

**ProFound - Search Result Summary**Version 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	1.90	<p><a href="#">FTTSGH1181</a> 1070076 1069615 [-1 L= 462 r=-1.186] (FTT1060c 1070067 1069615 -)  =====&gt;ref NP_253619.1  50S ribosomal protein L9 [Pseudomonas aeruginosa PAO1]gb AAG08317.1  50S ribosomal protein L9 [Pseudomonas aeruginosa PAO1] Score = 157 bits (396), Expect = 1e-37=====&gt;ref YP_170041.1  50S ribosomal protein L9 [Francisella tularensis subsp. tularensisSchu 4] Score = 287 bits (734), Expect = 8e-77</p>	51	5.6	16.38	
2	2.3e-006	0.51	<p><a href="#">FTTSGH1671</a> 1534332 1532923 [-1 L=1410 r=-1.210] (FTT1483c 1534332 1532923 -)  =====&gt;gb AAO90013.1  dihydrolipoamide dehydrogenase [Coxiella burnetii RSA 493]ref NP_819499.1  dihydrolipoamide dehydrogenase [Coxiella burnetii RSA 493] Score = 619 bits (1596), Expect = e-176=====&gt;ref YP_170418.1  dihydrolipoamide dehydrogenase [Francisella tularensis subsp. tularensis Schu 4] Score = 920 bits (2379), Expect = 0.0</p>	14	5.6	50.47	
3	2.6e-011	-	<p><a href="#">FTTSGH0495</a> 476164 477180 [+1 L=1017 r=-1.206] (FTT0459 476164 477180 +)  =====&gt;ref ZP_00636494.1  Peptidase S49 [Shewanella denitrificans OS-217]gb EAN68982.1  Peptidase S49 [Shewanella denitrificans OS-217] Score = 302 bits (774), Expect = 1e-80=====&gt;ref YP_169497.1  peptidase family S49 protein [Francisella tularensis subsp. tularensis Schu 4] Score = 658 bits (1697), Expect = 0.0</p>	7	9.1	38.10	
4	7.2e-012	-	<p><a href="#">FTTSGH1393</a> 1252948 1254090 [+1 L=1143 r=-1.227] (FTT1234 1252948 1254090 +)  =====&gt;ref YP_222152.1  choloylglycine hydrolase family protein [Brucella abortus biovar 1str. 9-941] Score = 166 bits (420), Expect = 1e-39=====&gt;ref YP_170192.1  choloylglycine hydrolase family protein [Francisella tularensis subsp. tularensis Schu 4] Score = 765 bits (1976), Expect = 0.0</p>	14	8.9	42.52	
5	4.5e-012	-	<p><a href="#">FTTSGH0194</a> 193789 194463 [+1 L= 675 r=-1.245] (FTT0179 193789 194463 +)  =====&gt;ref YP_126025.1  hypothetical</p>	16	9.1	25.99	

			protein lpl0663 [Legionella pneumophila str. Lens]emb CAH14897.1  hypothetical protein [Legionella pneumophila str. Lens] Score = 65.9 bits (159), Expect = 1e-09			
			<a href="#">FTTSGH1036</a> 941728 941132 [-2 L= 597 r=-1.203] (FTT0929 941911 941132 -) =====>ref ZP_00465325.1  3-hydroxybutyrate dehydrogenase			
6	5.7e-013	-	[Burkholderia cenocepacia HI2424]ref ZP_00458064.1  3-hydroxybutyrate dehydrogenase [Burkholderia cenocepacia AU 1054] Score = 244 bits (624), Expect = 9e-64	19	6.3	21.44
			<a href="#">FTTSGH1226</a> 1102566 1101550 [-1 L=1017 r=-1.193] (FTT1093c 1102512 1101550 -) =====>gb AAM50780.1  LD23608p [Drosophila melanogaster]Length = 320 Score = 317 bits (812), Expect = 4e-85=====>ref YP_170072.1			
7	4.5e-013	-	Transaldolase [Francisella tularensis subsp. tularensis Schu 4]emb CAG45726.1  Transaldolase [Francisella tularensis subsp. tularensis SCHU S4] Score = 622 bits (1603), Expect = e-177	13	6.9	38.00
			<a href="#">FTTSGH1017</a> 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			
8	2.0e-013	-	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 (1014), Expect = e-109	10	5.5	22.47
			<a href="#">FTTSGH0757</a> 706529 705165 [-3 L=1365 r=-1.217] (FTT0687c 706529 705165 -) =====>ref ZP_00419169.1  Heat shock protein HslU [Azotobacter vinelandii AvOP]gb EAM04539.1  Heat shock protein HslU [Azotobacter vinelandii AvOP] Score = 587 bits (1513), Expect = e-166=====>ref YP_169703.1			
9	5.3e-014	-	ATP-dependent protease, ATP-binding subunit [Francisella tularensissubsp. tularensis Schu 4] Score = 872 bits (2254), Expect = 0.0	8	5.9	51.22
			<a href="#">FTTSGH0534</a> 515335 515835 [+1 L= 501 r=-1.235] (FTT0495 515335 515835 +) =====>gb AAY91785.1  conserved			
10	3.3e-014	-	hypothetical protein [Pseudomonas fluorescens Pf-5]ref YP_259619.1  conserved	17	5.5	19.03

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

## NOTE:

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

**Input Summary**

**Search id** 20060404151141-1E60-192168001107  
**Sequences** 2053  
**Date & Time** Tue Apr 04 20:11:42 2006 UTC (Search Time: 0.28 sec.)  
**Sample ID** Schu4 242  
**Database** schu2K [..\databases\schu2k]  
**Taxonomy** -  
**Mass Range** 0 - 80 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)** 935.529 962.436 1057.622 1082.626 1087.566 1140.667 1199.681  
 1288.717 1308.721 1383.812 1431.826 1434.781 1470.792  
 1621.922 1638.873 1674.939 1717.883 1765.934 1838.944  
 1951.964 1994.006 2013.119 2251.160 2262.156 2270.256  
 2501.251 2705.046  
**Tolerance (mon)** 50.00 ppm  
**Number of**  
**Peptides** 27

Profound is provided under exclusive licence by Genomic Solutions Ltd.