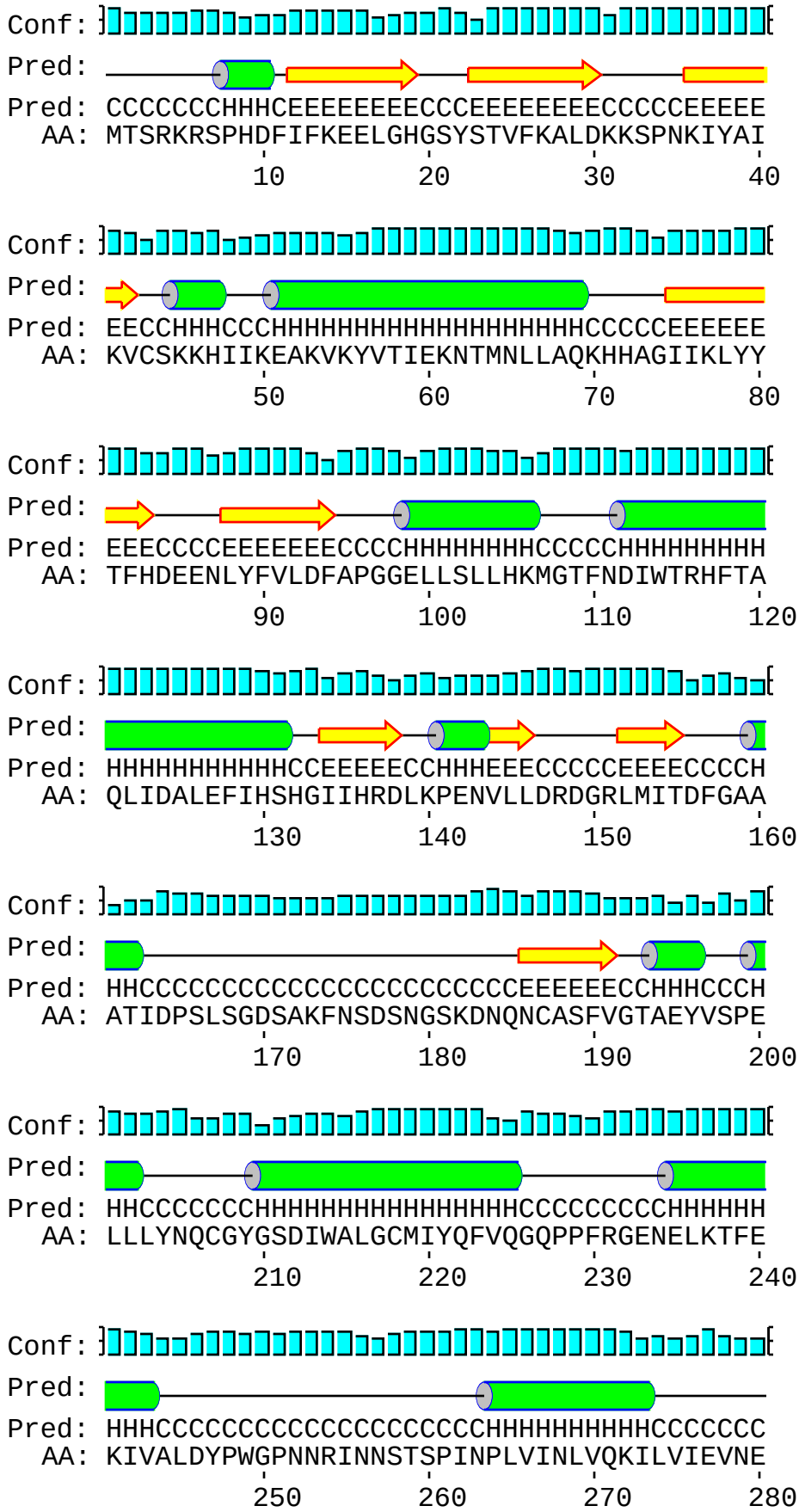
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Pred:
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10 20 30 40
Conf:
Pred:
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AA: KVCSKKHIIKEAKVKYVTIEKNTMNLLAQKHHAGIIKLYY
50 60 70 80
Conf:
Pred:
Pred: EEECCCCEEEEEEECCCCHHHHHHHHCCCCCHHHHHHHHH
AA: TFHDEENLYFVLDFAPGGELLSLLHKMGTFNDIWTRHFTA
90 100 110 120
Conf:
Pred:
Pred: HHHHHHHHHHHCCEEEEECCHHHEEECCCCCEEEECCCCH
AA: QLIDALEFIHSHGIIHRDLKPENVLLDRDGRLMITDFGAA
130 140 150 160
Conf:
Pred:
Pred: HHCCCCCCCCCCCCCCCCCCCCCCEEEEEECCHHHCCCH
AA: ATIDPSLSGDSAKFNSDSNGSKDNQNCASFVGTAEYVSPE
170 180 190 200
Conf:
Pred:
Pred: HHCCCCCCCHHHHHHHHHHHHHHHCCCCCCCCCHHHHHH
AA: LLLYNQCGYGSDIWALGCMIYQFVQGQPPFRGENELKTFE
210 220 230 240
Conf:
Pred:
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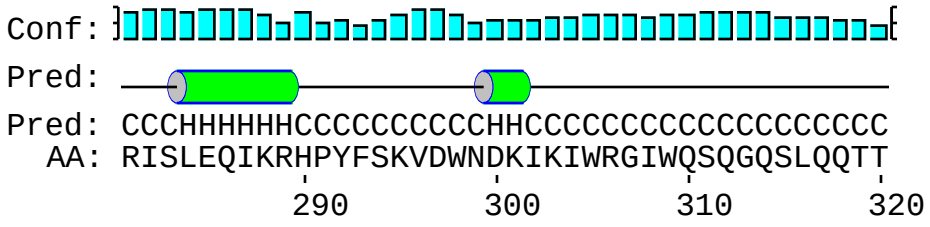
250 260 270 280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Pred:
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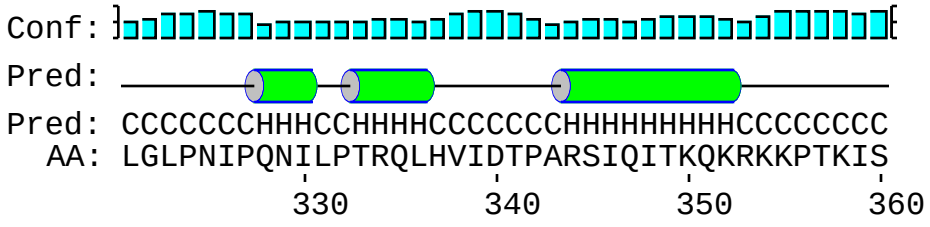
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Pred:
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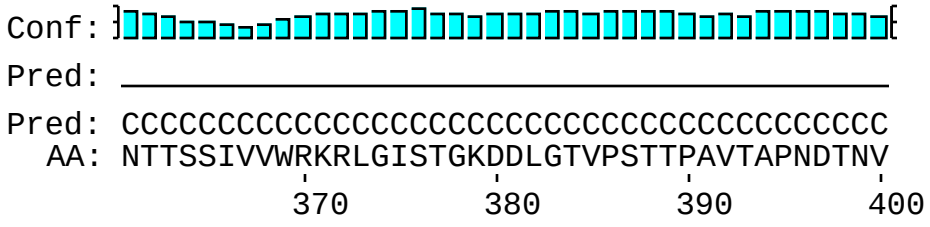
Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
AA: NTTSSIVVWRKRLGISTGKDDLGTVPSTTPAVTAPNDTNV
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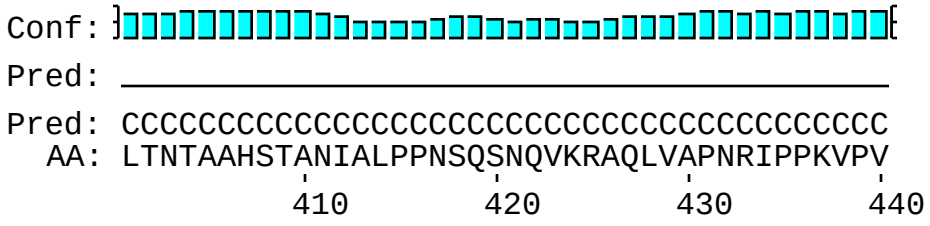
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Pred:
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AA: LTNTAAHSTANIALPPNSQSNQVKRAQLVAPNRIPPKVPV
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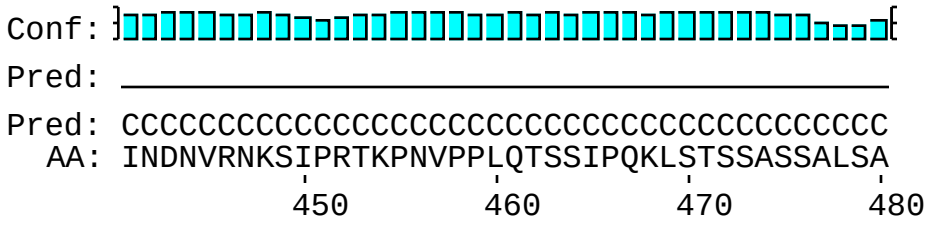
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Pred:
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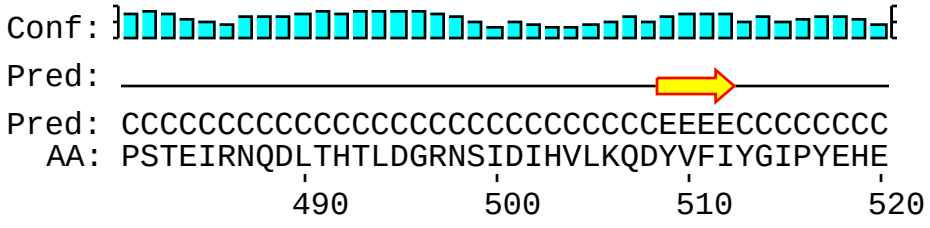
Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEEECCCCCCCC
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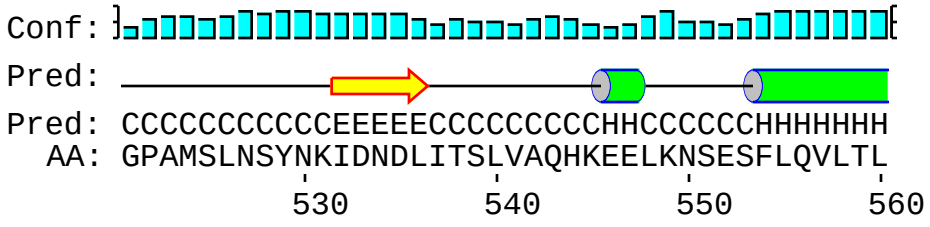
Conf:
Pred:
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530 540 550 560

Conf:
Pred:
Pred: HHHHHHCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHH
AA: KKSGMLSYKNTVMEGNDDQENKEHQMANIEDTDLSMYDFE
570 580 590 600

Conf:
Pred:
Pred: HHHHHHHHHHHHHHHHHCCEEEEEECCCCCCCCCCCCCCC
AA: FNELTRKGFLILEKYKNRIWFISLPSYSTLSKIPFNAVKS
610 620 630 640

Conf:
Pred:
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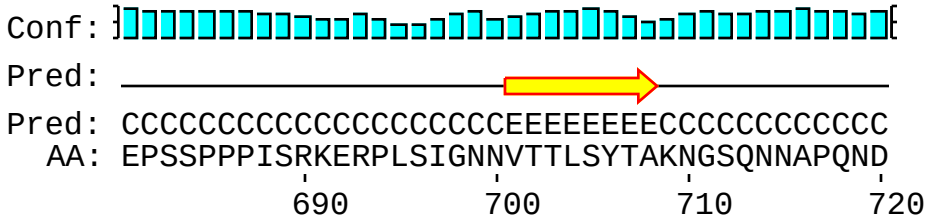
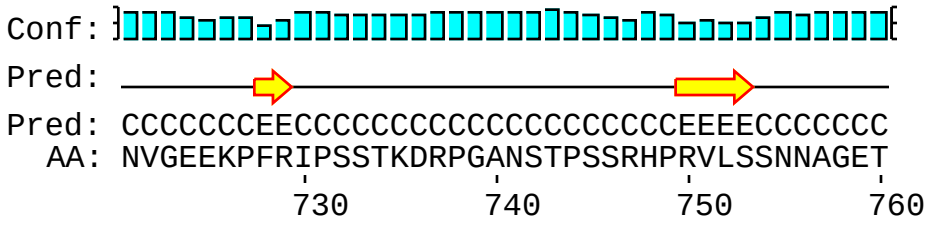
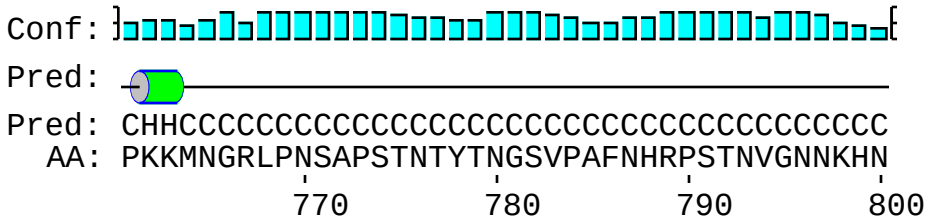
AA: STINNNENWVDCFFRARQLLEEKQILDKISNVSFDSKASS
650 660 670 680


Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCCCCEEEEEEEECCCCCCCCCCCC
AA: EPSSPPPISRKERPLSIGNNVTTLSYTAKNGSQNNAPQND
690 700 710 720


Conf:
Pred:
Pred: CCCCCCCEECCCCCCCCCCCCCCCCCCCCEEEECCCCCCC
AA: NVGEEKPFRIPSSTKDRPGANSTPSSRHPRVLSSNNAGET
730 740 750 760


Conf:
Pred:
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AA: PKKMNGRLPNSAPSTNTYTNGSVPAFNHRPSTNVGNNKHN
770 780 790 800

Conf:
Pred:
Pred: EEECCCCCCEEECCCCCCCCCEEEECCCCCCCCCCCCCCC
AA: ILTSKKQGSSVFSPSSSTTKPQIKTTGYRQPTPSPPLPQM
810 820 830 840

Conf:
Pred:
Pred: CCCCCHHHCCCCCCEEEECCCEEEEEEECCCCCCCCHHHH
AA: EFPTTREKYSAPSNMVISSSRYEVLHTLNNSQTNFDREIA
850
860
870
880
Conf:
Pred:
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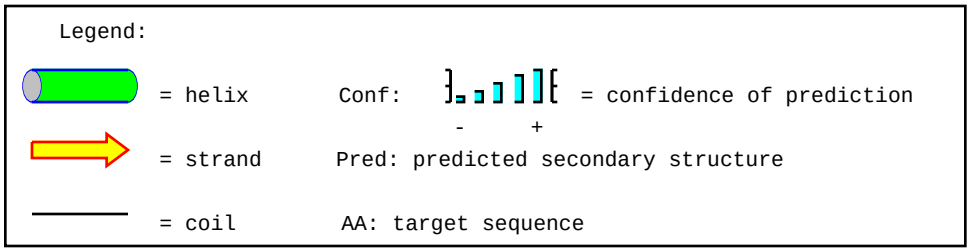
890


Legend:
= helix
Conf:
= confidence of prediction
-
+
= strand
Pred: predicted secondary structure
= coil
AA: target sequence