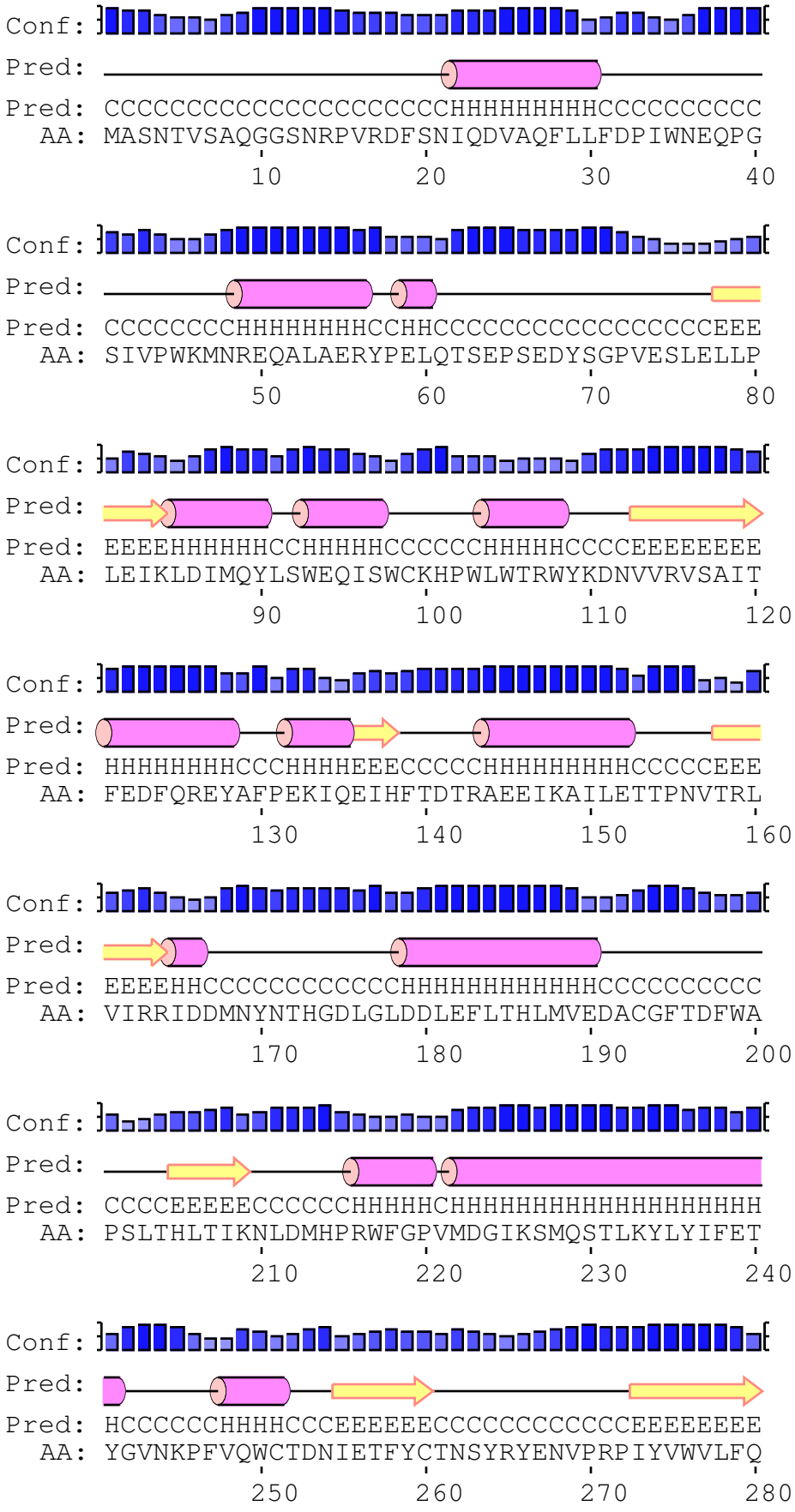
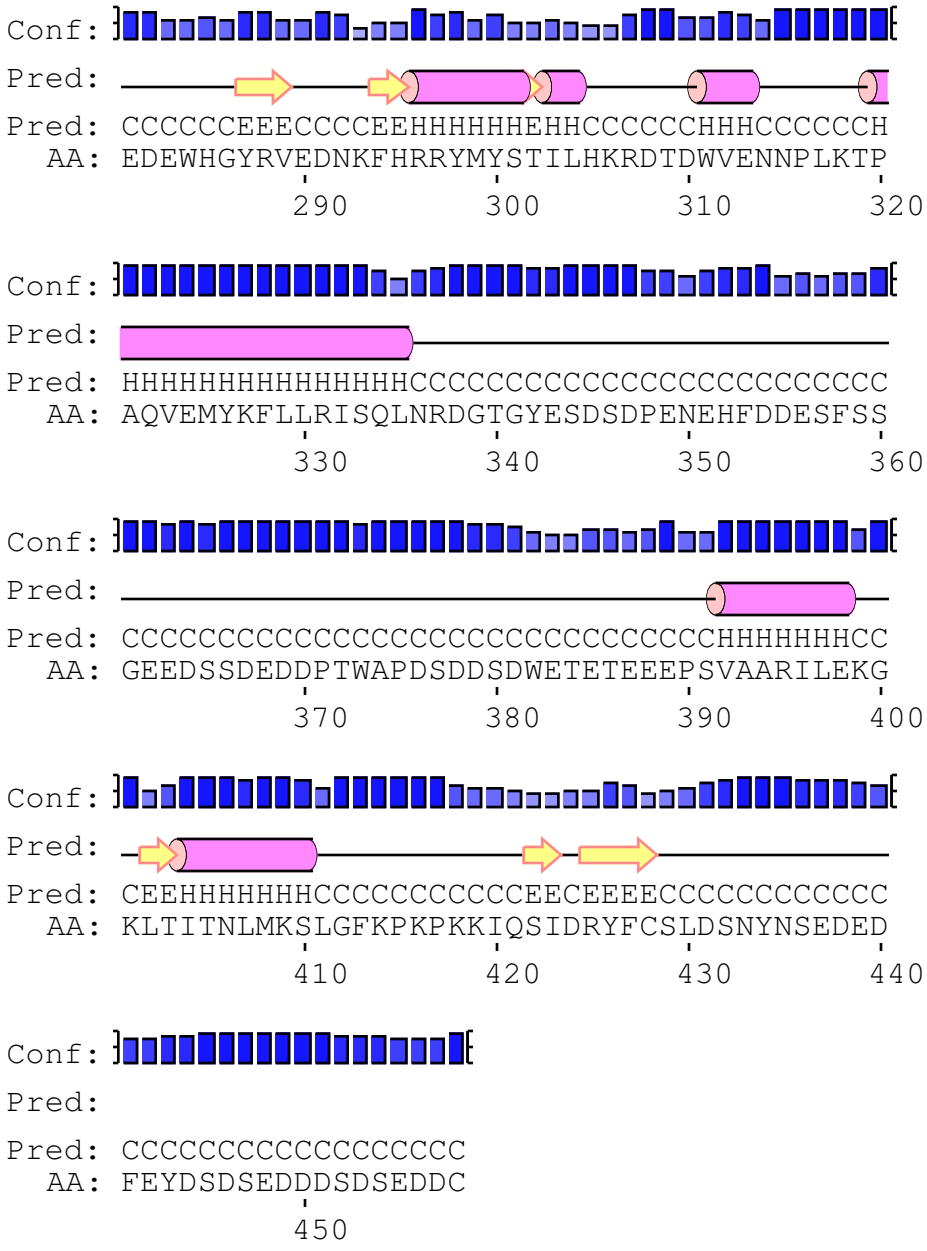

Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCCCCCHHHHHHHHHHCCCCCCCCCC
AA: MASNTVSAQGGSNRPVRDFSNIQDVAQFLLFDPIWNEQPG
10 20 30 40
Conf:
Pred:
Pred: CCCCCCCCHHHHHHHHHCCHHCCCCCCCCCCCCCCCCEEE
AA: SIVPWKMNREQALAERYPELQTSEPSEDYSGPVESLELLP
50 60 70 80
Conf:
Pred:
Pred: EEEEHHHHHHHCCHHHHHCCCCCCHHHHHCCCCEEEEEEEE
AA: LEIKLDIMQYLSWEQISWCKHPWLWTRWYKDNVVRVSAIT
90 100 110 120
Conf:
Pred:
Pred: HHHHHHHHCCCHHHHEEECCCCCHHHHHHHHHCCCCCEEE
AA: FEDFQREYAFPEKIQEIHFTDTRAEEIKAILETTPNVTRL
130 140 150 160
Conf:
Pred:
Pred: EEEEHHCCCCCCCCCCCCHHHHHHHHHHHHCCCCCCCCCC
AA: VIRRIDDMNYNTHGDLGLDDLEFLTHLMVEDACGFTDFWA
170 180 190 200
Conf:
Pred:
Pred: CCCCEEEEECCCCCCHHHHHCHHHHHHHHHHHHHHHHHH
AA: PSLTHLTIKNLDMHPRWFGPVMDGIKSMQSTLKYLYIFET
210 220 230 240
Conf:
Pred:
Pred: HCCCCCCHHHHCCCEEEEEECCCCCCCCCCCCCEEEEEEEE
AA: YGVNKPFVQWCTDNIETFYCTNSYRYENVPRPIYVWVLFQ
250 260 270 280



Legend:

= helix

= strand

= coil

Conf: = confidence of prediction

Pred: predicted secondary structure

AA: target sequence