

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	2.40	<p>FTTSGH1526 1399353 1398676 [-1 L= 678 r=-1.261] (FTT1358c 1400863 1399322 -) (FTT1357c 1399308 1398676 -)</p> <p>====>gb AAY51447.1 23 kDa protein [uncultured proteobacterium]gb AAY51446.1 23 kDa protein [uncultured proteobacterium] Score = 62.0 bits (149), Expect = 1e-08</p> <p>====>ref YP_170617.1 intracellular growth locus, subunit C [Francisella tularensissubsp. tularensis Schu 4] Score = 409 bits (1050), Expect = e-113</p> <p>====>gb AAP58964.1 IgLC [Francisella tularensis subsp. novicida]Length = 211 Score = 405 bits (1040), Expect = e-112</p> <p>FTTSGH1942 1792697 1792020 [-3 L= 678 r=-1.261] (FTT1713c 1794207 1792666 -) (FTT1712c 1792652 1792020 -)</p> <p>====>gb AAY51447.1 23 kDa protein [uncultured proteobacterium]gb AAY51446.1 23 kDa protein [uncultured proteobacterium] Score = 62.0 bits (149), Expect = 1e-08</p> <p>====>ref YP_170617.1 intracellular growth locus, subunit C [Francisella tularensissubsp. tularensis Schu 4] Score = 409 bits (1050), Expect = e-113</p> <p>====>gb AAP58964.1 IgLC [Francisella tularensis subsp. novicida]Length = 211 Score = 405 bits (1040), Expect = e-112</p>	36	8.7	24.26	
-	-	-	<p>FTTSGH1085 984281 985027 [+2 L= 747 r=-1.204] (FTT0972 984281 985027 +)</p> <p>====>ref ZP_00316715.1 COG0396: ABC-type transport system involved in Fe-S clusterassembly, ATPase component [Microbulbifer degradans Score = 337 bits (863), Expect = 3e-91</p> <p>====>ref YP_169961.1 ABC transporter, ATP-binding protein [Francisella tularensis subsp.tularensis Schu 4] Score = 484 bits (1247), Expect = e-136</p>	6	5.8	27.43	
3	1.1e-019	-	<p>FTTSGH1340 1202016 1202486 [+3 L= 471 r=-1.232] (FTT1186 1202016 1202486 +)</p>	15	10.2	17.94	

			=====>ref YP_047438.1 ssrA-binding protein (Small protein B) [Acinetobacter sp. ADP1]emb CAG69616.1 ssrA-binding protein (Small protein B) [Acinetobacter sp. ADP1] Score = 188 bits (477), Expect = 5e-47=====>ref YP_170148.1 SsrA (tmRNA)-binding protein [Francisella tularensis subsp.tularensis Schu 4] Score = 319 bits (817), Expect = 2e-86				
4	8.8e-020	-	FTTSGH0346 333070 333513 [+1 L= 444 r=-1.242] (FTT0319 333070 333513 +) =====>ref ZP_00281220.1 COG0756: dUTPase [Burkholderia fungorum LB400]Length = 148 Score = 181 bits (458), Expect = 8e-45=====>ref YP_169368.1 dUTP pyrophosphatase (Deoxyuridine 5'-triphosphatenucleotidohydrolase) [Francisella tularensis subsp. Score = 291 bits (745), Expect = 4e-78	29	5.4	15.92	
5	6.3e-020	-	FTTSGH0919 845068 844466 [-2 L= 603 r=-1.246] (FTT0828 845068 844475 -) =====>ref ZP_00168540.2 COG0436: Aspartate/tyrosine/aromatic aminotransferase [Ralstoniaeutropha JMP134] Score = 217 bits (552), Expect = 2e-55	16	5.2	23.02	
6	3.6e-020	-	FTTSGH0861 793422 793673 [+3 L= 252 r=-1.239] (FTT0773 793422 793673 +) =====>ref YP_069008.1 50S ribosomal protein L27 [Yersinia pseudotuberculosis IP 32953]ref NP_668010.1 50S ribosomal subunit protein L27 [Yersinia pestis KIM] Score = 133 bits (334), Expect = 2e-30=====>ref YP_169781.1 50S ribosomal protein L27 [Francisella tularensis subsp. tularensisSchu 4] Score = 176 bits (447), Expect = 1e-43	26	10.3	9.05	
7	2.6e-020	-	FTTSGH1867 1713885 1713244 [-1 L= 642 r=-1.259] (FTT1648c 1713885 1713244 -) =====>ref YP_192625.1 Orotidine 5'-phosphate decarboxylase [Gluconobacter oxydans 621H]gb AAW61969.1 Orotidine 5'-phosphate decarboxylase [Gluconobacter oxydans 621H] Score = 91.3 bits (225), Expect = 2e-17=====>ref YP_170557.1 Orotidine 5'-phosphate decarboxylase [Francisella tularensis subsp.tularensis Schu 4] Score = 426 bits (1096), Expect = e-118	10	6.2	23.82	
8	2.2e-020	-	FTTSGH1667 1530857 1530108 [-3 L= 750 r=-1.213] (FTT1478c 1530857 1530108 -) =====>gb AAO90028.1	10	5.9	28.17	

			3-deoxy-D-manno-octulosonate cytidyltransferase [Coxiellaburnetii RSA 493] Score = 250 bits (638), Expect = 3e-65====>ref YP_170414.1				
			3-deoxy-D-manno-octulosonate cytidyltransferase [Francisellatularensis subsp. tularensis Schu 4] Score = 485 bits (1249), Expect = e-136				
			FTTSGH1322 1188175 1187501 [-2 L= 675 r=-1.225] (FTT1173c 1188175 1187498 -) ====>gb AAN33167.1 putative type I specificity subunit HsdS [Campylobacter jejuni]gb AAN33159.1 putative type I specificity subunit HsdS [Campylobacter jejuni] Score = 102 bits (255), Expect = 7e-21				
9	1.9e-020	-		13	9.2	25.86	
			FTTSGH0560 535846 536433 [+1 L= 588 r=-1.195] (FTT0514 535837 536436 +) ====>ref NP_949656.1 L-lactate dehydrogenase [Rhodopseudomonas palustris CGA009]emb CAE29761.1				
10	1.2e-020	-	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	12	9.4	21.11	

NOTE:

1. To search again using [unmatched masses](#), click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id 20060404163001-1E00-192168001107

Sequences 1984

Date & Time Tue Apr 04 21:30:01 2006 UTC (Search Time: 0.17 sec.)

Sample ID Schu4 263

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) 803.514 1115.593 1132.601 1306.733 1330.710 1337.709
1354.738 1366.718 1419.114 1434.807 1475.761 1662.915
1670.469 1713.028 1724.894 1740.872 1834.899 1994.007
2444.278 2472.269 2800.474

Tolerance (mon) 50.00 ppm

Number of 21
Peptides

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