




Conf: 

Pred: _____

Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
 AA: MENLPPNRGMWNQEYSHGRISQSFRSAKPLLDRKRPIENA


10 20 30 40

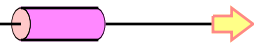
Conf: 

Pred: _____ 

Pred: CCCCCCCHHHHCCCCCCCCCCCCCCCCCCCCCCCCC
 AA: PNSSNPLPQRMKESMDTESVSHNINFNSTPLMELSANTPY


50 60 70 80


Conf: 

Pred: _____ 

Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHCCCCCEE
 AA: KRLKPEIESYADGHPGLRTPPPRFDLDKEIINGFQTDIY

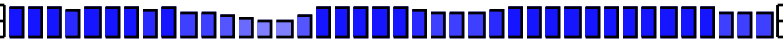
90 100 110 120


Conf: 

Pred: _____ 

Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHH
 AA: ADVGSLSEAFVTPKPERVTLNNGCSTSSILDDDFDDSI

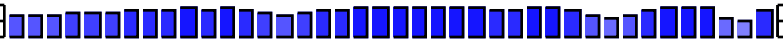
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
Conf: 

Pred: _____ 

Pred: HHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCC
 AA: LEEIDLICEQSARKAACQTPTTSIYQTPSKDNKSSDPKAS


170 180 190 200

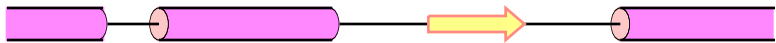
Conf: 

