



Email	l.a.kelley@imperial.ac.uk
Description	P77609
Date	Thu Jan 5 12:31:01 GMT 2012
Unique Job ID	Odd40488717d6cdd


Protein structure and disorder analysis of the N-terminal region of the protein. The top panel shows residues 1-60, and the bottom panel shows residues 70-110. Each panel includes the amino acid sequence, secondary structure (SS) with alpha-helices and beta-strands, confidence scores, and disorder predictions. The N-terminal region (1-60) contains several alpha-helices and a beta-strand, with a high confidence score. The C-terminal region (70-110) contains a beta-strand and a long loop, with a lower confidence score. Disorder predictions are shown as red bars below the sequence.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand