

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	9.2e-001	0.66	<p>FTTSGH1046 949339 948401 [-2 L= 939 r=-1.231] (FTT0937c 949339 948401 -) =====>gb AAO90528.1 biotin synthase [Coxiella burnetii RSA 493]ref NP_820014.1 biotin synthase [Coxiella burnetii RSA 493] Score = 365 bits (938), Expect = e-100 =====>ref YP_169930.1 biotin synthase [Francisella tularensis subsp. tularensis Schu 4]gb AAV29457.1 NT02FT0529 [synthetic construct] Score = 628 bits (1619), Expect = e-179</p> <p>FTTSGH0918 844295 843486 [-3 L= 810 r=-1.243] (FTT0828 844475 843486 -) =====>dbj BAC65229.1 </p> <p>L-aspartate-beta-decarboxylase [Pseudomonas dacunhae ATCC 21192]Length = 533 Score = 287 bits (734), Expect = 3e-76</p>	10	6.0	34.88	
2	5.9e-002	0.26	<p>FTTSGH1199 1083636 1083767 [+3 L= 132 r=-1.216] (None identical in .gff) =====>Hypothetical ORF FTTSGH1199</p> <p>FTTSGH0534 515335 515835 [+1 L= 501 r=-1.235] (FTT0495 515335 515835 +) =====>gb AAY91785.1 conserved hypothetical protein [Pseudomonas fluorescens Pf-5]ref YP_259619.1 conserved hypothetical protein [Pseudomonas fluorescens Pf-5] Score = 152 bits (383), Expect = 5e-36 =====>ref YP_169532.1 hypothetical protein FTT0495 [Francisella tularensis subsp. tularensis Schu 4] Score = 343 bits (881), Expect = 9e-94</p>	7	6.7	31.18	
3	1.9e-003	-	<p>FTTSGH1830 1681888 1682058 [+1 L= 171 r=-1.245] (FTT1618 1681888 1682058 +) =====>Hypothetical ORF FTTSGH1830</p> <p>FTTSGH1041 944978 945109 [+2 L= 132 r=-1.156] (FTT0933 944978 945109 +) =====>Hypothetical ORF FTTSGH1041</p> <p>FTTSGH1255 1127086 1126733 [-2 L= 354 r=-1.229] (FTT1116c 1127086 1126733 -) =====>gb AAQ59021.1 probable transmembrane protein [Chromobacterium violaceum ATCC12472] Score = 119 bits (297), Expect =</p>	30	6.2	4.88	
4	8.7e-004	-	<p>FTTSGH1830 1681888 1682058 [+1 L= 171 r=-1.245] (FTT1618 1681888 1682058 +) =====>Hypothetical ORF FTTSGH1830</p> <p>FTTSGH1041 944978 945109 [+2 L= 132 r=-1.156] (FTT0933 944978 945109 +) =====>Hypothetical ORF FTTSGH1041</p> <p>FTTSGH1255 1127086 1126733 [-2 L= 354 r=-1.229] (FTT1116c 1127086 1126733 -) =====>gb AAQ59021.1 probable transmembrane protein [Chromobacterium violaceum ATCC12472] Score = 119 bits (297), Expect =</p>	8	5.5	19.03	
5	7.5e-004	-	<p>FTTSGH1830 1681888 1682058 [+1 L= 171 r=-1.245] (FTT1618 1681888 1682058 +) =====>Hypothetical ORF FTTSGH1830</p> <p>FTTSGH1041 944978 945109 [+2 L= 132 r=-1.156] (FTT0933 944978 945109 +) =====>Hypothetical ORF FTTSGH1041</p> <p>FTTSGH1255 1127086 1126733 [-2 L= 354 r=-1.229] (FTT1116c 1127086 1126733 -) =====>gb AAQ59021.1 probable transmembrane protein [Chromobacterium violaceum ATCC12472] Score = 119 bits (297), Expect =</p>	12	6.7	6.30	
6	7.5e-004	-	<p>FTTSGH1830 1681888 1682058 [+1 L= 171 r=-1.245] (FTT1618 1681888 1682058 +) =====>Hypothetical ORF FTTSGH1830</p> <p>FTTSGH1041 944978 945109 [+2 L= 132 r=-1.156] (FTT0933 944978 945109 +) =====>Hypothetical ORF FTTSGH1041</p> <p>FTTSGH1255 1127086 1126733 [-2 L= 354 r=-1.229] (FTT1116c 1127086 1126733 -) =====>gb AAQ59021.1 probable transmembrane protein [Chromobacterium violaceum ATCC12472] Score = 119 bits (297), Expect =</p>	18	8.1	4.88	
7	7.4e-004	-	<p>FTTSGH1830 1681888 1682058 [+1 L= 171 r=-1.245] (FTT1618 1681888 1682058 +) =====>Hypothetical ORF FTTSGH1830</p> <p>FTTSGH1041 944978 945109 [+2 L= 132 r=-1.156] (FTT0933 944978 945109 +) =====>Hypothetical ORF FTTSGH1041</p> <p>FTTSGH1255 1127086 1126733 [-2 L= 354 r=-1.229] (FTT1116c 1127086 1126733 -) =====>gb AAQ59021.1 probable transmembrane protein [Chromobacterium violaceum ATCC12472] Score = 119 bits (297), Expect =</p>	14	9.8	12.85	

			4e-26====>ref YP_170090.1 preprotein translocase family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 223 bits (569), Expect = 1e-57					
			FTTSGH0218 218746 218952 [+1 L= 207 r=-1.257] (FTT0201 218746 218919 +)					
8	7.2e-004	-	====>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	12	9.9	7.46		
			FTTSGH0172 175037 174219 [-3 L= 819 r=-1.224] (FTT0159 175037 174219 -)					
9	6.5e-004	-	====>ref YP_169225.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 533 bits (1374), Expect = e-150	3	9.0	31.24		
			FTTSGH0753 700875 700060 [-1 L= 816 r=-1.240] (FTT0683c 700875 700060 -)					
10	6.0e-004	-	====>ref NP_790763.1 type IV pilus prepilin peptidase PilD [Pseudomonas syringae pv.tomato str. DC3000] Score = 231 bits (589), Expect = 2e-59====>ref YP_169699.1 Type IV pili leader peptidase and methylase. [Francisellatularensis subsp. tularensis Schu 4] Score = 557 bits (1436), Expect = e-157	5	9.3	31.22		

NOTE:

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

Input Summary

Search id 20060404161517-1D68-192168001107
Sequences 2059
Date & Time Tue Apr 04 21:15:17 2006 UTC (Search Time: 0.11 sec.)
Sample ID Schu4 257
Database schu2K [..\databases\schu2k]
Taxonomy -
Mass Range 0 - 40 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) 844.500 877.050 882.509 1016.543 1268.699 1555.841 1574.767
Tolerance (mon) 50.00 ppm

**Number of 7
Peptides**

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