

**Figure 3.6:** Alignments for ALDH (A), CtfA (B) and CtfB (C) from *C. beijerinckii* NRRL B592 and *C. beijerinckii* NRRL B593. "+" indicates conservative substitutions.

## BLAST 2 SEQUENCES RESULTS

VERSION BLASTP 2.0.9 [May-07-1999]

**A.**

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Query 1      ALDH from B592      Length   468  from:1 to = 468
Sbjct 1      ALDH from B593      Length   468  from:1 to = 468
Score = 922 bits (2357), Expect = 0.0
Identities = 455/468 (97%), Positives = 463/468 (98%)

Query: 1  MNKDTLIPTTKDLKVKTNGENINLNKKNYKDNSSCFGVFENVENAISSAVHAQKILSLHYTK 60
Sbjct: 1  MNKDTLIPTTKDLK+KTN ENINLNKKNYKDNSSCFGVFENVENAI+SAVHAQKILSLHYTK 60

Query: 61  EQREKIIITEIRKAALQNKEVLATMILEETHMGRYEDKILKHELVAKYTPGTEDLTTTAW 120
Sbjct: 61  EQREKIIITEIRKAAL+NKEVLATMILEETHMGRYEDKILKHELVAKYTPGTEDLTTTAW 120

Query: 121  GDNGLTVVEMSPYGVIGAITPSTNPTETVICNSIGMIAAGNAVVFNGHPCAKKCVAF 180
Sbjct: 121  GDNGLTVVEMSPYGVIGAITPSTNPTETVICNSIGMIAAGNAVVFNGHP AKKCVAF+E 180

Query: 181  MINKAIIISCGG PENLVTTIKNPTMESLDAIIKHPSIKLLCGTGGPGMVKTLLNSG 240
Sbjct: 181  MINKAIIISCGG PENLVTTIKNPTMESLDAIIKHPLIKLLCGTGGPGMVKTLLNSG 240

Query: 241  AGAGNPPVIVDDTADIEKAGRSIIIEGCSFDNNLPCIAEKEVVFVENVADDLISNML 300
Sbjct: 241  AGAGNPPVIVDDTADIEKAG+SIIIEGCSFDNNLPCIAEKEVVFVENVADDLISNML 300

Query: 301  VIINEDQVSKLIDLVLQKNNETQEYFINKKWVGKDAKFLDEIDVESPSNVKCIICE 360
Sbjct: 301  VIINEDQVSKLIDLVLQKNNETQEYFINKKWVGKDAKLF DEIDVESPSN+KCI+CE 360

Query: 361  NHPFVMTLMMPILPIVRVKDIDEAIIKYAKIAEQNRKHSAYIYSKNIDNLRNFERE 420
Sbjct: 361  NHPFVMTLMMPILPIVRVKDIDEA+KY KIAEQNRKHSAYIYSKNIDNLRNFERE 420

Query: 421  IFVKNAKSFAGVGYEAEAGFTTFTIAGSTGEGITSARNFTRQRRCVLAG 468
Sbjct: 421  IFVKNAKSFAGVGYEAEAGFTTFTIAGSTGEGITSARNFTRQRRCVLAG 468

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**B.**

Chapter III

**Query 1**            **CtfA** in B592            **Length**    217    from:1 to = 217

**Sbjct 1**            **CtfA** in B593            **Length**    217    from:1 to = 217

Score = 390 bits (991), Expect < e-108  
Identities = 216/217 (99.5%), Positives = 216/217 (99.5%)

Query: 1    MNKLVKLTDLKRIFKDGMTIMVGGFLDCGTPENIIDMLVDLNIKNLTIISNDTAFPNKGI 60  
          MNKLVKLTDLKRIFKDGMTIMVGGFLDCGTPENIIDMLVDLNIKNLTIISNDTAFPNKGI  
Sbjct: 1    MNKLVKLTDLKRIFKDGMTIMVGGFLDCGTPENIIDMLVDLNIKNLTIISNDTAFPNKGI 60

Query: 61    GKLIVNGQVSKVIAASHIGTNPETGKKMSSGELKVELSPQGTLIERIRAAGSGLGGVLTPT 120  
          GKLIVNGQVSKVIAASHIGTNPETGKKMSSGELKVELSPQGTLIERIRAAGSGLGGVLTPT  
Sbjct: 61    GKLIVNGQVSKVIAASHIGTNPETGKKMSSGELKVELSPQGTLIERIRAAGSGLGGVLTPT 120

Query: 121    GLGTIVEEGKKKVTIDGKEYLLELPLSADVSLIKGSIVDEFNGTFYRAATKNFNPYMAMA 180  
          GLGTIVEEGKKKVTI GKEYLLELPLSADVSLIKGSIVDEFNGTFYRAATKNFNPYMAMA  
Sbjct: 121    GLGTIVEEGKKKVTIGGKEYLLELPLSADVSLIKGSIVDEFNGTFYRAATKNFNPYMAMA 180

Query: 181    AKTVIVEAENLVKCEDLKRDAIMTPGVLVDYIVKEAA 217  
          AKTVIVEAENLVKCEDLKRDAIMTPGVLVDYIVKEAA  
Sbjct: 181    AKTVIVEAENLVKCEDLKRDAIMTPGVLVDYIVKEAA 217

**C.**

**Query 1**            **CtfB** in B592            **Length**    221    from:1 to = 221

**Sbjct 1**            **CtfB** in B593            **Length**    221    from:1 to = 221

Score = 423 bits (1077), Expect = e-118  
Identities = 214/221 (96%), Positives = 217/221 (97%)

Query: 1    LIVDKVLAKEIIAKRVAKELKKDQLVNLGIGLPTLVANYVPKEMNITFESENGMVGMAQM 60  
          LIVDKVLAKEIIAKRVAKELKK QLVNLGIGLPTLVANYVPKEMNITFESENGMVGMAQM  
Sbjct: 1    LIVDKVLAKEIIAKRVAKELKKGQLVNLGIGLPTLVANYVPKEMNITFESENGMVGMAQM 60

Query: 61    ASSGENDPDIINAGGEYVTLPLPQGSFFDSSMSFALIRGGHVDVAVLGALEVDEKGNLANW 120  
          ASSGENDPDIINAGGEYVTLPLPQG+FFDSS SFALIRGGHVDVAVLGALEVDE+GNLANW  
Sbjct: 61    ASSGENDPDIINAGGEYVTLPLPQGAFFDSSTSFALIRGGHVDVAVLGALEVDEEGNLANW 120

Query: 121    IVPNKIVPGMGAMDLAIGAKKIIIVAMQHTGKSKPKIVKKCTLPLTAKAQVDLIVTELCV 180  
          IVPNKIVPGMGAMDLAIGAKKIIIVAMQHTGK KPKIVKKCTLPLTAKAQVDLIVTELCV  
Sbjct: 121    IVPNKIVPGMGAMDLAIGAKKIIIVAMQHTGKGPKIVKKCTLPLTAKAQVDLIVTELCV 180

Query: 181    IDVTNDGLLLKEIHKDTTIDEIKFLTDADLIIPDNLKIMDI 221  
          IDVTNDGLL +EIHKDTTIDEIKFLTDADLIIPDNLKIMDI  
Sbjct: 181    IDVTNDGLLFREIHKDTTIDEIKFLTDADLIIPDNLKIMDI 221