

Search Info My Search

please fill in the fields bellow: ▼

Sample:

DB: ▼

Taxonomy: ▼

Protein Mass: - kDa

Protein pI: -

Expect: <: Show hits

Missed cleaves: ▼

Enzyme: ▼

Mods: ▼

Partial mods. ☐ Oxidize (M)

Tolerance: ☐ Da ☐ % ☒ ppm
average: mono:

Charge state: ☐ M ☒ MH+

Average masses: Mono masses:

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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	1.54	FTTSGH1181 1070076 1069615 [-1 L= 462 r=-1.186] (FTT1060c 1070067 1069615 -) ====>ref NP_253619.1 50S ribosomal protein L9 [Pseudomonas aeruginosa PAO1]gb AAG08317.1 50S ribosomal protein L9 [Pseudomonas aeruginosa PAO1] Score = 157 bits (396), Expect = 1e-37====>ref YP_170041.1 50S ribosomal protein L9 [Francisella tularensis subsp. tularensisSchu 4] Score = 287 bits (734), Expect = 8e-77	36	5.6	16.38	
2	1.0e-004	0.23	FTTSGH1393 1252948 1254090 [+1 L=1143 r=-1.227] (FTT1234 1252948 1254090 +) ====>ref YP_222152.1 choloylglycine hydrolase family protein [Brucella abortus biovar 1str. 9-941] Score = 166 bits (420), Expect = 1e-39====>ref YP_170192.1 choloylglycine hydrolase family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 765 bits (1976), Expect = 0.0	13	8.9	42.52	
3	5.2e-007	-	FTTSGH1220 1097865 1095853 [-1 L=2013 r=-1.237] (FTT1087c 1097865 1095853 -) ====>gb AAU37020.1 UvrD protein [Mannheimia succiniciproducens MBEL55E]ref YP_087605.1 UvrD protein [Mannheimia succiniciproducens MBEL55E] Score = 622 bits (1603), Expect = e-176====>ref YP_170066.1 ATP-dependent DNA helicase [Francisella tularensis subsp. tularensisSchu 4] Score = 1326 bits (3431), Expect = 0.0	3	6.2	78.20	
4	2.8e-007	-	FTTSGH2015 1860351 1857775 [-1 L=2577 r=-1.240] (FTT1769c 1860351 1857775 -) ====>ref YP_127052.1 endopeptidase Clp ATP-binding chain B (ClpB) [Legionella pneumophilastr. Lens] Score = 1098 bits (2841), Expect = 0.0====>ref YP_170660.1 ClpB protein [Francisella tularensis subsp. tularensis Schu 4]emb CAG46402.1 ClpB protein [Francisella tularensis subsp. tularensis SCHU S4] Score = 1655 bits (4285), Expect = 0.0	4	5.5	95.91	

			FTTSGH1781 1640746 1641828 [+1 L=1083 r=-1.220] (FTT1577 1640746 1641828 +) =====>ref YP_204773.1 carbohydrate binding domain protein [Vibrio fischeri ES114]gb AAW85885.1 carbohydrate binding domain protein [Vibrio fischeri ES114] Score = 54.7 bits (130), Expect = 5e-06=====>ref YP_170499.1 hypothetical protein FTT1577 [Francisella tularensis subsp.tularensis Schu 4] Score = 764 bits (1973), Expect = 0.0				
5	2.3e-007	-		9	5.1	41.25	
			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				
6	2.2e-007	-		22	9.5	13.51	
			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				
7	1.9e-007	-		15	6.1	25.97	
			FTTSGH0194 193789 194463 [+1 L= 675 r=-1.245] (FTT0179 193789 194463 +) =====>ref YP_126025.1 hypothetical protein lpl0663 [Legionella pneumophila str. Lens]emb CAH14897.1 hypothetical protein [Legionella pneumophila str. Lens] Score = 65.9 bits (159), Expect = 1e-09				
8	1.5e-007	-		12	9.1	25.99	
			FTTSGH1078 978100 977198 [-2 L= 903 r=-1.207] (FTT0965 978100 977198 -) =====>ref XP_307366.2 ENSANGP00000001972 [Anopheles gambiae str. PEST]gb EAA03109.2 ENSANGP00000001972 [Anopheles gambiae str. PEST] Score = 219 bits (559), Expect = 7e-56=====>ref YP_169955.1 conserved hypothetical membrane protein [Francisella tularensissubsp. tularensis Schu 4] Score = 566 bits (1459), Expect = e-160				
9	9.1e-008	-		11	10.1	31.65	
			FTTSGH1058 961036 959975 [-2 L=1062 r=-1.246] (FTT0947 960009 959497 -) (FTT0948 961036 959975 -) =====>emb CAC45719.1 PUTATIVE OXIDOREDUCTASE PROTEIN [Sinorhizobium				
10	9.1e-008	-		8	7.8	40.77	

meliloti]ref|NP_385246.1| PUTATIVE
 OXIDOREDUCTASE PROTEIN [Sinorhizobium
 meliloti 1021] Score = 328 bits (840),
 Expect = 2e-88====>ref|YP_169940.1|
 Aldo/keto reductase [Francisella tularensis
 subsp. tularensis Schu 4]emb|CAG45581.1|
 Aldo/keto reductase [Francisella tularensis
 subsp. tularensis SCHU Score = 729 bits
 (1882), Expect = 0.0

NOTE:

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

Input Summary

Search id 20060404123109-1928-192168001107
Sequences 1982
Date & Time Tue Apr 04 17:31:10 2006 UTC (Search Time: 0.27 sec.)
Sample ID Schu4 235
Database schu2K [..\databases\schu2k]
Taxonomy -
Mass Range 0 - 150 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) 935.478 962.444 1109.620 1140.661 1158.685 1302.768 1323.717
 1340.757 1357.777 1424.789 1431.857 1434.802 1493.779
 1621.954 1638.911 1674.971 1838.957 1940.935 1950.976
 1994.033 2013.168 2270.287 2501.236
Tolerance (mon) 50.00 ppm
Number of 23
Peptides

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