

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 | 1.18 | FTTSGH1181 1070076 1069615 [-1 L= 462 r=-1.186] (FTT1060c 1070067 1069615 -) =====>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=====>ref YP_170041.1 50S ribosomal protein L9 [Francisella tularensis subsp. tularensisSchu 4] Score = 287 bits (734), Expect = 8e-77 | 28 | 5.6 | 16.38 | |
| 2 | 1.1e-004 | - | FTTSGH1692 1555510 1556538 [+1 L=1029 r=-1.234] (FTT1501 1555510 1556538 +) =====>gb AAO36241.1 putative carbamoyl-phosphate synthase large chain [Clostridiumtetani E88] Score = 80.5 bits (197), Expect = 8e-14=====>ref YP_169534.1 hypothetical protein FTT0499 [Francisella tularensis subsp.tularensis Schu 4] Score = 194 bits (492), Expect = 5e-48 | 11 | 6.1 | 38.89 | |
| 3 | 3.3e-005 | - | FTTSGH1687 1550643 1549633 [-1 L=1011 r=-1.235] (FTT1496 1550643 1549633 -) =====>ref YP_170431.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 663 bits (1710), Expect = 0.0=====>ref YP_170535.1 hypothetical membrane protein [Francisella tularensis subsp.tularensis Schu 4] Score = 150 bits (380), Expect = 5e-35 | 10 | 6.5 | 37.74 | |
| 4 | 2.3e-005 | - | FTTSGH0202 200770 201657 [+1 L= 888 r=-1.275] (FTT0185 200770 201657 +) =====>ref ZP_00122127.1 COG1181: D-alanine-D-alanine ligase and related ATP-grasp enzymes[Haemophilus somnus 129PT] Score = 239 bits (610), Expect = 8e-62=====>ref YP_169246.1 D-alanine--D-alanine ligase B [Francisella tularensis subsp.tularensis Schu 4] Score = 583 bits (1504), Expect = e-165 | 10 | 5.2 | 32.75 | |
| 5 | 1.1e-005 | - | FTTSGH1036 941728 941132 [-2 L= 597 r=-1.203] (FTT0929 941911 941132 -) =====>ref ZP_00465325.1 3-hydroxybutyrate dehydrogenase | 14 | 6.3 | 21.44 | |

| | | | | | | | |
|----|----------|---|--|----|------|-------|---|
| | | | [Burkholderia cenocepacia HI2424]ref ZP_00458064.1 3-hydroxybutyrate dehydrogenase [Burkholderia cenocepacia AU 1054] Score = 244 bits (624), Expect = 9e-64 | | | | |
| 6 | 6.4e-006 | - | FTTSGH1206 1086581 1086465 [-3 L= 117 r=-1.319] [OlapWith _1236 L=59 S=98] (None identical in .gff) =====>Hypothetical ORF FTTSGH1206 | 38 | 6.2 | 4.43 | 🔴 |
| 7 | 6.3e-007 | - | FTTSGH0928 850799 851158 [+2 L= 360 r=-1.252] (FTT0834 850799 851158 +) =====>emb CAD75895.1 chorismate mutase [Rhodopirellula baltica SH 1]ref NP_868518.1 chorismate mutase [Rhodopirellula baltica SH 1] Score = 119 bits (299), Expect = 2e-26=====>ref YP_169839.1 chorismate mutase [Francisella tularensis subsp. tularensis Schu 4]gb AAV29324.1 NT02FT0715 [synthetic construct] Score = 236 bits (602), Expect = 2e-61 | 16 | 9.0 | 13.51 | 🔴 |
| 8 | 5.9e-007 | - | FTTSGH1078 978100 977198 [-2 L= 903 r=-1.207] (FTT0965 978100 977198 -) =====>ref XP_307366.2 ENSANGP00000001972 [Anopheles gambiae str. PEST]gb EAA03109.2 ENSANGP00000001972 [Anopheles gambiae str. PEST] Score = 219 bits (559), Expect = 7e-56=====>ref YP_169955.1 conserved hypothetical membrane protein [Francisella tularensissubsp. tularensis Schu 4] Score = 566 bits (1459), Expect = e-160 | 11 | 10.1 | 31.65 | 🔴 |
| 9 | 5.8e-007 | - | FTTSGH0151 151421 151888 [+2 L= 468 r=-1.262] (FTT0138 151421 151888 +) =====>ref NP_819268.1 preprotein translocase, SecE subunit [Coxiella burnetii RSA 493]gb AAO89782.1 preprotein translocase, SecE subunit [Coxiella burnetii RSA 493] Score = 77.0 bits (188), Expect = 2e-13=====>ref YP_169204.1 preprotein translocase, subunit E, membrane protein [Francisellatularensis subsp. tularensis Schu 4] Score = 304 bits (778), Expect = 7e-82 | 10 | 9.9 | 17.65 | 🔴 |
| 10 | 5.2e-007 | - | FTTSGH0194 193789 194463 [+1 L= 675 r=-1.245] (FTT0179 193789 194463 +) =====>ref YP_126025.1 hypothetical protein lpl0663 [Legionella pneumophila str. Lens]emb CAH14897.1 hypothetical protein [Legionella pneumophila str. Lens] Score = 65.9 bits (159), Expect = 1e-09 | 12 | 9.1 | 25.99 | 🔴 |

NOTE:

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

Input Summary

Search id 20060404155607-1E00-192168001107
Sequences 1985
Date & Time Tue Apr 04 20:56:08 2006 UTC (Search Time: 0.23 sec.)
Sample ID Schu4 251
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) 861.486 935.516 962.450 1140.701 1387.771 1431.870 1457.844
1622.004 1638.911 1661.022 1674.984 1703.189 1707.855
1838.974 1994.049 2013.170 2270.313 2501.276
Tolerance (mon) 100.00 ppm
Number of 18
Peptides

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