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Figure 1 displays the protein structure and disorder analysis of the human protein. The figure is organized into three panels, each showing a different segment of the protein sequence (1-180 residues) and its predicted secondary structure (SS) and disorder.

**Panel 1 (Top):** Shows the protein sequence (1-60 residues) and its predicted secondary structure (SS) and disorder. The sequence is: MQLNKKVLKGLMIALPVMIAAACSNNKNASNDGSEGLGAGTGMDANGGNGNMSSEEQARL. The SS is primarily alpha-helical, with a few beta-strands and loops. The disorder analysis shows that the protein is highly disordered, with a high disorder confidence score across most of the sequence.


**Panel 2 (Middle):** Shows the protein sequence (70-120 residues) and its predicted secondary structure (SS) and disorder. The sequence is: QMQQLQQNNIVYFDLDKYDIRSDFDAQMLDAHANFLRSNPSYKVTVEGHADERGTPEYNIS. The SS is primarily alpha-helical, with a few beta-strands and loops. The disorder analysis shows that the protein is highly disordered, with a high disorder confidence score across most of the sequence.


**Panel 3 (Bottom):** Shows the protein sequence (130-180 residues) and its predicted secondary structure (SS) and disorder. The sequence is: LGERRANAVKMYLQGKGVSAADQISIVSYGKEKPAVLGHDEAAYSKNRRAVLVY. The SS is primarily alpha-helical, with a few beta-strands and loops. The disorder analysis shows that the protein is highly disordered, with a high disorder confidence score across most of the sequence.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand