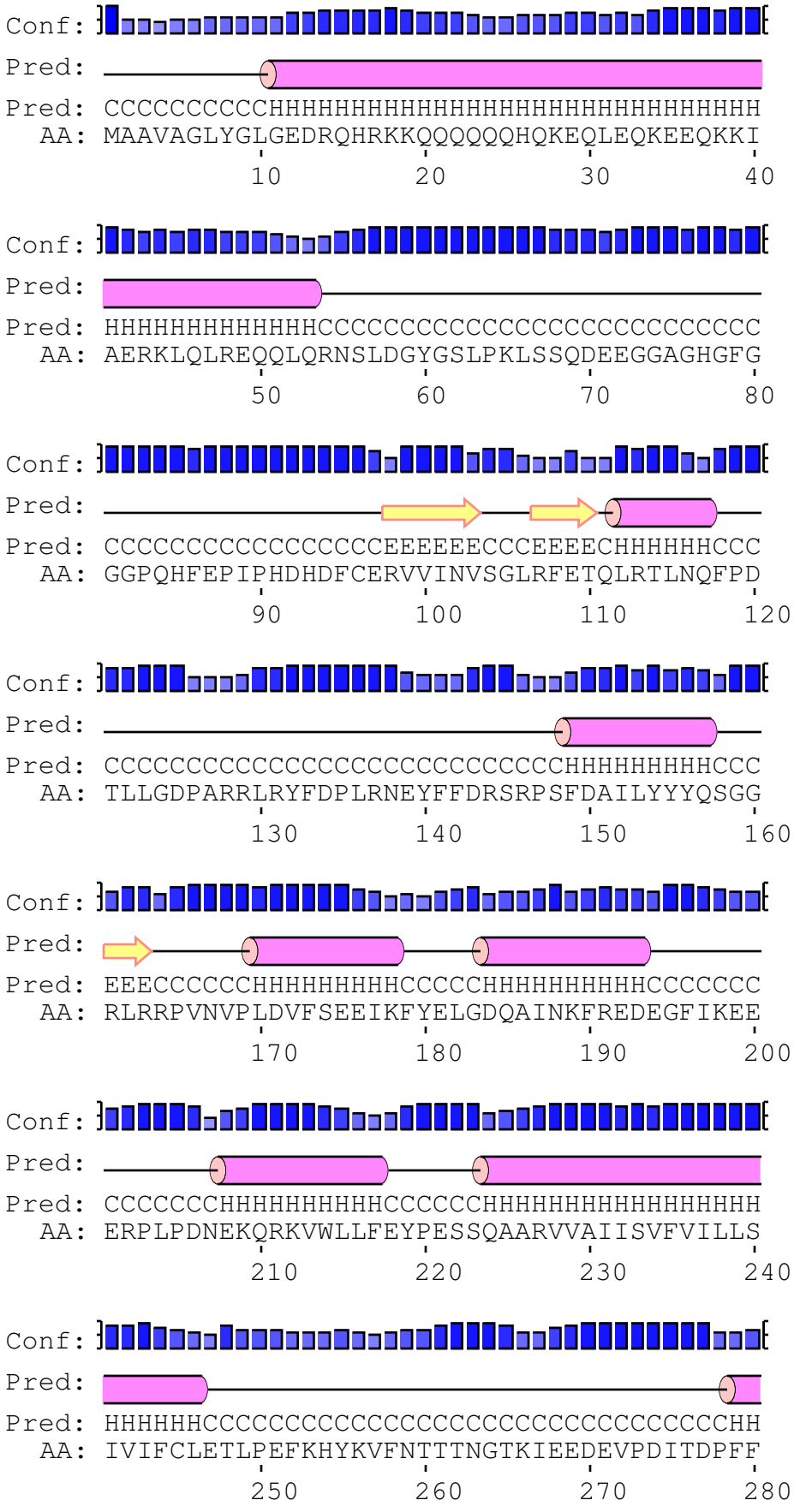
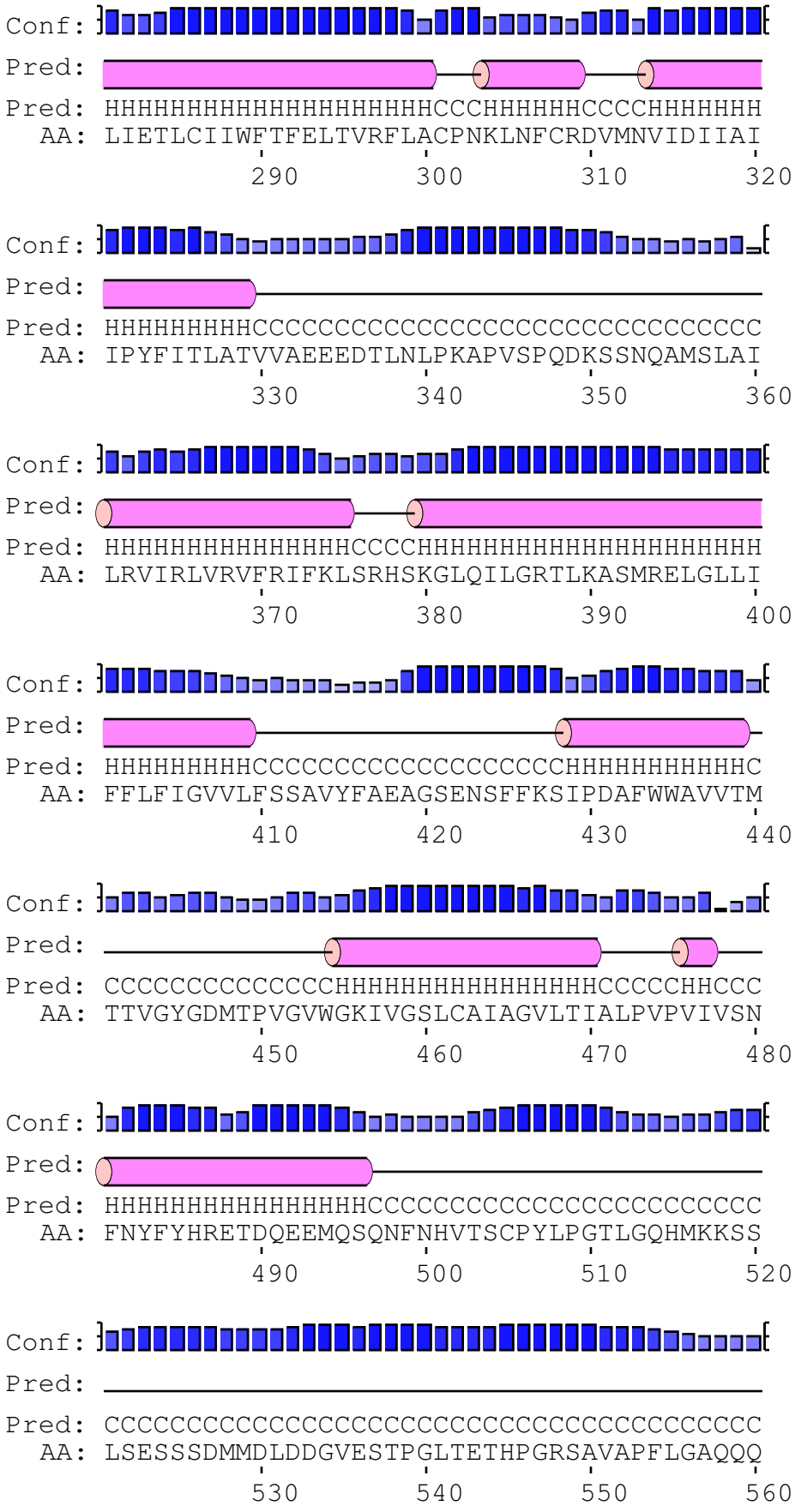
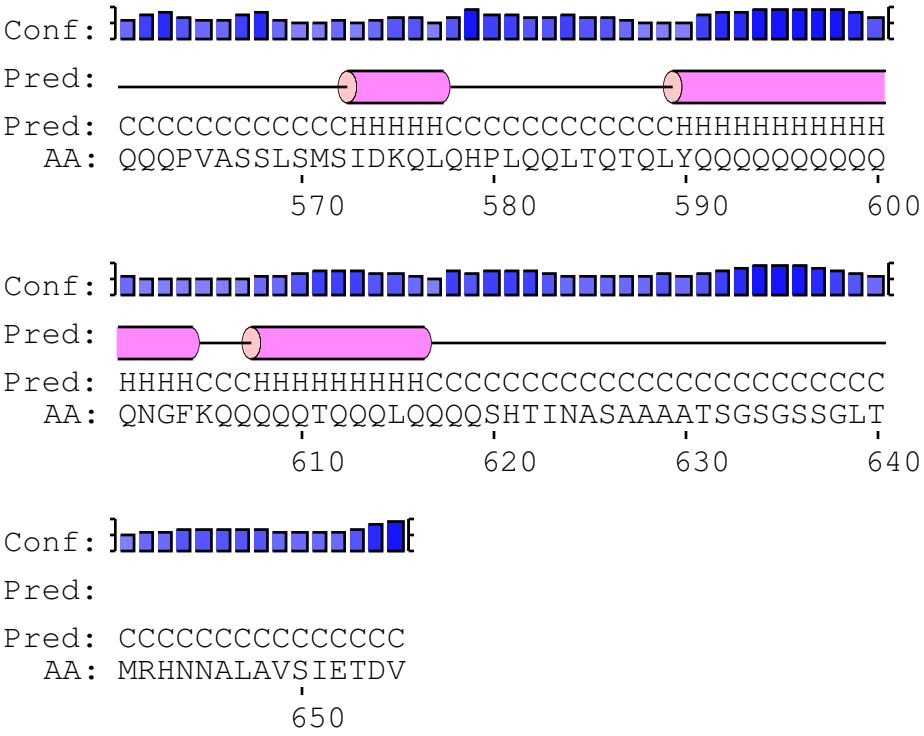

