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Protein structure prediction results for the protein sequence: MAGKFRCILLLIAGLFVSSLSYAENTEIPSEEGISLFDV EATLQPDGVL DIKENIHFQA.

The figure displays the sequence, secondary structure, SS confidence, disorder, and disorder confidence across the entire length of the protein (1-420 residues).

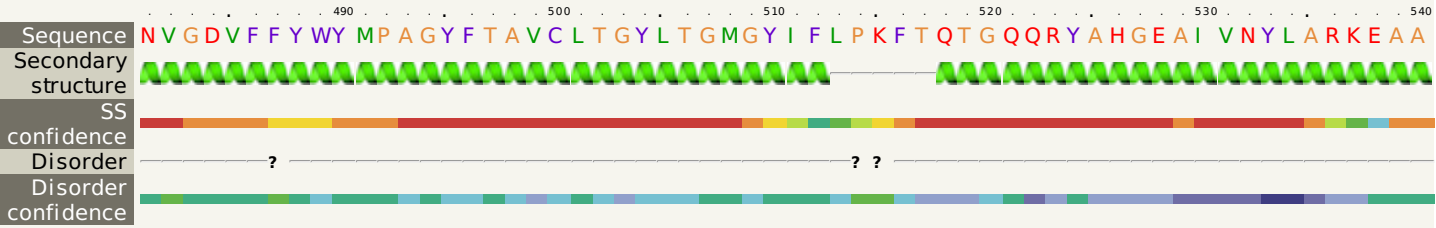
Sequence: MAGKFRCILLLIAGLFVSSLSYAENTEIPSEEGISLFDV EATLQPDGVL DIKENIHFQA

Secondary structure: The structure is shown as a series of blue arrows (alpha-helices) and green cylinders (beta-strands). The structure is primarily composed of alpha-helices, with a few beta-strands interspersed.

SS confidence: The confidence is shown as a bar chart with colors ranging from red (high confidence) to blue (low confidence). The confidence is generally high, with some lower confidence regions around residues 10-20 and 30-40.

Disorder: The disorder is indicated by question marks (?) along the sequence, suggesting regions of predicted disorder. Disordered regions are found at the N-terminus (residues 1-10), around residue 30, and at the C-terminus (residues 410-420).

Disorder confidence: The confidence for disorder is shown as a bar chart with colors ranging from red (high confidence) to blue (low confidence). The confidence is generally low, with some higher confidence regions around residues 10-20 and 30-40.



Confidence Key

High(9) Low (0)

? Disordered

Alpha helix

Beta strand