


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	2.35	<p>FTTSGH1433 1292668 1290743 [-2 L=1926 r=-1.202] (FTT1269c 1292668 1290743 -) =====>sp P48205 DNAK_FRATU Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDaprotein) (HSP70) Score = 1232 bits (3188), Expect = 0.0=====>ref YP_170225.1 Chaperone protein dnaK (heat shock protein family 70 protein)[Francisella tularensis subsp. tularensis Schu 4] Score = 1239 bits (3207), Expect = 0.0</p>	22	4.9	69.24	
2	3.4e-015	-	<p>FTTSGH1265 1134846 1136315 [+3 L=1470 r=-1.264] (FTT1125 1134846 1136315 +) =====>ref NP_804128.1 putative lipoprotein precursor [Salmonella enterica subsp. entericaserovar Typhi Ty2] Score = 244 bits (623), Expect = 5e-63=====>ref YP_170098.1 D-methionine binding transport protein, ABC transporter, membrane andperiplasmic protein [Francisella tularensis subsp. Score = 954 bits (2465), Expect = 0.0</p>	10	8.8	53.33	
3	1.2e-015	-	<p>FTTSGH1014 916820 917752 [+2 L= 933 r=-1.240] (FTT0908 916841 917752 +) =====>ref ZP_00046630.1 COG1475: Predicted transcriptional regulators [Lactobacillusgasseri] Score = 124 bits (310), Expect = 5e-27=====>ref YP_169905.1 chromosome partition protein B [Francisella tularensis subsp.tularensis Schu 4] Score = 591 bits (1524), Expect = e-168</p>	10	9.3	35.30	
4	8.3e-016	-	<p>FTTSGH1142 1035878 1035150 [-3 L= 729 r=-1.244] (FTT1024c 1035878 1035150 -) =====>ref YP_203771.1 ABC transporter ATP-binding protein [Vibrio fischeri ES114]gb AAW84883.1 ABC transporter ATP-binding protein [Vibrio fischeri ES114] Score = 342 bits (876), Expect = 8e-93=====>ref YP_170009.1 ABC transporter, ATP-binding protein [Francisella tularensis subsp.tularensis Schu 4] Score = 473 bits (1217), Expect = e-132</p>	21	8.9	27.14	
5	9.4e-017	-	<p>FTTSGH1054 956432 958192 [+2 L=1761 r=-1.224] (FTT0945 956432 958192 +) =====>gb EAM24719.1 </p>	7	6.8	68.39	

			Para-aminobenzoate synthase, component I [Chromohalobacter salexigensDSM 3043] Score = 335 bits (858), Expect = 4e-90====>ref YP_169938.1 chorismate binding family protein [Francisella tularensis subsp.tularensis Schu 4] Score = 1170 bits (3027), Expect = 0.0				
6	2.3e-017	-	FTTSGH0370 346535 347857 [+2 L=1323 r=-1.237] (FTT0345 346535 347857 +) ====>ref NP_931868.1 Preprotein translocase SecY subunit [Photorhabdus luminescens subsp.laumondii TTO1] Score = 516 bits (1328), Expect = e-145====>ref YP_169394.1 preprotein translocase, subunit Y, membrane protein [Francisellatularensis subsp. tularensis Schu 4] Score = 847 bits (2188), Expect = 0.0	9	9.7	48.45	●
7	2.3e-017	-	FTTSGH1110 1004724 1005953 [+3 L=1230 r=-1.207] (FTT0995 1004724 1005953 +) ====>ref ZP_00264965.1 COG0477: Permeases of the major facilitator superfamily [Pseudomonasfluorescens PfO-1] Score = 243 bits (619), Expect = 1e-62====>ref YP_169983.1 major facilitator superfamily (MFS) transport protein [Francisellatularensis subsp. tularensis Schu 4] Score = 791 bits (2043), Expect = 0.0	6	9.5	45.02	●
8	2.1e-017	-	FTTSGH1873 1719773 1718907 [-3 L= 867 r=-1.233] (FTT1652 1719773 1718907 -) ====>ref YP_124750.1 hypothetical protein lpp2445 [Legionella pneumophila str. Paris]emb CAH13598.1 hypothetical protein [Legionella pneumophila str. Paris] Score = 135 bits (341), Expect = 1e-30====>ref YP_170560.1 transcriptional regulator, LysR family [Francisella tularensissubsp. tularensis Schu 4] Score = 572 bits (1474), Expect = e-162	8	7.0	32.80	●
9	1.3e-017	-	FTTSGH0723 674250 674906 [+3 L= 657 r=-1.206] (FTT0654 674250 674906 +) ====>gb AAO07415.1 Uncharacterized protein [Vibrio vulnificus CMCP6]ref NP_762425.1 hypothetical protein VV20462 [Vibrio vulnificus CMCP6] Score = 207 bits (526), Expect = 3e-52====>ref YP_169672.1 DJ-1/Pfpl family protein [Francisella tularensis subsp. tularensisSchu 4] Score = 431 bits (1109), Expect = e-120	12	4.5	23.67	●

10 1.0e-017 - [FTTSGH1597](#) 1466658 1467557 [+3 L= 900
 r=-1.196] (FTT1415 1466658 1467557 +)
 =====>ref|YP_170358.1| hypothetical protein FTT1415 [Francisella tularensis
 subsp.tularensis Schu 4] Score = 593 bits
 (1528), Expect = e-168

10 7.1 33.71 

NOTE:

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

Input Summary

Search id 20060330141902-1840-192168001107
Sequences 1983
Date & Time Thu Mar 30 20:19:02 2006 UTC (Search Time: 0.33 sec.)
Sample ID Schu4 158
Database schu2K [..\databases\schu2k]
Taxonomy -
Mass Range 0 - 80 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) 958.511 1024.526 1211.648 1227.636 1249.661 1259.916
 1311.693 1313.696 1335.686 1456.833 1487.822 1510.767
 1539.849 1576.772 1593.772 1609.817 1654.849 1666.903
 1702.512 1749.924 1782.997 2094.963 2330.107 2526.228
 2885.315
Tolerance (mon) 100.00 ppm
Number of 25
Peptides

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