
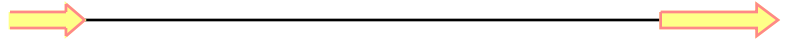



Conf: 

Pred: 

Pred: EEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEEEEEE

AA: LLLTRDGGNSNNESEIFRPGGGDMRDNWRSELYKYKVVKI

290 300 310 320





Conf: 

Pred: _

Pred: C

AA: E

Legend:

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