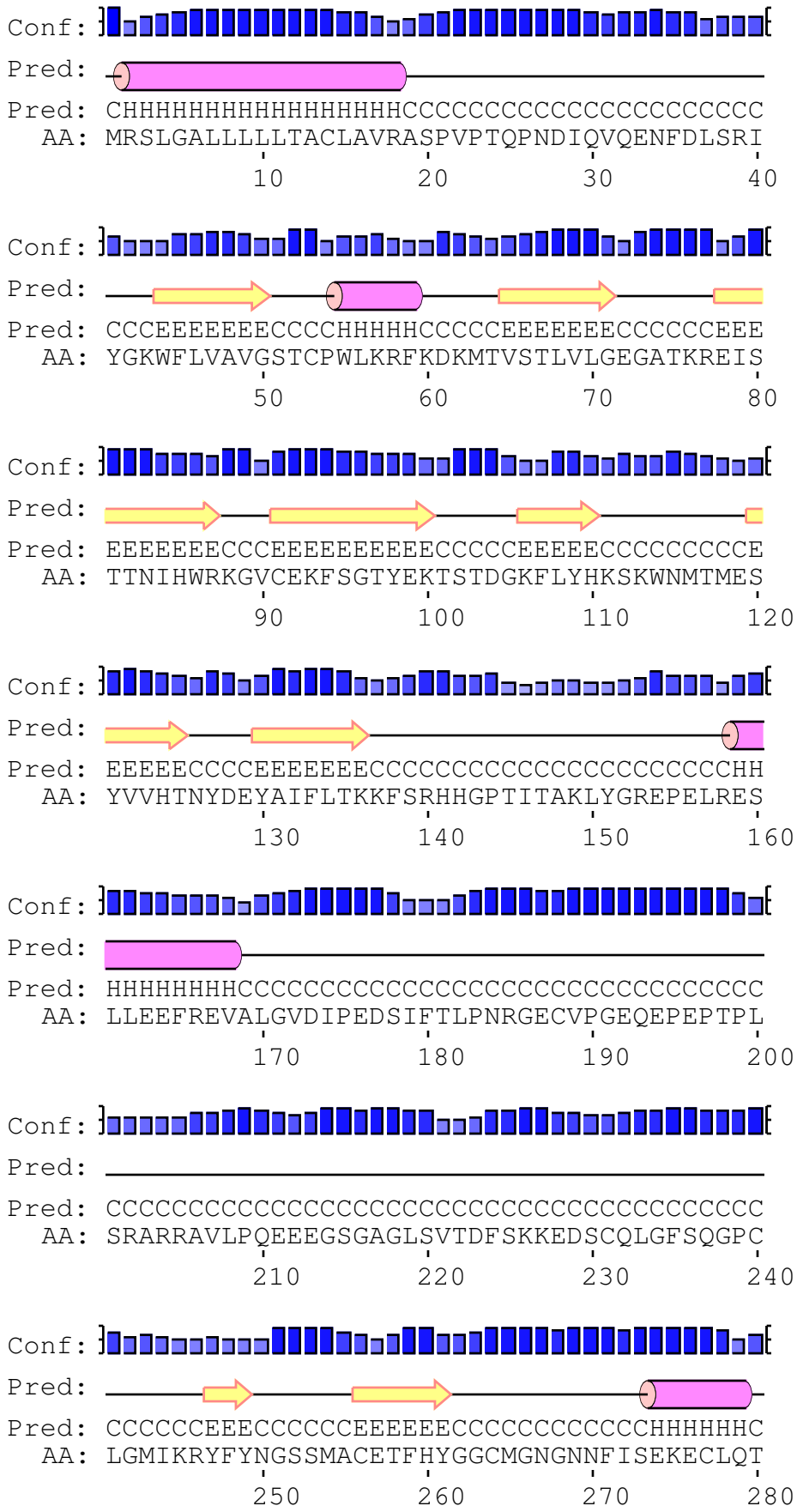
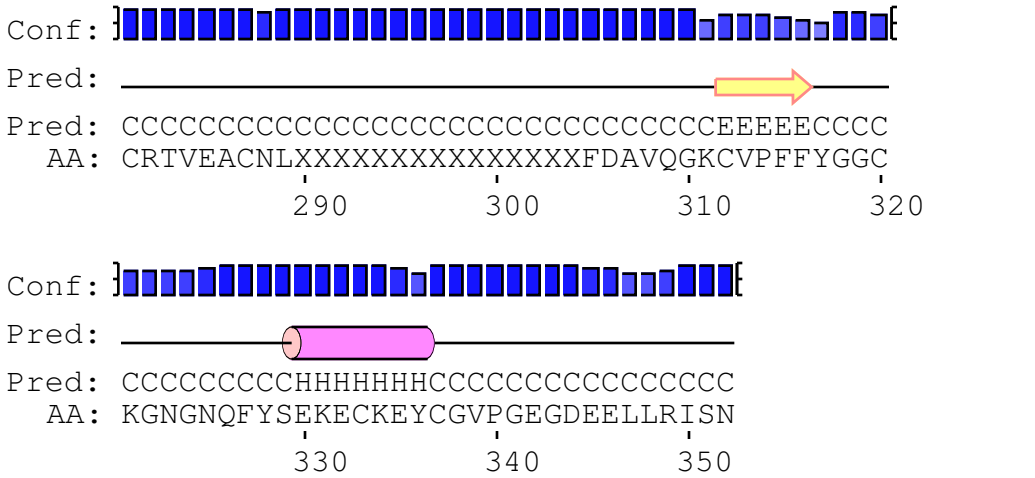
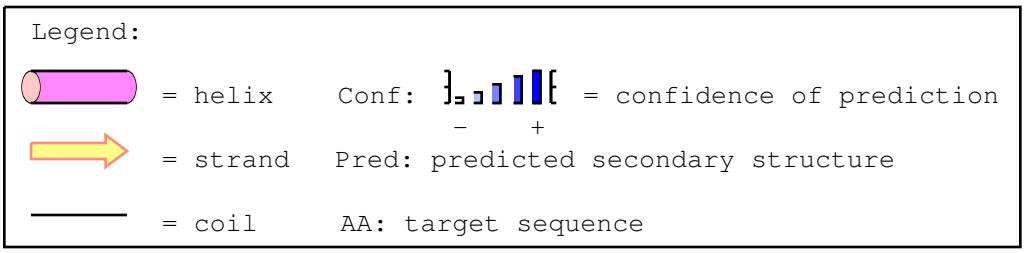

Conf:
Pred:
Pred: CHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCC
AA: MRSLGALLLLLTACLAVRASPVPTQPNDIQVQENFDLSRI
10 20 30 40
Conf:
Pred:
Pred: CCCEEEEEEECCCCHHHHHCCCCCEEEEEEECCCCCCEEE
AA: YGKWFLVAVGSTCPWLKRFKDKMTVSTLVLGEGATKREIS
50 60 70 80
Conf:
Pred:
Pred: EEEEEEECCCEEEEEEEEECCCCCEEEEECCCCCCCCCE
AA: TTNIHWRKGVCEKFSGTYEKTSTDGKFLYHKSKWNMTMES
90 100 110 120
Conf:
Pred:
Pred: EEEEECCCCEEEEEEECCCCCCCCCCCCCCCCCCCCCCHH
AA: YVVHTNYDEYAIFLTKKFSRHHGPTITAKLYGREPELRES
130 140 150 160
Conf:
Pred:
Pred: HHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
AA: LLEEFREVALGVDIPEDSIFTLPNRGECVPGEQEPEPTPL
170 180 190 200
Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
AA: SRARRAVLPQEEEGSGAGLSVTDFSKKEDSCQLGFSQGPC
210 220 230 240
Conf:
Pred:
Pred: CCCCCCEEECCCCCCEEEEEECCCCCCCCCCCCHHHHHHC
AA: LGMIKRYFYNGSSMACETFHYGGCMGNGNNFISEKECLQT
250 260 270 280


Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEEEECCCC
AA: CRTVEACNLXXXXXXXXXXXXXXXFDAVQGKCVPFFYGGC
290 300 310 320
Conf:
Pred:
Pred: CCCCCCCCCHHHHHHHCCCCCCCCCCCCCCCC
AA: KGNGNQFYSEKECKEYCGVPGEGDEELLRISN
330 340 350


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