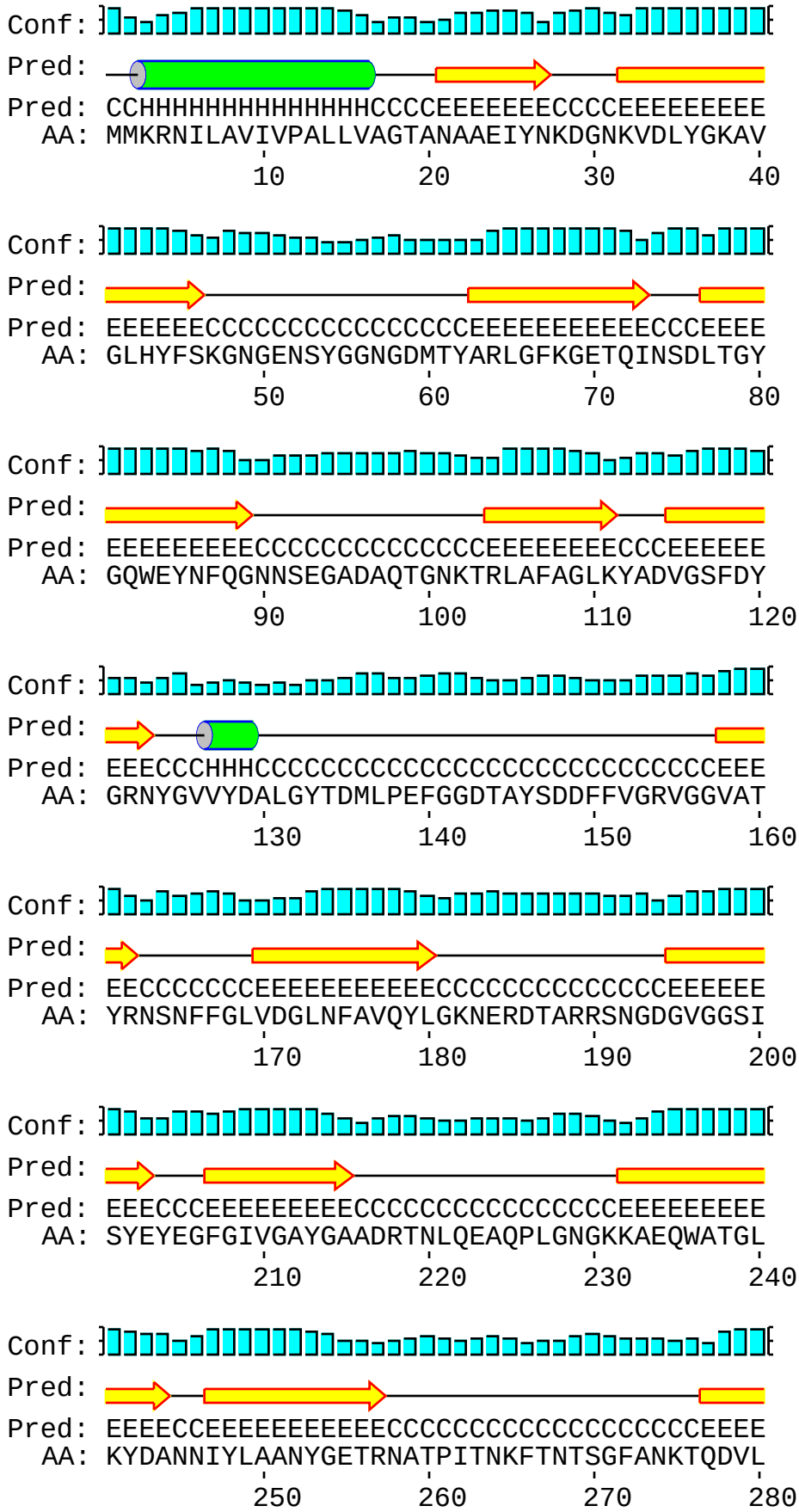
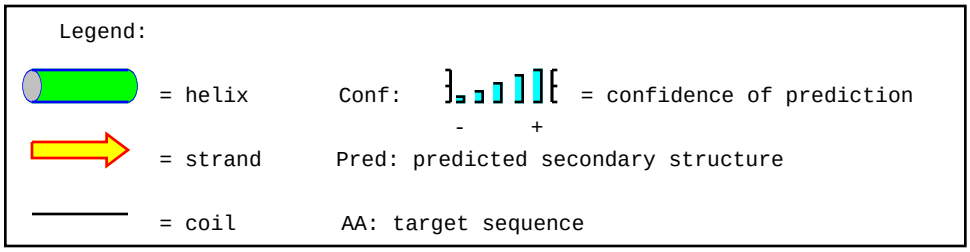

Conf:
Pred:
Pred: CCHHHHHHHHHHHHHHCCCCEEEEEEECCCCEEEEEEEEE
AA: MMKRNILAVIVPALLVAGTANAAEIYNKDGNKVDLYGKAV
10 20 30 40
Conf:
Pred:
Pred: EEEEEECCCCCCCCCCCCCCCEEEEEEEEEEEECCCEEEE
AA: GLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGY
50 60 70 80
Conf:
Pred:
Pred: EEEEEEEEECCCCCCCCCCCCCEEEEEEEEECCCEEEEEE
AA: GQWEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDY
90 100 110 120
Conf:
Pred:
Pred: EEECCCHHHCCCCCCCCCCCCCCCCCCCCCCCCCCEEE
AA: GRNYGVVYDALGYTDMLPEFGGDTAYSDDFFVGRVGGVAT
130 140 150 160
Conf:
Pred:
Pred: EECCCCCCCEEEEEEEEEECCCCCCCCCCCCCEEEEEE
AA: YRNSNFFGLVDGLNFAVQYLGKNERDTARRSNGDGVGGSI
170 180 190 200
Conf:
Pred:
Pred: EEECCCEEEEEEEECCCCCCCCCCCCCCCEEEEEEEEE
AA: SYEYEGFGIVGAYGAADRTNLQEAQPLGNGKKAEQWATGL
210 220 230 240
Conf:
Pred:
Pred: EEEECCEEEEEEEEECCCCCCCCCCCCCCCCCCCEEEE
AA: KYDANNIYLAANYGETRNATPITNKFTNTSGFANKTQDVL
250 260 270 280

Conf:
Pred:
Pred: EEEEEEECCEEEEEEEEEEECCCCCCCCCCCCEEEEEEEE
AA: LVAQYQFDFGLRPSIAYTKSKAKDVEGIGDVDLVNYFEVG
290 300 310 320
Conf:
Pred:
Pred: EEEEECCCEEEEEEEEEECCCCCCCCCCCCCEEEEEEEE
AA: ATYYFNKNMSTYVDYIINQIDSDNKLGVGSDDTVAVGIVY
330 340 350 360
Conf:
Pred:
Pred: EC
AA: QF


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