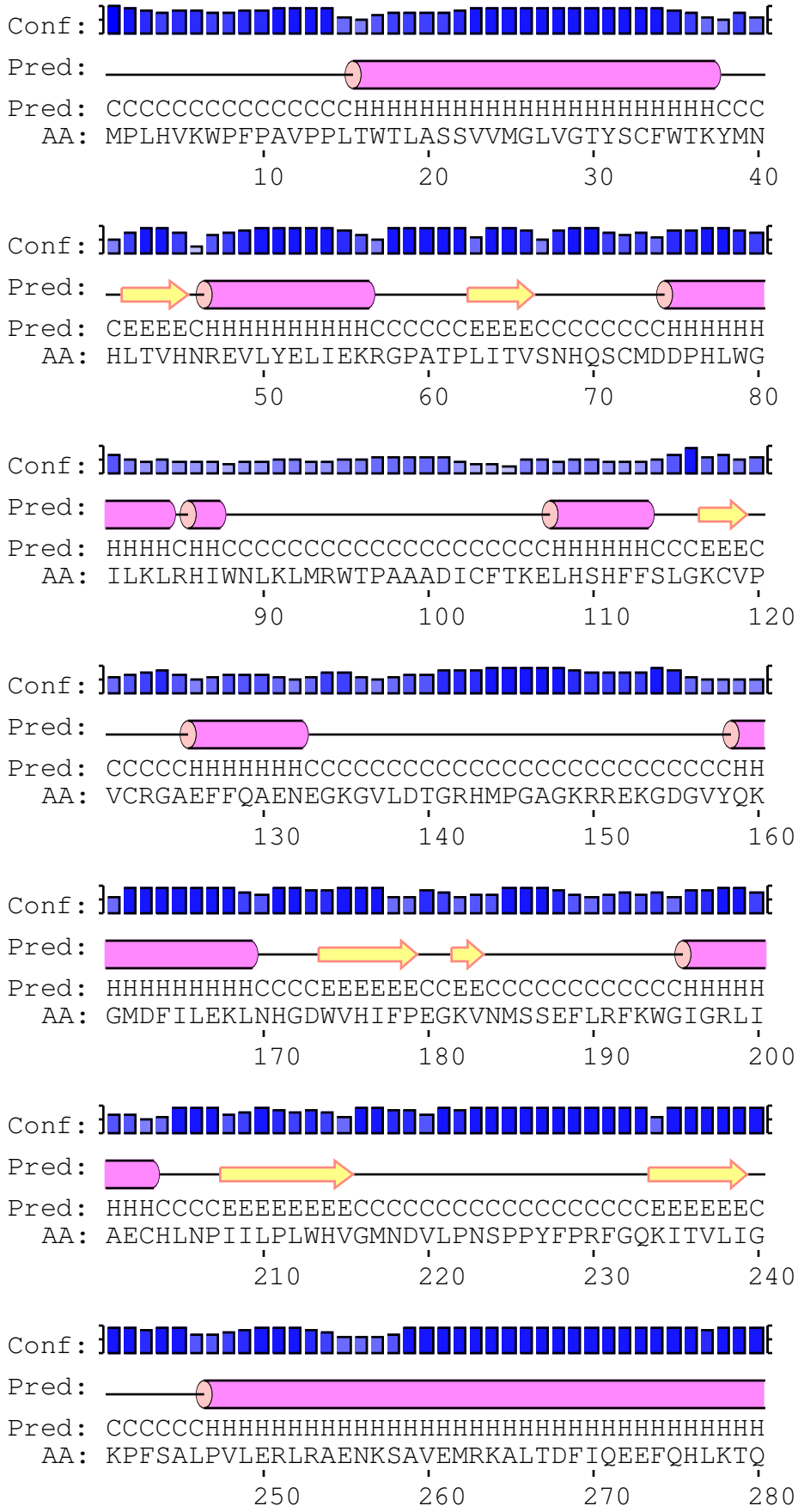
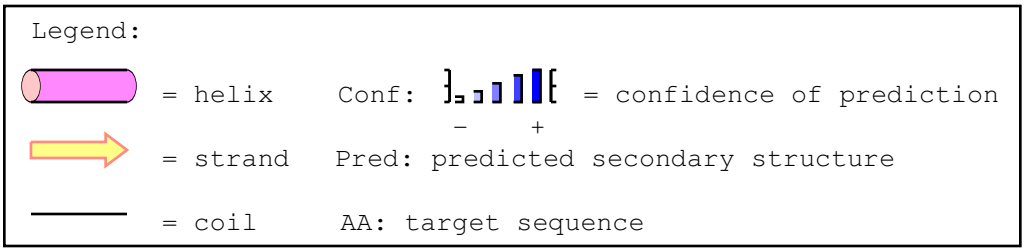

Conf:
Pred:
Pred: CCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHCCC
AA: MPLHVKWPFPAVPPLTWTLASSVVMGLVGTYSCFWTKYMN
10 20 30 40
Conf:
Pred:
Pred: CEEEECHHHHHHHHHHCCCCCCEEEECCCCCCCCHHHHHH
AA: HLTVHNREVLYELIEKRGPATPLITVSNHQSCMDDPHLWG
50 60 70 80
Conf:
Pred:
Pred: HHHHCHHCCCCCCCCCCCCCCCCCCCCHHHHHHCCCEEEC
AA: ILKLRHIWNLKLMRWTPAAADICFTKELHSHFFSLGKCVP
90 100 110 120
Conf:
Pred:
Pred: CCCCCHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCHH
AA: VCRGAEFFQAENEGKGVLDTGRHMPGAGKRREKGDGVYQK
130 140 150 160
Conf:
Pred:
Pred: HHHHHHHHHCCCCEEEEEECCEECCCCCCCCCCCCHHHHH
AA: GMDFILEKLNHGDWVHIFPEGKVNMSSEFLRFKWGIGRLI
170 180 190 200
Conf:
Pred:
Pred: HHHCCCCEEEEEEECCCCCCCCCCCCCCCCCCEEEEEEC
AA: AECHLNPIILPLWHVGMNDVLPNSPPYFPRFGQKITVLIG
210 220 230 240
Conf:
Pred:
Pred: CCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
AA: KPFSALPVLERLRAENKSAVEMRKALTDFIQEEFQHLKTQ
250 260 270 280

Conf:
Pred:
Pred: HHHHHHCCCCCC
AA: AEQLHNHLQPGR
290


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