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


- Sequence:** The amino acid sequence for the specified range, color-coded by type (e.g., red for acidic, blue for basic, green for polar, yellow for non-polar).
- Secondary structure (SS):** A representation of the local structure, showing alpha-helices (green cylinders) and beta-strands (blue arrows).
- confidence:** A bar representing the confidence in the secondary structure prediction, with colors indicating different levels of certainty (e.g., red for high, yellow for medium, green for low).
- Disorder:** A bar representing the predicted disorder of the protein, with colors indicating different levels of confidence (e.g., red for high, yellow for medium, green for low).
- Disorder confidence:** A bar representing the confidence in the disorder prediction, with colors indicating different levels of certainty (e.g., red for high, yellow for medium, green for low).


The protein is shown to have a complex structure with multiple alpha-helices and beta-strands. The disorder analysis indicates that the protein is highly disordered in several regions, particularly in the N-terminal and C-terminal regions, and in a central region (residues 70-120). The confidence in the disorder prediction is generally high, with some regions of lower confidence (yellow/green).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand