

Email	l.a.kelley@imperial.ac.uk
Description	P52132
Date	Thu Jan 5 12:05:37 GMT 2012
Unique Job ID	12f33cbd866485f6

Figure 1 displays the protein structure and disorder analysis of the human protein. The protein sequence is shown in the top panel, with residues numbered from 1 to 270. The secondary structure is predicted using the I-TASSER server, showing alpha-helices (green) and beta-strands (blue). The protein is annotated with various domains and motifs, including a coiled-coil domain (residues 1-60), a coiled-coil domain (residues 130-180), and a coiled-coil domain (residues 250-270). The protein is also annotated with various motifs, including a coiled-coil domain (residues 1-60), a coiled-coil domain (residues 130-180), and a coiled-coil domain (residues 250-270). The protein is shown in a ribbon diagram, with the N-terminal region (residues 1-60) and the C-terminal region (residues 130-180) highlighted in blue. The protein is annotated with various domains and motifs, including a coiled-coil domain (residues 1-60), a coiled-coil domain (residues 130-180), and a coiled-coil domain (residues 250-270). The protein is also annotated with various motifs, including a coiled-coil domain (residues 1-60), a coiled-coil domain (residues 130-180), and a coiled-coil domain (residues 250-270).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand