A.

```
>PHA00619 CRISPR-associated Cas4-like protein
  Probab=94.53  E-value=0.078  Score=42.16  Aligned_cols=78  Identities=27%  Similarity=0.323  Sum_probs=0.0

  Q ss_pred                eeccCCcccccccccc-ccCchHHHHHhhhcC-CcccchhHHHHHhcccchhHHHHHHHHHcCCcccccc------Chhh
  Q Wed_Aug_26_18:   11 YTIDENKEINSISAAD-TICPYRAYRSYHRKI-PIKIDDCKEARKIAGSMTHYVILRQLKEQGCETEKIV------DPEL   82 (113)
  Q Consensus        11 ytidenkeinsisaad-ticpyrayrsyhrki-pikiddckearkiagsmthyvilrqlkeqgcetekiv------dpel   82 (113)
                        |.+-+.+..+.|-+.| ..||-++|  |-++. |.+++.-.--+-+.|+..|-.+-+-|++.|.|+|+.|      +.++
  T Consensus        12 ~~~~~~~~~~~i~vTdl~~CpRk~~--~~~~~~~~~~~~~~~~~~~~~~G~~lHe~le~iLk~~g~e~E~eve~~~~~g~~I   89 (201)
  T PHA00619         12 YEIVSQNDLQTIWVTELSRCLRRSW--LMRKNGGVKLALEEAMKMHIGSGLHMRLQRILKKHGFETECRVERKTALGFEI   89 (201)
  T ss_pred                HhhcccCCCCEEEEeehhhCccHHH--HHHhCCcccccchhhHHHHhhHHHHHHHHHHHHHhCCceeEEEEEEEcCCCcEE


  Q ss_pred                cccccccc
  Q Wed_Aug_26_18:   83 KFRADAIC   90 (113)
  Q Consensus        83 kfradaic   90 (113)
                        +-|+|+++
  T Consensus        90 ~GrID~i~   97 (201)
  T PHA00619         90 VGKIDVYD   97 (201)
  T ss_pred                EEEEEEEe
```

B.

```
>4ic1_A CAS4, crispr, MCSG, exonuclease, PSI-biology, structural GEN unknown function; 2.35A {Sulfolobus solfataricus}
  Probab=96.31  E-value=0.0049  Score=40.81  Aligned_cols=67  Identities=24%  Similarity=0.339  Sum_probs=0.0

  Q ss_pred                eEEecccccccEEEEcCCeeEEEEcChHHHhhHHHHHHHHHHHhhCchhhhhhcCceeeehhhhhhhhcccc
  Q Thu_Aug_27_19:    2 YIALAGAERGHLIYINNGIRTTIQMDEEERVKITEYVRNLIRRIKNGEAVEERNRGIWCNICEFKAECNHKL   73 (74)
  Q Consensus         2 yialagaerghliyinngirttiqmdeeervkiteyvrnlirrikngeaveernrgiwcnicefkaecnhkl   73 (74)
                        |..+.....|-|+|++.+-...+..|++.+.+.   +.+.|+.|.++....  ..+-+|.-|.|+.-|..+.
  T Consensus       139 Y~~~~~~~~g~l~y~~~~~~~~~~~~~~~~~~~~~---l~~~i~~i~~~~~~P--~~~~~C~~C~~~~~C~~~~  205 (206)
  T 4ic1_A          139 YLWLFSAEKGILVYITPDRIAEYEINEPLDEAT---IVRLAEDTIMLQNSP--RFNWECKYCIFSVICPAKL  205 (206)
  T ss_dssp                HHHHHTCSEEEEEEEETTEEEEEEECCCCCHHH---HHHHHHHHHTTCSSS--SSTTSGGGCTTGGGCTTCC
  T ss_pred                HHHHHhccCcEEEEEeCCceEEEecCcchhHHH---HHHHHHHHHhcCCCC--CCCCCCCCCCcccccCCcc


>PHA00619 CRISPR-associated Cas4-like protein
  Probab=93.46  E-value=0.14  Score=38.31  Aligned_cols=67  Identities=19%  Similarity=0.303  Sum_probs=0.0

  Q ss_pred                eEEecccccccEEE-EcCCeeEEEEcChHHHhhHHHHHHHHHHHhhCchhhhhhc-Cceeeehhhhhhhh
  Q Thu_Aug_27_19:    2 YIALAGAERGHLIY-INNGIRTTIQMDEEERVKITEYVRNLIRRIKNGEAVEERN-RGIWCNICEFKAEC   69 (74)
  Q Consensus         2 yialagaerghliy-inngirttiqmdeeervkiteyvrnlirrikngeaveern-rgiwcnicefkaec   69 (74)
                        |+-+++++.|.|+| --++..-.|. +++....+.+-+..+.+-+++-..-+..- ...+|..|.|+.-|
  T Consensus       129 Yl~~l~~~~G~L~~V~~d~~~e~v~-~d~~e~el~~~~~~~l~~~l~~~~~p~~~p~~~~~C~~C~f~~~C  197 (201)
  T PHA00619        129 YIEMANAMAGYLIIVHADGRVEEIK-RDWSETDLENRANAFGISVEENILPPKKSKPDSECIECPFYNVC  197 (201)
  T ss_pred                HHHHHHHcCCEEEEEeCCCCeEEec-CchhHHHHHHHHHHHHHHHhccCCCCCCCCcCCCCCCCCCChhhc
```

Figure S1. Results of the HHpred search seeded with TP1 (A) and gp7 (B) sequences. H(h), α-helix; E(e), β-strand; C(c), coil.