

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	9.5e-001	0.55	<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>	11	5.6	17.51	
2	8.3e-003	-	<p>FTTSGH1088 986733 987059 [+3 L= 327 r=-1.258] (FTT0974 986280 987062 +) ====>dbj BAC74824.1 hypothetical protein [Streptomyces avermitilis MA-4680]ref NP_828289.1 hypothetical protein SAV7113 [Streptomyces avermitilis MA-4680] Score = 73.9 bits (180), Expect = 1e-12</p>	8	5.3	12.26	
3	7.3e-003	-	<p>FTTSGH0725 675747 676280 [+3 L= 534 r=-1.235] (FTT0656 675747 676280 +) ====>ref ZP_00581940.1 Crossover junction endodeoxyribonuclease RuvC [Shewanella balticaOS155] Score = 188 bits (477), Expect = 8e-47====>ref YP_169674.1 holliday junction endodeoxyribonuclease [Francisella tularensissubsp. tularensis Schu 4] Score = 345 bits (886), Expect = 3e-94</p>	7	9.8	19.18	
4	7.1e-003	-	<p>FTTSGH1506 1368817 1368440 [-2 L= 378 r=-1.214] (FTT1338 1368817 1368440 -) ====>ref YP_254429.1 translation initiation inhibitor [Staphylococcus haemolyticusJCSC1435] Score = 145 bits (365), Expect = 5e-34====>ref YP_170290.1 translation initiation inhibitor [Francisella tularensis subsp.tularensis Schu 4] Score = 246 bits (629), Expect = 1e-64</p>	11	5.5	13.73	
5	6.8e-003	-	<p>FTTSGH1446 1301460 1301296 [-1 L= 165 r=-1.193] [LowScoreBy _1484 L=38 S=38] (None identical in .gff) ====>ref YP_170238.1 hypothetical protein FTT1282 [Francisella tularensis subsp.tularensis Schu 4] Score = 90.9 bits (224), Expect = 1e-17</p>	11	10.0	6.36	

6	6.7e-003	-	FTTSGH1981 1831773 1831357 [-1 L= 417 r=-1.225] (FTT1741 1831794 1831354 -) ====>gb AAS73010.1 predicted NAD-dependent formate dehydrogenase [uncultured marinegamma proteobacterium EBAC20E09] Score = 234 bits (597), Expect = 6e-61	6	8.8	15.50	
7	4.9e-003	-	FTTSGH1289 1155426 1155923 [+3 L= 498 r=-1.217] (FTT1144 1155453 1155907 +) ====>ref NP_388300.1 hypothetical protein BSU04190 [Bacillus subtilis subsp. subtilisstr. 168] Score = 128 bits (321), Expect = 8e-29	5	8.4	19.13	
8	4.2e-003	-	FTTSGH0414 385686 386018 [+3 L= 333 r=-1.265] (FTT0383 385686 386018 +) ====>ref YP_169428.1 hypothetical protein FTT0383 [Francisella tularensis subsp.tularensis Schu 4] Score = 231 bits (590), Expect = 4e-60	11	10.5	13.33	

NOTE:

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

Input Summary

Search id 20060404163641-1D6C-192168001107
Sequences 2059
Date & Time Tue Apr 04 21:36:41 2006 UTC (Search Time: 0.05 sec.)
Sample ID Schu4 265
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) 774.518 877.117 899.450 962.490 975.365 1006.549 1209.709
 1339.011 1483.753 1510.823 1636.286 1668.180 1703.785
 1835.822
Tolerance (mon) 20.00 ppm
Number of 14
Peptides

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