

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	9.9e-001	0.76	<p>FTTSGH2019 1862587 1861781 [-2 L= 807 r=-1.224] (FTT1772c 1862587 1861781 -) =====>gb AAO11393.1 Tryptophan synthase alpha chain [Vibrio vulnificus CMCP6]ref NP_761866.1 Tryptophan synthase alpha chain [Vibrio vulnificus CMCP6] Score = 356 bits (914), Expect = 4e-97=====>ref YP_170662.1 tryptophan synthase alpha chain [Francisella tularensis subsp.tularensis Schu 4] Score = 526 bits (1355), Expect = e-148</p> <p>FTTSGH0555 532949 533809 [+2 L= 861 r=-1.242] (FTT0511 532949 533809 +) =====>ref YP_004327.1 pyridoxine biosynthesis protein [Thermus thermophilus HB27]gb AAS80700.1 pyridoxine biosynthesis protein [Thermus thermophilus HB27] Score = 406 bits (1043), Expect = e-112=====>ref YP_169546.1 Pyridoxine/pyridoxal 5-phosphate biosynthesis protein [Francisellatularensis subsp. tularensis Schu 4] Score = 558 bits (1437), Expect = e-157=====>sp O69190 PDXS_FRATU Pyridoxal biosynthesis lyase pdxSgb AAC18606.1 hypothetical protein IP1 [Francisella tularensis] Score = 461 bits (1185), Expect = e-128</p> <p>FTTSGH1454 1306629 1307195 [+3 L= 567 r=-1.254] (FTT1288 1306629 1307195 +) =====>ref NP_927602.1 hypothetical protein plu0239 [Photorhabdus luminescens subsp.laumondii TTO1] Score = 147 bits (372), Expect = 1e-34=====>ref YP_170243.1 conserved hypothetical membrane protein [Francisella tularensissubsp. tularensis Schu 4] Score = 374 bits (960), Expect = e-103=====>ref YP_170354.1 conserved hypothetical membrane protein [Francisella tularensissubsp. tularensis Schu 4] Score = 125 bits (314), Expect = 7e-28</p> <p>FTTSGH0169 171934 172515 [+1 L= 582 r=-1.220] (FTT0156 171934 172515 +) =====>ref YP_127873.1 hypothetical protein lpl2544 [Legionella pneumophila str.</p>	16	5.4	29.05	
2	5.5e-003	0.02		14	5.2	30.80	
3	9.4e-004	-		11	8.0	21.58	
4	7.4e-004	-		13	5.2	22.34	

			Lens]emb CAH16784.1 hypothetical protein [Legionella pneumophila str. Lens] Score = 102 bits (255), Expect = 5e-21====>ref YP_169222.1 acid phosphatase [Francisella tularensis subsp. tularensis Schu 4]emb CAG44789.1 acid phosphatase [Francisella tularensis subsp. tularensis SCHU S4] Score = 388 bits (997), Expect = e-107			
5	5.7e-004	-	FTTSGH1237 1112037 1112522 [+3 L= 486 r=-1.247] (FTT1101 1112007 1112525 +)====>gb AAC77123.1 orf, hypothetical protein; conserved protein, ferredoxin like[Escherichia coli K12] Score = 179 bits (455), Expect = 2e-44	15	9.1	18.28
6	4.8e-004	-	FTTSGH0514 495463 494684 [-2 L= 780 r=-1.201] (FTT0477c 495463 494684 -)====>ref YP_169515.1 Bifunctional protein, biotin-[acetylCoA carboxylase] holoenzymesynthetase; transcriptional repressor of biotin Score = 521 bits (1343), Expect = e-147	11	7.7	30.05
7	3.0e-004	-	FTTSGH1271 1143578 1144318 [+2 L= 741 r=-1.235] (FTT1131 1143578 1144321 +)====>ref YP_127901.1 hypothetical protein lpl2573 [Legionella pneumophila str. Lens]emb CAH16814.1 hypothetical protein [Legionella pneumophila str. Lens] Score = 120 bits (300), Expect = 5e-26	9	6.3	28.38
8	2.9e-004	-	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	17	6.2	19.78
9	1.6e-004	-	FTTSGH1017 919357 919944 [+1 L= 588 r=-1.229] (FTT0911 919357 919944 +)====>ref NP_798246.1 hypothetical protein VP1867 [Vibrio parahaemolyticus RIMD 2210633]dbj BAC60130.1 hypothetical protein [Vibrio parahaemolyticus RIMD 2210633] Score = 159 bits (401), Expect = 6e-38====>ref YP_169908.1 hypothetical protein FTT0911 [Francisella tularensis subsp.tularensis Schu 4] Score = 395 bits	12	5.5	22.47

			(1014), Expect = e-109	
			FTTSGH1816 1672528 1673349 [+1 L= 822	
			r=-1.210] (FTT1606 1672528 1673349 +)	
			====>gb AAN33522.1 septum	
			site-determining protein MinD [Brucella suis	
			1330]ref NP_699517.1 septum	
10	1.1e-004	-	site-determining protein MinD [Brucella suis	11 6.9 30.10 
			1330] Score = 330 bits (845), Expect =	
			4e-89====>ref YP_170522.1 septum	
			site-determining protein MinD [Francisella	
			tularensis subsp.tularensis Schu 4] Score =	
			528 bits (1360), Expect = e-149	

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

Input Summary

Search id 20060330152551-16EC-192168001107

Sequences 1985

Date & Time Thu Mar 30 21:25:51 2006 UTC (Search Time: 0.19 sec.)

Sample ID Schu4 174

Database schu2K [..\databases\schu2k]

Taxonomy -

Mass Range 0 - 35 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) 856.517 864.422 1140.730 1158.696 1174.777 1179.673 1199.697
1234.746 1263.768 1277.787 1434.837 1493.806 1621.952
1638.920 1669.907 1686.937 1702.167 1707.838 1838.984
1875.049 1994.039 2263.171

Tolerance (mon) 60.00 ppm

Number of 22

Peptides

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