




Conf: 

Pred: \_\_\_\_\_

Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  
 AA: MSRWKENASPLPLHPGGSS\$LLPRKRPPPSPPPPQPPCPP


10 20 30 40



Conf: 

Pred: \_\_\_\_\_ 

Pred: CCCCCCCCCHHHHHCCCCCCCCCCCCCCCCCCCCCCCC  
 AA: PRRPLADVTGNALRQRGSGGGGCGYGYSTPAPKAPRPSCR


50 60 70 80



Conf: 

Pred:  \_\_\_\_\_ 

Pred: EEECCCCCCHHHHHHHHHHHHHHHHHHHHHCCCCCCCC  
 AA: FLLDDDEGMDEAFLREVDAICEEHERSSARKDKEAGEAPP


90 100 110 120





Conf: 

Pred: \_\_\_\_\_  \_\_\_\_\_ 

Pred: CCCCCCCCCCCHHHHHHHHHHHHHCCCCCCCCCCHHHHH  
 AA: SIPSEPESGVSGDAFRKEENAIGEEGDAQPLATSQEEMED


130 140 150 160



Conf: 

Pred:  \_\_\_\_\_  \_\_\_\_\_  \_\_\_\_\_ 

Pred: HHHHHHHHHCCCCCCCCCEEECCCCCCHHCCCCCCHH  
 AA: ADEEEICELWFGDDSLPPAIS IATGGGEFEDAFWNISDIT


170 180 190 200



Conf: 

Pred:  \_\_\_\_\_ \_\_\_\_\_ 

Pred: HHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHH  
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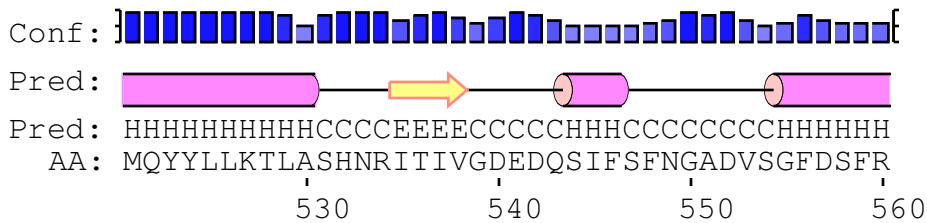
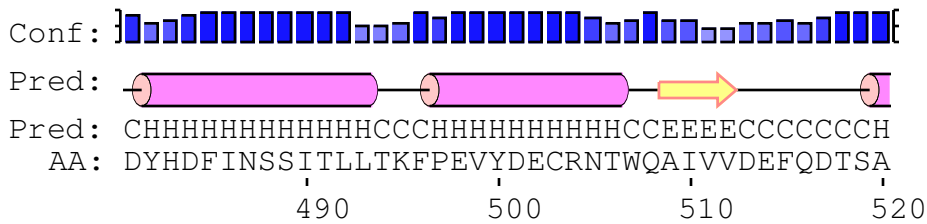
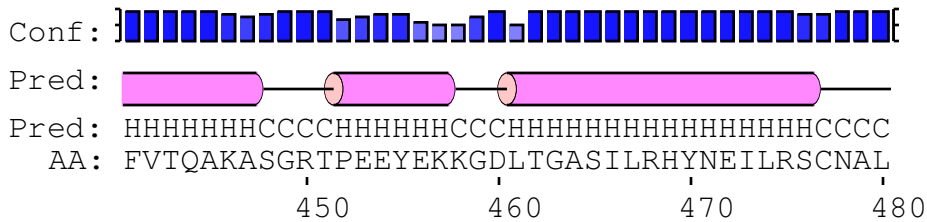
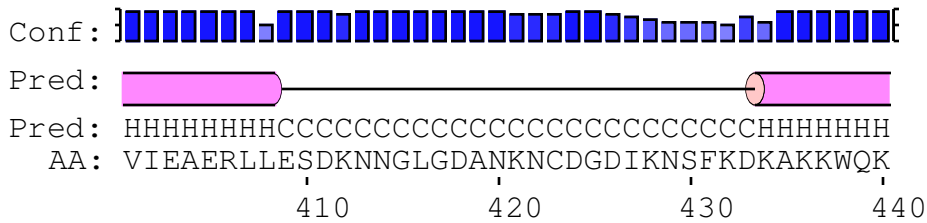
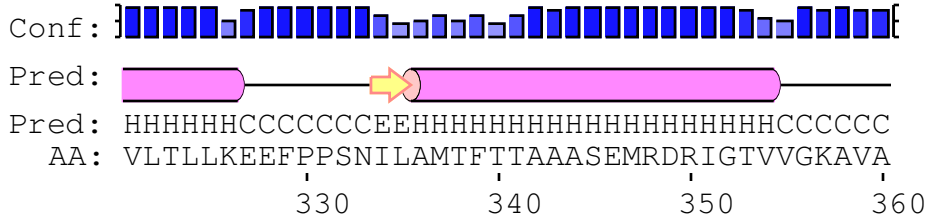
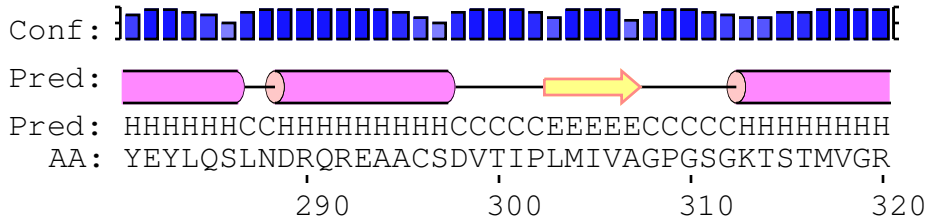
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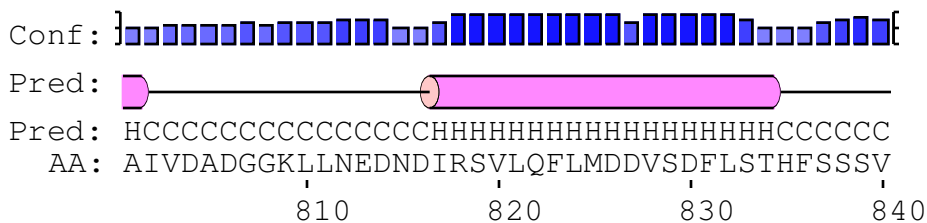
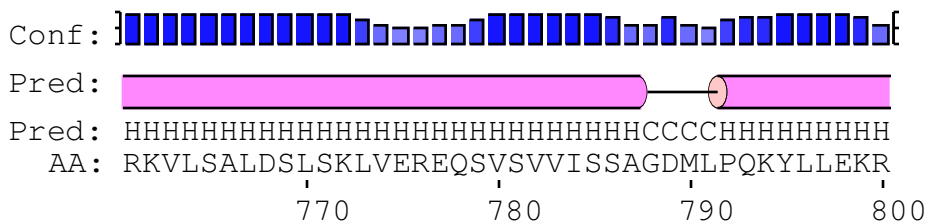
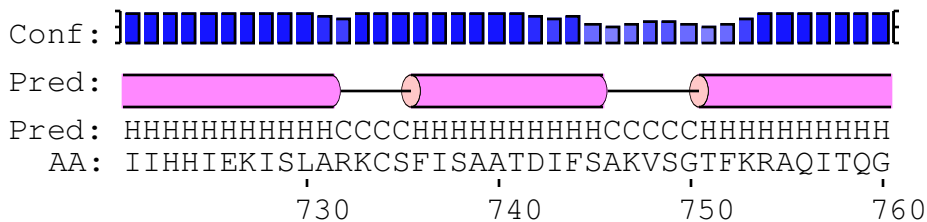
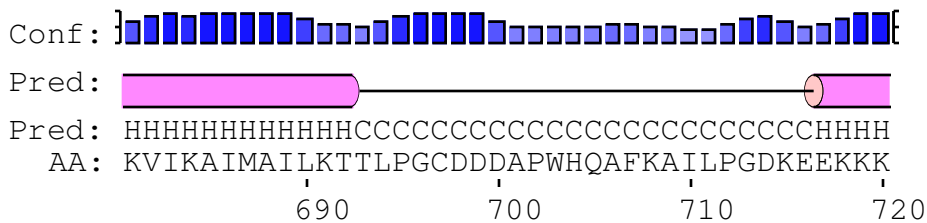
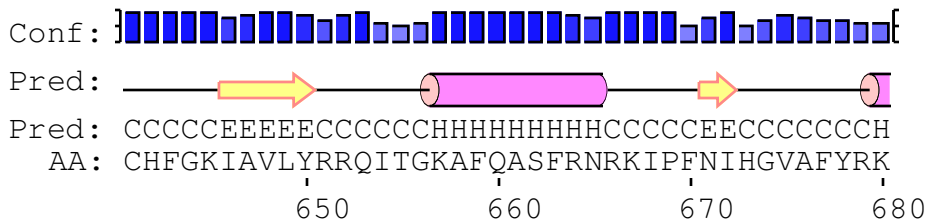
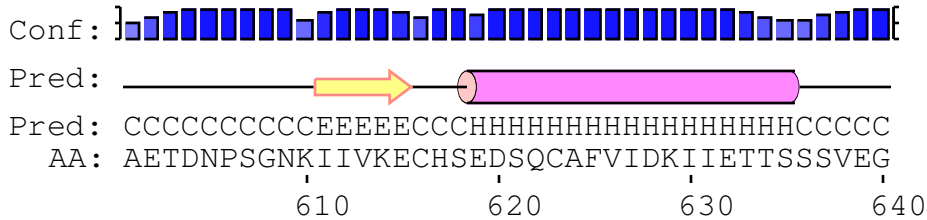
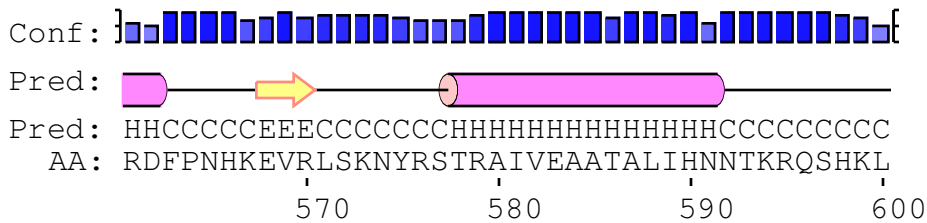
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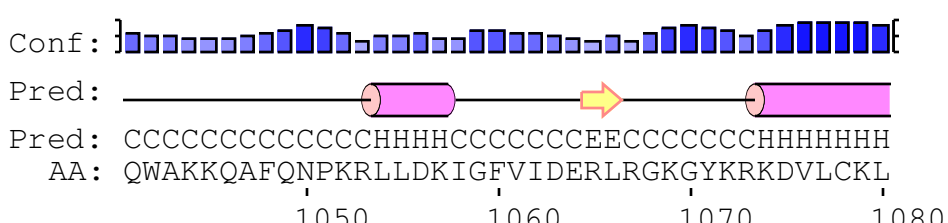
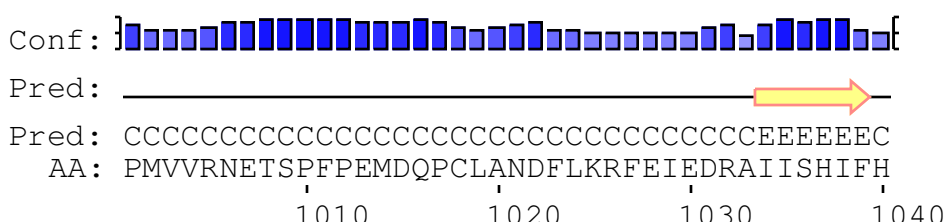
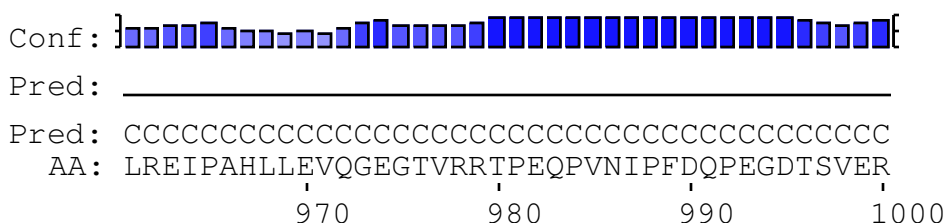
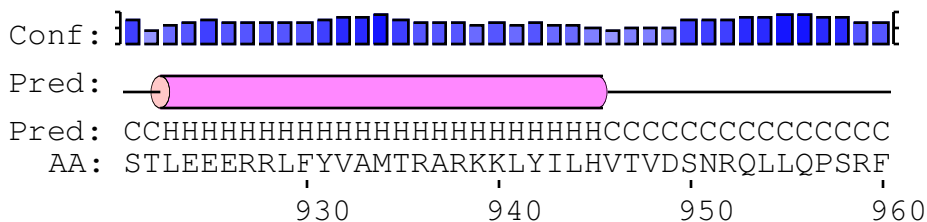
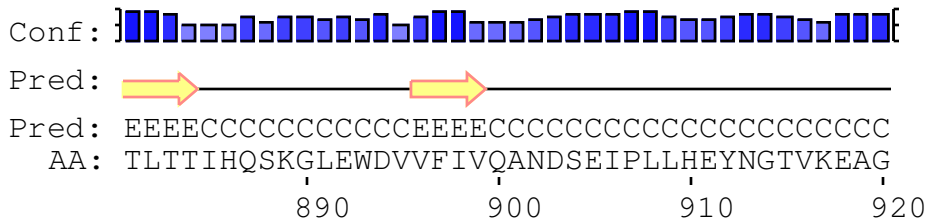
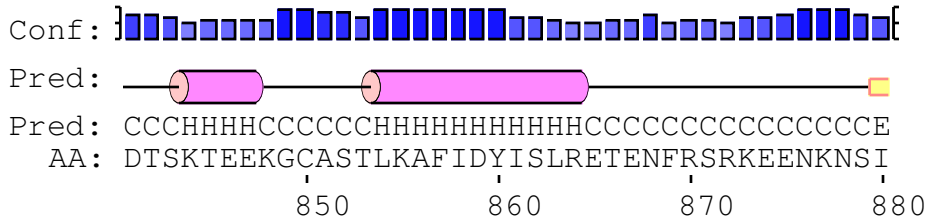
Pred:  \_\_\_\_\_ \_\_\_\_\_ 

