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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), plus a short segment (E L M Q F).

For each section, the following information is provided:


- Sequence:** The amino acid sequence is shown, with residue numbers indicated above the sequence.
- Secondary structure (SS):** The predicted secondary structure is shown, with green cylinders representing alpha-helices and blue arrows representing beta-strands.
- confidence:** A red bar indicates the confidence level for the secondary structure prediction.
- Disorder:** A line with question marks indicates regions of predicted disorder.
- Disorder confidence:** A bar with various colors (green, yellow, orange, red, blue, purple) indicates the confidence level for the disorder prediction.


The protein structure analysis shows that the protein is composed of several alpha-helices and beta-strands, with some regions marked as disordered. The disorder confidence analysis shows that the protein has a high confidence level for the disorder prediction in several regions.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand