

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	1.0e+000	1.07	<p>FTTSGH1740 1603293 1601866 [-1 L=1428 r=-1.216] (FTT1539 1603293 1601866 -) =====>ref ZP_00368662.1 probable periplasmic protein Cj0092 [Campylobacter lari RM2100]gb EAL55107.1 probable periplasmic protein Cj0092 [Campylobacter lari RM2100] Score = 152 bits (385), Expect = 2e-35=====>ref YP_170467.1 hypothetical protein FTT1539c [Francisella tularensis subsp.tularensis Schu 4] Score = 927 bits (2397), Expect = 0.0</p> <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> <p>FTTSGH0089 85720 86193 [+1 L= 474 r=-1.209] (FTT0083 85720 86193 +) =====>ref YP_126399.1 hypothetical protein lpl1042 [Legionella pneumophila str. Lens]emb CAH15277.1 hypothetical protein [Legionella pneumophila str. Lens] Score = 66.6 bits (161), Expect = 2e-10=====>ref YP_169157.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 313 bits (802), Expect = 1e-84</p> <p>FTTSGH0937 856027 856647 [+1 L= 621 r=-1.218] (FTT0842 856027 856647 +) =====>ref NP_670353.1 peptidoglycan-associated lipoprotein [Yersinia pestis KIM]ref NP_992404.1 peptidoglycan-associated lipoprotein Pal [Yersinia pestis biovar Score = 98.6 bits (244), Expect = 1e-19=====>ref YP_169847.1 Peptidoglycan-associated lipoprotein [Francisella tularensis subsp.tularensis Schu 4] Score = 421 bits (1083), Expect = e-117</p>	9	5.8	52.04	
2	3.2e-003	0.25		11	8.9	27.14	
3	7.7e-005	-		16	4.9	17.30	
4	1.4e-005	-		19	5.2	23.24	

5	1.4e-005	-	<p>FTTSGH1751 1610654 1611364 [+2 L= 711 r=-1.251] (FTT1549 1611324 1611776 +) (FTT1547 1610714 1611364 +) =====>gb AAK23408.1 cyclopropane-fatty-acyl-phospholipid synthase [Caulobacter crescentus CB15] Score = 192 bits (487), Expect = 1e-47</p>	13	7.9	27.29	
6	9.4e-006	-	<p>FTTSGH1831 1682071 1682829 [+1 L= 759 r=-1.235] (FTT1618 1682062 1682829 +) =====>ref ZP_00056223.2 COG0477: Permeases of the major facilitator superfamily[Magnetospirillum magnetotacticum MS-1] Score = 103 bits (257), Expect = 5e-21</p>	6	9.8	27.62	
7	2.4e-006	-	<p>FTTSGH0679 635695 634838 [-2 L= 858 r=-1.209] (FTT0615 635695 634838 -) =====>gb AAX87355.1 magnesium and cobalt efflux protein CorC [Haemophilus influenzae 86-028NP] Score = 210 bits (535), Expect = 4e-53=====>ref YP_169636.1 metal ion transporter protein [Francisella tularensis subsp. tularensis Schu 4] Score = 548 bits (1412), Expect = e-155</p>	8	4.8	32.16	
8	9.5e-007	-	<p>FTTSGH0738 685953 687125 [+3 L=1173 r=-1.240] (FTT0669 685953 687125 +) =====>dbj BAC24142.1 MagA protein [Magnetospirillum magnetotacticum]Length = 432 Score = 229 bits (583), Expect = 2e-58=====>ref YP_169686.1 Sodium/hydrogen exchanger family protein [Francisella tularensis subsp. tularensis Schu 4] Score = 734 bits (1896), Expect = 0.0</p>	6	9.1	42.77	
9	4.1e-007	-	<p>FTTSGH1961 1812058 1813386 [+1 L=1329 r=-1.250] (FTT1726 1812058 1813386 +) =====>ref ZP_00581771.1 Peptidase U32 [Shewanella baltica OS155]gb EAN43765.1 Peptidase U32 [Shewanella baltica OS155] Score = 558 bits (1438), Expect = e-157=====>ref YP_170628.1 protease yegQ [Francisella tularensis subsp. tularensis Schu 4]emb CAG46359.1 protease yegQ [Francisella tularensis subsp. tularensis SCHU S4] Score = 897 bits (2317), Expect = 0.0</p>	3	6.4	50.26	
10	3.6e-007	-	<p>FTTSGH0856 791118 791309 [+3 L= 192 r=-1.237] (FTT0770 791118 791684 +) =====>gb AAY82842.1 predicted 3-methyladenine DNA glycosylase [uncultured bacterium MedeBAC46A06] Score = 97.1 bits (240), Expect = 2e-19</p>	39	6.5	7.63	

NOTE:

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

Input Summary

Search id 20060330143627-184C-192168001107
Sequences 2059
Date & Time Thu Mar 30 20:36:27 2006 UTC (Search Time: 0.13 sec.)
Sample ID Schu4 162
Database schu2K [..\databases\schu2k]
Taxonomy -
Mass Range 0 - 55 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) 1093.482 1221.601 1365.847 1564.784 1581.883 1617.964
1639.914 1655.867 2341.658 2396.170 2979.389
Tolerance (mon) 50.00 ppm
Number of 11
Peptides

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