Conf:
Pred:
Pred: CCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
AA: MAAVAGLYGLGEDRQHRKKQQQQQQHQKEQLEQKEEQKKI
10
20
30
40
Conf:
Pred:
Pred: HHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCC
AA: AERKLQLREQQLQRNSLDGYGSLPKLSSQDEEGGAGHGFG
50
60
70
80
Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCEEEEEECCCEEEECHHHHHHCCC
AA: GGPQHFEPIPHDHDFCERVVINVSGLRFETQLRTLNQFPD
90
100
110
120
Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHHHHHHCCC
AA: TLLGDPARRLRYFDPLRNEYFFDRSRPSFDAILYYYQSGG
130
140
150
160
Conf:
Pred:
Pred: EEECCCCCCHHHHHHHHHCCCCCHHHHHHHHHHCCCCCCC
AA: RLRRPVNVPLDVFSEEIKFYELGDQAINKFREDEGFIKEE
170
180
190
200
Conf:
Pred:
Pred: CCCCCCCHHHHHHHHHHCCCCCCHHHHHHHHHHHHHHHH
AA: ERPLPDNEKQRKVWLLFEYPESSQAARVVAIISVFVILLS
210
220
230
240
Conf:
Pred:
Pred: HHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHH
AA: IVIFCLETLPEFKHYKVFNTTTNGTKIEEDEVPDITDPFF
250
260
270
280


Conf:
Pred:
Pred: HHHHHHHHHHHHHHHHHHHHCCCHHHHHHCCCCHHHHHHH
AA: LIETLCIIWFTFELTVRFLACPNKLNFCRDVMNVIDIIAI
290 300 310 320
Conf:
Pred:
Pred: HHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
AA: IPYFITLATVVAEEEDTLNLPKAPVSPQDKSSNQAMSLAI
330 340 350 360
Conf:
Pred:
Pred: HHHHHHHHHHHHHHHHCCCCHHHHHHHHHHHHHHHHHHH
AA: LRVIRLVRVFRIFKLSRHSKGLQILGRTLKASMRELGLLI
370 380 390 400
Conf:
Pred:
Pred: HHHHHHHHHCCCCCCCCCCCCCCCCCCCCHHHHHHHHHHC
AA: FFLFIGVVLFSSAVYFAEAGSENSFFKSIPDAFWWAVVTM
410 420 430 440
Conf:
Pred:
Pred: CCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHCCCCCHHCCC
AA: TTVGYGDMTPVGVWGKIVGSLCAIAGVLTIALPVPVIVSN
450 460 470 480
Conf:
Pred:
Pred: HHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCC
AA: FNYFYHRETDQEEMQSQNFNHVTSCPYLPGTLGQHMKKSS
490 500 510 520
Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
AA: LSESSSDMMDLDDGVESTPGLTETHPGRSAVAPFLGAQQQ
530 540 550 560




Legend:

= helix

= strand

= coil

Conf: = confidence of prediction

Pred: predicted secondary structure

AA: target sequence