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Description	P37056
Date	Thu Jan 5 11:54:44 GMT 2012
Unique Job ID	c90189a776958132

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 1 to 270. The secondary structure is predicted using a coiled-coil domain prediction method, showing several alpha-helices and beta-strands. 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 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