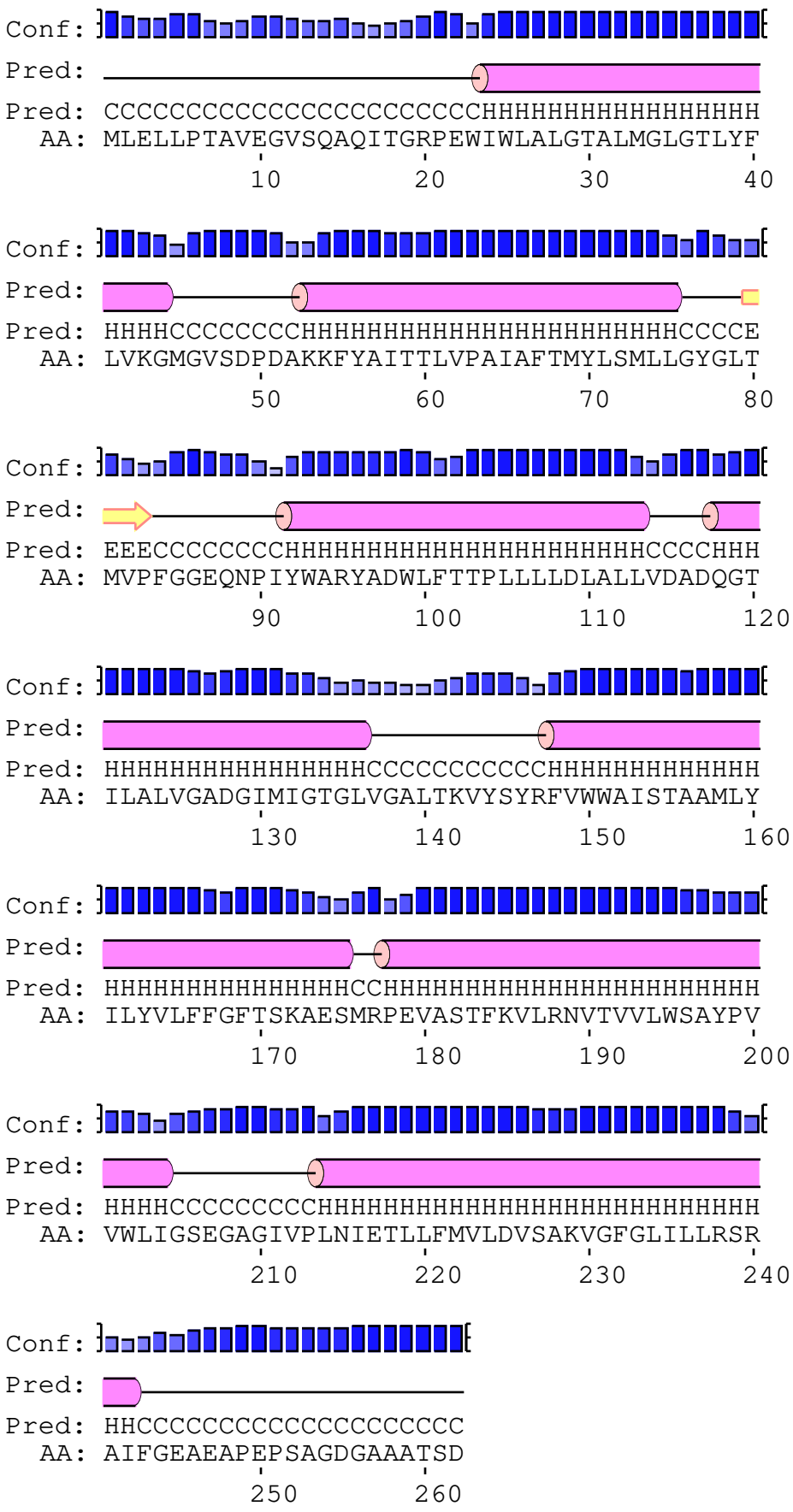
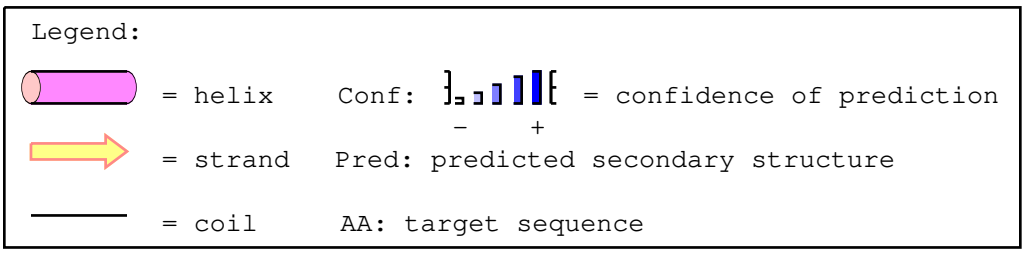

Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHH
AA: MLELLPTAVEGVSQAQITGRPEWIWLALGTALMGLGTLYF
10 20 30 40
Conf:
Pred:
Pred: HHHHCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHCCCCE
AA: LVKGMGVSDPDAKKFYAITTLVPAIAFTMYLSMLLGYGLT
50 60 70 80
Conf:
Pred:
Pred: EEECCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHCCCCHHH
AA: MVPFGGEQNPIYWARYADWLFTTPLLLLDLALLVDADQGT
90 100 110 120
Conf:
Pred:
Pred: HHHHHHHHHHHHHHHHHCCCCCCCCCCCHHHHHHHHHHHHH
AA: ILALVGADGIMIGTGLVGALTKVYSYRFVWWAISTAAMLY
130 140 150 160
Conf:
Pred:
Pred: HHHHHHHHHHHHHHHHCCHHHHHHHHHHHHHHHHHHHHHHH
AA: ILYVLFFGFTSKAESMRPEVASTFKVLRNVTVVLWSAYPV
170 180 190 200
Conf:
Pred:
Pred: HHHHCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHH
AA: VWLIGSEGAGIVPLNIETLLFMVLDVSAKVGFGLILLRSR
210 220 230 240
Conf:
Pred:
Pred: HHCCCCCCCCCCCCCCCCCCC
AA: AIFGEAEAPEPSAGDGAAATSD
250 260


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