

A

Score = 32.7 bits (73), Expect = 0.57, Method: Compositional matrix adjust.
Identities = 35/138 (26%), Positives = 52/138 (38%), Gaps = 27/138 (19%)

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Query 89 PAGTITVTEFFDYRCGYCRQATPAVLELVQKNPDIRLVLKDFVIFGNDSEAAARIALGAK 148
      P   +T F D CGYC +   + +   +R +   +D+E +   AK
Sbjct 104 PQEKHVITVFTDITCGYCHKLHEQMADYNALGITVRYLAFPRQGLSDAEKEMKAIWCAK 163

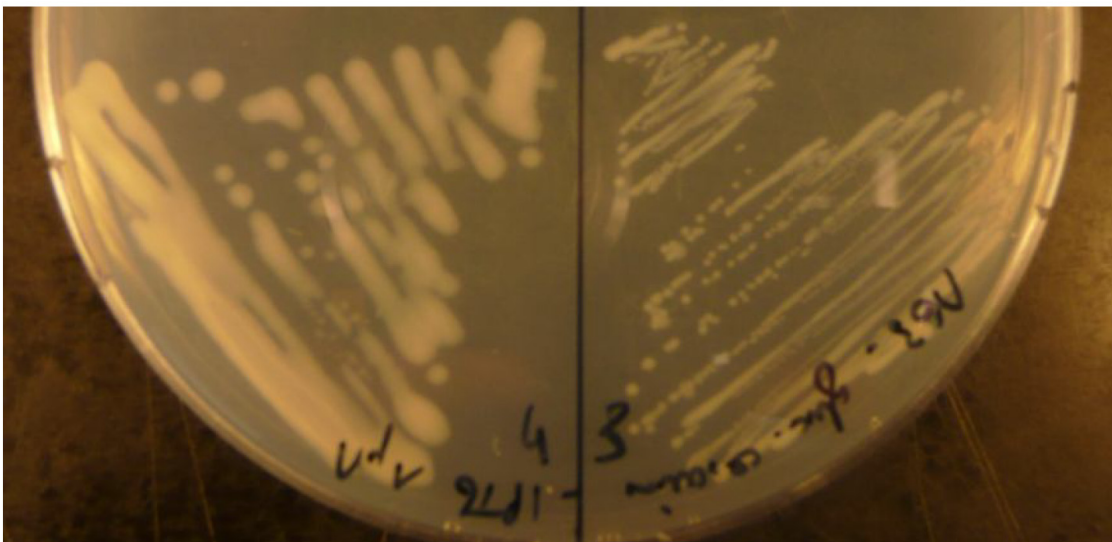
Query 149 DQGKSLELHKALMAENALDARGALRIAERLGI DMDKAKAVGESQAITQHLADTDALARAL 208
      D+ K           A D  A +   D+D           +AD AL  L
Sbjct 164 DKNK-----AFDDVMAGKSVAPASCDVD-----IADHYALGVQL 197

Query 209 NLSGTPAFIVGD-TLVPG 225           Cc ScsC
      +SGTPA ++ + TLVPG
Sbjct 198 GVSGTPAVVLSNGTLVPG 215           DsbC
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B

pDSW204::*dsbAss-Cc scsC-His*

pDSW204



PLD262: *dsbC mdoG E. coli*