

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	8.3e-001	1.10	<p>FTTSGH0402 373851 373432 [-1 L= 420 r=-1.195] (FTT0373c 373851 373432 -) =====>gb AAO90766.1 nucleoside diphosphate kinase [Coxiella burnetii RSA 493]ref NP_820252.1 nucleoside diphosphate kinase [Coxiella burnetii RSA 493] Score = 214 bits (546), Expect = 5e-55=====>ref YP_169420.1 nucleoside diphosphate kinase [Francisella tularensis subsp.tularensis Schu 4] Score = 273 bits (699), Expect = 9e-73</p> <p>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 protein FTT1624c [Francisella tularensis subsp.tularensis Schu 4] Score = 55.8 bits (133), Expect = 5e-07</p> <p>FTTSGH1993 1839942 1840415 [+3 L= 474 r=-1.213] (FTT1752 1839942 1840415 +) =====>ref ZP_00134369.1 COG0629: Single-stranded DNA-binding protein [Actinobacilluspleuropneumoniae serovar 1 str. 4074] Score = 137 bits (344), Expect = 1e-31=====>ref YP_170646.1 Single-strand binding protein [Francisella tularensis subsp.tularensis Schu 4] Score = 327 bits (839), Expect = 6e-89</p> <p>FTTSGH1091 988429 988575 [+1 L= 147 r=-1.276] (None identical in .gff) =====>Hypothetical ORF FTTSGH1091</p> <p>FTTSGH0940 858178 858354 [+1 L= 177 r=-1.246] (FTT0844 858178 858900 +) =====>Hypothetical ORF FTTSGH940</p> <p>FTTSGH0464 444629 444402 [-3 L= 228 r=-1.223] (FTT0429c 444629 444399 -) =====>gb AAN47234.1 beta-galactosidase I [Leptospira interrogans serovar lai str.56601] Score = 80.1 bits (196), Expect = 2e-14</p>	34	5.9	15.51	
2	1.7e-001	0.87		15	5.2	18.61	
3	2.4e-004	-		11	5.6	17.51	
4	6.6e-007	-		16	4.2	5.67	
5	3.6e-007	-		36	5.6	6.37	
6	3.4e-007	-		16	4.5	8.99	

7	3.3e-007	-	FTTSGH1946 1798614 1798522 [-1 L= 93 r=-1.236] (FTT1716 1798650 1798522 -) =====>Hypothetical ORF FTTSGH1946	26	9.7	3.35	
8	3.3e-007	-	FTTSGH1530 1405270 1405178 [-2 L= 93 r=-1.236] (FTT1361 1405306 1405178 -) =====>Hypothetical ORF FTTSGH1530	26	9.7	3.35	
9	3.0e-007	-	FTTSGH1246 1118948 1118502 [-3 L= 447 r=-1.266] (FTT1107c 1118948 1118538 -) (FTT1107c 1118538 1116997 -) =====>emb CAE09180.1 PUTATIVE CHOLINE TRANSPORTER [Wolinella succinogenes]ref NP_906280.1 PUTATIVE CHOLINE TRANSPORTER [Wolinella succinogenes DSM 1740] Score = 136 bits (342), Expect = 2e-31	9	5.5	16.68	
10	2.9e-007	-	FTTSGH0621 584188 583796 [-2 L= 393 r=-1.204] [DelayedBy _642 L=24] (FTT0567 584224 583793 -) =====>ref YP_095562.1 peptide transport protein, POT family [Legionella pneumophilasubsp. pneumophila str. Philadelphia 1] Score = 65.1 bits (157), Expect = 6e-10=====>ref YP_169702.1 Proton-dependent oligopeptide transport (POT) family protein[Francisella tularensis subsp. tularensis Schu 4] Score = 61.2 bits (147), Expect = 9e-09=====>ref YP_169991.1 Proton-dependent oligopeptide transporter (POT) family protein[Francisella tularensis subsp. tularensis Schu 4] Score = 51.2 bits (121), Expect = 9e-06	9	8.8	14.16	

NOTE:

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

Input Summary**Search id** 20060404164316-1B98-192168001107**Sequences** 2058**Date & Time** Tue Apr 04 21:43:16 2006 UTC (Search Time: 0.08 sec.)**Sample ID** Schu4 267 [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) 848.475 882.526 962.427 1006.545 1050.585 1224.654 1313.784
1509.834 1535.913 1577.731 1703.587 1729.816 1732.265
2001.997 2013.144 2299.145 2667.097 2679.152 2689.195
2721.199

Tolerance (mon) 30.00 ppm

Number of 20
Peptides

Profound is provided under exclusive licence by Genomic Solutions Ltd.