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Protein structure prediction results for the protein sequence MSISSKI RPTPRKPSRMATDHSFKMKKFYADPF AISI SLAI VSWVI AIGGSI SSASTNE. The figure displays the sequence, secondary structure, confidence, disorder, and disorder confidence across the entire protein length (1-600).

Sequence: MSISSKI RPTPRKPSRMATDHSFKMKKFYADPF AISI SLAI VSWVI AIGGSI SSASTNE

Secondary structure: The structure shows several alpha-helices (green cylinders) and beta-strands (blue arrows). Key features include a long alpha-helix from residue 10 to 60, a beta-strand at residue 70, and a long alpha-helix from residue 130 to 240.

SS confidence: The confidence score for the secondary structure prediction is shown as a bar chart below the sequence. It ranges from 0.0 (red) to 1.0 (green).

Disorder: The disorder prediction is shown as a bar chart below the sequence. It ranges from 0.0 (red) to 1.0 (green).

Disorder confidence: The confidence score for the disorder prediction is shown as a bar chart below the sequence. It ranges from 0.0 (red) to 1.0 (green).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand