



Email	l.a.kelley@imperial.ac.uk
Description	P39220
Date	Thu Jan 5 11:58:32 GMT 2012
Unique Job ID	5b6999045ef68bf5


Protein structure prediction and disorder analysis for the protein sequence. The image shows four segments of the protein, each with its amino acid sequence, secondary structure (SS), confidence, disorder, and disorder confidence. The protein is 210 residues long. The first segment (1-60) shows a beta-strand followed by a large alpha-helical region. The second segment (70-120) shows a beta-strand, an alpha-helical region, and a beta-strand. The third segment (130-180) shows a large beta-strand region followed by a small alpha-helical region. The fourth segment (190-210) shows a beta-strand followed by an alpha-helical region. Disorder analysis indicates several disordered regions, particularly in the first and third segments.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand