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Protein structure and disorder analysis for the full-length protein (1-120). The figure displays the amino acid sequence, secondary structure, and disorder predictions across the entire length of the protein.

Sequence: M S E A L K I L N N I R T L R A Q A R E C T L E T L E E M L E K L E V V V N E R R E E S A A A A E V E E R T R K L Q Q


Secondary structure: The structure is primarily composed of alpha-helices (green) and beta-strands (blue). The first 20 residues form a large alpha-helical domain, followed by a series of beta-strands and smaller alpha-helices.

SS confidence: The confidence is high (red) for most of the protein, with some lower confidence regions (yellow and green) in the first 20 residues.


Disorder: The protein is mostly ordered (red), with some disordered regions (yellow and green) in the first 20 residues.


Disorder confidence: The confidence is high (red) for most of the protein, with some lower confidence regions (yellow and green) in the first 20 residues.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand