


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	0.87	<p>FTTSGH1393 1252948 1254090 [+1 L=1143 r=-1.227] (FTT1234 1252948 1254090 +) ==>ref YP_222152.1 choloylglycine hydrolase family protein [Brucella abortus biovar 1str. 9-941] Score = 166 bits (420), Expect = 1e-39 ==>ref YP_170192.1 choloylglycine hydrolase family protein [Francisella tularensissubsp. tularensis Schu 4] Score = 765 bits (1976), Expect = 0.0</p> <p>FTTSGH1741 1603958 1603353 [-3 L= 606 r=-1.214] (FTT1540 1603958 1603353 -) ==>ref NP_716687.1 hypothetical protein SO1060 [Shewanella oneidensis MR-1]gb AAN54132.1 conserved hypothetical protein [Shewanella oneidensis MR-1] Score = 161 bits (408), Expect = 1e-38 ==>ref YP_170468.1 hypothetical protein FTT1540c [Francisella tularensis subsp.tularensis Schu 4] Score = 397 bits (1020), Expect = e-109</p> <p>FTTSGH1058 961036 959975 [-2 L=1062 r=-1.246] (FTT0947 960009 959497 -) (FTT0948 961036 959975 -) ==>emb CAC45719.1 PUTATIVE OXIDOREDUCTASE PROTEIN [Sinorhizobium meliloti]ref NP_385246.1 PUTATIVE OXIDOREDUCTASE PROTEIN [Sinorhizobium meliloti 1021] Score = 328 bits (840), Expect = 2e-88 ==>ref YP_169940.1 Aldo/keto reductase [Francisella tularensis subsp. tularensis Schu 4]emb CAG45581.1 Aldo/keto reductase [Francisella tularensis subsp. tularensis SCHU Score = 729 bits (1882), Expect = 0.0</p> <p>FTTSGH1075 975443 974334 [-3 L=1110 r=-1.225] (FTT0963c 975443 974334 -) ==>ref NP_439696.1 phospho-2-dehydro-3-deoxyheptonate aldolase [Haemophilus influenzaeRd KW20] Score = 384 bits (986), Expect = e-105 ==>ref YP_169953.1 Phospho-2-dehydro-3-deoxyheptonate aldolase [Francisella tularensissubsp. tularensis Schu 4] Score = 734 bits (1895), Expect = 0.0</p>	15	8.9	42.52	
2	1.4e-003	-		20	9.3	22.45	
3	5.2e-004	-		11	7.8	40.77	
4	2.8e-004	-		8	8.4	40.83	

			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				
5	2.5e-004	-	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 FTTSGH1107 1002015 1003202 [+3 L=1188 r=-1.210] (FTT0992 1002015 1003202 +) =====>ref ZP_00591623.1 MscS Mechanosensitive ion channel [Prosthecochloris aestuarii DSM271] Score = 306 bits (785), Expect = 6e-82=====>ref YP_169980.1 conserved hypothetical membrane protein [Francisella tularensis subsp. tularensis Schu 4] Score = 776 bits (2004), Expect = 0.0 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 tularensis subsp. tularensis Schu 4] Score = 374 bits (960), Expect = e-103=====>ref YP_170354.1 conserved hypothetical membrane protein [Francisella tularensis subsp. tularensis Schu 4] Score = 125 bits (314), Expect = 7e-28 FTTSGH0865 796770 795679 [-1 L=1092 r=-1.196] (FTT0776c 796770 795679 -) =====>ref YP_033771.1 Ribonuclease D [Bartonella henselae str. Houston-1]emb CAF27773.1 Ribonuclease D [Bartonella henselae str. Houston-1] Score = 156 bits (394), Expect = 1e-36=====>ref YP_169783.1 Ribonuclease D [Francisella tularensis subsp. tularensis Schu 4]emb CAG45409.1 Ribonuclease D [Francisella tularensis subsp. tularensis SCHU S4] Score = 719 bits (1856), Expect = 0.0 FTTSGH0635 594822 596192 [+3 L=1371 r=-1.223] (FTT0577 594822 596192 +) =====>ref YP_094826.1 L-serine dehydratase (iron, sulfur-dependent)	14	6.9	30.10	
6	1.6e-004	-		11	9.1	45.32	
7	1.2e-004	-		11	8.0	21.58	
8	1.1e-004	-		9	7.7	42.88	
9	8.2e-005	-		11	5.1	49.99	

				[Legionella pneumophila subsp. pneumophila str. Philadelphia 1] Score = 437 bits (1123), Expect = e-121====>ref YP_169601.1 L-serine dehydratase 1 [Francisella tularensis subsp. tularensis Schu4] Score = 916 bits (2367), Expect = 0.0	
				FTTSGH0803 750029 748998 [-3 L=1032 r=-1.215] (FTT0726 750029 748998 -)====>ref NP_773224.1 putative glycerophosphoryl diester phosphodiesterase [Bradyrhizobium japonicum USDA 110] Score = 215 bits (547), Expect = 2e-54====>ref YP_169739.1 glycerophosphoryl diester phosphodiesterase family protein [Francisella tularensis subsp. tularensis Schu 4] Score = 707 bits (1824), Expect = 0.0	
10	7.4e-005	-			15 5.4 39.02 

NOTE:

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

Input Summary

Search id 20060330145456-1C90-192168001107
Sequences 1986
Date & Time Thu Mar 30 20:54:56 2006 UTC (Search Time: 0.61 sec.)
Sample ID Schu4 166
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) 843.902 856.520 864.510 868.514 1158.680 1179.631 1208.717
1234.712 1255.550 1263.733 1277.759 1288.187 1307.747
1323.712 1340.744 1374.056 1383.829 1395.952 1405.736
1417.979 1427.112 1434.824 1457.810 1470.194 1493.777
1530.958 1554.924 1561.833 1621.915 1638.900 1702.431
1707.802 1838.941 1982.846 1993.970 2009.103 2249.065
2383.963 2501.339 2526.962 2705.061
Tolerance (mon) 50.00 ppm
Number of
Peptides 41

Profound is provided under exclusive licence by Genomic Solutions Ltd.