

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 | 1.72 | <p>FTTSGH1722 1584927 1582687 [-1 L=2241 r=-1.207] (FTT1526c 1584927 1582687 -) =====>ref ZP_00314716.1 COG2838: Monomeric isocitrate dehydrogenase [Microbulbifer degradans2-40] Score = 953 bits (2463), Expect = 0.0=====>ref YP_170456.1 isocitrate dehydrogenase [Francisella tularensis subsp. tularensisSchu 4] Score = 1476 bits (3821), Expect = 0.0</p> <p>FTTSGH0411 383364 382018 [-1 L=1347 r=-1.217] (FTT0380c 383364 382018 -) =====>emb CAA77805.1 Glutamate Dehydrogenase [Clostridium symbiosum]pir S22403 glutamate dehydrogenase (EC 1.4.1.2) - Clostridium symbiosum Score = 578 bits (1489), Expect = e-163=====>ref YP_169425.1 NAD(P)-specific glutamate dehydrogenase [Francisella tularensissubsp. tularensis Schu 4] Score = 905 bits (2338), Expect = 0.0</p> <p>FTTSGH1208 1087105 1087329 [+1 L= 225 r=-1.255] (FTT1075 1087105 1087329 +) =====>gb AAB91769.1 Y4mF [Rhizobium sp. NGR234]ref NP_443972.1 Y4mF [Rhizobium sp. NGR234] Score = 65.5 bits (158), Expect = 5e-10=====>ref YP_170054.1 transcriptional regulator [Francisella tularensis subsp. tularensisSchu 4] Score = 150 bits (379), Expect = 1e-35</p> <p>FTTSGH0961 874791 873898 [-1 L= 894 r=-1.214] (FTT0864 874791 873898 -) =====>ref ZP_00266545.1 COG0583: Transcriptional regulator [Pseudomonas fluorescens PfO-1]Length = 308 Score = 182 bits (463), Expect = 9e-45=====>ref YP_169866.1 transcriptional regulator, LysR family [Francisella tularensissubsp. tularensis Schu 4] Score = 584 bits (1505), Expect = e-165=====>ref YP_170510.1 transcriptional regulator, LysR family [Francisella tularensissubsp. tularensis Schu 4] Score = 158 bits (400), Expect = 2e-37</p> | 9 | 6.5 | 83.40 | |
| 2 | 3.0e-006 | - | | 10 | 6.5 | 49.09 | |
| 3 | 1.4e-006 | - | | 19 | 9.4 | 8.07 | |
| 4 | 5.9e-008 | - | | 6 | 6.9 | 33.54 | |

| | | | | | | | |
|---|----------|---|---|----|-----|-------|--|
| 5 | 2.3e-008 | - | <p>FTTSGH0649 609091 609678 [+1 L= 588 r=-1.246] (FTT0589 609091 609678 +) (FTT0590 609632 610111 +) ====>ref YP_169612.1 hypothetical protein FTT0589 [Francisella tularensis subsp.tularensis Schu 4] Score = 399 bits (1024), Expect = e-110</p> <p>FTTSGH0101 99108 97684 [-1 L=1425 r=-1.244] (FTT0094c 99108 97684 -) ====>ref YP_123578.1 hypothetical protein lpp1254 [Legionella pneumophila str. Paris]emb CAH12405.1 hypothetical protein [Legionella pneumophila str. Paris] Score = 219 bits (559), Expect = 1e-55====>ref YP_169166.1 sensor histidine kinase [Francisella tularensis subsp. tularensisSchu 4] Score = 935 bits (2417), Expect = 0.0</p> <p>FTTSGH1195 1079628 1078726 [-1 L= 903 r=-1.198] (FTT1069 1079628 1078726 -) ====>ref ZP_00346206.1 hypothetical protein Ddes02003716 [Desulfovibrio desulfuricans G20]Length = 221 Score = 76.6 bits (187), Expect = 9e-13====>ref YP_170049.1 hypothetical protein FTT1069c [Francisella tularensis subsp.tularensis Schu 4] Score = 587 bits (1513), Expect = e-166</p> <p>FTTSGH0796 743426 741204 [-3 L=2223 r=-1.247] (FTT0721c 743426 741204 -) ====>ref YP_069352.1 catalase; hydroperoxidase HPI(I) [Yersinia pseudotuberculosis IP32953] Score = 904 bits (2336), Expect = 0.0====>gb AAT77112.1 catalase-peroxidase precursor [Francisella tularensis subsp.tularensis] Score = 1529 bits (3959), Expect = 0.0</p> <p>FTTSGH1163 1053433 1054233 [+1 L= 801 r=-1.261] (FTT1042 1053433 1054233 +) ====>ref NP_249883.1 hypothetical protein PA1192 [Pseudomonas aeruginosa PAO1]gb AAG04581.1 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] Score = 366 bits (940), Expect = e-100====>ref YP_170025.1 hypothetical protein FTT1042 [Francisella tularensis subsp.tularensis Schu 4] Score = 536 bits (1381), Expect = e-151</p> | 14 | 9.7 | 22.59 | |
| 6 | 2.2e-008 | - | | 4 | 7.2 | 54.75 | |
| 7 | 1.7e-008 | - | | 8 | 6.1 | 34.66 | |
| 8 | 1.2e-008 | - | | 2 | 5.4 | 82.48 | |
| 9 | 8.0e-009 | - | | 7 | 8.5 | 30.88 | |

FTTSGH1595 1464938 1466065 [+2 L=1128
 r=-1.245] (FTT1413 1464938 1466065 +)
 =====>ref|ZP_00418113.1|
 Aminotransferase, class I and II [Azotobacter
 vinelandii AvOP]gb|EAM05749.1|
 Aminotransferase, class I and II [Azotobacter
 vinelandii AvOP] Score = 270 bits (691), 4 6.8 42.20 
 Expect = 5e-71=====>ref|YP_170356.1|
 Aminotransferase [Francisella tularensis
 subsp. tularensis Schu 4]emb|CAG46046.1|
 Aminotransferase [Francisella tularensis
 subsp. tularensis SCHU S4] Score = 758 bits
 (1957), Expect = 0.0

NOTE:

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

Input Summary

Search id 20060404123855-1D2C-192168001107
Sequences 1714
Date & Time Tue Apr 04 17:38:55 2006 UTC (Search Time: 0.19 sec.)
Sample ID Schu4 237
Database schu2K [..\databases\schu2k]
Taxonomy -
Mass Range 0 - 100 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) 868.527 882.550 927.556 1124.715 1173.717 1188.670 1350.806
 1516.835 1639.852 2361.198
Tolerance (mon) 60.00 ppm
Number of
Peptides 10

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