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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 sequence alignment, secondary structure prediction, and disorder analysis for a specific range of residues.

Top Section (Residues 1-60):

- Sequence:** MRSA D F S N P R I L S N L M S K S E K E K R A I I F N C R L N K G L Y V T S A C V S R S V F R C K Q E P L I E F
- Secondary structure:** The structure is shown as a series of green cylinders (alpha-helices) and blue arrows (beta-strands). The structure is highly disordered, with many regions of low confidence.
- SS confidence:** A bar chart showing the confidence of the secondary structure prediction. The confidence is generally low, with many regions marked as '???'.
- Disorder:** A bar chart showing the disorder analysis. The protein is highly disordered, with many regions marked as '???'.
- Disorder confidence:** A bar chart showing the confidence of the disorder analysis. The confidence is generally low, with many regions marked as '???'.

Bottom Section (Residues 70-100):

- Sequence:** V S P K M I A F V Q I D G R Y L T K M L T C D I H V R K E A K E G R G Y Q Q I H K L S
- Secondary structure:** The structure is shown as a series of green cylinders (alpha-helices) and blue arrows (beta-strands). The structure is more ordered than the top section, with a long alpha-helix and a short loop.
- SS confidence:** A bar chart showing the confidence of the secondary structure prediction. The confidence is generally higher than the top section, with fewer regions marked as '???'.
- Disorder:** A bar chart showing the disorder analysis. The protein is less disordered than the top section, with fewer regions marked as '???'.
- Disorder confidence:** A bar chart showing the confidence of the disorder analysis. The confidence is generally higher than the top section, with fewer regions marked as '???'.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand