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This figure provides a detailed view of the protein structure prediction results, showing the sequence, secondary structure, and disorder predictions across the entire length of the protein (residues 1 to 300).

The protein sequence is displayed at the top, with residues numbered from 1 to 300. The secondary structure is shown below the sequence, with alpha-helices represented by green cylinders and beta-strands by blue arrows. The disorder prediction is shown at the bottom, with a color scale indicating the confidence of the prediction (from 0 to 100%).

The protein structure is composed of several alpha-helices and beta-strands, with a significant region of disorder (residues 100-150) predicted with high confidence. The disorder prediction is shown as a color scale from 0 (blue) to 100 (red), with a green bar indicating the confidence of the prediction.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand