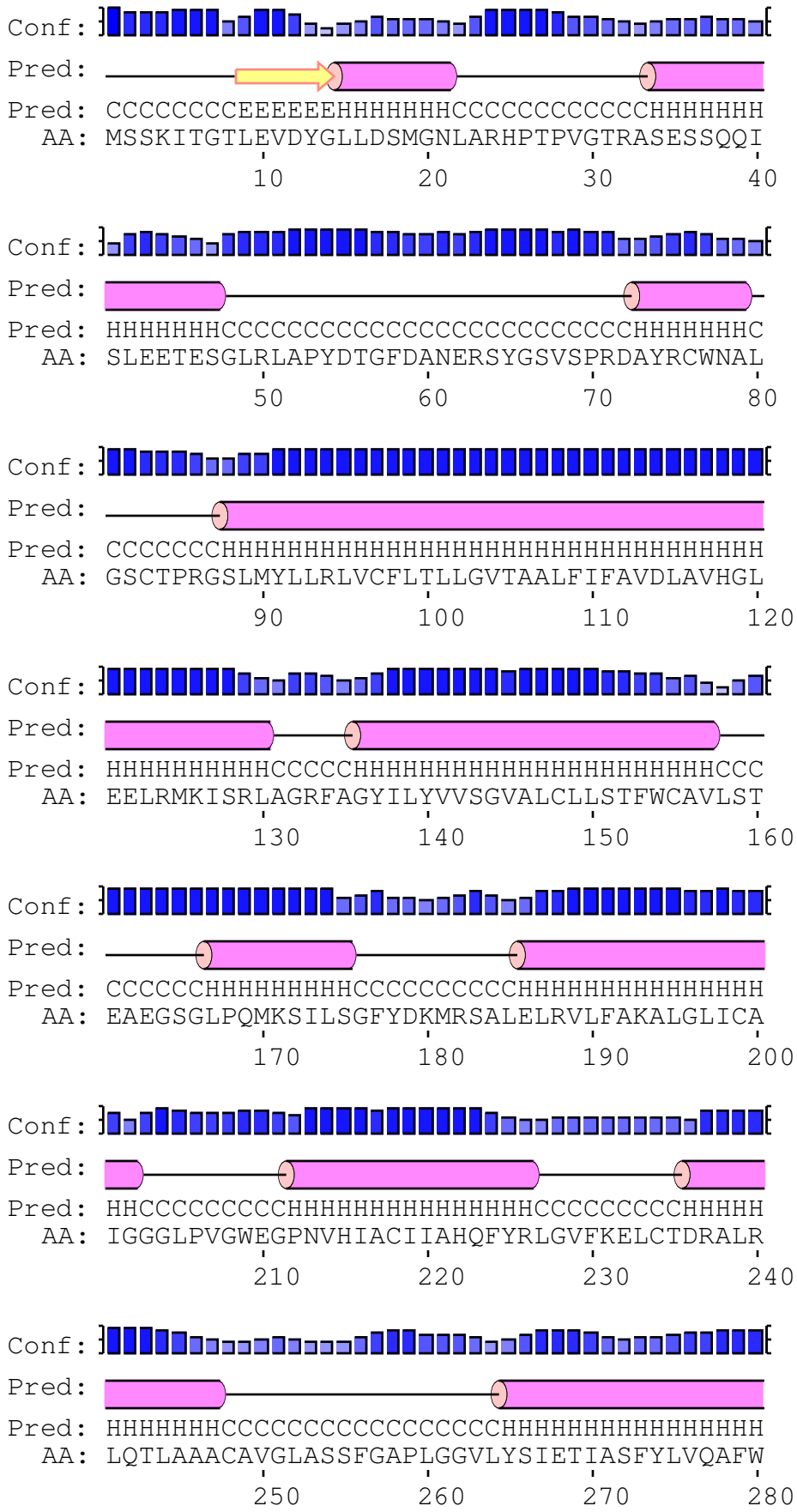
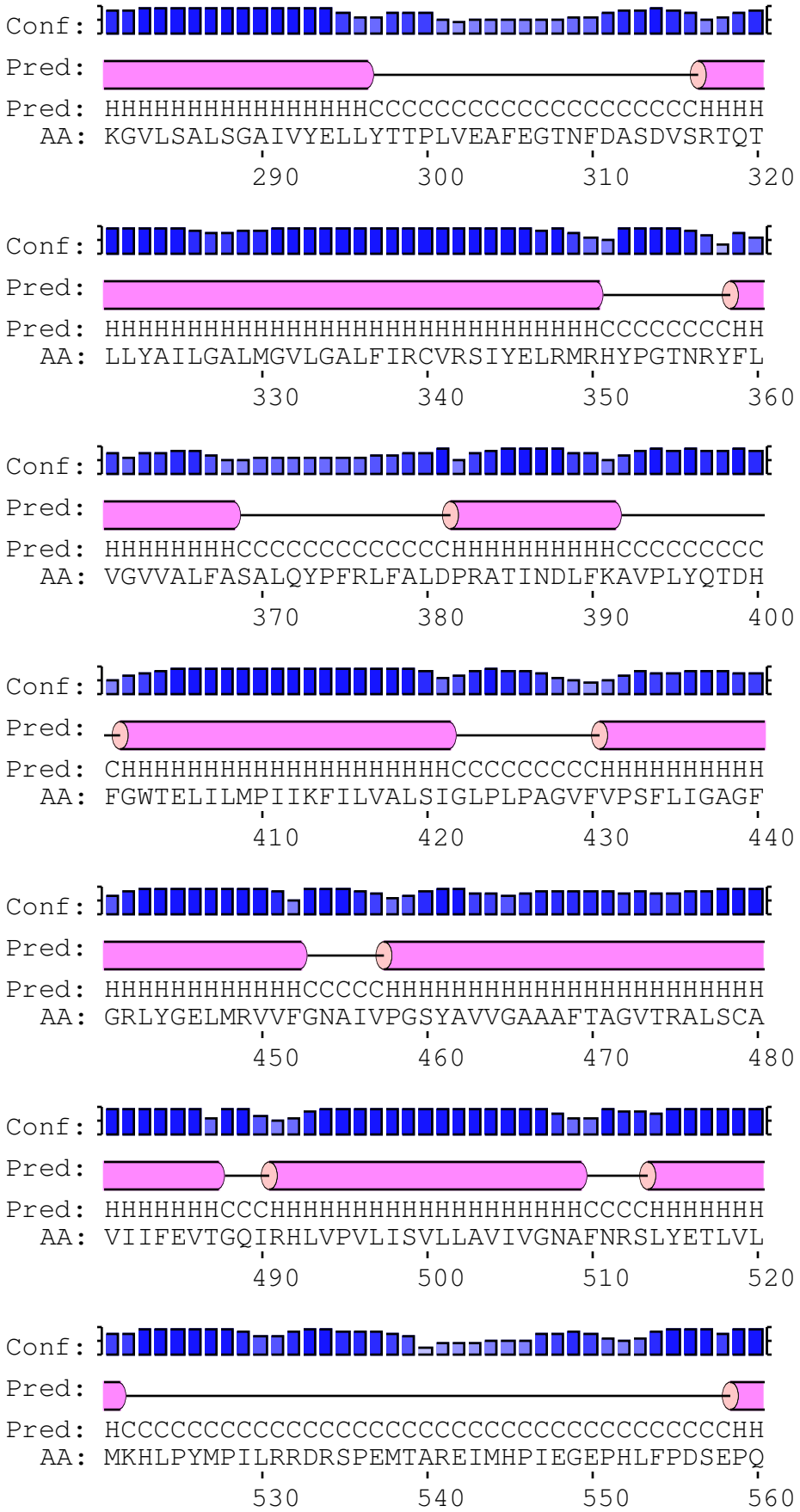
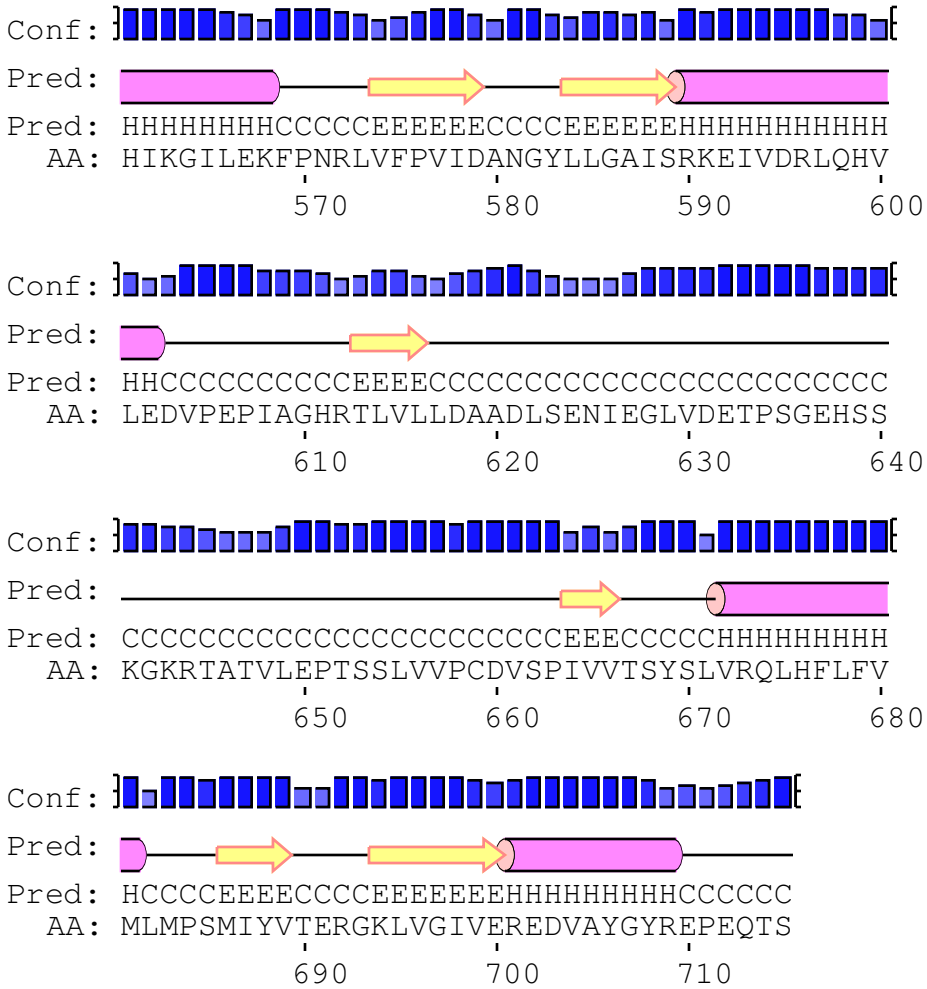

Conf:
Pred:
Pred: CCCCCCCCEEEEEEHHHHHHHCCCCCCCCCCCCHHHHHHH
AA: MSSKITGTLEVDYGLLDSMGNLARHPTPVGTRASESSQQI
10 20 30 40
Conf:
Pred:
Pred: HHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCHHHHHHHC
AA: SLEETESGLRLAPYDTGFDANERSYGSVSPRDAYRCWNAL
50 60 70 80
Conf:
Pred:
Pred: CCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
AA: GSCTPRGSLMYLLRLVCFLTLLGVTAALFIFAVDLAVHGL
90 100 110 120
Conf:
Pred:
Pred: HHHHHHHHHHCCCCCHHHHHHHHHHHHHHHHHHHHHCCC
AA: EELRMKISRLAGRFAGYILYVVSGVALCLLSTFWCAVLST
130 140 150 160
Conf:
Pred:
Pred: CCCCCCHHHHHHHHHCCCCCCCCCCHHHHHHHHHHHHHH
AA: EAEGSGLPQMKSILSGFYDKMRSALELRVLFAKALGLICA
170 180 190 200
Conf:
Pred:
Pred: HHCCCCCCCCCHHHHHHHHHHHHHHCCCCCCCCCHHHHH
AA: IGGGLPVGWEGPNVHIACIIAHQFYRLGVFKELCTDRALR
210 220 230 240
Conf:
Pred:
Pred: HHHHHHHCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHH
AA: LQTLAAACAVGLASSFGAPLGGVLYSIETIASFYLVQAFW
250 260 270 280


Conf:
Pred:
Pred: HHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCHHHH
AA: KGVLSALSGAIVYELLYTTPLVEAFEGTNFDASDVSRTQT
290 300 310 320
Conf:
Pred:
Pred: HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCCHH
AA: LLYAILGALMGVLGALFIRCVRSIYELRMRHYPGTNRYFL
330 340 350 360
Conf:
Pred:
Pred: HHHHHHHHCCCCCCCCCCCCCHHHHHHHHHHCCCCCCCCC
AA: VGVVALFASALQYPFRLFALDPRATINDLFKAVPLYQTDH
370 380 390 400
Conf:
Pred:
Pred: CHHHHHHHHHHHHHHHHHHHHCCCCCCCCCHHHHHHHHHH
AA: FGWTELILMPIIKFILVALSIGLPLPAGVFVPSFLIGAGF
410 420 430 440
Conf:
Pred:
Pred: HHHHHHHHHHHHCCCCCHHHHHHHHHHHHHHHHHHHHHH
AA: GRLYGELMRVVFGNAIVPGSYAVVGAAAFTAGVTRALSCA
450 460 470 480
Conf:
Pred:
Pred: HHHHHHHCCCHHHHHHHHHHHHHHHHHHHCCCCHHHHHHH
AA: VIIFEVTGQIRHLVPVLISVLLAVIVGNAFNRSLYETLVL
490 500 510 520
Conf:
Pred:
Pred: HCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHH
AA: MKHLPYMPILRRDRSPEMTAREIMHPIEGEPHLFPDSEPQ
530 540 550 560



Legend:

= helix

= strand

= coil

Conf: = confidence of prediction

Pred: predicted secondary structure

AA: target sequence