Pred: _____ 

Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCH
 AA: LDFRDVEKFEPDSNVKLLDEETPTIAADPALLNSMPDEC

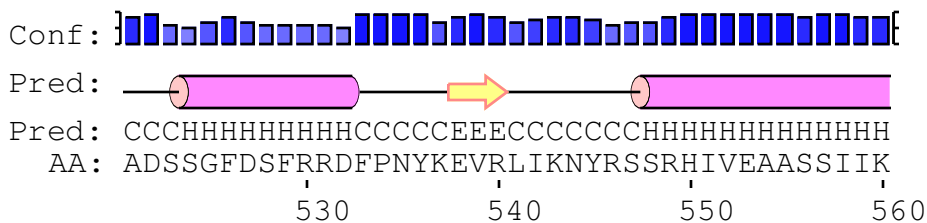
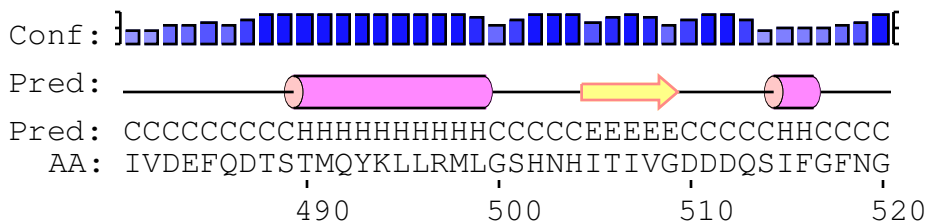
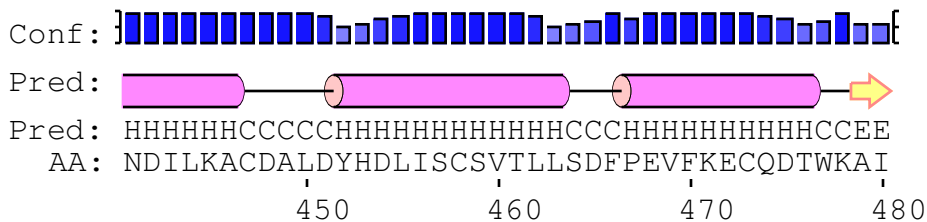
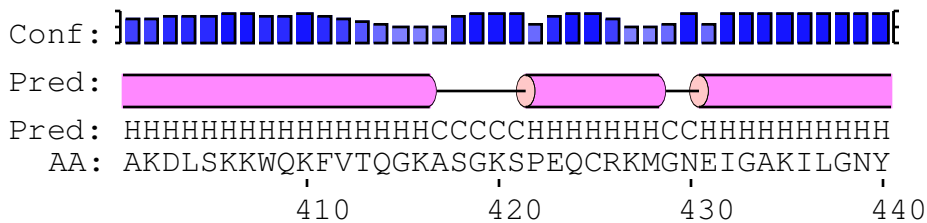
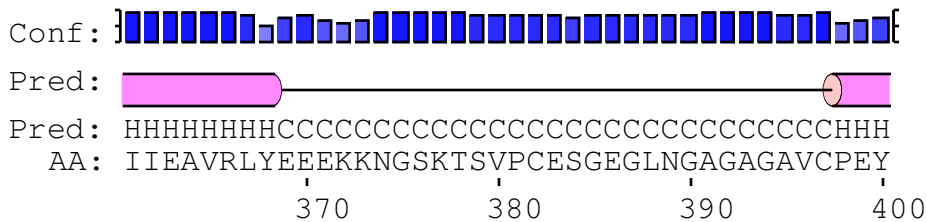
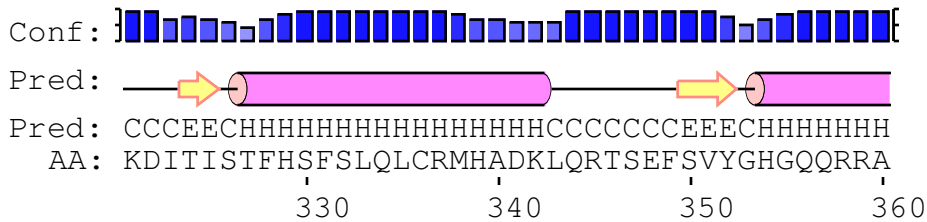
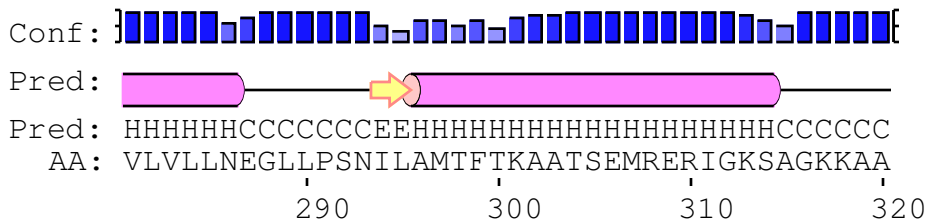
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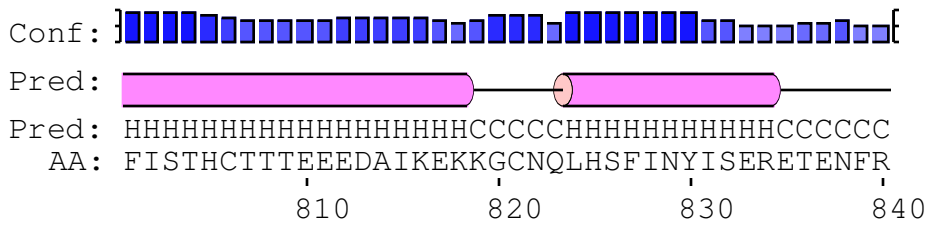
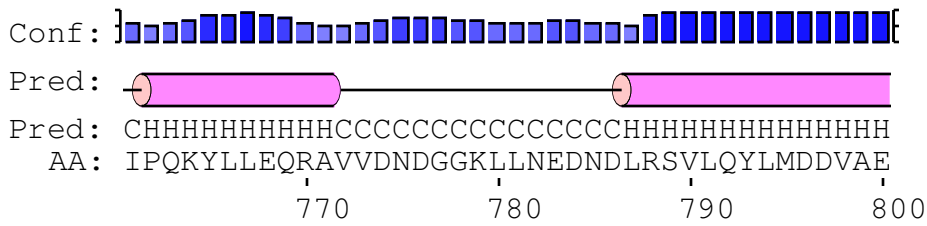
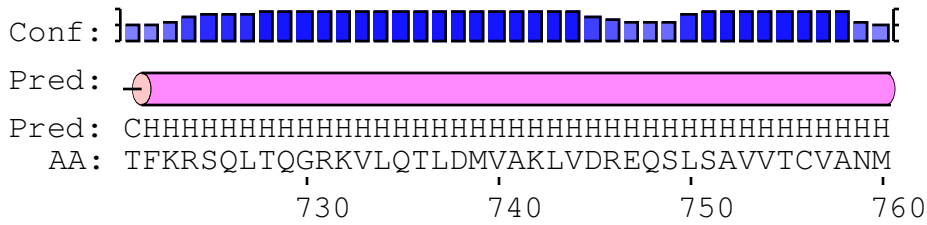
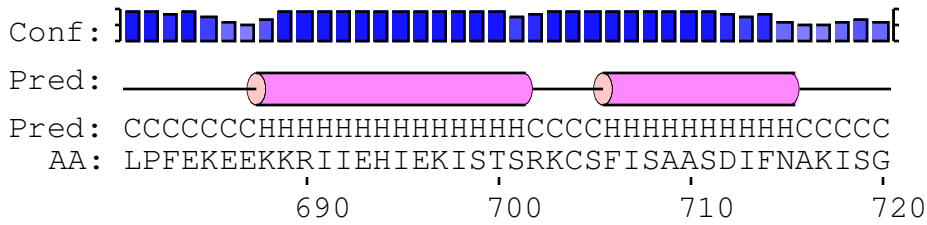
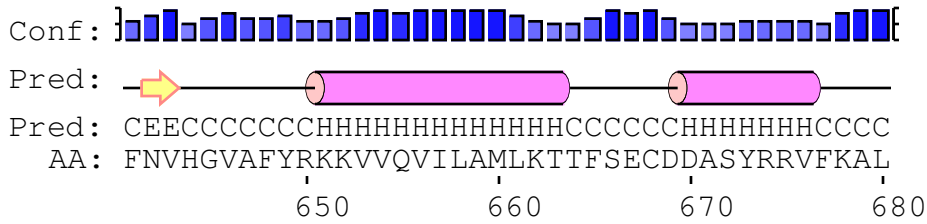
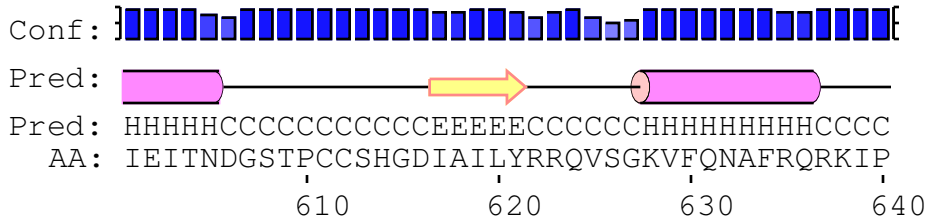
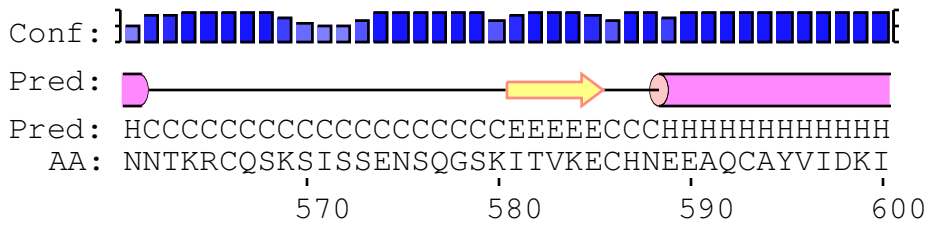
Conf: 

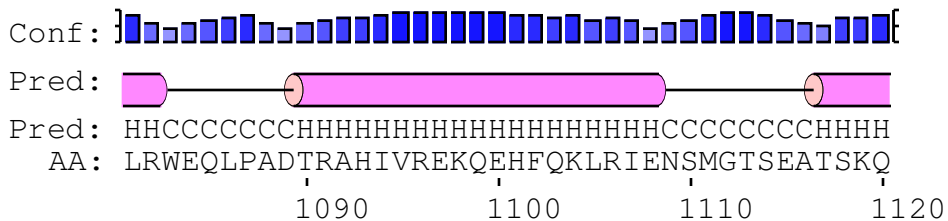
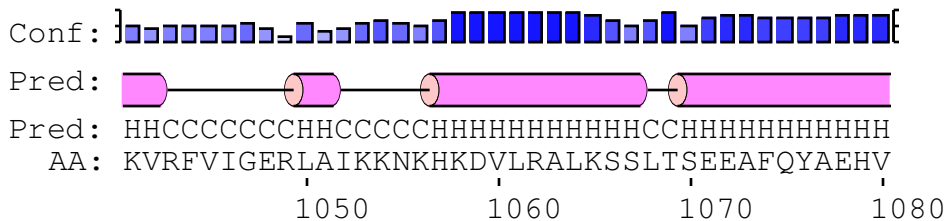
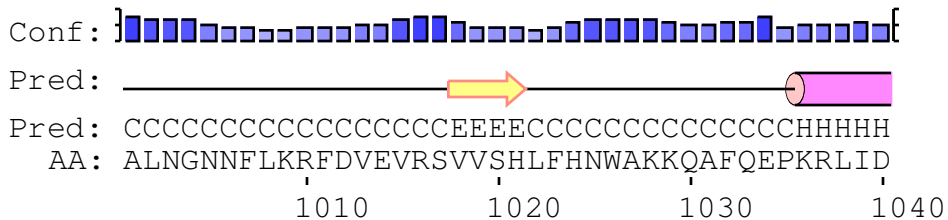
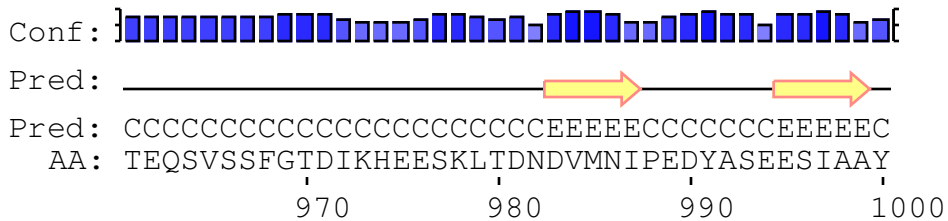
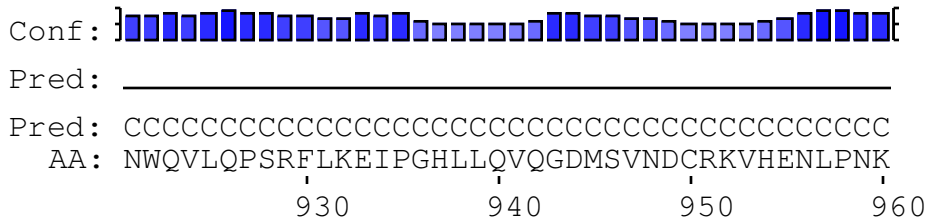
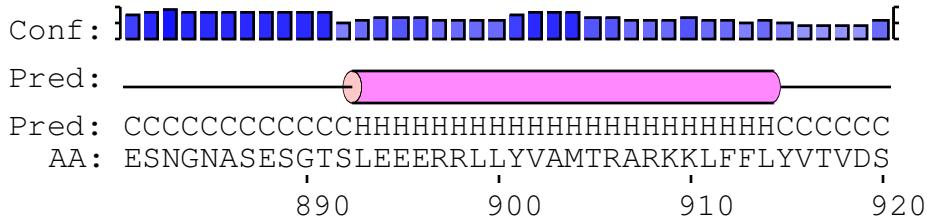
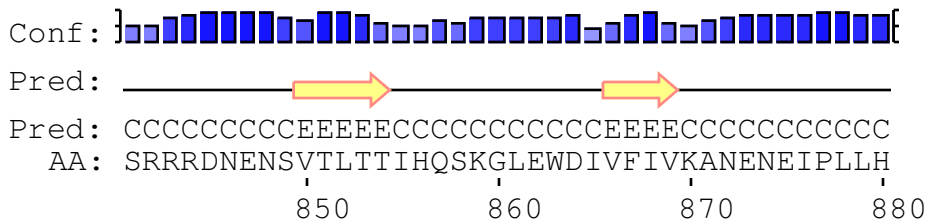
Pred: _____ 

