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Figure 1 displays the protein structure and disorder analysis of the human protein. The figure shows the full-length protein sequence (1-240 residues) and its predicted secondary structure (SS) and disorder. The sequence is color-coded (green for alpha-helices, red for beta-strands, and blue for loops). The SS is represented by a bar chart below the sequence, and the disorder is indicated by a bar chart below the SS. The protein is composed of several domains, including a coiled-coil domain (residues 1-120), a zinc finger domain (residues 121-180), and a C-terminal domain (residues 181-240). The disorder analysis shows that the protein is highly disordered, with many regions of low confidence in the disorder prediction.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand