


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	1.0e+000	2.40	<p>FTTSGH0150 150045 151226 [+3 L=1182 r=-1.259] (FTT0137 150045 151226 +) =====>gb AAM35853.1 elongation factor Tu [Xanthomonas axonopodis pv. citri str. 306]gb AAM35841.1 elongation factor Tu [Xanthomonas axonopodis pv. citri str. 306] Score = 673 bits (1737), Expect = 0.0=====>ref YP_169203.1 elongation factor Tu (EF-Tu) [Francisella tularensis subsp.tularensis Schu 4] Score = 788 bits (2034), Expect = 0.0</p> <p>FTTSGH0354 339314 340135 [+2 L= 822 r=-1.265] (FTT0328 339314 340135 +) =====>ref NP_715874.1 ribosomal protein L2 [Shewanella oneidensis MR-1]gb AAN53319.1 ribosomal protein L2 [Shewanella oneidensis MR-1] Score = 413 bits (1062), Expect = e-114=====>ref YP_169377.1 50S ribosomal protein L2 [Francisella tularensis subsp. tularensisSchu 4] Score = 555 bits (1430), Expect = e-157</p> <p>FTTSGH1260 1131189 1130089 [-1 L=1101 r=-1.241] (FTT1120c 1131189 1130089 -) =====>ref YP_156586.1 tRNA-guanine transglycosylase [Idiomarina loihiensis L2TR]gb AAV83037.1 tRNA-guanine transglycosylase [Idiomarina loihiensis L2TR] Score = 550 bits (1418), Expect = e-155=====>ref YP_170094.1 queuine tRNA-ribosyltransferase. [Francisella tularensis subsp.tularensis Schu 4] Score = 752 bits (1941), Expect = 0.0</p> <p>FTTSGH0019 13182 14477 [+3 L=1296 r=-1.222] (FTT0015 13182 14477 +) =====>ref NP_228901.1 adenylosuccinate lyase [Thermotoga maritima MSB8]gb AAD36171.1 adenylosuccinate lyase [Thermotoga maritima MSB8] Score = 320 bits (819), Expect = 8e-86=====>ref YP_169091.1 adenylosuccinate lyase [Francisella tularensis subsp. tularensis Schu4] Score = 849 bits (2193), Expect = 0.0</p>	40	5.1	43.39	
2	4.6e-023	-		22	11.1	30.37	
3	2.1e-023	-		21	8.9	41.48	
4	1.4e-023	-		7	6.1	49.36	

5	7.2e-024	-	<p>FTTSGH0069 64799 66172 [+2 L=1374 r=-1.243] (FTT0064 64799 66172 +) ====>ref ZP_00565839.1 ATP synthase F1, beta subunit [Methylobacillus flagellatus KT]gb EAN02168.1 ATP synthase F1, beta subunit [Methylobacillus flagellatus KT] Score 17 5.1 49.78 </p> <p>= 756 bits (1951), Expect = 0.0====>ref YP_169139.1 ATP synthase beta chain [Francisella tularensis subsp. tularensisSchu 4] Score = 894 bits (2309), Expect = 0.0</p>	
			<p>FTTSGH1132 1024994 1024272 [-3 L= 723 r=-1.169] (FTT1014 1024994 1024272 -) ====>ref NP_391652.1 hypothetical protein BSU37720 [Bacillus subtilis subsp. subtilisstr. 168] Score = 140 bits (353), Expect = 4e-32====>ref YP_169999.1 short chain dehydrogenase family protein 11 5.9 26.54 </p> <p>[Francisella tularensissubsp. tularensis Schu 4] Score = 470 bits (1209), Expect = e-131====>ref YP_169948.1 Short-chain dehydrogenase [Francisella tularensis subsp. tularensisSchu 4] Score = 106 bits (264), Expect = 7e-22</p>	
7	7.0e-025	-	<p>FTTSGH1822 1676491 1676781 [+1 L= 291 r=-1.209] (FTT1612 1676491 1676781 +) ====>ref YP_170527.1 hypothetical protein FTT1612 [Francisella tularensis subsp.tularensis Schu 4] Score = 196 bits (497), Expect = 2e-49 34 9.6 11.37 </p>	
			<p>FTTSGH0496 477191 478099 [+2 L= 909 r=-1.215] (FTT0460 477191 478099 +) ====>dbj BAC24241.1 holB [Wigglesworthia glossinidia endosymbiont of Glossinabrevipalpis] Score = 93.2 bits (230), 13 6.3 35.25 </p> <p>Expect = 1e-17====>ref YP_169498.1 DNA polymerase III, delta prime subunit [Francisella tularensissubsp. tularensis Schu 4] Score = 593 bits (1529), Expect = e-168</p>	
9	2.9e-025	-	<p>FTTSGH1712 1571663 1572232 [+2 L= 570 r=-1.223] (FTT1518 1571663 1572232 +) ====>ref NP_469414.1 hypothetical protein lin0068 [Listeria innocua Clip11262]emb CAC95301.1 lin0068 [Listeria innocua] Score = 156 bits (394), 13 9.6 21.74 </p> <p>Expect = 4e-37====>ref YP_170450.1 Methylated-DNA--protein-cysteine methyltransferase [Francisellatularensis subsp. tularensis Schu 4] Score = 384 bits (986), Expect = e-106</p>	

FTTSGH0321 308224 309000 [+1 L= 777
 r=-1.214] [DelayedBy _329 L=36] (FTT0294
 308194 309000 +)
 =====>ref|YP_125214.1| hypothetical
 protein lpp2912 [Legionella pneumophila str.
 Paris]emb|CAH14065.1| hypothetical protein 14 6.7 30.29 
 [Legionella pneumophila str. Paris] Score =
 177 bits (450), Expect =
 2e-43=====>gb|AAL06398.2| unknown
 [Francisella tularensis subsp.
 tularensis]Length = 271 Score = 543 bits
 (1398), Expect = e-153

NOTE:

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

Input Summary

Search id 20060330144555-19E4-192168001107

Sequences 1983

Date & Time Thu Mar 30 20:45:56 2006 UTC (Search Time: 0.31 sec.)

Sample ID Schu4 164

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) 814.925 848.154 854.588 867.517 974.406 1140.026 1156.616
 1199.699 1208.595 1233.665 1337.763 1373.887 1395.788
 1417.851 1419.354 1470.019 1486.858 1618.983 1634.829
 1666.673 1681.482 1696.983 1702.257 1765.797 1803.954
 1816.945 1820.009 1825.108 1834.218 1835.951 1840.131
 1920.796 1975.068 1991.104 2009.213 2163.231 2206.300
 2216.653 2236.102 2247.106 2256.846 2427.778 2482.282
 2498.309

Tolerance (mon) 100.00 ppm

Number of
Peptides 44

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