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Protein structure and disorder analysis for the full-length protein (1-200 residues). The figure displays the amino acid sequence, secondary structure (SS), confidence, and disorder predictions across the entire protein.

Sequence: MSIKNLPA DYLLAAQQGDI DKVKTC LALGV DINTCDRQ GKTAIT LASLYQQYACVQALID

Secondary structure (SS): The structure is primarily composed of alpha-helices (green cylinders) and loops (grey lines). Helices are observed in the N-terminal region (residues 10-20), the middle region (residues 30-40), and the C-terminal region (residues 110-120).

confidence: The confidence score is generally high, indicated by the red color in the confidence bar.

Disorder: The protein is predicted to be disordered, as indicated by the blue color in the disorder bar.

Disorder confidence: The disorder confidence is generally high, indicated by the blue color in the disorder confidence bar.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand