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Protein structure prediction results for the protein sequence MGI NNPI PRSLKSETKKA... showing sequence, secondary structure, SS confidence, disorder, and disorder confidence across 420 residues.

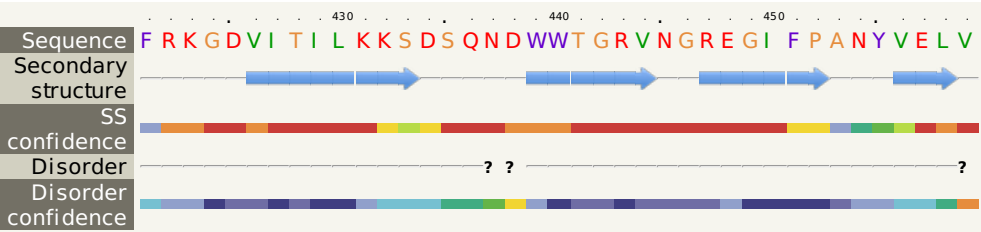
Sequence: MGI NNPI PRSLKSETKKA... (Residues 1-420)

Secondary structure: Alpha helices (green cylinders) and beta strands (blue arrows) are shown. Key features include a long alpha helix from residue 10 to 30, a beta strand at residue 40, and a long alpha helix from residue 110 to 120.

SS confidence: High confidence (green/yellow) is observed in the alpha helices and beta strands, while low confidence (red/orange) is seen in the loops and disordered regions.

Disorder: Disordered regions are indicated by question marks (?) along the sequence, particularly in the N-terminal region (residues 1-10) and the C-terminal region (residues 370-420).

Disorder confidence: High confidence (red/orange) is observed in the disordered regions, while low confidence (green/yellow) is seen in the structured regions.



Confidence Key

High(9) [red bar] [orange bar] [yellow bar] [light green bar] [green bar] [dark green bar] [blue bar] Low (0)

? Disordered

Alpha helix

Beta strand