


ProFound - Search Result SummaryVersion 2002.03.01
© 1997-2002 Proteometrics LLC**Protein Candidates**

Rank	Probability	Est'd Z	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	7.1e-001	0.42	<p>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 site-determining protein MinD [Brucella suis 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</p> <p>FTTSGH0998 901330 902370 [+1 L=1041 r=-1.211] (FTT0893 901330 902370 +) =====>ref YP_123967.1 Phosphoribosylformylglycinamide cyclo ligase [Legionellapneumophila str. Paris] Score = 361 bits (927), Expect = 2e-98=====>ref YP_169890.1 Phosphoribosylaminoimidazol (AIR) synthetase [Francisella tularensissubsp. tularensis Schu 4] Score = 693 bits (1788), Expect = 0.0</p> <p>FTTSGH1667 1530857 1530108 [-3 L= 750 r=-1.213] (FTT1478c 1530857 1530108 -) =====>gb AAO90028.1 3-deoxy-D-manno-octulosonate cytidyltransferase [Coxiellaburnetii RSA 493] Score = 250 bits (638), Expect = 3e-65=====>ref YP_170414.1 3-deoxy-D-manno-octulosonate cytidyltransferase [Francisellatularensis subsp. tularensis Schu 4] Score = 485 bits (1249), Expect = e-136</p> <p>FTTSGH0681 637131 636151 [-1 L= 981 r=-1.242] (FTT0617c 637131 636151 -) =====>ref YP_237414.1 PhoH-like protein [Pseudomonas syringae pv. syringae B728a]gb AAY39376.1 PhoH-like protein [Pseudomonas syringae pv. syringae B728a] Score = 342 bits (877), Expect = 1e-92=====>ref YP_169638.1 phoH-like protein [Francisella tularensis subsp. tularensis Schu 4]gb AAV29526.1 NT02FT0778 [synthetic construct] Score = 640 bits (1650), Expect = 0.0</p>	20	6.9	30.10	
2	2.3e-001	0.26		13	5.2	37.76	
3	2.0e-002	-		12	5.9	28.17	
4	4.8e-003	-		10	6.6	36.61	

5	4.0e-003	-	<p>FTTSGH2025 1867604 1867197 [-3 L= 408 r=-1.211] (FTT1777 1867604 1867197 -) ====>ref YP_170666.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 261 bits (667), Expect = 5e-69====>ref YP_170667.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 150 bits (380), Expect = 9e-36</p> <p>FTTSGH0899 830550 829951 [-1 L= 600 r=-1.216] (FTT0809c 830550 829951 -) ====>ref ZP_00316793.1 COG0353: Recombinational DNA repair protein (RecF pathway)[Microbulbifer degradans 2-40] Score = 201 bits (511), Expect = 1e-50====>ref YP_169816.1 Recombination protein recR [Francisella tularensis subsp.tularensis Schu 4] Score = 390 bits (1002), Expect = e-107</p> <p>FTTSGH0589 560380 559838 [-2 L= 543 r=-1.236] (FTT0539 560380 559637 -) ====>emb CAJ04249.1 ubiquitin-activating enzyme, putative [Leishmania major]Length = 276 Score = 174 bits (440), Expect = 2e-42</p> <p>FTTSGH0597 565308 565916 [+3 L= 609 r=-1.213] (FTT0546 565308 565916 +) ====>ref YP_169573.1 hypothetical protein FTT0546 [Francisella tularensis subsp.tularensis Schu 4] Score = 394 bits (1011), Expect = e-108====>ref YP_169570.1 hypothetical protein FTT0543 [Francisella tularensis subsp.tularensis Schu 4] Score = 68.2 bits (165), Expect = 2e-10</p> <p>FTTSGH0958 872090 871500 [-3 L= 591 r=-1.268] (FTT0861 872090 871500 -) ====>emb CAA36654.1 unnamed protein product [Dichelobacter nodosus]sp P17824 FMA2_BACNO Fimbrial protein precursor (Pilin) (Serogroup C2) Score = 50.1 bits (118), Expect = 4e-05====>ref YP_169863.1 Type IV pili fiber building block protein [Francisella tularensissubsp. tularensis Schu 4] Score = 382 bits (982), Expect = e-105====>ref YP_169885.1 Type IV pili fiber building block protein [Francisella tularensissubsp. tularensis Schu 4] Score = 50.4 bits (119), Expect = 3e-05</p>	23	6.5	14.52	
6	3.1e-003	-		14	5.8	22.00	
7	2.4e-003	-		18	8.7	19.60	
8	2.4e-003	-		13	7.8	22.61	
9	2.3e-003	-		15	9.8	21.93	

10 2.3e-003 - [FTTSGH1169](#) 1058317 1057958 [-2 L= 360
r=-1.234] (FTT1047 1058317 1057958 -)
====>ref|YP_170030.1| hypothetical protein FTT1047c [Francisella tularensis
subsp.tularensis Schu 4] Score = 229 bits
(583), Expect = 3e-59

12 9.5 13.51 

NOTE:

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

Input Summary

Search id 20060330150508-1238-192168001107

Sequences 1987

Date & Time Thu Mar 30 21:05:08 2006 UTC (Search Time: 0.25 sec.)

Sample ID Schu4 168 [Pass: 1]

Database SCHU2K [..\databases\schu2k]

Taxonomy -

Mass Range 0 - 50 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) 856.529 868.528 893.580 1158.663 1234.693 1277.731 1337.803
1375.635 1417.897 1457.777 1621.886 1638.859 1685.859
1707.787 1800.810 1834.261 1834.872 2206.352 2315.172
2483.123

Tolerance (mon) 100.00 ppm

Number of 20
Peptides

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