

Conf:

Pred:

Pred: CCHHHHHHHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHH
 AA: GNFVHAQELI LARLNHQLSP IGRPFQRAAFYFKEALQLLLH

Conf:

Pred:

Pred: HCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHH
 AA: MNMNNSSLALPGYS IIFKISAYKSFSEISPI LQFANFTCN

Pt-Sc

Conf:

Pred:

Pred: CCCCCCHHHHCCCEEEEECCCCCCHHHHHHHHHHHHHHHHH
 AA: MRAMP LAFED FQK GALD FS SSS SD SRQ FHHQQ HK EEQDW

Conf:

Pred:

Pred: HHHCCCCCCCCCCCCCECCCCCCCCCEEEEECCCCCCCCCCCC
 AA: LLSNSNRGNKKANCCYVGSATTEPT SVLDNRRSPSPPTSS

Conf:

Pred:

Pred: CCEEECCCCCCCCCCCCCECCCCCCCCCCCCCCCCCEEE
 AA: STLSSSLGGGSSATDITGVAATNASSNFP SVDITNTEKC

Conf:

Pred:

Pred: ECCCCHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHHHHHH
 AA: GGLGMEWESVLSGSPNGEQSLKLMGDTDDPSLGLNKI

Conf:

Pred:

Pred: HHHCHHHHHCCCCCCCCCCCCCCCCCEEECCCCCCCCCCCC
 AA: LHQDTEFNAGFGVVDQASLGFTETPTTSVSSNIDPFDVGNSS

Conf:

Pred:

Pred: CCCCCCCCCCCCCCHHHHHCCCCCCCCCCCCCCCCCCCC
 AA: ARLSGSNQNHIFSTAAANLSPFPFVFQPVFALDEKXP

Conf:

Pred:

Pred: EEECHHHHHHHHHHHCCCCCCCCCCCCCHHHHHHHHHHHHH
 AA: QIFSPQLIMNQNAQYQNPALFLPLSYAQMQVHQLLPPA

Conf:

Pred:

Pred: CCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHH
 AA: PPPPKRLNLGPNQKVPFSDSGQQELFLRRQPLQLQQQRE

Conf:

Pred:

Pred: HRCCEHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
 AA: TMGVTTTATKQKLVNDELANQQLQQAITDQIFKASELIET

Conf:

Pred:

Pred: CCHHHHHHHHHHHHHHHHHCCCCCHHHHHHHHHHHHHHHHHHH
 AA: GNFVHAQELI LARLNHQLSP IGRPFQRAAFYFKEALQLLLH

Conf:

Pred:

Pred: HCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHH
 AA: MNMNNSSLALPGYS IIFKISAYKSFSEISPI LQFANFTCN

Conf:

Pred:

Pred: HHHHHHHHCCCEEEEECCCCCCHHHHHHHHHHHHHHHHHHH
 AA: QALLEAFEGCNRIH IIDFDIGYGGQWASLMQELVLRSEGP

Conf:

Pred:

Pred: CEEEEEEECCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHH
 AA: PSLKITAFASPS THDEL EL SFTREN LKHFASEINMPFELE

Conf:

Pred:

Pred: ECCCCHHHHHHHHHHHCCCCCCCCCEEECCCHHHHHCCCCCH
 AA: ILSLEALNSASLALPFRGLESEATAVNLP IGTFCNYPATF

Conf:

Pred:

Pred: HHHHHHHHHHHHHHHHHCCCCCEEEEECCCCCHHHHHHHHHHHHH
 AA: PSVLCEVFKQLKPKIKLVVSLDRGQDR TDVFPFHHTIHALOSVY

Conf:

Pred:

Pred: HHHHHHHHHHHHHHHHHCCCCCHHHHHHHHHHHHHHHHHHHHHHHHH
 AA: SCLLESLEDAVIVNL DALQR IERFLVYPCIEKIVLGRHRSF

Conf:

Pred:

Pred: CCHHHHHHHHHHHHHHHHHCEEEEEECHHHHHHHHHHHHHHHHH
 AA: ERLFPWKSLFMQSQFAPLITFSNFTESQADCLVQRTPVKKGTE

Conf:

Pred:

Pred: EEEEECCCCCEEEECCEEEEEEESB00
 AA: HVEKRQSSLYFCWQRKELI LATAWR

Legend:

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

