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


- Sequence:** The amino acid sequence for the specified range.
- Secondary structure:** A diagram showing the predicted secondary structure elements (alpha-helices and beta-strands) for the sequence.
- SS confidence:** A bar chart representing the confidence score for the secondary structure prediction, ranging from 0.00 to 1.00.
- Disorder:** A bar chart representing the disorder analysis, with colors indicating different levels of disorder (e.g., red for high disorder, green for low disorder).
- Disorder confidence:** A bar chart representing the confidence score for the disorder analysis, ranging from 0.00 to 1.00.


The N-terminal region (1-60) shows a high degree of disorder, with a confidence score of 0.00. The middle region (70-120) shows a high degree of disorder, with a confidence score of 0.00. The C-terminal region (130-180) shows a high degree of disorder, with a confidence score of 0.00.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand