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Protein structure prediction results for the protein sequence: ML S F L W D L A S F I V A L G V L I T V H E F G H F W V A R R C G V R V E R F S I G F G K A L W R R T D K L G T E Y V.

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

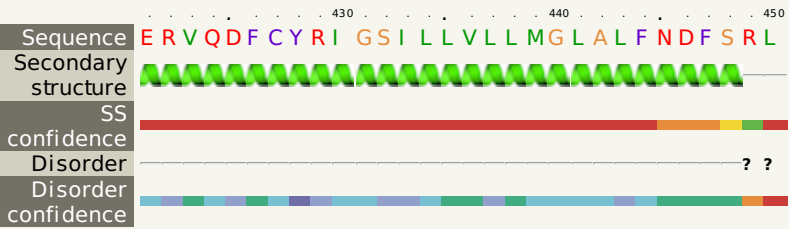
Sequence: ML S F L W D L A S F I V A L G V L I T V H E F G H F W V A R R C G V R V E R F S I G F G K A L W R R T D K L G T E Y V

Secondary structure: The structure is primarily composed of alpha-helices (green) and beta-strands (blue). Key features include a long alpha-helix from residue 1 to 30, a beta-strand at 35, and a large alpha-helical region from 70 to 120. A beta-strand is also present at 130. The structure continues with a mix of helices and strands until residue 420.

SS confidence: The confidence is generally high, indicated by the green and yellow colors in the bar chart, with some lower confidence regions (red/orange) around residues 30-40 and 130-140.

Disorder: The protein is mostly ordered, with some disorder indicated by question marks in the bar chart, particularly in the regions around residues 30-40 and 130-140.

Disorder confidence: The confidence is generally high, indicated by the green and yellow colors in the bar chart, with some lower confidence regions (red/orange) around residues 30-40 and 130-140.



Confidence Key

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

? Disordered

Alpha helix

Beta strand