

Pred: 

Pred: CCCCHHHHHCCCCCCCCHHCCCCCCCCCCCCCCCCCCCC
AA: MTQEPFREELAYDRMPTLERGRQDPASYAPDAKPSDLQLS

10 20 30 40

Conf: } { }

Pred: 

Pred: CCCCCCCCHHHHHHHHHHCCCCC
AA: KRLPPCFSHKTWVF SVLMGAASW

50 60

Legend:

 = helix Conf:  = confidence of prediction

 = strand Pred: predicted secondary structure

— = coil AA: target sequence