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Figure 1 displays the protein structure and disorder analysis of the human protein. The figure is organized into three main sections, each corresponding to a different range of residues (1-60, 70-120, and 130-180). Each section contains four rows of information:


- Sequence:** The amino acid sequence for the specified residue range, color-coded by chemical properties.
- Secondary structure:** A diagram showing the predicted secondary structure elements (alpha-helices in green, beta-strands in blue) and loops (grey).
- SS confidence:** A bar representing the confidence in the secondary structure prediction, with colors indicating different levels of confidence.
- Disorder:** A bar representing the predicted disorder of the protein, with colors indicating different levels of confidence.


The protein is a single-chain protein with a total length of 180 residues. The structure analysis shows that the protein is primarily composed of alpha-helices and beta-strands, with some disordered regions. The disorder analysis indicates that the protein is mostly disordered, with some regions of high confidence in being ordered (e.g., residues 1-10, 11-20, 131-140, 141-150, 151-160, 161-170, 171-180).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand