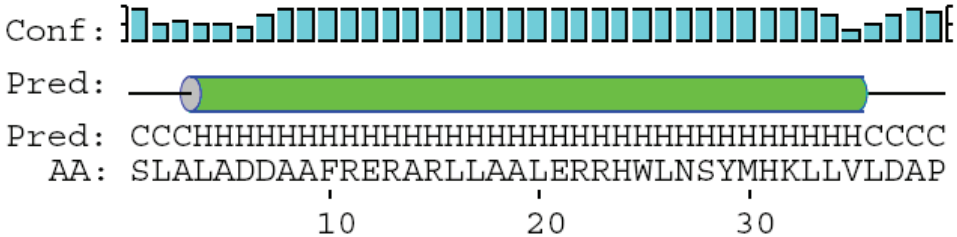
Conf:
Pred:
Pred: CCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCC
AA: SLALADDAAFRERARLLAALERRHWLNSYMHKLLVLDAP
10
20
30
Legend:
= helix
Conf:
= confidence of prediction
-
+
= strand
Pred: predicted secondary structure
= coil
AA: target sequence