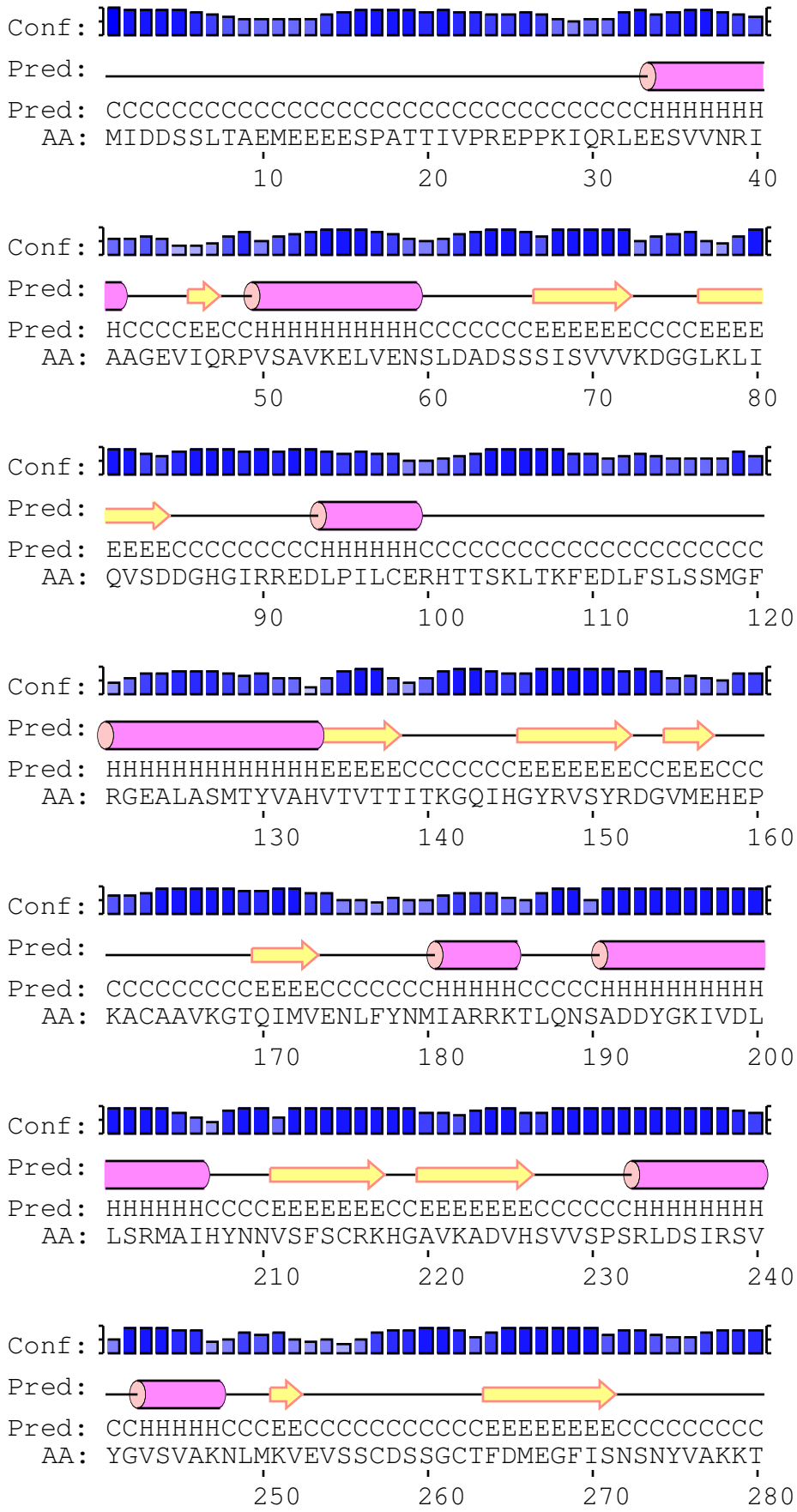
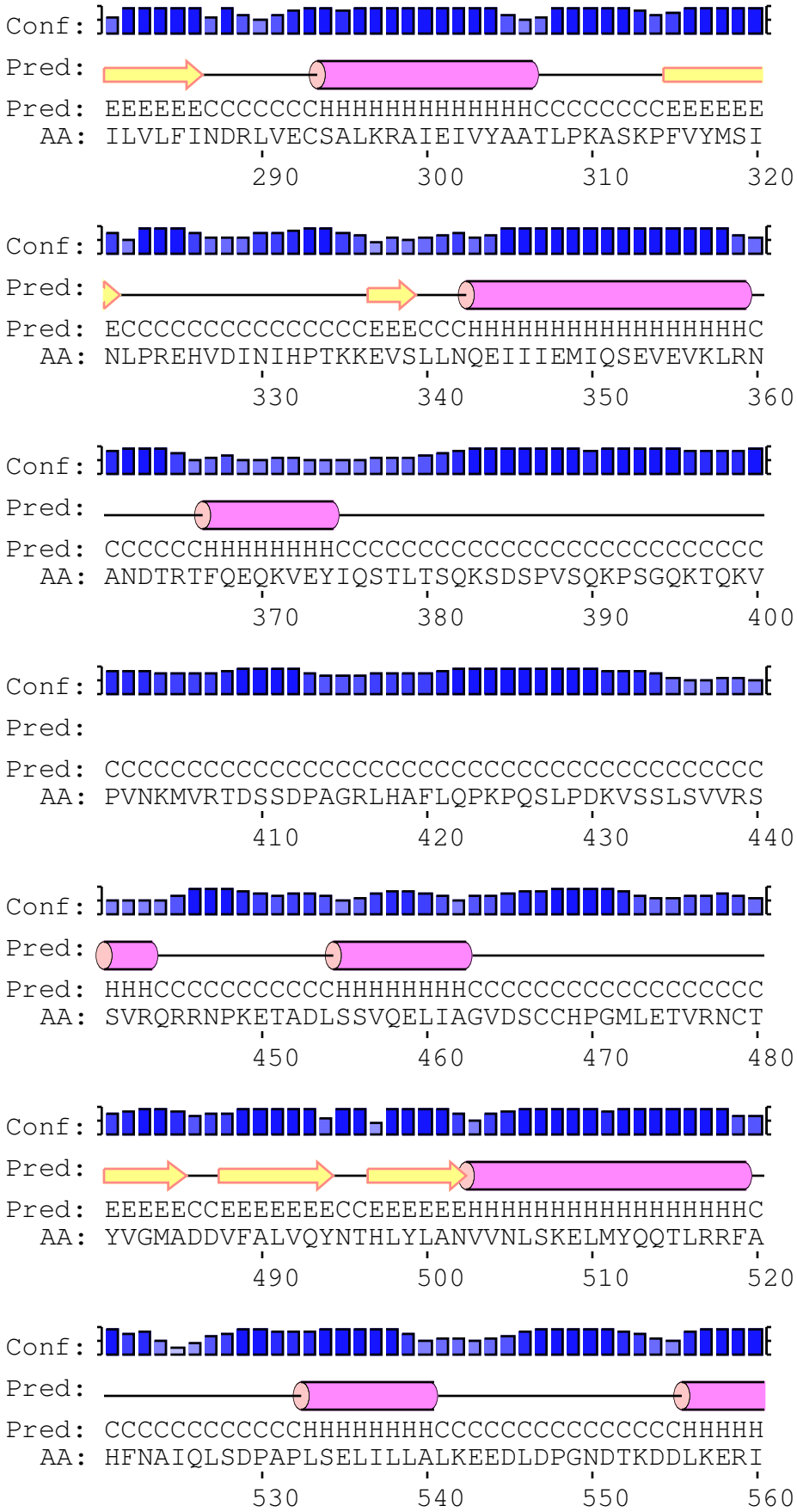
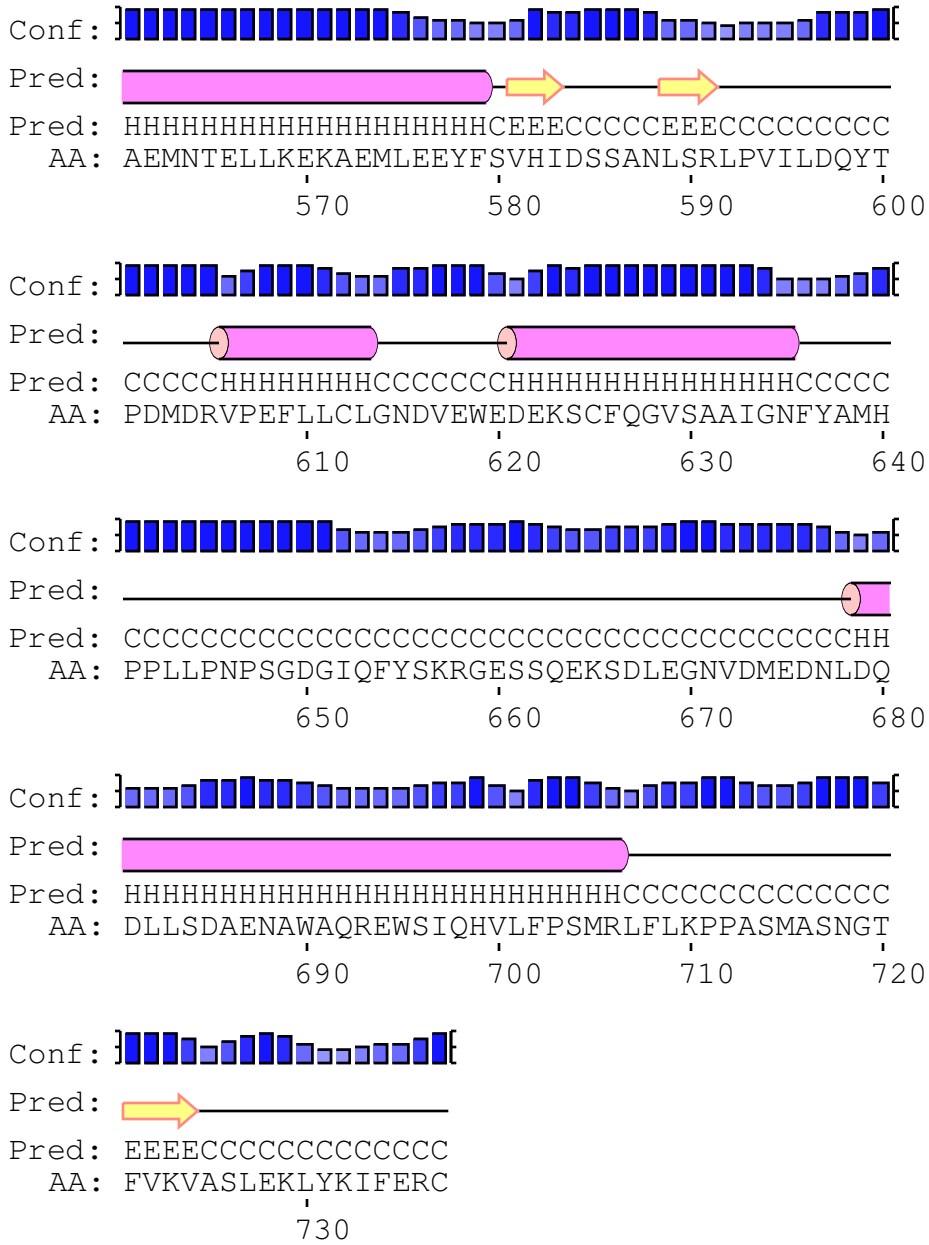
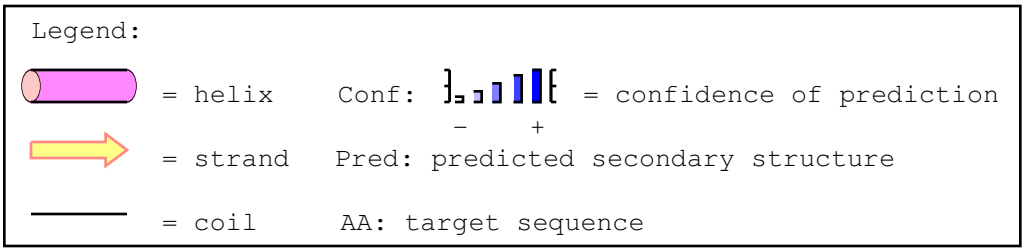

Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHHHH
AA: MIDDSSLTAEMEEEESPATTIVPREPPKIQRLEESVVNRI
10 20 30 40
Conf:
Pred:
Pred: HCCCCEECCHHHHHHHHHCCCCCCCEEEEECCCCEEEE
AA: AAGEVIQRPVSAVKELVENSLDADSSSISVVVKDGGLKLI
50 60 70 80
Conf:
Pred:
Pred: EEEECCCCCCCCCHHHHHHCCCCCCCCCCCCCCCCCCCC
AA: QVSDDGHGIRREDLPILCERHTTSKLTKFEDLFSLSSMGF
90 100 110 120
Conf:
Pred:
