

**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	2.32	<b>FTTSGH0150</b> 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 <b>FTTSGH0601</b> 567978 569411 [+3 L=1434 r=-1.226] [DelayedBy _620 L=18] (FTT0550 567978 569411 +) (FTT0549 567545 568015 +) ====>ref ZP_00586126.1  TPR repeat [Shewanella amazonensis SB2B]gb EAN39373.1  TPR repeat [Shewanella amazonensis SB2B] Score = 88.2 bits (217), Expect = 6e-16====>ref YP_169577.1  hypothetical protein FTT0550 [Francisella tularensis subsp.tularensis Schu 4] Score = 933 bits (2412), Expect = 0.0====>ref YP_170465.1  hypothetical protein FTT1537c [Francisella tularensis subsp.tularensis Schu 4] Score = 179 bits (454), Expect = 2e-43 <b>FTTSGH1233</b> 1110999 1110709 [-1 L= 291 r=-1.209] [DelayedBy _1266 L=42] (FTT1099 1111041 1110709 -) ====>ref YP_170077.1  hypothetical protein FTT1099c [Francisella tularensis subsp.tularensis Schu 4] Score = 194 bits (493), Expect = 7e-49 <b>FTTSGH1786</b> 1646966 1646526 [-3 L= 441 r=-1.246] (FTT1582 1647014 1646526 -) ====>ref ZP_00143306.1  TYPE III RESTRICTION-MODIFICATION SYSTEM METHYLATION SUBUNIT[Fusobacterium nucleatum subsp. vincentii ATCC 49256] Score = 90.5 bits (223), Expect = 1e-17 <b>FTTSGH1267</b> 1137666 1138421 [+3 L= 756 r=-1.232] (FTT1127 1137666 1138421 +) ====>ref ZP_00521456.1  Rhodanese-like [Solibacter usitatus Ellin6076]gb EAM59572.1	30	5.1	43.39	
2	2.2e-012	-		10	7.6	54.31	
3	5.1e-013	-		19	9.7	11.37	
4	2.2e-013	-		24	4.8	16.51	
5	4.8e-014	-		15	6.6	28.19	

			Rhodanese-like [Solibacter usitatus Ellin6076] Score = 140 bits (352), Expect = 5e-32====>ref YP_170100.1  Rhodanese-like family protein [Francisella tularensis subsp.tularensis Schu 4] Score = 509 bits (1310), Expect = e-143			
6	3.9e-014	-	FTTSGH1597 1466658 1467557 [+3 L= 900 r=-1.196] (FTT1415 1466658 1467557 +) ====>ref YP_170358.1  hypothetical protein FTT1415 [Francisella tularensis subsp.tularensis Schu 4] Score = 593 bits (1528), Expect = e-168	10	7.1	33.71
7	3.5e-014	-	FTTSGH0179 182142 181489 [-1 L= 654 r=-1.205] (FTT0166 182142 181489 -) ====>ref NP_754917.1  Hypothetical protein yfgM [Escherichia coli CFT073]gb AAN81485.1  Hypothetical protein yfgM [Escherichia coli CFT073] Score = 58.5 bits (140), Expect = 1e-07====>ref YP_169232.1  conserved hypothetical membrane protein [Francisella tularensissubsp. tularensis Schu 4] Score = 425 bits (1092), Expect = e-118	13	9.5	24.48
8	3.2e-014	-	FTTSGH1650 1514722 1514093 [-2 L= 630 r=-1.240] (FTT1463c 1514707 1514093 -) ====>dbj BAB07435.1  galactosyltransferase [Bacillus halodurans C-125]ref NP_244583.1  galactosyltransferase [Bacillus halodurans C-125] Score = 270 bits (690), Expect = 2e-71====>ref YP_170400.1  galactosyl transferase [Francisella tularensis subsp. tularensisSchu 4] Score = 419 bits (1076), Expect = e-116	15	9.5	23.83
9	3.0e-014	-	FTTSGH1400 1260817 1262067 [+1 L=1251 r=-1.224] (FTT1241 1260817 1262067 +) ====>ref YP_149642.1  serine hydroxymethyltransferase [Salmonella enterica subsp. entericaserovar Paratyphi A str. ATCC 9150] Score = 574 bits (1479), Expect = e-162====>ref YP_170199.1  serine hydroxymethyltransferase [Francisella tularensis subsp.tularensis Schu 4] Score = 833 bits (2151), Expect = 0.0	6	6.6	45.30
10	3.0e-014	-	FTTSGH1551 1422264 1423520 [+3 L=1257 r=-1.207] (FTT1377 1422264 1423520 +) ====>emb CAD14756.1  PROBABLE 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE II [Ralstoniasolanacearum] Score = 506 bits (1304), Expect = e-142====>ref YP_170326.1	8	5.8	44.06

3-oxoacyl-[acyl-carrier-protein] synthase II  
[Francisella tularensissubsp. tularensis Schu 4]  
Score = 835 bits (2156), Expect = 0.0

## NOTE:

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

**Input Summary**

**Search id** 20060404153651-1A78-192168001107

**Sequences** 2058

**Date & Time** Tue Apr 04 20:36:52 2006 UTC (Search Time: 0.17 sec.)

**Sample ID** Schu4 246 [Pass: 1]

**Database** SCHU2K [..\databases\schu2k]

**Taxonomy** -

**Mass Range** 0 - 55 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)** 882.520 963.562 975.069 1199.706 1233.662 1243.624 1309.634  
1311.640 1652.918 1696.957 1816.871 1920.532 1940.934  
1975.000 1993.976 2009.131 2024.025 2163.170 2482.184

**Tolerance (mon)** 50.00 ppm

**Number of** 19  
**Peptides**

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