


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	2.23	<p>FTTSGH1358 1220376 1219657 [-1 L= 720 r=-1.229] (FTT1201 1220376 1219657 -) =====>gb AAF96951.1 oxidoreductase, short-chain dehydrogenase/reductase family [Vibrio cholerae 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</p> <p>FTTSGH1267 1137666 1138421 [+3 L= 756 r=-1.232] (FTT1127 1137666 1138421 +) =====>ref ZP_00521456.1 Rhodanese-like [Solibacter usitatus Ellin6076]gb EAM59572.1 Rhodanese-like [Solibacter usitatus Ellin6076] Score = 140 bits (352), Expect = 5e-32 =====>ref YP_170100.1 Rhodanese-like family protein [Francisella tularensis subsp. tularensis Schu 4] Score = 509 bits (1310), Expect = e-143</p> <p>FTTSGH0508 489503 489937 [+2 L= 435 r=-1.258] (FTT0471 489503 489937 +) =====>ref NP_892505.1 Dehydroquinase class II [Prochlorococcus marinus subsp. pastorisstr. CCMP1986] Score = 171 bits (434), Expect = 5e-42 =====>ref YP_169509.1 3-dehydroquinase dehydratase, type II [Francisella tularensis subsp. tularensis Schu 4] Score = 293 bits (750), Expect = 1e-78</p> <p>FTTSGH0693 649910 650236 [+2 L= 327 r=-1.257] (FTT0630 649910 650236 +) =====>gb AAK02990.1 Hfq [Pasteurella multocida subsp. multocida str. Pm70]ref NP_245843.1 Hfq [Pasteurella multocida subsp. multocida str. Pm70] Score = 120 bits (302), Expect = 1e-26 =====>ref YP_169651.1 host factor I for bacteriophage Q beta replication [Francisella tularensis subsp. tularensis Schu 4] Score = 220 bits (560), Expect = 1e-56</p>	30	6.1	25.97	
2	7.2e-009	-		19	6.6	28.19	
3	1.3e-010	-		21	6.0	16.31	
4	1.0e-010	-		21	4.9	12.51	

5	3.1e-011	-	<p>FTTSGH1630 1492446 1492766 [+3 L= 321 r=-1.253] (FTT1445 1492446 1492766 +) =====>ref ZP_00465503.1 Thioredoxin [Burkholderia cenocepacia HI2424]ref ZP_00457921.1 Thioredoxin [Burkholderia cenocepacia AU 1054] Score = 139 bits (349), Expect = 4e-32=====>ref YP_170383.1 Thioredoxin [Francisella tularensis subsp. tularensis Schu 4]emb CAG46078.1 Thioredoxin [Francisella tularensis subsp. tularensis SCHU S4] Score = 223 bits (567), Expect = 2e-57</p> <p>FTTSGH0039 33957 34442 [+3 L= 486 r=-1.269] (FTT0035 33957 34442 +) =====>ref YP_096782.1 NADH dehydrogenase I, E subunit [Legionella pneumophila subsp.pneumophila str. Philadelphia 1] Score = 168 bits (426), Expect = 5e-41=====>ref YP_169111.1 NADH dehydrogenase I, E subunit [Francisella tularensis subsp.tularensis Schu 4] Score = 326 bits (836), Expect = 1e-88</p> <p>FTTSGH0352 338373 338993 [+3 L= 621 r=-1.247] (FTT0326 338373 338993 +) =====>ref YP_128562.1 putative ribosomal protein L4 [Photobacterium profundum SS9]emb CAG18760.1 putative ribosomal protein L4 [Photobacterium profundum SS9] Score = 239 bits (610), Expect = 4e-62=====>ref YP_169375.1 50S ribosomal protein L4 [Francisella tularensis subsp. tularensisSchu 4] Score = 397 bits (1020), Expect = e-109</p> <p>FTTSGH1912 1757082 1756468 [-1 L= 615 r=-1.212] (FTT1687c 1757082 1756468 -) =====>ref YP_131672.1 Putative glucose inhibited division protein B [Photobacteriumprofundum SS9] Score = 169 bits (427), Expect = 7e-41=====>ref YP_170592.1 methyltransferase glucose-inhibited cell division protein[Francisella tularensis subsp. tularensis Schu 4] Score = 405 bits (1041), Expect = e-112</p> <p>FTTSGH0652 611224 611907 [+1 L= 684 r=-1.218] [LowScoreBy _674 L=34 S=21] (FTT0592 611224 611907 +) =====>ref ZP_00532300.1 Carbonate dehydratase [Chlorobium phaeobacteroides BS1]gb EAM63340.1 Carbonate dehydratase [Chlorobium phaeobacteroides BS1] Score =</p>	30	4.7	12.02	
6	2.7e-011	-		22	5.0	18.15	
7	1.5e-011	-		11	9.8	22.50	
8	1.2e-011	-		7	7.8	23.52	
9	4.9e-012	-		10	7.0	25.41	

223 bits (567), Expect =
5e-57====>ref|YP_169615.1| carbonic
anhydrase [Francisella tularensis subsp.
tularensis Schu4] Score = 468 bits (1204),
Expect = e-131
FTTSGH1693 1556638 1556730 [+1 L= 93
r=-1.164] [ShorterThan _1734 L=74 S=99] **58** 4.9 3.68 
(FTT1501 1556542 1556730 +)
====>Hypothetical ORF FTTSGH1693

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

Input Summary

Search id

20060404162736-1F0C-192168001107

Sequences

1986

Date & Time

Tue Apr 04 21:27:36 2006 UTC (Search Time: 0.20 sec.)

Sample ID

Schu4 262

Database

schu2K [..\databases\schu2k]

Taxonomy

-

Mass Range

0 - 30 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)

930.556 1036.617 1307.703 1320.658 1383.740 1385.788
1424.852 1473.859 1487.795 1541.891 1621.839 1638.897
1657.825 1703.315 1707.802 1838.945 1845.866 1851.941
1893.068 1940.956 1993.968 2222.059 2286.131 2369.002
2383.923 2398.987 2501.218 2705.111

Tolerance (mon)

50.00 ppm

Number of Peptides

28

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