Pred: HHHHHHHHHHHHHEEEEECCCCCCCEEEEEEECCEEECCC
AA: RGEALASMTYVAHVTVTTITKGQIHGYRVSYRDGVMEHEP
130 140 150 160
Conf:
Pred:
Pred: CCCCCCCCCEEEECCCCCCCHHHHHCCCCCHHHHHHHHHH
AA: KACAAVKGTQIMVENLFYNMIARRKTLQNSADDYGKIVDL
170 180 190 200
Conf:
Pred:
Pred: HHHHHHCCCCEEEEEEECCEEEEEECCCCCCHHHHHHHH
AA: LSRMAIHYNNVSFSCRKHGAVKADVHSVVSPSRLDSIRSV
210 220 230 240
Conf:
Pred:
Pred: CCHHHHHCCCEECCCCCCCCCCCEEEEEEEECCCCCCCCC
AA: YGVSVAKNLMKVEVSSCDSSGCTFDMEGFISNSNYVAKKT
250 260 270 280


Conf:
Pred:
Pred: EEEEEECCCCCCCHHHHHHHHHHHHHCCCCCCCCEEEEEE
AA: ILVLFINDRLVECSALKRAIEIVYAATLPKASKPFVYMSI
290 300 310 320
Conf:
Pred:
Pred: ECCCCCCCCCCCCCCCEEECCCHHHHHHHHHHHHHHHHHHC
AA: NLPREHVDINIHPTKKEVSLLNQEIIIEMIQSEVEVKLRN
330 340 350 360
Conf:
Pred:
Pred: CCCCCCHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCC
AA: ANDTRTFQEQKVEYIQSTLTSQKSDSPVSQKPSGQKTQKV
370 380 390 400
Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
AA: PVNKMVRTDSSDPAGRLHAFLQPKPQSLPDKVSSLSVVRS
410 420 430 440
Conf:
Pred:
Pred: HHHCCCCCCCCCCCHHHHHHHHCCCCCCCCCCCCCCCCCC
AA: SVRQRRNPKETADLSSVQELIAGVDSCCHPGMLETVRNCT
450 460 470 480
Conf:
Pred:
Pred: EEEEECCEEEEEEECCEEEEEEHHHHHHHHHHHHHHHHHHC
AA: YVGMADDVFALVQYNTHLYLANVVNLSKELMYQQTLRRFA
490 500 510 520
Conf:
Pred:
Pred: CCCCCCCCCCCCHHHHHHHHCCCCCCCCCCCCCCCHHHHH
AA: HFNAIQLSDPAPLSELILLALKEEDLDPGNDTKDDLKERI
530 540 550 560





Analysis performed with the use of PSIPRED Protein Structure Prediction Server

Citation: Bryson K, McGuffin LJ, Marsden RL, Ward JJ, Sodhi JS. & Jones DT. (2005)
Protein structure prediction servers at University College London.
Nucl. Acids Res. 33(Web Server issue):W36-38