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Figure 1 displays the protein structure and disorder analysis for the 180-residue protein. The figure is organized into three main sections corresponding to residue ranges 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.
- Secondary structure:** A representation of the protein's fold, showing alpha-helices (green cylinders) and beta-strands (blue arrows).
- SS (Solvent Accessibility):** A bar chart indicating the relative solvent accessibility of each residue, with red representing high accessibility and yellow representing low accessibility.
- confidence:** A bar chart showing the confidence in the structural predictions, with red indicating high confidence and yellow indicating lower confidence.
- Disorder:** A bar chart indicating regions of intrinsic disorder, with red representing high disorder and yellow representing lower disorder.
- Disorder confidence:** A bar chart showing the confidence in the disorder predictions, with red indicating high confidence and yellow indicating lower confidence.

The overall protein structure is highly disordered, with many residues marked as '??' in the disorder analysis, suggesting a lack of a fixed three-dimensional structure. The secondary structure elements are primarily located in the C-terminal region (residues 130-180).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand