

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	9.9e-001	0.75	FTTSGH2047 1882631 1883056 [+2 L= 426 r=-1.197] (FTT1794 1882631 1883056 +) ====>ref YP_247020.1 Small heat shock protein [Rickettsia felis URRWXCal2]gb AAY61855.1 Small heat shock protein [Rickettsia felis URRWXCal2] Score = 116 bits (291), Expect = 2e-25====>ref YP_170678.1 heat shock protein [Francisella tularensis subsp. tularensis Schu4] Score = 287 bits (734), Expect = 8e-77	20	5.6	16.69	
2	2.3e-003	-	FTTSGH0094 93225 92773 [-1 L= 453 r=-1.231] (FTT0089 93297 92773 -) ====>ref ZP_00376095.1 putative transmembrane protein [Erythrobacter litoralis HTCC2594]gb EAL75573.1 putative transmembrane protein [Erythrobacter litoralis HTCC2594] Score = 86.3 bits (212), Expect = 3e-16	15	6.0	17.46	
3	1.8e-003	-	FTTSGH0578 550618 550187 [-2 L= 432 r=-1.251] (FTT0529c 550618 550238 -) (FTT0529c 550238 549570 -) ====>gb AAU37742.1 DinP protein [Mannheimia succiniciproducens MBEL55E]ref YP_088327.1 DinP protein [Mannheimia succiniciproducens MBEL55E] Score = 153 bits (386), Expect = 2e-36	19	9.2	16.20	
4	1.5e-003	-	FTTSGH1001 905381 905869 [+2 L= 489 r=-1.243] (FTT0896 905381 905869 +) ====>ref NP_254113.1 phosphoribosylaminoimidazole carboxylase, catalytic subunit[Pseudomonas aeruginosa PAO1] Score = 218 bits (556), Expect = 4e-56====>ref YP_169893.1 phosphoribosylaminoimidazole carboxylase,catalytic subunit[Francisella tularensis subsp. tularensis Schu 4] Score = 323 bits (828), Expect = 1e-87	6	5.8	17.18	
5	4.8e-004	-	FTTSGH1688 1551127 1550627 [-2 L= 501 r=-1.227] (FTT1497 1551127 1550627 -) ====>ref YP_170432.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 318 bits (814), Expect = 5e-86====>ref YP_170537.1 hypothetical	10	5.2	18.61	

			protein FTT1624c [Francisella tularensis subsp.tularensis Schu 4] Score = 55.8 bits (133), Expect = 5e-07				
			FTTSGH0492 475129 474839 [-2 L= 291 r=-1.212] (FTT0456 475129 474839 -) =====>ref YP_095944.1 hypothetical protein lpg1927 [Legionella pneumophila subsp.pneumophila str. Philadelphia 1] Score = 112 bits (279), Expect = 5e-24=====>ref YP_169494.1 UPF0269 family protein [Francisella tularensis subsp. tularensisSchu 4] Score = 205 bits (521), Expect = 4e-52				
6	8.5e-005	-		7	7.8	11.77	
			FTTSGH1091 988429 988575 [+1 L= 147 r=-1.276] (None identical in .gff) =====>Hypothetical ORF FTTSGH1091	16	4.2	5.67	
			FTTSGH1530 1405270 1405178 [-2 L= 93 r=-1.236] (FTT1361 1405306 1405178 -) =====>Hypothetical ORF FTTSGH1530	26	9.7	3.35	
			FTTSGH1946 1798614 1798522 [-1 L= 93 r=-1.236] (FTT1716 1798650 1798522 -) =====>Hypothetical ORF FTTSGH1946	26	9.7	3.35	
			FTTSGH0218 218746 218952 [+1 L= 207 r=-1.257] (FTT0201 218746 218919 +) =====>ref YP_204026.1 serine transporter [Vibrio fischeri ES114]gb AAW85138.1 serine transporter [Vibrio fischeri ES114] Score = 73.6 bits (179), Expect = 2e-12	12	9.9	7.46	
10	2.5e-006	-					

NOTE:

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

Input Summary**Search id** 20060404164606-1D0C-192168001107**Sequences** 2058**Date & Time** Tue Apr 04 21:46:06 2006 UTC (Search Time: 0.11 sec.)**Sample ID** Schu4 268 [Pass: 1]**Database** SCHU2K [..\databases\schu2k]**Taxonomy** -**Mass Range** 0 - 20 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) 855.385 882.529 910.458 962.442 978.450 1050.569 1086.586
1305.694 1352.695 1535.915 1674.937 1784.831 1827.909
1835.608 2041.137 2252.243 2255.512 2286.298 2298.280
2807.302
Tolerance (mon) 40.00 ppm
Number of 20
Peptides

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