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Figure 1 displays the protein structure and disorder analysis of the 200-residue protein. The protein is composed of several alpha-helices and beta-strands, with some regions being disordered. The disorder predictions are shown as red and green bars, indicating different levels of disorder confidence.

The figure is divided into four panels, each showing a different segment of the protein. Each panel includes the amino acid sequence, secondary structure (SS) prediction, confidence scores, and disorder predictions.

Panel 1 (Residues 1-60): The sequence is ML A F C R S S L K S K K Y I I L L A L A A I A G L G T H A A W S S N G L P R I D N K T L A R L A Q Q H P V V V L F R. The secondary structure shows several alpha-helices. The disorder prediction shows a high confidence region (red) from residue 1 to 10, followed by a low confidence region (green) from residue 11 to 60.

Panel 2 (Residues 70-120): The sequence is H A E R C D R S T N Q C L S D K T G I T V K G T Q D A R E L G N A F S A D I P D F D L Y S S N T V R T I Q S A T W F S A. The secondary structure shows several alpha-helices. The disorder prediction shows a high confidence region (red) from residue 70 to 100, followed by a low confidence region (green) from residue 101 to 120.

Panel 3 (Residues 130-180): The sequence is G K K L T V D K R L L Q C G N E I Y S A I K D L Q S K A P D K N I V I F T H N H C L T Y I A K D K R D A T F K P D Y L D. The secondary structure shows several alpha-helices. The disorder prediction shows a high confidence region (red) from residue 130 to 150, followed by a low confidence region (green) from residue 151 to 180.

Panel 4 (Residues 190-200): The sequence is G L V M H V E K G K V Y L D G E F V N H. The secondary structure shows a beta-strand. The disorder prediction shows a high confidence region (red) from residue 190 to 200.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand