2 L= 291 r=-1.212] (FTT0456 475129 474839 -) =====>ref YP_095944.1 hypothetical protein lpg1927 [Legionella pneumophila subsp.pneumophila str. Philadelphia 1] Score = 112 bits (279), Expect = 5e-24=====>ref YP_169494.1 UPF0269 family protein [Francisella tularensis subsp. tularensisSchu 4] Score = 205 bits (521), Expect = 4e-52</p> <p>FTTSGH2058 1892386 1890893 [-2 L=1494 r=-1.197] (FTT1804c 1892386 1890893 -) =====>ref ZP_00317701.1 COG1530: Ribonucleases G and E [Microbulbifer degradans 2-40]Length = 492 Score = 469 bits (1208), Expect = e-131=====>ref YP_170686.1 Ribonuclease</p>	13	6.1	27.69
7	7.6e-005	-		9	5.4	39.02
8	5.2e-005	-		4	6.4	68.04
9	4.7e-005	-		16	7.8	11.77
10	4.2e-005	-		5	5.2	57.48

G [Francisella tularensis subsp. tularensis
Schu 4]emb|CAG46437.1| Ribonuclease G
[Francisella tularensis subsp. tularensis SCHU
S4] Score = 976 bits (2524), Expect = 0.0

NOTE:

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

Input Summary

Search id 20060404151301-0F3C-192168001107

Sequences 2055

Date & Time Tue Apr 04 20:13:02 2006 UTC (Search Time: 0.22 sec.)

Sample ID Schu4 242 [Pass: 2]

Database SCHU2K [..\databases\schu2k]

Taxonomy -

Mass Range 0 - 80 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) 962.436 1057.622 1082.626 1140.667 1199.681 1288.717
1308.721 1434.781 1470.792 1638.873 1674.939 1838.944
1951.964 1994.006 2501.251 2705.046

Tolerance (mon) 50.00 ppm

Number of 16
Peptides

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