


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	2.20	<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>	15	4.9	69.24	
2	4.0e-008	-	<p>FTTSGH1110 1004724 1005953 [+3 L=1230 r=-1.207] (FTT0995 1004724 1005953 +) =====>ref ZP_00264965.1 COG0477: Permeases of the major facilitator superfamily [Pseudomonas fluorescens PfO-1] Score = 243 bits (619), Expect = 1e-62 =====>ref YP_169983.1 major facilitator superfamily (MFS) transport protein [Francisella tularensis subsp. tularensis Schu 4] Score = 791 bits (2043), Expect = 0.0</p>	6	9.5	45.02	
3	2.4e-009	-	<p>FTTSGH1054 956432 958192 [+2 L=1761 r=-1.224] (FTT0945 956432 958192 +) =====>gb EAM24719.1 Para-aminobenzoate synthase, component I [Chromohalobacter salexigens DSM 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</p>	6	6.8	68.39	
4	3.9e-010	-	<p>FTTSGH2037 1874713 1875234 [+1 L= 522 r=-1.231] (FTT1786 1874749 1875234 +) (FTT1786 1874256 1874747 +) =====>emb CAG37026.1 conserved hypothetical protein [Desulfotalea psychrophila LSv54]ref YP_066033.1 hypothetical protein DP2297 [Desulfotalea psychrophila LSv54] Score = 154 bits (390), Expect = 9e-37</p>	16	8.6	19.88	
5	1.9e-010	-	<p>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</p>	8	7.0	32.80	

		[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				
		FTTSGH0167 170083 170958 [+1 L= 876 r=-1.257] (FTT0154 170083 170958 +) =====>ref NP_716579.1				
		integrase/recombinase XerD [Shewanella oneidensis MR-1]gb AAN54024.1				
6	1.7e-010	- integrase/recombinase XerD [Shewanella oneidensis MR-1] Score = 315 bits (807), Expect = 1e-84====>ref YP_169220.1	10	9.4	33.33	🔴
		Integrase/recombinase [Francisella tularensis subsp. tularensisSchu 4] Score = 580 bits (1494), Expect = e-164				
		FTTSGH0818 757925 758569 [+2 L= 645 r=-1.202] (FTT0736 757925 758569 +) =====>emb CAG35120.1 hypothetical protein [Desulfotalea psychrophila LSv54]ref YP_064127.1 hypothetical protein DP0391 [Desulfotalea psychrophila LSv54]				
7	1.5e-010	- DP0391 [Desulfotalea psychrophila LSv54] Score = 69.7 bits (169), Expect = 6e-11====>ref YP_169747.1 hypothetical protein FTT0736 [Francisella tularensis subsp.tularensis Schu 4] Score = 433 bits (1114), Expect = e-120	8	9.4	24.01	🔴
		FTTSGH1631 1492812 1494071 [+3 L=1260 r=-1.281] (FTT1446 1492812 1494071 +) =====>ref YP_156742.1 Transcription termination factor rho [Idiomarina loihiensis L2TR]gb AAV83193.1 Transcription				
8	7.1e-011	- termination factor rho [Idiomarina loihiensis L2TR] Score = 623 bits (1607), Expect = e-177====>ref YP_170384.1 transcription termination factor Rho [Francisella tularensis subsp.tularensis Schu 4] Score = 815 bits (2106), Expect = 0.0	9	5.8	47.11	🔴
		FTTSGH0934 853523 854431 [+2 L= 909 r=-1.226] [Contains _959] (FTT0839 853523 854431 +) ====>ref XP_656020.1				
		hypothetical protein 19.t00007 [Entamoeba histolytica HM-1:IMSS]gb EAL50634.1				
9	6.5e-011	- hypothetical protein 19.t00007 [Entamoeba histolytica HM-1:IMSS] Score = 109 bits (272), Expect = 1e-22====>ref YP_169844.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 578 bits (1490), Expect = e-164	8	9.7	34.55	🔴

[FTTSGH0523](#) 504863 506662 [+2 L=1800
 r=-1.241] (FTT0486 504863 506662 +)
 =====>ref|ZP_00315672.1| COG0323:
 DNA mismatch repair enzyme (predicted
 ATPase) [Microbulbiferdegradans 2-40] Score **5** 6.4 68.04 
 = 523 bits (1346), Expect =
 e-146=====>ref|YP_169524.1| DNA
 mismatch repair protein [Francisella
 tularensis subsp. tularensisSchu 4] Score =
 1183 bits (3061), Expect = 0.0

NOTE:

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

Input Summary

Search id 20060404124128-1D40-192168001107
Sequences 1983
Date & Time Tue Apr 04 17:41:28 2006 UTC (Search Time: 0.20 sec.)
Sample ID Schu4 238
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) 958.537 1140.746 1211.688 1313.755 1470.888 1487.859
 1510.833 1619.894 1749.975 1800.947 1835.298 2386.848
 2526.218
Tolerance (mon) 100.00 ppm
Number of 13
Peptides

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