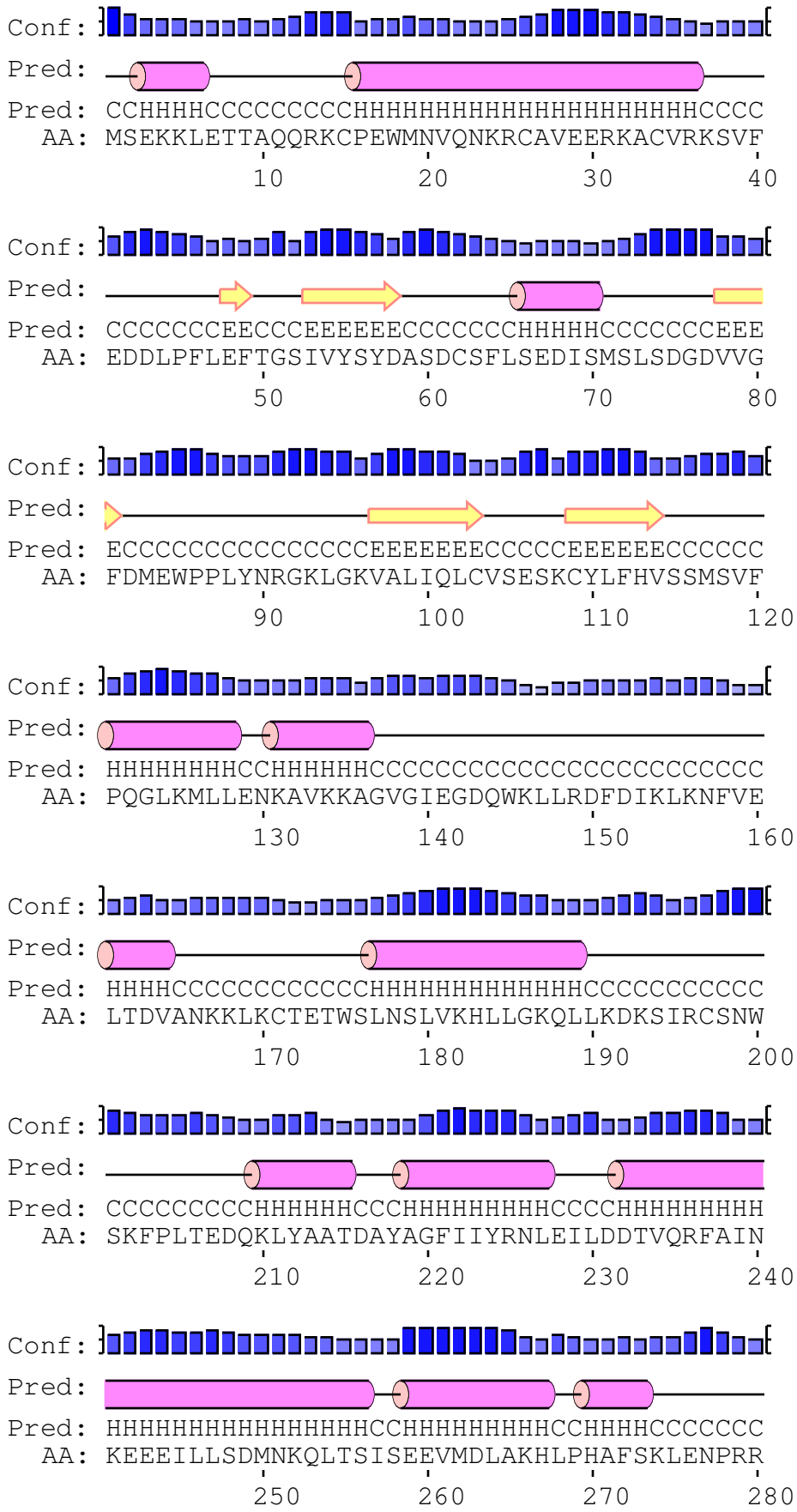
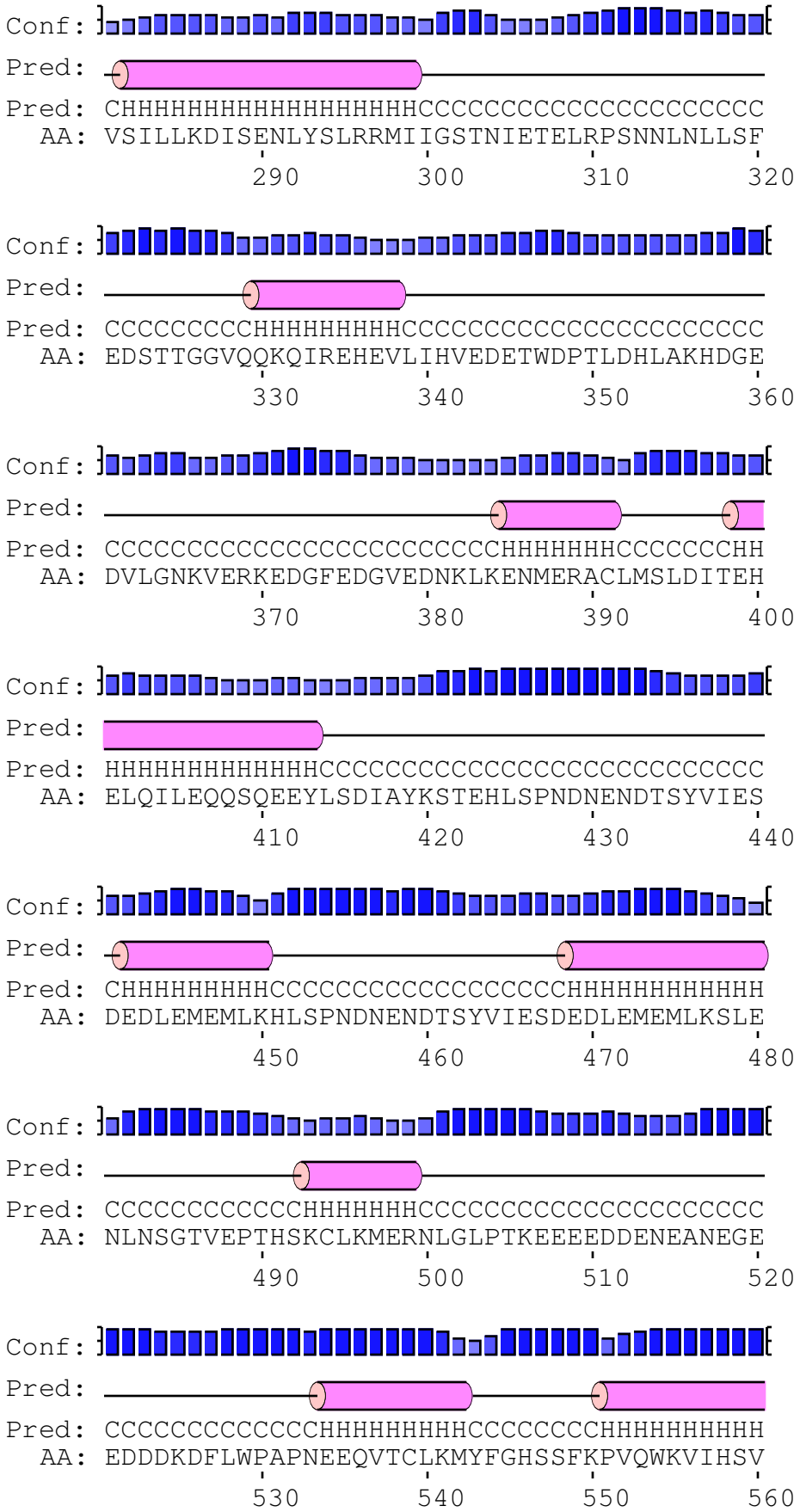
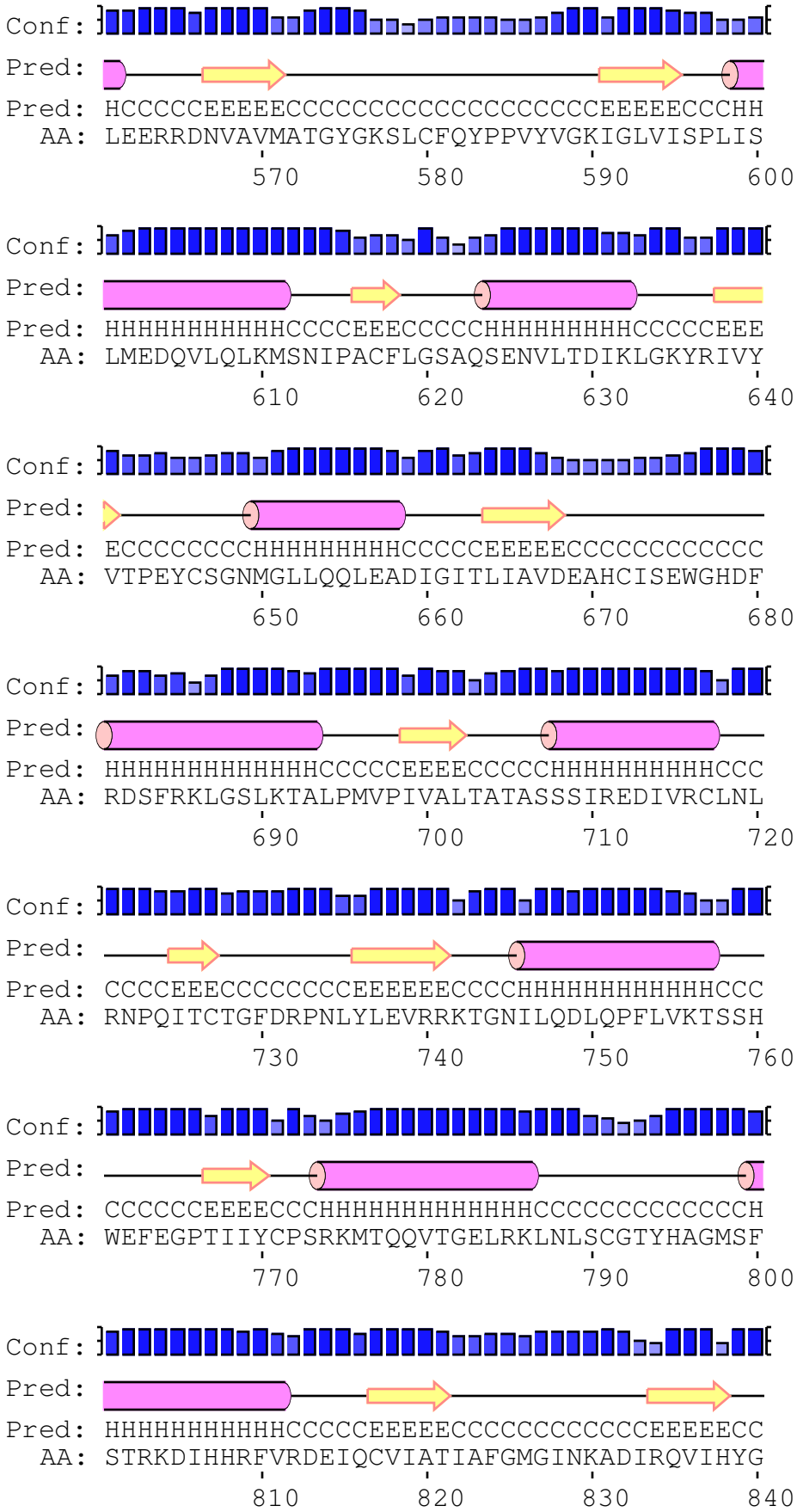
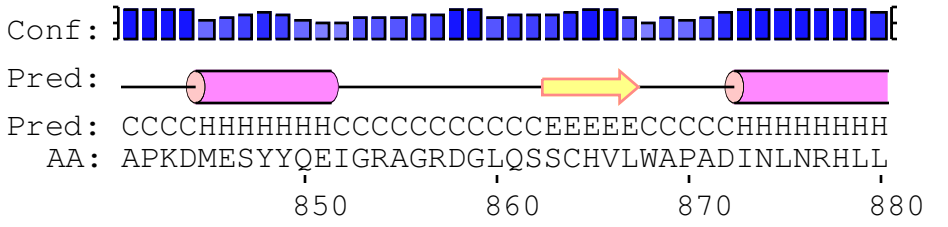
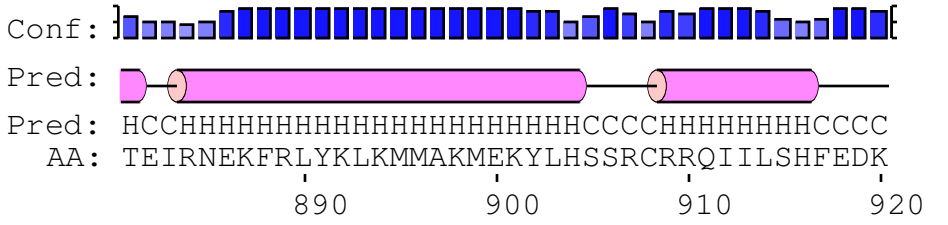
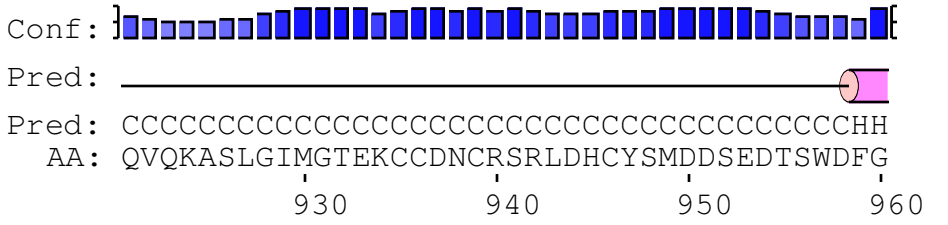

Conf:
Pred:
Pred: CCHHHHCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHCCCC
AA: MSEKKLETTAQQRKCPEWMNVQNKRCAVEERKACVRKSVF
10 20 30 40
Conf:
Pred:
Pred: CCCCCCCEECCCEEEEECCCCCCCHHHHHCCCCCCCEEE
AA: EDDLPFLEFTGSIVYSYDASDCSFLSEDISMSLSDGDVVG
50 60 70 80
Conf:
Pred:
Pred: ECCCCCCCCCCCCCCCEEEEEECCCCCEEEEECCCCCC
AA: FDMEWPPLYNRGKLGKVALIQLCVSESKCYLFHVSSMSVF
90 100 110 120
Conf:
Pred:
Pred: HHHHHHHHCCHHHHHCCCCCCCCCCCCCCCCCCCCCCC
AA: PQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKLKNFVE
130 140 150 160
Conf:
Pred:
Pred: HHHHCCCCCCCCCCCCHHHHHHHHHHHHCCCCCCCCCC
AA: LTDVANKKLKCTETWSLNSLVKHLLGKQLLKDKSIRCSNW
170 180 190 200
Conf:
Pred:
Pred: CCCCCCCCCHHHHHHCCCHHHHHHHHCCCCHHHHHHHH
AA: SKFPLTEDQKLYAATDAYAGFIIYRNLEILDDTVQRFAIN
210 220 230 240
Conf:
Pred:
Pred: HHHHHHHHHHHHHHHHCCHHHHHHHHCCHHHHCCCCCC
AA: KEEEILLSDMNKQLTSISEEVMDLAKHLPHAFSKLENPRR
250 260 270 280

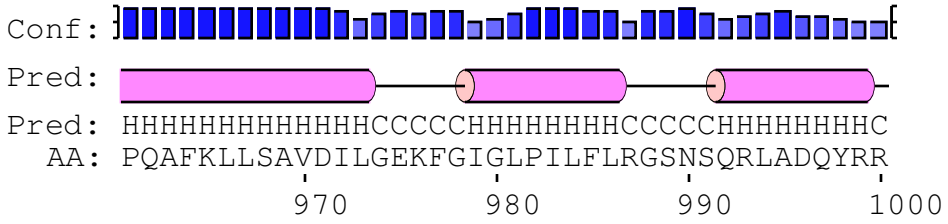

Conf:
Pred:
Pred: CHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCC
AA: VSILLKDISENLYSLRRMIIGSTNIETELRPSNNLNLLSF
290 300 310 320
Conf:
Pred:
Pred: CCCCCCCCCHHHHHHHHHCCCCCCCCCCCCCCCCCCCCC
AA: EDSTTGGVQQKQIREHEVLIHVEDETWDPTLDHLAKHDGE
330 340 350 360
Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCCCCCCCCHHHHHHHCCCCCCCHH
AA: DVLGNKVERKEDGFEDGVEDNKLKENMERACLMSLDITEH
370 380 390 400
Conf:
Pred:
Pred: HHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCC
AA: ELQILEQQSQEEYLSDIAYKSTEHLSPNDNENDTSYVIES
410 420 430 440
Conf:
Pred:
Pred: CHHHHHHHHHCCCCCCCCCCCCCCCCCCHHHHHHHHHHH
AA: DEDLEMEMLKHLSPNDNENDTSYVIESDEDLEMEMLKSLE
450 460 470 480
Conf:
Pred:
Pred: CCCCCCCCCCCCHHHHHHHCCCCCCCCCCCCCCCCCCCC
AA: NLNSGTVEPTHSKCLKMERNLGLPTKEEEEDDENEANEGE
490 500 510 520
Conf:
Pred:
Pred: CCCCCCCCCCCCCHHHHHHHHHCCCCCCCCHHHHHHHHHH
AA: EDDDKDFLWPAPNEEQVTCLKMYFGHSSFKPVQWKVIHSV
530 540 550 560

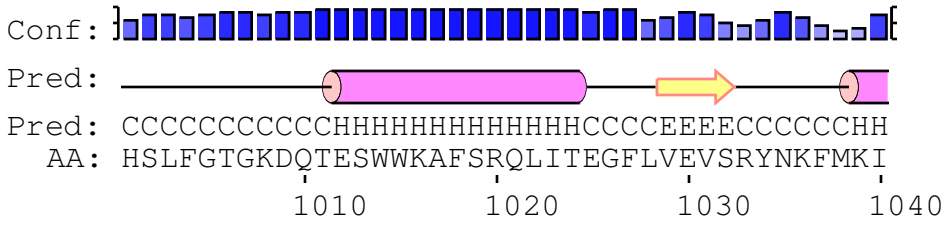

Conf:
Pred:
Pred: HCCCCCEEEEECCCCCCCCCCCCCCCCCCCEEEEECCCHH
AA: LEERRDNVAVMATGYGKSLCFQYPPVYVGKIGLVISPLIS
570 580 590 600
Conf:
Pred:
Pred: HHHHHHHHHHHCCCCEEECCCCCHHHHHHHHHCCCCCEEE
AA: LMEDQVLQLKMSNIPACFLGSAQSENVLTDIKLGKYRIVY
610 620 630 640
Conf:
Pred:
Pred: ECCCCCCCCHHHHHHHHHCCCCCEEEEECCCCCCCCCCCC
AA: VTPEYCSGNMGLLQQLEADIGITLIAVDEAHCISEWGHDF
650 660 670 680
Conf:
Pred:
Pred: HHHHHHHHHHHHHCCCCCEEEECCCCCHHHHHHHHHCCC
AA: RDSFRKLGSLKTALPMVPIVALTATASSSIREDIVRCLNL
690 700 710 720
Conf:
Pred:
Pred: CCCCEEECCCCCCCCEEEEECCCCHHHHHHHHHHHCCC
AA: RNPQITCTGFDRPNLYLEVRRKTGNILQDLQPFLVKTSSH
730 740 750 760
Conf:
Pred:
Pred: CCCCCCEEEECCCHHHHHHHHHHHHCCCCCCCCCCCCCH
AA: WEFEGPTIIYCPSRKMTQQVTGELRKLNLSCGTYHAGMSF
770 780 790 800
Conf:
Pred:
Pred: HHHHHHHHHHHCCCCCEEEEECCCCCCCCCCCCEEEECC
AA: STRKDIHHRFVRDEIQCVIATIAFGMGINKADIRQVIHYG
810 820 830 840

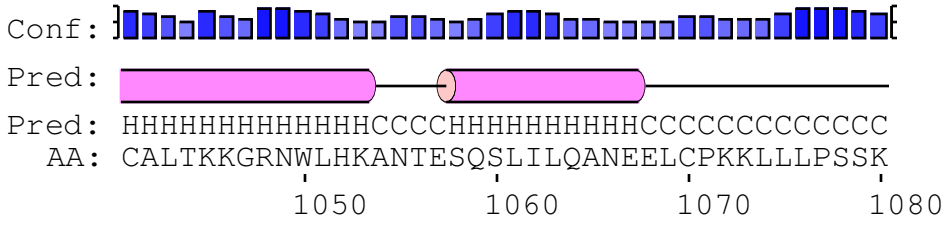

Conf:
Pred:
Pred: CCCCHHHHHHHCCCCCCCCCCCEEEEECCCCCHHHHHHHH
AA: APKDMESYYQEIGRAGRDGLQSSCHVLWAPADINLNRHLL
850 860 870 880

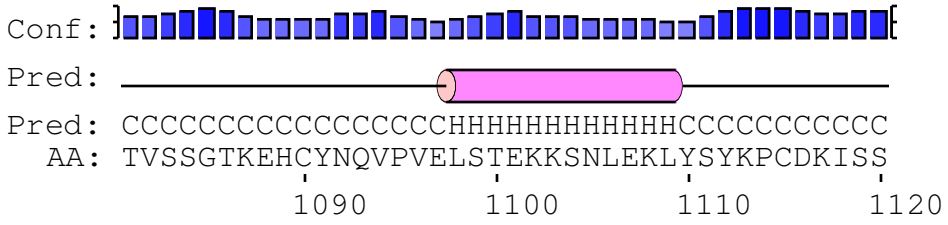

Conf:
Pred:
Pred: HCCHHHHHHHHHHHHHHHHHHHHHCCCCHHHHHHHHCCCC
AA: TEIRNEKFRLYKLKMMAKMEKYLHSSRCRRQIILSHFEDK
890 900 910 920

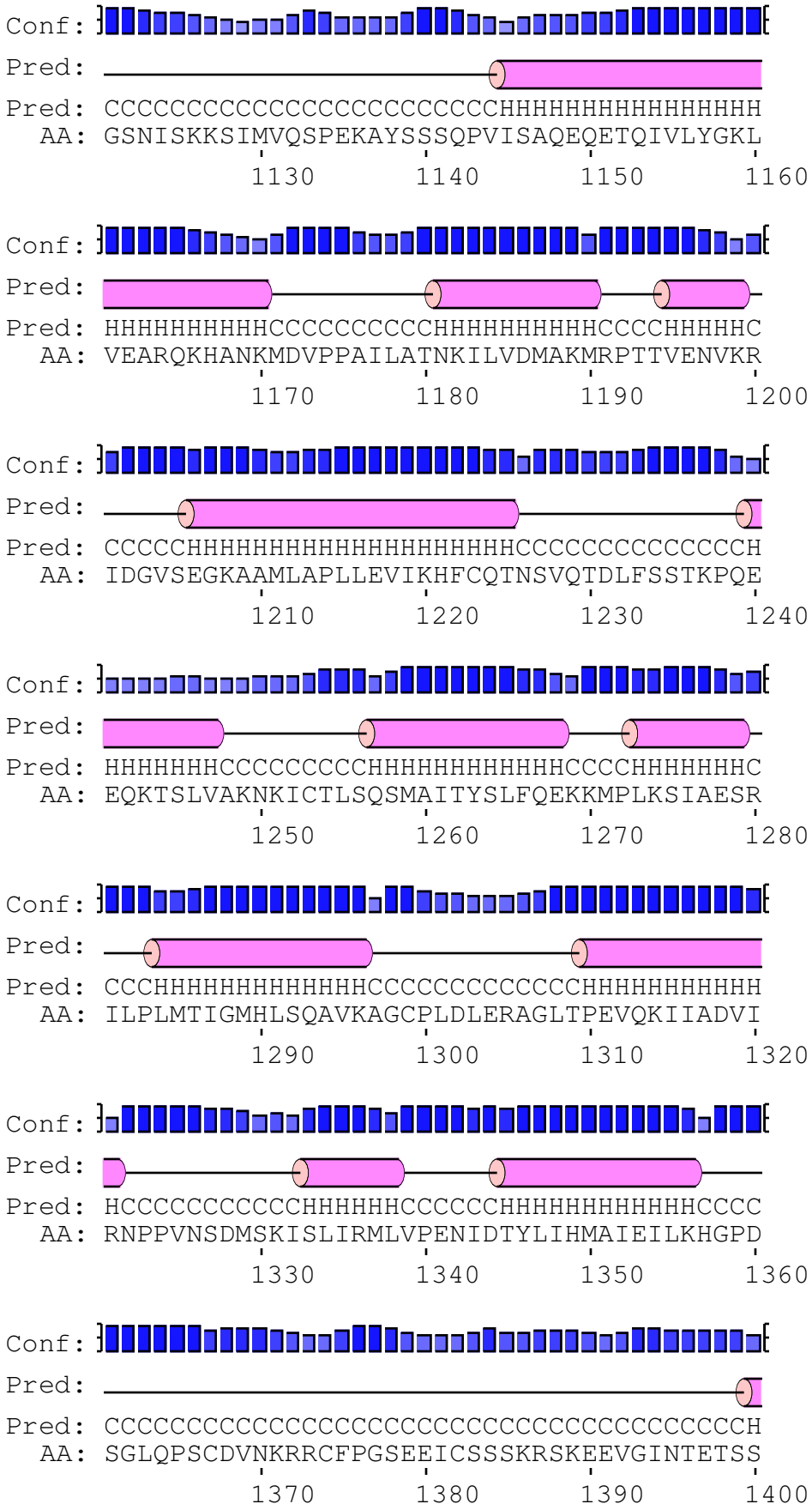

Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHH
AA: QVQKASLGIMGTEKCCDNCRSRLDHCYSMDDSEDTSWDFG
930 940 950 960

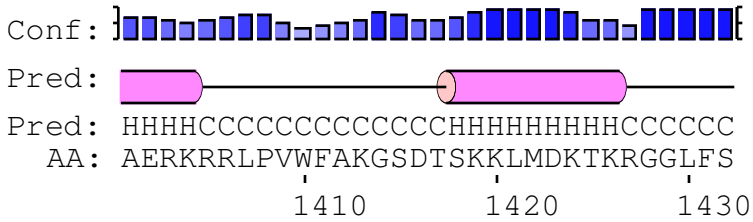

Conf:
Pred:
Pred: HHHHHHHHHHHHHCCCCCHHHHHHHHCCCCCHHHHHHHHC
AA: PQAFKLLSAVDILGEKFGIGLPILFLRGSNSQRLADQYRR
970 980 990 1000

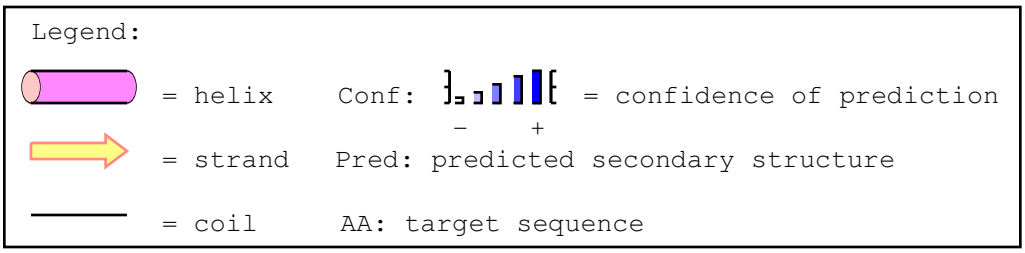

Conf:
Pred:
Pred: CCCCCCCCCCCHHHHHHHHHHHHHCCCCEEEECCCCCCHH
AA: HSLFGTGKDQTESWWKAFSRQLITEGFLVEVSRYNKFMKI
1010 1020 1030 1040


Conf:
Pred:
Pred: HHHHHHHHHHHHHCCCCHHHHHHHHHCCCCCCCCCCCCC
AA: CALTKKGRNWLHKANTESQSLILQANEELCPKKLLLPSSK
1050 1060 1070 1080


Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCHHHHHHHHHHHHCCCCCCCCCCC
AA: TVSSGTKEHCYNQVPVELSTEKKSNLEKLYSYKPCDKISS
1090 1100 1110 1120


Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHH
AA: GSNISKKSIMVQSPEKAYSSSQPVISAQEQETQIVLYGKL
1130 1140 1150 1160
Conf:
Pred:
Pred: HHHHHHHHHHCCCCCCCCCCHHHHHHHHHHCCCCHHHHHC
AA: VEARQKHANKMDVPPAILATNKILVDMAKMRPTTVENVKR
1170 1180 1190 1200
Conf:
Pred:
Pred: CCCCCHHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCH
AA: IDGVSEGKAAMLAPLLEVIKHFCQTNSVQTDLFSSTKPQE
1210 1220 1230 1240
Conf:
Pred:
Pred: HHHHHHHCCCCCCCCCHHHHHHHHHHHHCCCCHHHHHHHC
AA: EQKTSLVAKNKICTLSQSMAITYSLFQEKKMPLKSIAESR
1250 1260 1270 1280
Conf:
Pred:
Pred: CCCHHHHHHHHHHHHHCCCCCCCCCCCCCHHHHHHHHHHH
AA: ILPLMTIGMHLSQAVKAGCPLDLERAGLTPEVQKIIADVI
1290 1300 1310 1320
Conf:
Pred:
Pred: HCCCCCCCCCCCHHHHHHCCCCCCHHHHHHHHHHHHCCCC
AA: RNPPVNSDMSKISLIRMLVPENIDTYLIHMAIEILKHGPD
1330 1340 1350 1360
Conf:
Pred:
Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCH
AA: SGLQPSCDVNKRRCFPGSEEICSSSKRSKEEVGINTETSS
1370 1380 1390 1400


Conf:
Pred:
Pred: HHHHCCCCCCCCCCCCCHHHHHHHHHCCCCCC
AA: AERKRRLPVWFAKGSDTSKKLMDKTKRGGLFS
1410
1420
1430


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