

prof_sim alignment

c.69.1.10 281 aa <-> c.69.1.12 277 aa score 123.3 p-value 2.41e-03

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225  VLVFHGRQDRIVPLD.TSLYLTKHLKHAELVVLD 257
      .L: HG  DR.:P.. T.   .K L. AE.V. .
220  ALILHGTGDRTLPIENTARVFHKALPSAEYVEVE 253

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36% identity in 33 aa overlap

prof_ss alignment (predicted ss)

c.69.1.10 281 aa <-> c.69.1.12 277 aa score 137.2 p-value 6.44e-04

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52  LAENFFVVPDLIGFGQSEYPETYPGHIMSWVGMRVEQILGLMNHFGIEKSHIVGNSMGGAVTLQLVVEA.PERFDKVAL 130
      L.. . V:. D  GFGQS. P T  G. .   ... :.... . . . .VG S.G:   . V .. . R  KVA:
47  LDAGYRVITYDRRGFGQSSQPTT..GYDYD...TFAADLNTVLETLDLQDAVLVGSTGTGEVARYVSSYGTARIAKVAF 121

131  MGSV.....GAPMNARPPELARLLAFYADPRLTPYRELIHSFVYDPENFPGMEEIVKSRFEVANDPEVRRIQEVM.. 200
      . S:      P  A P E.      . . . . . D  F  ...      . . . . . R  .E..
122  LASLEPFLKTDNDNPDGAAPQEF.....FDGIVA AVKADRYAF..YTGFNFDFYNLDENLGTRISEEAVRN 185

201  ..FESMKAGMESLVIPPAT.....LGR LPHDVLVFHGRQDRIVPLD.TSLYLTKHLKHAELVVLD 257
      .. G... . P.T      : R.   .L: HG  DR.:P.. T.   .K L. AE.V...
186  SWNTAASGGFFAAAAAPT TWYTD FRADIPRIDVPALILHGTGDRTLPIENTARVFHKALPSAEYVEVE 253

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24% identity in 185 aa overlap

prof_ss alignment (true ss)

c.69.1.10 281 aa <-> c.69.1.12 277 aa score 280.8 p-value 7.79e-10

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29  VVLLHGAGPGAHAASNW.RPIIPDLAENFFVVPDLIGFGQSEYPETYPGHIMSWVGMRVEQILGLMNHFGIEKSHIVGN 107
      VVL.HG P .   ...W R ..  L.. . V:. D  GFGQS. P T  G. .   ... :.... . . . .VG
26  VVLIHGF.PLS..GHSWERQSAALLDAGYRVITYDRRGFGQSSQPTT..GYDYD...TFAADLNTVLETLDLQDAVLVG 97

108  SMGGAVTLQLVVE.APERFDKVALMGSV.....GAPMNARPPELARLL..AFYADPRLTPYRELIHSFVYDPENFPG 176
      S.G:   . . V . . . R. KVA:. S:      P  A P E.   :  A  AD R . Y... .F Y   . .G
98  STGTGEVARYVSSYGTARIAKVAFLASLEPFLKTDNDNPDGAAPQEFFD GIVA AVKAD.RYAFYTGFNFDF.YNLDENLG 175

177  M...EEIVKSRFEVAND...PEVRRIQEVMFESMKAGMESLVIPPATLGR LPHDVLVFHGRQDRIVPLD.TSLYLTKHLK 249
      EE.V.. .A   . . . . .A .... :P      .L: HG  .DR.:P.. T.   .K L.
176  TRISEEAVRNSWNTAASGGFFAAAAAPT TWYTD FRADIPRIDVP.....ALILHGTGDRTLPIENTARVFHKALP 245

250  HAELVVLDRCGHWAQLERWDAMG PMLME 277
      AE:V...  H      ... . L..
246  SAEYVEVEGAPHGLLWTHAE EVNTALLA 273

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26% identity in 229 aa overlap