

ProFound - Search Result Summary

Version 2002.03.01

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Protein Candidates

Rank	Probability	Est'd Z	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	9.6e-001	1.13	<p>FTTSGH1302 1168674 1168147 [-1 L= 528 r=-1.212] (FTT1155c 1168674 1168147 -) ==>ref YP_094966.1 shikimate kinase [Legionella pneumophila subsp. pneumophila str.Philadelphia 1] Score = 206 bits (525), Expect = 2e-52==>ref YP_170122.1 shikimate kinase I [Francisella tularensis subsp. tularensis Schu4] Score = 338 bits (868), Expect = 3e-92</p> <p>FTTSGH0066 61794 62315 [+3 L= 522 r=-1.226] (FTT0061 61794 62315 +) ==>ref YP_044976.1 membrane-bound ATP synthase , F1 sector, delta-subunit[Acinetobacter sp. ADP1] Score = 125 bits (314), Expect = 6e-28==>ref YP_169136.1 ATP synthase delta chain [Francisella tularensis subsp. tularensisSchu 4] Score = 335 bits (858), Expect = 5e-91</p> <p>FTTSGH1786 1646966 1646526 [-3 L= 441 r=-1.246] (FTT1582 1647014 1646526 -) ==>ref ZP_00143306.1 TYPE III RESTRICTION-MODIFICATION SYSTEM METHYLATION SUBUNIT[Fusobacterium nucleatum subsp. vincentii ATCC 49256] Score = 90.5 bits (223), Expect = 1e-17</p> <p>FTTSGH0758 707088 706540 [-1 L= 549 r=-1.189] (FTT0688c 707088 706540 -) ==>ref YP_114446.1 ATP-dependent protease HslV [Methylococcus capsulatus str. Bath]gb AAU91756.1 ATP-dependent protease HslV [Methylococcus capsulatus str. Bath] Score = 221 bits (564), Expect = 7e-57==>ref YP_169704.1 ATP-dependent protease, proteasome-related peptidase subunit[Francisella tularensis subsp. tularensis Schu 4] Score = 353 bits (906), Expect = 1e-96</p> <p>FTTSGH0225 224989 224510 [-2 L= 480 r=-1.212] (FTT0206 225061 224510 -) ==>ref YP_125044.1 hypothetical protein lpp2739 [Legionella pneumophila str. Paris]emb CAH13892.1 hypothetical protein [Legionella pneumophila str. Paris] Score =</p>	32	5.5	19.72	
2	4.3e-002	0.68		28	5.8	19.18	
3	1.9e-005	-		1	4.8	16.51	
4	7.2e-006	-		13	6.2	19.78	
5	9.4e-007	-		18	9.1	18.41	

162 bits (410), Expect = 3e-39							
6	7.0e-008	-	FTTSGH0502 481750 481935 [+1 L= 186 r=-1.353] [Vote] (FTT0465 481750 481935 +) =====>ref YP_169503.1 hypothetical protein FTT0465 [Francisella tularensis subsp.tularensis Schu 4] Score = 124 bits (311), Expect = 9e-28	27	8.1	6.18	
7	2.2e-008	-	FTTSGH0493 475434 475123 [-1 L= 312 r=-1.278] (FTT0457c 475434 475123 -) =====>gb AAK02485.1 unknown [Pasteurella multocida subsp. multocida str. Pm70]ref NP_245338.1 hypothetical protein PM0401 [Pasteurella multocida subsp. multocida Score = 117 bits (292), Expect = 1e-25=====>ref YP_169495.1 anaerobic sulfite reductase subunit [Francisella tularensis subsp.tularensis Schu 4] Score = 212 bits (540), Expect = 2e-54	13	6.3	11.83	
8	2.2e-008	-	FTTSGH2002 1847287 1847433 [+1 L= 147 r=-1.218] [ShadowedBy _2054] (None identical in .gff) =====>ref YP_170650.1 B-type cytochrome [Francisella tularensis subsp. tularensis Schu 4]emb CAG46391.1 B-type cytochrome [Francisella tularensis subsp. tularensis SCHU Score = 101 bits (251), Expect = 8e-21	37	10.5	5.24	
9	2.1e-008	-	FTTSGH0542 520151 520408 [+2 L= 258 r=-1.230] (FTT0500 520151 520408 +) =====>ref YP_169535.1 hypothetical protein FTT0500 [Francisella tularensis subsp.tularensis Schu 4] Score = 174 bits (440), Expect = 1e-42	12	5.6	9.81	
10	1.8e-008	-	FTTSGH1383 1242217 1241891 [-2 L= 327 r=-1.249] (FTT1225 1242217 1241891 -) =====>ref YP_170183.1 hypothetical protein FTT1225c [Francisella tularensis subsp.tularensis Schu 4] Score = 212 bits (539), Expect = 3e-54	17	5.4	12.59	

NOTE:

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

Input Summary

Search id 20060404163301-1DDC-192168001107

Sequences 2059

Date & Time Tue Apr 04 21:33:01 2006 UTC (Search Time: 0.08 sec.)

Sample ID Schu4 264

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) 815.653 962.459 975.262 1088.630 1185.683 1268.669 1338.848
1399.828 1434.835 1471.177 1562.860 1636.092 1667.991
1690.933 1796.898 1818.886 1824.992 1835.632 2255.257
Tolerance (mon) 40.00 ppm
Number of 19
Peptides

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