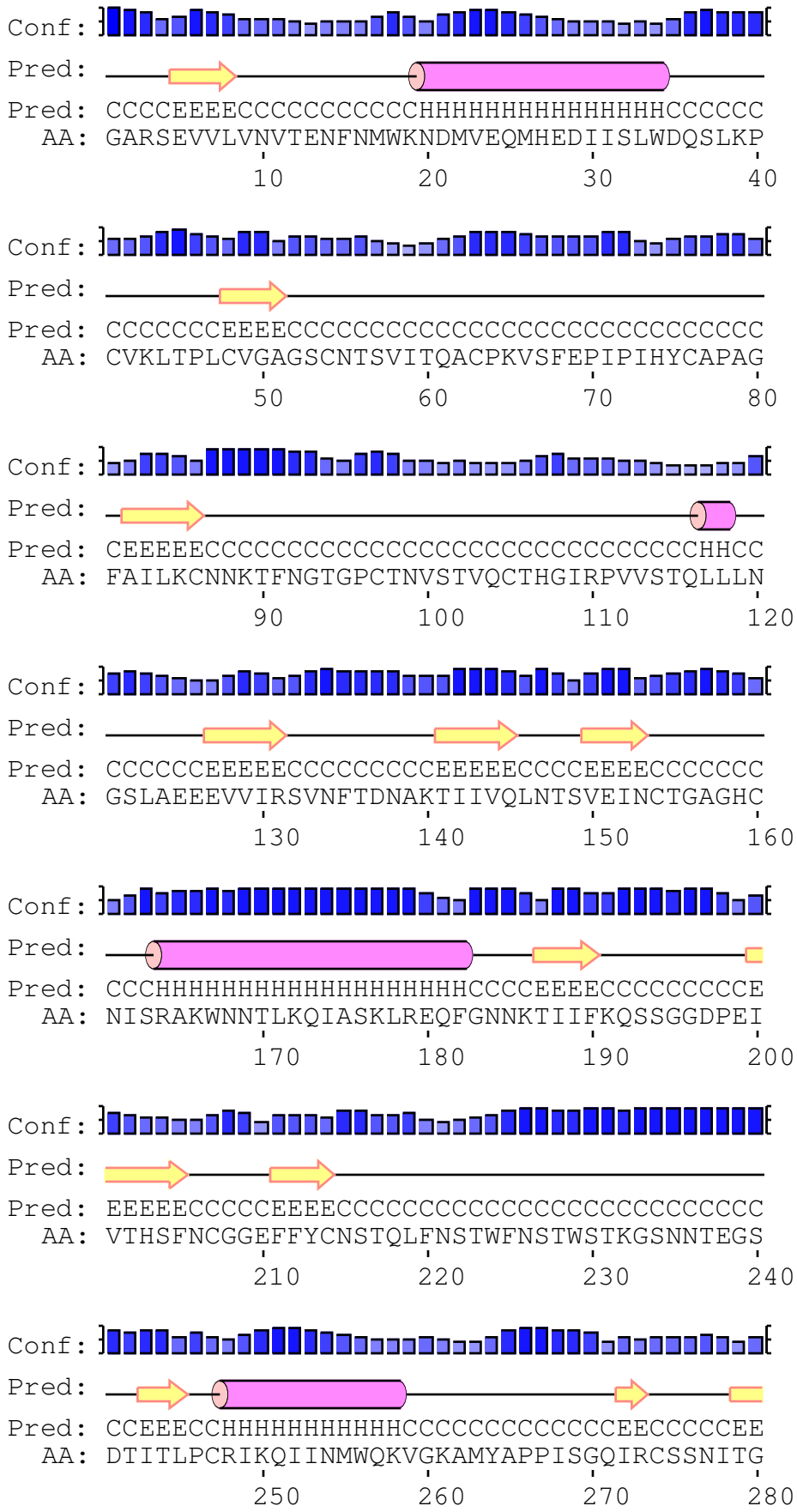
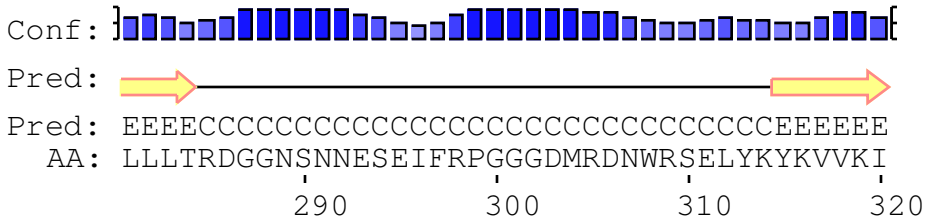
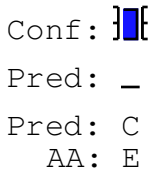
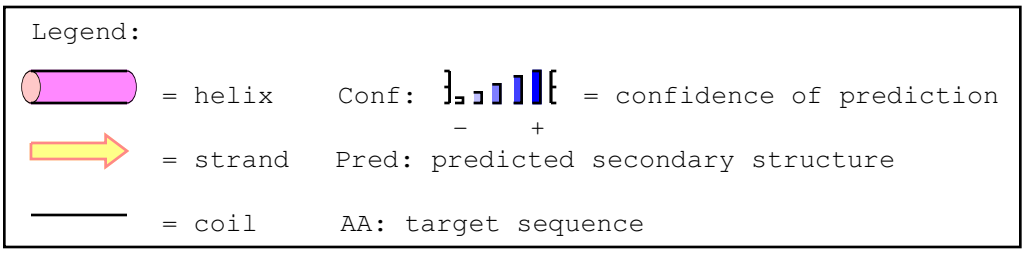

Conf:
Pred:
Pred: CCCCEEEECCCCCCCCCCCHHHHHHHHHHHHHHHCCCCCC
AA: GARSEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKP
10 20 30 40
Conf:
Pred:
Pred: CCCCCCCEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCC
AA: CVKLTPLCVGAGSCNTSVITQACPKVSFEPIPIHYCAPAG
50 60 70 80
Conf:
Pred:
Pred: CEEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHCC
AA: FAILKCNNKTFNGTGPCTNVSTVQCTHGIRPVVSTQLLLN
90 100 110 120
Conf:
Pred:
Pred: CCCCCCCEEEEECCCCCCCCCEEEEECCCCEEEECCCCCCC
AA: GSLAEEEVVIRSVNFTDNAKTIIVQLNTSVEINCTGAGHC
130 140 150 160
Conf:
Pred:
Pred: CCCHHHHHHHHHHHHHHHHHHCCCCEEEECCCCCCCCCE
AA: NISRAKWNNTLKQIASKLREQFGNNKTIIFKQSSGGDPEI
170 180 190 200
Conf:
Pred:
Pred: EEEEECCCCCEEEECCCCCCCCCCCCCCCCCCCCCCCCC
AA: VTHSFNCGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGS
210 220 230 240
Conf:
Pred:
Pred: CCEEECCHHHHHHHHHHCCCCCCCCCCCCCEECCCCCEE
AA: DTITLPCRIKQIINMWQKVGKAMYAPPISGQIRCSSNITG
250 260 270 280


Conf:
Pred:
Pred: EEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEEEEE
AA: LLLTRDGGNSNNESEIFRPGGGDMRDNWRSELYKYKVVKI
290
300
310
320


Conf:
Pred: _
Pred: C
AA: E


Legend:
= helix
Conf:
= confidence of prediction
-
+
= strand
Pred: predicted secondary structure
= coil
AA: target sequence