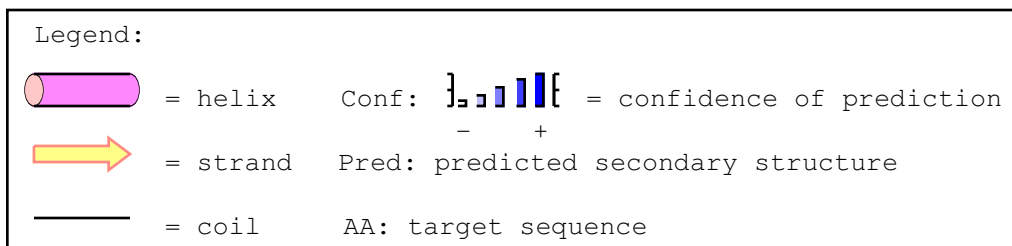
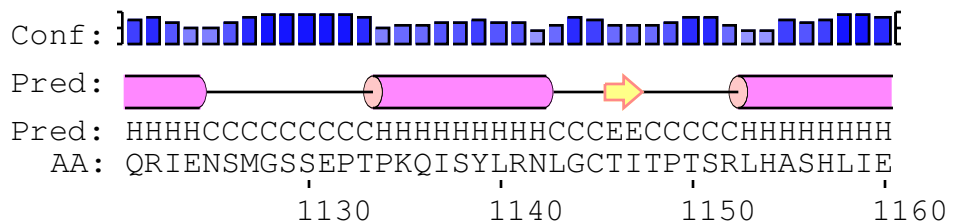
Pred: HHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCH  
 AA: DAFLEDLDAIHQGDATKGQEEPQETELEIEENEGCVPKKY

250 260 270 280









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