

Key

Pred: Predicted secondary structure (H=helix, E=strand, C=coil)

AA: Target sequence

Conf: 951133221000113860667899999999830247777678762257663012122222
Pred: CCCHHHHHHCEEECCCCHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCHHHHHHHH
AA: ML SRLFRMHGLFVASHPWEIVGTVTLTICMMSMNMFTGNKICGWN YECPKFEEDVLSS
10 20 30 40 50 60

Conf: 468999999999999998610203453131678899999999999999999961766430
Pred: HHHHHHHHHHHHHHHHHHHHCCHHHHCCHHHHHHHHHHHHHHHHHHHHHHHHCCCCC
AA: DIIILTITRCIAILYIYFQFNLRQLGSKYILGIAGLFTIFSSFFVSTVVIHFLDKELTG

70 80 90 100 110 120

Conf: 332120200013230799999999971478887789999999998899999999999999
Pred: HHHHHHHEEEEECCCHHHHHHHHHHHCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
AA: LNEALPFFLLIDLSTLAKFALSSNSQDEVRENIARGMAILGPTFTLDALVECLVIG
 130 140 150 160 170 180

[illegible][illegible][illegible]

Conf: 10132100032775311257678765666666540013156677788886531010565
Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCECCCCCCCCCCCCCECCCCC
AA: QKKVPDNCCRREPLVRNNQKCDSEVEETGINRERKVEVIKPLVAETDTPNRATFVVGNS

370 380 390 400 410 420

Conf: 55677655678765334788888614655652253356777778999998627763012
Pred: CCCCCCCCCCCCCCCCCCCCCCHHHHHHHHCCCCCCCCCHHHHHHHHHCCCCHHH
AA: SLLDTSSVLVTQEPEIELPREPRNEECLQILGNAEKGAFLSDAEIIQLVNAKHIPAYK
430 440 450 460 470 480

