



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