

prof_sim alignment

a.4.5.12 100 aa <-> a.4.5.7 120 aa score 145.6 p-value 5.90e-05

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1   VPKRVYWEMLATNLTKEYVRTRRALILEILIKAGSLKIEQIQDNLKKLGFD....EVIETIENDIKGLINTGIF..IEI   74
   V .R . . . .T..E   R   L..L           E .. ..K..GF   EV ... .   L.. GI.  I.:
11  VKQRAFLKLYMITMTEQE.....RLYGLKLL.....EVLRSEFKEIGFKPNHTEVYRSLHE....LLDDGILKQIKV   73

75  KGRFYQLKD HIL.QF   88
   K .   .L... :L QF
74  KKEGAKLQEVVLYQF   88
  
```

30% identity in 71 aa overlap

prof_ss alignment (true ss)

a.4.5.12 100 aa <-> a.4.5.7 120 aa score 161.5 p-value 1.31e-05

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20  VRTRRALILEILI.....KAGSLKI.EQIQDNLKKLGFD EVIETIENDIKGLINTGIF..IEIKGR.....FYQLKD   83
   V..R  L L ..      .   LK. E .... K..GF           :   .. L.. GI   I.:K .           .YQ.KD
11  VKQRAFLKLYMITMTEQERLYGLKLLEVL RSEFKEIGFKPNHTEVYRSLHELDDGILKQIKVKKEGAKLQEVVLYQFKD   90
  
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29% identity in 64 aa overlap