

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	1.31	<p>FTTSGH1924 1763981 1764265 [+2 L= 285 r=-1.205] (FTT1695 1763981 1764265 +) =====>ref NP_954379.1 chaperonin, 10 kDa [Geobacter sulfurreducens PCA]gb AAR36729.1 chaperonin, 10 kDa [Geobacter sulfurreducens PCA] Score = 130 bits (328), Expect = 1e-29=====>ref YP_170600.1 Chaperonin protein, groES [Francisella tularensis subsp. tularensisSchu 4] Score = 186 bits (471), Expect = 3e-46=====>emb CAA67359.1 groES [Francisella tularensis]sp P94797 CH10_FRATU 10 kDa chaperonin (Protein Cpn10) (groES protein) Score = 184 bits (468), Expect = 6e-46</p> <p>FTTSGH1506 1368817 1368440 [-2 L= 378 r=-1.214] (FTT1338 1368817 1368440 -) =====>ref YP_254429.1 translation initiation inhibitor [Staphylococcus haemolyticusJCSC1435] Score = 145 bits (365), Expect = 5e-34=====>ref YP_170290.1 translation initiation inhibitor [Francisella tularensis subsp.tularensis Schu 4] Score = 246 bits (629), Expect = 1e-64</p> <p>FTTSGH1447 1301423 1301557 [+2 L= 135 r=-1.168] [OlapWith _1483 L=38 S=61] [DelayedBy _1483 L=108] (FTT1282 1301315 1301557 +) =====>ref YP_170238.1 hypothetical protein FTT1282 [Francisella tularensis subsp.tularensis Schu 4] Score = 93.2 bits (230), Expect = 2e-18</p> <p>FTTSGH0576 549173 549547 [+2 L= 375 r=-1.224] (FTT0528 549173 549547 +) =====>ref YP_169559.1 hypothetical protein FTT0528 [Francisella tularensis subsp.tularensis Schu 4] Score = 256 bits (655), Expect = 1e-67</p> <p>FTTSGH0481 460514 460693 [+2 L= 180 r=-1.200] (FTT0445 460499 460696 +) =====>emb CAD78259.1 ABC transporter ATP-binding protein uup-1 [Rhodopirellula balticaSH 1] Score = 50.1 bits (118), Expect = 2e-05</p>	28	5.5	10.23	
2	7.7e-005	-		25	5.5	13.73	
3	4.4e-005	-		20	10.1	5.51	
4	1.3e-005	-		15	8.7	14.33	
5	2.4e-007	-		17	4.4	7.21	

6	2.3e-007	-	FTTSGH1062 963421 963146 [-2 L= 276 r=-1.257] (FTT0950 963385 963149 -) =====>Hypothetical ORF FTTSGH1062	20	9.2	10.02	
7	1.7e-007	-	FTTSGH0602 569775 570107 [+3 L= 333 r=-1.239] (FTT0551 569775 570080 +) =====>ref YP_095379.1 L-lysine dehydrogenase [Legionella pneumophila subsp. pneumophilastr. Philadelphia 1] Score = 77.0 bits (188), Expect = 2e-13	13	5.1	12.67	
8	1.4e-007	-	FTTSGH0790 737241 737498 [+3 L= 258 r=-1.224] (FTT0717 737241 737483 +) =====>emb CAE10530.1 FORMYLTETRAHYDROFOLATE DEFORMYLASE [Wolinella succinogenes]ref NP_907630.1 FORMYLTETRAHYDROFOLATE DEFORMYLASE [Wolinella succinogenes DSM Score = 80.5 bits (197), Expect = 1e-14	16	9.0	10.13	
9	1.4e-007	-	FTTSGH1123 1019568 1019428 [-1 L= 141 r=-1.248] [ShadowedBy _1153] (None identical in .gff)=====>ref YP_169992.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 94.7 bits (234), Expect = 7e-19	28	9.8	5.20	
10	1.3e-007	-	FTTSGH0933 853737 853543 [-1 L= 195 r=-1.249] [ShadowedBy _960] (None identical in .gff)=====>ref YP_169844.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 124 bits (312), Expect = 7e-28	15	10.2	7.47	

NOTE:

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

Input Summary

Search id 20060330160314-1D10-192168001107

Sequences 2059

Date & Time Thu Mar 30 22:03:15 2006 UTC (Search Time: 0.06 sec.)

Sample ID Schu4 188

Database schu2K [..\databases\schu2k]

Taxonomy -

Mass Range 0 - 15 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)	1142.669	1158.679	1174.681	1208.619	1288.066	1337.819
	1373.929	1395.810	1417.895	1419.417	1470.057	1486.922
	1510.910	1523.190	1618.999	1634.887	1666.780	1701.677
	1702.347	1800.044	1816.724	1833.554	1945.999	2129.707
	2168.083	2184.117	2528.295	2538.669	2555.418	

Tolerance (mon) 70.00 ppm

Number of 29
Peptides

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