

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	8.7e-001	0.47	FTTSGH0729 678247 679656 [+1 L=1410 r=-1.200] (FTT0659 678247 679656 +) =====>ref ZP_00634898.1 Protein of unknown function DUF195 [Shewanella denitrificans OS-217]gb EAN70605.1 Protein of unknown function DUF195 [Shewanella denitrificans OS-217] Score = 364 bits (935), Expect = 3e-99=====>ref YP_169676.1 DNA recombination protein RmuC family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 908 bits (2347), Expect = 0.0	10	6.3	54.32	
2	5.9e-002	0.08	FTTSGH0430 401042 399927 [-3 L=1116 r=-1.255] (FTT0399 401042 399927 -) =====>gb AAV93113.1 BNR/Asp-box repeat protein [Pseudomonas fluorescens Pf-5]ref YP_260949.1 BNR/Asp-box repeat protein [Pseudomonas fluorescens Pf-5] Score = 153 bits (387), Expect = 8e-36=====>ref YP_169444.1 BNR/Asp-box repeat protein [Francisella tularensis subsp. tularensisSchu 4] Score = 751 bits (1939), Expect = 0.0	8	9.5	42.50	
3	3.5e-002	0.01	FTTSGH1401 1262352 1263611 [+3 L=1260 r=-1.230] (FTT1242 1262352 1263611 +) =====>ref YP_170200.1 hypothetical protein FTT1242 [Francisella tularensis subsp.tularensis Schu 4] Score = 826 bits (2133), Expect = 0.0=====>ref YP_170201.1 FAD binding family protein [Francisella tularensis subsp. tularensisSchu 4] Score = 90.5 bits (223), Expect = 1e-16	9	7.1	45.93	
4	7.1e-003	-	FTTSGH0506 487872 488657 [+3 L= 786 r=-1.251] (FTT0469 487872 488657 +) =====>gb AAQ57800.1 dimethyladenosine transferase [Chromobacterium violaceum ATCC12472] Score = 211 bits (537), Expect = 2e-53=====>ref YP_169507.1 dimethyladenosine transferase , kasugamycin resistance [Francisellatularensis subsp. tularensis Schu 4] Score = 512 bits (1318), Expect = e-144	12	9.5	29.74	

5	3.1e-003	-	<p>FTTSGH1490 1350607 1351182 [+1 L= 576 r=-1.203] (FTT1323 1350607 1351182 +) ====>ref ZP_00155943.1 COG0742: N6-adenine-specific methylase [Haemophilus influenzaeR2846] Score = 143 bits (361), Expect = 3e-33====>ref YP_170276.1 Methylase [Francisella tularensis subsp. tularensis Schu 4]gb AAV29509.1 NT02FT0419 [synthetic construct] Score = 374 bits (960), Expect = e-103</p> <p>FTTSGH0649 609091 609678 [+1 L= 588 r=-1.246] (FTT0589 609091 609678 +) (FTT0590 609632 610111 +) ====>ref YP_169612.1 hypothetical protein FTT0589 [Francisella tularensis subsp.tularensis Schu 4] Score = 399 bits (1024), Expect = e-110</p> <p>FTTSGH1217 1093653 1092796 [-1 L= 858 r=-1.191] (FTT1084c 1093653 1092796 -) ====>ref NP_931129.1 recombinaison associated protein [Photorhabdus luminescens subsp.laumondii TTO1] Score = 135 bits (339), Expect = 2e-30====>ref YP_170063.1 recombination associated protein [Francisella tularensis subsp.tularensis Schu 4] Score = 568 bits (1465), Expect = e-161</p> <p>FTTSGH1262 1132633 1132166 [-2 L= 468 r=-1.276] (FTT1122 1132633 1132166 -) ====>ref YP_170095.1 hypothetical lipoprotein [Francisella tularensis subsp. tularensisSchu 4] Score = 319 bits (817), Expect = 2e-86====>ref YP_169520.1 hypothetical lipoprotein [Francisella tularensis subsp. tularensisSchu 4] Score = 80.1 bits (196), Expect = 2e-14</p> <p>FTTSGH1450 1304044 1303157 [-2 L= 888 r=-1.233] (FTT1285 1304044 1303157 -) ====>ref YP_047298.1 putative transcriptional regulator [Acinetobacter sp. ADP1]emb CAG69476.1 putative transcriptional regulator [Acinetobacter sp. ADP1] Score = 111 bits (277), Expect = 3e-23====>ref YP_170241.1 LysR transcriptional regulator family protein [Francisellatularensis subsp. tularensis Schu 4] Score = 583 bits (1504), Expect = e-165</p> <p>FTTSGH0560 535846 536433 [+1 L= 588 r=-1.195] (FTT0514 535837 536436 +) ====>ref NP_949656.1 L-lactate dehydrogenase [Rhodopseudomonas palustris</p>	12	9.5	21.63	
6	3.0e-003	-		4	9.7	22.59	
7	3.0e-003	-		11	4.7	32.92	
8	2.9e-003	-		13	6.6	16.83	
9	2.4e-003	-		7	8.5	33.73	
10	2.2e-003	-		13	9.4	21.11	

CGA009]emb|CAE29761.1| L-lactate
dehydrogenase [Rhodopseudomonas palustris
CGA009] Score = 191 bits (485), Expect =
1e-47====>ref|YP_169352.1| L-lactate
dehydrogenase [Francisella tularensis subsp.
tularensisSchu 4] Score = 169 bits (429),
Expect = 4e-41

NOTE:

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

Input Summary

Search id 20060404153232-16C4-192168001107
Sequences 2058
Date & Time Tue Apr 04 20:32:32 2006 UTC (Search Time: 0.20 sec.)
Sample ID Schu4 245 [Pass: 1]
Database SCHU2K [..\databases\schu2k]
Taxonomy -
Mass Range 0 - 55 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) 864.467 868.484 882.512 996.563 1141.604 1183.696 1261.709
1314.696 1450.783 1495.779 1547.806 1685.880 1802.840
1940.966 2313.157
Tolerance (mon) 50.00 ppm
Number of
Peptides 15

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