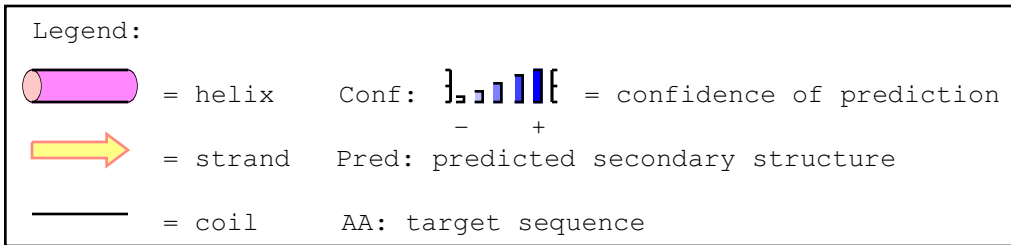
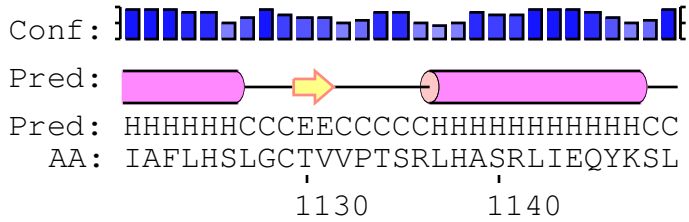
Pred: HHHHCCCHHHHHHHHHCCCCCEEEEEECCCCHHHHHHH
 AA: SKYMLSLNDRQRDAACSNI STPLMVIAGPGSGKTSTMVGR

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