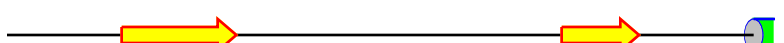


Conf: 
 Pred: _____
 Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
 AA: MGSNKS PKDASQRRRSLEPAENVHGAGGGAFPASQTPSK
 10 20 30 40

Conf: 
 Pred: _____
 Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
 AA: PASADGHRGPSAAFAPAAAE PKLFGGFNSSDTVTSPQRAG
 50 60 70 80

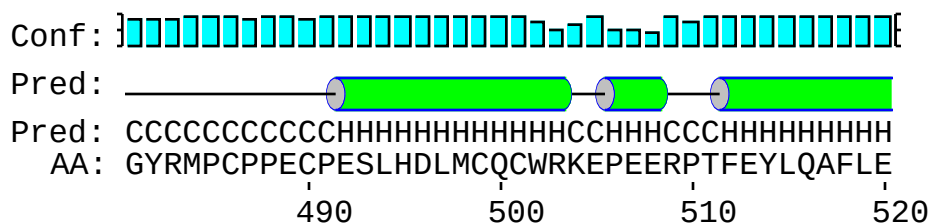
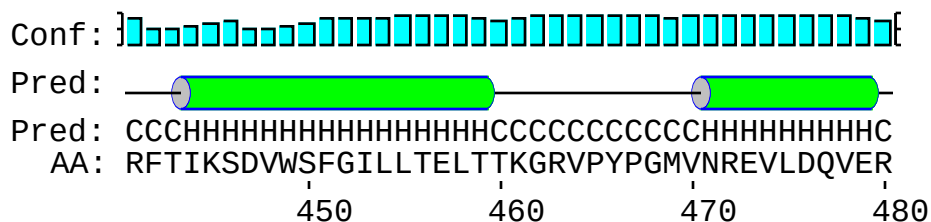
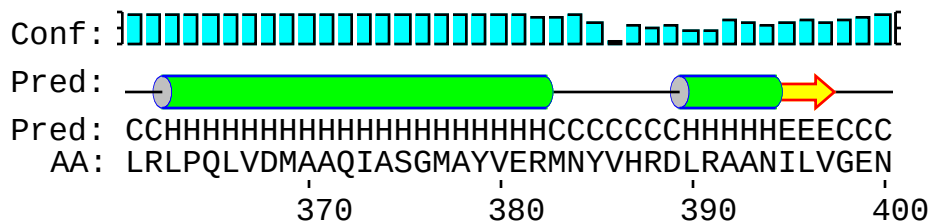
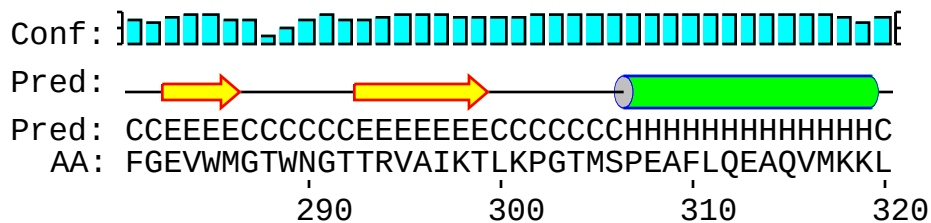
Conf: 
 Pred: 
 Pred: CCCCCEEEEEECCCCCCCCCCCCCCCCCEEECCCCCH
 AA: PLAGGVTTFVALYDYESRTETDLSFKKGERLQIVNNTEGD
 90 100 110 120

Conf: 
 Pred: 
 Pred: HHHHHCCCCCEEECCCCCCCCCCCCCCCCCCCCCHHH
 AA: WWLAHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRE
 130 140 150 160

Conf: 
 Pred: 
 Pred: HHHHHCCCCCCCCCEEECCCCCCCCCEEECCCCC
 AA: SERLLLNAENPRGTFVRESETTKGAYCLSVSDFDNAKGL
 170 180 190 200

Conf: 
 Pred: 
 Pred: CEEEEEECCCCCEEECCCCCCCCCHHHHHHHHHCCCC
 AA: NVKHYKIRKLDSGGFYITSRTQFNSLQQLVAYYSKHADGL
 210 220 230 240

Conf: 
 Pred: 
 Pred: CCCCCCCCCCCCCCCCCCCCCCHHHHEEEEEECCCC
 AA: CHRLTTVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQGC
 250 260 270 280



Legend:



= helix



= strand



= coil

Conf:  = confidence of prediction
- +

Pred: predicted secondary structure

AA: target sequence