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Figure 1 displays the protein structure and disorder analysis for the N-terminal region of the protein. The figure is divided into two main sections, each showing a different segment of the protein sequence.

Top Section (Residues 1-60):

- Sequence:** MMI RERI EEKLR AAF QP VFL E VVDE S Y R H N V P A G S E S H F K V V L V S D R F T G E R F L N R H R M I
- Secondary structure:** The structure is shown as a green ribbon diagram. It features several alpha-helices and beta-strands, with a blue arrow indicating a beta-strand.
- SS confidence:** A bar chart showing the confidence of the secondary structure prediction. The confidence is generally high, with some lower values in the middle of the segment.
- Disorder:** A bar chart showing the disorder analysis. The protein is highly disordered in the N-terminal region (residues 1-60), indicated by red and yellow bars.
- Disorder confidence:** A bar chart showing the confidence of the disorder analysis. The confidence is generally high, with some lower values in the middle of the segment.

Bottom Section (Residues 70-100):

- Sequence:** Y S T L A E E L S T T V H A L A L H T Y T I K E W E G L Q D T V F A S P P C R G A G S I A
- Secondary structure:** The structure is shown as a green ribbon diagram. It features several alpha-helices and beta-strands, with a blue arrow indicating a beta-strand.
- SS confidence:** A bar chart showing the confidence of the secondary structure prediction. The confidence is generally high, with some lower values in the middle of the segment.
- Disorder:** A bar chart showing the disorder analysis. The protein is less disordered in the C-terminal region (residues 70-100), indicated by blue and green bars.
- Disorder confidence:** A bar chart showing the confidence of the disorder analysis. The confidence is generally high, with some lower values in the middle of the segment.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand