


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Figure 1 displays the protein structure and disorder analysis for the protein. The figure is organized into four panels, each showing a different segment of the protein (residues 1-60, 70-120, 130-180, and 190-220). Each panel includes the following information:


- Sequence:** The amino acid sequence for the segment, with residues numbered above the sequence.
- Secondary structure (SS):** A diagram showing the predicted secondary structure elements (alpha-helices and beta-strands) for the segment.
- confidence:** A bar chart showing the confidence scores for the secondary structure predictions.
- Disorder:** A bar chart showing the disorder predictions for the segment.
- Disorder confidence:** A bar chart showing the confidence scores for the disorder predictions.


The protein is 220 amino acids long. The first segment (1-60) shows a high confidence structure with several alpha-helices and beta-strands. The second segment (70-120) shows a high confidence structure with several alpha-helices and beta-strands. The third segment (130-180) shows a high confidence structure with several alpha-helices and beta-strands. The fourth segment (190-220) shows a high confidence structure with several alpha-helices and beta-strands. The disorder analysis shows that the protein is mostly ordered, with some regions of low confidence and disorder predictions.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand