

Legend:

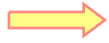


= helix

Conf:



= confidence of prediction



= strand

Pred: predicted secondary structure



= coil

AA: target sequence

Analysis performed with the use of PSIPRED Protein Structure Prediction Server

Citation: Bryson K, McGuffin LJ, Marsden RL, Ward JJ, Sodhi JS. & Jones DT. (2005)
Protein structure prediction servers at University College London.
Nucl. Acids Res. 33(Web Server issue):W36-38