

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	2.16	<p>FTTSGH1060 962552 962130 [-3 L= 423 r=-1.188] (FTT0949 962552 962130 -) =====>gb AAO08511.1 Unknown [Vibrio vulnificus CMCP6]ref NP_763521.1 hypothetical protein VV21653 [Vibrio vulnificus CMCP6] Score = 52.0 bits (123), Expect = 6e-06</p>	38	6.6	16.10	
2	1.0e-007	-	<p>FTTSGH1596 1466068 1466547 [+1 L= 480 r=-1.240] (FTT1414 1466068 1466547 +) =====>ref YP_170357.1 hypothetical protein FTT1414 [Francisella tularensis subsp.tularensis Schu 4] Score = 328 bits (842), Expect = 3e-89</p>	10	9.6	18.44	
3	9.0e-009	-	<p>FTTSGH1420 1282524 1282943 [+3 L= 420 r=-1.212] (FTT1260 1282524 1282943 +) =====>ref YP_170218.1 hypothetical lipoprotein [Francisella tularensis subsp. tularensisSchu 4] Score = 289 bits (740), Expect = 2e-77</p>	9	5.8	16.02	
4	3.5e-009	-	<p>FTTSGH1019 920785 921249 [+1 L= 465 r=-1.251] (FTT0913 920785 921249 +) =====>ref YP_169910.1 hypothetical protein FTT0913 [Francisella tularensis subsp.tularensis Schu 4] Score = 313 bits (803), Expect = 8e-85</p>	17	8.6	17.90	
5	3.5e-010	-	<p>FTTSGH0819 758671 758847 [+1 L= 177 r=-1.193] (None identical in .gff) =====>Hypothetical ORF FTTSGH819</p>	24	4.7	6.99	
6	2.4e-010	-	<p>FTTSGH1533 1406455 1406667 [+1 L= 213 r=-1.297] (FTT1362 1406455 1406601 +) (FTT1362 1406603 1407331 +) =====>gb AAT45388.1 unknown [Francisella tularensis subsp. holarctica]Length = 278 Score = 87.0 bits (214), Expect = 2e-16 =====>gb AAT45387.1 unknown [Francisella tularensis subsp. holarctica]Length = 278 Score = 87.0 bits (214), Expect = 2e-16</p>	24	7.9	7.95	
7	2.4e-010	-	<p>FTTSGH1949 1799799 1800011 [+3 L= 213 r=-1.297] (FTT1717 1799947 1800675 +) (FTT1717 1799799 1799945 +) =====>gb AAT45388.1 unknown [Francisella tularensis subsp.</p>	24	7.9	7.95	

			holarctica]Length = 278 Score = 87.0 bits (214), Expect = 2e-16====>gb AAT45387.1 unknown [Francisella tularensis subsp. holarctica]Length = 278 Score = 87.0 bits (214), Expect = 2e-16 FTTSGH0008 7959 8291 [+3 L= 333 r=-1.218] (FTT0008 7959 8252 +) =====>gb AAO77255.1 glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482]ref NP_811061.1 glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] Score = 53.1 bits (126), Expect = 3e-06 FTTSGH0447 427438 427575 [+1 L= 138 r=-1.139] (FTT0415 427438 427575 +) =====>ref ZP_00279281.1 COG0448: ADP-glucose pyrophosphorylase [Burkholderia fungorumLB400] Score = 61.2 bits (147), Expect = 9e-09 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				
8	2.4e-010	-		20	8.8	12.63	
9	2.1e-010	-		50	4.9	5.10	
10	1.8e-010	-		12	9.9	7.46	

NOTE:

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

Input Summary**Search id** 20060404165711-1BE4-192168001107**Sequences** 2058**Date & Time** Tue Apr 04 21:57:11 2006 UTC (Search Time: 0.11 sec.)**Sample ID** Schu4 272**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) 882.536 948.483 1060.613 1066.528 1157.616 1307.723 1323.689
1346.792 1383.736 1406.749 1434.747 1563.825 1657.840
1716.875 1790.928 1794.865 1828.907 1838.015 1994.025
2249.105 2299.153 2383.973 2510.134 2705.166

Tolerance (mon) 30.00 ppm

Number of 24
Peptides

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