

**ProFound - Search Result Summary**


Version 2002.03.01

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**Protein Candidates**

Rank	Probability	Est'd Z	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	1.0e+000	1.61	<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>	12	5.6	50.47	
2	1.3e-006	-	<p><a href="#">FTTSGH0473</a> 452620 453273 [+1 L= 654 r=-1.229] (FTT0439 452620 453273 +)  =====&gt;emb CAG76519.1  probable tRNA/rRNA methyltransferase [Erwinia carotovora subsp.atroseptica SCRI1043] Score = 174 bits (440), Expect = 2e-42=====&gt;ref YP_169479.1  tRNA/rRNA methyltransferase [Francisella tularensis subsp.tularensis Schu 4] Score = 428 bits (1101), Expect = e-119</p>	16	7.8	23.67	
3	9.3e-007	-	<p><a href="#">FTTSGH1704</a> 1565788 1566669 [+1 L= 882 r=-1.279] (FTT1511 1565788 1566669 +)  =====&gt;gb AAO90839.1  membrane protein, putative [Coxiella burnetii RSA 493]ref NP_820325.1  membrane protein, putative [Coxiella burnetii RSA 493] Score = 206 bits (523), Expect = 1e-51=====&gt;ref YP_170445.1  conserved hypothetical membrane protein [Francisella tularensissubsp. tularensis Schu 4] Score = 570 bits (1469), Expect = e-161</p>	12	9.7	33.02	
4	9.1e-007	-	<p><a href="#">FTTSGH1821</a> 1675823 1676488 [+2 L= 666 r=-1.244] (FTT1611 1675823 1676488 +)  =====&gt;ref YP_094879.1  signal peptide protein, toluene tolerance protein Ttg2D [Legionellapneumophila subsp. pneumophila str. Philadelphia 1] Score = 77.0 bits (188), Expect = 4e-13=====&gt;ref YP_170526.1  conserved hypothetcial protein [Francisella tularensis subsp.tularensis Schu 4] Score = 441 bits (1134), Expect = e-123</p>	9	9.6	25.53	
5	2.8e-007	-	<p><a href="#">FTTSGH1847</a> 1696986 1696351 [-1 L= 636 r=-1.213] (FTT1632 1696986 1696351 -)  =====&gt;gb AAO91263.1  conserved</p>	5	6.0	23.49	

			hypothetical protein [Coxiella burnetii RSA 493]ref NP_820749.1  hypothetical protein CBU1769 [Coxiella burnetii RSA 493] Score = 160 bits (406), Expect = 2e-38====>ref YP_170545.1  conserved hypothetical protein [Francisella tularensis subsp.tularensis Schu 4] Score = 430 bits (1105), Expect = e-119			
6	2.8e-007	-	<a href="#">FTTSGH1032</a> 936176 937114 [+2 L= 939 r=-1.201] (FTT0925 936176 937114 +)====>gb AAP96735.1  methionyl-tRNA formyltransferase [Haemophilus ducreyi 35000HP]ref NP_874346.1  methionyl-tRNA formyltransferase [Haemophilus ducreyi 35000HP] Score = 284 bits (727), Expect = 2e-75====>ref YP_169921.1  Methionyl-tRNA formyltransferase [Francisella tularensis subsp.tularensis Schu 4] Score = 628 bits (1620), Expect = e-179 <a href="#">FTTSGH0530</a> 512981 512058 [-3 L= 924 r=-1.237] (FTT0492c 512981 512058 -)====>ref NP_799897.1  transcriptional regulator, LysR family [Vibrio parahaemolyticusRIMD 2210633] Score = 195 bits (496), Expect = 1e-48====>ref YP_169530.1  transcriptional regulator, LysR family [Francisella tularensissubsp. tularensis Schu 4] Score = 617 bits (1592), Expect = e-175 <a href="#">FTTSGH1908</a> 1753817 1754716 [+2 L= 900 r=-1.245] (FTT1684 1753817 1754716 +)====>ref YP_122688.1  hypothetical protein lpp0348 [Legionella pneumophila str. Paris]emb CAH11496.1  hypothetical protein [Legionella pneumophila str. Paris] Score = 176 bits (445), Expect = 1e-42====>ref YP_170589.1  transcription regulator [Francisella tularensis subsp. tularensisSchu 4] Score = 592 bits (1527), Expect = e-168 <a href="#">FTTSGH1956</a> 1807479 1805992 [-1 L=1488 r=-1.240] (FTT1721c 1807479 1805992 -)====>ref YP_149816.1  amidophosphoribosyltransferase [Salmonella enterica subsp. entericaserovar Paratyphi A str. ATCC 9150] Score = 555 bits (1431), Expect = e-156====>ref YP_170623.1  Amidophosphoribosyltransferase [Francisella tularensis subsp.tularensis Schu 4] Score = 995 bits (2573), Expect = 0.0	9	8.7	35.31
7	2.5e-007	-		5	8.6	35.74
8	2.2e-007	-		8	9.3	34.13
9	1.7e-007	-		7	6.7	55.33

FTTSGH0021 15179 16717 [+2 L=1539  
 r=-1.221] (FTT0017 15179 16717 +)  
 =====>ref|YP\_125645.1| hypothetical  
 protein lpl0278 [Legionella pneumophila str.  
 Lens]emb|CAH14509.1| hypothetical protein  
 10 1.0e-007 - [Legionella pneumophila str. Lens] Score = 6 8.7 58.94   
 195 bits (496), Expect =  
 3e-48=====>ref|YP\_169093.1| conserved  
 hypothetical membrane protein [Francisella  
 tularensissubsp. tularensis Schu 4] Score =  
 986 bits (2548), Expect = 0.0

## NOTE:

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

**Input Summary**

**Search id** 20060330143315-1C90-192168001107  
**Sequences** 2057  
**Date & Time** Thu Mar 30 20:33:16 2006 UTC (Search Time: 0.13 sec.)  
**Sample ID** Schu4 161  
**Database** schu2K [..\databases\schu2k]  
**Taxonomy** -  
**Mass Range** 0 - 60 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)** 720.162 775.499 1087.632 1191.471 1337.883 1373.997 1383.895  
 1395.894 1417.998 1470.142 1634.994 1666.863 1702.442  
 1766.032 1800.162 1834.408 2207.661 2217.037 2262.231  
**Tolerance (mon)** 90.00 ppm  
**Number of** 19  
**Peptides**

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